SUPPLEMENTAL INFORMATION

Propranolol Decreases Fear Expression by Modulating Fear Memory Traces

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SUPPLEMENTAL METHODS

Genotyping

Genotyping was performed as previously described (1).

Behavioral Assays

Contextual Fear Conditioning (CFC)

A 4-shock CFC paradigm was administered as previously described (1). Briefly, mice were brought into the behavior room in a home cage, with normal lights on, and were placed in a CFC box scented with lemon (context A), to be administered 4 shocks at 180, 240, 300, and 360 s after placement into the context. Context re-exposure (RE) occurred 30 minutes or 5 days following CFC training, and each RE session lasted for 3 minutes. All sessions were scored for freezing using FreezeFrame4 (Actimetrics, Wilmette, IL).

Cued Fear Conditioning (FC)

A 4-shock cued FC was administered as previously described (2). Briefly, mice were placed in context A (identical to the CFC context) and were administered four 20 s tones (80 db, 2kHz) at 180, 260, 370, and 435 s after placement into the context. Each tone was co-terminated with a 2 s shock at 0.75 mA. The entire testing session lasted 485 s.

Five days later, to test how retrieval of cued FC is affected by prior administration of propranolol, mice were brought to the behavior room this time with red lights on, in paper buckets instead of a home cage, were injected with either saline or propranolol (10 mg/kg) and were placed in a novel context (context B) scented with anise, with a plastic floor covered with bedding, rounded walls, and cleaned with Sani-Cloth wipes. Mice were administered tones at 180, 260, 370, and 435 s. Twenty-four hours later they were tested again in context B, after drug washout,

with tones presented in the same manner, and 24 hours after this they were placed back in context A, where FC had taken place, for 8 min, without presentation of tones.

Context Fear Discrimination (CFD)

A 4-shock CFC paradigm was administered as previously described (1). Five days later, mice were administered saline or propranolol (10 mg/kg) and placed back in the aversive context A, for 3 min, and then 40 minutes later placed in context B (novel), as described above, for 3 min, to assess fear generalization. Thirty-five days after CFC mice were placed back in context A for 3 min to assess whether the prior administration of propranolol or saline before RE1 produced effects in long term memory (LTM).

Social Memory Recognition

Male mice were individually housed overnight. The next day mice were placed in a clean home cage with an ovariectomized (OVX) female mouse for 10 minutes of recorded interaction. Afterwards, each male mouse and the respective female mouse they were presented to were cohoused for 4 days, to allow formation of a consolidated social memory. After 4 days the mice were tested for social recognition. On the test day, the mice were separated and individually housed for 1.5 h, then they were administered either saline or propranolol (10 mg/kg) and immediately placed in an arena with 2 mesh cups on opposite sides, one with the familiar OVX female mouse, and one with a novel OVX female mouse. Time spent actively exploring each cup was quantified.

Elevated Plus Maze (EPM)

To test the effect of propranolol on anxiety, mice were administered with saline or propranolol before EPM testing 5 days after mice had undergone CFC. Testing was performed as previously described (3). Briefly, the maze is a plus-cross-shaped apparatus consisting of 4 arms, two open

and two enclosed by walls, linked by a central platform at a height of 50 cm from the floor. Mice were individually placed in the center of the maze facing an open arm and were allowed to explore the maze for 5 min. The time spent in and the number of entries into the open arms was used as an index of anxiety. Videos were scored using ANY-maze behavior tracking software (Stoelting, Wood Dale, IL).

Open Field (OF)

To test the effect of propranolol on anxiety on more than one assay, mice were administered with saline or propranolol before OF testing 5 days after mice had undergone CFC. The OF assay was administered as previously described (3). Briefly, motor activity was quantified in Plexiglas open field boxes 43×43 cm^2 (MED Associates, Georgia, VT). Mice were individually placed in the center of the OF box and allowed to explore the field for 10 min. A periphery area and a center area were defined, with the center square consisting of 4 lines 10 cm from the wall. Distance traveled, speed, freezing, time spent in the center, time spent in the periphery, entries into the center, and entries into the periphery were quantified. Videos were scored using ANY-maze behavior tracking software (Stoelting, Wood Dale, IL).

Ovariectomy (OVX)

Female mice were OVX as described (4), at least 2 weeks before being housed with a male mouse for the social recognition task. In brief, a 5 mm transverse skin incision in the mid-dorsal thoracolumbar region of the back was created followed by a second incision halfway down the side of the abdominal wall in the dorsolateral musculature to enter the abdominal cavity in the periovarian fat pad. To exteriorize the ovary, preovarian fat was grasped using tissue forceps, the pedicle was ligated and excised between the uterine horn and fallopian tube. The procedure was performed on both sides. After surgery, mice were returned to their home cage and monitored for the following 3 days until recovery from surgery.

Memory Trace Tagging

For all memory trace tagging experiments, mice were placed into a separate housing room in a fresh cage the night before the 4-OHT injection (Day 1). The next day, mice were injected with 4-OHT (10 mg/ml, 2 mg per mouse) and administered CFC training 5 h later (Day 2). Following the behavioral task, mice were housed in a dark room for that night and the following 3 days (Days 3-5). Mice were taken out of the dark on the morning of Day 5, cages were changed, and they were returned to the normal colony room. All precautions to prevent disturbances to the ArcCreER^{T2} x eYFP mice during dark housing were taken in order to reduce off-target labeling. Mice were re-exposed to the CFC context and euthanized 1 h following context exposure to allow for visualization of IEG (e.g., c-Fos) protein expression.

Immunohistochemistry

Mice were deeply anesthetized, and brains were processed as previously described in (1, 5, 6). Brains were then frozen in optimal cutting temperature (OCT) medium and sliced into 100 µm sections using a cryostat. An iDISCO-based immunohistochemistry protocol was performed (6). Briefly, sections were washed in 1X phosphate buffered saline (PBS) in 3 increments of 10 min each, then dehydrated in 50% MeOH for 2.5 h. Sections were then washed in 0.2% PBS with TritonX-100 (PBST) in 3 increments of 10 min each and placed in blocking solution (6% normal donkey serum (NDS) / 10% dimethyl sulfoxide (DMSO) / 84% PBST) for 2 h. After blocking, sections were washed in 3 increments of 10 min each in 1X PBS / 0.2% Tween-20 / 10 µg/ml heparin (PTwH). Sections were then incubated in a solution of primary antibody chicken polyclonal anti-GFP (1:500, Abcam, Cambridge, MA) and rabbit polyclonal IgG anti-c-Fos (1:5000 / 3% NDS / 5% DMSO / 92% PTwH, SySy, Goettingen, Germany) for 3 days at 4˚C. On day 4, sections were washed in 3 increments of 10 min each in PTwH and incubated in secondary antibody solution consisting of Alexa 647 conjugated Donkey Anti-Rabbit IgG (1:500, Life

Technologies, Carlsbad, CA) and Cy2 conjugated Donkey Anti-Chicken IgG (1:250, Jackson ImmunoResearch, West Grove, PA) in 3% NDS / 97% PTwH overnight. The next day, sections were washed in 3 increments of 10 min each in PTwH, then washed in 3 increments of 10 min each in 1X PBS. Sections were mounted on slides and allowed to dry for approximately 20 min before adding mounting medium Fluoromount G (Electron Microscopy Sciences, Hatfield, PA) and a coverslip.

Confocal Microscopy

All samples were imaged on a confocal scanning microscope (Leica TCS SP8, Leica Microsystems Inc., Wetzlar, Germany) with 2 simultaneous PMT detectors, as previously described (6). Fluorescence from Cy2 was excited at 488 nm and detected at 500–550 nm, and Alexa Fluor 647 was excited at 634 nm and detected at 650–700 nm. Sections were imaged with a dry Leica 20× objective (NA 0.70, working distance 0.5 mm), with a pixel size of 1.08 × 1.08 μm^2, a z step of 3 µm, and z-stack of 27 µm. Fields of view were stitched together to form tiled images by using an automated stage and the tiling function and algorithm of the LAS X software.

Cell Quantification

Manual cell counting

An investigator blind to treatment counted $eYFP^+$ and $c\text{-}Fos^+$ immunoreactive cells bilaterally in the granule cell layer (GCL) of the DG or in the pyramidal layer (PL) of CA3 throughout the entire rostro-caudal axis of the hippocampus (HPC) (2). Cells were counted bilaterally using Fiji (5) and normalized to the area of the GCL or PL. The average $eYFP^+$ and $c\text{-}Fos^+$ cells per mm^2 are presented in **Figure S11**.

Automated cell counting

Cells were automatically quantified in 3D using custom scripts in Fiji, with slight variations depending on the label. c-Fos$^+$ cells were identified by first passing the image through a bandpass filter in Fourier space, subtracting the background using a rolling ball algorithm, and identifying the cells using the 3D Local Maxima Fast Filter, 3D Spot Segmentation, and 3D Manager plugins in the 3D ImageJ suite (7). eYFP$^+$ cells were identified by subtracting the background, blurring the image with a Gaussian kernel, thresholding the image for the 1% brightest pixels, and using the thresholded regions as a mask for identifying the cells with the Classic Watershed plugin in the MorphoLibJ suite (8). Co-labeled cells were identified using the 3D MultiColoc plugin in the 3D ImageJ suite (9), which uses the label images created during segmentation of the individual labels to efficiently identify overlapping objects. In order to maximize the precision of the automated counts, all segmented objects were filtered by size, shape, and intensity variation. To ensure that only true co-labeled cells were identified, the co-labeled cells were additionally filtered by the amount of overlap between the objects identified in each individual channel.

Registration to an Anatomical Atlas

Immunohistochemistry-labeled coronal brain sections were aligned to an anatomical atlas using the WholeBrain package in R (10). The atlas plate most closely corresponding to each section was chosen, and WholeBrain was used to automatically align the brain section to the corresponding atlas plate. All sections were manually curated to ensure an accurate fit, and when necessary, the correspondence points automatically generated by WholeBrain were manually adjusted. In some cases, due to uneven cutting or damage to the section, different hemispheres from the same section were aligned to different atlas plates, or only regions of interest were precisely curated. In all such cases, misaligned or damaged regions were excluded from further analysis.

Data Integration and Analysis

Cell information, including location, intensity, and size, were imported into R from Fiji and copied into the WholeBrain object corresponding to the appropriate section. WholeBrain was then used to convert the image coordinates of each cell into atlas coordinates and determine which brain region contained each cell. Data for each label and the co-labeled cells were imported separately but handled in parallel. Cells mapping to areas not expected to contain cells, such as fiber tracts and ventricles, or mapping outside the identified regions of the atlas, were excluded. Additionally, cells mapping to cortical layer 1 were also excluded, due both to this being a dendritic layer that should not contain cell bodies and to uneven antibody labeling at the edge of the sections leading to a high number of false positives in this layer. The area of each region in the original image (using the registered coordinates) was calculated using Gauss's area formula. Areas and cell counts were aggregated across layers to yield a single value per region, and aggregate areas were converted to volumes and used to normalize the aggregate cell counts for each region. Normalized counts (cells per mm^3) were used in all further analyses.

Network Analysis

Cross-correlations between all pairs of regions for each label were calculated in R, using the rcorr function in the Hmisc package. Pearson's correlations were computed in all cases. Because the c-Fos and Arc-driven eYFP labels are both activity dependent, the correlations between regions are akin to functional connections, and the correlation data can be visualized and interpreted as a functional network, with regions as nodes and the correlation value determining the weight of the edges between region nodes (11, 12). Since pairwise correlations were calculated for all pairs, the initial functional network is necessarily complete, with all nodes connected to all other nodes. In order to be able to interpret the networks and discover the most salient features, correlations with an absolute R value lower than 0.5 were dropped.

