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### Global effects of land use on local terrestrial biodiversity 15

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- 63 Human activities, especially conversion and degradation of habitats, are causing global
- 64 biodiversity declines. How local ecological assemblages are responding is less clear a
- 65 concern given their importance for many ecosystem functions and services. We analyze
- 66 a terrestrial assemblage database of unprecedented geographic and taxonomic coverage
- 67 to quantify local biodiversity responses to land-use and related changes. In the worst-
- 68 impacted habitats, these pressures reduce within-sample species richness by an average
- 69 of 76.5%, total abundance by 39.5% and rarefaction-based richness by 40.3%. We
- 70 estimate that, globally, these pressures have already slightly reduced average within-
- sample richness (by 13.6%), total abundance (10.7%) and rarefaction-based richness
- 72 (8.1%), with changes showing marked spatial variation. Rapid further losses are
- 73 predicted under a business-as-usual land-use scenario: within-sample richness is
- 74 projected to fall by a further 3.4% globally by 2100, with losses concentrated in
- 75 biodiverse but economically poor countries. Strong mitigation can deliver much more
- positive biodiversity changes (up to a 1.9% average increase) that are less strongly
   related to countries' socioeconomic status.
- 78

79 Biodiversity faces growing pressures from human actions, including habitat conversion and

- degradation, habitat fragmentation, climate change, harvesting and pollution<sup>1</sup>. As a result,
   global assessments show that species' extinction risk is increasing on average while
- global assessments show that species extinction risk is increasing on average while
   population sizes are declining<sup>1,2</sup>. Such assessments have usually focused on data-rich
- vertebrates, so might not reflect broader biodiversity<sup>3</sup>. Furthermore, most have concentrated
- 84 on the global status of species, whereas the long-term security of many ecosystem functions
- and services especially in changing environments is likely to depend upon local
- 86 biodiversity<sup>4–6</sup>. Average trends in local diversity remain unclear: analyses of temporal
- 87 changes in assemblages have suggested no systematic change in species richness<sup>7,8</sup>, but the
- available times-series data might under-represent transitions between land-use types<sup>9</sup> and
- population time series suggest vertebrate populations have declined sharply in recent
   decades<sup>3</sup>.
- 91 Spatial comparisons provide an alternative source of evidence on how human pressures 92 affect biodiversity, assuming that differences in pressures have caused observed biodiversity 93 differences between otherwise matched sites<sup>10–12</sup>. The prevalence of published spatial 94 comparisons makes it possible to go beyond particular taxa or regions<sup>11,12</sup> to develop global, 95 taxonomically representative models. Furthermore, the willingness of many researchers to 96 share their raw data makes it possible to consider multiple aspects of biodiversity, rather than 97 the single, simple metrics of most existing models<sup>10</sup> which cannot capture all key aspects of 98 diversity<sup>13</sup>.
- We present the most geographically and taxonomically representative models to date of how several aspects of the composition and diversity of terrestrial assemblages respond to

101 multiple human pressures. The explanatory variables in our models most directly measure

- 102 land use and infrastructure, but might correlate<sup>14,15</sup> with two other important pressures –
- 103 harvesting and invasive species for which comparable high-resolution spatial data are
- 104 unavailable globally. We exclude climate change effects because they are not captured well
- by spatial comparisons. We use our models to infer past net changes in assemblages since
- 106 1500, project future changes over this century under different socioeconomic scenarios of 107 land use, and relate projected national changes in local biodiversity to socioeconomic
- 108 variables and natural biodiversity.
- 109 Our models of local within-sample species richness (hereafter 'richness'), rarefaction-110 based species richness (hereafter 'rarefied richness'), total abundance, compositional turnover 111 and average organism size are based on among-site comparisons of ecological assemblage composition collated from the literature as part of the PREDICTS project<sup>16</sup>. The dataset 112 consisted of 1,130,251 records of abundance and 320,924 of occurrence or species richness at 113 114 11,525 sites (2-360 sites per study, median 15; Figure 1a). These data, from 284 publications (see Methods), represent 26,953 species -1.4% of the number formally described<sup>17</sup> – and 13 115 116 of the 14 terrestrial biomes (Extended Data Figure 1). Each site was scored for six putative pressures: land use<sup>11</sup> and use intensity<sup>18</sup>, land-use history<sup>19</sup>, human population density<sup>20</sup>, proximity to roads<sup>21</sup>, and accessibility from the nearest large town. Random effects in our 117 118 119 models accounted for study-level differences in response variables and sampling methods,
- 120 and for the within-study spatial arrangement of sites.
- 121

## 122 Effects of pressures on site-level diversity

123

124 Local richness, rarefied richness and total abundance were most strongly influenced by land 125 use and land-use intensity: they were substantially lower in most other land-use types than in 126 primary vegetation, especially in intensively-used areas (Figure 1; see Supplementary 127 Information for statistics and coefficient estimates). These results extend those of previous, geographically or taxonomically restricted, meta-analyses (e.g. refs. 11,22). Other variables 128 129 were weaker as main effects, but showed stronger effects in interaction (Extended Data 130 Figure 2) and were often significant overall (see Supplementary Information). Richness and 131 total abundance tended to be slightly lower at the highest human population densities, and 132 richness was lower nearer to roads and in more accessible sites (Figure 1). Differences in richness were not driven solely by differences in abundance: rarefied richness<sup>23</sup> (see Methods 133 134 for details) showed weaker but mostly similar patterns, although the effects of variables other 135 than land use and land-use intensity were not significant (Extended Data Figure 3a,b). Under 136 the worst combinations of pressures, our models estimated richness, rarefied richness and 137 total abundance to be 76.5%, 40.3% and 39.5% lower, respectively, than in minimally 138 impacted sites. Effects of pressures on vertebrate, invertebrate and plant richness were 139 statistically indistinguishable (P > 0.05; results not shown). The modelled coefficients were 140 robust to efforts to correct for publication bias (Extended Data Figure 4). As with all studies 141 based on data from the literature, unpublished data are almost unrepresented. Coefficients 142 were also robust under cross-validation (Extended Data 3c,d), and the model residuals 143 showed little spatial autocorrelation (Extended Data Figure 5).

The importance of secondary vegetation for conservation is hotly debated<sup>11,24,25</sup>, and is crucial because this land-use will soon become the most widespread type<sup>26</sup>. We find that the answer depends strongly on the secondary vegetation's maturity: early-stage communities tend to be less diverse than those in primary vegetation and are compositionally distinct, but these differences are much reduced in mature secondary vegetation (Figures 1 & 2; we caution though that not all data sources clearly distinguished mature secondary from primary vegetation). This successional rise in diversity accords with a recent meta-analysis of plant
 communities over time<sup>7</sup>.

Net changes in diversity provide an incomplete view of the effects of human activities
on biodiversity because they ignore replacement of original species by newcomers<sup>8</sup>. We
therefore analysed how land use affects similarity in species composition between sites.
Communities under the same land use were, unsurprisingly, the most similar (Figure 2a).
Across land uses, communities in primary vegetation were most like those in secondary

vegetation, while plantation forest, pasture and cropland communities formed a different,human-dominated, cluster (Figure 2b).

