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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.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
☐	☒	An indication of 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 statistics 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
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	Imaging data was collected through the use of MATLAB 2012b running ScanIMAGE. Animal behavior was monitored through Ethovision software.
Data analysis	Custom software was used to analyze fluorescence lifetime imaging experiments. It has been described in detail in the paper and will be made available if requested. Statistics were completed using GraphPad Prism as described.

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 upon request. 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 datasets generated during and/or the code used to analyze the data in the current study are available from the corresponding author on reasonable request.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

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

Sample size	No statistical tests were done to predetermine sample size, however approximate sample size was predetermined by experience with similar published data.
Data exclusions	Individual neurons used for structural plasticity data was excluded if there were obvious signs of poor neuron health such as dendritic beading or blebbing. Individual spines were excluded if there was significant focal drift during the imaging session. FLIM data was excluded if the noise in the baseline was more than 0.1 ns due to low photon count. No animals were excluded from behavioral studies.
Replication	All attempts at replication were successful.
Randomization	Samples were allocated to groups by genotype as applicable, littermate controls of other genotype were used when possible, when not possible animals of the closest age were used. For in-vitro studies, neurons were assigned to different groups to randomly interleave control and experimental groups from slices prepared from the same animals. Experiments from control and experimental groups were randomly interleaved during experimentation with the exception that each block of experiments began with one neuron from the control group to ensure technical success of experiments.
Blinding	Behavioral experiments were double blinded. For in-vitro experiments, data collection and analysis were not performed blind to the conditions of the experiments.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☐	☒ Unique biological materials
☒	☐ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☒	☐ Human research participants

Methods

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

Unique biological materials

Policy information about availability of materials

Obtaining unique materials	No restrictions. Plasmids designed for this study will be deposited on Addgene.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	HeLa cell lince (ATCC® CCL-2) purchased from ATCC
Authentication	This cell line was not authenticated as the nature of the cell line was irrelevant to the research done.
Mycoplasma contamination	Cell lines were not tested for Mycoplasma contamination
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used

Animals and other organisms

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

Laboratory animals	P3-P8 mouse pups from both sexes were used for organotypic slices for imaging studies. P30-P50 mice of both sexes were used for acute slices for electrophysiological studies. 2- 4 month old male mice were used for behavioral studies. -Nontransgenic animals, C57Bl/6N Crl, were received from Charles River Lab. -PKCα KO 129/sv and PKCβ KO 129/sv animals were developed by Dr. Michael Lietges as previously described 58,59. Animals were crossed to C57Bl/6N Crl and are on a mixed background. For all experiments WT littermates were used as controls for KO animals. -PKCγ KO animals were developed by Dr. Susumu Tonegawa as previously described 53 and received from Jackson Labs B6;129P2-Prkcgtm1Stl/J Stock No: 002466. Animals were crossed with C57Bl/6N Crl and are on a mixed background. For all experiments WT littermates were used as controls for KO animals. -Double (β, γ) knockout and triple (α, β, γ) KO animals were bred by crossing single KO animals. Breeding pairs were KO on one or two genes and Het on the remaining. A parallel WT control line was bred to match offspring by strain and generation. -TrkBF616A C57bl/6 mutant mice were developed and provided by Dr. David Ginty as previously described 50. -BDNF fl/fl C57bl/6 mice were developed and provided by Dr. Luis Parada as previously described 60.
Wild animals	Study did not involve wild animals.
Field-collected samples	Study did not involve samples collected from the field.