Statistical Analysis

All data were analyzed using Prism 7.0 or 8.0. and R 3.6.3. Alpha was set to 0.05 for all analyses. For the behavioral data, the effect of Drug was analyzed using a *t*-test, using two-way analysis of variance (ANOVA) to assess the effects of Drug, Time, and of their interaction where appropriate. Post-hoc Sidak's Multiple Comparison's test was used to correct for multiple comparisons when a significant effect was found in the two-way ANOVA. Data analysis of the cell count data was conducted entirely in R using the tidyverse packages to organize the data and base R functions to perform the statistical tests. The effect of Drug on average levels of c-Fos+, eYFP+ or co-labeled cells was analyzed using *t*-tests. Because each of the regions was selected according to an *a priori* hypothesis regarding its involvement in extinction behavior, multiple comparisons correction is unnecessary for the count comparisons (13, 14). Pearson correlations between regions were calculated using the Hmisc package and p-values for each correlation were determined using a one-sample *t*-test. Consistent with a published study that performed similar analysis (11), no correction for multiple comparisons was done, and reported p-values are uncorrected. Networks were constructed using igraph and tidygraph packages. All statistical tests and *p* values are listed in **Tables S2-S4**.

SUPPLEMENTAL FIGURES

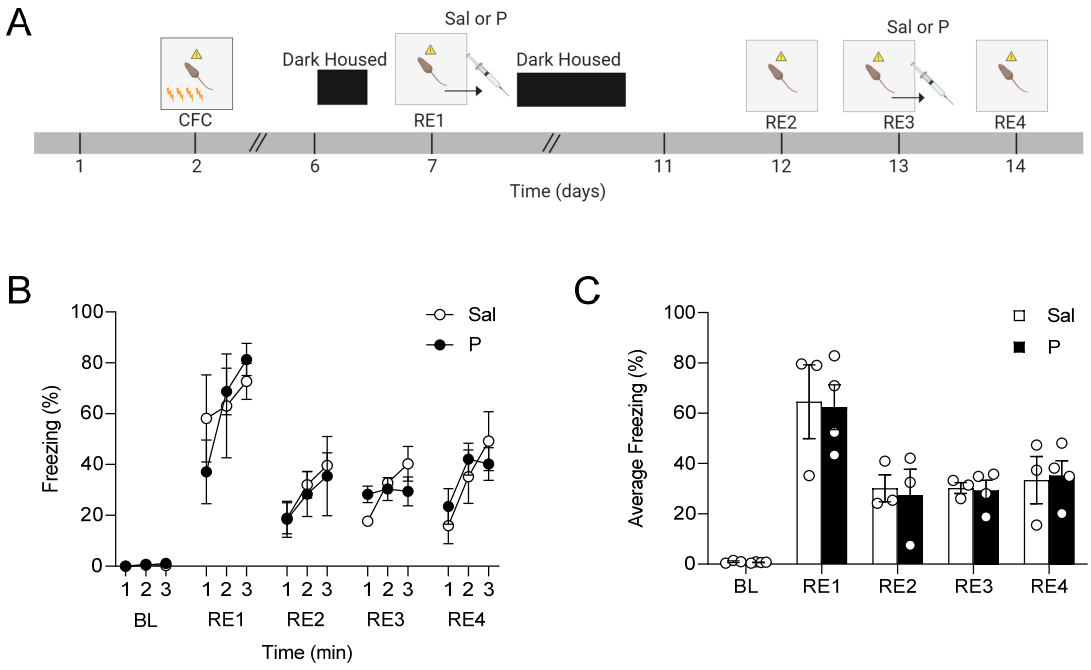

Figure S01. Multiple injections of propranolol do not increase the efficacy when administered post context re-exposure. (A) Experimental design. **(B)** An injection of propranolol following RE1 and an injection of propranolol following RE3 does not impact fear expression during RE2, RE3, or RE4. **(C)** Average freezing percentages do not differ between saline- and propranolol-injected mice. (n = 3-4 male mice per group). Sal, Saline; P, Propranolol; CFC, contextual fear conditioning; RE, context re-exposure; min, minutes.

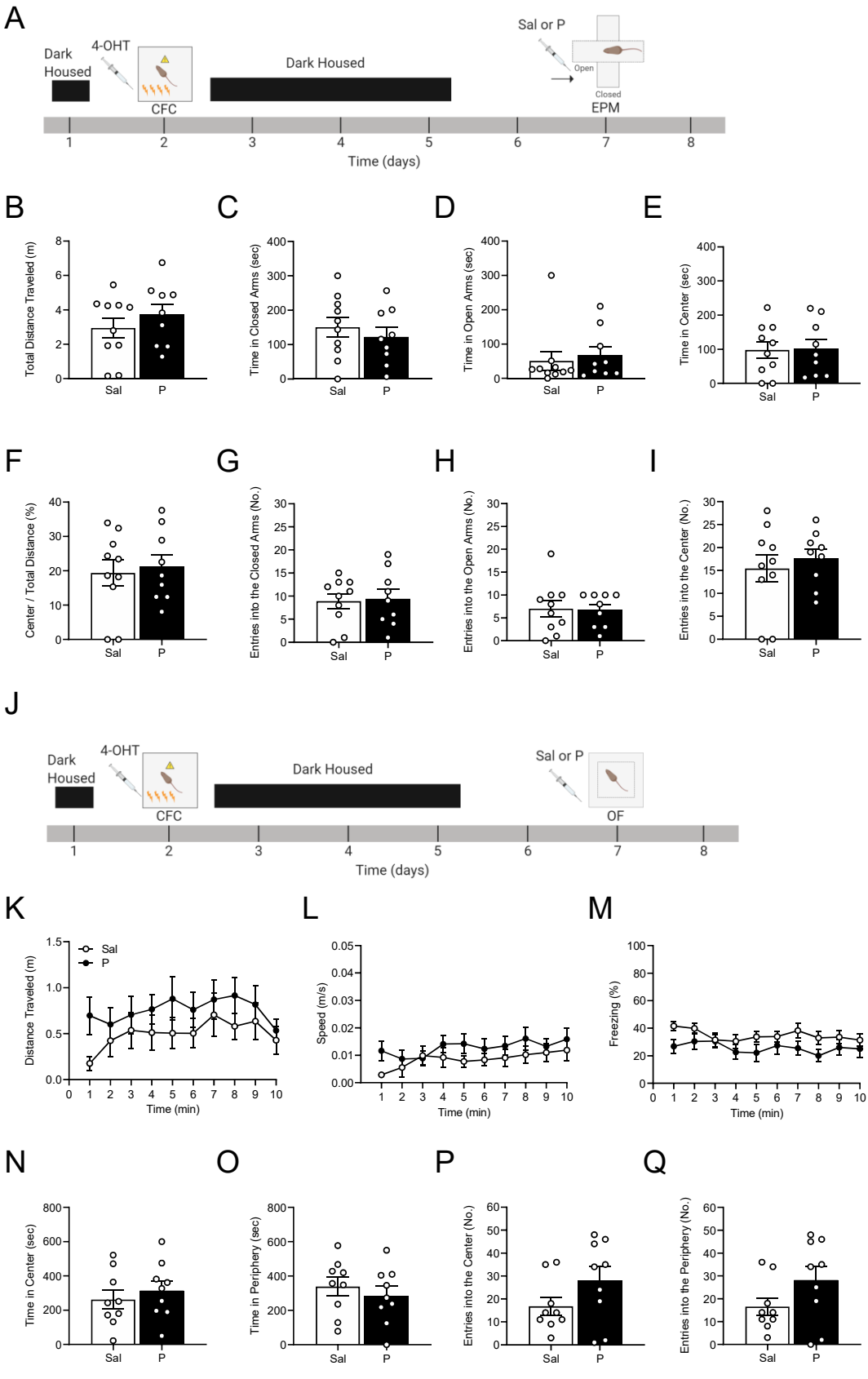
A
Dark Housed
4-OHT
CFC
Dark Housed
Sal or P
Open
Closed
EPM
1 2 3 4 5 6 7 8
Time (days)
B
Total Distance Traveled (m)
Sal P
C
Time in Closed Arms (sec)
Sal P
D
Time in Open Arms (sec)
Sal P
E
Time in Center (sec)
Sal P
F
Center / Total Distance (%)
Sal P
G
Entries into the Closed Arms (No.)
Sal P
H
Entries into the Open Arms (No.)
Sal P
I
Entries into the Center (No.)
Sal P
J
Dark Housed
4-OHT
CFC
Dark Housed
Sal or P
OF
1 2 3 4 5 6 7 8
Time (days)
K
Sal
P
Distance Traveled (m)
Time (min)
L
Speed (m/s)
Time (min)
M
Freezing (%)
Time (min)
N
Time in Center (sec)
Sal P
O
Time in Periphery (sec)
Sal P
P
Entries into the Center (No.)
Sal P
Q
Entries into the Periphery (No.)
Sal P

Figure S02. Administration of propranolol is not anxiolytic in 129S6/SvEv mice. (A) Experimental design. Injection of propranolol prior to the EPM does not impact **(B)** total distance travelled, **(C)** time in closed arms, **(D)** time in open arms, **(E)** time in the center, **(F)** the percent of time spent in the center/total distance, **(G)** entries into the closed arms, **(H)** entries into the open arms, or **(I)** entries into the center. **(J)** Experimental design. Injection of propranolol prior to the OF does not impact **(K)** distance traveled, **(L)** speed, **(M)** freezing behavior, **(N)** time in center, **(O)** time in periphery, **(P)** entries into the center, or **(Q)** entries into the periphery. (n = 9-10 male mice per group). Sal, Saline; P, Propranolol; CFC, contextual fear conditioning; EPM, elevated plus maze; m, meters; sec, seconds; No., number; OF, open field; m/s, meters/second; min, minutes.

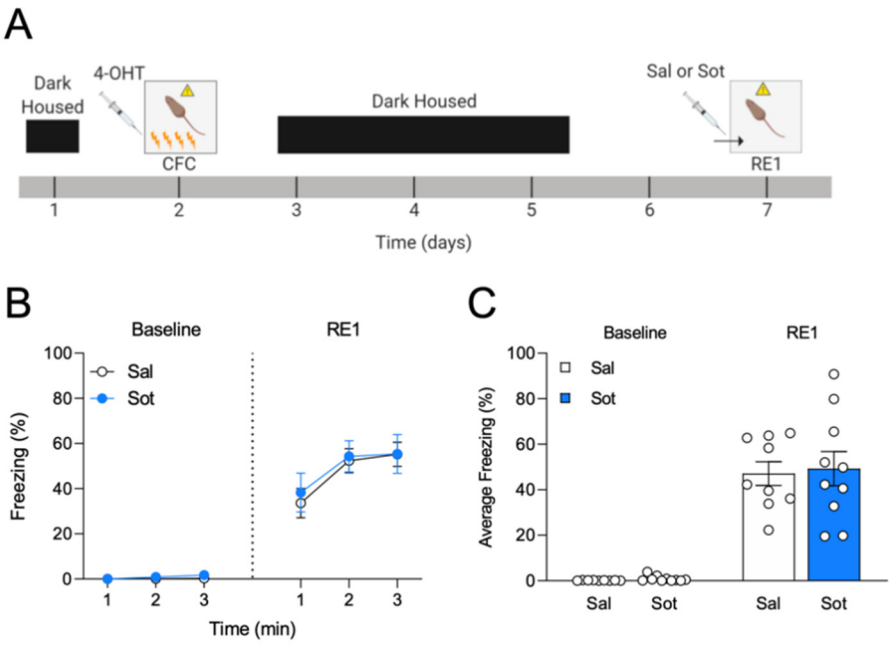

Figure S03. Administration of sotalol does not decrease fear expression in 129S6/SvEv mice. (A) Experimental design. **(B)** Injection of sotalol prior to RE1 does not decrease freezing behavior. **(C)** Injection of sotalol prior to RE1 does not impact average freezing behavior. (n = 9-10 male mice per group). Sal, Saline; Sot, Sotalol; 4-OHT, 4-hydroxytamoxifen; CFC, contextual fear conditioning; RE1, context re-exposure 1; min, minutes.