Anthropogenic pressures can affect ecosystem functions and services more strongly 159 than changes in species diversity would imply, if species' responses depend on their traits<sup>27</sup>. Large size is often linked to species' declines<sup>28,29</sup> and is important for some ecosystem 160 161 processes<sup>30</sup>. We combined abundance data with species' average sizes to calculate site-level 162 community-weighted mean plant height and animal mass. As in local studies<sup>29</sup>, mean plant 163 164 height was lower in human-dominated land uses than in primary and secondary vegetation, 165 and tended to decline with increasing human population density (Figure 1d). Most field studies focused on particular plant taxa, so this difference does not simply reflect tree 166 167 removal. Average animal mass did not change consistently with land use or human 168 population density, but increased with proximity to roads (Figure 1d).

Models like ours that substitute space for time ignore time lags in biotic changes, which can be important<sup>31</sup>. We also assume that land uses are situated randomly within studies relative to sites' intrinsic suitability for biodiversity. Adding global data on other important pressures as they become available, and also incorporating climate change, will give a more complete picture of human impacts on local biodiversity.

- 175 Global effects on local diversity to date
- 176

177 By applying our model for within-sample species richness – the most widely used and 178 understood biodiversity measure - to maps of current pressure variables, we estimate the 179 global pattern of net local changes to date in plot-level richness (Figure 3; we did not estimate 180 total richness within the  $0.5^{\circ} \times 0.5^{\circ}$  grid cells). Human-dominated areas are inferred to have 181 lost much more local diversity than have regions where more natural vegetation remains. The worst-affected cells showed a 31% reduction in average local richness – probably enough to 182 impact ecosystem functioning substantially<sup>5</sup>. Local richness increased in 1.7% of cells (by  $\leq$ 183 184 4.8%). Total abundance and rarefied richness showed broadly similar patterns, although less 185 pronounced in the latter case (Extended Data Figure 6).

We applied our models to global spatial estimates of how land use and human population changed from 1500-2005<sup>26</sup> (see Methods) to infer the global history of local biodiversity change. We focus on within-sample species richness because of its wide use and easy interpretation. Our inferences incorporate uncertainty in model parameter estimates, but not in the trajectories of the drivers themselves (which have not been assessed<sup>32</sup>) nor effects of changes in roads and accessibility, for which temporal estimates could not be obtained.

192 Richness is estimated to have declined most rapidly in the 19<sup>th</sup> and 20<sup>th</sup> centuries 193 (Figure 4), with other metrics showing similar responses (Extended Data Figure 6). By 2005, 194 we estimate that land use and related pressures had reduced local richness by an average of 195 13.6% (95% CI: 9.1 – 17.8%) and total abundance by 10.7% (95% CI: 3.8% gain – 23.7% 196 reduction) compared with what they would have been in the absence of human effects. 197 Approximately 60% of the decline in richness was independent of effects on abundance: 198 average rarefied richness has fallen by 8.1% (95% CI: 3.5 – 12.9%). Although these confidence limits omit uncertainty in the projections of land use and other pressures, there is
 less uncertainty in estimates of current pressure levels than in changes over time<sup>33</sup>.

Our inferences contrast with two recent analyses of community time series<sup>7,8</sup>, which 201 suggested no overall trend in local diversity, and with the Living Planet Index<sup>3</sup> which, based 202 203 on vertebrate population time series, reports a much more rapid decline in abundance than we 204 infer. Although time series potentially provide a more direct view of temporal trends than our 205 space-for-time approach, the available data might under-represent transitions between landuse types<sup>9</sup>. On the other hand, our approach may underestimate additions of species through 206 207 climate change and species invasion (although accessibility and proximity to roads may partly capture the latter  $^{14,15}$ ). 208

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## 210 Global and national projections to 2095

211 Global changes in local diversity from 2005 to 2095 were projected using estimated land use

and human population from the four Intergovernmental Panel on Climate Change

213 Representative Concentration Pathway (RCP) scenarios<sup>26</sup>, which correspond to different

214 intensities of global climate change (Table 1). Although these estimates have limitations $^{32}$ ,

they are the most consistent available, are widely-used<sup>34</sup>, and are consistent with the

216 historical estimates <sup>26</sup>. However, they – like all other global land-use projections – include no

estimate of uncertainty; therefore, each of our projections must be viewed as the predicted

218 biodiversity outcome under one particular set of land-use assumptions.

219 Projected net changes in average local diversity to 2095 vary widely among scenarios 220 (Figure 4; Extended Data Figure 6). The scenario with the least climate change (IMAGE 2.6) yields the second-worst outcome for biodiversity, because it assumes rapid conversion of 221 primary vegetation – especially in the tropics – to crops and biofuels<sup>26</sup> (Table 1, Extended 222 223 Data Figure 7). These projections do not imply that low-emission scenarios must entail large 224 losses of biodiversity, but instead reflect that scenario's mitigation strategy. Indeed, in 225 MiniCAM 4.5 (where mitigation is through carbon markets, crop improvements and diet 226 shifts: Table 1), average richness is projected to increase (though other diversity metrics 227 respond more weakly: Extended Data Figure 6). The worst biodiversity outcomes arise from 228 the scenario with most climate change – MESSAGE 8.5 – in which rapid human population 229 growth drives widespread agricultural expansion (Table 1; Extended Data Figure 7). This scenario, which has been characterised as 'business-as-usual'<sup>35</sup>, most closely matches recent 230 trends in emissions<sup>36</sup> and gives the worst outcomes even though our projections omit direct 231 232 climate impacts on local assemblages.

233 The global projections hide wide regional and national variation (Figure 5; Extended 234 Data Figure 8). Projections for 2095 under 'business-as-usual' (MESSAGE 8.5) are strongly 235 inequitable, presenting serious challenges for both sustainable development and global 236 conservation of biodiversity (Figure 5a). Under this scenario, European and North American 237 countries – typically with a high Human Development Index (HDI), low native biodiversity 238 and widespread historical land conversion – are mostly projected to gain in local richness by 239 2095. More naturally biodiverse but less economically developed Southeast Asian and 240 especially sub-Sharan African countries, with more natural and semi-natural habitat, will 241 suffer the greatest losses (Figure 5a; Extended Data Figure 8f).

Such globally inequitable outcomes might be avoidable: the best scenario for
biodiversity (MiniCAM 4.5; Figure 4) yielded country-level outcomes that are relatively
independent of HDI, native species richness (Figure 5b) and past changes (Extended Data
Figure 8e). For local richness, outcomes under MiniCAM4.5 were better than MESSAGE 8.5
for 93% of countries worldwide (Figure 5c).

