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Supplementary Videos: 0

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	Wilcoxon signed rank test, two-sided	Fig. legend and Results para 1	29	sessions in 5 mice	Fig. legend and Results para 1	error bars are mean +/- SEM; raw values are shown with superimposed grey lines	Fig. legend, Fig. 1d	P = 0.0006	Fig. legend and Results para 1	Z = -3.43	
+ -	2c	Kruskall Wallis one-way analysis of variance followed by Tukey's post-hoc tests	Fig. legend	531	place cells	Fig. legend; # of cells for each distance point is shown on the graph	Boxplots showing median and data dispersion (min and max values)	Fig. legend, Fig. 2c	P = 2.4e-64; post hoc tests P<0.001 for all comparisons to illuminated shank; P>0.05 for the others	Fig. legend	chi-square = 303 df = 530	
+ -	2g	Kruskall Wallis test followed by Tukey's post-hoc tests	Fig. legend	283, 81, 167	control, delayed, silenced place cells	Fig. legend	Boxplots showing median and data dispersion (min and max values)	Fig. legend, Fig. 2h	P = 2.6e-78	Fig. legend	chi-square = 357.3 df = 530	
+ -	3d	Kruskall Wallis test followed by Tukey's post-hoc tests	Fig. legend and Results para 3	283, 81, 167	control, delayed, silenced place cells	Fig. legend	Cumulative distribution	Results	Kruskall Wallis: P = 0.002; post-hoc tests: silenced vs control: P = 0.008; delayed vs control: P = 0.62; silenced vs delayed: P = 0.007	Fig. legend and Results	chi-square = 12.35 df = 530	
+ -	3e	Chi square test followed by two-sided Fisher's exact tests with Bonferroni correction	Fig. legend and Results para 3	283, 81, 167	control, delayed, silenced place cells	# of cells with or without overlapping place fields also shown in Fig. 3e and in Results	Proportions from contingency data with raw # of cells in each group displayed in the figure	Fig. 3e	chi square test on the 3 groups: P = 5.8e-4; post-hoc Fisher's exact tests: P = 0.004 (control vs silenced); P = 0.04 (delayed vs silenced); P = 1 (control vs delayed)	Fig. legend and Results	chi-square = 11.85 df = 2	
+ -	4a	Wilcoxon signed rank test, two-sided	Fig. legend and Results para 6	283	control place cells	Fig. legend and Results	Full distribution is shown in dot plot (except one outlier included in statistical analysis)	Fig. 4a legend	P = 0.007	Fig. legend and Results	Z = -2.70	
+ -	4b	Wilcoxon signed rank test, two-sided	Fig. legend	81	delayed silenced place cells	Fig. legend	Full distribution is shown in dot plot	Fig. 4b legend	P = 0.13	Fig. legend	Z = -1.50	

