nature portfolio

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Last updated by author(s):	Aug 22, 2022

Reporting Summary

Nature Portfolio 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 Portfolio policies, see our <u>Editorial Policies</u> and the <u>Editorial Policy Checklist</u>.

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

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1010	an statistical analyses, commit that the following items are present in the ligare regend, table regend, main text, or internous section.
n/a	Confirmed
\boxtimes	\Box 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
\boxtimes	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.
\boxtimes	A description of all covariates tested
\boxtimes	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)
\boxtimes	For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
\boxtimes	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
\boxtimes	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
\boxtimes	\square Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated
	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection

For the imaging, the control of the hardware are part of our open-source microscope control project developed in Python available at https://github.com/TestaLab, additional LabVIEW code for FPGA control is available upon request.

Data analysis

Code for simulation of STARSS experiments is available at https://github.com/TestaLab, any other script and small piece of code is available upon request.

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 and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio 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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

No restriction on data availability. Minimal datasets are available on Zenodo (10.5281/zenodo.7010471). All code and raw data are available upon request.

Field-spe	ecific reporting		
<u> </u>	ne 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		
	the document with all sections, see <u>nature.com/documents/nr-reporting-summary-flat.pdf</u>		
Tot a reference copy of t	the document with an sections, see <u>nature, confuded unions of reporting-summary-nat, pur</u>		
Life scier	nces study design		
All studies must dis	close on these points even when the disclosure is negative.		
Sample size	No sample size dependent statistical testing was performed.		
Data exclusions	No data were excluded from the analysis.		
Replication	The STARSS curve presented were reproducible in different days of recording and for extended times after system alignment. System alignment was stable over time for the full day of recording.		
Randomization	No allocation into experimental group were performed		
Blinding	No allocation into experimental group were performed		
Reportin	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, sed 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 & ex	perimental systems Methods		
n/a Involved in th	n/a Involved in the study		
Antibodies	ChIP-seq		
☐ X Eukaryotic	cell lines Flow cytometry		
	ogy and archaeology MRI-based neuroimaging		
	d other organisms		
	earch participants		
Clinical dat			
Dual use re	esearch of concern		
Antibodies			
Antibodies used	Polyclonal antisera raised against recombinant HIV-1 capsid (CA) (sheep; in house) or GFP (rabbit; in house); secondary antibodies		
	donkey anti-sheep IgG DyLight 680 (#613-744-168; Rockland Immunochemicals, USA), IRdye800CW donkey anti-rabbit IgG (#926-32213; LI-COR Biosciences). Recombinant Anti-GFP antibody [EPR14104] (ab183734) was used to decorate rsEGFP2 coated		
	silica beads.		
Validation	The in-house antibodies have tested and used in many publications over the past 20 years. Here are few examples: doi.org/10.10 j.cell.2021.01.025, doi.org/10.7554/eLife.41800, doi:10.1038/nature13838. We think that a formal validation is not necessary in case.		
Eukaryotic c	all lines		
Policy information Cell line source(s			
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Policy information about <u>cert lines</u>		
Cell line source(s)	ATCC	
Authentication	None of the cell lines used were authenticated.	
Mycoplasma contamination	All cell lines were tested negative for mycoplasma contamination.	
Commonly misidentified lines (See <u>ICLAC</u> register)	HEK293T cells were validated in 2017 by Eurofins Medigenomics Forsensic GmbH (Ebersberg, Germany).	