247 Under AIM 6.0, most Afrotropical countries are projected to gain in local richness but
248 heavy losses are inferred for the Indo-Malay region (Extended Data Figure 8). Projections

- under IMAGE 2.6 are spatially similar to those under MESSAGE 8.5. The land-use change
- 250 caused by the biofuels-based strategy in IMAGE 2.6 is projected to have a major negative
- 251 impact overall on terrestrial biodiversity (Extended Data Figure 8).
- 252
- 253 *Conclusions*

Many assessments of the state of biodiversity have focused on global metrics such as rates of species extinction<sup>37</sup>, but resilient delivery of ecosystem functions and services is more likely to depend on local diversity<sup>4–6</sup>. Our models suggest land-use changes and associated pressures strongly reduce local terrestrial biodiversity, and we estimate global average reductions to date of 13.6% in within-sample species richness, 10.7% in total abundance and 8.1% in rarefaction-based species richness (Figs. 3 and 4). Climate change, which we could

not include in our framework, is likely to exacerbate losses, especially under business-as usual<sup>38</sup>, although direct effects of climate change will increase local diversity in some
 maions<sup>8</sup>

262  $regions^8$ .

It is important to remember that the habitat conversion and associated changes that 263 264 reduced local biodiversity had largely positive consequences for people: agricultural intensification underpinned many countries' development. However, benefits have not been 265 shared equally among or within countries<sup>39</sup>. Losses of local species richness exceeding 20% 266 267 are likely to substantially impair the contribution of biodiversity to ecosystem function and services, and thus to human well-being<sup>5</sup>. We estimate that reductions in average plot-level 268 269 species richness currently exceed this level for 28.4% of grid cells, increasing to 41.5% of 270 cells by 2095 under 'business-as-usual' (note that we do not estimate or project total richness 271 across the cell). Importantly, our projections suggest that such widespread large losses are not 272 inevitable. With concerted action and the right societal choices, global sustainability of local 273 biodiversity may be an achievable goal.

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# **Supplementary Information** is linked to the online version of the paper at

- 387 www.nature.com/nature.
- 388

389 Additional references can be found in the Supplementary Information.

390

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- 423 T.N., L.N.H. and A.P. wrote the manuscript with contributions from G.M.M., L.B., D.W.P.,
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- 425 and S.T.; T.N. and L.N.H. contributed equally to the study.
- 426

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- 431
- 432 Tables
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- 434

# Table 1. Key features of the four Representative Concentration Pathways (RCP)scenarios (land-use and human-population assumptions are detailed in ref. 26, energyassumptions in refs. 40–42, and climate implications in ref. 43).

| Scenario    | Land use (see also<br>Extended Data Figure 7)   | Climate and energy   | Human population  |
|-------------|---|--|---|
| IMAGE 2.6   | Agriculture moves from<br>developed to developing<br>countries. Large increase<br>in area of biofuel<br>plantations. Urban extent<br>assumed constant.  | Increased energy<br>efficiency. Increased use<br>of carbon capture and<br>storage, nuclear,<br>renewable energy and<br>biofuels. Approximately<br>1 °C temperature increase<br>by 2100 compared to pre-<br>industrial.   | 10.1 billion by 2100 (UN<br>Medium variant, 2010)                                 |
| MiniCAM 4.5 | Carbon pricing leads to<br>preservation of primary<br>forest and expansion of<br>secondary forest. Crop<br>yield increases, improved<br>agricultural efficiency<br>and dietary shifts lead to<br>decreases in cropland and<br>pasture areas. Small<br>increase in area of biofuel<br>plantations. Urban extent<br>assumed constant. | Decline in overall energy<br>use. Decreased use of<br>fossil fuels and increase<br>in nuclear and renewable<br>energy, and in carbon<br>capture and storage.<br>Moderate increase in use<br>of biofuels, but limited by<br>availability of biomass.<br>Approximately 1.75 °C<br>temperature increase by<br>2100.         | Peaks above 9 billion<br>around 2065, then<br>declines to 8.7 billion by<br>2095. |
| AIM 6.0     | Urban area increases<br>owing to human<br>population growth.<br>Cropland area increases<br>to meet food demand.<br>Pasture area declines<br>strongly.   | Approximately 2.5 °C temperature increase by 2100.   | 9.1 billion by 2100 (UN<br>Medium variant, 2004)                                  |
| MESSAGE 8.5 | Increasing crop yields<br>and intensification<br>account for much of the<br>increased production<br>required, but area of<br>cropland and, to a lesser<br>extent, pasture increases<br>rapidly. Small increase in<br>area of biofuel<br>plantations. Urban area<br>increases owing to<br>increased population.                      | Small improvements in<br>efficiency leading to high<br>demand for energy.<br>Conventional oil and gas<br>become scarce, leading to<br>shift in favour of<br>unconventional and<br>carbon-intensive fossil<br>fuels. Moderate increase<br>in use of biofuels.<br>Approximately<br>4 °C increase in<br>temperature by 2100 | 12 billion by 2100.   |

- 440 **Figure legends**
- 441
- 442 Figure 1. Locations of sites and responses of four metrics of local diversity to human
- **pressures. a.** Sites used in the models. Responses<sup>44</sup> of richness, **b**, total abundance, **c**, and 443
- community-weighted mean organism size plant height (crosses) and animal mass 444
- 445 (triangles), **d**, to anthropogenic variables. Error bars show 95% confidence intervals. Primary
- 446 = primary vegetation, YSV = young secondary vegetation, ISV = intermediate secondary
- vegetation, MSV = mature secondary vegetation, Plantation = plantation forest. Land-use 447 448 intensity: minimal (circle), light (triangle), intense (diamond), and combined light and intense
- (square). HPD = human population density<sup>45</sup>, PR = proximity to roads<sup>46</sup> (as  $-\log(\text{distance to})$ 449
- nearest road)), ACC = accessibility to humans<sup>47</sup> (as  $-\log(\text{travel time to nearest major city}))$ 450
- are shown as fitted effects from a model with no interactions between continuous effects and 451
- 452 land use, at the lowest (L), median (M) and highest (H) values in the dataset. Sample sizes are 453 given in full in the Methods (Table S2).
- 454
- 455 Figure 2. Similarity in assemblage composition as a function of land use. a, Average
- 456 dissimilarity of species composition (1 - Sortenson Index) between pairs of sites within and
- among land uses (shown relative to the similarity between pairs of primary-vegetation sites): 457
- 458 blue and red colours indicate, respectively, more and less similar composition; numbers
- 459 indicate numbers of studies within which comparisons could be made. b, Clustering of land-
- 460 use types based on average compositional dissimilarity; urban sites were excluded owing to 461 the small sample size. Land-use labels as in Figure 1.
- 462
- 463 Figure 3. Net change in local richness caused by land use and related pressures by 2000. Projections used an IMAGE reference scenario<sup>10</sup>. The baseline landscape was assumed to be 464 entirely uninhabited, unused primary vegetation. Shown using a Lambert Cylindrical Equal-465 Area projection at  $0.5^{\circ} \times 0.5^{\circ}$  resolution. 466
- 467

468 Figure 4. Projected net change in local richness from 1500 to 2095. Future projections 469 were based on the four RCP scenarios (Table 1). Historical (shading) and future (error bars) 470 uncertainty is shown as 95% confidence intervals, rescaled to zero in 2005. The baseline for 471 projections is a world entirely composed of uninhabited, unused primary vegetation; thus, the 472 value at 1500 is not constrained to be zero because by then non-primary land uses were 473 present - and in some regions widespread. The global average projection for MESSAGE 8.5 474 does not join the historical reconstruction because that scenario's human-population 475 projections start in 2010 and because human population and plantation-forest extent have not 476 been harmonized among scenarios.