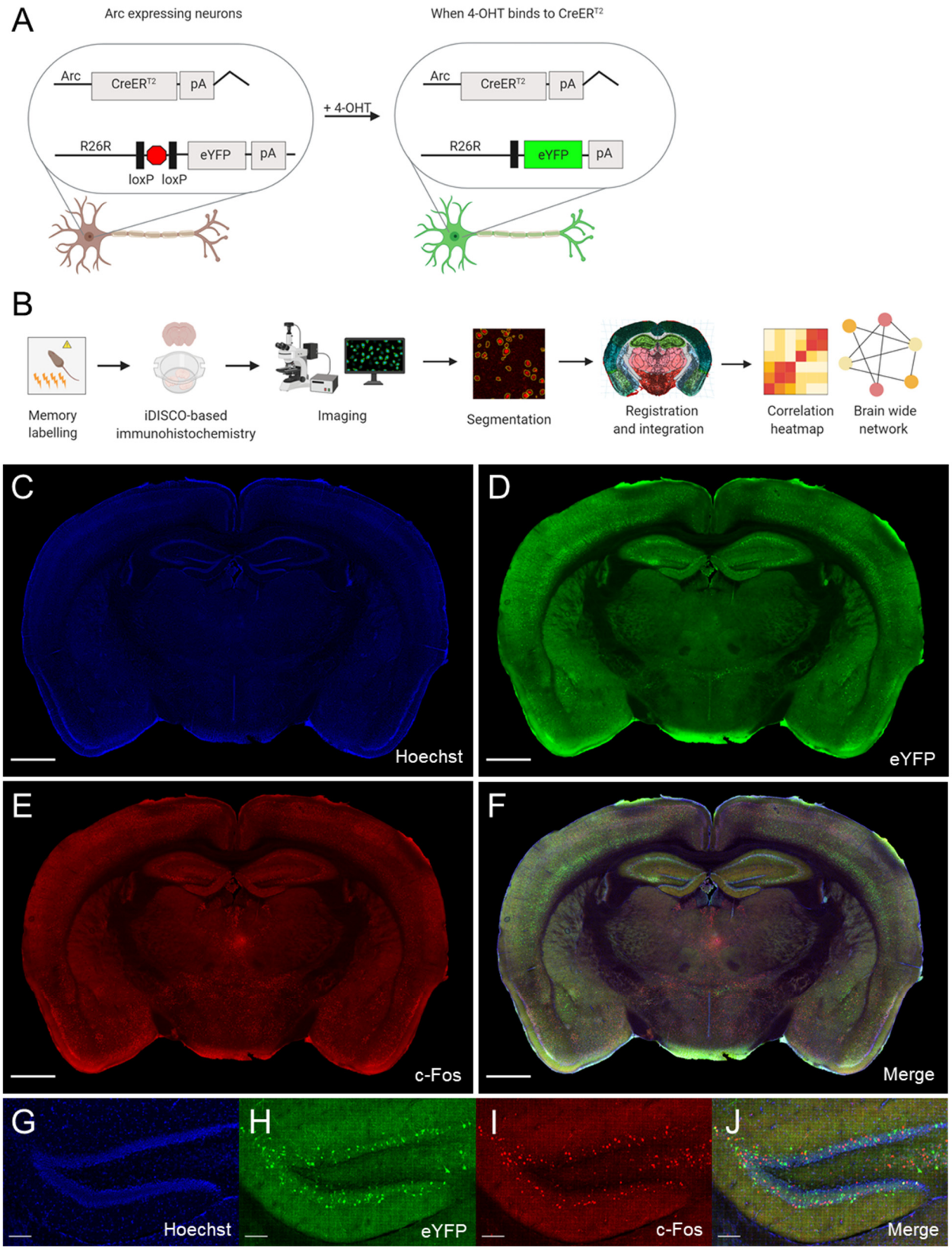
A
Arc expressing neurons
When 4-OHT binds to CreER^{T2}
Arc
CreER^{T2}
pA
+ 4-OHT
R26R
eYFP
loxP loxP
B
Memory labelling
iDISCO-based immunohistochemistry
Imaging
Segmentation
Registration and integration
Correlation heatmap
Brain wide network
C
Hoechst
D
eYFP
E
c-Fos
F
Merge
G
Hoechst
H
eYFP
I
c-Fos
J
Merge

Figure S04. ArcCreER^{T2} x eYFP mice experimental design for memory trace tagging. (A) Genetic design. **(B)** Experimental design for memory trace tagging, immunolabeling, brain-wide imaging of thick sections, automated quantification, and registration to atlas**.** Tissue section labelled for **(C)** Hoechst, **(D)** eYFP, **(E)** c-Fos, and **(F)** merged image acquired at 20x magnification. Scale bar **(C-F)** = 1000 μm. Magnification of the DG labeling with **(G)** Hoechst, **(H)** eYFP, **(I)** c-Fos, and **(J)** merged image. Scale bar **(G-J)** = 100 μm.

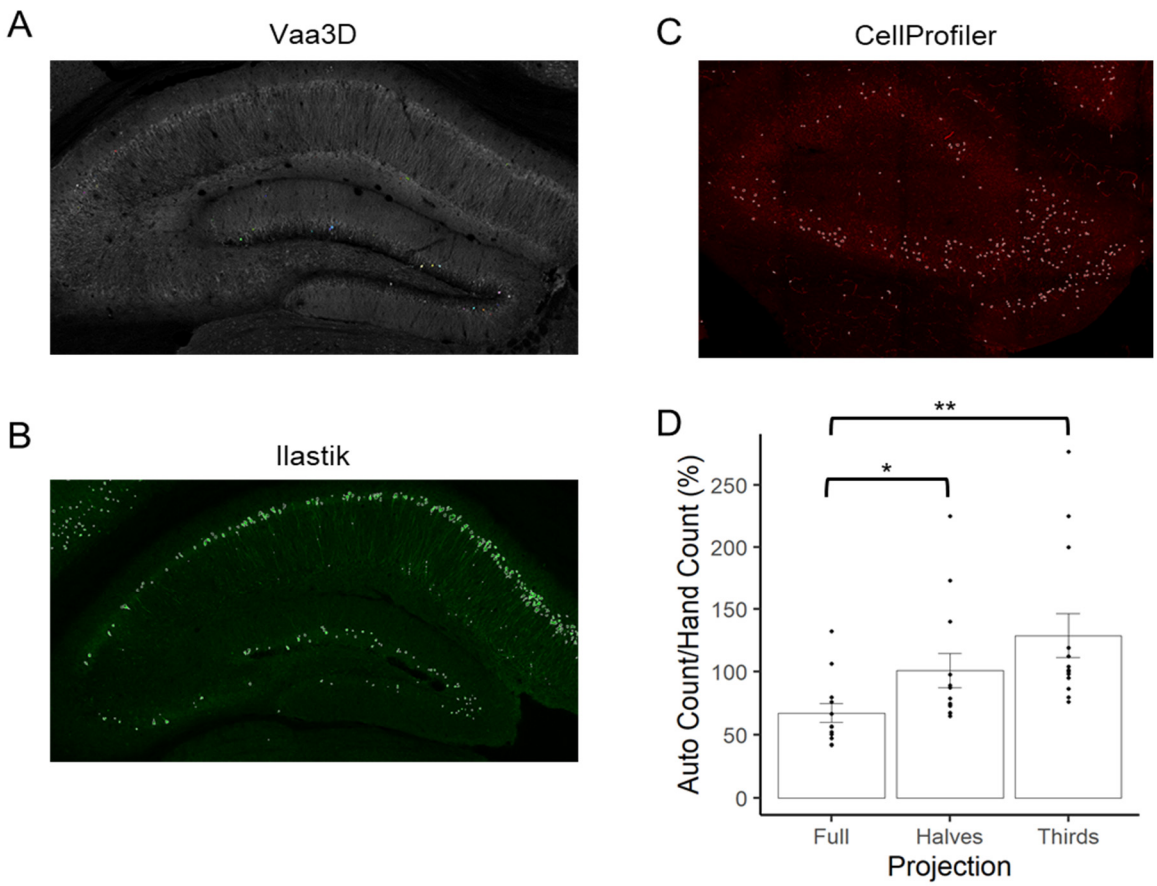

Figure S05. Initial attempts at development of segmentation pipeline. (A) Vaa3D produced good segmentation results for c-Fos but was too difficult to incorporate with the rest of the pipeline. **(B)** After months of training, Ilastik produced comparable eYFP segmentation results to the final pipeline but was labor and computationally intensive to run. CellProfiler produced sufficient segmentation results for c-Fos **(C)** but could not quantify cells in 3D. Therefore, in order to count 3D image stacks, the stack had to be subdivided and flattened. **(D)** Further analysis showed that the number of cells identified increased depending on how the stack was subdivided (full stack vs. halves vs. thirds), making the results unreliable. * $p < 0.05$, ** $p < 0.01$.

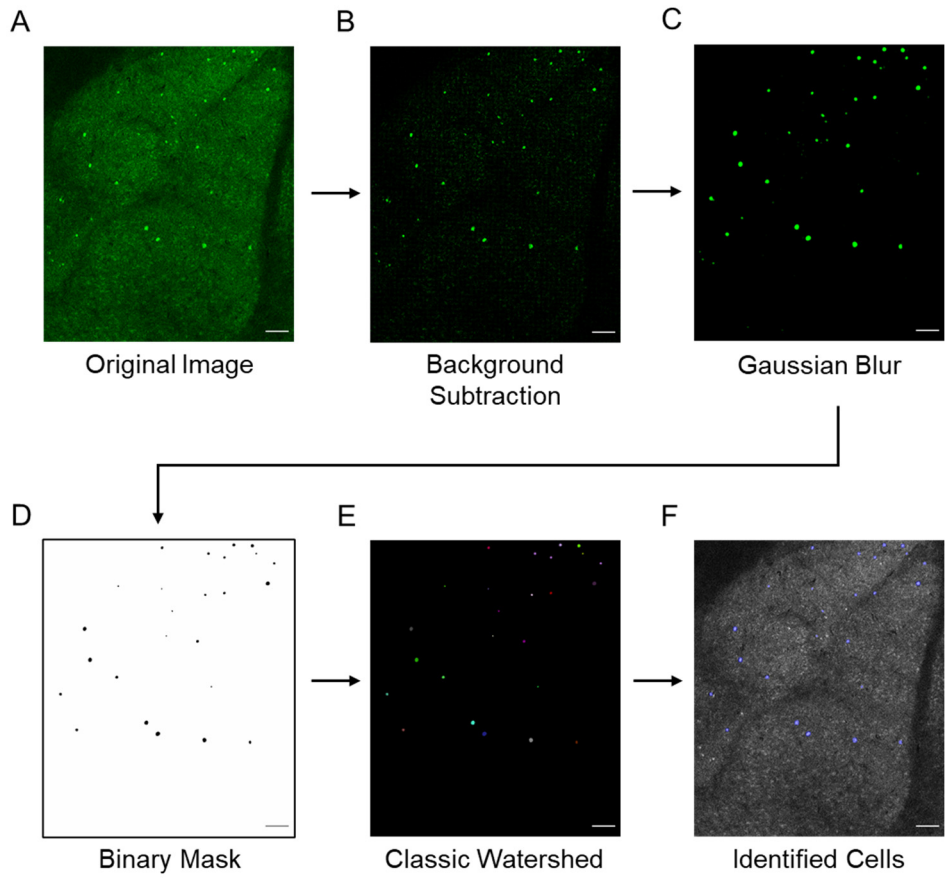

Figure S06. Segmentation of eYFP^{+} cells. Original image **(A)** is pre-processed to reduce background **(B)** and noise **(C)**, then thresholded for the brightest 1% of pixels to create a binary mask **(D)**. Binary mask and pre-processed image are used to identify cells with the classic watershed algorithm in MorphoLibJ. **(E)** Each object is assigned a unique label that can be mapped to different colors. **(F)** Identified cells are indicated as a blue overlay on the original image. Scale bar = 100 μm.

