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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	No commercial, open source or custom code was used in data collection.
Data analysis	All software and code used during the data collection are available from the corresponding author on reasonable request, and the list is as following: R software (version 4.2.1, R Foundation for Statistical Computing, Vienna, Austria), Seurat package (v4.0.0), SingleR（v1.4.1）, inferCNV package, scran package, pySCENIC (version 0.10.2), monocle2 package, CytoTRACE package and image J software.

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 raw sequence data have been deposited in the Genome Sequence Archive (Genomics, Proteomics & Bioinformatics 2021) in National Genomics Data Center (Nucleic Acids Res 2024), China National Center for Bioinformation / Beijing Institute of Genomics, Chinese Academy of Sciences (GSA-Human: HRA009572) that are

publicly accessible at https://ngdc.cncb.ac.cn/gsa-human. The source data for the graphs has been uploaded on GitHub (https://github.com/Cedar98/SCNECC_single_cell_analysis.git).

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	A total of 69 women with neuroendocrine cervical carcinoma participated in our study. Since this is a kind of gynecological cancer occur only in women, there is no sex- or gender-based analyses in our study.
Reporting on race, ethnicity, or other socially relevant groupings	All enrolled patients are Chinese women. Since our study only focus on the tumor biology of neuroendocrine cervical carcinoma, there is no socially groupings in the research.
Population characteristics	The relevant clinicopathological characteristics have been listed as supplementary table 1 in our study.
Recruitment	All patients were enrolled from the Obstetrics and Gynecology Hospital of Fudan University and Informed consent was obtained before sampling. Since neuroendocrine cervical carcinoma is an rare gynecological malignancy, all applicable patients were enrolled.
Ethics oversight	This study was approved by the Ethics Committee of the Obstetrics and Gynecology Hospital of Fudan University (2023-41).

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	Since neuroendocrine cervical carcinoma is an rare gynecological malignancy, all applicable patients were enrolled in our study. Previous single-cell sequencing researches usually enrolled 5-10 samples, of which our study has fulfilled the sequencing size for this rare cancer.
Data exclusions	No data were excluded from the analyses.
Replication	The analyses of single-cell sequencing data and experiments with cell lines were taken more than three times to confirm reproducibility. The Immunohistochemical staining of formalin-fixed, paraffin-embedded sections were replicated in the same patients for more than three times, and kept more than ten sections of every patients for subsequent validation.
Randomization	The samples from tumor tissues and normal adjacent tissues were allocated into two experimental group in our study and need no randomization.
Blinding	The study was not blinded, since the tumor and normal adjacent tissues were automatedly grouped and did not undergo randomization.

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 primary antibodies used in western blotting targeted β-actin (AA128-1, Beyotime), GAPDH (#5174, Cell Signaling), ASCL1 (A10669, ABclonal), NEUROD1 (ab109224, Abcam), POU2F3 (#36135, Cell Signaling), YAP1 (A1002, ABclonal), TOP2A (ab52934, Abcam), SLFN11 (#34858, Cell Signaling), MTOR (A11354, ABclonal), and PDGFRA (A2103, ABclonal). And the primary antibodies used in immunohistochemical staining against ASCL1 (PHA1199, Abmart), NEUROD1 (A16927, ABclonal), POU2F3 (#36135, Cell Signaling), and YAP1 (A1002, ABclonal).

Validation: All antibodies used in this study were validated on the manufacturer's website.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s): Human SCNECC cell line TC-YIK was from Typical Culture Collection Center in Wuhan, whereas human cervical epithelial cell line Ect-1, human keratinocytes cell line Hacat, and human cervical cancer cell lines Hela and SiHa were from Authenticated Cell Cultures Collection in Shanghai.

Authentication: All cell lines were authenticated by short tandem repeat profiling.

Mycoplasma contamination: All cell lines were confirmed mycoplasma-free before experiments.

Commonly misidentified lines (See ICLAC register): There is no commonly misidentified cell lines used in this study.

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.*