- 477
- 478 Figure 5. Biodiversity projections at the country level. a-b, Country-level projections of 479 average net local richness change between 2005 and 2095 under the worst (a, MESSAGE
- 480 8.5) and best (b, MiniCAM 4.5) RCP scenarios for biodiversity, shown in relation to the
- 481 Human Development Index. Colours indicate biogeographic realms; colour intensity reflects
- 482 natural vertebrate species richness (more intense = higher richness); point size is proportional
- 483 to (log) country area. c, Correlation between projected richness changes under the MiniCAM
- 484 4.5 and MESSAGE 8.5 scenarios, with dashed line showing equality; colours as in **a and b**;
- 485 colour intensity is proportional to the HDI (more intense = higher index).
- 486
- 487 **Methods**
- 488

- 489 Data collation
- 490

491 Between March 2012 and April 2014 we collated among-site comparisons of ecological 492 assemblage composition from published studies (or from unpublished datasets where the 493 methods have been published) examining the effect of human activities on more than one 494 named taxon. A full description of how the dataset was assembled and curated is presented elsewhere<sup>16</sup>. We define sites to be in the same study if they were sampled using the same 495 496 methodology and the data were reported in the same paper; therefore, some publications 497 contain multiple studies. After six months of broad searching, we targeted efforts towards 498 under-represented taxa, habitat types, biomes and regions. We accepted data only from 499 published or in-press papers, or data collected using a published methodology, and we 500 required that the data providers agreed to our making their data publicly available at the end 501 of the PREDICTS (Projecting Responses of Ecological Diversity In Changing Terrestrial 502 Systems) project in 2015. We accepted data only where abundance, occurrence or richness 503 had been measured at two or more sampling locations and/or times, and where all sites were 504 sampled using the same sampling procedure and with either the same effort or site-specific 505 data on effort. We used geographical coordinates preferentially from the paper or supplied by 506 data providers; but where coordinates were not thus available, we georeferenced them from maps in the papers. The final dataset came from 378 studies<sup>49-332</sup> and two unpublished 507 datasets (M. E. Hanley, 2005 and 2011) that were collected with published methods<sup>146</sup>. 508

509 Studies compared from 2 to 360 sites (median = 15; 82% had  $\geq$  5 sites); most sampled 510 species from multiple families but fewer than half sampled multiple orders. Over 70% of sites 511 were from studies that sampled entire communities within a taxonomic group rather than a 512 target list of species. Removing studies having a target list did not substantially alter model 513 coefficients (results not shown) and increased the projected global net average loss of local 514 species richness until 2005 by 0.6%. Sites varied in the maximum linear extent sampled 515 (median 106 m; interquartile range 50 m to 354 m). Model coefficients for the approximately 516 50% of studies that reported maximum linear extent were robust to its inclusion in the models 517 (results not shown).

518 The great majority of listed taxa were species-level, although many could not be given explicit species identifications (e.g. morpho-species)<sup>16</sup>; henceforth we refer to distinct taxa in 519 520 our dataset as species. We matched taxonomic names given in the source paper to the Catalogue of Life 2013 Annual Checklist (COL)<sup>333</sup>, obtaining the full taxonomic 521 522 classification. In order to relate the taxonomic names to species-level trait databases, we 523 generated, for each taxon, a 'best-guess' Latin binomial as: a) the taxon name from COL if 524 the COL query returned a species-level identification; b) the first two words of the text 525 returned by the COL query if this was a sub-species designation; c) the first two words of the 526 taxon name in the source publication if the COL query returned neither a species or sub-527 species name, and the taxon name in the source publication contained two or more words. 528 Taxa that met none of these criteria were not matched to trait data, but were included in the 529 calculation of richness and total abundance, and for estimating turnover in community 530 composition among sites.

The resulting data set contained data for 26,953 species at 11,525 sites. For many highdiversity taxa, the database contains data for more than 1% of the number of species thought to have been formally described (Extended Figure 1a). The distribution of sites among major biomes is roughly proportional to the amount of terrestrial net primary productivity (NPP) fixed within each biome (Extended Figure 1b).

- 536
- 537 Site-level composition and diversity538

We computed four site-level biodiversity metrics: within-sample species richness, total
abundance, rarefaction-based richness and community-weighted mean organism size. These
were calculated as follows.

- 542
  543 Within-sample species richness was calculated as the number of differently-named taxa
  544 recorded at a given site in a standardised sampling unit (a measure also known as species
  545 density<sup>334</sup>). We gave precedence to the author's classification of species, even where a search
  546 of global databases revealed potential synonymies, because only certain taxonomic groups
  547 could be reliably matched to accepted taxonomies.
- 548 This measure of richness is appropriate for conservation questions but among site-549 differences could be due to effects on numbers of individuals as well as to changes in the shape of the species accumulation curve<sup>334</sup>. We therefore also calculated **rarefaction-based** 550 **species richness** by taking 1000 random samples of *n* individuals from each site, where *n* is 551 552 the smallest total number of individuals recorded at any site within its study, and calculating 553 the mean species richness across samples. This index could only be calculated for sites 554 where, in addition to the criteria above being met, abundance was recorded as number of 555 individuals. Rarefied species richness was rounded to the nearest integer for analysis with 556 Poisson errors.
- 557

558 Total abundance was calculated as the sum of the measures of abundance of all taxa at a 559 site; we were thus unable to estimate abundance for sites where only species occurrence or 560 overall richness or diversity had been recorded (17% of sites). Some abundance metrics -561 those not reported as densities per unit time, distance, area or volume sampled - were 562 sensitive to sampling effort. When a study reported any of these metrics and sampling effort varied among sites within a study, we corrected the raw abundance measurements for the 563 564 sampling effort expended at each sampling location and time; this was done by rescaling the sampling efforts within each study, so that the most heavily sampled site had a value of one, 565 and then dividing the raw abundance measurements by this relative sampling effort. The 566 567 rescaling was performed to prevent introducing additional heterogeneity in the modelled abundance values. 568

