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	n/a
Data analysis	1. RNA-seq mapping: STAR v2.4.2a, GATK v4.0 2. Gene expression: RSEM v1.2.21 3. RNA editing site identification: GATK v4.0 4. RNA editing site clustering: DBSCAN v1.1-3, R v3.6 5. Neural cell type enrichment analysis: Bioconductor v3.5, EWCE v1.0.0 6. Characterization of dsRNA features: ViennaRNA v2.4.10 7. qRT-PCR analysis: Graph Pad PRISM 8 8. Enrichment analysis of dsRNAs in GWAS signal: PLINK version 1.9 Computational codes used in this study are available at https://github.com/vargasliqin/editome.

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 accession number for the sequencing data reported in this paper is GEO: GSE155964, which is public as of Aug31 2025

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	All experiments such as qPCR and luciferase assay were carried out with duplicates (generally n=3 unless otherwise specified) to ensure the conclusion is accurate.
Data exclusions	no data was excluded
Replication	Each experiment includes multiple replicates and controls to ensure the accuracy. Major experiments such as ADAR complementation assay, NPC differentiation have been repeated at least twice and the results were reproducible.
Randomization	Randomization is irrelevant because no group allocation was performed
Blinding	Blinding is irrelevant because no group allocation was performed

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
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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

Antibodies

Antibodies used	Flag (Sigma: F3165; clone M2) ADAR1 (Santa Cruz Biotechnology, sc-73408), MAVS (Santa Cruz Biotechnology sc-166583, clone E3) MDA5 (Invitrogen 700360, clone 33H12L34), GAPDH (Thermo Fisher: MA5-15738; clone GA1R) Actin (Thermo Fisher, MA5-11869; clone ACTIN05(C4)). goat anti-mouse-HRP (Thermo Fisher Cat, # 31444) goat anti-rabbit-HRP (Thermo Fisher, Cat# 31460). goat anti-mouse IgG alexa fluor 488 (Thermo Fisher, A-11001)

Validation

Flag (Sigma: F3165; clone M2) RRID:AB_259529
ADAR1 (Santa Cruz Biotechnology, sc-73408),RRID:AB_2222767
MAVS (Santa Cruz Biotechnology sc-166583, clone E3), RRID:AB_2012300
MDA5 (Invitrogen 700360, clone 33H12L34), RRID: AB_2532316
GAPDH (Thermo Fisher: MA5-15738; clone GA1R), RRID:AB_10977387
Actin (Thermo Fisher, MA5-11869; clone ACTIN05(C4)). RRID: AB_11004139
goat anti-mouse-HRP (Thermo Fisher Cat, # 31444), RRID: AB_228321
goat anti-rabbit-HRP (Thermo Fisher, Cat# 31460). RRID:AB_228341
goat anti-mouse IgG alexa fluor 488 (Thermo Fisher, A-11001). RRID: AB_2534069

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	HEK293T, human ESC
Authentication	none were authenticated
Mycoplasma contamination	The cell lines were not tested for mycoplasma contamination
Commonly misidentified lines (See ICLAC register)	HEK is commonly misidentified as HEK293T