

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](#).

Please do not complete any field with "not applicable" or n/a. Refer to the help text for what text to use if an item is not relevant to your study. For final submission: please carefully check your responses for accuracy; you will not be able to make changes later.

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	Western blotting: The target protein was detected using an ECL chemiluminescent substrate kit (YEASEN, Shanghai, China) and visualized with a ChemiDoc XRS+ imaging system (Bio-Rad, USA). Quantitative qRT-PCR was conducted with SYBR Green Premix Pro Taq HS qPCR Kit (Accurate Biology, Hunan, China) on a CFX Connect Real-Time PCR System (Bio-Rad,CA, USA). The images of Immunohistochemistry (IHC), Transwell, and colony formation assays were acquired using a microscope (Carl Zeiss, Oberkochen, Germany) and analyzed with ImageJ (National Institutes of Health, Bethesda, MD, USA) and Image-Pro Plus 6.0 software (Media Cybernetics, Rockville, MD, USA). CCK8 and ELISA: Optical density (OD) values were measured using a Multiskan SkyHigh microplate reader (Thermo Fisher Scientific, Waltham, MA, USA). UHPLC-MS/MS analysis was performed using a Vanquish UHPLC system coupled with an Orbitrap Q Exactive series mass spectrometer (Thermo Fisher). RNA-seq was performed on the MGISEQ-2000RS platform. The sequencing data was filtered with SOAPnuke (v1.5.6) to obtain the clean data. The differential gene expression analysis was performed using the DESeq2 (v1.4.5).
Data analysis	Statistical analysis and data visualization carried out in this study was performed by GraphPad Prism 9.

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](#)

Raw sequence data of RNA-seq have been deposited in the Gene Expression Omnibus (GEO) database (accession number GSE263382). All materials and data are available upon request from the corresponding authors.

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	In this study, sex was defined based on biological characteristics such as chromosomal, gonadal, and anatomical factors. A total of 40 participants were included in the study. The distribution by sex is as follows: 28 males, 12 females. These numbers are detailed in Table 1.
Reporting on race, ethnicity, or	This study does not include any socially constructed or socially relevant categorization variables. Our research primarily focuses on biomedical factors. Therefore, we did not employ variables such as race, ethnicity, or socioeconomic status.
Population characteristics	Our study enrolled 40 patients (Clinical stage II,n=8; Clinical stage III and IV,n=32). The clinical characteristics, including age, sex, clinical stage, tumor invasion, and lymph node metastasis, are displayed in Table 1.
Recruitment	A cohort of 40 NPC patients who were first diagnosed between 2018 and 2022 at the First Affiliated Hospital of Nanchang University was recruited for this study, and their formalin-fixed paraffin-embedded (FFPE) specimens were obtained from the Pathology Department (Table 1). All cases have not undergone preoperative radiotherapy, chemotherapy, or interventional therapy. All patients have signed informed consent.
Ethics oversight	The protocol of human sample usage and the informed consent were approved by the Ethical Review Board of the First Affiliated Hospital of Nanchang University[(2024)CDYFYLK(02-030)].

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

Life sciences study design

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

Sample size	In our study, a formal sample size calculation was not performed. We included 40 NPC patients, whose demographic and clinical characteristics were fully documented. We are confident that the sample size used in our study is adequate for the aims of our analysis.
Data exclusions	No data were excluded from the analysis.
Replication	All attempts at replication were successful. For in vitro assays, the experiment was repeated at least three times. For in vivo assays, we replicated the finding in six mice.
Randomization	As this was a controlled laboratory study with in vitro/in vivo models, we did not apply randomization to the allocation of experimental groups.
Blinding	In our study, blinding was not applied to group allocation during data collection or analysis due to the nature of the experimental setup. The investigators were aware of the group assignments because the treatments required direct handling, making blinding impractical.

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-PSAT1 (#20180-1-AP, 1:1500), anti-Arg1 (#16001-1-AP, 1:1000), anti-iNOS (#80517-1-RR, 1:1000), anti-Flag (66008-4-Ig, 1:5000), anti-HA (66006-2-Ig, 1:5000), anti-H3 (17168-1-AP, 1:5000), anti-LDHA (19987-1-AP, 1:2000), anti-RXR (14684-1-AP, 1:1000), HRP-conjugated Goat Anti-Mouse IgG(H+L) (#SA00001-1, 1:2000), and HRP-conjugated Goat Anti-Rabbit IgG(H+L) (#SA00001-2, 1:2000) were obtained from Proteintech; anti-PKM2 (#4053, 1:1000) was purchased from Cell Signaling Technology (USA); anti-ACTB (#TA310155, 1:2000) was purchased from Origene (USA); and anti-pan-Klac (1401RM, 1:1000) was obtained from PTM Bio (China); anti-APOE (1:300, #A0304, ABclonal)

