

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	Excel Version 16.89
Data analysis	R version 4.4.1; for Remote Sensing and Image Processing: SNAP version 11.0, ACOLITE version 20231023.0, QGIS version 3.40; Protist community's assessment: Demultiplexing and length filtering were performed with OBITOOLS. The taxonomic assignment was conducted using the RDP Classifier with the SILVA 138 reference database. The codes that support the findings of the current study are available in the supplementary information and from the corresponding author (R.B.) (by mail at riccardo.bentivogli4@unibo.it).

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](#)

Environmental datasets and derived data products supporting the findings of this study are available in the Zenodo repository at <https://doi.org/10.5281/zenodo.18376796>. Raw sequencing data have been deposited in the European Nucleotide Archive under study accession PRJEB107152 and will be publicly released upon publication of this article.

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

Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used. Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.

Reporting on race, ethnicity, or other socially relevant groupings

Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status). Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.) Please provide details about how you controlled for confounding variables in your analyses.

Population characteristics

Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."

Recruitment

Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.

Ethics oversight

Identify the organization(s) that approved the study protocol.

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

This study examines the short-term ecological impacts of the extreme flood event of May 2023 in Emilia-Romagna (Italy) on inland and marine ecosystems. It evaluates post-flood changes in both continental and marine water characteristics, as well as the response of aquatic communities to assess ecosystem resilience and identify indicators of disturbance and recovery.

Research sample

Environmental water quality data were collected from inland (river) and marine monitoring stations across the Emilia-Romagna region (Italy) during and after the 2023 flood events. The dataset includes measurements from multiple stations along the river-to-sea continuum, capturing spatial variability across freshwater and coastal systems. Sampling points were selected based on existing monitoring networks to represent the affected hydrological system and its connectivity from inland to marine environments. The dataset includes physicochemical and biological parameters obtained from routine monitoring programs and targeted post-event sampling campaigns.

Sampling strategy

Sampling was conducted using established environmental monitoring protocols from regional observation networks. No formal

Sampling strategy	statistical methods were used to predetermine sample size, as the study relies on observational data collected across available monitoring stations and time points. Sampling locations and frequency were determined by the operational design of the monitoring programs and by the timing of the flood events. The resulting dataset provides representative coverage of the spatial and temporal variability of water quality across inland and marine environments affected by the flood.
Data collection	Fieldwork was carried out by trained researchers following standardized protocols. Water samples were collected manually and stored in sterile, labeled containers. Analytical procedures, including chemical characterization of water, DNA extraction, algae identification, were performed in duplicate, using reference materials to assess analytical performance.
Timing and spatial scale	Sampling took place in May, June and October 2023, at various intervals following the major flood event across both marine and inland areas of the Emilia-Romagna coast. The total area covered was approximately 200 km2
Data exclusions	No data were excluded from the analysis. All collected samples were processed and any uncertainty in species identification or data quality was reported in the results or supplementary information.
Reproducibility	The study utilized standardized and replicable methods for all analyses. While it captured a post-event dynamic, the findings establish a valuable baseline for future monitoring and comparative studies.
Randomization	Randomization was not applicable due to the targeted nature of environmental sampling in response to a natural disaster. However, sampling locations were selected to represent a range of impacted habitats.
Blinding	Blinding was not used, as the study involved field-based environmental monitoring. All data were processed according to objective protocols to minimize bias.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions	Samples and measurements were collected in three different campaigns after a major flooding of the area.
Location	The sampling campaigns covered both marine and continental waters within a square bounded by the following coordinates: northwest vertex at 44.583589, 12.094051 and southeast vertex at 44.438970, 12.416782.
Access & import/export	All sampled locations were freely accessible and did not require special permissions. The continental stations were reached by car, while marine stations were accessed by boat.
Disturbance	No disturbance was caused by the sampling campaigns, as all stations were situated within freely accessible park areas

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		Methods	
n/a	Involved in the study	n/a	Involved in the study
☒	☐ Antibodies	☒	☐ ChIP-seq
☒	☐ Eukaryotic cell lines	☒	☐ Flow cytometry
☒	☐ Palaeontology and archaeology	☒	☐ MRI-based neuroimaging
☒	☐ Animals and other organisms		
☒	☐ Clinical data		
☒	☐ Dual use research of concern		
☒	☐ Plants		

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.