

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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☐ | ☒ 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
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ 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 radio frequency data were acquired using Texas Instruments AWR 6843 FMCW radar device. The clinical ECGs were collected by the clinical-grade 12-lead ECG device. The daily life long-term 3-lead ECGs were obtained using Sid Medical HA301B holter device. Code was written using Python version 3.9 (python software Foundation, PyTorch version 2.0.1) and Matlab R2021a. Code is available for non-commercial research purpose at https://github.com/zhangbinbin18/RF-HRV .
Data analysis	The radio frequency data were stored as a digital BIN file, and all files were transmitted to the University of Science and Technology of China Intelligent Perception Lab (Anhui, Hefei, China). These source radio frequency BIN files were preprocessed using the commercially available Matlab R2021a and stored as MAT file. The radar MAT data were then used for algorithm testing. We reported HRV monitoring performance using HRV error. All analyses were completed using Matlab R2021a. Code is available for non-commercial research purpose at https://github.com/zhangbinbin18/RF-HRV .

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](#)

The minimum dataset supporting the findings and the released code has been deposited in (<https://doi.org/10.24433/CO.9082638.v2>). Additional data are available under restricted access due to privacy regulations. Access requests can be directed to the corresponding author, with an expected response time of up to 60 days. Requesters should sign a data use agreement and submit a research proposal specifying the intended use. Access approval is contingent upon an ethical review to ensure compliance with institutional policies and legal requirements. Approved data use will be restricted to non-commercial research purposes.

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

Sex was assigned based on the government-issued ID. The datasets used in the cohorts have sex distributions reported in the paper. Sex-based analysis was not reported because sex was unrelated to system implementation or deployment. Self-identification gender was not collected from the patients.

Reporting on race, ethnicity, or other socially relevant groupings

Race, ethnicity, and other socially relevant groupings were not collected from the patients and were unrelated to model implementation or deployment.

Population characteristics

Our test data covers human subjects aged 3 to 94 years, with an average age of 55 years. Overall, the younger subjects had healthier cardiovascular systems and were mostly normal. After excluding subjects with motion or improperly attached electrode pads, our cohort included 6,222 subjects (55% females, 45% males).

Recruitment

We recruited 7,090 outpatient volunteers in the hospital and 2 long-term monitoring volunteers at home. Informed consent was obtained from all volunteers. All data were de-identified. There were no selective exclusion criteria based on sex, race, or acuity of illness. However, 868 subjects in the hospital were excluded solely due to unstable electrode placement during data collection; the number of eligible subjects in the hospital is 6,222. Participants received no compensation for their participation.

Ethics oversight

The project was conducted after ethics review by the Ethics Review Board of The First Affiliated Hospital of the University of Science and Technology of China. When registering, all participants agreed that their data could be used for scientific research and signed an informed consent form. Participants received no compensation for their participation.

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

Life sciences study design

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

Sample size

The sample size for this study was determined with the aim of covering a diverse population across various diseases, thereby ensuring data diversity. Over a period of more than six months, a total of 7,090 cases were collected. After excluding 868 cases that did not meet the study criteria, all remaining 6222 eligible data were used in the analysis. The dataset from 6,222 outpatients contains 186,660 seconds of data. The data (55% female) was collected at the First Affiliated Hospital of USTC. For long-term monitoring, we recruited 2 subjects who experienced discomfort and had scheduled medical check-ups. Prior to their appointments, we deployed our radio monitoring system in their sleep environment and collected overnight radio signal recordings during sleep. We continuously collected data from a specific subject for 21 consecutive nights, totaling 453,600 seconds of data. For more details and demographics of the outpatient dataset, please see manuscript Table 1. Since our system does not require training data, all data are used as test data.

No formal sample size calculation was performed prior to data collection. However, the sample size is considered sufficient due to the extensive collection period and the intentional inclusion of diverse cases, which enhances the generalizability and robustness of the findings.

Data exclusions

Data from 868 participants were excluded due to loosening of the electrode pads when capturing the ground-truth ECG.

Replication	Replication were conducted on data from 6,222 outpatients and data from a specific subject across 21 consecutive nights.
Randomization	Randomization was not relevant to this study.
Blinding	Blinding was not relevant to this study.

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

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.