nature portfolio

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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	No data was collected for this protocol. All data were previously published, and the original publication describing the data is noted in the text.
Data analysis	This manuscript is a protocol for how to analyze multi-omics datasets with software that we created. All software is open-source, and we provided Github repository URLs in the code availability statement at the end of the manuscript.

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 datasets used in this protocol are from a previously published study that collected multi-omics data from islet tissue (transcriptomics and proteomics) and plasma (lipidomics) from human donors undergoing pancreatic surgery30. The example datasets used in this protocol are integrated as examples throughout the four web-tools. The unprocessed matrices are included as examples in ExpressAnalyst (www.expressanalyst.ca) and MetaboAnalyst (www.metaboanalyst.ca). Lists of significant features are included as examples in OmicsNet (www.omicsnet.ca). Normalized matrices are included as examples in OmicsAnalyst (www.omicsanalyst.ca). See the Materials section for further information about the example datasets.

Human research participants

Policy information about studies involving human research participants and Sex and Gender in Research.

Reporting on sex and gender	Metadata describing sex was not provided by the authors who originally published the data re-analyzed in this protocol manuscript, for what we assume are privacy reasons as identification with sex alongside the other provided metadata is highly possible. However, our manuscript clearly describes how sex can be statistically accounted for during analysis (step 8).
Population characteristics	This protocol re-analyzed previously published data. All metadata made publicly available by the original authors is provided to researchers executing the protocol (diabetes diagnosis, age, oral glucose tolerance test, HbA1c levels, BMI).
Recruitment	No new data was collected in this work, therefore no recruitment was performed.
Ethics oversight	Only previously published, publicly available data was analyzed, therefore there was no ethics approval process.

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	This protocol re-analyzed previously published data, so we did not perform any experimental design.
Data exclusions	In this protocol, we followed sample exclusions as described in the original study.
Replication	This manuscript is a software protocol for analyzing data from the life sciences. No new data was collected, thus no attempts were made to replicate findings.
Randomization	This protocol re-analyzed previously published data, so we did not perform any experimental design.
Blinding	This protocol re-analyzed previously published data, so we did not perform any experimental design.

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

Methods

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