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Supplementary Figures: 10

Supplementary Tables: 2

Supplementary Videos: NA

Reporting Checklist for Nature Neuroscience

This checklist is used to ensure good reporting standards and to improve the reproducibility of published results. For more information, please read Reporting Life Sciences Research.

Please note that in the event of publication, it is mandatory that authors include all relevant methodological and statistical information in the manuscript.

Statistics reporting, by figure

- Please specify the following information for each panel reporting quantitative data, and where each item is reported (section, e.g. Results, & paragraph number).
- Each figure legend should ideally contain an exact sample size (n) for each experimental group/condition, where n is an exact number and not a range, a clear definition of how n is defined (for example x cells from x slices from x animals from x litters, collected over x days), a description of the statistical test used, the results of the tests, any descriptive statistics and clearly defined error bars if applicable.
- For any experiments using custom statistics, please indicate the test used and stats obtained for each experiment.
- Each figure legend should include a statement of how many times the experiment shown was replicated in the lab; the details of sample collection should be sufficiently clear so that the replicability of the experiment is obvious to the reader.
- For experiments reported in the text but not in the figures, please use the paragraph number instead of the figure number.

Note: Mean and standard deviation are not appropriate on small samples, and plotting independent data points is usually more informative. When technical replicates are reported, error and significance measures reflect the experimental variability and not the variability of the biological process; it is misleading not to state this clearly.

		TEST USED		n			DESCRIPTIVE STATS (AVERAGE, VARIANCE)		P VALUE		DEGREES OF FREEDOM & F/t/z/R/ETC VALUE	
	FIGURE NUMBER	WHICH TEST?	SECTION & PARAGRAPH #	EXACT VALUE	DEFINED?	SECTION & PARAGRAPH #	REPORTED?	SECTION & PARAGRAPH #	EXACT VALUE	SECTION & PARAGRAPH #	VALUE	SECTION & PARAGRAPH #
example	1a	one-way ANOVA	Fig. legend	9, 9, 10, 15	mice from at least 3 litters/group	Methods para 8	error bars are mean +/- SEM	Fig. legend	p = 0.044	Fig. legend	F(3, 36) = 2.97	Fig. legend
example	results, para 6	unpaired t-test	Results para 6	15	slices from 10 mice	Results para 6	error bars are mean +/- SEM	Results para 6	p = 0.0006	Results para 6	t(28) = 2.808	Results para 6

		TEST USED		n			DESCRIPTIVE STATS (AVERAGE, VARIANCE)		P VALUE		DEGREES OF FREEDOM & F/t/z/R/ETC VALUE	
	FIGURE NUMBER	WHICH TEST?	SECTION & PARAGRAPH #	EXACT VALUE	DEFINED?	SECTION & PARAGRAPH #	REPORTED?	SECTION & PARAGRAPH #	EXACT VALUE	SECTION & PARAGRAPH #	VALUE	SECTION & PARAGRAPH #
+ -	1d	rank sum test	Results	data: 9803 shuffle: 9803*5000	9803 out of 9818 candidate events during eight Sleep1 epoch produce real number correlation values (see Methods)	Methods	median	Results	top: p=0.08 bottom: p=1	Results		
+ -	2c	rank sum test	Figure legends	9818 vs. 4438	number of candidate events during eight Sleep1 epoch and Run 1 epoch	Methods	median, SEM	Figure legends	p<10^-10	Figure legends		
+ -	3, 4e-g, 5c, 6e-g,7,S8d,S9	shuffle test	Figure legends	5000 times the number of candidate events reported	Candidate events from 8 recording sessions from 4 rats	Methods			on Figure			
+ -	5a	rank sum test	Figure legends	sal vs. cpp: 10081 vs. 10291 for Run 1;11745 vs. 12238 for Run2;11338 vs. 12667 for Run3	Decoded time bins from 7 saline and 7 cpp recording sessions from 4 rats	Figure legends	median, SEM	Figure legends	p=0.0837 for Run1; p=0.4171 for Run2; p=0.0704 for Run3	Figure legends		
+ -	8a	rank sum test	Figure legends	56	Rate of trajectory events in every 5 minutes during 45min of Sleep3 from 7 saline and 7 cpp recording sessions of 4 rats	Figure legends	median, SEM		p=0.0742 for track1; p=1.73*10^-4 for track2; p=1.22*10^-11 for track3	Figure lengends		
+ -	S9	rank sum test	Figure legends	sal vs. cpp: 10081 vs. 10291 for Run 1;11745 vs. 12238 for Run2;11338 vs. 12667 for Run3	Decoded time bins from 7 saline and 7 cpp recording sessions from 4 rats	Figure legends	median, SEM	Figure legends	p=0.0837 for Run1; p<10^-10 for Run2 and Run3	Figure legends		
+ -	S3	Kruskal-Wallis test	Figure legends	787 place fields (remapping: 72 place cells)	Number of place cells from 7 saline recording sessions from 4 rats	Figure legends	H	Figure legends	Firing rate: p=0.1514; Remapping: p=2.785*10^-10; Place field size: p=0.0793; Sparsity: p=0.5593	Figure legends	Firing rate: H(2)=4.98; Remapping: H(5)=53.4; Place field size: H(2)=5.07; Sparsity: H(2)=1.16	Figure legends