569

570 Community-weighted mean organism size was calculated as the arithmetic mean of logtransformed height of plants (available for 4,235 species in our dataset) or the log-571 572 transformed body mass or volume of vertebrates, beetles and hoverflies (5,236 species) present at a site, weighted by abundance<sup>335</sup>. Plant height data were taken from the TRY 573 database<sup>336</sup>; for 61 species where plant vegetative height data were unavailable, we estimated 574 it from generative height from a regression across the 2,554 species with estimates of both 575 traits ( $R^2 = 0.91$ ). Data on vertebrate body mass were taken from the PanTHERIA database 576 for mammals<sup>337</sup>, from BirdLife International's World Bird Database for birds, and from a 577 wide range of published and grey-literature sources for amphibians <sup>338–384</sup>. Length data for 578 reptiles were taken from published<sup>385,386</sup> and unpublished (S. Meiri & A. Feldman, 579 unpublished data) sources, and converted to estimates of body mass using published length-580 mass allometries<sup>387,388</sup>. Arthropod size data (beetles and hoverflies) were collated from published sources<sup>389,390</sup>. Beetle length and amphibian snout-vent length values were raised to 581 582 the power three so that they had the same dimensionality as the other animal size measures. 583 584 For both plant height and vertebrate body mass, missing values were interpolated as the 585 average values for congeners, since both of these traits are strongly conserved 586 phylogenetically (Pagel's  $\lambda = 0.98, 0.997, 0.93, 0.89$  for plant height, vertebrate body mass, 587 beetle body length and hoverfly thorax volume, respectively). 588

## 589 Human pressure data

590

591 While many human pressures can impact local biodiversity, we focus on those that can 592 be obtained for sites around the world and for which, as far as possible, spatiotemporal data 593 are available for 1500-2095; this focus enables us to use our statistical models as a basis for 594 projecting responses through time. Each site was assigned to one of eight land-use classes 595 based on the description of the habitat given in the source paper (see Extended Data Table 1 596 for definitions): primary vegetation, secondary vegetation (subdivided into mature, intermediate or young secondary vegetation), plantation forest, cropland, pasture and urban<sup>16</sup>. 597 598 These classes were selected to match the land-use classification adopted in the 599 Intergovernmental Panel on Climate Change Representative Concentration Pathways scenarios<sup>26</sup> in order to facilitate the projection of our models onto these scenarios. Sites were 600 also assigned to a level of human intensity of use - minimal, light or intense - within each 601 602 major land-use class, also based on the description of the habitat in the source paper (see 603 Extended Data Table 1 for definitions). The factors that determined this level depended on 604 the land-use class (e.g. bushmeat extraction and limited logging in primary and secondary 605 vegetation; or stocking density and chemical inputs in pasture; Extended Data Table 1). Sites that could not be classified for land-use and use intensity were excluded from the analyses. 606 607 The final dataset contained the following numbers of sites in each land use and land-use 608 intensity level: Primary vegetation, minimal use – 1546 (from 183 studies), light use – 860 609 (76 studies), intense use – 449 (33 studies); mature secondary vegetation, minimal use – 198 610 (52 studies), light/intense use – 213 (23 studies); intermediate secondary vegetation, minimal 611 use – 404 (55 studies), light/intense use – 269 (30 studies); young secondary vegetation, 612 minimal use -431 (50 studies), light/intense use -331 (34 studies); plantation forest, 613 minimal use – 356 (47 studies), light use – 402 (42 studies), intense use – 238 (29 studies); 614 cropland, minimal use -427 (45 studies), light use -632 (43 studies), intense use -703 (36 studies); pasture, minimal use - 525 (43 studies), light use - 434 (52 studies), intense use -615 174 (23 studies); and urban, minimal use - 174 (23 studies), light use - 244 (26 studies), 616 617 intense use - 195 (18 studies).

We overlaid our sites with available global data sets to obtain site-level estimates of 618 human population density<sup>45</sup>, distance to the nearest road<sup>46</sup> and estimated travel time to nearest population centre with greater than 50,000 inhabitants<sup>47</sup>. For distance to nearest road, the map 619 620 621 of roads was first projected onto a Berhmann equal-area projection. These operations were 622 carried out using Python code implemented using the arcpy Python module in ArcMap Version  $10.0^{391}$ . In the main figures, the inverses of distance to roads and travel time to major 623 population centre (proximity to roads and accessibility) were presented so that high values 624 625 corresponded to higher hypothesized human impact. To estimate the history of human use of 626 the landscapes within which sites were located, we calculated the number of years since the 30-arc-second grid cell containing each site became 30% covered by human land uses 627 (cropland, pasture and urban), according to the HYDE model<sup>48</sup>. Collinearity among variables 628 629 describing anthropogenic change was low: the highest correlation was between land use and human population density (Pearson  $R^2 = 0.31$ ). 630

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- 632

633 Modelling site-level diversity, composition and turnover634

The response of site-level diversity to the measures of anthropogenic change was
 modelled using generalized linear mixed effects models, implemented in the lme4 package
 Version 1.0-5<sup>44</sup> in R Version 3.0.2<sup>392</sup>. We first compared candidate random-effects structures
 using the full candidate fixed-effects structure<sup>393</sup>. Random-intercept terms considered in all

639 models were the identity of study from which data were taken, to account for study-level 640 differences in the response variables and sampling methods used, and – within-study – the spatial block in which the site was located, to account for the spatial arrangement of sites. For 641 models of species richness (within-sample and rarefied), we also fitted an observation-level 642 random effect (i.e. site identity) to account for the overdispersion present<sup>394</sup>. We also 643 644 considered random slopes, with respect to study, of each of the main fixed effects (land use, 645 land-use intensity, human population density, distance to nearest road, travel time to nearest 646 major city and time since the landscape was majority converted to human uses). Random 647 effects were retained or discarded based on Akaike Information Criterion values.

648 Once the best random-effects structure had been selected, we performed backward 649 stepwise model simplification to select the best fixed-effects structure (see 'Full Statistical Results')<sup>393</sup>. Human population density, distance to roads, travel time to nearest major city 650 and time since major human use of the landscape were log transformed in the analyses, with a 651 652 value of 1 added to human population density, travel time to nearest major city and time since major landscape conversion to deal with zero values. These four variables were fitted as 653 654 continuous effects, with quadratic polynomials for human population, distance to roads and 655 travel time to nearest major city, and as a linear effect for time since human landscape conversion. For variables fitted as quadratic polynomials, we also tested linear effects during 656 657 the backward stepwise model selection. All continuous variables were rescaled prior to 658 analysis so that values ranged between zero and one. Interaction terms were tested first, and 659 then removed to test the main effects. All main effects that were part of significant interaction 660 terms were retained in the final models regardless of their significance as main effects. For 661 the model of community-weighted mean body mass and plant height, because the number of 662 sites with data was smaller than for the other metrics, only land use (excluding urban sites, which were few), human population density and distance to roads, and no interactions, were 663 664 fitted (for the model of plant height, sample sizes in each land use were: primary vegetation – 634 sites, secondary vegetation – 851 sites, plantation forest – 222 sites, cropland – 72 sites, 665 pasture – 412 sites; and for the model of animal mass: primary vegetation – 1728 sites, 666 667 secondary vegetation - 805 sites, plantation forest - 602 sites, cropland - 641 sites, pasture -440 sites). The decision whether or not to retain terms was based on likelihood ratio tests. 668 669 The coefficient estimates of the best models are shown in Figure 1b-d and Extended Data 670 Figure 2, and the formulae and statistical results are shown in the Supplementary Information. To test for spatial autocorrelation in the residuals of the final best models, we 671 calculated Moran's I values and associated P-values, separately for each study considered in the models, using the spdep package Version 0.5-68<sup>395</sup> in R; the distribution of P-values 672 673 across studies was used as an indication of whether spatial autocorrelation was likely to cause 674 675 a problem. This revealed that the residuals showed little spatial autocorrelation (Extended 676 Data Figure 5). We used cross validation to assess the robustness of model parameter 677 estimates, first based on dividing the studies randomly into 10 equal-sized sets and dropping 678 each set in turn (Extended Data Figure 3c), and secondly based on leaving out the studies 679 from each biome in turn (Extended Data Figure 3d). 680