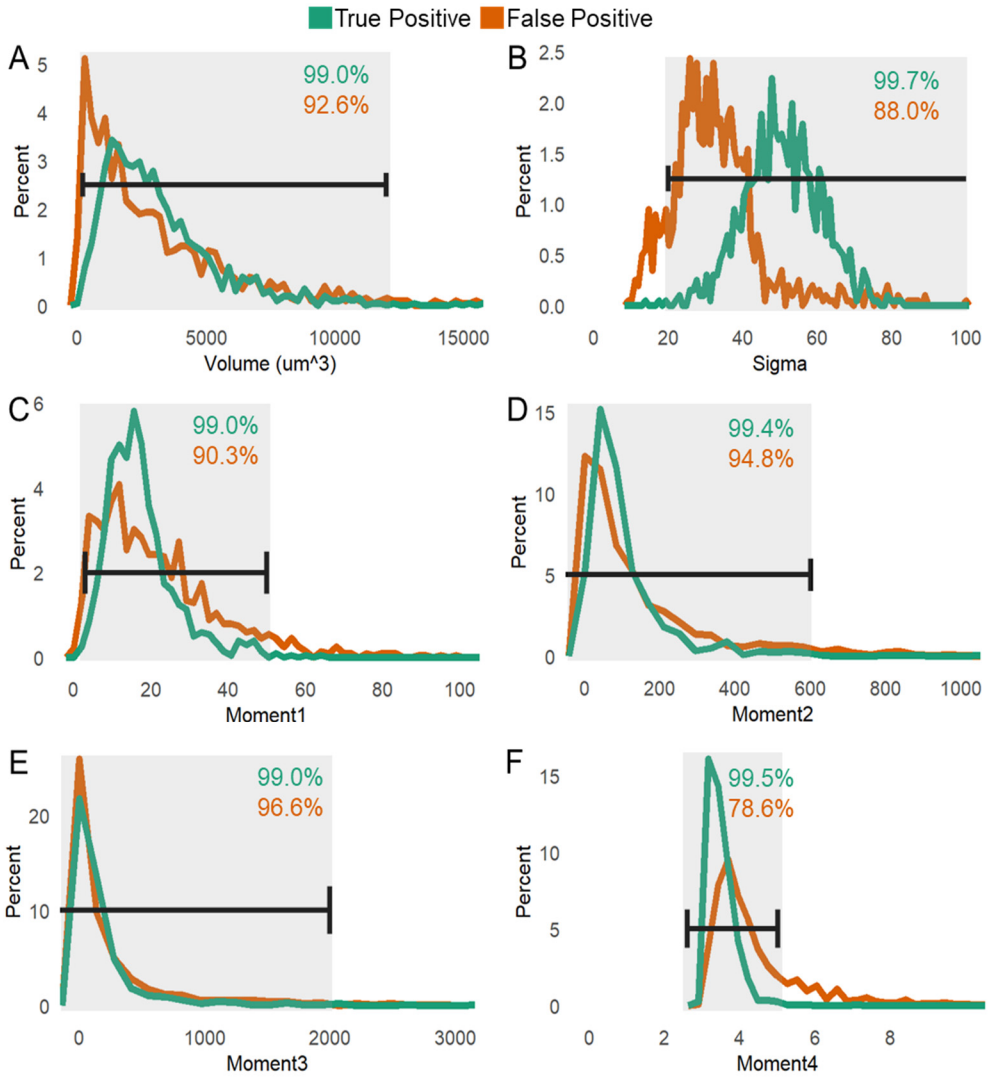

Figure S07. Filtering of eYFP counts. Initial eYFP segmentation is filtered to eliminate false positives using six metrics. Segmented objects are filtered according to size **(A)**, variance **(B)**, and shape **(C-F)**. Moments 1-4 are shape descriptors based on order 2 moments. True positive and false positive distributions were determined via manual curation of a representative subset of segmented objects. Shaded area indicates values for which objects were kept; percentages indicate proportion of objects that are maintained by the filter.

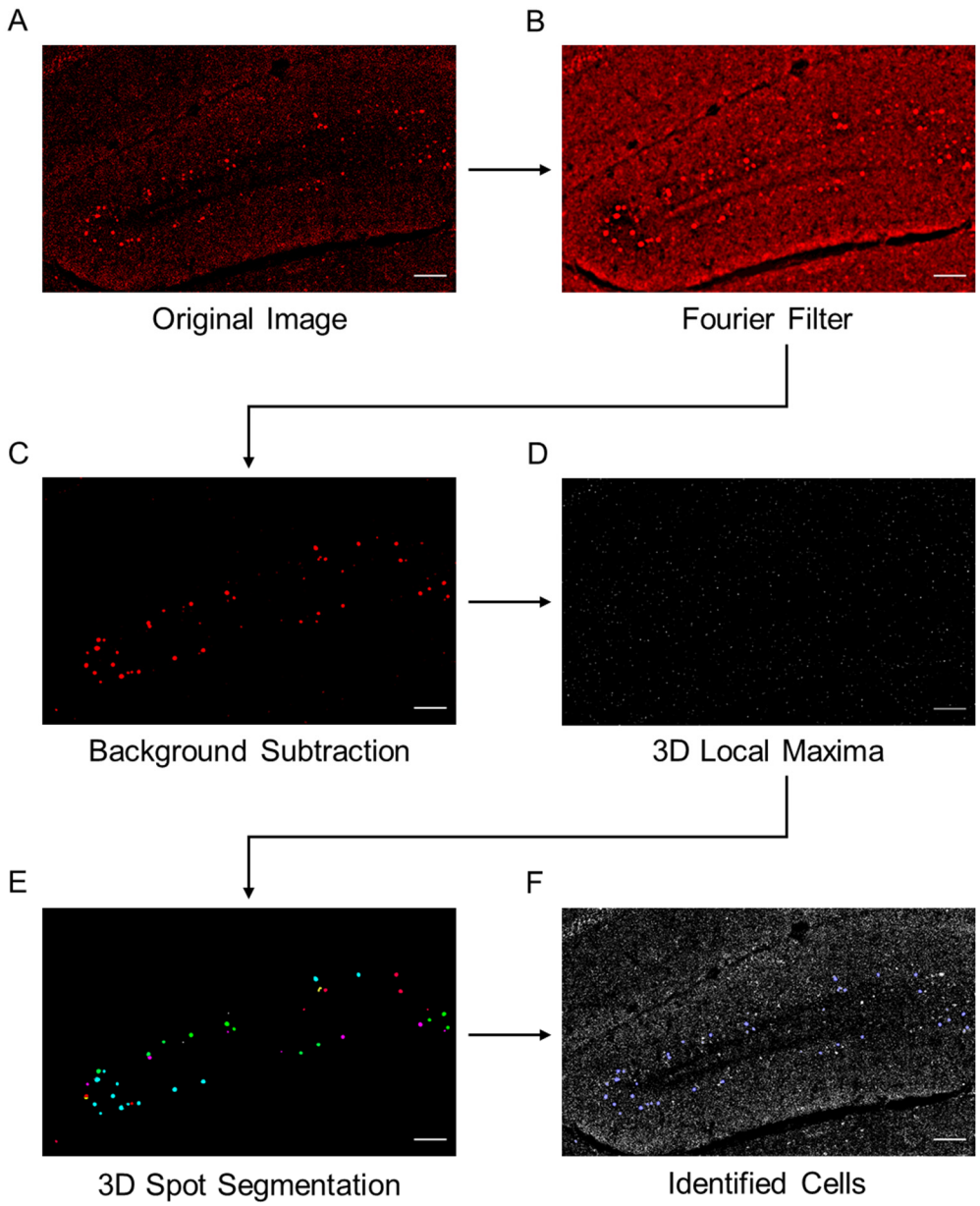

Figure S08. Segmentation of c-Fos$^+$ cells. Original image **(A)** is pre-processed to smooth out noise **(B)** and reduce background **(C)**. 3D Fast Filters plugin is used to identify local maxima in the pre-processed image **(D)**, and 3D Spot Segmentation plugin is used to identify cells **(E)**, using the local maxima image as seeds. Each object is assigned a unique label that can be mapped to different colors. **(F)** Identified cells are indicated as a blue overlay on the original image. Scale bar = 100 μm.

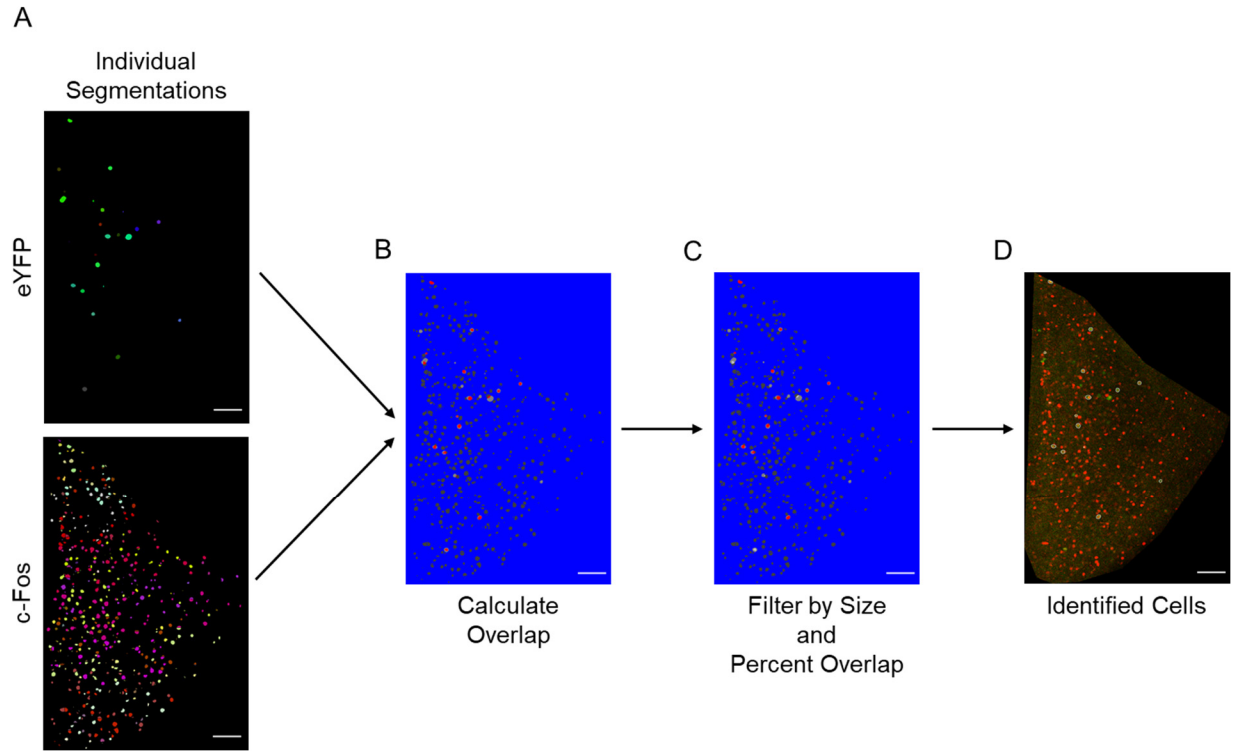

Figure S09. Identification of co-labeled cells. Using the c-Fos and eYFP segmentations **(A)**, overlapping objects are calculated **(B)**, and then filtered by size and percent of overlap to identify true co-labeled cells **(C)**. In **(B-C)**, red regions indicate areas of overlap, dark grey regions are segmented c-Fos$^+$ cells, and light grey regions are segmented eYFP$^+$ cells. White areas are overlaps that do not correspond to co-labeled cells and are removed by the filter. **(D)** Identified co-labeled cells are outlined in white. Scale bar = 100 μm.

