

Life Sciences Reporting Summary

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► Experimental design

1. Sample size

Describe how sample size was determined.

The removal experiments established on these islands are the longest running biodiversity manipulation experiments in existence that include repetitions of the same treatments across contrasting ecosystems. The first of these experiments consists of full factorial removals of three dominant ericaceous dwarf shrub species (*Vaccinium myrtillus*, *Vaccinium vitis-idaea* and *Empetrum hermaphroditum*) across 30 independent islands. The other consists of full factorial removals of three plant functional groups (tree roots, mosses and dwarf shrubs) on each island. Both experiments in combination yield a total of 420 plots.

2. Data exclusions

Describe any data exclusions.

We tackled the outlier issue by removing extreme values following the outlier labelling rule with a tuning parameter of $g = 2$ (L413-L414 in the manuscript). (Hoaglin & Iglewicz, 1987 - Journal of the American Statistical Association)

3. Replication

Describe whether the experimental findings were reliably reproduced.

Island archipelagos are ideal model systems for understanding the effects of biodiversity loss, because each island operates as an independent replicate ecosystem, thus allowing us to address questions at ecologically meaningful spatial scales ($n = 10$ per island size class). We believe that findings are reliably reproduced.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

All plots were randomly assigned with each island.

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

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Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or the Methods section if additional space is needed).

n/a Confirmed

- ☐ ☒ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
- ☐ ☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly.
- ☐ ☒ A statement indicating how many times each experiment was replicated
- ☐ ☒ The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
- ☐ ☒ A description of any assumptions or corrections, such as an adjustment for multiple comparisons
- ☐ ☒ The test results (e.g. p values) given as exact values whenever possible and with confidence intervals noted
- ☐ ☒ A summary of the descriptive statistics, including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
- ☐ ☒ Clearly defined error bars

See the web collection on [statistics for biologists](#) for further resources and guidance.

► Software

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

7. Software

Describe the software used to analyze the data in this study.

R studio and R 3.4.1

For all studies, we encourage code deposition in a community repository (e.g. GitHub). Authors must make computer code available to editors and reviewers upon request. The *Nature Methods* [guidance for providing algorithms and software for publication](#) may be useful for any submission.

► Materials and reagents

Policy information about [availability of materials](#)

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.

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9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

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10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

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b. Describe the method of cell line authentication used.

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c. Report whether the cell lines were tested for mycoplasma contamination.

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d. If any of the cell lines used in the paper are listed in the database of commonly misidentified cell lines maintained by [ICLAC](#), provide a scientific rationale for their use.

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► Animals and human research participants

Policy information about [studies involving animals](#); when reporting animal research, follow the [ARRIVE guidelines](#)

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.

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12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

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