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☐ Initial submission ☐ Revised version ☒ Final submission

Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form is intended for publication with all accepted life science papers and provides structure for consistency and transparency in reporting. Every life science submission will use this form; some list items might not apply to an individual manuscript, but all fields must be completed for clarity.

For further information on the points included in this form, see Reporting Life Sciences Research. For further information on Nature Research policies, including our data availability policy, see Authors & Referees and the Editorial Policy Checklist.

Experimental design

1. Sample size

Describe how sample size was determined.

No statistical methods were used for determining sample size. The number of cell lines was based on the number of cryostocks used for other experiments in the laboratory of Dr. Cyril Benes.

2. Data exclusions

Describe any data exclusions.

The cell lines BT474 and UACC893 were excluded from the analysis because of a very weak correlation between proteome and mRNA expression profiles (Klijn et al. (2015) Nat Biotechnol 33, 306).
The proteome profiles for the cell line T47D were excluded from further analysis as the correlation of the proteome profiles from the analysis of biological replicates was very weak.
See Supplementary Table 1.

3. Replication

Describe whether the experimental findings were reliably reproduced.

Each cell line proteome was mapped as biological duplicate and the reproducibility is reported in Supplementary Figure 3.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

N/A

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

N/A

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
☐	☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒ A statement indicating how many times each experiment was replicated
☐	☒ The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
☐	☒ A description of any assumptions or corrections, such as an adjustment for multiple comparisons
☐	☒ The test results (e.g. *P* values) given as exact values whenever possible and with confidence intervals noted
☐	☒ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
☐	☒ Clearly defined error bars

See the web collection on statistics for biologists for further resources and guidance.

Software

Policy information about availability of computer code

7. Software

Describe the software used to analyze the data in this study.	Excel (2013), JMP (2014,2015,2016), Sequest, Core Proteomcs Data Analysis Platform (in-house developed by the laboratory of Steven Gygi at Harvard Medical School), Cytoscape, R cor.prob function

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* guidance for providing algorithms and software for publication provides further information on this topic.

Materials and reagents

Policy information about availability of materials

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.	Only commonly available cell lines were used for the study.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).	N/A

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.	All cell lines were obtained from commercial repositories through the HMS LINCS program. From the authenticated stocks cell lines were received at MGH. Cell lines were expanded and frozen stocks created using media recommended by the repository. All frozen stocks were created within a month of culture. From frozen stocks cells were not continuously kept in culture for more than 3 months to perform experiments.
b. Describe the method of cell line authentication used.	No further authentication was performed.
c. Report whether the cell lines were tested for mycoplasma contamination.	All cell lines were tested for mycoplasma contamination prior to freezing and again at the time of thawing prior to perform experiments.
d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.	N/A

Animals and human research participants

Policy information about studies involving animals; when reporting animal research, follow the ARRIVE guidelines

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.	N/A

Policy information about studies involving human research participants

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.	N/A