+ -	4c	Wilcoxon signed rank test, two-sided	Fig. legend and Results para 6	167	silenced place cells	Fig. legend and Results	Full distribution is shown in dot plot (except one outlier included in statistical analysis)	Fig. 4c legend	P = 0.86	Fig. legend and Results	Z = -0.17	
+ -	5e	Kruskall Wallis test followed by Tukey's post-hoc tests	Fig. legend and Results para 7	24, 6, 16	ensembles of control, delayed and silenced place cells	Fig. legend and Results	Full distribution is shown in dot plot; superimposed bars represent mean +/- SEM	Fig. 5e, Results	Kruskall Wallis: P = 0.009; Post-hoc tests: silenced vs control: P = 0.01; delayed vs control: P = 0.94; silenced vs delayed: P = 0.07	Fig. legend and Results	chi-square = 0.009 df = 45	
+ -	6b	Wilcoxon signed rank test, two-sided	Fig. legend and Results para 8	6, 15	Pairs of simultaneously recorded control-delayed ensembles; pairs of control-silenced ensembles	Fig. legend and Results	error bars are mean +/- SEM; raw values are shown with superimposed grey lines	Fig. 6b legend	P = 0.84 (control-delayed pairs); P = 0.015 (control-silenced pairs)	Fig. legend and Results	Ctrl-Silenced pairs: signed rank = 102; Ctrl-delayed pairs: signed rank = 9	
+ -	6c	Mann and Whitney U test	Fig. legend and Results para 8	6, 15	Differences values calculated for simultaneously recorded ensembles	Fig. legend and Results	Full distribution is shown in dot plot; superimposed bars represent mean +/- SEM	Fig. 6c legend	P = 0.047	Fig. legend and Results	Z = -1.99	
+ -	Supp 5c	Mann and Whitney U test	Fig. legend	19, 32	control and silenced pyramidal cells	Fig. legend	boxplots showing median and data dispersion (min and max values)	Supp Fig. 3c legend	P = 1.7e-7	Fig. legend	Z = 5.23	
+ -	Supp 10a	Chi-square test	Fig. legend	460, 129, 273	control, delayed and silenced pyramidal cells	Fig. legend	Proportions from contingency data with raw cell counts in legend	Fig. legend	P = 0.56	Fig. legend	df = 2 chi-square = 1.17	
+ -	Supp 10b	Kruskall Wallis test	Fig. legend	283, 81, 167	control, delayed, silenced place cells	Fig. legend	Cumulative distribution	Supp Fig. 4b legend	P = 0.67	Fig. legend	df = 1061 chi-square = 3.23	
+ -	Supp 10c	Kruskall Wallis test	Fig. legend	283, 81, 167	control, delayed, silenced place cells	Fig. legend	Cumulative distribution	Supp Fig. 4c legend	P = 0.41	Fig. legend	df = 1061 chi-square = 5.08	
+ -	Supp 10d	Chi-square tests	Fig. legend	460, 129, 273	control, delayed and silenced pyramidal cells	Fig. legend	Proportions from contingency data combined for all recorded cells in each group per exploration epoch	Supp Fig. 4d	P = 0.84 (control); P = 0.90 (delayed); P = 0.61 (silenced)	Fig. legend	df = 1; chi2 = 0.04 (control); chi2 = 0.02 (delayed); chi2 = 0.27 (silenced)	
+ -	Supp 10e	Chi-square test	Fig. legend	276, 79, 149	place cells in pre-exploration epoch from control, delayed and silenced groups	Fig. legend	Proportions from contingency data combined for all recorded cells in the 3 groups	Supp Fig. 4e	P = 0.76	Fig. legend	df = 2 chi-square = 0.56	
+ -	Supp 10f	Chi-square test	Fig. legend	273, 80, 155	place cells in post-exploration epoch from control, delayed and silenced groups	Fig. legend	Proportions from contingency data combined for all recorded cells in the 3 groups	Supp Fig. 4f	P = 0.13	Fig. legend	df = 2 chi-square = 4.02	
+ -	Supp 12a	Wilcoxon signed rank test, two-sided	Fig. legend	6	pairs of control-delayed ensembles	Fig. legend	error bars are mean +/- SEM; raw values are shown with superimposed grey lines	Supp Fig. 6a legend	P = 0.84	Fig. legend	signed rank = 10	

