

# Causal claims, causal assumptions and protected area impact

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To effectively conserve biodiversity, policymakers must know the extent to which protected areas (PAs) benefit biodiversity. By leveraging impressive datasets on three measures of biodiversity for Southeast Asia, Brodie et al.<sup>1</sup> claim to have detected a positive impact of protection within PAs, and spillovers of these impacts into the wider landscape. We argue that their analyses do not provide strong evidence about the benefits of PAs for biodiversity because their design cannot eliminate the most likely rival explanations for the patterns observed in the data, and their interpretations of the two tests for spillovers are flawed. Our concerns have important implications for balancing the trade-offs between investing in more PAs and managing the existing network better, as well as for the better use of causal inference methods in conservation science.

To quantify the impacts of protection, one must compare biodiversity in protected locations to plausible estimates of biodiversity in the same locations had they not been protected<sup>2,3</sup>. This is often done via comparison with unprotected sites. Where treatment assignment is non-random (as is the case for PAs), a clear understanding of the process by which some sites came to be protected while others did not is important for identifying potential confounders that could affect both the likelihood of a site being protected and the observed patterns of diversity<sup>4</sup>. The analysis by Brodie et al.<sup>1</sup> controls for three confounding variables: two at the site level (3D forest structure and accessibility), and one at the country level (Human Development Index). This design depends on the assumption that after controlling for these three variables, PAs are designated as if random<sup>5</sup>. In other words, the authors assume that once they control for these three variables, protected and unprotected sites would have equivalent levels of diversity prior to protection, and so any observed difference in diversity would be caused by protection. We believe that this assumption is questionable for two reasons.

First, forest structure and accessibility are measured post-protection, and so cannot represent sites in their pre-protection state. In the directed acyclic graph given in Extended Data Fig. 2 of the main paper<sup>1</sup>, forest structure and accessibility are shown to affect both the selection of protected sites and diversity at the protected sites (we show a simplified version in Supplementary Fig. 1a). We agree that pre-protection forest structure and accessibility could be confounders. However, data for these variables were taken from recent measurements, decades after most PAs were designated (the average PA designation date was 1989). This is a problem because forest structure and accessibility are likely to themselves be affected by protection, for instance by reducing deforestation or influencing the construction

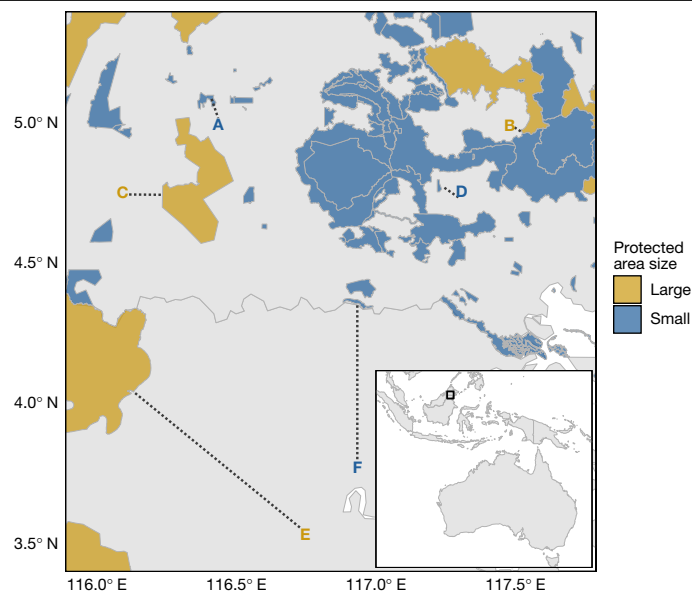
of roads<sup>6</sup>; placing them on the causal path from protection to diversity. Controlling for post-protection accessibility and forest structure introduces bias through two well-known mechanisms (blocking mediator pathways and introducing collider bias (Supplementary Information, section 1)), meaning that the direction and magnitude of the relationship between protection and diversity cannot be reliably estimated<sup>7</sup>.

Second, even if data for these variables had been measured before protection, it is not reasonable to assume that forest structure, accessibility and Human Development Index, as relevant as they are, are sufficient to control for the complex spatial patterns in biodiversity. Using only these three variables does, therefore, not enable one to eliminate the rival explanation that biodiversity was higher in sites selected for protection than those that were not selected, and thus the observed patterns were driven by processes that took place prior to protection. This is particularly problematic because principles of conservation prioritization and planning suggest that PAs are likely to be placed in areas with higher biodiversity<sup>8–10</sup>. In a supplementary analysis, Brodie et al.<sup>1</sup> claim that PAs were not designated with biodiversity in mind by reporting that post-protection diversity measures are not correlated with the age of the PAs. However, one cannot draw inferences about how past biodiversity affected PA placement using the correlation between current biodiversity and the age of protected sites.

