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Reporting Summary

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Statistics	
For all statistical analyse	es, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.
n/a Confirmed	
The exact samp	ole size (n) for each experimental group/condition, given as a discrete number and unit of measurement
A statement or	n whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
	test(s) used AND whether they are one- or two-sided sts should be described solely by name; describe more complex techniques in the Methods section.
A description o	of all covariates tested
🔲 🗶 A description o	of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
	on of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
	nesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted exact values whenever suitable.
For Bayesian a	nalysis, information on the choice of priors and Markov chain Monte Carlo settings
For hierarchica	and complex designs, identification of the appropriate level for tests and full reporting of outcomes
Estimates of ef	fect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated
'	Our web collection on statistics for biologists contains articles on many of the points above.
Software and co	ode
	t availability of computer code
Data collection	in vitro data were collected in Clampfit 10.4. Animal behaviors were collected using Ethovision video tracking software (Noldus).
Data analysis	in vitro data were analyzed in Clampfit 10.4. Statistic analyses were performed using Sigmaplot 14.
	m algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. eposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.
Data	
- Accession codes, unic - A list of figures that h	t <u>availability of data</u> nclude a <u>data availability statement</u> . This statement should provide the following information, where applicable: que identifiers, or web links for publicly available datasets lave associated raw data restrictions on data availability
The data that support the	findings of this study are available from the corresponding authors upon reasonable request.
Field-specif	fic reporting
Please select the one be	elow that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

Ecological, evolutionary & environmental sciences

Behavioural & social sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

	ices stady design
All studies must dis	close on these points even when the disclosure is negative.
Sample size	Sample size for each experiment is indicated in the figure legend for each experiment. The sample size was chosen based on previous experience for each experiment to yield high power to detect specific effects (Qin et al, JN 2012; Qin et al, Neuron, 2015). No statistical methods were used to predetermine sample size.
Data exclusions	no data were excluded except unhealthy cells for EP recording as described in methods: Series resistance was compensated at \sim 50% and monitored during the process, cells with series resistances larger than 25 M Ω were excluded.
Replication	All attempts for replication were successful. Numbers of cells and mice for replicates are indicated in the figure legends.
Randomization	Animals were chosen based on correct genotypes. Animal pairs from the same litters were compared to decrease variance in age and rearing. Each experiment contained animals from at least two different litters to ensure that the differences can be observed in different litters. Within each group, all mice and cells were randomly selected.
Blinding	Investigators are blinded for genotypes for electrophysiological recording, behvaior and immunohistological studies.
We require information	g for specific materials, systems and methods on from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, ed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.
Materials & exp	perimental systems Methods
n/a Involved in th	e study n/a Involved in the study
Antibodies	ChIP-seq
x Eukaryotic	cell lines
▼ Palaeontolo	ogy MRI-based neuroimaging
Animals an	d other organisms
Human res	earch participants
Clinical data	a
Antibodies	
Antibodies used	Parvalbumin (Swant PV235, 500x), the neuronal marker NeuN (Millipore MAB377, anti-mouse, 500x), cFos (Santa Cruz, sc52, rabbit, 50x) Cy2-, Cy3-conjugated secondary antibodies (Jackson Labs, 1000x dilution).
Validation	Cruz et al, 2017 Frontiers Cell Neu. PMID: 28769762; Schwaller B., et al. 1999, Am. J. Physiol. PMID: 9950767
– Animals and	other organisms
Policy information a	about studies involving animals; ARRIVE guidelines recommended for reporting animal research
Laboratory anima	Experimental mice included both males and females, between the ages of 2-4 months. PV-Cre mice (gift from Dr. Sylvia Arber, Jackson Lab # 017320) to LMO4flox/flox mice (gift from Dr. Jane Visvader). PTP1Bflox/flox mice (gift from Dr. Benjamin Neel, Jackson Lab #012679). All mice were bred on the C57BL6 background for over 12 generations.
- Wild animals	NA.
Field-collected sa	mples NA.
Ethics oversight	All procedures for animal use were approved by the University of Ottawa Animal Care and Veterinary Service, and were

Note that full information on the approval of the study protocol must also be provided in the manuscript.