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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 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 (*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	Data were recorded using NIS-Elements Advance Research software v4.60.00, HC Image 4.5, OmniPlex system 1.6.0, and MATLAB 2014b.
Data analysis	Data were analyzed offline using NIS-Elements Advance Research software v4.60.00, OriginPro 8 (OriginLab), C, Excel 2016 (Microsoft), ImageJ(Fiji) 1.52i, Python 3.6.8. and 3.7.1, BoxPlotR, and MATLAB 2017a, 2018a, 2018b.

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

Code availability. Computer codes used to generate results for this study are available at https://github.com/HanLabBU/somarchon-imaging.
Data availability. The data that support the findings of this study are available from the corresponding author upon reasonable request; raw data essential to the work is avalible online at nature.com. Sequences of the reported proteins are available at Genbank at the following accession codes: SomArchon MN091368; SomArchon-P2A-CoChR-KV2.1motif, MN091369.

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 estimate sample size for animal studies throughout. We did not perform a power analysis, since our goal was to create a new technology; in the reference (Dell, R. B., Holleran, S. & Ramakrishnan, R. Sample size determination. ILAR. J. 43, 207–213 (2002)), as recommended by the NIH, "In experiments based on the success or failure of a desired goal, the number of animals required is difficult to estimate..." As noted in the aforementioned paper, "The number of animals required is usually estimated by experience instead of by any formal statistical calculation, although the procedures will be terminated [when the goal is achieved]." These numbers reflect our past experience in developing neurotechnologies.
Data exclusions	Voltage imaging datasets with significant motion or where no spikes were detected were excluded from analysis. Significant motion was defined as a shift for more than 20 µm in any direction. In Extended Data Figure 1i,j,k data points that corresponded to overlapping neurites were excluded. Data exclusion criteria were not pre-established.
Replication	All attempts at replication were successful. The detailed experimental protocols are provided to facilitate replication by others.
Randomization	There were no treatment conditions to compare in this study. All recording sessions were randomly performed with different voltage sensors or in different brain regions. On recording days, cultured cells or brain slices expressing specific sensors were known. On in vivo recording days, mouse conditions were known. Voltage trace extraction and subsequent analysis were performed with the investigators unaware of specific mouse conditions. For analysis of movement modulation of striatal neuron spiking, a computer algorithm was used to identify periods with different movement parameters. For analysis of spike-phase relationships, or subthreshold membrane voltage relationships, a computer algorithm was used across all conditions. For histology,- sections were selected and images were taken from slides by a researcher not aware of the conditions or antibody used. Cells were also counted and quantified from these sections by a researcher blinded to the experimental conditions or antibody used.
Blinding	

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

Antibodies

Antibodies used	Primary antibodies anti-GFAP (1:250, Clone N206/A8, Neuromab) and anti-IBa1 (1:500, 019-19741, Wako Chemicals) and secondary antibodies Alexa Fluor 568 (1:1000, Goat anti-Mouse IgG (H+L) Cross-Adsorbed Secondary Antibody, A11004, InVitrogen) 633 secondary antibodies (1:1000, Goat anti-Rabbit IgG (H+L) Cross-Adsorbed Secondary Antibody, A21070, InVitrogen)were used in the study.
Validation	For anti-GFAP please see: http://neuromab.ucdavis.edu/datasheet/N206A_8.pdf For anti IBa1, please see: http://www.e-reagent.com/uh/Shs.do?now=1550070200673 Validation methods are references in Methods.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	Species, strain, sex, and age are reported for each experiment in the Methods
Wild animals	The study did not involve wild animals

Field-collected samples	This study did not involve samples collected in the field.
Ethics oversight	Boston University Institutional Animal Care and Use and Biosafety Committee, Massachusetts Institute of Technology Institutional Animal Care and Use and Biosafety Committee

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