

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

- ☐ ☒ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- ☐ ☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☐ ☒ The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- ☐ ☒ A description of all covariates tested
- ☐ ☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- ☐ ☒ 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)
- ☐ ☒ For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- ☒ ☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- ☒ ☐ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- ☒ ☐ 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

No custom code was used to collect the data.

Data analysis

We used R version 4.0.5 to perform the statistical analyses. We provide the following code availability statement in the manuscript: "We provide the code, Demo code file, phylogenetic tree, and README file, that we used for the statistical analyses, in Zenodo43 (<https://zenodo.org/records/14834543>)."

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](#)

We provide the following data availability statement in the manuscript:

"The data used in this study are available in Zenodo43 (<https://zenodo.org/records/14834543>). This Zenodo dataset consists of data from various sources.

Specifically, the primary diet data are from sources noted in Supplementary Data 8-9. The diet percentages are from Jin Song et al.⁸². The mean plasma glucose concentration data are from the ZIMS database (<https://www.species360.org/>). The neoplasia prevalence data are from the literature^{7,12,44}. Body mass, gestation length or incubation length, and maximum lifespan data are from the literature^{44,86,87}, and species domestication data are also from the literature^{4,12}. Information and instructions for generating figures can be found in the Source Data file."

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	Not applicable
Reporting on race, ethnicity, or other socially relevant groupings	Not applicable
Population characteristics	Not applicable
Recruitment	Not applicable
Ethics oversight	Not applicable

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)

Life sciences study design

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

Sample size	We used all the samples that were available in the publicly available datasets (cancer prevalence data and glucose concentration data).
Data exclusions	In the methods section we mention that: "In the trophic level analyses, we only included trophic levels that had at least 10 species to improve the power of the analyses." "In the analyses of these diet percentages, we only included diets with a percentage of $\geq 10\%$. We removed diets (fish, nectar, scavenger, unknown vertebrates) with a sample size smaller than 10 species to improve the power of the analyses." "In all the above analyses, we excluded species for which the percentage of that food type in their diet was 0% because: (1) we were interested in the effects of eating a particular food type on neoplasia prevalence and plasma glucose concentrations; and (2) one can already identify the 0% data from our figures and analyses of the other diet types - for example, if a species consumes 100% fruit, it does not consume any of the other food types, in other words the consumption of endothermic vertebrates, ectothermic vertebrates, fish, invertebrates, nectar, plants, scavenging items, seeds, and unknown vertebrates is 0%." and "Each species' neoplasia and malignancy prevalence is based on data from necropsies of at least 20 individuals in that species. These data are from several zoological and veterinary institutions. The choice of a 20-necropsy threshold is a compromise between accuracy of the prevalence estimates and the number of species in the analysis."
Replication	Replication was not applicable to this study since a second dataset on cancer prevalence or plasma glucose concentration was not available.
Randomization	Not applicable.
Blinding	The pathologists originally assessing which animal had or did not have a neoplasm/malignancy were not aware of this idea to perform this study.

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 & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Plants

Seed stocks

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.

Novel plant genotypes

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.

Authentication

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.