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Reporting Summary

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For	all st	tatistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.
n/a	Coi	nfirmed
	×	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
x		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 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

For MRI data, ParaVision®5 - Bruker, Germany Data collection

For calcium, AcqKnowledge Acquisition & Analysis Software, BIOPAC system (MP150 System, BIOPAC Systems, USA).

Data analysis AFNI(Analysis of Functional NeuroImages), NIH

MATLABR2016a

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 can be provided upon email request to the corresponding author. Excel files are included for each quantitative plot included in main figures. Source data underlying Figs 2F, 4C, 5C, 5E, 5G, 5H and 5I are provided as a Source Data file. The data presented in the figures and other summary level data are contained within the Supplementary Files.

Field-spe	cific repo	orting
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.		
x Life sciences	Behav	ioural & social sciences
For a reference copy of t	he document with all sect	tions, see nature.com/documents/nr-reporting-summary-flat.pdf
Life scier	nces stud	y design
All studies must dis	close on these point	ts even when the disclosure is negative.
Sample size	A total of 37 male Sp	rague–Dawley rats were used in this study. P19
Data exclusions	For rats died during t	the middle of fMRI experiments or low expression of virus, the data were not included for analysis.
Replication	Yes. See Figure 2 and	5.
Randomization	N/A	
Blinding	N/A	
Reportin	g for spec	cific materials, systems and methods
		some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material,
		study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.
	perimental syste	
n/a Involved in th	•	n/a Involved in the study ChIP-seq
x Eukaryotic		Flow cytometry
x Palaeontol	ogy	MRI-based neuroimaging
Animals an	d other organisms	
	earch participants	
Clinical dat	a	
Animals and	other organi	isms
Policy information	about <u>studies involv</u>	ing animals; ARRIVE guidelines recommended for reporting animal research
Laboratory anima	A total of 37 male Sprague—Dawley rats were used in this study. P19	
Wild animals	N/A	
Field-collected sa	amples N/A	
Ethics oversight All surgical and experimental procedures reported in this paper were approved by the local authorities (Regierungspraesidi		
		en Referat 35, Veterinärwesen, Leiter Dr. Maas) and were in full compliance with the guidelines of the European inity (EUVD 86/609/EEC) for the care and use of laboratory animals. P19
Note that full information on the approval of the study protocol must also be provided in the manuscript.		
Magnetic re	conanco ima	ging
Magnetic resonance imaging Experimental design		
•	Experimental design Design type Task, Block design	
Design specifications P25		

N/A

Behavioral performance measures

Acquisition			
Imaging type(s)	P24-25		
Field strength	P24, 14 T		
Sequence & imaging parameters	P24-25		
Area of acquisition	P24-25, a whole brain scan and images for individual arterioles and venules in rat hippocampus were used.		
Diffusion MRI Used	X Not used		
Preprocessing			
Preprocessing software	AFNI, P26		
Normalization	Included in the standard AFNI code.		
Normalization template	Included in the standard AFNI code.		
Noise and artifact removal	Included in the standard AFNI code.		
Volume censoring	N/A		
Statistical modeling & inference			
Model type and settings	Included in the standard AFNI code.		
Effect(s) tested	N/A		
Specify type of analysis: Whole	brain ROI-based 🗷 Both		
Anatomica	al location(s) Hippocampus and barrel cortex. Based on brain atlas (Paxinos&Watson), sixth edition.		
Statistic type for inference (See <u>Eklund et al. 2016</u>)	Cluster-wise (>20 voxels). Detailed p-values are included.		
Correction	FDR based correction.		
Models & analysis			
n/a Involved in the study			
Anatomica Statistic type for inference (See Eklund et al. 2016) Correction Models & analysis	Cluster-wise (>20 voxels). Detailed p-values are included. FDR based correction.		

ı/a	Involved in the study	
X	Functional and/or effective connectivity	
X	Graph analysis	
X	Multivariate modeling or predictive analysi	