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Reporting Summary

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 Authors & Referees and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒	A description of all covariates tested
☐	☒	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 hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐	Estimates of effect 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 code

Policy information about availability of computer code

Data collection	For acquisition of sequencing data, the commercially available Illumina NextSeq 500 platform was used with accompanying software. For acquisition of qPCR data, the commercially available StepOnePlus platform was used with accompanying software. For image acquisition, Zen (Zeiss) or pylon 6.1.0 (Basler) was used.
Data analysis	For data analysis, custom python code was used (python 3.7) or R code (R 3.4.1, https://www.r-project.org/), integrated into the anaconda distribution 1.9.7. Additionally, the following software packages were used: Mapping to the zebrafish genome (GRCz11, https://www.ncbi.nlm.nih.gov/assembly/GCA_000002035.4/) was done using the STAR 2.7 algorithm (https://github.com/alexdobin/STAR). Reads were counted using featureCount 1.6.3 (http://subread.sourceforge.net/). Annotation of the genes was performed by scraping information from ENSEMBL (https://www.ensembl.org/index.html) using biomaRt (http://www.biomart.org/). Differential expression analysis was done using edgeR 3.11 (10.18129/B9.bioc.edgeR). For video analysis, common functions of the OpenCV platform (3.4.9 and following releases) were used (https://opencv.org/). Additional code that was used in this study is available from https://github.com/Anneser/SensingOthers/.

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

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

All data is provided in this paper or the accompanying supplementary tables S1 (sequencing data) and S2 (raw data for qPCR experiments). All sequencing data has

been made available under the SRA BioProject PRJNA627056. Gene annotation was performed using the publicly available ENSEMBL database (https://www.ensembl.org/Danio_rerio/Info/Index). The Z-Brain atlas can be downloaded from https://github.com/owenrandlett/Z-Brain. Gene expression data from Raj et al. are available under the Omnibus accession number GSE105010.

Field-specific 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.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

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

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Sample size was determined prior to experiments using the E-equation method.
Data exclusions	No data was excluded from analysis except for data in supplemental figure 6 d, in which animals that did not move over the imaging period were excluded from further analysis (pre-established criterion).
Replication	All replicates for all experiments were performed as biological replicates that showed a consistent effect. For Next-Generation-Sequencing, 4 - 6 replicates were used. For qPCR experiments, 2 - 15 replicates were used. For imaging experiments, 4 - 18 animals were imaged.
Randomization	For all experiments, animals were selected from a batch of eggs at 2 dpf. The only exclusion criteria were obvious malformations. After removal of these deformed animals, eggs were then sorted into the different conditions (e.g. isolated vs social) in batches of 10 (10 consecutive animals went into the same condition). We assumed that within one clutch of eggs all animals are equivalent and by alternating the condition into which the animals were sorted across different batches we used a blocked design to prevent potential confounders.
Blinding	The researchers sorted the animals into different categories (e.g. isolated vs social) and by the very nature of the experiments (e.g. different number of animals within a tank or dish) could not be blinded to the conditions during experiment and data acquisition. To account for this, all experiments were performed in a paired design (e.g. RNA extraction was done simultaneously on all animals derived from one batch) and analyzed with minimal human interference (e.g. automatic tracking of animals with OpenCV, automatic determination of threshold cycle in qPCR).

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.

Materials & experimental systems

n/a	Involved in the study
☐	☒ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	1) anti-PTH2 (custom, this study); 2) anti-TH (custom, Ryu lab), ; 3) anti-OXT (custom, Ryu lab); 4) anti-znp1 (Synaptic Systems cat. no 106002, lot 1-27).
Validation	1) custom antibody, was validated by co-staining with corresponding in-situ-probe, which clearly labeled the same population of cells. In accordance with the findings described in our study, the antibody signal increases if the specimen has been raised with conspecifics. 2) custom antibody, was reported to overlap with TH and dopamine transporter in-situ signal. Introduced in Ryu et al., 2007 (http://dx.doi.org/10.1016/j.cub.2007.04.003). 3) custom antibody, introduced in Herget et al. 2014 (https://doi.org/10.1002/cne.23480). Specificity was confirmed by loss of signal in oxytocin-morpholino injected 3 dpf larvae. 4) commercial antibody, polyclonal rabbit serum. Specificity was demonstrated by loss of signal in knock-out animals.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	The study included zebrafish (strain Konstanz and nacre (mitfa-/-)) of both sexes ranging from the larval to the adult stage. In particular, animals at age 5, 7, 14, 21, 28 dpf and 3 mpf were used. Additionally, artemia salina (larval stage) was used in this study.
Wild animals	The study did not include wild animals.
Field-collected samples	The study did not included field-collected samples.
Ethics oversight	All animal procedures conformed to the institutional guidelines of the Max Planck Society and were approved by the Regierungspräsidium Darmstadt, Germany (governmental ID: V 54-19 c 20/15-F126/1016 and V 54-19 c 20/15- F126/1013).

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