Validation

Anti-PSAT1: rabbit polyclonal antibody; reactivity: human, mouse, Rat; applications: western blot, immunohistochemistry, immunofluorescence, Co-immunoprecipitation, enzyme-linked immunosorbent assay (ELISA).
 Anti-ARG1: rabbit Polyclonal antibody(16001-1-AP); reactivity: human, mouse, Rat, pig, bovine; applications: western blot, immunohistochemistry, immunofluorescence, Co-immunoprecipitation, ELISA.
 Anti-iNOS: rabbit recombinant antibody (80517-1-RR), reactivity: human, mouse, Rat ; applications: western blot, immunohistochemistry and ELISA.
 Anti-Flag: mouse monoclonal (66008-4-Ig); reactivity: recombinant protein; applications: western blot, immunohistochemistry, immunofluorescence, Co-immunoprecipitation, Chromatin immunoprecipitation, RNA immunoprecipitation.
 Anti-Flag: rabbit polyclonal (20543-1-AP); reactivity: recombinant protein; applications: western blot, immunohistochemistry, immunofluorescence, Co-immunoprecipitation, Chromatin immunoprecipitation.
 Anti-HA (66006-2-Ig): mouse monoclonal; reactivity: recombinant protein; applications: western blot, immunofluorescence, Co-immunoprecipitation, Chromatin immunoprecipitation, RNA immunoprecipitation, ELISA, and Proximity Ligation Assay.
 Anti-HA: rabbit polyclonal (51064-2-AP); reactivity: recombinant protein; applications: western blot, immunofluorescence, Co-immunoprecipitation, Chromatin immunoprecipitation.
 Anti-H3: rabbit polyclonal antibody (17168-1-AP); reactivity: human, mouse; applications: western blot, immunohistochemistry, immunofluorescence, Co-immunoprecipitation, Chromatin immunoprecipitation, and ELISA.
 Anti-LDHA: rabbit Polyclonal (19987-1-AP); reactivity: human, mouse, Rat; applications: western blot, immunohistochemistry, immunofluorescence, Co-immunoprecipitation, ELISA.
 Anti-RXR (14684-1-AP): domestic rabbit monoclonal; reactivity: human, mouse, Rat; applications: western blot, immunohistochemistry, immunofluorescence, Co-immunoprecipitation, ELISA.
 HRP-conjugated Goat Anti-Mouse IgG(H+L) (SA00001-1): reactivity: mouse; applications: western blot, ELISA.
 HRP-conjugated Goat Anti-Rabbit IgG(H+L) (SA00001-2): reactivity: mouse; applications: western blot, ELISA.
 Anti-PKM2: domestic rabbit monoclonal (4053); reactivity: human, mouse, rat and monkey; applications: Western Blotting, Immunoprecipitation, Immunohistochemistry, Immunofluorescence, Flow Cytometry.
 Anti-ACTB: mouse monoclonal (TA310155); reactivity: human, mouse, rat, monkey and dog; applications: western blotting.
 Anti-APOE: rabbit polyclonal(A0304); reactivity: human, mouse, rat; applications: Western Blotting, Immunoprecipitation, Immunohistochemistry, Immunofluorescence, ELISA.
 Anti-pan-Klac: rabbit monoclonal (1401RM); reactivity: all; Applications: western blot, immunohistochemistry, immunofluorescence, Co-immunoprecipitation, Flow Cytometry.

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)

Human NPC cell lines C666-1 and HK1 were obtained from Shanghai Jingyuan Biotechnology (China).The human monocyte cell line THP-1 cell was purchased from Procell (China).

Authentication

All cell lines were authenticated using STR method before experiments.

Mycoplasma contamination

All cell lines were tested negative for mycoplasma contamination.

Commonly misidentified lines
(See [ICLAC](#) register)

This study do not use misidentified cell lines.

Palaeontology and Archaeology

Specimen provenance *Provide provenance information for specimens and describe permits that were obtained for the work (including the name of the*

Specimen deposition *Indicate where the specimens have been deposited to permit free access by other researchers.*

Dating methods *If new dates are provided, describe how they were obtained (e.g. collection, storage, sample pretreatment and measurement), where*

☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

Ethics oversight *Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance*

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Animals and other research organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research, and [Sex and Gender in Research](#)

Laboratory animals *The male BALB/c nude mice (4-6 weeks old) were purchased from GemPharmatech (China) and were raised under pathogen-free conditions.*

Wild animals *This study did not involve wild animals.*

Reporting on sex *The male BALB/c nude mice (4-6 weeks old) were purchased from GemPharmatech (China).*

Field-collected samples *This study did not involve samples collected from the field.*

Ethics oversight *Mice experiments were carried out in accordance with the guidelines approved by the Institutional Animal Care and Use Committee (IACUC) of the First Affiliated Hospital of Nanchang University (CDYFY-IACUC-202307QR007).*

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Clinical data

Policy information about [clinical studies](#)

All manuscripts should comply with the ICMJE [guidelines for publication of clinical research](#) and a completed [CONSORT checklist](#) must be included with all submissions.

