nature portfolio

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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	Datasets are available on the Zenodo platform: 10.5281/zenodo.14526072. Source data of graphs in figures are provided as a Source Data file.
Data analysis	Code (in Python) is available at https://gitlab.pasteur.fr/mbenimam/spatiopath (DOI: 10.5281/zenodo.14520113). The method for spatial analysis is also implemented as a plugin Spatiopath on the Icy software (https://icy.bioimageanalysis.org/).

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

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implemented as a plugin Spatiopath on the Icy software (https://icy.bioimageanalysis.org/). Instructions for installation and for running the code are provided in the README files therein.

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	We have information about the sex of the patients included in this study. However, sex is not a relevant parameter for the analysis, and we do not wish to disclose the sex of the two included patients to protect patients' identity. Consent has not been obtained nor requested for sharing of individual-level data.
Reporting on race, ethnicity, or other socially relevant groupings	N.A.
Population characteristics	The eight patients included in the study were diagnosed with lung squamous cells carcinoma and operated at Oslo University Hospital. We do not wish to disclose any additional population characteristics data to protect patients' identity. Consent has not been obtained nor requested for sharing of individual-level data.
Recruitment	Tumor specimens were obtained from NSCLC patients diagnosed with TNM stage 1a/1b and who underwent tumor resection at the Department of Cardiothoracic Surgery at Oslo University Hospital, Ullevål hospital, Oslo, Norway, during the period 01.01.2000-31.12.2008. These patients had not received neoadjuvant chemotherapy, preoperative radiotherapy, or immunosuppressive therapy. The pathological TNM stage (pTNM) was determined for all tumor specimens by two lung pathologists based on histopathologic criteria according to the 8th edition of Union for International Cancer Control TNM staging system and 2015 World Health Organization guidelines.
Ethics oversight	The study was reviewed and approved by The Norwegian Regional Ethical Committee (ref: 2019/352).

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

Life sciences study design

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

Sample size	We analyzed the data from n=8 patients
Data exclusions	No data were excluded
Replication	Images and code are available for a sake of results' reproducibility
Randomization	N/A
Blinding	N/A

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

Antibodies

Antibodies used

Anti-CD3 monoclonal antibody (clone 2GV6, Roche, cat. no. 790-4341)
Anti-tryptase monoclonal antibody (clone EPR8476, Abcam, cat. no. ab134932)
Anti- Cytokeratins monoclonal antibodies (clones AE1/AE3/PCK26, Roche, cat. no. 760-2135)

Validation

We used validated commercial antibodies. Isotype- and concentration-matched irrelevant antibodies were used as negative controls.

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, mosiacism, off-target gene editing) were examined.