

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 (<i>n</i>) 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> 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 <i>d</i> , Pearson's <i>r</i>), 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	Thermo Q Exactive tune Application (version 172.16.0.200) and Thermo Scientific Xcalibur (version 4.1) were used for the control of mass spectrometer and data collection.
Data analysis	The code and applet written in this study have been uploaded on GitHub which can be downloaded at https://github.com/HuXiaoyu-TJU/A-comprehensive-landscape-of-human-organ-N-glycoproteome. Glyco-Decipher (version 1.0.4, https://github.com/DICP-1809/Glyco-Decipher/releases), pGlyco (version 3.1, https://github.com/pFindStudio/pGlyco3/releases), FragPipe (version 22.0, https://github.com/Nesvilab/FragPipe/releases) were used to search datasets. Skyline (version 24.1, https://skyline.ms/project/home/software/Skyline/begin.view) were used for quantitative extracted ion chromatograms of each ID. Post-analysis statistics was conducted using Python (version 3.9.13, Anaconda version 23.7.4, https://www.anaconda.com/) and R (version 4.4.1, https://cran.r-project.org/mirrors.html). Packages "tidyverse (version 2.0.0)", "factoextra (version 1.0.7)", "tidyr (version 1.3.1)", "dplyr (version 1.1.4)" were used for data analysis. "RColorBrewer (version 1.1-3)", "ComplexUpset (version 1.3.3)", "ggplot2 (version 3.5.1)", "pheatmap (version 1.0.12)", "ComplexHeatmap (version 2.20.0)", "svglite (version 2.1.3)", "motifStack (version 1.42.0)" were used for data visualization. Package "scikit-learn" (v1.3.0) was used for machine learning pipelines, feature selection, and model evaluation. "pandas" and "numpy" were utilized for data manipulation and numerical computations. "matplotlib" was employed for data visualization and ROC curve generation.

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 raw LC-MS/MS datasets from analysis of intact N-glycopeptides enriched from the 18 human organs/tissues have been uploaded to the Pride (<https://www.ebi.ac.uk/pride/>) under accession code PXD070547 [<https://www.ebi.ac.uk/pride/archive/projects/PXD070547>].

The skyline files were uploaded to <https://panoramaweb.org/Tongji%20University%20-%20Tian-BAMS/N-glycoproteome%20of%2018%20human%20organs/project-begin.view>

The merged search results of gPeptide, Glyco-Decipher, FragPipe and pGlyco were provided in Supplementary Data 7.

Protein database is from the UniProt (<https://www.uniprot.org/>) Homo sapiens reference proteome (version 2023-07-28, containing 20,423 protein sequences) .

Glygen (<https://glygen.org/home/>) and GlyConnect (<https://glyconnect.expasy.org/all/compositions?f=glycan%3DN-linked&p=0>) database of human N-glycans were downloaded for comparison with this study.

Source data are provided with this paper. Unless otherwise stated, all data supporting the results of this study can be found in the article, supplementary, and source data 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

Sex was determined based on self-reported medical records. A specific sex and gender-based statistical analysis was not carried out in this study. The primary objective of this research was to establish a baseline, organ-specific N-glycoproteome atlas across human tissues. Given the limited sample size per individual organ (n = 2 to 6 subjects per organ), the study lacks the statistical power required to robustly detect and report sex- or gender-specific glycosylation differences.

Reporting on race, ethnicity, or other socially relevant groupings

All participants are asian-pacific.

Population characteristics

The study included a total of 74 subjects. The cohort consisted of 45 males and 29 females. The participants' ages ranged from 32 to 66 years old (median age: 48). Sex and gender information was determined based on self-reported medical records. Participants were not compensated for their inclusion in this retrospective study. Sample size was determined based on the maximum available high-quality clinical residual specimens for each organ to ensure broad representativeness. No statistical method was used to pre-determine sample size.

Recruitment

All human tissue samples utilized in this study were residual specimens obtained following routine diagnostic biopsies or surgical procedures, exclusively after the completion of requisite clinical pathological examinations.

Ethics oversight

The experiments were performed in accordance with the Code of Ethics of the World Medical Association (Declaration of Helsinki) and approved by the Ethics Committee of the First Affiliated Hospital of Nanjing Medical University (2202-SR-598). The requirement for specific informed consent for this study was waived. This waiver was granted because (i) all participants had previously signed a broad informed consent form upon admission or during the diagnostic procedure, explicitly agreeing that their residual clinical specimens could be utilized for future medical research; and (ii) the research utilized fully de-identified and anonymized residual samples post-pathological examination, posing no more than minimal risk to the subjects and involving no sensitive personal or genetic information. The study procedures strictly adhere to the current ethical regulations and guidelines in China.

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 The study included a total of 74 subjects. The cohort consisted of 45 males and 29 females. There were 2-6 samples in each organ.

Data exclusions No data were excluded in analysis.

Replication Each organ was obtained from 2 to 6 subjects, and each sample underwent 1 to 3 technical replications.

Randomization	Sample processing sequence was randomized.
Blinding	Researchers were blinded to specific patient identities during data analysis (due to anonymization).

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.