+ -	S7	Kruskal-Wallis test	Figure legends	742 place fields (remapping: 70) place cells	Number of place cells from 7 cpp recording sessions from 4 rats	Figure legends	H	Figure legends	Firing rate: p=0.083; Remapping: p=9.732*10^-10; Place field size: p=0.0329; Sparsity: p<10^-10	Figure legends	Firing rate: H(2)=3.78; Remapping: H(5)=50.75; Place field size: H(2)=6.83; Sparsity: H(2)=155.24	Figure legends
+ -	S2	Kruskal-Wallis test	Figure legends	7 recording sessions, 3 different runs for each	7 recording sessions, 3 different runs for each	Figure legends	H	Figure legends	p=0.39 for saline; p=0.13 for D-CPPene	Figure legends	H(2)=1.87 for saline; H(2)=4.01 for D-CPPene	Figure legends
+ -	S4-a	rank sum test	Figure legends	data: 8310 shuffle: 8310*5000	8310 out of 9818 candidate events during eight Sleep1 epoch produce real number correlation values when down sample to 15 cells (see Methods)	Figure legends	median	Figure legends	top: p=0.75 bottom: p<1			
+ -	1d	Levene's test	Results	data: 9803 shuffle: 9803*5000	9803 out of 9818 candidate events during eight Sleep1 epoch produce real number correlation values (see Methods)	Methods			top:p=0.44 bottom: p=0.77	Results		
+ -	1d	Kolmogorov-Smirnov test	Results	data: 9803 shuffle: 9803*5000	9803 out of 9818 candidate events during eight Sleep1 epoch produce real number correlation values (see Methods)	Methods			top: p=0.122 bottom: p=0.998	Results		
+ -	1d	Monte-Carlo P-Value	Results	data: 9803 shuffle: 9803*5000	9803 out of 9818 candidate events during eight Sleep1 epoch produce real number correlation values (see Methods)	Methods			top: p>0.1 bottom: p>0.9	Results		
+ -	S4-a	Kolmogorov-Smirnov test	Figure legends	data: 8310 shuffle: 8310*5000	8310 out of 9818 candidate events during eight Sleep1 epoch produce real number correlation values when down sample to 15 cells (see Methods)	Methods			left: p=0.81 right: p=1	Results		
+ -	S4-a	Monte-Carlo P-Value	Figure legends	data: 8310 shuffle: 8310*5000	8310 out of 9818 candidate events during eight Sleep1 epoch produce real number correlation values when down sample to 15 cells (see Methods)	Methods			left: p>0.4 right: p=1	Figure legends		

+ -	S4-c	Kolmogorov -Smirnov test	Figure legends	data: 8051 shuffle: 8051*5000	8051 out of 9818 candidate events during eight Sleep1 epoch produce real number correlation values when using down-sampled cells with Lratio less than or equal to median value (see Methods)	Methods			left: p=0.6 right: p=1	Figure legends		
+ -	S4-c	Kolmogorov -Smirnov test	Figure legends	data: 8051 shuffle: 8051*5000	8051 out of 9818 candidate events during eight Sleep1 epoch produce real number correlation values when using down-sampled cells with Lratio less than or equal to median value (see Methods)	Methods			left: p>0.1 right: p=1	Figure legends		
+ -	S4-c	ranksum test	Figure legends	data: 8051 shuffle: 8051*5000	8051 out of 9818 candidate events during eight Sleep1 epoch produce real number correlation values when using down-sampled cells with Lratio less than or equal to median value (see Methods)	Methods	meidan	Figure legends	left: p=0.4 right: p=1	Figure legends		

Representative figures

1. Are any representative images shown (including Western blots and immunohistochemistry/staining) in the paper?

   If so, what figure(s)?

Figure 1b, 4a, S1, S3 are representative place fields from individual recording sessions.
Figure 1c is an individual candidate event.
Figure 2a,b, 4b, 4c, 4d, 5b, 6b, 6c, 6d, 7, S7c are decoding example of trajectory events from individual recording sessions.

2. For each representative image, is there a clear statement of how many times this experiment was successfully repeated and a discussion of any limitations in repeatability?

   If so, where is this reported (section, paragraph #)?

Yes. Group data results are described immediately following the description of the representative data in the manuscript.

Statistics and general methods

1. Is there a justification of the sample size?

   If so, how was it justified?

   Where (section, paragraph #)?

