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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	
☐	☒	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	*Provide a description of all commercial, open source and custom code used to collect the data in this study, specifying the version used OR state that no software was used.*
Data analysis	No novel software or algorithms were developed for this study. All bioinformatic analyses were performed using publicly available software: UMI-tools v1.1.1, Trim Galore v0.6.6, FastQC v0.11.9, MultiQC v1.9 and v1.11, Bismark v0.23.1, methylKit v0.9.5, Ontologizer, Circos, and R v4.3.2 (stats and dplyr packages). Custom Python scripts used for diversity-base trimming (provided by NuGen/Tecan) and DMR annotation were developed solely for routine data preprocessing and annotation and do not represent novel software or algorithms.

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

Raw bisulfite sequencing data have been deposited in the NCBI Sequence Read Archive (SRA) under 711 accession number XXXXX (The code will be provided after acceptance)

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	Research was performed on a marine plant
Reporting on race, ethnicity, or other socially relevant groupings	Research was performed on a marine plant
Population characteristics	Research was performed on a marine plant
Recruitment	Research was performed on a marine plant
Ethics oversight	Research was performed on a marine plant

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

Ecological, evolutionary & environmental sciences study design

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

Study description	Sediment and horizontal rhizome fragments of similar size, bearing one apical shoot and 6–7 vertical shoots, were collected by SCUBA diving on 2 May 2023 from a shallow monospecific meadow of Cymodocea nodosa in the Mar Menor coastal lagoon (Spain). Fragments were transferred to the mesocosm facility within 2 h of collection. Twelve independent 200-L tanks were used as experimental units (n = 4 per treatment): primed (P), not-primed (NP), and control conditions. Plants were acclimated for 10 days under environmental conditions matching those at the collection site (25 °C, salinity 43, maximum irradiance 200 µmol photons m^{-2} s^{-1}, 14 h:10 h light photoperiod). Temperature was then gradually increased to 28 °C at a rate of 1 °C day^{-1}. Thermal priming was applied by increasing temperature in P tanks from 28 to 34 °C at 2 °C day^{-1}, maintaining this temperature for 4 days, and subsequently returning to 28 °C. The priming phase lasted 8 days. Shoots present during the priming period were defined as "old shoots", whereas shoots produced after priming were defined as "new shoots". The apical shoot was marked after priming to track shoot development and assess potential transmission of stress memory. Plants were maintained under control conditions for 37 days to allow new shoot formation. Subsequently, primed and not-primed plants were exposed to a thermal triggering treatment (35 °C for 10 days) to evaluate priming acquisition and the transfer of thermal memory from old to new shoots. Leaf samples were collected from both old and new shoots across experimental conditions for subsequent analyses.
Research sample	The research material consisted of rhizome fragments bearing apical shoots of the seagrass Cymodocea nodosa, collected from the Mar Menor Lagoon (Spain). Following the experimental treatments, leaf samples were collected from selected shoots for DNA analysis. Samples were immediately preserved at −80 °C until further molecular processing.
Sampling strategy	Leaves were collected from individual shoots for molecular analyses. Five biological replicates were analysed, following experimental designs previously applied in seagrass studies and selected to provide an adequate representation of the biological variability required to address the objectives of this study. This represents the first study investigating DNA methylation patterns in Cymodocea nodosa using randomly collected plant material.
Data collection	Cymodocea nodosa rhizome fragments were collected by SCUBA diving by members of the research team who are authors of the

Data collection	present study. All biological material used in the experiment, including leaf samples collected for subsequent molecular analyses, was collected by the authors during the experimental procedures.
Timing and spatial scale	The biological material analysed in this study was collected at the end of the experimental period (5 July 2023) and immediately processed for subsequent molecular analyses.
Data exclusions	no data were excluded from the analysis
Reproducibility	To ensure reproducibility, all experimental procedures were conducted following a predefined experimental design with clearly defined biological material, environmental conditions, and sampling procedures. Cymodocea nodosa rhizome fragments of comparable size and developmental stage were collected from the same meadow in the Mar Menor Lagoon (Spain) and randomly assigned to experimental tanks. The experiment was performed using independent replicate tanks as experimental units (n = 4 per treatment).All environmental parameters were controlled and recorded throughout the experiment, including temperature and salinity. Temperature treatments were applied following predefined rates of increase and exposure durations, and all plants were maintained under identical conditions except for the thermal priming treatment.
Randomization	A total of 12 independent tanks were used in the experiment, with four tanks randomly assigned to each experimental condition (Primed, Not-Primed, and Control; n = 4 tanks per treatment). Tanks were considered the true experimental units. Multiple shoots were sampled and analysed for physiological and DNA methylation measurements, all measurements obtained from shoots within the same tank were averaged to generate a single value per experimental unit. For molecular analysis, n = 5 were analized.
Blinding	No blinding was applied during data acquisition because the experimental treatments involved controlled temperature manipulations that required continuous monitoring and management of the experimental conditions. However, samples were processed using standardized protocols, and all molecular analyses were performed following the same procedures across experimental groups. Data processing and statistical analyses were conducted using predefined procedures based on the experimental design.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions	The study was not conducted directly in the field. Rhizome fragments of the seagrass species of interest were collected and immediately transferred to the mesocosm facility, where they were maintained under environmental conditions matching those recorded at the sampling site (25 °C temperature and salinity 43).
Location	Spain, coordinates 37.771219, -0.755790
Access & import/export	Sampling was performed upon obtaining sampling permit from the competent Regional Authorities, requested from the Spanish Oceanographic Institute of the CSIC (Murcia, Spain)
Disturbance	The collection of Cymodocea nodosa material was designed to minimize disturbance to the natural meadow. Only a limited number of rhizome fragments of comparable size were collected from a shallow monospecific meadow in the Mar Menor Lagoon, representing a small fraction of the local plant population.

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	Horizontal rhizome fragments of similar size, bearing one apical shoot and 6–7 vertical shoots, were collected by SCUBA diving on 2 May 2023 from a shallow monospecific meadow of Cymodocea nodosa in the Mar Menor coastal lagoon (Spain).
Novel plant genotypes	not applicable
Authentication	not applicable