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	No software was used.
Data analysis	The methods of ST-GEARS is packaged, and distributed as an open-source, publicly available repository: https://github.com/STOmics/ST-GEARS. All software used to analyze data in this study are open-sourced Python packages, including anndata==0.9.2, numpy==1.22.4, pandas==1.4.3, scipy==1.10.1, matplotlib==3.5.2, k3d==2.15.3

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 used in this research were collected from published sources. DLPFC data was obtained from the research: Transcriptome-scale Spatial Gene Expression in the Human Dorsolateral Prefrontal Cortex, with data downloading link of http://research.libd.org/spatialLIBD/index.html; Drosophila embryo and Drosophila larva

data were collected from High-resolution 3d Spatiotemporal Transcriptomic Maps of Developing Drosophila Embryos and Larvae, with the dataset link of https://db.cngb.org/stomics/datasets/STDS0000060. Mouse hippocampus data was collected from research: Slide-seq: A scalable technology for measuring genome-wide expression at high spatial resolution, with the dataset link of: https://singlecell.broadinstitute.org/single_cell/study/SCP354/slide-seq-study. Mouse brain data was collected from research: Modular cell type organization of cortical areas revealed by in situ sequencing. The download link is: https://data.mendeley.com/datasets/8bhhk7c5n9/1. All datasets were generated on Spatial Transcriptomics platform, with DLPFC data generated by Visium technology of 10x Genomics, Mouse brain data generated by BARseq of Cold Spring Harbor Laboratory, while Drosophila embryo and larva generated by Stereo-seq technology of BGI.

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	Neither human participants nor human data is involved in this study.
Reporting on race, ethnicity, or other socially relevant groupings	Neither human participants nor human data is involved in this study.
Population characteristics	Neither human participants nor human data is involved in this study.
Recruitment	Neither human participants nor human data is involved in this study.
Ethics oversight	Neither human participants nor human data is involved in 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	Our research involves only method proposal and study. Sample size of 5 with 78 sections in total were chosen to study effect of our method, in consideration of sample size of other comparable method studies.
Data exclusions	No data were excluded from the analyses.
Replication	All attempts at replication were successful.
Randomization	This is not relevant to our study, because our study on our method's effect is completed by applying the method on each sample, and comparing the results with profiles before application.
Blinding	This is not relevant to our study, because group allocation is not relevant to our research our study on our method's effect is completed by applying the method on each sample, and comparing the results with profiles before application.

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

Plants

Seed stocks	Plants were not involved in the study.
Novel plant genotypes	Plants were not involved in the study.
Authentication	Plants were not involved in the study.