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	DIA-NN version 1.8.1, Python version 3.11.5, kneed version 0.8.5, pandas version 2.1.4, numpy version 1.24.3, scipy version 1.11.1, pingouin version 0.5.3, seaborn version 0.12.2, matplotlib version 3.7.2, statsmodels version 0.14.0, sklearn version 1.3.0, sklearn2pmml version 0.105.2, shap version 0.43.0, fastcluster version 1.2.6, networkx version 3.1, umap version 0.5.5, R version 4.2.1, RStudio version 2021.09.2 Build 382, ROCR version 1.0-11, nnls version 1.4, glmnet version 4.1-4, glmnetUtils version 1.1.8, pROC version 1.18.0, Matrix version 1.5.1, leaps version 3.1, MASS version 7.3-58.1, broom version 1.0.0, Cytoscape version 3.10.1, Android Studio Iguana version 2023.2.1, pmml-android version https://github.com/loopGod/pmml-android
Data analysis	Custom code used in this study is available at: https://zenodo.org/records/11002015.

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 proteomics data have been deposited in the iProX integrated Proteome resources (https://www.iprox.cn/page/home.html; accession number IPX0008492000).

Human research participants

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

Reporting on sex and gender	All participants are pregnant female.
Population characteristics	Participants included women with spontaneous preterm birth (sPTB) who delivered at < 37 weeks of gestation, and women with full-term birth (FTB) who delivered at ≥ 37 weeks.
Recruitment	Pregnant women who came into the clinic with a previous history of PTB, late miscarriage, or cervical surgery were defined as increased-risk, or with suspected symptoms and signs of PTB, such as contractions, abdominal cramps, back pain, or increased pelvic pressure between 16+0 and 36+6 weeks of gestation, and those without symptoms or such history were assigned as low-risk control group, matched by gestational age at sampling.
Ethics oversight	IRB of Research Ehics Committee of 5 hospitals and BGI Research provided 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

Life sciences study design

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

Sample size	806 participants
Data exclusions	Women were excluded from the study if they experienced vaginal bleeding or had an iatrogenic preterm birth due to conditions such as preeclampsia, severe fetal growth restriction, fetal distress, placental abruption, placenta previa, or chromosomal abnormalities, as identified during the follow-up assessments
Replication	Biological replication
Randomization	The proteomics data were acquired in a randomized sequence for all samples
Blinding	The investigators were blinded to group allocation during data collection and/or analysis

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

Antibodies

Antibodies used

LUM: Human Lumican DuoSet ELISA, catalog number: DY2846-05, lot number: P358379, DouSet ELISA Ancillary Reagent Kit 2 category number: DY008B, lot number: P368843; Recombinant Human Lumican Protein, CF, category number: 2846-LU-050, lot number: NEA0822101; TIMP1: Human TIMP-1 Quantikine ELISA Kit, category number: DTM100, lot number: P364674; Quantikine Immunoassay Control Set 651 for Human TIMP1, category number: QC173, lot number: 651-230605; FN1: Human Fibronectin Quantikine ELISA Kit, category number: DFBN10, lot number: P368799, Quantikine Immunoassay Control Set 834 for Human Fibronectin, category number QC200, lot number: 834-180605; B2M: Human beta 2-Microglobulin Parameter Assay Kit, category number: KGE019, lot number: 360653, Parameter Immunoassay Control Set 916 for Human B2M, category number: QC224, lot number: 916-180508; AMBP: Human alpha 1-Microglobulin ELISA Kit (Colorimetric), catalog number: NBP2-60496, lot number: 041392209R;

Validation

The ELISA and QC kits mentioned above are utilized for the quantitative determination of concentrations for Human Lumican/Tissue Inhibitor of Metalloproteinases 1/Fibronectin/beta 2-Microglobulin/alpha 1-Microglobulin proteins in human samples. The ELISA kits' characteristics, including sensitivity, specificity, precision, assay range, recovery, linearity, calibration, cross-reactivity, and interference, were validated as described in the product datasheets.