***eLife’s* transparent reporting form**

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
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No statistical method was used to predetermine sample size. See the section Materials and Methods – Statistical analyses for a description of the statistical analyses.

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* You should report how often each experiment was performed
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* Criteria for exclusion/inclusion of data should be clearly stated
* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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A detailed description of the optimization conditions can be found in supplementary table 1.

Description of the technical and biological variability calculations can be found in materials and methods section “healthy donors”, supplementary figure 6 and figure legend of figure 2. The core set analysis is described in supplementary figure 7.

The mass spectrometry data are available via ProteomeXchange with identifier PXD010899.

Reviewer account details:

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* Statistical analysis methods should be described and justified
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* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
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(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

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* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
* Indicate if masking was used during group allocation, data collection and/or data analysis

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This information can be found in materials and methods section “mother and child cohort” ,“healthy donors cohort” and “female longitudinal” respectively. No randomization was performed and no masking was used during group allocation and analysis.

**Additional data files (“source data”)**

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
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Please indicate the figures or tables for which source data files have been provided:

Source data for figure 1, 3 and 4 can be found as supplementary tables.

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