

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 [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	The custom wearable sensing system was designed using Altium Designer. Digital data encoding and real-time wireless transmission from the Hall-effect sensor array were managed via custom C/C++ firmware and a Python-based FastAPI server (v0.100+). Structural and chemical characterization data were collected using specialized instrument software, including Asylum Research Cypher ES for MFM, Quantum Design MPMS-3 for SQUID magnetometry, and NIS-Elements for confocal imaging. Histological quantification and cell viability analysis were performed using ImageJ (NIH, v1.53).Phillips EPIQ 7 Ultrasound System S5-1 probe for pig's echocardiograph.
Data analysis	The cardiac volumetric reconstruction was performed using a custom-developed algorithm, PAGO-DeMag, implemented in Python. The custom code for the PAGO-DeMag algorithm and the real-time analytics platform is available in the following public repository: https://github.com/sxing1208/MagCNWeb . For per-atom magnetic moment prediction, the open-source FT-ChemBERTa model (based on the ChemBERTa-2 foundation) was utilized. The ChemBERTa model used for magnetic moment prediction is an open-source tool available at https://github.com/deepchem/deepchem . Finite element analysis (FEA) for mechanical deployment and strain distribution was conducted using Abaqus/Standard 2019, while time-resolved magnetic-field mapping was simulated in COMSOL Multiphysics 6.3. First-principles density functional theory (DFT) calculations were performed using the Vienna Ab initio Simulation Package (VASP). Circuit validation was conducted via LTSpice transient simulations. Statistical analyses and machine-learning pipeline for rhythm classification (CNN and MLP branches) were implemented using Python (TensorFlow/Keras).All commercial software used in this study is available from the respective vendors.Statistical analyses were performed using GraphPad Prism 9.

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](#)

All data generated or analyzed during this study are included in this published article and its supplementary information files.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender

Reporting on race, ethnicity, or other socially relevant groupings

Population characteristics

Recruitment

Ethics oversight

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

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](https://www.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

Data exclusions

Replication

Randomization

Blinding

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
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Antibodies

Antibodies used	Live/Dead Cell Imaging Kit (R37601, Thermo Fisher Scientific), CCK-8 assay (CK04-01, Dojindo) , anti- α SMA (ab5694 abcam), anti-F4/80 (ab6640 abcam)
Validation	All antibodies are commercially available. Antibodies were validated for indicated species and applications, as appropriate, according to the manufacturer's specification sheet and supported by relevant citations on their product pages.

Animals and other research organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research, and [Sex and Gender in Research](#)

Laboratory animals	porcine model (Yorkshire, 18.5~24.2 kg) ; Wistar rats (250–300 g); Charles River Laboratories
Wild animals	No wild animals were used in this study.
Reporting on sex	Both female and male animals were used for all experiments
Field-collected samples	The study did not involve field-collected samples.
Ethics oversight	All animal procedures were conducted in accordance with the guidelines and regulations of the Institutional Animal Care and Use Committee (IACUC) of Columbia University (Protocol No. AC-AABY0652, AC-AABY0651). All experimental protocols adhered to institutional ethical standards for animal research.

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

Plants

Seed stocks	Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.
Novel plant genotypes	Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.
Authentication	Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.