   Even if no sample size calculation was performed, authors should report why the sample size is adequate to measure their effect size.

Firstly, we examined hippocampal replay while the animal explored a novel environment, under which abundant hippocampal replays has been reported (Foster and Wilson 2006). Also our high density recording technique allows us to accurately track representation change of neuronal activities between conditions (before or after experience, and drug versus saline). Additionally, we adopted a simple spatial task such that an individual animal's behavior was not significantly different with others.

2. Are statistical tests justified as appropriate for every figure? Where (section, paragraph #)?	Yes. All statistical methods are explained in the figure legends and/or in the methods section.
a. If there is a section summarizing the statistical methods in the methods, is the statistical test for each experiment clearly defined?	Yes.
b. Do the data meet the assumptions of the specific statistical test you chose (e.g. normality for a parametric test)? Where is this described (section, paragraph #)?	Yes. Monte-carlo simulations are as described in the manuscript. Non-parametric tests, e.g. Wilcoxon Rank Sum test and Kruskal-Wallis test, are also used as the data does not meet the assumption of normality.
c. Is there any estimate of variance within each group of data? Is the variance similar between groups that are being statistically compared? Where is this described (section, paragraph #)?	Our shuffle procedure, e.g. Monte-carlo simulation directly estimates the expected replays by chance, where the variance can be accessed though its distribution. The shuffle method is described in detail in the Methods section.
d. Are tests specified as one- or two-sided?	NA
e. Are there adjustments for multiple comparisons?	NA
3. Are criteria for excluding data points reported? Was this criterion established prior to data collection? Where is this described (section, paragraph #)?	No data points were excluded.
4. Define the method of randomization used to assign subjects (or samples) to the experimental groups and to collect and process data. If no randomization was used, state so. Where does this appear (section, paragraph #)?	All animals underwent all the relevant conditions in a balanced manner, e.g. pre-drug and post-drug epochs within each recording day, and saline and drug conditions on different days with the sequence balanced and/or repeated.
5. Is a statement of the extent to which investigator knew the group allocation during the experiment and in assessing outcome included? If no blinding was done, state so. Where (section, paragraph #)?	NA. no blinding.
6. For experiments in live vertebrates, is a statement of compliance with ethical guidelines/regulations included? Where (section, paragraph #)?	Methods paragraph 1.
7. Is the species of the animals used reported? Where (section, paragraph #)?	Species reported in abstract, as well as in Methods.
8. Is the strain of the animals (including background strains of KO/transgenic animals used) reported? Where (section, paragraph #)?	NA

9. Is the sex of the animals/subjects used reported?

   Where (section, paragraph #)?

   Methods paragraph 1. Male.

10. Is the age of the animals/subjects reported?

    Where (section, paragraph #)?

    Methods paragraph 1. 10-20 weeks old.

11. For animals housed in a vivarium, is the light/dark cycle reported?

    Where (section, paragraph #)?

    No. Standard (e.g. non-reversed, 12h cycle was used).

12. For animals housed in a vivarium, is the housing group (i.e. number of animals per cage) reported?

    Where (section, paragraph #)?

    No. Single housing is standard for implantation experiments.

13. For behavioral experiments, is the time of day reported (e.g. light or dark cycle)?

    Where (section, paragraph #)?

    Time of day was approximately the same each session, and during the day, as standard.

14. Is the previous history of the animals/subjects (e.g. prior drug administration, surgery, behavioral testing) reported?

    Where (section, paragraph #)?

    Yes. Sleep 1 and Run 1 data are all prior to drug administration and are compared throughout all figures.

    a. If multiple behavioral tests were conducted in the same group of animals, is this reported?

       Where (section, paragraph #)?

       NA. All animals underwent the same behavioral tests.

15. If any animals/subjects were excluded from analysis, is this reported?

    Where (section, paragraph #)?

    NA

    a. How were the criteria for exclusion defined?

       Where is this described (section, paragraph #)?

       NA

    b. Specify reasons for any discrepancy between the number of animals at the beginning and end of the study.

       Where is this described (section, paragraph #)?

       NA

Reagents

1. Have antibodies been validated for use in the system under study (assay and species)?

   NA

   a. Is antibody catalog number given?

      Where does this appear (section, paragraph #)?

      NA

b. Where were the validation data reported (citation, supplementary information, Antibodypedia)?

Where does this appear (section, paragraph #)?

NA

2. Cell line identity

a. Are any cell lines used in this paper listed in the database of commonly misidentified cell lines maintained by ICLAC and NCBI Biosample?

Where (section, paragraph #)?

NA

b. If yes, include in the Methods section a scientific justification of their use--indicate here in which section and paragraph the justification can be found.

NA

c. For each cell line, include in the Methods section a statement that specifies:

- the source of the cell lines
- have the cell lines been authenticated? If so, by which method?
- have the cell lines been tested for mycoplasma contamination?

