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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	NIS-Elements (v5.21, Nikon), OlyVIA 3.2 (Olympus). No custom code or scripts were developed or used in this study.
Data analysis	Image analysis: ImageJ (NIH,USA), XPS peak deconvolution: PeakFit (MagicPlot Systems, LLC). RNA-seq reads were quality-checked with FastQC, trimmed with Fastp (v0.23.1), aligned with STAR, and quantified using Salmon. Normalization and analysis were done with Python ("conorm" package) and ExDEGA (Ebiogen Inc., Korea). ATAC-seq reads were aligned using Bowtie2 (v2.3.4.3), filtered with Picard (v2.27.5) and SAMtools (v1.17). Tn5 bias was corrected with deepTools (v3.5.2). Peaks were called with MACS2 (v2.2.8), annotated with ChIPseeker (v1.36.0), analyzed with edgeR (v3.42.4), and motif enrichment was done using HOMER (v4.11.1). Graphing, and visualization: Origin (9.0, OriginLab Corp., USA) and GraphPad Prism (8.4.3; GraphPad Software, USA). Illustrations: Blender (Blender Foundation, Netherlands), Adobe Illustrator (Adobe, USA), BioRender (Canada, version), ChemDraw (25.0, Revvity Signals Software, USA). No custom code or scripts were developed or used in this study.

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 data supporting the findings of this study are available within the manuscript and its supplementary information. The transcriptomics data generated in this study have been deposited in the Gene Expression Omnibus (GEO) database under accession codes: GSE315168 (mRNA-seq), GSE315167 (ATAC–seq), GSE320430 (ChIP–seq), and GSE319127 for GeoMx spatial transcriptomics. Source data are 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	n/a
Reporting on race, ethnicity, or other socially relevant groupings	n/a
Population characteristics	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.

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 statistical method was used to predetermine sample size. Sample sizes were chosen based on previous studies using similar experimental designs and were sufficient to detect biologically relevant differences.
Data exclusions	No data were excluded from the analyses.
Replication	All experiments were repeated multiple times independently and were subjected to statistical analysis.
Randomization	Experimental animals were randomly allocated to groups. For imaging-based analyses, multiple fields of view were randomly selected.
Blinding	Experiments were not blinded. Most measurements were objective and equipment-based, and some procedures required knowing the group assignments.

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
[ ]	[x] Antibodies
[ ]	[x] Eukaryotic cell lines
[x]	[ ] Palaeontology and archaeology
[ ]	[x] Animals and other organisms
[x]	[ ] Clinical data
[x]	[ ] Dual use research of concern
[x]	[ ] Plants

Methods

n/a	Involved in the study
[ ]	[x] ChIP-seq
[x]	[ ] Flow cytometry
[x]	[ ] MRI-based neuroimaging

Antibodies

Antibodies used

Primary antibodies: Ki67 (Abcam, Cat. No. ab16667; 1:100), H3ac3 (Sigma-Aldrich, Cat. No. 06-599; 1:100-1:500), H3K9me3 (Novus, Cat. No. NBP1-30141; 1:100), H3K4me3 (Active Motif, Cat. No. 39159; 1:100), H3K27me3 (Cell Signaling, Cat. No. 9733; 1:100), iNOS (Abcam, Cat. No. ab178945; 1:100), CD206 (ICC; Thermo Fisher, Cat. No. MA5-28581; 1:100), CD206 (IHC; Cell Signaling, Cat. No. 24595; 1:400), p-STAT1 Ser727 (Cell Signaling, Cat. No. 9177; 1:100), p-NFκB p65 (Cell Signaling, Cat. No. 3031; 1:100), LOX (Abcam, Cat. No. ab174316; 1:100), VEGF (Thermo Fisher, Cat. No. MA5-13182; 1:100), CD86 (Thermo Fisher, Cat. No. MA5-32078; 1:200), 8-OHdG (Santa Cruz, Cat. No. sc-66036; 1:100), CD31 (Abcam, Cat. No. ab281583; 1:4000), and F4/80 (Santa Cruz, Cat. No. sc-377009; 1:50).