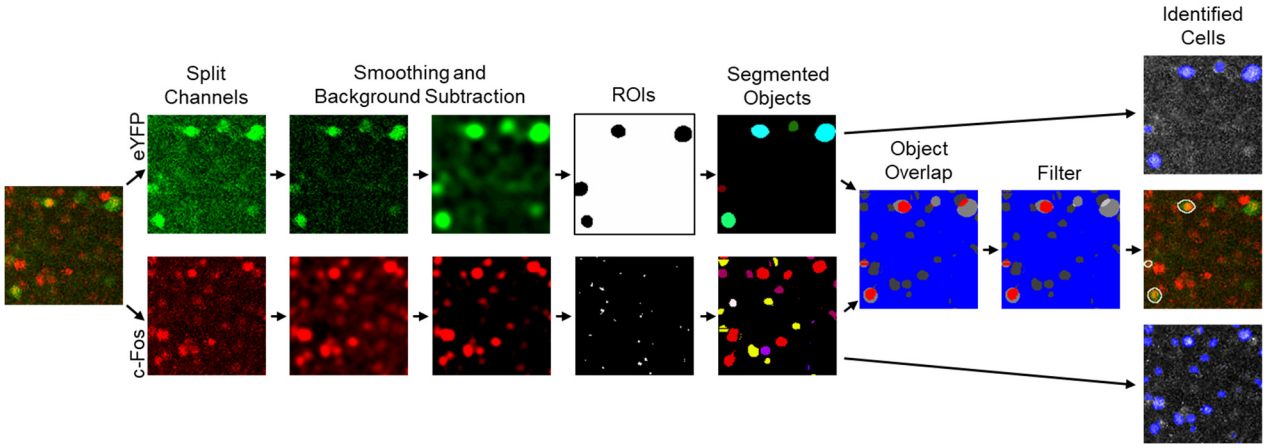

Figure S10. Overview of complete segmentation protocol. Original image is split into individual channels and run through the segmentation process for each channel. The segmented images produced by each process, to identify eYFP$^+$ and c-Fos$^+$ cells, are used to determine the co-labeled population (eYFP$^+$ and c-Fos$^+$), which are shown here encircled in white.

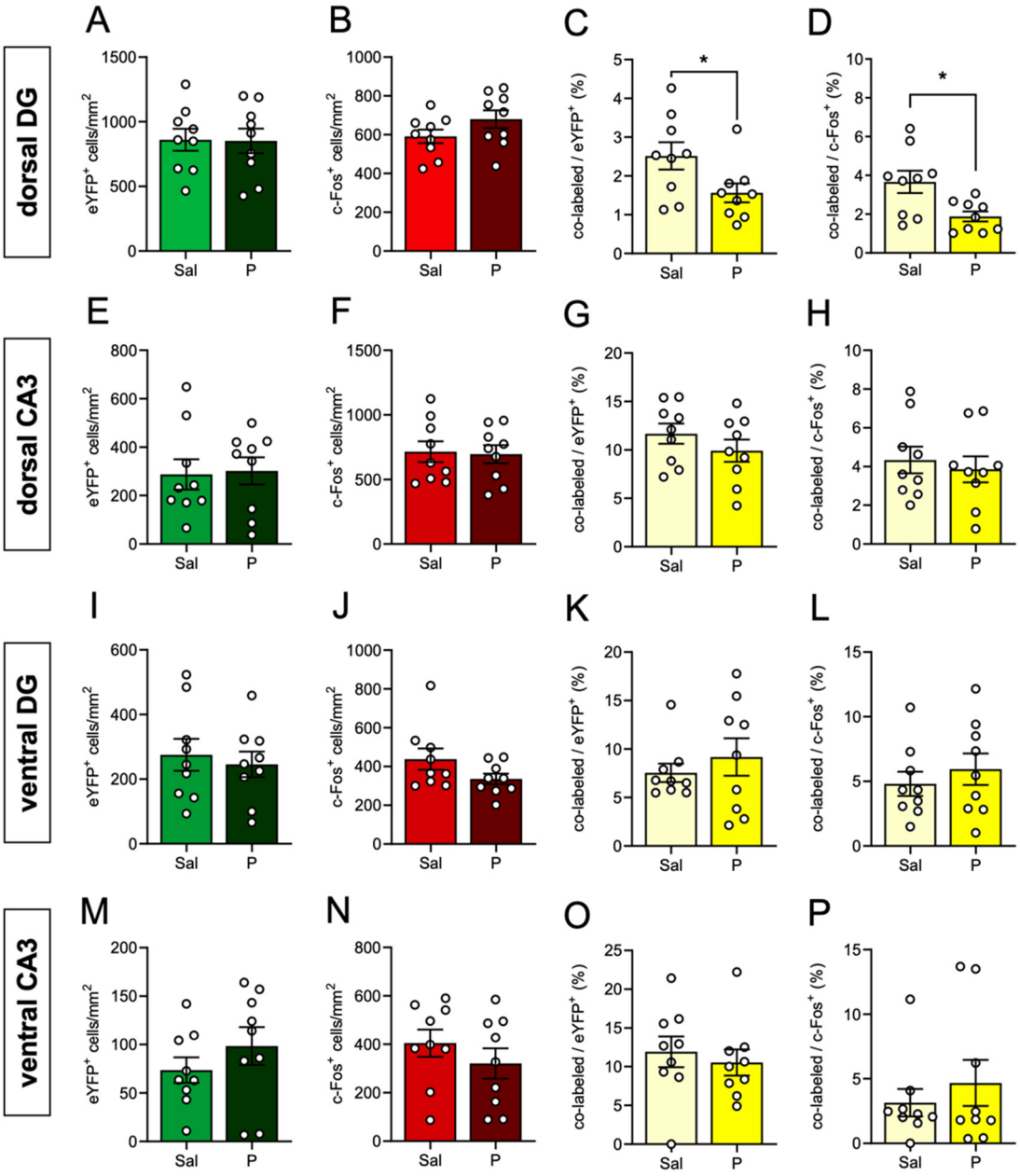

Figure S11. Administration of propranolol decreases fear expression and alters memory traces in the dorsal dentate gyrus of ArcCreER^{T2} x eYFP mice as assessed by manual hand counting. The number of **(A)** eYFP$^+$ cells or **(B)** c-Fos$^+$ cells does not differ in the dDG following administration of propranolol. The percentage of **(C)** co-labeled/eYFP$^+$ cells and **(D)** co-labeled/c-Fos$^+$ cells significantly decreases in the dDG following administration of propranolol. The number of **(E)** eYFP$^+$ cells or **(F)** c-Fos$^+$ cells does not differ in dCA3 following administration of

propranolol. The percentage of **(G)** co-labeled/eYFP$^+$ cells and **(H)** co-labeled/c-Fos$^+$ cells does not differ in dCA3 following administration of propranolol. The number of **(I)** eYFP$^+$ cells or **(J)** c-Fos$^+$ cells does not differ in the vDG following administration of propranolol. The percentage of **(K)** co-labeled/eYFP$^+$ cells and **(L)** co-labeled/c-Fos$^+$ cells does not differ in the vDG following administration of propranolol. The number of **(M)** eYFP$^+$ cells or **(N)** c-Fos$^+$ cells does not differ in vCA3 following administration of propranolol. The percentage of **(O)** co-labeled/eYFP$^+$ cells and **(P)** co-labeled/c-Fos$^+$ cells does not differ in vCA3 following administration of propranolol. (n = 9 male mice per group). * $p < 0.05$, ** $p < 0.01$. eYFP, enhanced yellow fluorescent protein; Sal, Saline; P, Propranolol.

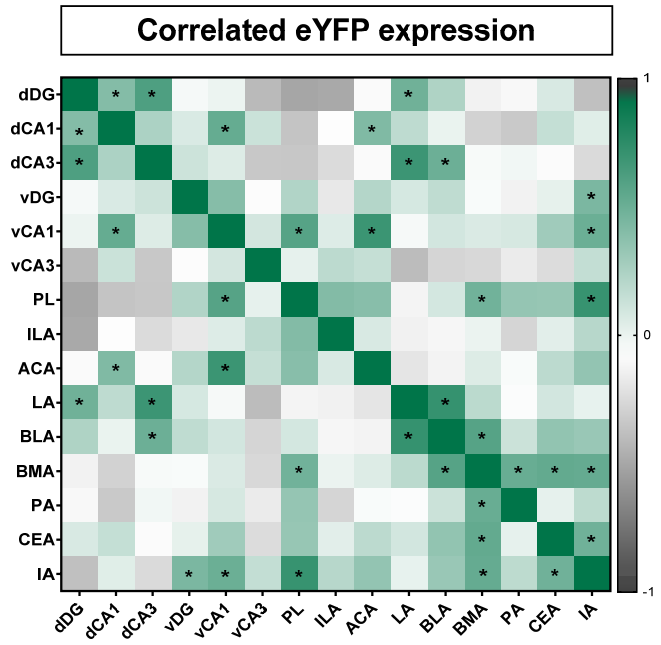

Figure S12. Correlations of activity between hippocampal, prefrontal, and amygdalar regions during encoding. Correlations of the number of eYFP$^+$ cells (tagged during CFC memory encoding) between brain regions. Square color reflects the Pearson correlation coefficient and asterisks represent a significant correlation. dDG, dorsal dentate gyrus; dCA1, dorsal CA1; dCA3, dorsal CA3; vDG, ventral dentate gyrus; vCA1, ventral CA1; vCA3, ventral CA3; PL, prelimbic area; ILA, infralimbic area; ACA, anterior cingulate area; LA, lateral amygdalar nucleus; BLA, basolateral amygdalar nucleus; BMA, basomedial amygdalar nucleus; PA, posterior amygdalar nucleus; CEA, central amygdalar nucleus; IA, intercalated amygdalar nucleus; FRZ, average freezing (%) during RE1. * $p < 0.05$

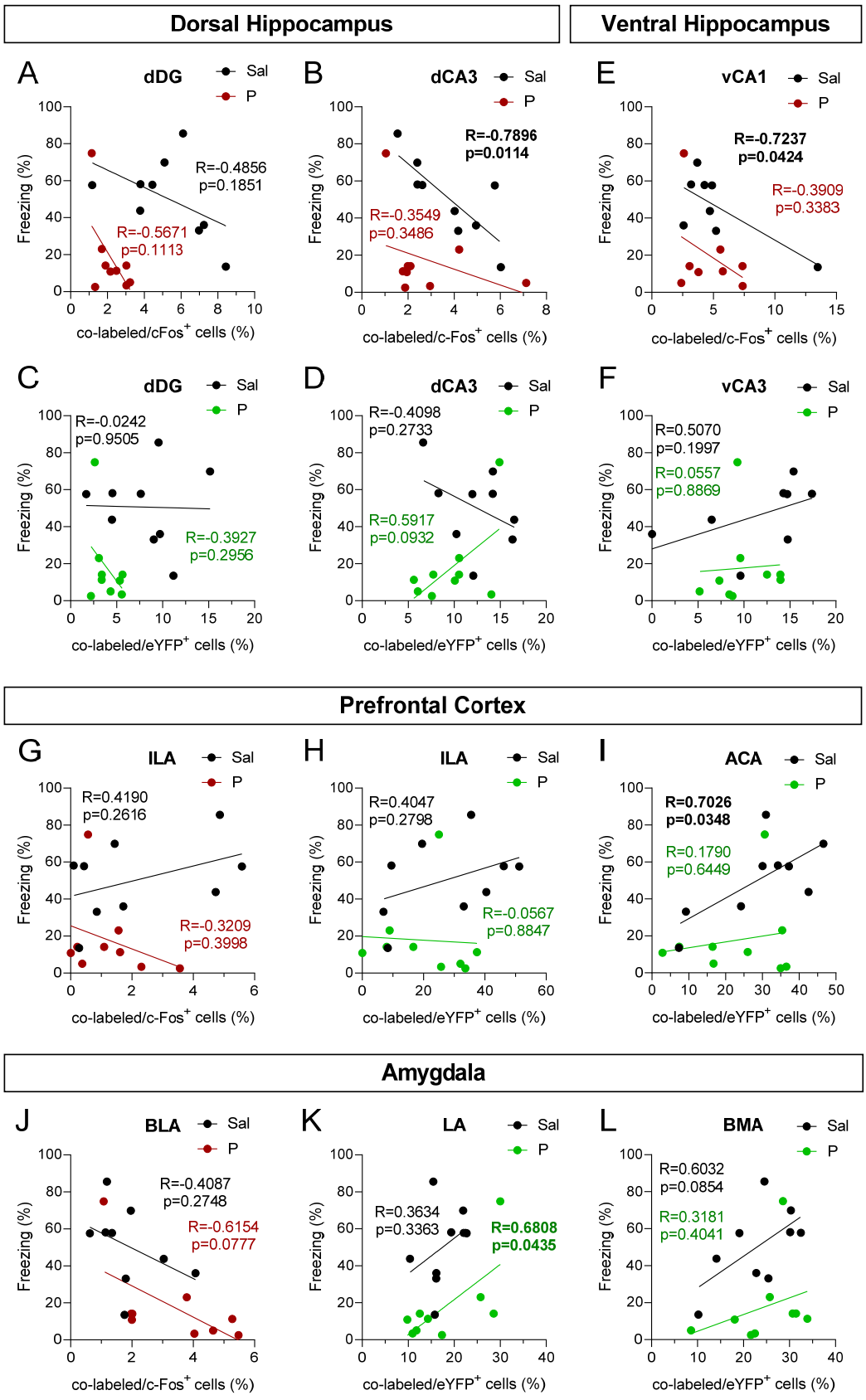
Dorsal Hippocampus
Ventral Hippocampus
A
dDG
Sal
P
R=-0.4856
p=0.1851
R=-0.5671
p=0.1113
B
dCA3
R=-0.7896
p=0.0114
R=-0.3549
p=0.3486
E
vCA1
R=-0.7237
p=0.0424
R=-0.3909
p=0.3383
C
R=-0.0242
p=0.9505
R=-0.3927
p=0.2956
D
R=-0.4098
p=0.2733
R=0.5917
p=0.0932
F
vCA3
R=0.5070
p=0.1997
R=0.0557
p=0.8869
Freezing (%)
co-labeled/cFos+ cells (%)
co-labeled/c-Fos+ cells (%)
co-labeled/eYFP+ cells (%)
Prefrontal Cortex
G
ILA
R=0.4190
p=0.2616
R=-0.3209
p=0.3998
H
R=0.4047
p=0.2798
R=-0.0567
p=0.8847
I
ACA
R=0.7026
p=0.0348
R=0.1790
p=0.6449
Amygdala
J
BLA
R=-0.4087
p=0.2748
R=-0.6154
p=0.0777
K
LA
R=0.3634
p=0.3363
R=0.6808
p=0.0435
L
BMA
R=0.6032
p=0.0854
R=0.3181
p=0.4041

