# 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 <u>Editorial Policies</u> and the <u>Editorial Policy Checklist</u>.

#### **Statistics**

For a	Il statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.
n/a	Confirmed
	$\boxtimes$ The exact sample size ( <i>n</i> ) for each experimental group/condition, given as a discrete number and unit of measurement
	igee 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.
$\boxtimes$	A description of all covariates tested
$\boxtimes$	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. <i>F</i> , <i>t</i> , <i>r</i> ) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable</i> .
$\boxtimes$	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
$\boxtimes$	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
	$\boxtimes$ Estimates of effect sizes (e.g. Cohen's <i>d</i> , Pearson's <i>r</i> ), 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 <u>availability of computer code</u>	
Data collection	Confocal fluorescence microscopy images were acquired and analyzed using Leica TCS SP8 STED.	
Data analysis	Mass spectrometry were then analyzed with an Orbitrap Classic mass spectrometry (Thermo Fisher Scientific Inc., MA, USA). Identification and quantification of the sample products were performed using MaxQuant version 1.5.0.30. The quantification for the proteins by western blot was performed by Image J version 1.51j8. All statistical analyses were performed using either GraphPad Prism 7 version 1.0 (GraphPad Software, Inc., La Jolla, CA, USA) or the Partek <sup>®</sup> Genomics Suite <sup>®</sup> version 7.0 (Partek Incorporated, St. Louis, MO, 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 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 authors declare that all quantifications supporting the findings of this study are available within the paper, Source Data and the Supplementary Information files. Source data are provided with this paper. The RNA sequencing data generated in this study have been deposited in the GEO database under accession code: GSE182102 [https://www.ncbi.nlm.nih.gov/bioproject/?term=GSE182102]. The SILAC proteomics data of SRSF10 interactors generated in this study have been deposited in the PRIDE database under accession code: PXD030800 [https://www.ebi.ac.uk/pride/archive/projects/PXD030800/private]. The microarray data have

been deposited in the ArrayExpress public database under accession code: E-MEXP-84 [https://www.ebi.ac.uk/arrayexpress/experiments/E-MEXP-84/] and E-TABM-292 [https://www.ebi.ac.uk/arrayexpress/experiments/E-TABM-292/]. The SREK1L binding sites on the B-T mRNA were predicted by RNA-Protein Interaction Prediction (RPISeq) online database [http://pridb.gdcb.iastate.edu/RPISeq/about.php].

## 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 <u>nature.com/documents/nr-reporting-summary-flat.pdf</u>

# Life sciences study design

All studies must dis	sclose on these points even when the disclosure is negative.
Sample size	No statistical methods were used to pre-determine sample size. For animal works and RIP experiments, minimum sample sizes for individual experiments were determined not on the basis of a statistical method, but based on previous experience and report (Nat Commun . 2019 Mar 22;10(1):1353).
Data exclusions	no data were excluded
Replication	no experiments shown failed to replicated. All expeirments were replicated by at least three independent experments performed on different days.
Randomization	No specific randomization method was used to allocate mice into different treatment groups.
Blinding	Blinding was not necessary because experimental conditions were well-controlled and experimental results were quantitative and did not require subjective interpretation or analysis.

# Reporting for specific materials, systems and methods

**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	n/a	Involved in the study
	Antibodies	$\boxtimes$	ChIP-seq
	Eukaryotic cell lines	$\boxtimes$	Flow cytometry
$\boxtimes$	Palaeontology and archaeology	$\boxtimes$	MRI-based neuroimaging
	Animals and other organisms		
	Human research participants		
$\boxtimes$	Clinical data		
$\boxtimes$	Dual use research of concern		
	•		

### Antibodies

Antibodies used The antibodies used in this studies were all listed in Supplementary table 5. 1) antibodies used for immunoblot: Cat. No Antibody Lot No. Species dilution Company and description HPA037674 SREK1 R35896 Rabbit 1/1000 Sigma-Aldrich, for Fig. 5G, Fig. 3E (ab-2) #2118 GAPDH (14C10) 10 Rabbit 1/5000 Cell Signaling Technology T6199 α-Tubulin (DM1A) R11234 Mouse 1/5000 Sigma-Aldrich sc-393594 UPF1 L1217 Mouse 1/2000 Santa Cruz Biotechnology sc-374557 SMG1 K2817 Mouse 1/1000 Santa Cruz Biotechnology sc-515722 MOV10 H0916 Mouse 1/1000 Santa Cruz Biotechnology sc-393905 RUVBL1 H0217 Mouse 1/1000 Santa Cruz Biotechnology sc-374135 RUVBL2 K2817 Mouse 1/1000 Santa Cruz Biotechnology sc-374230 UPF2 H1417 Mouse 1/1000 Santa Cruz Biotechnology sc-398821 UPF3 G3117 Mouse 1/1000 Santa Cruz Biotechnology sc-271405 MAGOH/B G0210 Mouse 1/1000 Santa Cruz Biotechnology sc-514050 GNL2 I1217 Mouse 1/1000 Santa Cruz Biotechnology sc-514308 SEC13 G2617 Mouse 1/1000 Santa Cruz Biotechnology sc-32318 PABPC1 L2216 Mouse 1/1000 Santa Cruz Biotechnology HPA053805 SRSF10 R71755 Rabbit 1/1000 Sigma-Aldrich