Publication bias is a potential problem for any large-scale synthesis of data from many publications. In standard meta-analyses, funnel plots<sup>396</sup> can be used to test for any 681 682 relationship between standard error and effect size, as a bias in effect sizes at high standard 683 error toward more positive or more negative effects indicates a likely effect of publication 684 bias. Creating funnel plots for our data was more complicated because ours was a site-level 685 analysis of raw diversity estimates rather than a traditional meta-analysis. Instead we 686 generated individual models relating diversity to land use for each study that sampled at least two sites within each of at least two land-use types. We focused on land use because: a) there 687 were a small number of sites included in most within-study models; and 2) the original 688

689 studies focused on effects of land use - not generally on land-use intensity, human population 690 density or distance to roads – and thus any effect of publication bias would likely be seen in the land-use coefficients. Funnel plots were generated by plotting, for each land-use type, the 691 692 estimated model coefficients against the associated standard errors (Extended Data Figure 4). 693 There were some indications of an effect of publication bias, with less certain coefficient 694 estimates tending to have more negative estimates for some of the land uses (Extended Data 695 Figure 4). On the other hand, study-level random slopes of human-dominated land uses 696 tended to be more negative for studies that sampled more sites (Extended Data Figure 4). It is 697 important to emphasize that in a site-level analysis like ours, studies with fewer sites have 698 less weight in the models. Modelled coefficient estimates were generally robust to the 699 removal of these studies (Extended Data Figure 4). Basing projections on coefficient 700 estimates from models where small studies were excluded led to a less than 1% change in the 701 estimated global richness values (results not shown). As with all studies based on data from 702 the literature, we under-represent unpublished data.

703 To model turnover of species composition between pairs of sites, we calculated average 704 dissimilarity<sup>23</sup> in the lists of present species (1 - Sørensen index) between all pairs of sites 705 within each study. For this analysis, we were only able to consider studies with more than one 706 site in at least one of the land-use types considered. Once compositional similarity had been 707 calculated for every pair of sites within each study, the average compositional similarity was 708 calculated for every pair of land-use types considered within each study (including 709 comparisons between sites in the same land-use type). Finally, the average compositional 710 similarity was calculated for each pair of land-use types across all studies. To visualize the 711 clustering of different land-use types in terms of community composition, we performed a 712 hierarchical complete-linkage cluster analysis on the compositional dissimilarity (i.e. 1 – similarity) matrix, using the helust function in R Version  $3.0.2^{392}$ . To test whether differences 713 in the average geographic distance between pairs of sites in different land-use combinations 714 715 affected these results, we correlated average compositional similarity with average distance 716 between sites, for all pairwise combinations of land use (including comparisons of a land-use 717 type with itself). Correlations between average distance and average community similarity were only very weakly negative ( $R^2 = 0.001$ ), suggesting they do not strongly distort the 718 comparisons of community composition. However, the fact that some land uses tend to occur 719 720 more closely together than others could influence the diversity patterns seen in our models, if 721 some land uses are typically close to high-diversity habitats and so are more likely to benefit 722 from dispersal. For example, sites in secondary vegetation and plantation forest were closer, 723 on average, to primary vegetation sites than were those in cropland, pasture and urban 724 (average distances to sites in primary vegetation were: other primary vegetation sites = 7.38725 km, mature secondary vegetation = 4.4 km, intermediate secondary vegetation = 3.9 km, young secondary vegetation = 6.9 km, plantation forest = 4.2 km, cropland = 16.4 km, 726 727 pasture = 10.1 km, and urban = 11.4 km). Accounting for distance in such already-complex 728 models is not computationally tractable. In making the projections, we therefore implicitly 729 assume that the average distances will not change (i.e. that secondary vegetation and 730 plantation forests will remain closer to primary vegetation than cropland, pasture and urban 731 habitats).

732

Projecting the Models onto Spatial Estimates of Anthropogenic Variables734

735 We projected the best overall models of richness (within-sample and rarefied), 736 abundance and community-weighted mean organism size onto estimates of land use, land-use 737 intensity and human population density at  $0.5^{\circ} \times 0.5^{\circ}$  resolution, using historical estimates 738 for 1500 to 2005, and four Representative Concentration Pathways scenarios of future changes (IMAGE 2.6, MiniCAM 4.5, AIM 6.0 and MESSAGE 8.5; the names refer to the
 integrated assessment models used and the numbers to the amount of radiative forcing
 assumed in 2100)<sup>397</sup>. In the absence of global projections, proximity to roads and accessibility
 were omitted from our projections.

743 Estimates of land use for both the historical reconstruction and the future scenarios 744 were taken from the harmonized land-use data accompanying the scenarios<sup>26</sup>. Estimates of 745 the stage of secondary vegetation (young, intermediate or mature) are not available directly in 746 the RCP land-use data. However, these data contain estimates of the transition each year 747 between secondary vegetation and all other land-use types. To convert this into an estimate of 748 the proportion of secondary vegetation in each of the stages of maturity, we considered any 749 transition to secondary vegetation to result in secondary vegetation of age zero. Each year, 750 this age was then incremented by one. In the absence of better information, any transitions 751 from secondary vegetation to any other land-use type were assumed to be drawn evenly from 752 the ages currently represented. For the purposes of the projections, secondary vegetation was 753 considered to be young until an age of 30 years, intermediate between 30 years and 100 754 years, and mature thereafter. We developed C# code to convert land-use transitions into 755 estimates of the stage structure of secondary vegetation.

756 Gridded temporal estimates of human population density were directly available for the 757 HYDE historical scenario and MESSAGE future scenario. Human population trajectories in 758 the MiniCAM model were resolved only to the level of United Nations regions<sup>41</sup>; we 759 therefore downscaled these to grid cells assuming no temporal change in the spatial pattern of relative population density within regions compared to present day patterns<sup>45</sup>, which is the 760 method used in other RCP-scenario land-use models lacking human population data resolved 761 to grid cells<sup>26</sup>. Gridded estimates of human population from the MESSAGE model were 762 763 downloaded from http://www.iiasa.ac.at/web-apps/ggi/GgiDb/. For the scenarios for which human population projections were not available (IMAGE and AIM), we used country-level 764 estimates from the 'medium' scenario of the United Nations population division<sup>398</sup>, which 765 gives the closest global predictions of future human population to those assumed by IMAGE 766 767 and AIM<sup>26</sup>. These country-level estimates were downscaled to grid cells using the same 768 method as for MiniCAM's regional projections.

