

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	Data was collected using the Enable Medicine Platform and Akoya PhenoCycler-Fusion platform.
Data analysis	For model training the primary libraries used are Pytorch, Weights and Biases, numpy, and pandas. For evaluation and analysis, matplotlib, scikit-learn, scipy, and pytorch-geometric were used. For a full list of libraries used and the specific version numbers, please refer to the Gitlab repository. Name: torch Version: 2.7.1 Name: torchvision Version: 0.22.1 Name: pandas Version: 2.2.3 Name: wandb Version: 0.18.3 Name: numpy Version: 1.26.4 Name: scikit-image Version: 0.24.0 Name: ome-zarr Version: 0.10.2 Name: fastparquet

Version: 2023.7.0
 Name: matplotlib
 Version: 3.5.2
 Name: scikit-learn
 Version: 1.1.3
 Name: scipy
 Version: 1.10.0

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 code and data used to produce the analysis for this manuscript are available at <https://gitlab.com/enable-medicine-public/rosie>. All data are available in the main text or the supplementary materials.

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 analysis was not performed as this information was not available to the researchers.
Reporting on race, ethnicity, or other socially relevant groupings	Race, ethnicity, and other socially relevant groups were not available to the researchers as well so no analysis was done.
Population characteristics	Banked samples were collected in an unbiased manner from patients from the corresponding clinical sites.
Recruitment	The data were made available to the researchers through academic collaborators who had collected this data prior to this study. Samples were chosen as an unbiased representation of patients served at each of the clinical sites in the study, without regards to demographic or clinical covariates.
Ethics oversight	Sample collections were approved by institutional review boards at the clinical sites where the data were collected. IRB approval was obtained from the study sites for each of the evaluation datasets: UChicago - IRB protocol (13-1297) was approved by U of Chicago BSD/UCMC Institutional Review Board. Informed consent was not required in this retrospective study of anonymized samples. Stanford - IRB protocol (IRB-8) was approved by the Stanford University Institutional Review Board. Informed consent was not required in this retrospective study of anonymized samples. Ochsner - IRB protocol (10515) was approved by the Fred Hutchinson Cancer Center Institutional Review Board. Informed consent was not required in this retrospective study of anonymized samples. Tuebingen - Patients gave written informed consent and the use of their tissue samples and data was approved by the local Ethics Committee of the Canton of Bern (KEK 200/2014).

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 No sample size was calculated; it was determined based on available training and test data.

Data exclusions	No exclusions
Replication	We perform significance tests on the predicted samples, as well as validating the results across a diverse set of samples.
Randomization	Training and test splits were determined based on unique slide coverslips and studies.
Blinding	No blinding since this is a retrospective analysis

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

The proteins that was stained for in this study are: DAPI, CD45, CD68, CD14, PD1, FoxP3, CD8, HLA-DR, PanCK, CD3e, CD4, aSMA, CD31, Vimentin, CD45RO, Ki67, CD20, CD11c, Podoplanin, PDL1, GranzymeB, CD38, CD141, CD21, CD163, BCL2, LAG3, EpCAM, CD44, ICOS, GATA3, Gal3, CD39, CD34, TIGIT, ECad, CD40, VISTA, HLA-A, MPO, PCNA, ATM, TP63, IFNg, Keratin8/18, IDO1, CD79a, HLA-E, CollagenIV, CD66

The corresponding antibodies assays are listed here: <https://www.akoyabio.com/phenocycler/assays/antibodies/>

Additional antibody information is provided at: <https://gitlab.com/enable-medicine-public/rosie/-/blob/main/Antibody%20Information.xlsx>

Validation

Validation of antibody staining is detailed in the manuscript under Methods.

Plants

Seed stocks

N/A

Novel plant genotypes

N/A

Authentication

N/A