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Mehdi Tafti

Corresponding author(s): NCOMMS-19-39487C

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## Reporting Summary

x Life sciences

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see <u>Authors & Referees</u> and the <u>Editorial Policy Checklist</u>.

Statistics				
For all statistical analys	es, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.			
n/a Confirmed				
The exact sam	ple size $(n)$ for each experimental group/condition, given as a discrete number and unit of measurement			
A statement o	n whether measurements were taken from distinct samples or whether the same sample was measured repeatedly			
<b> </b>	test(s) used AND whether they are one- or two-sided ests should be described solely by name; describe more complex techniques in the Methods section.			
A description	of all covariates tested			
A description	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons			
	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)			
For null hypot	hesis 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	analysis, information on the choice of priors and Markov chain Monte Carlo settings			
For hierarchic	al and complex designs, identification of the appropriate level for tests and full reporting of outcomes			
Estimates of e	ffect 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 c	ode			
Policy information abou	ut availability of computer code			
Data collection	EMBLATM hardware was used for signal acquisition and Somnologica- 3TM (Medcare) software for data analysis. High-resolution CCD cameras (Panasonic WV-CP500) were used for high-quality, horizontal (side-view) video recording.			
Data analysis	Signal processing and data analysis was performed using custom written algorithms in MATLAB R2015a software. GraphPad prism 8 was used for statistical analysis.			
For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.				
Data				
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We (the authors) declare	that the data supporting the findings of our study are available within the paper and its supplementary information files.			
Field-speci	fic reporting			

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

Ecological, evolutionary & environmental sciences

Behavioural & social sciences

#### Life sciences study design

were blind during the EEG scoring.

All studies must dis	sclose on these points even when the disclosure is negative.
Sample size	we determined the sample size based on experiences during last 25 years of animal experimentation work and our published literatures (Vassalli et al, 2013 brain, Maret et al, 2007, PNAS). We did not use statistical test to determine sample size.
Data exclusions	Animals without correct, enough and local expression of viral particles were removed from analysis. Animals with good EEG, EMG and video recording were kept for the analysis and the rest were excluded. Good EEG, EMG and video recording means that any mice with high quality EEG but disrupted EMG and vice versa and also the same for video recording were excluded. This step was done before moving to analysis part. During video analysis, animals without normal behavior (e.g. sick behavior), were excluded from the study.
Replication	Under investigation
Randomization	All genotypes were randomly distributed for recording. This means that in each seri of recording we had different combination of the genotypes. Vigilance state scoring was done blindly.

### Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed 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.

People who performed sleep deprivation and viral injection were totally blind to the genotype of the animals. In the analysis the investigators

Materials & experimental systems		Methods	
n/a Involved in the study	n/a	Involved in the study	
☐ <b>X</b> Antibodies	×	ChIP-seq	
<b>▼</b> Eukaryotic cell lines	×	Flow cytometry	
<b>▼</b> Palaeontology	x	MRI-based neuroimaging	
Animals and other organisms			
Human research participants			
<b>▼</b> Clinical data			
·			

#### **Antibodies**

Blinding

Antibodies used

Antibodies used are mouse-anti-TPH (sigma, Cat# T0678), Rat-anti-mCHERRY (life technologies, Cat# M11217) and Chicken-anti-GFP (Aves Labs, Cat# 1020), Rabbit-anti-CRE (Novagen, Cat# 69050-3).

Validation

The antibodies that we used, all are commercially-available, and were used according to manufacturer's instructions. mCherry Antibody (M11217) in IF

U2OS cells were transduced using an adenoviral construct expressing mCherry. A) Native expression of mCherry detected post-transduction using Texas Red filters (562 nm/624 nm) B) Anti-Cherry antibody added and cells imaged using the Cy5 filter set (628 nm/692 nm) C) mCherry expression detected by adding anti-mCherry and Alexa Fluor® 647 goat anti-rat (Product # A-21247).

Anti-checken-GFP: Antibodies were analyzed by western blot analysis (1:5000 dilution) and immunohistochemistry (1:500 dilution) using transgenic mice expressing the GFP gene product. Western blots were performed using BlokHen® (Aves Labs) as the blocking reagent, and HRP-labeled goat anti-chicken antibodies (Aves Labs, Cat. #H-1004) as the detection reagent. Immunohistochemistry used tetramethyl rhodamine-labeled anti-chicken IgY.

Rabbit-anti-CRE: Evaluated by Western Blotting with Recombinant Cre-His. Western Blotting Analysis: Representative lot data. Recombinant Cre-His loaded at 20 ng/lane (Lane 1) and 10 ng/lane (Lane 2) was probed with Cat. No. 69050-3, Anti-Cre (1:10,000 dilution). Proteins were visualized using a Donkey Anti-Rabbit secondary antibody conjugated to HRP and a chemiluminescence detection system. Arrow indicates Cre (~39 kDa).

Validation of TPH antibody has been reported in 68 published papers based on the company website.

#### Animals and other organisms

Policy information about <u>studies involving animals</u>; <u>ARRIVE guidelines</u> recommended for reporting animal research

Laboratory animals the following mouse lines were used in our study:

Hcrt knock out mice (Chemelli, 1999) 5HTT knouk out mice (Bengel, 1998)

Hcrtr1/Hcrtr2 double-floxed mice (Vassalli et al, 2015; Li et al 2018).

All analyzed mice were male and at the age between 12-14 week old.

Wild animals No wild animals were used in this study.

Field-collected samples No field collected samples were used in this study.

Ethics oversight All animal procedures followed Swiss federal laws and were approved by the State of Vaud Veterinary Office.

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