Figure S13. Correlations between memory trace reactivation and freezing levels. Memory trace reactivation levels normalized to either c-Fos$^+$ or eYFP$^+$ cells were correlated with freezing levels during RE1. Here, the brain regions in which there was a correlation with R>0.5 or R<-0.5 for at least one of the groups, or that had differences in c-Fos$^+$ or reactivation cells between groups are shown. Correlations between memory trace reactivation and freezing levels for dDG and dCA3 in the dorsal HPC **(A-D)**, for vCA1 and vCA3 **(E-F)**, for ILA and ACA **(G-I)**, and for BLA, LA and BMA **(J-L)**. dDG, dorsal dentate gyrus; dCA3, dorsal CA3; vCA1, ventral CA1; vCA3, ventral CA3; ILA, infralimbic area; ACA, anterior cingulate area; LA, lateral amygdalar nucleus; BLA, basolateral amygdalar nucleus; BMA, basomedial amygdalar nucleus.

Table S01. Numbers of mice in each group.

Experiment	Mice	Group	n	Figure
Delayed, after RE1	129S6/SvEv	Saline	8	1A-1C
		Propranolol	10	
Delayed, before RE1		Saline	9	1D-1F
		Propranolol	10	
Immediate, after RE1		Saline	8	1G-1I
		Propranolol	7	
Immediate, before RE1		Saline	9	1J-1L
		Propranolol	10	
Cued fear conditioning		Saline	10	2B-2C
		Propranolol	11	
		Saline	5	2D-2E
		Propranolol	5	
Fear generalization		Saline	6	3B-3C
		Propranolol	6	
Social recognition		Saline	4	3E-3G
		Propranolol	5	
Delayed, before RE1	ArcCreERT2 x eYFP	Saline	9	4B
		Propranolol	9	
Multiple injections	129S6/SvEv	Saline	3	S1B-S1C
		Propranolol	4	
Delayed, before EPM		Saline	10	S2A-S2I
		Propranolol	9	
Delayed, before OF		Saline	9	S2J-S2Q
		Propranolol	9	
Delayed, before RE1		Saline	9	S3A-S3C
		Sotalol	10	

Table S02. Statistical analysis summary for all behavioral tests.

Cohort	Strain	Behavioral Paradigm	Abbreviation	Trial	Measurement	Statistical Test	Comparison	F	t	° of freedom	p	*	Fig.
Propranolol after delayed RE1	129S6/SvEv mice	Contextual Fear Conditioning	CFC	Baseline	Freezing per min (%)	2way ANOVA	Drug	1.672		1, 16	0.2144	ns	
							Time	0.6979		2, 32	0.5050	ns	
							Drug x Time	1.32		2, 32	0.2813	ns	
				RE1	Freezing per min (%)	2way ANOVA	Drug	1.121		1, 16	0.3054	ns	
							Time	67.16		2, 32	<0.0001	***	1B
							Drug x Time	1.721		2, 32	0.1950	ns	
				RE2	Freezing per min (%)	2way ANOVA	Drug	6.73		1, 16	0.8119	ns	
							Time	25.97		2, 32	<0.0001	***	
							Drug x Time	0.2619		2, 32	0.7712	ns	
				Baseline	Average Freezing (%)	*t*-test	Drug		1.293	16	0.2144	ns	
				RE1	Average Freezing (%)	*t*-test	Drug		1.059	16	0.3054	ns	1C
				RE2	Average Freezing (%)	*t*-test	Drug		0.2419	16	0.8119	ns	
Propranolol before delayed RE1				Baseline	Freezing per min (%)	2way ANOVA	Drug	0.08008		1 , 17	0.7806	ns	
							Time	1.771		2, 34	0.1854	ns	
							Drug x Time	1.572		2, 34	0.2224	ns	
				RE1	Freezing per min (%)	2way ANOVA	Drug	23.86		1, 17	0.0001	***	
							Time	3.155		2, 34	0.0553	ns	
							Drug x Time	1.581		2, 34	0.2206	ns	
					Minute 1	Multiple Comparisons (Sidak)	Sal vs. Prop min 1		2.119	51	0.1125	ns	1E
					Minute 2		Sal vs. Prop min 2		3.62	51	0.0020	**	
					Minute 3		Sal vs. Prop min 3		4.311	51	0.0002	***	
				RE2	Freezing per min (%)	2way ANOVA	Drug	0.05913		1, 17	0.8108	ns	
							Time	22.45		2, 34	<0.0001	****	
							Drug x Time	1.446		2, 34	0.2496	ns	
				Baseline	Average Freezing (%)	*t*-test	Drug		0.283	17	0.7806	ns	
				RE1	Average Freezing (%)	*t*-test	Drug		4.885	17	0.0001	***	1F
				RE2	Average Freezing (%)	*t*-test	Drug		0.2432	17	0.8108	ns	
Propranolol after immediate RE1				Baseline	Freezing per min (%)	2way ANOVA	Drug	1.19E-06		1, 13	0.9991	ns	
							Time	0.5469		2, 26	0.5852	ns	
							Drug x Time	0.9209		2, 26	0.4108	ns	
				RE1	Freezing per min (%)	2way ANOVA	Drug	2.145		1, 13	0.1668	ns	
							Time	23.87		2, 26	<0.0001	***	1H
							Drug x Time	1.962		2, 26	0.1609	ns	
				RE2	Freezing per min (%)	2way ANOVA	Drug	0.006994		1, 13	0.9346	ns	
							Time	22.33		2, 26	<0.0001	***	
							Drug x Time	0.02629		2, 26	0.9741	ns	
				Baseline	Average Freezing (%)	*t*-test	Drug		0.001089	13	0.9991	ns	
				RE1	Average Freezing (%)	*t*-test	Drug		1.465	13	0.1668	ns	1I
				RE2	Average Freezing (%)	*t*-test	Drug		0.08363	13	0.9346	ns	
Propranolol before immeidate RE1				Baseline	Freezing per min (%)	2way ANOVA	Drug	6.147		1, 17	0.0239	*	
							Time	0.6853		2, 34	0.5108	ns	
							Drug x Time	0.1872		2, 34	0.8302	ns	
				RE1	Freezing per min (%)	2way ANOVA	Drug	2.023		1, 17	0.1731	ns	
							Time	3.894		2, 34	0.0300	*	1K
							Drug x Time	1.716		2, 34	0.1951	ns	
				RE2	Freezing per min (%)	2way ANOVA	Drug	3.067		1, 17	0.0979	ns	
							Time	9.166		2, 34	0.0007	***	
							Drug x Time	0.9685		2, 34	0.3899	ns	
				Baseline	Average Freezing (%)	*t*-test	Drug		2.479	17	0.0239	*	
				RE1	Average Freezing (%)	*t*-test	Drug		1.422	17	0.1731	ns	1L
				RE2	Average Freezing (%)	*t*-test	Drug		1.751	17	0.0979	ns	
Propranolol before cued fear test	129S6/SvEv mice	Cued Fear Conditioning	Cued FC	Conditioning	Freezing per min (%)	2way ANOVA	Drug	1.405		1, 20	0.2498	ns	
							Time	104		4, 80	<0.0001	***	2B
							Drug x Time	1.303		4, 80	0.2762	ns	
			Cued FC	Tone Test 1	Freezing per min (%)	2way ANOVA	Drug	23.41		1, 19	0.0001	***	
							Time	9.696		4, 76	<0.0001	***	
							Drug x Time	3.162		4, 76	0.0185	*	
						Multiple comparisons (Sidak's)	BL		0.3212	95	0.9990	ns	
							T1		2.749	95	0.0353	*	2C
							T2		4.027	95	0.0006	***	
							T3		3.99	95	0.0007	***	
							T4		3.763	95	0.0014	**	
			Cued FC	Tone Test 2	Freezing per min (%)	2way ANOVA	Drug	9.664		1, 8	0.0145	*	
							Time	2.015		4, 32	0.116	ns	
							Drug x Time	1.007		4, 32	0.4183	ns	
						Multiple comparisons (Sidak's)	BL		1.677	40	0.4142	ns	
							T1		2.81	40	0.0376	*	2D
							T2		2.165	40	0.1691	ns	
							T3		2.603	40	0.0629	ns	
							T4		0.6414	40	0.9758	ns	
			Cued FC	Context Test	Average Freezing (%)	*t*-test	Drug		4.272	8	0.0027	**	2E