769 Land-use intensity was an important explanatory variable in our models, but global 770 maps of land-use intensity are not available. We therefore generated global estimates of current land-use intensity based on a map of 'Global Land Systems'<sup>359</sup>, which divides coarse 771 772 land-use types into sub-categories based on levels of cropland intensity, livestock densities 773 and human population density. We mapped each Global Land Systems class onto one or 774 more relevant combinations of our classes of land use and land-use intensity (Extended Data 775 Table 2). The Global Land Systems dataset has a spatial resolution of 5 arc-minutes. To calculate the proportion of each  $0.5^{\circ}$  cell occupied by each land use and land-use intensity 776 777 combination we calculated the proportion of 5-arc-minute cells within each  $0.5^{\circ}$  cell 778 containing matching Global Land Systems categories (see legend of Extended Data Table 2 779 for details).

780 To generate past and future estimates of land-use intensity, we modelled the current 781 proportion of each land-use type estimated to be under minimal, light or intense levels of 782 intensity within each grid cell (one model for each intensity level), as a function of the 783 prevalence of the land-use type within each cell and human population density, with the 784 relationships allowed to vary among the 23 United Nations (UN) sub-regions (i.e. we fitted 785 interaction terms between UN sub-region and both the prevalence of each land-use type and 786 human population density). UN sub-region data were taken from the world borders shapefile Version 0.3 (http://thematicmapping.org/downloads/world\_borders.php) and converted to a 787  $0.5^{\circ} \times 0.5^{\circ}$  raster using ArcMap Version  $10.0^{391}$ . The models were developed using 788

generalized linear models with a binomial distribution of errors, implemented in the lme4
package Version 1.0-5<sup>44</sup> in R Version 3.0.2<sup>392</sup>. The resulting models explained between
30.6% and 76.7% of the deviance in estimated current levels of intensity. Past and future
land-use intensities were estimated by applying the models to the same past and future
estimates of land use and human population density as above.

794 The scenarios gave the proportion of each grid cell estimated to be occupied by each 795 combination of land use and land-use intensity. We did not attempt to resolve human 796 population density within grid cells for our historical estimates or forecasts, thereby assuming 797 it to be spatially (not temporally) constant within each cell. The coefficients from the models 798 of site-level diversity were thus applied to each combination of land use and intensity within 799 each cell, with the same human population density estimate across all combinations. All 800 predictions were expressed as a percentage net change compared with a baseline before 801 human land-use impacts on biodiversity, in which all land use was assumed to be primary 802 vegetation of minimal intensity of use, and with a human population density of zero. Each 803 cell's average value of net biodiversity change was calculated as the area-weighted mean 804 value across all land uses and intensities. Global average values were calculated as mean 805 values across all cells, weighted by cell area and an appropriate weighting factor to account 806 for the fact that cells have different baseline levels of diversity. The weighting factors applied 807 were: terrestrial vertebrate species richness in the case of richness, and net primary 808 production (NPP) in the case of total abundance. No weighting factor was applied for 809 projections of community-weighted mean plant height. Terrestrial vertebrate species richness 810 was estimated by overlaying extent-of-occurrence range maps for mammals, birds, amphibians and reptiles, using Python code written by ourselves and implemented in ArcMap 811 Version  $10.0^{391}$ . Data on Net Primary Production were estimates of potential NPP (i.e. in the 812 813 absence of human impacts) from the Lund-Postdam-Jena (LPJ) Dynamic Global Vegetation Model<sup>400</sup>. 814 815 The 95% confidence intervals around the projected values of biodiversity for each

816 combination of pressure variables were estimated based on uncertainty in the modelled 817 coefficients. We were unable to conduct multi-model averaging to account for uncertainty in 818 the structure of the models (i.e. projections were based only on the final best model) because 819 applying such complex mixed-effects models, based on such large datasets, to multiple 820 scenarios of human pressure at a global scale was intractable both in terms of time and computer-memory requirements. We were also unable to account for uncertainty in the 821 822 trajectories of the human pressure variables, because uncertainty estimates are not available 823 for any of the variables considered.

824 To estimate average biodiversity change in individual countries, we intersected the gridded projections with the world borders shapefile (see above) using the extract function in 825 the raster package Version  $2.2-12^{401}$  in R Version  $3.0.2^{392}$ . Mean values across the cells 826 associated with each country were calculated, weighted by cell area. To interpret the 827 828 outcomes for countries in terms of their natural biodiversity, we related the country-level 829 projections to estimates of average natural vertebrate species richness (see above). To 830 interpret the outcomes for countries in terms of their socio-economy, we related the 831 projections to estimates of the Human Development Index, which is an indicator of 832 education, life expectancy, wealth and standard of living (https://data.undp.org/).

833

## 834 Extended Data Legends

835

# 836 Extended Data Figure 1. Taxonomic and geographic representativeness of the dataset

used. a, The relationship between the number of species represented in our data and the
 number estimated to have been described<sup>17</sup>, for 47 major taxonomic groups; lines show (from

- 839 bottom to top) 0.1%, 1% and 10% representation of described species in our dataset; magenta
- = invertebrates, red = vertebrates, green = plants, blue = fungi, and grey = all other taxonomic groups. **b**, the relationship across biomes<sup>402</sup> between the percentage of global terrestrial net 840
- 841 primary production and the number of sites in our dataset; A = tundra, B = boreal forests and 842
- taiga, C = temperate conifer forests, D = temperate broadleaf and mixed forests, E = montane 843
- grasslands and shrublands, F = temperate grasslands, savannas and shrublands, G = 844
- 845 Mediterranean forests, woodlands and scrub, H = deserts and xeric shrublands, J = tropical
- 846 and subtropical grasslands, savannas and shrublands, K = tropical and subtropical coniferous
- 847 forests, M = tropical and subtropical dry broadleaf forests, N = tropical and subtropical moist
- 848 broadleaf forests, P = mangroves; note that the flooded grasslands and savanna biome is not
- 849 represented in the dataset; grey line show 1:1 line.
- 850

### 851 Extended Data Figure 2. Detailed response of local diversity to human pressures.

- 852 Modelled effects (controlling for land use) of human population density (HPD), distance to 853 nearest road, time since 30% conversion of a landscape to human uses (TSC) and time to
- 854 nearest population centre with greater than 50,000 inhabitants (a-d), interactions between
- 855 pairs of these variables (e), and interactions between these variables and land use (f-i) on site-
- level diversity: **a-c**, **f**, **g**, within-sample species richness; **e**, **h**, **i**, total abundance; and **d**, 856
- 857 community-weighted mean vertebrate body mass. Shaded polygons in **a-d** show 95%
- 858 confidence intervals. For clarity, shaded polygons in **f-i** are shown as  $\pm 0.5 \times \text{SEM}$ .
- 859 Confidence intervals in e are omitted. Rugs along the x axes in the line graphs show the
- 860 values of the explanatory variables represented in the dataset used for modelling. Only
- 861 significant effects are shown. Note that distance to nearest road and travel time to major
- 862 population centre measures are the raw (log-transformed) values fitted in the models rather
- than the proximity to roads and accessibility values (obtained as 1 minus the former values) 863
- 864 presented in Figure 1. Sample sizes are given in full in the Methods.
- 865

Extended Data Figure 3. Robustness of modelled effects of human pressures. a, Effects 866 of land use, human population density (HPD) and proximity to nearest road (PR) on 867 rarefaction-based species richness. b, To test that any differences between these results and 868 869 the results for within-sample species richness presented in the main manuscript were not 870 because rarefied species richness could only be calculated with a smaller dataset, we also show modelled effects on within-sample species richness with the same reduced dataset. **c-d**. 871 872 Cross-validated robustness of coefficient estimates for land use and land-use intensity: 873 crosses show 95% confidence intervals around the coefficient estimates under ten-fold cross-874 validation, excluding data from approximately 10% of studies at a time (c), and under 875 geographical cross-validation, excluding data from one biome at a time (**d**); colours, points, 876 error bars and land-use labels are as in Figure 1 in the main text. Primary, primary vegetation; 877 YSV, young secondary vegetation; ISV, intermediate secondary vegetation; MSV, mature 878 secondary vegetation; plantation, plantation forest. Sample sizes are given in full in the 879 Methods.