We show that the conclusions regarding the benefit of protection presented by Brodie et al. change with only a small amount of unobserved confounding (see Supplementary Information, section 2). A confounder that explains just 14% (for species richness and phylogenetic diversity) and 8% (for functional richness) of the residual variance in protection and post-protection diversity would be sufficient to make the estimated effect of PAs indistinguishable from zero. Therefore, the conclusions about PA impact are fragile to minor violations of the assumption that bias can be eliminated using only these three confounders, even under the assumption that the data were from pre-protection years.

These two design limitations not only weaken the claims about the magnitudes of the impacts inside PAs, but they also weaken the headline claims of positive spillover effects from PAs to the surrounding landscape. Brodie et al. acknowledge that inferring causality from the data is challenging in the context of spillover effects but, given the spatial dependence between a PA and its surroundings, the same problems of controlling for confounding bias in the within-protected design also affect the spillover design. If PAs are more likely to be designated in areas of high biodiversity, then it is also likely that similar

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**Fig. 1** Illustration of why the approach to answering the question ‘Is diversity higher nearer large PAs, relative to small PAs?’ is inappropriate. Maps shows actual PAs in Malaysia and Indonesia (see Supplementary Information, section 3 for details), coloured to indicate whether they are large (>500 km<sup>2</sup>) or small (<500 km<sup>2</sup>). We have overlaid hypothetical sites, coloured by their nearest area, to demonstrate how exposure to protection is not consistent within or between groups. Sites in the ‘large’ group can be very near to or very far from PAs (B versus E), and can be surrounded on one or many sides by protection (B versus C), whereas sites in the ‘small’ group can be much nearer a large PA than either sites in that same group (D versus F) or sites in the ‘large’ group (A versus E). We acknowledge we have selected example sites to make our point; it would be valuable to see the true configuration of sites to establish the magnitude of the problem.

areas surrounding those PAs will have higher biodiversity than areas further away, even without any spillover effect<sup>11</sup>.

Moreover, even if such confounding effects were not a serious source of bias, the results do not support the claim that areas around PAs have higher biodiversity than the surrounding landscape. To quantify spillover, Brodie et al.<sup>1</sup> present two tests. The first test examines diversity in unprotected sites that are adjacent to large PAs (more than 500 km<sup>2</sup>) or small PAs (less than 500 km<sup>2</sup>). However, all unprotected sites are included in this analysis, regardless of distance to nearest PA or how many other PAs they are near to. This means that sites in both groups can vary hugely in the number and size of PAs that they could experience spillover from, and how far they are from these areas (Fig. 1). We would not expect spillover to be more similar within each of these groupings than between them (for a full exploration, see Supplementary Information, section 3). The second test explores whether average diversity in unprotected sites within 2 km of a PA is larger than average diversity in unprotected sites further away (note that although this 2 km threshold is not specified in the main text, it is apparent from the Extended Data and code<sup>3</sup>; see Supplementary Information, section 3). However, among the six estimated differences in diversity, five are statistically non-significant at conventional levels, indicating no evidence of spillover.

We strongly agree with Brodie et al.<sup>1</sup> that PAs matter. Their data confirm that protected sites in Southeast Asia harbour more bird diversity than unprotected sites. This observation provides a strong argument for investment in maintaining the globally important biodiversity in these sites. We also agree that expanding protection will probably be necessary given the large gaps in the global network of PAs<sup>12</sup> and

current state of biodiversity<sup>13</sup>. However, their analysis cannot tell us how much more biodiversity exists within and outside the study sites because of protection, nor can it tell us how much more biodiversity will exist in future if the area under protection were expanded. Causal inference from observational data is difficult. Sometimes available data and study designs will not allow the causal question to be answered, however relevant it may be to policy.

## Online content

Any methods, additional references, Nature Portfolio reporting summaries, source data, extended data, supplementary information, acknowledgements, peer review information; details of author contributions and competing interests; and statements of data and code availability are available at <https://doi.org/10.1038/s41586-024-08512-8>.

## Reporting summary

Further information on research design is available in the Nature Portfolio Reporting Summary linked to this article.

## Data availability

Data used in this paper are from Brodie et al.<sup>1</sup>.

## Code availability

The code to support our analyses is presented in the Supplementary Information.

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**Author contributions** All authors contributed equally to developing and writing this response. H.W. conducted all analyses.

