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 <u>Editorial Policies</u> and the <u>Editorial Policy Checklist</u>.

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St	at	ıctı	CS

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.
\times	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>
\boxtimes	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 <u>statistics for biologists</u> contains articles on many of the points above.
So	ftware and code

Policy information about availability of computer code

Data collection

This study selected dataset GSE139829 for single-cell RNAseq analysis

Data analysis

All sc-RNAseq analysis was performed using on the Seurat (version 5.0) package. Bulk RNAseq analysis was performed using STAR aligner (version 2.7.9a).

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 WGS, bulk RNAseq, and sc-RNAseq data generated during this study will be made publicly available upon acceptance for publication.

Research involving numan participants, their data, or biological material
Policy information about studies with <u>human participants or human data</u> . See also policy information about <u>sex, gender (identity/presentation), and sexual orientation</u> and <u>race, ethnicity and racism</u> .
No and the second and the second and an also be and an also in the second and an also also also also also also also also

and sexual orientation and	d <u>race, ethnicity and racism</u> .		
Reporting on sex and ge	nder No sex-based and gender-based analysis was performed, not relevant and outside the study scope.		
Reporting on race, ethn other socially relevant groupings	icity, or No race-based analysis was performed, not relevant and outside the study scope.		
Population characteristi	cs N/A		
Recruitment	N/A		
Ethics oversight	N/A		
Note that full information on	the approval of the study protocol must also be provided in the manuscript.		
<u>Field-specifi</u>	c reporting		
Please select the one belo	w that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.		
X Life sciences	Behavioural & social sciences Ecological, evolutionary & environmental sciences		
For a reference copy of the docur	ment with all sections, see <u>nature.com/documents/nr-reporting-summary-flat.pdf</u>		
Life science:	s study design		
All studies must disclose c	on these points even when the disclosure is negative.		
	e size was estimated using the ANOVA degrees of freedom (E), which fell within a range of 10–20. This approach adhered to the 3R ole, and the final number of samples was further determined in conjunction with other relevant studies to ensure robust experimental		
Data exclusions No dat	ta were excluded		
Replication A mini	inimum of three repetition of each experiment were conducted.		
Randomization Sampl	amples were not randomized because it was not relevant to the experimental design of this study.		
Blinding Blindin	Blinding was not used in this study.		
Reporting fo	or specific materials, systems and methods		
	authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, levant 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 & experim	ental systems Methods		
n/a Involved in the study	/a Involved in the study		
Antibodies ChIP-seq			
	Eukaryotic cell lines Flow cytometry		
Palaeontology and archaeology MRI-based neuroimaging Animals and other organisms			
Animals and other Clinical data	organisms		

Antibodies

Dual us

Dual use research of concern

Antibodies used

BAP1 (Cell Signaling Technology, Rabbit mAb #13271), β -actin (Santa Cruz, sc-47778 AF680), Anti-rabbit IgG, HRP-linked Antibody (Cell Signaling Technology, 7074).

Eukaryotic cell lines

Policy information about <u>cell lines and Sex and Gender in Research</u>

N/A

Melan-a, a murine melanocyte cell line was purchased from Sigma-Aldrich (SCC202) Cell line source(s)

Authentication Melan-a cells were purchased directly from Sigma-Aldrich and used at early passage. We performed morphological checks

and confirmed the expression of melanocyte-specific markers

The cell lines were tested for mycoplasma contamination and resulted negative Mycoplasma contamination

Commonly misidentified lines (See ICLAC register)

Animals and other research organisms

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

C57BL/6 mice Laboratory animals

Wild animals This study did not involve wild animals

female and male Reporting on sex

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

All animal experiments were conducted with approval from Singapore's Institutional Animal Care and Use Committee (IACUC) under Ethics oversight reference number 2022/SHS/1756.

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

Plants

N/A Seed stocks

N/A Novel plant genotypes

N/A Authentication