

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 (<i>n</i>) 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 <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☐	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>
☒	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 <i>d</i> , Pearson's <i>r</i>), 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	/
Data analysis	/

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 needed to evaluate the conclusions in the paper are present in the paper and/or the Supplementary Materials. Additional data related to this paper may be requested from the authors.

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

/

Reporting on race, ethnicity, or other socially relevant groupings

/

Population characteristics

/

Recruitment

/

Ethics oversight

/

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](https://www.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

The determination of sample size is designed according to the existing literature by searching the literature. All results are expressed as the mean $\pm$ SD, as indicated. Statistical analyses were performed using GraphPad Prism 8. A one-way ANOVA with Tukey's post-hoc test was used to evaluate statistically significant differences in multiple group data ($P > 0.05$ (n.s.), $*P < 0.05$, $**P < 0.01$, $***P < 0.001$). Two-sided unpaired t-tests and two-sided paired t-tests were used to evaluate statistically significant differences between the two groups ($P > 0.05$ (n.s.), $*P < 0.05$, $**P < 0.01$, $***P < 0.001$) (n.s., not significant).

Data exclusions

Some data were excluded because there were obvious individual differences, and the data were quite different from other samples in this group. Exclusion criteria were not established in advance.

Replication

The experiment will be repeated for 3 or more times, and the standard deviation will be displayed after analysis. For each experiment, statistical analysis is shown in the legend.

Randomization

The sample was randomly assigned.

Blinding

No blind method was used in the research. At the beginning of the experiment, the groups were randomly divided, but in the subsequent experiment, the situation of each group of mice will be recorded, and investigators will inevitably know during the data collection and/or analysis.

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

Occludin Rabbit pAb : Abclonal, clone name A2601, lot number 3600002467;
TGF beta 1 Rabbit pAb : Abclonal, clone name A2124, lot number 5500009529;
α-Smooth Muscle Actin (ACTA2) Rabbit pAb : Abclonal, clone name A7248, lot number 5500019521;
ZO-1 Polyclonal antibody : Proteintech Group, clone name 21773-1-AP, lot number 00144045.

Validation

Occludin Rabbit pAb : <https://abclonal.com.cn/catalog/A2601> ;
TGF beta 1 Rabbit pAb : <https://abclonal.com.cn/catalog/A2124>;
α-Smooth Muscle Actin (ACTA2) Rabbit pAb : <https://abclonal.com.cn/catalog/A7248>;
ZO-1 Polyclonal antibody : <https://ptgcn.com/products/ZO1-Antibody-21773-1-AP.htm>.

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)

CCD-18CO (CRL-1459) cell lines were obtained from the American Type Culture Collection (ATCC). NCM460 cell lines were obtained from In Cell (San Antonio, TX) and cultured according to the method of manufacturer.

Authentication

Cell lines have been authenticated by short tandem repeat profiling, and the results were compared with reference database.

Mycoplasma contamination

All cell lines tested negative for mycoplasma contamination.

Commonly misidentified lines
(See [ICLAC](#) register)

No commonly misidentified cell lines were used.

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

BALB/c and C57bl/6j mice (female, 6 weeks old, 18–20 g)

Wild animals

This study did not involve wild animals

Reporting on sex

The findings are applicable to any gender. Gender was not considered in the research design.

Field-collected samples

When extracting the colon protein and homogenizing the tissue, the colon tissue should be placed at 4°C. For fecal collection and RNA sequencing, samples should be stored at -80°C.

Ethics oversight

All animal experiments were approved by the Institutional Animal Care and Use Committee of Hefei University of Technology (No. HFUT20220305003).

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Plants

Seed stocks

/

Novel plant genotypes

/

Authentication

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