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## Additional information

**Supplementary information** The online version contains supplementary material available at <https://doi.org/10.1038/s41586-024-08512-8>.

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# Reply to: Causal claims, causal assumptions and protected area impact

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REPLYING TO: J. Geldmann et al. *Nature* <https://doi.org/10.1038/s41586-024-08512-8> (2025).

In the accompanying Comment, Geldmann et al.<sup>1</sup> incorrectly claim that protected area (PA) efficacy cannot be established without biodiversity data that predates establishment of the PA. Spatial correlates of diversity are known as a result of centuries of ecological research; our analyses controlled for these factors in a variety of ways in order to isolate the impacts of protection per se on bird and mammal biodiversity. The proposition of Geldmann et al. that our results are biased because PAs were established in areas with high natural biodiversity ignores these analytical controls, is naive to the realities of on-the-ground conservation, and has been disproved by recent research. Although we look forward to future work that improves on our predictions, our study provides robust estimates of the biodiversity impacts of PAs across hyperdiverse Southeast Asia<sup>2</sup>—information that is critically needed to support large-scale conservation objectives.

Geldmann et al.<sup>1</sup> correctly state that the strongest causal inference is derived when treatments (PA status, in this case) are assigned randomly and prior to the onset of a study. In conservation, however, this is frequently unfeasible, such as for PAs that were established before the invention of robust biodiversity sampling methods (for example, before the camera trapping used in our study). We overcame this issue by assigning treatments as if they were random relative to pre-existing biodiversity across the landscape by controlling for confounding factors that would have driven spatial variation in pre-establishment diversity. Geldmann et al.<sup>1</sup> are of the opinion that controlling for these factors is not sufficient because some were measured after rather than before PA establishment. This claim is not relevant for many of the fundamental determinants of diversity, including latitude, longitude, elevation and general climatic conditions, which have not changed over the relevant timescales.

For the few temporally dynamic variables, the key consideration is whether changes over time would bias the results in ways that would reduce the effect sizes reported. Namely, forest structure and accessibility are temporally dynamic, but there is no evidence or intuition that these have changed in consistently biasing ways that would affect

our inference. Geldmann et al.<sup>1</sup> conflate this absence of evidence with evidence of absence. Accessibility, in particular, has changed in predictable ways across the globe; areas that were accessible in the past are now even more so, and historically remote areas are now more accessible than they were<sup>3</sup>. In short, accessibility values have increased everywhere, but relative differences in accessibility across space have changed much less—this renders pre-establishment accessibility values highly correlated with post-establishment values, negating the critique of Geldmann et al.

The assertion by Geldmann et al. that diversity must be measured before the PA is established<sup>1</sup> ignores centuries of ecological research. Ecologists have been studying the spatial distribution of diversity since the inception of the field. The naturally driven spatial variation in tropical forest biodiversity is well known to be strongly linked to elevation, topography and climate<sup>4–6</sup>. In the directed acyclic graphs for our structural causal modelling (Extended Data Fig. 2 in ref. 2), elevation, topographic position index (TPI) and bioclimate were all included as influencers of forest structure, which was included in our linear mixed-effects models. Although forest structure values have changed over time, the influences of elevation, topography and climate have not.

As a follow-up analysis in response to the critique by Geldmann et al., we re-ran our mixed-effects models to explicitly include other known and temporally static correlates of diversity—elevation and TPI—as covariates. The prediction of Geldmann et al. would be that this would reduce the PA coefficients and render them non-significant. Instead, the PA coefficients increased in the bird functional richness model, changed only slightly in the species richness and phylogenetic diversity models, and remained highly significant in all cases (Table 1). Climate, another major correlate of diversity, covaries strongly with other variables in our models. Across bird sampling locations, the first principle component of the 35 bioclimatic variables from WorldClim<sup>7</sup> is highly correlated with latitude ( $r = 0.89$ ), which is included in our models, and the second principle component is correlated with elevation ( $r = -0.80$ ), which we tested in the follow-up analysis above. Climate changes are experienced

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**Table 1 | Changes to bird ‘protected area’ model coefficients when adding elevation and TPI to the linear mixed-effects models**

	$\beta$ (standard error; <i>P</i> value)	
	Analysis without elevation and TPI	Analysis with elevation and TPI
Species richness	24.72 (4.95; <0.001)	25.54 (4.99; <0.001)
Functional richness	25.78 (6.52; <0.001)	29.08 (6.29; <0.001)
Phylogenetic diversity	0.38 (0.07; <0.001)	0.38 (0.07; <0.001)

at larger spatiotemporal scales than our paired inside-versus-outside treatment points<sup>8,9</sup>; therefore, as with accessibility, by accounting for differences seen today we are also accounting for differences that were likely to be present several decades ago when PAs were established. Overall, these analyses highlight that analysis of temporally static covariates generates similarly strong results to those in our original Article<sup>2</sup>, again negating the critique.