+ -	Supp 12b	Wilcoxon signed rank test, two-sided	Fig. legend	15	pairs of control-silenced ensembles	Fig. legend	error bars are mean +/- SEM; raw values are shown with superimposed grey lines	Supp Fig. 6b legend	P = 0.02	Fig. legend	signed rank = 100	
+ -	Supp 12c	Mann-Whitney U test	Fig. legend	6 , 15	Difference values computed for pairs of ensembles	Fig. legend	Full distribution is shown in dot plot; superimposed bars represent mean +/- SEM	Supp Fig. 6c legend	P = 0.047	Fig. legend	Z = -1.99	
+ -	Supp 9a	Mann-Whitney U test	Fig. legend	240, 377	"ripple-delayed" and "ripple-locked" place cells with identifiable light-response	Fig. legend	Boxplots showing median and data dispersion (min and max values)	Fig. legend	P = 0.07	Fig. legend	Z = -1.83	
+ -	Supp 9b	Chi-square test	Fig. legend	369, 601	"ripple-delayed" and "ripple-locked" PYR cells	Fig. legend	Contingency data with raw cell counts in legend	Fig. legend	P = 0.22	Fig. legend	chi-square = 1.54 df = 1	
+ -	Supp 9c	Kruskall Wallis test	Fig. legend	247, 385	"ripple-delayed" and "ripple-locked" place cells	Fig. legend	Cumulative distribution	Fig. legend	P = 0.92	Fig. legend	df = 1263 chi-square = 0.49	
+ -	Supp 9d	Kruskall Wallis test	Fig. legend	247, 385	"ripple-delayed" and "ripple-locked" place cells	Fig. legend	Cumulative distribution	Fig. legend	P = 0.59	Fig. legend	df = 1263 chi-square = 1.9	
+ -	Supp 9e	Chi-square tests	Fig. legend	369, 601	"ripple-delayed" and "ripple-locked" PYR cells	Fig. legend	Contingency data		P = 0.64 (delayed); P = 0.86 (locked)	Fig. legend	delayed: chi-square = 0.21 ,df = 1; locked: chi-square = 0.03, df = 1	
+ -	Supp 9f	Wilcoxon signed rank test, two-sided	Fig. legend	247	"ripple-delayed" place cells	Fig. legend	Full distribution is shown in dot plot (except one outlier included in statistical analysis)		P = 6.6e-5	Fig. legend	Z = -3.99	
+ -	Supp 9g	Wilcoxon signed rank test, two-sided	Fig. legend	385	"ripple-locked" place cells	Fig. legend	Full distribution is shown in dot plot (except two outliers included in statistical analysis)		P = 0.49	Fig. legend	Z = -0.69	
+ -	Supp 9h	Mann-Whitney U test	Fig. legend and Results	247, 385	"ripple-delayed" and "ripple-locked" place cells	Fig. legend and Results	Cumulative curve	Fig. legend	P = 0.007	Fig. legend and Results	Z = 2.71	
+ -	Supp 9i	Pearson's test	Fig. legend	240, 377	"ripple-delayed" and "ripple-locked" place cells with identifiable light-response	Fig. legend	Full distributions are shown in dot plots	Supp. Fig. 7i	P = 0.2 for ripple-locked and ripple-delayed units	Fig. legend	R = -0.09 (delayed) and R = 0.07 (locked)	Fig. legend
+ -	Supp 9j	Chi-square test	Fig. legend	247, 385	"ripple-delayed" and "ripple-locked" place cells	Fig. legend	Contingency data combined for all recorded cells in the 3 groups: raw number of cells in each group in the figure	Supp. Fig. 7j	P = 0.07	Fig. legend	chi-square = 3.21 df = 1	
+ -	Supp 9k	Mann-Whitney U test	Fig. legend	74, 166	"ripple-delayed" place cells (no ov, ov) - identifiable light response	Fig. legend	Boxplots showing median and data dispersion (min and max values)	Fig. legend	P = 0.58	Fig. legend	Z = 0.55	
+ -	Supp 9l	Mann-Whitney U test	Fig. legend	140, 237	"ripple-locked" place cells (no ov, ov) - identifiable light response	Fig. legend	Boxplots showing median and data dispersion (min and max values)	Fig. legend	P = 0.005	Fig. legend	Z = -2.76	

