nature portfolio

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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	SwissTargetPrediction (https://www.swisstargetprediction.ch/), Targetnet (https://targetnet.scbdd.com/), SEA (https://sea.bkslab.org/), CHEMBL (https://www.ebi.ac.uk/chembl/) - for target acquisition for Anoplin OMIM(https://www.omim.org/), NCBI(https://static.pubmed.gov/portal/portal.fcgi/), GeneCards(https://www.genecards.org/),Disgenet(https://disgenet.com/) - for target acquisition for human non-small cell lung cancer STRING(https://cn.string-db.org/) - for obtaining PPI network analysis UniProt(https://www. uniprot.org/), RCSB PDB (http://www.rcsb.org/) - for obtaining protein structure Metascape(https://metascape.org/) - for obtaining GO.KEGG analysis
Data analysis	Analytical HPLC - Agilent 1260 Infinity II system and EClassical 3200 Liquid Chromatography system - for data representation MestReNova -12.0.0 for data representation Graphpad Prism ver 10.1.2 - for generating graphs Cytoscape ver 3.7.1- for screening of PPI networks MOE ver 2024- for molecular docking

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

Full experimental procedures and the data supporting the findings of this study are available within in this article and its Supplementary Information. All data are available from the corresponding author upon request. Source data has been provided with this paper.

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	Not applicable as human participants are not a part of this study
Reporting on race, ethnicity, or other socially relevant groupings	Not applicable as human participants are not a part of this study
Population characteristics	Not applicable as human participants are not a part of this study
Recruitment	Not applicable as human participants are not a part of this study
Ethics oversight	Not applicable as human participants are not a part of this study

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 calculation was performed. Each cyclic peptide was synthesized in multiple independent batches. Cell based assays were performed in three independent biological experiments.
Data exclusions	All data included unless otherwise specified.
Replication	Synthesis of cyclic peptides was performed in multiple independently runs and proved to be reliable. For cell based assays, experiments were carried out as independent biological replicates on multiple occasions.
Randomization	Not applicable.
Blinding	Not applicable.

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: MOUSE ANTI-HUMAN INTEGRIN a-V MONOCLONAL ANTIBODY MCE MAB1978 LM142 2931241
Anti-Mouse IgG (whole molecule) - Peroxidase antibody produced in rabbit IgG fraction of antiserum A9044-2ML 0000435602

Validation: Validation stated in manufacturers' websites and previous publications.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s): Cells were obtained from Guangzhou Xinyuan Technology Co., Ltd., including A549-Luc cells (human non-small-cell lung carcinoma, catalog no. XY-1034), Caco-2 cells (human colorectal adenocarcinoma, catalog no. XY-0268), and A498 cells (human renal carcinoma, catalog no. XY-0586), MCF-10A cells (human normal breast epithelial cells, catalog no. XY-0328).

Authentication: The cell lines were purchased directly from the commercial source (Xinyuan Company) and were used without further authentication in our laboratory.

Mycoplasma contamination: All cell lines tested negative for mycoplasma contamination.

Commonly misidentified lines (See ICLAC register): Neither of the cell lines used in this study is listed in the ICLAC database of commonly misidentified cell lines.

Plants

Seed stocks: Not applicable

Novel plant genotypes: Not applicable

Authentication: Not applicable

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: A549-Luc cells were seeded in triplicate in 6-well plates at a density of 150000 cells/well and cultured to 90% confluence in RPMI-1640 medium supplemented with 10% fetal bovine serum. Peptides P25, 25a, 25b, 25c (dissolved in RPMI-1640 medium containing 0.1% DMSO via 5-minute sonication) were administered at a final concentration of 50 μM (1 mL/well). After 2, 4, 6, 8, 10 hours of incubation, the supernatant was aspirated, and cells were trypsinized with 0.25% trypsin-EDTA for

	2 minutes at 37 °C under 5% CO_2. Detached cells were collected, centrifuged at 1000 rpm for 3 minutes at room temperature, washed three times with pre-warmed PBS, resuspended in 1 mL PBS, and filtered through a 40 µm nylon mesh. Flow cytometry analysis was performed on a BD LSRII system (excitation wavelength: 488 nm, detection channel: FITC). Data were analyzed using FlowJo v10.8.14.
Instrument	FongCyte™ flow cytometer
Software	Flow v10.8.14
Cell population abundance	A549-Luc cells were seeded in triplicate in 6-well plates at a density of 150000 cells/well and cultured to 90% confluence
Gating strategy	Forward scatter (FSC) and side scatter (SSC) were first used to exclude debris and aggregates and to identify the cells population. Doublets were eliminated using FSC-H versus FSC-A plots. Within the single-cell gate, live cell were selected. For functional assays, all the live cells were considered under the gate

☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.