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Corresponding author(s): Su Ryon Shin, Yu Shrike Zhang NP-PI180508B

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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	The MATLAB codes can be accessed through key references and the Zhang Lab website (https://shrikezhang.com/publications/opensource).
Data analysis	No new data were collected and they were referenced from the key references. Full descriptions were presented in the key references.

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

Most data associated with this protocol can be found in the Key References. Additional datasets that support this protocol are available from the corresponding authors upon reasonable request. All requests for raw and analyzed data and materials will be promptly reviewed by the Brigham and Women's Hospital to verify whether the request is subject to any intellectual property or confidentiality obligations. Any data and materials that can be shared will be released via a Material Transfer Agreement.

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	Performance of independent experiments were set up in at least three or more replicates, based on a sample size calculated using power analysis from anticipated results (means and standard deviations) from the key references. Zhang, Y.S., et al. Multisensor-integrated organs-on-chips platform for automated and continual in situ monitoring of organoid behaviors. Proc Natl Acad Sci U S A 114, E2293-E2302 (2017). DOI: 10.1073/pnas.1612906114. Shin, S.R., et al. Label-Free and Regenerative Electrochemical Microfluidic Biosensors for Continual Monitoring of Cell Secretomes. Adv Sci (Weinh) 4, 1600522 (2017). DOI:10.1002/advs.201600522. Shin, S.R., et al. Aptamer-Based Microfluidic Electrochemical Biosensor for Monitoring Cell-Secreted Trace Cardiac Biomarkers. Anal Chem 88, 10019-10027 (2016). DOI:10.1021/acs.analchem.6b02028.
Data exclusions	For electrochemical measurements the samples were excluded from the analysis when leakages from the sensing chips were observed; otherwise, all the data were included.
Replication	Fully functional sensors, electrochemical chips, and breadboard have to be thoroughly evaluated before running the experiment to ensure replication. The experimental reagents should only be used during the established time frame after preparation and if stored under the appropriate conditions.
Randomization	In this article, we present the protocol for the development of a electrochemically affinity based biosensor. Validation of biomarker sensitivity and specificity has been previously reported. Zhang, Y.S., et al. Multisensor-integrated organs-on-chips platform for automated and continual in situ monitoring of organoid behaviors. Proc Natl Acad Sci U S A 114, E2293-E2302 (2017). DOI: 10.1073/pnas.1612906114. Shin, S.R., et al. Label-Free and Regenerative Electrochemical Microfluidic Biosensors for Continual Monitoring of Cell Secretomes. Adv Sci (Weinh) 4, 1600522 (2017). DOI:10.1002/advs.201600522. Shin, S.R., et al. Aptamer-Based Microfluidic Electrochemical Biosensor for Monitoring Cell-Secreted Trace Cardiac Biomarkers. Anal Chem 88, 10019-10027 (2016). DOI:10.1021/acs.analchem.6b02028.
Blinding	This article is a descriptive protocol for the development of a electrochemically affinity based biosensor. No need for blinding for the data collection or device preparation.

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

Antibodies

Antibodies used	Albumin biotinylated antibody and full-length protein from Albumin ELISA kit (Abcam cat. no. ab108788, RRID: AB_2876883); Glutathione S-transferase-alpha (GST-α) biotinylated antibody and full-length protein from GST-α ELISA kit (Abcam, cat. no. ab173835, RRID: AB_2876882); CK-MB full-length protein from CK-MB ELISA kit (Abcam, ab193696, RRID: AB_2876884)
Validation	Initial detection of the liver associated secretomes via GST-α and albumin antibody affinity in our electrochemical platform was

Validation	validated by our team in the paper: Shin, S.R., et al. Label-Free and Regenerative Electrochemical Microfluidic Biosensors for Continual Monitoring of Cell Secretomes. Adv Sci (Weinh) 4, 1600522 (2017). We reported the multiplexed electrochemical biosensor capability of continuous detection of the same antibodies in the paper: Zhang, Y.S., et al. Multisensor-integrated organs-on-chips platform for automated and continual in situ monitoring of organoid behaviors. Proc Natl Acad Sci U S A 114, E2293-E2302 (2017).