+ -	Supp 9o	Mann-Whitney U test	Fig. legend	12, 19	"ripple-delayed" and "ripple-locked" ensembles of place cells	Fig. legend and Results	Full distribution is shown in dot plot; superimposed bars represent mean +/- SEM	Fig. legend	P = 0.009	Fig. legend and Results	Z = 2.62	
+ -	Supp 15a	Kruskall Wallis test	Fig. legend	283, 81, 167	control, delayed, silenced place cells	Fig. legend	Full distribution is shown in dot plot	Supp. Fig. 8a	P = 0.02	Fig. legend	df = 1061 chi-square = 14.05	
+ -	Supp 15b	Kruskall Wallis test	Fig. legend	272, 80, 153	control place cells with place fields both in pre and post	Fig. legend	Full distribution is shown in dot plots	Supp. Fig. 8b legend	P = 0.09 (i) P = 0.07 (ii) P = 0.08 (iii)	Fig. legend	df = 1035, chi-square = 9.98(i); 10.85(ii), 10.74(iii)	
+ -	Supp 7a	Wilcoxon signed-rank	Fig. legend	7 sessions	sessions with ripple-delayed paradigms only	Fig. legend	All individual data points are shown with blue lines	Supp. Fig. 9a legend	P = 0.05	Fig. legend	signed rank = 2	
+ -	Supp 7b	Wilcoxon signed-rank	Fig. legend	13 sessions	sessions with ripple-locked paradigms only	Fig. legend	All individual data points are shown with green lines	Supp. Fig. 9b legend	P = 0.08	Fig. legend	signed rank = 20	
+ -	Supp 7d	Mann-Whitney U test	Fig. legend	7, 13	sessions with ripple-delayed or locked paradigms	Fig. legend	All individual data points are shown	Supp. Fig. 9d	P = 0.70	Fig. legend	Z = 0.40	
+ -	Supp 7e	Mann-Whitney U test with Bonferroni correction	Fig. legend	7,13	sessions with ripple-delayed or locked paradigms	Fig. legend	Lines with shaded areas show mean ± SEM		P>0.5 for all trials	Fig. legend		
+ -	Supp 4	Pearson's test	Fig. legend	81, 167	delayed and silenced place cells	Fig. legend	Full distributions are shown in dot plots	Supp. Fig. 11	P = 0.70 (delayed) and 1.16e-05 (silenced)	Fig. and fig legend	r = 0.04 (delayed) and 0.34 (silenced)	
+ -	Supp 11a	Kruskall Wallis test	Fig. legend	283, 81, 167	control, delayed, silenced place cells	Fig. legend	Boxplots showing median and data dispersion (min and max values)		P = 0.90	Fig. and fig legend	df = 530, chi-square = 11.52	
+ -	Supp 11b	Kruskall Wallis test	Fig. legend	283, 81, 167	control, delayed, silenced place cells	Fig. legend	Boxplots showing median and data dispersion (min and max values)		P = 0.17	Fig. and legend	df = 530, chi-square = 3.53	
+ -	Supp 11c	Pearson's tests	Fig. legend	531, 283, 81, 167	all, control, delayed, silenced place cells	Fig. legend	Full distributions are shown in dot plots	Supp. Fig. 12c and legend	P = 0.16(all), 0.85(control), 0.17(delayed), 0.05(silenced)	Fig. and legend	r = -0.06(all), 0.01(control), -0.15(delayed), -0.15(silenced)	
+ -	Supp 11d	Pearson's tests	Fig. legend	531, 283, 81, 167	all, control, delayed, silenced place cells	Fig. legend	Full distributions are shown in dot plots	Supp. Fig. 12d and legend	P = 0.91(all), 0.99(control), 0.86(delayed), 0.51(silenced)	Fig. and legend	r = 0(all), 0(control), -0.02(delayed), 0.05(silenced)	
+ -	Supp 2a	Kruskall Wallis test	Fig. legend	264, 81, 135	control, delayed, silenced place cells	Fig. legend	Cumulative curve		P = 0.01	Fig. and fig legend	df = 479, chi-square = 8.41	
+ -	Supp 2b	Chi-square test	Fig. legend	264, 81, 135	control, delayed, silenced place cells	Fig. and legend	Contingency data combined for all recorded cells in the 3 groups: raw number of cells in each group in the figure	Supp. Fig. 13b	P = 0.002	Fig. legend	chi-square = 9.31, df = 2	
+ -	Supp 2c	Wilcoxon signed-rank	Fig. legend	264	control place cells	Fig. legend	Full distributions are shown in dot plots	Supp. Fig. 13c	P = 0.009	Fig. and legend	signed rank = 14242	
+ -	Supp 2d	Wilcoxon signed-rank	Fig. legend	81	delayed place cells	Fig. legend	Full distributions are shown in dot plots	Supp. Fig. 13d	P = 0.13	Fig. and legend	signed rank = 1341	
+ -	Supp 2e	Wilcoxon signed-rank	Fig. legend	135	silenced place cells	Fig. legend	Full distributions are shown in dot plots	Supp. Fig. 13e	P = 0.91	Fig. and legend	signed rank = 4539	

