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PXD identifier(s) must be provided in the manuscript abstract. In your abstract, please include the following sentence: "The proteomic data has been deposited to the ProteomeXchange Consortium via the xxx (e.g. PRIDE, MassIVE, etc.) partner repository with the data set identifier PXDxxxxxx".

Credentials to access the non-public data should be provided in the Materials and Methods at the time of submission. A condition of acceptance is to allow public access to the data sets via a PDX identifier at the time of publication. Manuscripts will not be reviewed if the data have not been deposited – the data can remain password protected until acceptance but before the paper is in press, the password protection must be lifted and the data publicly available.

Please ensure to use the most recent version of the neXtProt or UniProt reference proteome for all informatics. For protein identification, ≥ two uniquely mapping, non-fully nested peptides of length ≥ 9 are required.

Describe in detail the calculation of FDRs at the PSM, peptide, and protein levels. Report the PSM-, peptide-, and protein-level FDR values along with the total number of expected true positives and false positives at each level. Present large-scale results thresholded at equal to or lower than 1% protein-level global FDR. If any large-scale datasets are individually thresholded and then combined, calculate the new, higher peptide- and protein-level FDRs for the combined result.

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Amino acid and nuclei sequences
Sequences should be computer printed using a monospace font and high quality printer. They should be assembled as a camera-ready figure, not a table, so that the alignment can be maintained.

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