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Reporting Summary

Nature Research 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 Research 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	RNA-seq data shown in this paper have been deposited in GEO under accession code GSE100756. Source data for Fig. 3, 4a, 8b, and Fig. 7c-d, 9b-d are included in Source Data files individually. Source data files for other figures can be accessed via the supporting primary research article.
Data analysis	All the qRT-PCR data were analyzed using GraphPad PRISM 7. Software used to analyze the MS data are as followed: MaxQuant (v1.6.17), DEP package (v1.12.0), InterProScan (v5.47-82.0). Software used to analyze the RNA sequencing data are described under accession code GSE100756 in GEO.

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 Research 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 list of figures that have associated raw data
- A description of any restrictions on data availability

It has been described in the section of Data availability statement.

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 methods were used to predetermine sample sizes. We chose the sample size based on the cell numbers.
Data exclusions	No data were excluded.
Replication	Optimization of EU incorporation (Fig. 3), silver staining (Fig. 4a-b) in 16-hour RICK and short-labelling RICK, Western Blotting (Fig. 4c) in 16-hour RICK were performed at least 3 times independently, but only one representative experiment is shown in each respective figure. qRT-PCR for diverse RNA species captured by RICK (Fig. 6) and quantification of RNAs and proteins captured by 16-hour RICK and short-labelling RICK (Fig. 8c) were repeated 3 times independently.
Randomization	Samples were not randomized for the experiments. In addition, more than three researchers in our lab have repeated this method independently.
Blinding	No blinding was used because our experimental designs excluded the possibility of biased data collection or analysis. Additionally, more than three researchers in our lab have repeated this method independently.

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	Anti-DDX5 (ab21696; 1:2000), anti-PTBP1 (ab5642; 1:1000), anti-HNRNPK (ab39975; 1:2000), Rabbit Anti-Mouse IgG (HRP) (ab6728; 1:5000), Goat Anti-Rabbit IgG (HRP) (ab6721; 1:5000), Donkey Anti-Goat IgG (HRP) (ab6885; 1:3000) were purchased from Abcam; Anti-β-Actin (A2228; 1:2000) and Anti-β-Tubulin (T0198; 1:2000) were purchased from Sigma-Aldrich; Pol II Antibody (sc-899; 1:1000) was purchased from Santa Cruz Biotechnology. All antibodies were used for Western Blotting. A list of antibodies is also included in Table 3.
Validation	All antibodies were used for Western Blot detection according to the manufacturer's instruction. Antibodies were considered valid when the bands on the immunoblot membrane were observed with the right size compared to the manufacturer's results.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	HeLa cells and E14gt2a mESCs were purchased from American Type Culture Collection (cat. no. CCL-2 and CRL-1821, respectively).
Authentication	Gene expression by qRT-PCR of mouse ESC lysates was used to confirm the expression of specific pluripotency genes. No other cell line authentication was performed.

Mycoplasma contamination	Cells were monthly checked and were devoid of mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	No.