Fear Generalization	129S6/SvEv mice	Contextual Fear Conditioning	CFC	RE1 (A)	Freezing per min (%)	2way ANOVA	Drug	5.148		1,10	0.0467	*	3B
							Time	9.773		2,20	0.0011	**	
							Drug x Time	0.001061		2,20	0.9989	ns	
			CFC	(B)	Freezing per min (%)	2way ANOVA	Drug	0.1512		1,10	0.7055	ns	
							Time	6.665		2,20	0.0061	**	
							Drug x Time	0.3443		2,20	0.7129	ns	
			CFC	LTM (A)	Freezing per min (%)	2way ANOVA	Drug	0.471		1,10	0.5081	ns	
							Time	10.3		2,20	0.0008	***	
							Drug x Time	3.23		2,20	0.0609	ns	
			CFC	RE1 (A)	Average Freezing (%)	*t*-test	Saline vs. Propranolol		2.269	10	0.0467	*	
			CFC	(B)	Average Freezing (%)	*t*-test	Saline vs. Propranolol		0.3889	10	0.7055	ns	3C
			CFC	LTM (A)	Average Freezing (%)	*t*-test	Saline vs. Propranolol		0.6863	10	0.5081	ns	
Propranolol before Social Recognition test	129S6/SvEv mice	Social Recognition	SR	Total Exploration	Exploration Time (sec)	Mixed-effects model	Drug	0.3376		1, 14	0.5705	ns	3E
							Familiar vs. Novel	7.19		1, 14	0.0179	*	
							Drug x Familiar vs. Novel	4.55E-05		1, 14	0.9947	ns	
				Familiar Female	Exploration Time (sec)	2way ANOVA	Drug	2.137		1, 80	0.1477	ns	3F
							Time	0.8158		9, 80	0.6032	ns	
							Drug x Time	0.4555		9, 80	0.8999	ns	
				Novel Female	Exploration Time (sec)	2way ANOVA	Drug	0.2554		1, 80	0.6147	ns	3G
							Time	0.4539		9, 80	0.9009	ns	
							Drug x Time	0.5929		9, 80	0.7993	ns	
Propranolol immediately before RE1	ArcCreERT2 x eYFP mice	Contextual Fear Conditioning	CFC	Baseline	Average Freezing (%)	*t*-test	Saline vs. Propranolol		0.498	16	0.6253	ns	4B
				RE1	Average Freezing (%)	*t*-test	Saline vs. Propranolol		3.185	16	0.0058	**	
					b								
Propranolol immediately after RE1 and RE3 (repeated exposures)	129S6/SvEv mice	Contextual Fear Conditioning	CFC	Baseline	Freezing per min (%)	2way ANOVA	Drug	0.395		1, 5	0.5572	ns	S1B
							Time	3.444		2, 10	0.0728	ns	
							Drug x Time	1.988		2, 10	0.1876	ns	
				RE1	Freezing per min (%)	2way ANOVA	Drug	0.01879		1, 5	0.8963	ns	
							Time	12.74		2, 10	0.0018	**	
							Drug x Time	3.835		2, 10	0.0580	ns	
				RE2	Freezing per min (%)	2way ANOVA	Drug	0.05721		1, 4	0.8227	ns	
							Time	12.65		2, 8	0.0033	**	
							Drug x Time	0.1453		2, 8	0.8670	ns	
				RE3	Freezing per min (%)	2way ANOVA	Drug	0.03133		1, 5	0.8664	ns	
							Time	6.051		2, 10	0.0190	*	
							Drug x Time	4.722		2, 10	0.0360	*	
				RE4	Freezing per min (%)	2way ANOVA	Drug	0.0323		1, 5	0.8644	ns	
							Time	21.88		2, 10	0.0002	***	
							Drug x Time	2.845		2, 10	0.1052	ns	
				Baseline	Average Freezing (%)	*t*-test	Drug		0.8996	5	0.4096	ns	S1C
				RE1	Average Freezing (%)	*t*-test	Drug		0.1371	5	0.8963	ns	
				RE2	Average Freezing (%)	*t*-test	Drug		0.2392	4	0.8227	ns	
				RE3	Average Freezing (%)	*t*-test	Drug		0.177	5	0.8664	ns	
				RE4	Average Freezing (%)	*t*-test	Drug		0.1797	5	0.8644	ns	
Propranolol immediately before the EPM	129S6/SvEv mice	Elevated Plus Maze	EPM		Total Distance Traveled (m)	*t*-test	Drug		0.9273	17	0.3668	ns	S2B
					Time in Closed Arms (sec)	*t*-test	Drug		0.7063	17	0.4896	ns	S2C
					Time in Open Arms (sec)	*t*-test	Drug		0.4668	17	0.6466	ns	S2D
					Time in Center (sec)	*t*-test	Drug		0.09594	17	0.9247	ns	S2E
					Center / Total Distance (%)	*t*-test	Drug		0.3504	17	0.7303	ns	S2F
					Entries into the Closed Arms (No.)	*t*-test	Drug		0.2116	17	0.8349	ns	S2G
					Entries into the Open Arms (No.)	*t*-test	Drug		0.1018	17	0.9201	ns	S2H
					Entries into the Center (No.)	*t*-test	Drug		0.6217	17	0.5424	ns	S2I
Propranolol immediately before the OF		Open Field	OF		Total Distance Traveled (m)	2way ANOVA	Drug	1.496		1, 16	0.2390	ns	S2K
							Time	2.018		9, 144	0.0412	*	
							Drug x Time	0.5638		9, 144	0.8249	ns	
					Speed (m/s)	2way ANOVA	Drug	1.475		1, 16	0.2422	ns	S2L
							Time	2.087		9, 144	0.0343	*	
							Drug x Time	0.697		9, 144	0.7108	ns	
					Freezing (%)	2way ANOVA	Drug	2.441		1, 16	0.1377	ns	S2M
							Time	1.845		9, 144	0.0650	ns	
							Drug x Time	0.8624		9, 144	0.5604	ns	
					Time in Center (sec)	*t*-test	Drug		0.687	16	0.5019	ns	S2N
					Time in Periphery (sec)	*t*-test	Drug		0.687	16	0.5019	ns	S2O
					Entries into the Center (No.)	*t*-test	Drug		1.602	16	0.1287	ns	S2P
					Entries into the Periphery (No.)	*t*-test	Drug		1.635	16	0.1215	ns	S2Q

Sotalol immediately before RE1	129S6/SvEv mice	Contextual Fear Conditioning	CFC	Baseline	Freezing per min (%)	2way ANOVA	Drug	2.858		1, 17	0.1092	ns	S3B
							Time	3.384		2, 34	0.0457	*	
							Drug x Time	1.6		2, 34	0.2167	ns	
			CFC	RE1	Freezing per min (%)	2way ANOVA	Drug	0.05676		1, 17	0.8145	ns	
							Time	20.01		2, 34	<0.0001	***	
							Drug x Time	0.2223		2, 34	0.8019	ns	
			CFC	Baseline	Average Freezing (%)	*t*-test	Saline vs. Sotalol		1.691	17	0.1092	ns	S3C
			CFC	RE1	Average Freezing (%)	*t*-test	Saline vs. Sotalol		0.2383	17	0.8145	ns	

Table S03. Statistical analysis summary for cell quantification data.

Cohort	Strain	Cell counts	Measurement	Brain Region	Comparison	t	º of freedom	p	*	Figure
Propranolol before RE1	ArcCreERT2 x eYFP mice	eYFP	eYFP+ cells/mm3	dDG	Drug	-1.2949	12.3551	0.2190	ns	4D
				dCA1	Drug	-1.6702	14.5793	0.1162	ns	
				dCA3	Drug	-0.0383	9.3391	0.9702	ns	
				vDG	Drug	0.1898	11.6316	0.8527	ns	4I
				vCA1	Drug	-0.3692	10.8104	0.7191	ns	
				vCA3	Drug	1.2067	13.7477	0.2479	ns	
				PL	Drug	1.3518	14.0000	0.1979	ns	5B
				ILA	Drug	-0.3939	15.5442	0.6990	ns	
				ACA	Drug	-0.4934	15.289	0.6288	ns	
				LA	Drug	0.8874	10.3825	0.3949	ns	5G
				BLA	Drug	1.5122	12.5377	0.1553	ns	
				BMA	Drug	1.073	12.348	0.3038	ns	
				PA	Drug	0.7246	11.3891	0.4833	ns	
				CEA	Drug	-0.6269	12.0137	0.5424	ns	
				IA	Drug	1.2434	11.7871	0.2379	ns	
		c-Fos	c-Fos+/mm3	dDG	Drug	-0.6431	14.4019	0.5303	ns	4E
				dCA1	Drug	-1.2562	15.4783	0.2277	ns	
				dCA3	Drug	-1.8793	15.1725	0.0795	ns	
				vDG	Drug	-0.644	11.1918	0.5325	ns	4J
				vCA1	Drug	0.6939	13.3071	0.4997	ns	
				vCA3	Drug	0.811	14.363	0.4306	ns	
				PL	Drug	-1.0961	12.826	0.2932	ns	5C
				ILA	Drug	-2.5495	11.0461	0.0269	*	
				ACA	Drug	-1.4632	13.6823	0.1660	ns	
				LA	Drug	-2.3152	14.0286	0.0363	*	5H
				BLA	Drug	-0.4605	15.8732	0.6514	ns	
				BMA	Drug	0.985	12.2654	0.3437	ns	
				PA	Drug	0.6708	15.4071	0.5123	ns	
				CEA	Drug	1.387	15.6271	0.1849	ns	
				IA	Drug	0.7242	11.6518	0.4832	ns	
		co-labeled cells / c-Fos	co-labeled cells/c-Fos+ cells (%)	dDG	Drug	-3.8375	9.886	0.0033	*	4F
				dCA1	Drug	-2.0836	10.94	0.0615	ns	
				dCA3	Drug	-1.2064	15.6758	0.2455	ns	
				vDG	Drug	0.0308	15.9719	0.9758	ns	4K
				vCA1	Drug	-0.0586	15.6579	0.9540	ns	
				vCA3	Drug	0.1932	14.6472	0.8495	ns	
				PL	Drug	0.749	15.5811	0.4650	ns	5D
				ILA	Drug	-1.1684	12.0585	0.2652	ns	
				ACA	Drug	-0.2722	15.9365	0.7890	ns	
				LA	Drug	1.528	8.751	0.1618	ns	5I
				BLA	Drug	2.2864	13.7791	0.0386	*	
				BMA	Drug	1.1462	12.3623	0.2734	ns	
				PA	Drug	-0.9579	13.5745	0.3548	ns	
				CEA	Drug	-0.026	15.938	0.9796	ns	
				IA	Drug	1.7364	10.3878	0.1120	ns	
		co-labeled cells/eYFP	co-labeled cells/eYFP+ cells (%)	dDG	Drug	-2.9244	9.6487	0.0157	*	4G
				dCA1	Drug	-1.6934	14.0993	0.1123	ns	
				dCA3	Drug	-1.6447	15.9698	0.1196	ns	
				vDG	Drug	-0.3333	14.1975	0.7437	ns	4L
				vCA1	Drug	-0.4986	10.8928	0.6280	ns	
				vCA3	Drug	-0.912	12.4035	0.3791	ns	
				PL	Drug	-0.3388	15.974	0.7391	ns	5E
				ILA	Drug	-0.9819	14.9393	0.3418	ns	
				ACA	Drug	-0.9962	15.9162	0.3341	ns	
				LA	Drug	0.0397	11.8622	0.9690	ns	5J
				BLA	Drug	0.4837	14.8423	0.6356	ns	
				BMA	Drug	0.362	15.9733	0.7221	ns	
				PA	Drug	-1.381	13.9174	0.1890	ns	
				CEA	Drug	0.6292	15.9875	0.5381	ns	
				IA	Drug	1.7948	13.0441	0.0959	ns	

Cohort	Strain	Cell Count	Measurement	Brain Region	Comparison	t	° of freedom	p	*	Fig.
Propranolol immediately before RE1	ArcCreERT2 x eYFP mice	eYFP	eYFP+ cells/mm2	dDG	Drug	0.07028	16	0.9448	ns	S10A
				dCA3	Drug	0.1744	16	0.8637	ns	S10E
				vDG	Drug	0.4661	16	0.6474	ns	S10I
				vCA3	Drug	1.056	16	0.3065	ns	S10M
		c-Fos	c-Fos+ cells/mm2	dDG	Drug	1.525	16	0.1469	ns	S10B
				dCA3	Drug	0.1862	16	0.8546	ns	S10F
				vDG	Drug	1.667	16	0.1149	ns	S10J
				vCA3	Drug	1.002	16	0.3314	ns	S10N
		co-labeled / eYFP	co-labeled / eYFP (%)	dDG	Drug	2.228	16	0.0406	*	S10C
				dCA3	Drug	1.133	16	0.2741	ns	S10G
				vDG	Drug	0.7593	16	0.4587	ns	S10K
				vCA3	Drug	0.5361	16	0.5993	ns	S10O
		co-labeled / c-Fos	co-labeled / c-Fos (%)	dDG	Drug	2.814	16	0.0125	*	S10D
				dCA3	Drug	0.496	16	0.6266	ns	S10H
				vDG	Drug	0.7393	16	0.4704	ns	S10L
				vCA3	Drug	0.7398	16	0.4701	ns	S10P

Table S04. Statistical analysis summary for correlation analysis.

