

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	numpy=1.20.3 pandas=2.0.3
Data analysis	numpy=1.20.3 matplotlib= 3.7.2 scikit-learn =1.3.0 pandas =2.0.3 lifelines = 0.27.8 (https://lifelines.readthedocs.io/en/latest/)

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](#)

All benchmark datasets used in this paper are publicly available. For the processed RNA-seq data and corresponding survival outcome of HCC transcriptome dataset, the TCGA-LIHC cohort data was downloaded from <https://portal.gdc.cancer.gov/projects/TCGA-LIHC>. Grinchuk et al's cohort was downloaded from <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE76427>. Fujimoto et al's cohort data was downloaded from <https://docs.icgc-argo.org/docs/data-access/icgc-25k-data>. Roessler et al's cohort data was downloaded from <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse14520>. Hoshida et al's cohort data was

downloaded from <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE10143>. For breast cancer dataset, one can download RNA-seq, survival outcome, cohort and clinical information from https://www.cbiportal.org/study/summary?id=brca_metabric. For Melanoma transcriptome dataset, Liu et al's cohort data was download from https://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?study_id=phs000452.v3.p1. Hugo et al's cohort data was downloaded from <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=gse78220>. Gide et al's cohort data was downloaded from <https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJEB23709>. Riaz et al's cohort data was downloaded from <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE91061>. Van et al's cohort was downloaded from https://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?study_id=phs000452.v2.p1. For lung cancer clinical dataset, one could download the clinical and survival outcome data from <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6777828/>. All data source used in this paper are listed in Supplementary material Table A1. The simulated data is generated when running the source code. The preprocessed data of real-world data is available at: <https://github.com/googlebaba/Stable-Cox>.

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 N/A. The study does not involve human research participants and sex and gender related study.

Reporting on race, ethnicity, or other socially relevant groupings N/A. The study does not involve race, ethnicity, or other socially relevant groupings.

Population characteristics N/A. The study does not involve human research participants.

Recruitment Used publicly available data. Didn't recruit any participants.

Ethics oversight Used publicly available data. No study protocol approval is needed.

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 In this work, we usually select the cohort with the largest sample size among candidate cohorts as the training set and the remaining cohorts are set as validation and test cohorts. Training on larger cohort could result in more confident results.

Data exclusions No data were excluded in our analysis.

Replication In our work, we validate the model's performance using the average value from multiple independent testing cohorts to draw robust results.

Randomization For simulated data, we generate it with 10 different seeds for each experiment.

Blinding N/A. Our study does not involve group allocation.

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	Involvement 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	Involvement in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Plants

Seed stocks

N/A. We do not use this kind of dataset.

Novel plant genotypes

N/A. Not related to this work.

Authentication

N/A. Not related to this work.