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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 our Editorial Policies 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	In the conventional sense, no software was used for data collection. However, simulated datasets were created using custom codes on Python platform. The details will be made available with the codes shared with the editor and reviewers according to the software policy.
Data analysis	In the conventional sense, data analysis for generating box plots have been done using custom codes in Python. Deep learning codes have been generated in Python on Keras. Codes of all these will be made available to the editor and reviewers according to the software policy.

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 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

Accession codes will be made available before publication. All the raw microscopy data used in this paper will be made open access. There are no restrictions on data availability in our current knowledge.

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	In our case, the conventional sample size pertaining life sciences does not apply. Our sample size is typically determined by the number of images in the training or test datasets. These have been explicitly included in the paper.
Data exclusions	No data was excluded from the analysis
Replication	In the sense of conventional life sciences jargon, replication does not apply. Replication in the sense of deep learning applies in the conventional sense and has been verified through cross-validation.
Randomization	In the sense of conventional life sciences jargon, randomization does not apply. Randomization as relevant to machine learning has been incorporated using standard mechanisms.
Blinding	Our data does not require blinding of the investigators.

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 and archaeology
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	H9c2 (2-1) Rat DB1X heart myoblast; Cataloge No: 88092904 ; Lot No. 08G008 P+8 ; Source: ECACC; European Collection of Authenticated Cell Cultures; The MCC13 cell line was a gift from Professor Ugo Moens, Molecular Inflammation Research Group, UiT, and originated from Professor Baki Akguel, University of Cologne, Institute of Virology, Germany.
Authentication	H9c2 (2-1) cell line was authenticated by DNA fingerprinting and quality controlled by source (ECACC) as stated in the Certificate of analysis for lot no 08G008; The MCC13 cells line was not authenticated.
Mycoplasma contamination	H9c2 (2-1) cells tested negative for mycoplasma; the MCC13 cell line was not tested for mycoplasma.
Commonly misidentified lines (See ICLAC register)	Not relevant for any cell line used.