			All mice				
	Region 1	Region 2	r	n	p	*	Figure
Correlation of EYFP levels during CFC encoding	dCA1	dDG	0.4803	18	0.0436	*	S12
	dCA3	dDG	0.6895	18	0.0015	*	
	LA	dDG	0.5586	18	0.0160	*	
	dDG	dCA1	0.4803	18	0.0436	*	
	vCA1	dCA1	0.5985	16	0.0143	*	
	ACA	dCA1	0.4955	18	0.0365	*	
	dDG	dCA3	0.6895	18	0.0015	*	
	LA	dCA3	0.7599	18	0.0003	*	
	BLA	dCA3	0.5745	18	0.0126	*	
	IA	vDG	0.5121	16	0.0426	*	
	dCA1	vCA1	0.5985	16	0.0143	*	
	PL	vCA1	0.6591	14	0.0104	*	
	ACA	vCA1	0.7650	16	0.0006	*	
	IA	vCA1	0.5762	16	0.0195	*	
	vCA1	PL	0.6591	14	0.0104	*	
	BMA	PL	0.5517	16	0.0267	*	
	IA	PL	0.7810	16	0.0004	*	
	dCA1	ACA	0.4955	18	0.0365	*	
	vCA1	ACA	0.7650	16	0.0006	*	
	dDG	LA	0.5586	18	0.0160	*	
	dCA3	LA	0.7599	18	0.0003	*	
	BLA	LA	0.7883	18	0.0001	*	
	dCA3	BLA	0.5745	18	0.0126	*	
	LA	BLA	0.7883	18	0.0001	*	
	BMA	BLA	0.6609	18	0.0028	*	
	FRZ	BLA	-0.5573	18	0.0163	*	
	PL	BMA	0.5517	16	0.0267	*	
	BLA	BMA	0.6609	18	0.0028	*	
	PA	BMA	0.5888	18	0.0101	*	
	CEA	BMA	0.6092	18	0.0073	*	
	IA	BMA	0.6017	18	0.0083	*	
	BMA	PA	0.5888	18	0.0101	*	
	BMA	CEA	0.6092	18	0.0073	*	
	IA	CEA	0.5575	18	0.0162	*	
	vDG	IA	0.5121	16	0.0426	*	
	vCA1	IA	0.5762	16	0.0195	*	
	PL	IA	0.7810	16	0.0004	*	
	BMA	IA	0.6017	18	0.0083	*	
	CEA	IA	0.5575	18	0.0162	*	
	BLA	FRZ	-0.5573	18	0.0163	*	

			Saline-administered mice					Propranolol-administered mice				
	Region 1	Region 2	r	n	p	*	Figure	r	n	p	*	Figure
Correlation of c-Fos levels during CFC retrieval	dCA1	dDG	0.7186	9	0.0292	*	6A	0.7176	9	0.0295	*	6B
	PL	dDG	-0.0709	8	0.8675			-0.9202	8	0.0012	*	
	dDG	dCA1	0.7186	9	0.0292	*		0.7176	9	0.0295	*	
	vCA1	dCA1	0.7879	8	0.0202	*		-0.1347	8	0.7504		
	PL	dCA1	-0.7226	8	0.0429	*		-0.7381	8	0.0365	*	
	vCA3	dCA3	0.4052	8	0.3193			-0.7307	9	0.0253	*	
	LA	dCA3	0.7764	9	0.0139	*		0.3738	9	0.3216		
	BMA	dCA3	0.8164	9	0.0073	*		0.0177	9	0.9639		
	CEA	dCA3	0.7447	9	0.0213	*		-0.0381	9	0.9225		
	vCA3	vDG	0.8449	8	0.0083	*		-0.1385	8	0.7435		
	PL	vDG	0.8532	7	0.0146	*		0.1290	7	0.7828		
	dCA1	vCA1	0.7879	8	0.0202	*		-0.1347	8	0.7504		
	LA	vCA1	0.7285	8	0.0404	*		0.2066	8	0.6235		
	dCA3	vCA3	0.4052	8	0.3193			-0.7307	9	0.0253	*	
	vDG	vCA3	0.8449	8	0.0083	*		-0.1385	8	0.7435		
	PL	vCA3	0.7545	7	0.0500	*		0.1522	8	0.7189		
	ILA	vCA3	-0.0916	8	0.8293			0.7096	9	0.0322	*	
	dDG	PL	-0.0709	8	0.8675			-0.9202	8	0.0012	*	
	dCA1	PL	-0.7226	8	0.0429	*		-0.7381	8	0.0365	*	
	vDG	PL	0.8532	7	0.0146	*		0.1290	7	0.7828		
	vCA3	PL	0.7545	7	0.0500	*		0.1522	8	0.7189		
	IA	PL	0.3417	8	0.4075			0.7235	8	0.0425	*	
	vCA3	ILA	-0.0916	8	0.8293			0.7096	9	0.0322	*	

	IA	PL	0.3417	8	0.4075			0.7235	8	0.0425	*	
	vCA3	ILA	-0.0916	8	0.8293			0.7096	9	0.0322	*	
	dCA3	LA	0.7764	9	0.0139	*		0.3738	9	0.3216		
	vCA1	LA	0.7285	8	0.0404	*		0.2066	8	0.6235		
	BMA	BLA	0.7851	9	0.0122	*		0.7603	9	0.0174	*	
	IA	BLA	0.7597	9	0.0176	*		0.3169	9	0.4060		
	dCA3	BMA	0.8164	9	0.0073	*		0.0177	9	0.9639		
	BLA	BMA	0.7851	9	0.0122	*		0.7603	9	0.0174	*	
	CEA	BMA	0.8612	9	0.0029	*		0.2183	9	0.5726		
	IA	BMA	0.7422	9	0.0220	*		0.7328	9	0.0247	*	
	dCA3	CEA	0.7447	9	0.0213	*		-0.0381	9	0.9225		
	BMA	CEA	0.8612	9	0.0029	*		0.2183	9	0.5726		
	PL	IA	0.3417	8	0.4075			0.7235	8	0.0425	*	
	BLA	IA	0.7597	9	0.0176	*		0.3169	9	0.4060		
	BMA	IA	0.7422	9	0.0220	*		0.7328	9	0.0247	*	
Correlation of co-labeling/eYFP(%) levels during CFC retrieval	LA	dDG	0.0233	9	0.9525		7A	-0.7113	9	0.0317	*	7B
	IA	dDG	-0.8267	9	0.0060	*		-0.2277	9	0.5556		
	BLA	dCA1	0.7801	9	0.0131	*		0.2138	9	0.5806		
	vCA1	vDG	0.8895	8	0.0031	*		-0.2104	8	0.6170		
	vCA3	vDG	0.7365	8	0.0372	*		-0.0910	8	0.8303		
	CEA	vDG	0.5609	8	0.1481			-0.7641	8	0.0273	*	
	vDG	vCA1	0.8895	8	0.0031	*		-0.2104	8	0.6170		
	vCA3	vCA1	0.7488	8	0.0325	*		-0.2443	8	0.5598		
	vDG	vCA3	0.7365	8	0.0372	*		-0.0910	8	0.8303		
	vCA1	vCA3	0.7488	8	0.0325	*		-0.2443	8	0.5598		
	BLA	vCA3	0.3193	8	0.4408			0.7204	9	0.0286	*	
	BMA	vCA3	0.5145	8	0.1920			0.9267	9	0.0003	*	
	ILA	PL	0.7787	8	0.0228	*		0.8220	8	0.0123	*	
	PL	ILA	0.7787	8	0.0228	*		0.8220	8	0.0123	*	
	FRZ	ACA	0.7026	9	0.0348	*		0.1790	9	0.6449		
	dDG	LA	0.0233	9	0.9525			-0.7113	9	0.0317	*	
	FRZ	LA	0.3634	9	0.3364			0.6809	9	0.0435	*	
	dCA1	BLA	0.7801	9	0.0131	*		0.2138	9	0.5806		
	vCA3	BLA	0.3193	8	0.4408			0.7204	9	0.0286	*	
	BMA	BLA	0.6923	9	0.0388	*		0.7785	9	0.0135	*	
	IA	BLA	-0.6776	9	0.0449	*		0.3074	9	0.4211		
	vCA3	BMA	0.5145	8	0.1920			0.9267	9	0.0003	*	
	BLA	BMA	0.6923	9	0.0388	*		0.7785	9	0.0135	*	
	vDG	CEA	0.5609	8	0.1481			-0.7641	8	0.0273	*	
	dDG	IA	-0.8267	9	0.0060	*		-0.2277	9	0.5556		
	BLA	IA	-0.6776	9	0.0449	*		0.3074	9	0.4211		
	ACA	FRZ	0.7026	9	0.0348	*		0.1790	9	0.6449		
	LA	FRZ	0.3634	9	0.3364			0.6809	9	0.0435	*	
Correlation of co-labeling/c-Fos(%) levels during CFC retrieval	ACA	dDG	-0.8606	9	0.0029	*	7C	-0.3393	9	0.3717		7D
	PA	dDG	-0.1521	9	0.6960			0.6665	9	0.0499	*	
	vCA3	dCA1	0.0933	8	0.8261			0.6938	9	0.0382	*	
	IA	dCA1	0.2640	9	0.4925			0.7273	9	0.0264	*	
	LA	dCA3	-0.1721	9	0.6579			0.7209	9	0.0284	*	
	FRZ	dCA3	-0.7896	9	0.0114	*		-0.3549	9	0.3486		
	CEA	vDG	-0.0399	8	0.9253			-0.7361	8	0.0373	*	
	ILA	vCA1	-0.1942	8	0.6450			0.8132	8	0.0141	*	
	FRZ	vCA1	-0.7237	8	0.0424	*		-0.3909	8	0.3383		
	dCA1	vCA3	0.0933	8	0.8261			0.6938	9	0.0382	*	
	BLA	vCA3	-0.7955	8	0.0182	*		0.3312	9	0.3840		
	BMA	vCA3	-0.8459	8	0.0081	*		0.0715	9	0.8550		
	IA	vCA3	-0.2990	8	0.4719			0.8104	9	0.0081	*	
	ILA	PL	0.9774	8	<0.0001	*		0.5704	8	0.1398		
	BMA	PL	0.2606	8	0.5331			0.7863	8	0.0207	*	
	vCA1	ILA	-0.1942	8	0.6450			0.8132	8	0.0141	*	
	PL	ILA	0.9774	8	<0.0001	*		0.5704	8	0.1398		
	ACA	ILA	0.6576	9	0.0542			0.8488	9	0.0038	*	
	BLA	ILA	-0.0771	9	0.8437			0.6819	9	0.0431	*	
	BMA	ILA	0.1967	9	0.6120			0.6998	9	0.0359	*	
	dDG	ACA	-0.8606	9	0.0029	*		-0.3393	9	0.3717		
	ILA	ACA	0.6576	9	0.0542			0.8488	9	0.0038	*	
	BLA	ACA	-0.2954	9	0.4403			0.7032	9	0.0346	*	
	CEA	ACA	0.1631	9	0.6749			0.7470	9	0.0207	*	
	IA	ACA	0.6858	9	0.0414	*		0.5263	9	0.1455		
	dCA3	LA	-0.1721	9	0.6579			0.7209	9	0.0284	*	
	vCA3	BLA	-0.7955	8	0.0182	*		0.3312	9	0.3840		

PL	BMA	0.2606	8	0.5331		0.7863	8	0.0207	*
ILA	BMA	0.1967	9	0.6120		0.6998	9	0.0359	*
BLA	BMA	0.8619	9	0.0028	*	0.4531	9	0.2206	
PA	BMA	-0.5838	9	0.0988		0.6758	9	0.0457	*
dDG	PA	-0.1521	9	0.6960		0.6665	9	0.0499	*
BMA	PA	-0.5838	9	0.0988		0.6758	9	0.0457	*
vDG	CEA	-0.0399	8	0.9253		-0.7361	8	0.0373	*
ACA	CEA	0.1631	9	0.6749		0.7470	9	0.0207	*
IA	CEA	0.5915	9	0.0934		0.7359	9	0.0238	*
dCA1	IA	0.2640	9	0.4925		0.7273	9	0.0264	*
vCA3	IA	-0.2990	8	0.4719		0.8104	9	0.0081	*
ACA	IA	0.6858	9	0.0414	*	0.5263	9	0.1455	
CEA	IA	0.5915	9	0.0934		0.7359	9	0.0238	*
dCA3	FRZ	-0.7896	9	0.0114	*	-0.3549	9	0.3486	
vCA1	FRZ	-0.7237	8	0.0424	*	-0.3909	8	0.3383	

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