

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 (<i>n</i>) 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 <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☒	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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
☒	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 <i>d</i> , Pearson's <i>r</i>), 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	No software was used to collect data.
Data analysis	We used R studio (version 4.3.1) to analyze data with Seurat (version 5.1), ggplot2 (version 3.5.1), ggpubr (version 0.6.0), harmony (version 1.2.3), tidyverse (version 2.0.0), ggbreak (version 0.1.4) and reshape2 (version 1.4.4) packages. Code availability section is included.

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](#)

Data availability section is in the manuscript.

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	Sex and gender were not used in the manuscript.
Reporting on race, ethnicity, or other socially relevant groupings	Race, ethnicity, or other socially relevant groupings were not used in the manuscript.
Population characteristics	Population characteristics were not used in the manuscript.
Recruitment	Recruitment was not used in the manuscript.
Ethics oversight	Mesothelioma IRB protocol: Lab08-0380; lung adenocarcinoma IRB protocol: PA15-1112 UT MD Anderson Cancer Center

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)

Life sciences study design

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

Sample size	2 lung adeno-carcinoma TMA blocks with 22 patients' FFPE samples were constructed. 2 mesothelioma TMA blocks with 22 patients' FFPE samples were constructed.
Data exclusions	There is not data exclusions.
Replication	TMA blocks were sectioned. All assays were performed using serial sections of TMAs to replicate spatial information with different assays.
Randomization	There is not randomization in the manuscript.
Blinding	Investigators were blinded in the data analysis. Investigators were not blinded to group allocation during data collection.

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	SYTO13 (DNA, Nanostring, 121301310, concentration 500nM with 1:10 dilution), panCK (PanCK AF532: Clone: AE1 + AE3; Novus NBP2-33200AF532; nanoString 121300320-020223; concentration at 0.5 µg/ml with 1:40 dilution), CD3E (CD3 AF647: Clone: UMAB54; Origene AC211369; CG223985F005AF; concentration at 0.5 µg/ml with 1:2000 dilution) , CD68 (CD68 AF594: Clone: KP1; Santa Cruz AF594; E3024; dilution 0.5 µg/ml with 1:400 dilution)
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Validation	We validated the standard fluorescence assay of The GeoMx DSP assay using human tonsil tissue, we used the best assay conditions that displayed the higher signal to noise ratio and alignment with expected biological patterns. Antibodies were validated to use in human tissue. (https://brd.nci.nih.gov/brd/sop/show/3105 , https://pubmed.ncbi.nlm.nih.gov/36100434/)
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Plants

Seed stocks	<i>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.</i>
Novel plant genotypes	<i>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.</i>
Authentication	<i>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.</i>