To summarize, we thoroughly accounted for proxies for (that is, correlates of) pre-establishment biodiversity in our original Article<sup>2</sup> and in the follow-up analyses above. There are still additional factors (as is always the case in science) that could have affected pre-establishment diversity and were not included in our models. However, for the omission of these factors to bias our results along the lines that Geldmann et al. suggest<sup>1</sup>, they would somehow have to be: correlated with the eventual locations of PAs, but uncorrelated with latitude, longitude, elevation, topography, climate, human accessibility, human development, forest height, forest cover, forest vertical complexity and tree leaf density (that is, the covariates that we tested or are highly correlated with the ones that we tested). It is difficult to imagine what factors could realistically meet these criteria. Geldmann et al. apparently could not imagine any either, as their simulation analysis used non-specific ‘unobserved confounding variables’ rather than any real biophysical metrics<sup>1</sup>. Their simulation is therefore abstract, implausible and not relevant to our empirical analyses.

Geldmann et al. propose a rival hypothesis that “diversity was higher in sites selected for protection than those that were not selected”<sup>1</sup>. Although modern systematic conservation prioritization strategies are intended to do exactly this, such methods were not in use decades ago when the majority of Southeast Asia’s PAs were established. PA establishment has been based much more on sociopolitical and economic considerations—such as targeting areas unsuitable for logging or agriculture—than ecological concerns<sup>3</sup>. As a result, current PA coverage is an exceedingly poor reflection of historic underlying diversity<sup>10,11</sup>. Indeed, an analysis of global PAs found that “both old and new protected areas did not target places with high concentrations of threatened vertebrate species. Instead, they appeared to be established in locations that minimize conflict with agriculturally suitable lands”<sup>12</sup>. Finally, tropical vertebrate diversity has been very difficult to quantify until recently, and so could not have been included in conservation prioritization analyses even if such analyses had occurred. If managers had wanted to establish PAs in high-diversity areas, they would have had to use proxies such as elevation, topography, bioclimate and accessibility—the very factors that we controlled for.

We acknowledged in our original Article that establishing causality between PAs and spillover was problematic<sup>2</sup>, but our stated justification for this analysis was to compare whether the data were consistent with patterns of spillover rather than to directly infer causality. Therefore, the claim in our abstract—“Rather than PAs generating leakage that deteriorated ecological conditions elsewhere, our results are consistent with PAs inducing spillover that benefits biodiversity in surrounding areas”—is valid.

Geldmann et al. bring up “the same problems of controlling for confounding bias”<sup>1</sup> that we refute above. They also suggest that there are

difficulties in measuring spillover within the spatially complex constellation of PAs in the region, which we agree with and had discussed in our Article<sup>2</sup>. Indeed, we hope that our results spur further research on the patterns and mechanisms of spillover, which could result from animal demography and investment in outreach or enforcement targeted at large reserves, with the influences of these management strategies (for example, reduced hunting, alternative employment in the PA or associated ecotourism) permeating into surrounding areas. Finally, Geldmann et al. appear to have misunderstood another test that we performed—we did not actually assess “whether average diversity in unprotected sites within 2 km of a PA is larger than average diversity in unprotected sites farther away”<sup>1</sup>, but rather tested the effects of ‘distance to PA’ as a continuous variable. We found a general lack of relationship between this variable and diversity but, as we stated in our paper, “Straight-line distance does not account for how topography, forest quality, human infrastructure, or hunting might affect animal movement out of protected areas and across the landscape, and so is only a very crude metric of PA proximity”.

Causal inference is always stronger if multiple lines of evidence can be brought to bear for any particular question. We do not claim that our Article<sup>2</sup> singlehandedly justifies the entire United Nations 30 × 30 enterprise<sup>13</sup>. However it does provide an important contribution to a broader literature that strongly supports the case that PAs enhance biodiversity conservation. The expansion and effective management of PAs is critical, given that the current global protected estate is not sufficiently large<sup>14</sup>, ecologically representative<sup>11</sup> or well-connected<sup>15,16</sup> to achieve the desired mitigation of the extinction crisis. Geldmann et al. apparently agree, despite the fact that biodiversity (and thus the most urgent need for new PAs) is concentrated in the Global South, whereas the pre-establishment diversity data that they consider so indispensable are essentially restricted to a tiny set of non-threatened species at a handful of sites in wealthy nations<sup>17</sup>.