880

881 Extended Data Figure 4. Tests of the potential for publication bias to influence the

882 richness models and projections. Left-hand panels (a, d, g, j, m) show funnel plots of the relationship between the standard error around coefficient estimates (inversely related to the 883

884 size of studies) and the coefficient estimates themselves for each coarse land-use type; there

- 885 is evidence for publication bias with respect to some of the land-use types, as indicated by an
- 886 absence of points on one or other side of zero for studies with large standard errors (but note
- that small studies are down-weighted in the model); red points show studies with more than 5 887
- 888 sites in the land use in question (10 for secondary vegetation and plantation forest because

889 there were more sites for these land uses and some studies with between 5 and 10 sites

- 890 showed variable responses); horizontal dashed lines show the modelled coefficients for each
- 891 land use. Central panels (**b**, **e**, **h**, **k**, **n**) show the relationship between study size (log-
- 892 transformed total number of sites) and the random slope of the land use in question with 893 respect to study identity, from a random-slopes-and-intercepts model; where a significant
- 894 relationship was detected using a linear model, fitted values and 95% confidence intervals are
- 895 shown as a red dashed line and red dotted lines, respectively; conversely to what would be
- 896 expected if publication bias was present, where significant relationships between study size
- 897 and random slopes were detected, these were negative (i.e. larger studies detected more
- 898 negative effects). Right-hand panels (c, f, i, l, o) show the robustness of modelled coefficients
- 899 to removal of studies with few sites in a given land use (black points in the left-hand panels);
- 900 left-hand error bars show coefficient estimates for all studies and right-hand error bars show
- 901 coefficient estimates for studies with more than 5 sites in that land use (10 for secondary 902 vegetation and plantation forest).
- 903

904 Extended Data Figure 5. Tests for spatial autocorrelation in the model residuals. For the 905 four main modelled metrics of site-level diversity —  $\mathbf{a}$ , within-sample species richness;  $\mathbf{b}$ , 906 total abundance; c, community-weighted mean plant-height; and d, community-weighted

907 mean animal mass — histograms of P-values from sets of Moran's tests for spatial

908 autocorrelation in the residuals of the best models for individual studies. The percentage of

- 909 studies with significant spatial autocorrelation (P < 0.05; indicated by vertical red line) is
- 910 shown.
- 911

912 Extended Data Figure 6. Current, past and future projections of all metrics of local

- 913 biodiversity. Net change in local diversity caused by land use and related pressures by 2000 under an IMAGE reference scenario<sup>10</sup>: **a**, richness; **b**, rarefied richness; **c**, total abundance; 914 and **d**, community-weighted mean plant height. Note that the values used to divide the 915
- colours are the same in all panels, but that the maximum and minimum values are different, 916
- 917 as indicated in the legends. Historical and future estimates of net change in local diversity 918 from 1500-2095, based on estimates of land-use, land-use intensity and human population
- 919 density from the four Representative Concentration Pathways (RCP) scenarios (Table 1): e,
- 920 richness; f, total abundance; and g, community-weighted mean plant height; historical
- 921 (shading) and future (error bars) uncertainty shown as 95% confidence intervals, with
- 922 uncertainty rescaled to be zero in 2005 to show uncertainty in past and future change
- 923 separately; the global average projection for the MESSAGE scenario does not directly join 924 the historical reconstruction because projections start in 2010 (human population estimates
- 925 are available at 15-year intervals) and because human population (and thus land-use intensity)
- 926 and plantation-forest extent have not been harmonized among scenarios. In panel  $\mathbf{e}$ , the
- 927 dashed line shows projected diversity change under land-use change only (i.e. without land-
- 928 use intensity and human population density, the projections of which involved simplifying
- 929 assumptions), and the dotted line shows projections of rarefaction-based species richness.
- 930
- 931 Extended Data Figure 7. Reconstructed and projected total global land-use areas under
- 932 the Representative Concentration Pathways (RCP) scenarios. a, estimated total area of
- 933 the major land-use types. **b-f**, estimated total area of secondary vegetation in different stages 934 of recovery.
- 935

### 936 Extended Data Figure 8. Biodiversity projections at the country level. a-d, Country-level

- 937 projections of net change in local richness between 2005 and 2095 under the four RCP
- 938 scenarios (a, IMAGE 2.6; b, MiniCAM 4.5; c, AIM 6.0; and d, MESSAGE 8.5), shown in

- 939 relation to the Human Development Index (an indicator of education, life expectancy, wealth
- 940 and standard of living) in the most recent year for which data are available. e-f, Country-level
- 941 projections of net change in local richness between 2005 and 2095 under the best- and worst-
- 942 performing RCP scenarios in terms of biodiversity (e. MiniCAM 4.5; f, MESSAGE 8.5), 943 shown in relation to past change in biodiversity from a baseline with no human land-use
- 944 effects to 2005 according to the HYDE land-use reconstruction. Colours indicate
- 945 biogeographic realms (key in **b**); colour intensity reflects native vertebrate species richness
- 946 (more intense = higher species richness); point size is proportional to (log) country area.
- 947
- 948 949

#### 950 Extended Data Table 1. Land use and land-use intensity classification definitions (from 951 ref. 16).

952

### 953 Extended Data Table 2. Conversion between Global Land Systems dataset and our

954 intensity classification for each major land-use type. To estimate proportional coverage of each intensity class for each land-use type in the  $0.5^{\circ} \times 0.5^{\circ}$  grid cells used for projection, we 955 calculated the number of finer-resolution Global Land Systems<sup>399</sup> cells with a matching 956 957 intensity class for the land-use type in question, as a proportion of Global Land Systems cells matching any intensity class for the land-use type in question. For example, to calculate the 958 959 proportion of urban land that is under intense use, we divided the number of cells with a 960 Global Land Systems classification of 'urban' by the number of cells classified as 'urban' or 961 'peri-urban and villages'. None of the Global Land Systems classes could inform about the 962 intensity of plantation forest, and so we assumed that any plantation forest was composed of 963 equal proportions under minimal, light and intense use.

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