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	In this study, the following commercial, open-source, and custom code were used to collect and process the data:Bulk RNA-SeqBase Quality Analysis: FastQC (version 0.11.2)Data Quality Control: fastp (version 0.14.0)Alignment Tools:Tophat (version 2.0.13)HISAT2 (version 2.1.0)Alignment Quality Control: RSeQC (version 2.6.4)Transcript Assembly: StringTie (version 1.3.3b)Quantification: StringTie (version 1.3.3b), featureCounts (version 2.0.0)scRNA-SeqData Quality Control and Initial Statistics: CellRanger (version 3.1.0)Spatial TranscriptomicsData Quality Assessment: FastQC (version 0.11.2)Spatial Data Analysis: Space Ranger (version 1.1.0)
Data analysis	In this study, the following tools were used for data analysis:Seurat (version 4.2.1): Used for normalizing the data, estimating the variance of raw filtered data, and identifying the most variable genes. Seurat is widely applied in both single-cell and spatial transcriptomics data analysis.10X Genomics Cell Ranger (version 3.1.0): Used to process raw BCL files into FASTQ files, perform alignment, and quantify gene expression counts, primarily applied in preprocessing single-cell RNA-seq data.DoubletFinder (version 2.0.3): Used to identify and filter out doublets (artificially formed cell pairs) in single-cell RNA-seq data, ensuring higher accuracy in downstream analyses.limma (version 3.32.10) and edgeR (version 3.18.1): These tools were used for differential expression analysis, comparing gene expression differences between experimental groups, commonly applied in bulk RNA-seq data analysis.CellChat (version 1.5.0): Used for cell-cell communication analysis, leveraging ligand-receptor interaction networks to infer signaling pathways between different cell types.AUCell (version 1.18): Used to calculate the Area Under the Curve (AUC) for gene set enrichment analysis, evaluating gene set activity across individual cells.SCENIC (version 1.1.2): Used to infer transcription factor (TF) networks, helping to identify key regulatory transcription factors and their influence on gene expression programs.

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 associated with this study are present in the main text or the Supplementary Materials. All materials and primary data used in this study are available upon request. The raw sequence data of the ST sequencing, snRNA-seq, and bulk RNA-seq reported in this paper have been deposited in the Genome Sequence Archive at National Genomics Data Center China 75, 76, National Center for Bioinformation/Beijing Institute of Genomics, Chinese Academy of Sciences (GSA: CRA011548, OMIX008153 and OMIX008150).

Human research participants

Policy information about studies involving human research participants and Sex and Gender in Research.

Reporting on sex and gender	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 the sample size.
Data exclusions	In single-cell sequencing, data exclusions are applied to improve data quality:Retain cells with fewer than 7500 genes detected: This filters out empty GEMs and doublet-containing GEMs, ensuring only valid single cells are included. Retain cells with mitochondrial gene transcripts < 5%: This helps exclude dead or low-quality cells. Only retain single cells predicted by DoubletFinder: This ensures that doublets (cells mistakenly captured together) are removed, preserving the accuracy of the analysis.
Replication	For the 10x Visium ST with SNL surgery on SC (lumbar enlargement), there are 2 replicates per group, each replicate from 1 mouse. For the snRNA-seq with SNI surgery on L3-L5 DRG and SC (ipsi lumbar enlargement), there is 1 replicate per group, each repliacate from 3 mice. For the bulk RNA-seq with SNL surgery on SC (ipsi lumbar enlargement), there are 3 replicates per group, each replicate from 1 mouse. For the bulk RNA-seq with SNI surgery on L3-L5 DRG, there are 3 replicates per group, each replicate from 3 mice.
Randomization	Animals are randomly assigned to different experimental groups (Sham, SNL; Sham SNI;), ensuring that each animal has an equal chance of being allocated to any group.
Blinding	Blinding is not typically applicable in sequencing experiments where the process is automated and the samples are handled by machines.

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

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used

Complement component 1q (C1Q, rabbit, 1:200, Abcam, Cambridge, UK, ab182451, RRID:AB_2732849), Choline transporter 1 (CHT1, rabbit, 1:200, Millipore, Chicago, USA, ABN458), Protein kinase C gamma (PKC γ, SC-211, rabbit, 1: 500, Santa Cruz Biotechnology, CA, USA, RRID:AB_632234), Neuronal nuclear protein (NeuN, mouse, 1:1000, Millipore, Chicago, USA, MAB377, RRID:AB_2298772), Glial fibrillary acidic protein (GFAP, mouse, 1:1000, Millipore, Chicago, USA, MAB360, RRID:AB_11212597), Ionized calcium-binding adaptor molecule 1 (IBA-1, goat, 1: 500, Abcam, Cambridge, UK, ab5076, RRID:AB_2224402), Calcitonin gene-related peptide (CGRP, goat, 1:300, Abcam, Cambridge, UK, ab36001, RRID:AB_725807), and the 200 kD neurofilament protein (NF200, mouse, 1:2000, Millipore, Chicago, USA, MAB5266, RRID:AB_2149763).

Validation

All the primary antibodies listed have been validated for use in immunofluorescence on mouse tissue. This validation is ensured by the manufacturers and is further supported by the Research Resource Identifiers (RRIDs) provided for each antibody. Our previous study, as well as this one, has confirmed that these antibodies are specific to their targets in mouse tissue immunofluorescence.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	HEK293T
Authentication	N/A
Mycoplasma contamination	Negative
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	Adult (6-8 week old) male ICR mice and C57BL/6J mice used for ST, bulk RNA-seq or snRNA-seq were purchased from the Experimental Animal Center of Nantong University and Jiangsu Wukong Biotechnology Co. (Nanjing, China). Cx3cr1-GFP mice (005582, B6.129P2(Cg)-Cx3cr1tm1Litt/J, RRID:IMSR_JAX:005582) were obtained from Jackson Lab (Bar Harbor, ME, USA).
Wild animals	N/A
Reporting on sex	All data in this study collected from Male mice.
Field-collected samples	N/A
Ethics oversight	All experiments conformed to the NIH Guide for Care and Use of Laboratory Animals and the Committee for Research and Ethical Issues of IASP guidelines and were approved by the Animal Care and Use Committee of Nantong University and Zhejiang University (IACUC20220210-2001 and AIRB-2023-0881).

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