

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	SpikeGLX, Kilosort 2.0, Phy2, pyBpod
Data analysis	custom Python (version 3.12) and MATLAB (2023b) code. Code to reproduce the figures is available here: https://osf.io/fap2s/ . Code to fit behavioral models is available here: https://github.com/int-brain-lab/ibl-changeoint . Code to fit encoding models is available here: https://github.com/BalzaniEdoardo/PGAM .

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](#)

Raw data can be accessed following instructions here: <https://osf.io/fap2s>. summary data to reproduce the figures is available here: <https://osf.io/fap2s/>

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	N/A
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

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](#)

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Sample size is equivalent or larger to that of IBL et al., 2021 (most similar report)
Data exclusions	Individual mice were removed from behavioral analyses within the “biased blocks” (i.e., where the probability of the grating alternated between being 80% left vs. 80% right hemifield) if they did not reach proficiency (80% correct on 100% contrast stimuli) in the “unbiased” version of the task. This resulted in 8% of animals being removed from the behavioral results report below. Neurons were not analyzed if they were localized to a brain region with less than 40 units / area in any of the 4 genotypes tested. No other data were excluded.
Replication	Results are replicated across 3 different mouse models of ASD.
Randomization	Animals were visually identical, data was collected by hypothesis-naive experimenter.
Blinding	Animals were visually identical, data was collected by hypothesis-naive experimenter. Names used internally were not indicative of underlying genotype.

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		Methods	
n/a	Involved in the study	n/a	Involved in the study
☒	☐ Antibodies	☒	☐ ChIP-seq
☒	☐ Eukaryotic cell lines	☒	☐ Flow cytometry
☒	☐ Palaeontology and archaeology	☒	☐ MRI-based neuroimaging
☐	☒ Animals and other organisms		
☒	☐ Clinical data		
☒	☐ Dual use research of concern		
☒	☐ Plants		

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	In addition to wildtype control animals (n = 15), three different monogenetic mouse models of ASD were used. Fmr1 KO25 (male are Fmr1-/y, female are Fmr1-/-, no sex difference, n = 19; JAX 003025) mice have a neomycin resistance cassette replacing exon 5 of the fragile X mental retardation syndrome 1. Cntnap2tlacZ/tlacZ(n = 21; JAX 028635) mice26 have a dysfunctional contactin associated protein-like 2 gene by replacement of the exon 1 on the Cntnap2 gene. Shank3B+/- (n = 20; JAX 017688) mice have a neocassette replacing the PDZ domain (exons 13-16) on the Shank3 gene, resulting in altered expression of the synaptic scaffolding protein expressed in the post-synaptic density of excitatory synapses. All animals were between 10 and 29 weeks old.
Wild animals	No wild animals were used in this study.
Reporting on sex	In addition to wildtype control animals (n = 15), three different monogenetic mouse models of ASD were used. Fmr1 KO25 (male are Fmr1-/y, female are Fmr1-/-, no sex difference, n = 19; JAX 003025) mice have a neomycin resistance cassette replacing exon 5 of the fragile X mental retardation syndrome 1. Cntnap2tlacZ/tlacZ(n = 21; JAX 028635) mice26 have a dysfunctional contactin associated protein-like 2 gene by replacement of the exon 1 on the Cntnap2 gene. Shank3B+/- (n = 20; JAX 017688) mice have a neocassette replacing the PDZ domain (exons 13-16) on the Shank3 gene, resulting in altered expression of the synaptic scaffolding protein expressed in the post-synaptic density of excitatory synapses. All animals were between 10 and 29 weeks old.
Field-collected samples	No field-collected samples were used here.
Ethics oversight	All procedures performed in this study were approved the Institutional Animal Care and Use Committee (IACUC) at New York University (protocol number: 18-1868)

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

Plants

Seed stocks	NA
Novel plant genotypes	NA
Authentication	NA