

Reporting Summary

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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
<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. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P 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 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

This work is the initial description of the setup and software used for collecting the data (Live Mouse Tracker, running on the ICY platform: De Chaumont F, Dallongeville S, Chenouard N, Hervé N, Pop S, Provoost T, et al. Icy: an open bio- image informatics platform for extended reproducible research. Nat Methods. 2012; 9: 690–696. doi: 10.1038/nmeth.2075).

Data analysis

We used Python 3.6 (Python Software Foundation. Python Language Reference, version 3.6; available at <http://www.python.org>) to compute distances and SAP in the experiments. We used R 3.3.1 for graphical representation and statistics (R Core Team (2016). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <https://www.R-project.org/>). Part of the analyses (direction of approaches, group formation) were computed on the ICY platform (De Chaumont F, Dallongeville S, Chenouard N, Hervé N, Pop S, Provoost T, et al. Icy: an open bio- image informatics platform for extended reproducible research. Nat Methods. 2012; 9: 690–696. doi: 10.1038/nmeth.2075). Analysis codes are available on GitHub.

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

The authors declare that all the data supporting the findings of this study are available within the paper and its Supplementary Information. Full datasets (databases and films) generated during and/or analysed during the study are available in the Live Mouse Tracker website repository, <https://livemousetracker.org>. Full source code is available at <http://icy.bioimageanalysis.org/plugins/livemousetracker>. It includes Java code. This also includes CAD hardware resource files.

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 work was explorative; therefore, we did not estimate the sample size needed. Given the complexity of the behavioral traits examined, we did not have any previous experiments that could provide us with a reasonable effect size to be expected. For the single-object exploration, we studied 10 Shank2+/+ and 8 Shank2-/- female mice in a first cohort; 12 Shank2+/+ and 7 Shank2-/- female mice in a second Shank2 cohort and 8 Shank2+/+; 8 Shank2-/- male mice in a second Shank2 cohort and 7 Shank3+/+ and 12 Shank3-/- female mice. For the paired-object exploration, we used 12 Shank2+/+ and 12 Shank2-/- female mice from the first cohort and 13 Shank2+/+ and 11 Shank2-/- from the second cohort. For the long-term recordings of groups, we tested nine groups of four Shank2 mice, meaning 18 Shank2+/+ mice and 18 Shank2-/- mice. We also tested six groups of four Shank3 mice, meaning 12 Shank3+/+ and 12 Shank3-/- female mice.
Data exclusions	No data were excluded from the analyses.
Replication	We replicated nine times the experiment of the long-term recordings of a group of four mice for the Shank2 model and six times for the Shank3 model. Data gathered were consistent between all groups within each model.
Randomization	For the single and dyadic object exploration, animals underwent behavioral tests in random order, without knowledge of their genotype. The experimenter was not aware of the genotype at the moment of testing. Genotypes were uncovered only at the end of the analyses. For the long-term recordings, mice were distributed in the different groups according to their genotype (two wild-type and two mutant mice per group). We also avoided (as much as mouse availability allowed) placing littermates in the same group. Genotypes were uncovered only at the end of the analyses computations.
Blinding	Blinding was used in the single and dyadic object exploration tests. Mice were genotyped at weaning, 2 months before the start of the experiments. At the time of experiment, the experimenter was blinded to the genotype of the tested animals. Blinding was not relevant for the long-term monitoring of animals. These animals were recorded without human intervention, only through the tracking system presented in this work.

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

We studied mice mutated in Shank2 or Shank3, two genes associated with ASD risk (Schmeisser et al. 2012 Nature). These mouse lines were generated on a C57BL/6J background. We studied adult females aged between 3 and 12 months of age and adult males aged between 3–6 months. The same animals underwent single-object exploration, dyadic-object exploration and the long-term monitoring study for the Shank2 mice. Shank3 mice underwent single-object exploration and long-term monitoring study (project accepted under the reference 2013-85 by the ethical committee of the Institut Pasteur CETEA n°89).

Wild animals

This study did not involve wild animals.

Field-collected samples

This study did not involve samples collected from the field.

Ethics oversight

This project was accepted under the reference 2013-85 by the ethical committee of the Institut Pasteur CETEA n°89.

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