# 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.

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

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n/a	Со	nfirmed
	X	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.
x		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.
x		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
x		Estimates of effect sizes (e.g. Cohen's $d$ , Pearson's $r$ ), indicating how they were calculated
,		Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.

#### Software and code

Policy information about availability of computer code

Data collection No custom code used in this manuscript.

Data analysis Statistical analyses were assessed using Prism software 9 version 9.3.1 (GraphPad Software, Inc, La Jolla, CA, USA).

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 <u>data availability statement</u>. 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 RNA-Seq dataset generated during the sequencing procedure is deposited in the Gene Expression Omnibus database (access number GSE247670), the mass spectrometry proteomics and peptidomics datasets have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository (access numbers PXD046940, PXD046506) and available from the corresponding author upon request.

# Research involving human participants, their data, or biological material

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#### **Antibodies**

Antibodies used

The detailed full list of antibodies, use and dilutions are included as Supplementary Table 3.

Validation

The validation includes examination of several cell lines and/or tissues of known expression levels allows accurate determination of species cross-reactivity and verifies specificity.

Treatment of cell lines with growth factors, chemical activators or inhibitors, which induce or inhibit target expression, verifies specificity. Phosphatase treatment confirms phospho-specificity.

The use of siRNA transfection or knockout cell lines verifies target specificity. Side-by-side comparison of lots to ensures lot-to-lot

Optimal dilutions and buffers are predetermined, positive and negative cell extracts are specified, and detailed protocols are already optimized.

Cell Signaling Technology provide a validation procedure and statement. Antibody validations can also be found at the company website in the data sheet for each antibody online (https://www.cellsignal.com/).

Santa Cruz Biotechnology antibody validations can be found at the company website in the data sheet for each antibody (https:// www.scbt.com/home).

BD Biosciences antibody validations can be found at the company website in the data sheet for each antibody (https:// www.bdbiosciences.com/en-us).

Bio-Rad provide a validation procedure and statement. Antibody validations can also be found at the company website in the data sheet for each antibody online (https://www.bio-rad-antibodies.com/primary-antibodies-monoclonal-polyclonal.html).

Thermo Fisher Scientific validations can be found at the company website in the data sheet for each antibody (https:// www.thermofisher.com/us/en/home.html).

Sigma-Aldrich provide a validation statement. Antibody validations can also be found at the company website in the data sheet for each antibody online (https://www.sigmaaldrich.com/US/en/products).

R&D Systems validations can be found at the company website in the data sheet for each antibody (https://www.rndsystems.com/ products/antibodies#quality).

### Eukaryotic cell lines

Cell line source(s)

Policy information about cell lines and Sex and Gender in Research

HepG2 cell line (# HB-8065; ATCC), Cellosaurus HLE (CVCL\_1281), Cellosaurus HuH-6 (CVCL\_4381), hESC H1 (WiCell).

Authentication As per company authentication description. The authentication was not performed in our laboratory.

Mycoplasma contamination We have performed rutin mycoplasma tests in our cell lines. No contaminations have been detected.

Commonly misidentified lines (See ICLAC register)

None.

### Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals

Ptprk knockout mice were generated at The Jackson Laboratory (Ptprk-8356J-M669 project) by CRISPR/Cas9 technology and were bred on a pure C57BL/6N background. The duration for which the animals were subjected to the experimental diets ranged from 4 to 40 weeks.

Wild animals

No wild animals were used in our studies.

Reporting on sex

Both male and female mice have been used in our studies. The information is provided in the figure legends.

Field-collected samples

No field collected samples were used in our study.

Ethics oversight

Liver samples were collected after approval of the Hôpital Erasme Ethics Committee (Brussels, Belgium). Written informed consent was obtained from each participant. The study was conducted with the approved human ethics by the Comité d'Ethique hospitalofacultaire Erasme Université libre de Bruxelles (PI Gurzov approval Ref P2019/498). Mice were housed and managed in compliance with the Belgian Regulations for Animal Care, and the animal protocols underwent approval from the Commision d'Ethicque du Bien-Être Animal (CEBEA), Faculté de Médecine, Université libre de Bruxelles (dossier No. 732).

Note that full information on the approval of the study protocol must also be provided in the manuscript.

# Plants

Seed stocks	No seed stocks were used in our studies.
Novel plant genotypes	No plants were used in our studies.
Authentication	No authentication was required in our studies.