+ -	Supp 2f	Kruskall Wallis test	Fig. legend	21, 6, 13	ensembles of control, delayed, silenced place cells	Fig. legend	All individual data points are shown		P = 0.024	Fig. and legend	df = 39, chi-square = 7.46	
+ -	Supp 2g	Mann-Whitney U test	Fig. legend	6, 12	pairs of control-delayed ensembles, pairs of control-silenced ensembles	Fig. legend	All individual data points are shown	Supp. Fig. 13g	P = 0.03	Fig. and legend	ranksum: 91	
+ -	Supp 13a	Mann-Whitney U test with Bonferroni correction	Fig. legend	10, 29	sessions with cued or non-cued versions of the task	Fig. legend	Lines with shaded areas show mean ± SEM		P<0.05 for trials marked with black dot	Fig. and legend		
+ -	Supp 13b	Kruskall Wallis test and Tukey's post-hoc tests	Fig. legend	121, 72, 283, 167, 81	control place cells in cued version, silenced in cued version, control in non-cued version, silenced in non-cued, delayed in non-cued	Fig. and legend	Cumulative distributions for the 5 groups		P = 7.89e-06	Fig, and legend	df = 723, chi-square = 28.98	
+ -	Supp 11e	Pearson's tests	Fig. legend	283, 81, 167	control, delayed, silenced place cells	Fig. legend	Full distributions are shown in dot plots	Supp. Fig. 15	P = 0.41 (control), 0.57 (delayed), 0.42 (silenced)	Fig and fig. legend	r = -0.05 (control), -0.06 (delayed and silenced)	
+ -	Supp 17a	Kruskall Wallis tests	Fig. legend	257, 161,79	control, delayed ans silenced place cells recorded during sleep	Fig. legend	Boxplots showing median and data dispersion (min and max values)		P = 0.73 (rates), 0.66 (participation), 0.79 (counts), 0.66 (gains)	Fig and legend	df = 496; chi-square = 0.65(rates), 0.83(participation), 0.46(counts), 0.82(gains)	
+ -	Supp 14b	Pearson' s test	Fig. legend	497	place cells from 3 groups	Fig. legend	Full distributions are shown in dot plots		P = 0.36	Fig and legend	r = -0.04	
+ -	Supp 14c	Pearson's test	Fig. legend	497	place cells from 3 groups	Fig. legend	Full distributions are shown in dot plots		P = 0.35	Fig and legend	r = -0.04	
+ -	Supp 14d	Pearson' s test	Fig. legend	497	place cells from 3 groups	Fig. legend	Full distributions are shown in dot plots		P = 0.39	Fig and legend	r = -0.04	
+ -	Supp 14e	Pearson's test	Fig. legend	497	place cells from 3 groups	Fig. legend	Full distributions are shown in dot plots		P = 0.32	Fig and legend	r = -0.04	
+ -	Supp 8a	Chi-square test	Fig. legend	283, 81, 167	control, delayed, silenced place cells	Fig. legend	Contingency data combined for all recorded cells in the 3 groups: raw number of cells in each group in the figure		P = 0.001	Fig. legend	chi-square = 10.31, df = 2	
+ -	Supp 8b	Chi-square test	Fig. legend	283, 81, 167	control, delayed, silenced place cells	Fig. legend	Contingency data combined for all recorded cells in the 3 groups: raw number of cells in each group in the figure		P = 0.002	Fig. legend	chi-square = 9.93, df = 2	
+ -	Supp 7c	Wilcoxon signed rank test, two-sided	Fig. legend	29	sessions in 5 mice	Fig. legend	error bars are mean +/- SEM; raw values are shown with superimposed lines		P = 0.0006	Fig and Fig. legend	Z = -3.43	
+ -	Supp 2a	Kruskall Wallis test	Fig. legend	264, 81, 135	control, delayed, silenced place cells from CamKII-cre::Arch mice only	Fig. legend	Cumulative curve		P = 0.01	Fig. and fig legend	df = 479, chi-square = 8.41	

Representative figures

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

   If so, what figure(s)?

Fig. 2e
Fig. 3a-c
Fig. 5b
Fig. 6a

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 #)?

The representative images are presented for illustration purposes, not as final evidence. The corresponding statistics for group data are included in the same figures.

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.

No statistical methods were used to pre-determine sample sizes, but our sample sizes are similar to those generally employed in the field.