Fig 3E)
<u> </u>
a - light chain (HRP) GR1190308-3 Rat Abcam IB, 1/5000
G light chain (HRP) GR122803-1 Mouse Abcam IB, 1/5000
00
a037674 ss/gapdh-14c10-rabbit-mab/2118 /t6199
pa053805
o1-antibody-clone-1a6-elisa-if-immunofluorescence-wb-
021593
PA034829
ody-ab21679.html
tml
-ab175205
REK1-SFRS12-Antibody-Polyclonal/A305-105A
ntibody
; onoclonal-1871-mouse-kappa-light-chain-hrp-ab99617.htm
; onoclonal-1871-mouse-kappa-light-chain-hrp-ab99617.htm
; onoclonal-1871-mouse-kappa-light-chain-hrp-ab99617.htm
; onoclonal-1871-mouse-kappa-light-chain-hrp-ab99617.htm com/Mouse-monoclonal-SB62a-Rabbit-IgG-light-chain-HRP ling-control-ab89984.html a/f9291
; onoclonal-1871-mouse-kappa-light-chain-hrp-ab99617.html com/Mouse-monoclonal-SB62a-Rabbit-IgG-light-chain-HRP ling-control-ab89984.html

Validation

### Eukaryotic cell lines

Policy information about <u>cell lines</u>	
Cell line source(s)	The Hep3B (HB-8064), HepG2 (HB-8065), PLC/PRF/5(CRL-8024), SNU449 (CRL-2234), SK-Hep-1(HTB-52) and HEK-293T (CRL-3216) were obtained from American Tissue Culture (ATCC). Huh7 (JCRB0403), Huh1 (JCRB0199), HLE (JCRB0404), JHH2 (JCRB1028), JHH4 (JCRB0435), JHH5 (JCRB1029), JHH7 (JCRB1031) were obtained from Japanese Collection of Research Biosources Cell Bank (JCRB). SNU354 (KCLB00354), SNU368 (KCLB00368), SNU387 (KCLB00387), SNU398 (KCLB00398), SNU423 (KCLB00423), SNU449 (KCLB00449), SNU739 (KCLB00739), SNU761 (KCLB00761), SNU878 (KCLB00878), SNU886 (KCLB00886) cell lines were obtained from Korean Cell Line Bank (KCLB). The HCCLM3, Mahlavu and BEL7404 cells were gifts from Dr. John M Luk.
Authentication	Hep3B and HCCLM3 cells were examined by short tandem repeat analysis with the Geneprint 10 System Kit (Promega), the rest cell lines were not authenticated.
Mycoplasma contamination	all cell lines were tested negative for mycoplasma by every month monitoring.
Commonly misidentified lines (See <u>ICLAC</u> register)	No commonly misidentified cell lines were used.

### Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	5-7 week-old male BALB/c-Nude or C57BL/6 mice were purchased from INVIVOS PTE Ltd and housed in the animal facility at NCCS with the conditions: temperature range 19-26 °C, temperature fluctuations within bandwidth 3-4 °C, humidity range 50-70%, light intensity 300-350 lux at 1 meter above the floor, uniform 12 hours light/dark daily lighting cycle, ventilation 15-20 air change per hour.
Wild animals	no wild animals were used.
Field-collected samples	no filed-collected samples were used.
Ethics oversight	Mice were maintained according to protocols and ethical regualtions approved by SingHealth Institutional Animal Care and Use Committee (IACUC).

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

### Human research participants

Policy information about studies involving human research participants					
Population characteristics	The collection of tissues from HCC patients was approved by the SingHealth Centralized Institutional Review Board (CIRB), and all tissues studied were provided by the SingHealth Tissue Repository.				
Recruitment	NA				
Ethics oversight	SingHealth Centralized Institutional Review Board				

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