Clinical trial registration *Provide the trial registration number from ClinicalTrials.gov or an equivalent agency.*

Study protocol *Note where the full trial protocol can be accessed OR if not available, explain why.*

Data collection *Describe the settings and locales of data collection, noting the time periods of recruitment and data collection.*

Outcomes *Describe how you pre-defined primary and secondary outcome measures and how you assessed these measures.*

Dual use research of concern

Policy information about [dual use research of concern](#)

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes
☒	☐ Public health
☒	☐ National security
☒	☐ Crops and/or livestock
☒	☐ Ecosystems
☒	☐ Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes
☒	☐ Demonstrate how to render a vaccine ineffective
☒	☐ Confer resistance to therapeutically useful antibiotics or antiviral agents
☒	☐ Enhance the virulence of a pathogen or render a nonpathogen virulent
☒	☐ Increase transmissibility of a pathogen
☒	☐ Alter the host range of a pathogen
☒	☐ Enable evasion of diagnostic/detection modalities
☒	☐ Enable the weaponization of a biological agent or toxin
☒	☐ Any other potentially harmful combination of experiments and agents

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

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

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

ChIP-seq

Data deposition

☐ Confirm that both raw and final processed data have been deposited in a public database such as [GEO](#).

☐ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links

For "Initial submission" or "Revised version" documents, provide reviewer access links. For your "Final submission" document,

Files in database submission

Provide a list of all files available in the database submission.

Genome browser session
(e.g. [UCSC](#))

Provide a link to an anonymized genome browser session for "Initial submission" and "Revised version" documents only, to enable peer review. Write "no longer applicable" for "Final submission" documents.

Methodology

Replicates

Describe the experimental replicates, specifying number, type and replicate agreement.

Sequencing depth

Describe the sequencing depth for each experiment, providing the total number of reads, uniquely mapped reads, length of reads and

Antibodies

Describe the antibodies used for the ChIP-seq experiments; as applicable, provide supplier name, catalog number, clone name, and lot number.

Peak calling parameters

Specify the command line program and parameters used for read mapping and peak calling, including the ChIP, control and index files

Data quality

Describe the methods used to ensure data quality in full detail, including how many peaks are at FDR 5% and above 5-fold enrichment.

Software

Describe the software used to collect and analyze the ChIP-seq data. For custom code that has been deposited into a community

Flow Cytometry

Plots

Confirm that:

- ☐ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).
- ☐ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).
- ☐ All plots are contour plots with outliers or pseudocolor plots.
- ☐ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

- Sample preparation *Describe the sample preparation, detailing the biological source of the cells and any tissue processing steps used.*
- Instrument *Identify the instrument used for data collection, specifying make and model number.*
- Software *Describe the software used to collect and analyze the flow cytometry data. For custom code that has been deposited into a*
- Cell population abundance *Describe the abundance of the relevant cell populations within post-sort fractions, providing details on the purity of the*
- Gating strategy *Describe the gating strategy used for all relevant experiments, specifying the preliminary FSC/SSC gates of the starting cell*
- ☐ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.

Magnetic resonance imaging

Experimental design

- Design type *Indicate task or resting state; event-related or block design.*
- Design specifications *Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial*
- Behavioral performance measures *State number and/or type of variables recorded (e.g. correct button press, response time) and what statistics were used*

Acquisition

- Imaging type(s) *Specify: functional, structural, diffusion, perfusion.*
- Field strength *Specify in Tesla*
- Sequence & imaging parameters *Specify the pulse sequence type (gradient echo, spin echo, etc.), imaging type (EPI, spiral, etc.), field of view, matrix size,*
- Area of acquisition *State whether a whole brain scan was used OR define the area of acquisition, describing how the region was determined.*
- Diffusion MRI ☐ Used ☐ Not used

Preprocessing

- Preprocessing software *Provide detail on software version and revision number and on specific parameters (model/functions, brain extraction,*
- Normalization *If data were normalized/standardized, describe the approach(es): specify linear or non-linear and define image types used for*
- Normalization template *Describe the template used for normalization/transformation, specifying subject space or group standardized space (e.g.*
- Noise and artifact removal *Describe your procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and*
- Volume censoring *Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.*

Statistical modeling & inference

- Model type and settings *Specify type (mass univariate, multivariate, RSA, predictive, etc.) and describe essential details of the model at the first and*
- Effect(s) tested *Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA*
- Specify type of analysis: ☐ Whole brain ☐ ROI-based ☐ Both
- Statistic type for inference *Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.*
- (See [Eklund et al. 2016](#))
- Correction *Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).*

Models & analysis

n/a	Involvement in the study
☐	☐ Functional and/or effective connectivity
☐	☐ Graph analysis
☐	☐ Multivariate modeling or predictive analysis

Functional and/or effective connectivity	<i>Report the measures of dependence used and the model details (e.g. Pearson correlation, partial correlation,</i>
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Graph analysis	<i>Report the dependent variable and connectivity measure, specifying weighted graph or binarized graph,</i>
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Multivariate modeling and predictive analysis	<i>Specify independent variables, features extraction and dimension reduction, model, training and evaluation</i>
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