This information is stated in the "online Methods" section, paragraph entitled "Statistical analyses".

2. Are statistical tests justified as appropriate for every figure?

   Where (section, paragraph #)?

Yes

   a. If there is a section summarizing the statistical methods in the methods, is the statistical test for each experiment clearly defined?

This information is stated in the "online Methods" section, paragraph entitled "Statistical Analyses" .

   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 #)?

Our data did not follow normal distributions, therefore non parametric tests were used (see online Methods, "Statistical Analyses" section).

   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 #)?

All tests are non-parametric

   d. Are tests specified as one- or two-sided?

Yes. All tests are two-sided unless indicated, as stated in the online Methods ("Statistical Analyses" section). One-sided Wilcoxon signed rank tests are only used to assess whether the cell is suppressed or activated by the light stimuli.

   e. Are there adjustments for multiple comparisons?

Yes. Tukey's post-hoc tests are used following Kruskall Wallis tests (Fig. 2c; 2h; 3d; 5e) and Bonferroni correction is applied following chi square tests (Fig. 3e).

3. To promote transparency, *Nature Neuroscience* has stopped allowing bar graphs to report statistics in the papers it publishes. If you have bar graphs in your paper, please make sure to switch them to dot-plots (with central and dispersion statistics displayed) or to box-and-whisker plots to show data distributions.	We used cumulative distributions, dot plots or box plots (with central and dispersion statistics) in our figures. Bar plots are only used in combination with the complete distribution of the values (grey lines superimposed).
4. Are criteria for excluding data points reported? Was this criterion established prior to data collection? Where is this described (section, paragraph #)?	Outlier data points are not displayed in Figure 4a and 4c and Supplementary Figure 7f and 7g but these data are included in the statistical analyses. Excluding the outlier values does not impact the conclusions. This information is reported in the corresponding figure legends and in the online Methods section ("Statistical analyses").
5. 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 #)?	As presented in Supplementary Table 1, the two different types of stimulations ("delayed" or "locked" relative to SPW-R detection) were used in the same animal subjects, either in different recording sessions or in combination. Each paradigm was used in a pseudo-randomized manner (as stated in the online Methods).
6. 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 #)?	Analysis of place cells properties (remapping, place field characteristics) was done blindly relative to the cell categories these cells belonged to (control, delayed and silenced groups - approach 1 - or ripple-locked or ripple-delayed groups -approach 2-). This is stated in the online Methods ("Statistical analyses" section).
7. For experiments in live vertebrates, is a statement of compliance with ethical guidelines/regulations included? Where (section, paragraph #)?	Yes. All experiments were approved by the Institutional Animal Care and Use Committee of New York University Medical Center. This information is reported in the online Methods section, paragraph "Subjects and electrode implantation"
8. Is the species of the animals used reported? Where (section, paragraph #)?	Yes. As reported in the main text and in the online Methods ("Subjects and electrode implantation") sections, mice were used for this study.
9. Is the strain of the animals (including background strains of KO/ transgenic animals used) reported? Where (section, paragraph #)?	Yes. This information is reported in the online Methods section, paragraph "Subjects and electrode implantation"
10. Is the sex of the animals/subjects used reported? Where (section, paragraph #)?	Yes. This information is reported in the online Methods section, paragraph "Subjects and electrode implantation"
11. Is the age of the animals/subjects reported? Where (section, paragraph #)?	"3-5 months old". This information is reported in the online Methods section, paragraph "Subjects and electrode implantation"
12. For animals housed in a vivarium, is the light/dark cycle reported? Where (section, paragraph #)?	"All mice were [...] maintained on a 12h:12h light-dark cycle (lights on at 07:00 a.m.)". This information is reported in the online Methods section, paragraph "Pre-training"

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

    Where (section, paragraph #)?

"Maximum 5 adult mice per cage; housed individually after surgery". This information is reported in the online Methods section, paragraph "Pre-training".

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

    Where (section, paragraph #)?

"All experiments were done during the day (light-cycle)". This information is reported in the online Methods section, paragraph "Pre-training"

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

    Where (section, paragraph #)?