Therefore, and contrary to the claims of Geldmann et al., our results do in fact provide robust estimates of the biodiversity impacts of PAs across hyperdiverse Southeast Asia. All scientific estimates are imperfect, and we look forward to new research that improves on our predictions and updates the state of knowledge in the field. For now, massive global changes and the urgency of implementing the 30 × 30 commitment require policymakers to use the best available information at any given time. Our study provides a timely update to the state of the science for tropical PAs and biodiversity.

## Methods

We compared mixed-effects models based on propensity score-matched data, as described in our original Article<sup>2</sup>, with and without elevation and topographic position index as additional covariates.

## Online content

Any methods, additional references, Nature Portfolio reporting summaries, source data, extended data, supplementary information, acknowledgements, peer review information; details of author contributions and competing interests; and statements of data and code availability are available at <https://doi.org/10.1038/s41586-024-08513-7>.

## Reporting summary

Further information on research design is available in the Nature Portfolio Reporting Summary linked to this article.

## Data availability

Data are available at <https://doi.org/10.6084/m9.figshare.22527298.v1> (ref. 18).

## Code availability

Analysis code is available at <https://doi.org/10.5281/zenodo.13742402> (ref. 19).

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**Competing interests** The authors declare no competing interests.

### Additional information

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## Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

### Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- |                                     |                                     |  |
|-------------------------------------|-------------------------------------|--|
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | The exact sample size ( $n$ ) for each experimental group/condition, given as a discrete number and unit of measurement  |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly  |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | The statistical test(s) used AND whether they are one- or two-sided<br><i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>   |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | A description of all covariates tested   |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons  |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals) |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | For null hypothesis testing, the test statistic (e.g. $F$ , $t$ , $r$ ) with confidence intervals, effect sizes, degrees of freedom and $P$ value noted<br><i>Give <math>P</math> values as exact values whenever suitable.</i>                            |
| <input checked="" type="checkbox"/> | <input type="checkbox"/>            | For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings   |
| <input checked="" type="checkbox"/> | <input type="checkbox"/>            | For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes   |
| <input checked="" type="checkbox"/> | <input type="checkbox"/>            | Estimates of effect sizes (e.g. Cohen's $d$ , Pearson's $r$ ), indicating how they were calculated   |

*Our web collection on [statistics for biologists](#) contains articles on many of the points above.*

### Software and code

Policy information about [availability of computer code](#)

Data collection

NA

Data analysis

R v4.4.1

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

### Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

Data are available at [doi.org/10.6084/m9.figshare.22527298.v1](https://doi.org/10.6084/m9.figshare.22527298.v1)

## Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender	NA
Reporting on race, ethnicity, or other socially relevant groupings	NA
Population characteristics	NA
Recruitment	NA
Ethics oversight	NA

Note that full information on the approval of the study protocol must also be provided in the manuscript.

## Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

Life sciences       Behavioural & social sciences       Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

## Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	Data on bird observations from 1079 sampling locations plus data on mammal detections on camera traps from 1365 sampling locations
Research sample	All species detected at each sampling location (excluding domestic species and those with ambiguous taxonomic identification)
Sampling strategy	All records were used, except as noted above
Data collection	Bird data were downloaded from eBird website; mammal data were collected by individual authors Bird data were downloaded from eBird website; mammal data were collected by individual authors
Timing and spatial scale	ata restricted to 2014-2022. The spatial scale was Southeast Asia as shown in our Fig. 2 of the original article
Data exclusions	3-6 data points excluded (depending on analysis) to improve normality of residuals, as described in our original article
Reproducibility	Non-experimental
Randomization	Non-experimental
Blinding	NA

Did the study involve field work?  Yes  No

## Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

## Materials &amp; experimental systems

n/a	Involvement
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern
<input checked="" type="checkbox"/>	<input type="checkbox"/> Plants

## Methods

n/a	Involvement
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

## Animals and other research organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research, and [Sex and Gender in Research](#)

Laboratory animals	NA
Wild animals	Animals were observed non-invasively. No animals were handled, caught, or harmed
Reporting on sex	NA
Field-collected samples	NA
Ethics oversight	ethical oversight not required for compilation of previously collected (non-invasive) data

Note that full information on the approval of the study protocol must also be provided in the manuscript.

## Plants

Seed stocks	<i>Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.</i>
Novel plant genotypes	<i>Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.</i>
Authentication	<i>Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.</i>