

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 checked="" type="checkbox"/>	The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
<input checked="" type="checkbox"/>	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
<input checked="" type="checkbox"/>	The statistical test(s) used AND whether they are one- or two-sided <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
<input checked="" type="checkbox"/>	A description of all covariates tested
<input checked="" type="checkbox"/>	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
<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 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 <i>Give P values as exact values whenever suitable.</i>
<input checked="" type="checkbox"/>	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
<input checked="" type="checkbox"/>	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
<input checked="" 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 We used Microsoft Excel and GIS Software (ArcGIS & QGIS) to collect the relevant data

Data analysis To analyze the data in this study we used Python code (Python version 3.10.6) within the anaconda distribution.

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](#)

The dataset containing the primary and additional grapevine varieties cultivated in each PDO is available at <https://doi.org/10.5281/zenodo.7257126>. The dataset containing the exposure, sensitivity and adaptive capacity indicators is available at <https://doi.org/10.5281/zenodo.7341521>

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender	This information has not been collected
Population characteristics	See above
Recruitment	See above
Ethics oversight	See above

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	We analyzed the climate change vulnerability of the 1174 European PDO regions by clustering them into homogeneous groups based on their exposure, sensitivity and adaptive capacity.
Research sample	We used all the wine PDO regions within the European Union which is a total of 1174 regions. We used a database that we created and that is freely available online, related descriptions and link for download can be found here: https://doi.org/10.1038/s41597-022-01513-0
Sampling strategy	Since our study aim was to understand climate change impacts on high-quality wine production in Europe, we focused on PDO regions because they have the strongest link to a defined production area and its climate. To have a comprehensive overview, we included all available PDO regions in our study.
Data collection	The data was collected from different sources: statistical databases, regulatory documents and geo-data repositories. The data collection was carried out by S.T., S.C. and T.M.
Timing and spatial scale	The data related to this publication was collected and processed during the period January 2022 - August 2022. The spatial scale strongly depends on the indicator; some were available at the national scale while others were available at the municipality level. For the aim of this study all the indicators were standardized at the scale of each PDO
Data exclusions	No data was excluded from the analysis
Reproducibility	The main calculations were performed in the ArcGIS and QGis software, and in the python programming language. The code for the clustering and vulnerability calculation can be found at the following link: https://doi.org/10.5281/zenodo.7341521
Randomization	We performed a statistical clustering to aggregate our samples into homogeneous groups. The code we used can be found at the following link: https://doi.org/10.5281/zenodo.7341521
Blinding	Blinding was not relevant for our study

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 & experimental systems

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

Methods

n/a	Involved in the study
<input checked="" type="checkbox"/>	ChIP-seq
<input checked="" type="checkbox"/>	Flow cytometry
<input checked="" type="checkbox"/>	MRI-based neuroimaging