Secondary antibodies: Donkey Anti-Rabbit IgG (H+L) Alexa Fluor Plus 488 (Thermo Fisher, Cat. No. A32790), Donkey Anti-Mouse IgG (H+L) Alexa Fluor 488 (Thermo Fisher, Cat. No. A-21202), Goat Anti-Rabbit IgG (H+L) Alexa Fluor 488 (Abcam, Cat. No. ab150077), Donkey Anti-Mouse IgG (H+L) Alexa Fluor Plus 594 (Thermo Fisher, Cat. No. A32744), Donkey Anti-Rabbit IgG (H+L) Alexa Fluor 594 (Thermo Fisher, Cat. No. A-21207), Donkey anti-Rabbit IgG (H+L) Alexa Fluor 594 (Jackson ImmunoResearch, Cat. No. 711-585-152), Donkey anti-Mouse IgG (H+L) Alexa Fluor 594 (Jackson ImmunoResearch, Cat. No. 715-585-150), Anti-Rabbit EnVision+ System-HRP Labelled Polymer (Agilent Dako, Cat. No. K4003), and Anti-Mouse EnVision+ System-HRP Labelled Polymer (Agilent Dako, Cat. No. K4001).

Validation

All primary antibodies were commercially validated by the suppliers for use in immunohistochemistry and immunocytochemistry. Validation details, including species reactivity, recommended dilutions and application, are available on the respective manufacturer websites.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)

Human Dermal Fibroblasts (HDF, PCS 201 012, ATCC, USA), Human Umbilical Vein Endothelial Cells (HUVEC, PCS 100 013, ATCC, USA), and RAW 264.7 murine macrophage cells (TIB 71, ATCC, USA). HDF and HUVEC cells are of human origin; RAW 264.7 is derived from Mus musculus (mouse).

Authentication

All cell lines were purchased from ATCC and no additional authentication was performed in our laboratory.

Mycoplasma contamination

The cell lines were obtained from ATCC, which verifies that cell lines are free of mycoplasma at the time of distribution. The cell lines were not re-tested for mycoplasma contamination in our laboratory.

Commonly misidentified lines
(See ICLAC register)

n/a

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

5-week-old male Sprague–Dawley (SD) rats (Rattus norvegicus, outbred) were obtained from Daehan Biolink Co. (DBL; Eumseong, Republic of Korea)

Wild animals

n/a

Reporting on sex

Sex-based analysis was not conducted because the study design and objectives focused on overall mechanistic trends rather than sex-specific variation.

Field-collected samples

n/a

Ethics oversight

All the experiments were conducted following the protocols approved by the Animal Care and Use Committee at Dankook University, Republic of Korea (DKU-24-051)

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

Plants

Seed stocks	n/a
Novel plant genotypes	n/a
Authentication	n/a

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 *May remain private before publication.*	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE320430
Files in database submission	Raw ChIP-seq FASTQ files (H3ac ChIP and Input), processed peak files (BED), and signal tracks (BigWig).
Genome browser session (e.g. UCSC)	A genome browser session can be created and provided upon request.

Methodology

Replicates	Every ChIP seq analysis performed with two technical replicate independent ChIP-seq experiments.
Sequencing depth	ChIP-seq libraries were sequenced to high depth across all samples. For the sGel group, sGel_ID yielded 135,297,440 total reads, of which 133,764,256 reads were retained after processing, while sGel_ID-1 generated 128,955,232 total reads with 127,305,326 processed reads. For the sCuNZ group, sCuNZ_ID produced 106,528,524 total reads and 105,462,246 processed reads, whereas sCuNZ_ID-1 yielded 76,393,712 total reads with 75,531,938 processed reads. In the iGel group, iGel_ID generated 151,454,854 total reads, with 150,524,332 reads retained after processing, and iGel_ID-1 produced 142,968,028 total reads with 141,948,532 processed reads. For the iCuNZ group, iCuNZ_ID yielded 149,164,054 total reads and 148,154,324 processed reads, while iCuNZ_ID-1 generated 121,003,010 total reads with 120,111,890 processed reads.
Antibodies	H3ac (Sigma-Aldrich, Cat. No. 06-599)
Peak calling parameters	Peaks were called using MACS2 callpeak v2.2.8, keeping all duplicates and using the mouse genome size option. BAMPE was used for paired-end samples and input samples were used as control.
Data quality	ChIP-seq data quality was evaluated as per ENCODE standards. Namely, for each sample we considered the following parameters: total depth, number of peaks, fraction of reads in peaks.
Software	Fastp v0.23.1, bowtie2 v2.3.4.3, samtools v1.17, ENCODE blacklist regions v2.0, Bedtools v2.26.0, MACS v2.2.8