Where (section, paragraph #)?

NA

Data deposition

Data deposition in a public repository is mandatory for:

a. Protein, DNA and RNA sequences
b. Macromolecular structures
c. Crystallographic data for small molecules
d. Microarray data

Deposition is strongly recommended for many other datasets for which structured public repositories exist; more details on our data policy are available here. We encourage the provision of other source data in supplementary information or in unstructured repositories such as Figshare and Dryad.

We encourage publication of Data Descriptors (see Scientific Data) to maximize data reuse.

1. Are accession codes for deposit dates provided?

Where (section, paragraph #)?

NA

Computer code/software

Any custom algorithm/software that is central to the methods must be supplied by the authors in a usable and readable form for readers at the time of publication. However, referees may ask for this information at any time during the review process.

1. Identify all custom software or scripts that were required to conduct the study and where in the procedures each was used.

We use Matlab to analyze all the spikes and LFP data acquired during each recording session. We carefully explained and referenced the algorithms in the methods section.

2. If computer code was used to generate results that are central to the paper's conclusions, include a statement in the Methods section under "**Code availability**" to indicate whether and how the code can be accessed. Include version information as necessary and any restrictions on availability.	Matlab programs can be provided upon request.

Human subjects

1. Which IRB approved the protocol? Where is this stated (section, paragraph #)?	NA
2. Is demographic information on all subjects provided? Where (section, paragraph #)?	NA
3. Is the number of human subjects, their age and sex clearly defined? Where (section, paragraph #)?	NA
4. Are the inclusion and exclusion criteria (if any) clearly specified? Where (section, paragraph #)?	NA
5. How well were the groups matched? Where is this information described (section, paragraph #)?	NA
6. Is a statement included confirming that informed consent was obtained from all subjects? Where (section, paragraph #)?	NA
7. For publication of patient photos, is a statement included confirming that consent to publish was obtained? Where (section, paragraph #)?	NA

fMRI studies

For papers reporting functional imaging (fMRI) results please ensure that these minimal reporting guidelines are met and that all this information is clearly provided in the methods:

1. Were any subjects scanned but then rejected for the analysis after the data was collected?	NA
a. If yes, is the number rejected and reasons for rejection described? Where (section, paragraph #)?	NA

2. Is the number of blocks, trials or experimental units per session and/or subjects specified? Where (section, paragraph #)?	NA
3. Is the length of each trial and interval between trials specified?	NA
4. Is a blocked, event-related, or mixed design being used? If applicable, please specify the block length or how the event-related or mixed design was optimized.	NA
5. Is the task design clearly described? Where (section, paragraph #)?	NA
6. How was behavioral performance measured?	NA
7. Is an ANOVA or factorial design being used?	NA
8. For data acquisition, is a whole brain scan used? If not, state area of acquisition.	NA
a. How was this region determined?	NA
9. Is the field strength (in Tesla) of the MRI system stated?	NA
a. Is the pulse sequence type (gradient/spin echo, EPI/spiral) stated?	NA
b. Are the field-of-view, matrix size, slice thickness, and TE/TR/flip angle clearly stated?	NA
10. Are the software and specific parameters (model/functions, smoothing kernel size if applicable, etc.) used for data processing and pre-processing clearly stated?	NA
11. Is the coordinate space for the anatomical/functional imaging data clearly defined as subject/native space or standardized stereotaxic space, e.g., original Talairach, MNI305, ICBM152, etc? Where (section, paragraph #)?	NA
12. If there was data normalization/standardization to a specific space template, are the type of transformation (linear vs. nonlinear) used and image types being transformed clearly described? Where (section, paragraph #)?	NA
13. How were anatomical locations determined, e.g., via an automated labeling algorithm (AAL), standardized coordinate database (Talairach daemon), probabilistic atlases, etc.?	NA

14. Were any additional regressors (behavioral covariates, motion etc) used?	NA
15. Is the contrast construction clearly defined?	NA
16. Is a mixed/random effects or fixed inference used?	NA
a. If fixed effects inference used, is this justified?	NA
17. Were repeated measures used (multiple measurements per subject)?	NA
a. If so, are the method to account for within subject correlation and the assumptions made about variance clearly stated?	NA
18. If the threshold used for inference and visualization in figures varies, is this clearly stated?	NA
19. Are statistical inferences corrected for multiple comparisons?	NA
a. If not, is this labeled as uncorrected?	NA
20. Are the results based on an ROI (region of interest) analysis?	NA
a. If so, is the rationale clearly described?	NA
b. How were the ROI's defined (functional vs anatomical localization)?	NA
21. Is there correction for multiple comparisons within each voxel?	NA
22. For cluster-wise significance, is the cluster-defining threshold and the corrected significance level defined?	NA

Additional comments

Additional Comments	NA