"All mice were free from prior manipulation before being included in this study". This information is reported in the online Methods section, paragraph "Pre-training"

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

       Where (section, paragraph #)?

N/A

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

    Where (section, paragraph #)?

No animal was excluded from the analyses.

    a. How were the criteria for exclusion defined?

       Where is this described (section, paragraph #)?

N/A

    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 #)?

N/A

Reagents

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

N/A

    a. Is antibody catalog number given?

       Where does this appear (section, paragraph #)?

N/A

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

       Where does this appear (section, paragraph #)?

N/A

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 #)?

N/A

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.

N/A

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 #)?

N/A

Data availability

Provide a Data availability statement in the Methods section under "Data availability", which should include, where applicable:
• Accession codes for deposited data
• Other unique identifiers (such as DOIs and hyperlinks for any other datasets)
• At a minimum, a statement confirming that all relevant data are available from the authors
• Formal citations of datasets that are assigned DOIs
• A statement regarding data available in the manuscript as source data
• A statement regarding data available with restrictions

See our data availability and data citations policy page for more information.

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.

Where is the Data Availability statement provided (section, paragraph #)?

The data that support the findings of this study are available from the corresponding author on request. Our laboratory is a member of the NeuroData Without Borders (NWB) initiative. After publication we routinely make our data publicly available (CRCNS.org) and this will also be the case for this article.

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.

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.

The code that was used to generate results of this study are available from the corresponding author upon request. Multiple analyses were done with the FMAToobox available in open access to the following address: http://fmatoolbox.sourceforge.net/

Human subjects

1. Which IRB approved the protocol?

   Where is this stated (section, paragraph #)?

N/A

2. Is demographic information on all subjects provided?

   Where (section, paragraph #)?

3. Is the number of human subjects, their age and sex clearly defined?

   Where (section, paragraph #)?

4. Are the inclusion and exclusion criteria (if any) clearly specified?

   Where (section, paragraph #)?

5. How well were the groups matched?

   Where is this information described (section, paragraph #)?

6. Is a statement included confirming that informed consent was obtained from all subjects?

   Where (section, paragraph #)?

7. For publication of patient photos, is a statement included confirming that consent to publish was obtained?

   Where (section, paragraph #)?

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?	N/A
a. If yes, is the number rejected and reasons for rejection described? Where (section, paragraph #)?	
2. Is the number of blocks, trials or experimental units per session and/or subjects specified? Where (section, paragraph #)?	
3. Is the length of each trial and interval between trials specified?	
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.	
5. Is the task design clearly described? Where (section, paragraph #)?	
6. How was behavioral performance measured?	
7. Is an ANOVA or factorial design being used?	
8. For data acquisition, is a whole brain scan used? If not, state area of acquisition.	
a. How was this region determined?	
9. Is the field strength (in Tesla) of the MRI system stated?	
a. Is the pulse sequence type (gradient/spin echo, EPI/spiral) stated?	
b. Are the field-of-view, matrix size, slice thickness, and TE/TR/flip angle clearly stated?	
10. Are the software and specific parameters (model/functions, smoothing kernel size if applicable, etc.) used for data processing and pre-processing clearly stated?	

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 #)?

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 #)?

13. How were anatomical locations determined, e.g., via an automated labeling algorithm (AAL), standardized coordinate database (Talairach daemon), probabilistic atlases, etc.?

14. Were any additional regressors (behavioral covariates, motion etc) used?

15. Is the contrast construction clearly defined?

16. Is a mixed/random effects or fixed inference used?

    a. If fixed effects inference used, is this justified?

17. Were repeated measures used (multiple measurements per subject)?

    a. If so, are the method to account for within subject correlation and the assumptions made about variance clearly stated?

18. If the threshold used for inference and visualization in figures varies, is this clearly stated?

19. Are statistical inferences corrected for multiple comparisons?

    a. If not, is this labeled as uncorrected?

20. Are the results based on an ROI (region of interest) analysis?

    a. If so, is the rationale clearly described?

    b. How were the ROI's defined (functional vs anatomical localization)?

21. Is there correction for multiple comparisons within each voxel?

22. For cluster-wise significance, is the cluster-defining threshold and the corrected significance level defined?

Additional comments

Additional Comments