

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 [Authors & Referees](#) 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	Behavioral measurement: UMATracker (http://ymnk13.github.io/UMATracker/)
Data analysis	Microarray analysis: GeneSpring (version 14.9) Canonical pathway analysis: Ingenuity pathway analysis (version 01-12) Quality control: FastQC (version 0.11.5, http://www.bioinformatics.babraham.ac.uk/projects/fastqc/) Read trimming: Trimmomatic (version 0.32), FASTX-Toolkit (version 0.0.13, http://hannonlab.cshl.edu/fastx_toolkit/index.html) Genome-guided assembly: HISAT2 (version 2.0.5), TopHat (version 2.1.0) Read counting: StringTie (version 1.3.3b), cufflinks (version 2.2.1) Behavioral analysis: UMATracker (http://ymnk13.github.io/UMATracker/)

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/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

Raw data of microarray data, RNA-seq and Ribo-seq data have been deposited at the NCBI Gene Expression Omnibus (accession number GSE119905).

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	No formal sample size calculation was performed. We determined sample size based on standards established in the field. For experiments using animals, the minimum number of animals necessary to achieve the scientific objectives was used.
Data exclusions	No data were excluded from the analysis.
Replication	In the SD to LD transition microarray experiment, we have used 2 pooled sample composed of 3 individual females for each time point (Total 108 females). In the experiments using LDAIR-null fish, 3 pooled sample composed of 3 individual females were used for each genotype (wildtype 9 fish and knockout 9 fish) (Total 18 females). In the strand specific RNA-seq, 2 pooled sample composed of 3 individual females were used (Total 6 females). In the ribosome profiling experiment, 2 pooled sample composed of 10 individual females were used (Total 20 females). In the qPCR experiment, 3 fish were used for each genotype (Total 6 females) In the behavior test, 16-20 females were used for each genotype.
Randomization	Animals were randomly allocated to groups.
Blinding	In the behavior test, investigator was blind to group allocation and data collection.

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
☐	☒ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

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

Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals	Medaka fish (<i>Oryzias latipes</i>) were obtained from a local dealer ((Fuji 3A Project, Nagoya, Japan) and kept under SD (short day; 10 h light / 14 h dark; 26°C) conditions or LD(long day; 16 h light / 8 h dark; 26°C) conditions in a housing system (MEITO system, Meito Suien; LP-30LED-8CTAR, NK system). Adult females were used in all experiments.
Wild animals	The study did not involve wild animals.
Field-collected samples	The study did not involve samples collected from the field.
Ethics oversight	Animals were treated in accordance with the guidelines of Nagoya University and the National Institutes of Natural Sciences. All experimental protocols were approved by the Animal Experiment Committee of Nagoya University and the National Institutes of Natural Sciences.

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