nature portfolio

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Last updated by author(s): Oct 30, 2023

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.

Statistics

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

n/a	Confirmed	
☐	☒	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.*
☐	☒	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.*
☒	☐	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
☒	☐	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	Image Lab Touch (version 2.0.0.25, BioRad), Image Studio (3.1, LI-COR), Zeiss Zen Blue Edition (version 3.6.1), DeltaVision softWoRx.
Data analysis	Proteomic data were analysed using Mascot Server from Matrix Science (version 2.2.06) and Scaffold from Proteome Software (version 4.8.4). Imaris 9, Huygens (Version 16.10.1p4), ImageJ (Version 1.54f), FIJI (Version 2.9.0/1.53t), Image Studio (31., LI-COR), GraphPad Prism (Versions 9.5.1 & 10.1.0)

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

Mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the MassIVE partner repository (doi:10.25345/C5BG2HM8B) and are publicly available. All other data supporting the findings this study are available within the paper, Supplementary Information and Source Data files. Further

information and requests for resources and reagents should be directed to the Lead Contacts, Tero Järvinen (tero.jarvinen@tuni.fi) and Mark Morgan (mark.morgan@liverpool.ac.uk).

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	N/A
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

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

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 nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	No sample size was not predetermined for this study. The sample size was based on previous studies (including in vivo wound healing studies and cell biological, biochemical and imaging techniques) that were sufficient to detect minimal biologically relevant differences between experimental conditions at the 5% significance level.
Data exclusions	No data was excluded from analyses.
Replication	In vivo: Three different peptide treatment trials were carried out to confirm the outcome. The primary treatment outcome was also confirmed when SDC WT vs. KO mice were tested (in WT mice). All attempts of replication were successful. For cell biological, biochemical and imaging experiments: Number of independent biological replicate experiments are stated in figure legends. For quantitative analysis of imaging or biochemical experiments, data from all independent replicate experiments were merged, without exclusion of datapoints, and means +/- SEM are presented. For cell migration analysis, data from a single representative replicate experiment is shown.
Randomization	In vivo: The animals were randomized to different treatment groups just before the treatment was started, i.e 24 h after the surgical procedure (randomization was based on housing cages). In vitro: Randomisation of sample allocation was not relevant to the cell biological, biochemical or microscopy experiments. For comparative experiments in vitro, the same number of cells were randomly apportioned to each sample/group.
Blinding	In vivo: Yes. Both morphological and histological evaluations of skin wounds were performed from coded samples. The investigators were blinded to group allocation. In vitro: Experiments were performed non-blinded to experimental group allocation, as complicated experimental design rendered blinding unfeasible.

Behavioural & social sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	*Briefly describe the study type including whether data are quantitative, qualitative, or mixed-methods (e.g. qualitative cross-sectional, quantitative experimental, mixed-methods case study).*
Research sample	*State the research sample (e.g. Harvard university undergraduates, villagers in rural India) and provide relevant demographic information (e.g. age, sex) and indicate whether the sample is representative. Provide a rationale for the study sample chosen. For studies involving existing datasets, please describe the dataset and source.*

Sampling strategy	*Describe the sampling procedure (e.g. random, snowball, stratified, convenience). Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient. For qualitative data, please indicate whether data saturation was considered, and what criteria were used to decide that no further sampling was needed.*
Data collection	*Provide details about the data collection procedure, including the instruments or devices used to record the data (e.g. pen and paper, computer, eye tracker, video or audio equipment) whether anyone was present besides the participant(s) and the researcher, and whether the researcher was blind to experimental condition and/or the study hypothesis during data collection.*
Timing	*Indicate the start and stop dates of data collection. If there is a gap between collection periods, state the dates for each sample cohort.*
Data exclusions	*If no data were excluded from the analyses, state so OR if data were excluded, provide the exact number of exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.*
Non-participation	*State how many participants dropped out/declined participation and the reason(s) given OR provide response rate OR state that no participants dropped out/declined participation.*
Randomization	*If participants were not allocated into experimental groups, state so OR describe how participants were allocated to groups, and if allocation was not random, describe how covariates were controlled.*

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	*Briefly describe the study. For quantitative data include treatment factors and interactions, design structure (e.g. factorial, nested, hierarchical), nature and number of experimental units and replicates.*
Research sample	*Describe the research sample (e.g. a group of tagged Passer domesticus, all Stenocereus thurberi within Organ Pipe Cactus National Monument), and provide a rationale for the sample choice. When relevant, describe the organism taxa, source, sex, age range and any manipulations. State what population the sample is meant to represent when applicable. For studies involving existing datasets, describe the data and its source.*
Sampling strategy	*Note the sampling procedure. Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient.*
Data collection	*Describe the data collection procedure, including who recorded the data and how.*
Timing and spatial scale	*Indicate the start and stop dates of data collection, noting the frequency and periodicity of sampling and providing a rationale for these choices. If there is a gap between collection periods, state the dates for each sample cohort. Specify the spatial scale from which the data are taken*
Data exclusions	*If no data were excluded from the analyses, state so OR if data were excluded, describe the exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.*
Reproducibility	*Describe the measures taken to verify the reproducibility of experimental findings. For each experiment, note whether any attempts to repeat the experiment failed OR state that all attempts to repeat the experiment were successful.*
Randomization	*Describe how samples/organisms/participants were allocated into groups. If allocation was not random, describe how covariates were controlled. If this is not relevant to your study, explain why.*
Blinding	*Describe the extent of blinding used during data acquisition and analysis. If blinding was not possible, describe why OR explain why blinding was not relevant to your study.*

Did the study involve field work? ☐ Yes ☐ No

Field work, collection and transport

Field conditions	*Describe the study conditions for field work, providing relevant parameters (e.g. temperature, rainfall).*
Location	*State the location of the sampling or experiment, providing relevant parameters (e.g. latitude and longitude, elevation, water depth).*
Access & import/export	*Describe the efforts you have made to access habitats and to collect and import/export your samples in a responsible manner and in compliance with local, national and international laws, noting any permits that were obtained (give the name of the issuing authority, the date of issue, and any identifying information).*
Disturbance	*Describe any disturbance caused by the study and how it was minimized.*

Reporting for specific materials, systems and 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
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used

Primary antibodies for immunohistochemistry: rabbit anti-mouse Ki67 (M7249 TEC-3, 1:200, Bethyl Laboratories, Montgomery, TX); rat anti-CD31 (550274, 1:50, BD Biosciences); rat anti-F4/80 (MF48000 BM8, 1:50, Life Technologies Ltd); rabbit anti-cytohesin-2 (N7, 1:100, generous gift from Dr. H. Sakagami); rabbit anti-Arf6 (PA1-093, 1:400, Invitrogen, Carlsbad, CA); anti-α-smooth muscle actin (α-SMA) (ab5694, 1:100, Abcam, Cambridge, UK); rat anti-mouse-Syndecan-4 (KY/8.2, 1:100 BD Biosciences); rabbit anti-cytokeratin 17 (ab53707, 1:50, Abcam); rabbit anti-fibronectin (ab2413, 1:100, Abcam); rabbit anti-fluorescein (71-1900, 1:200, Invitrogen).

Primary antibodies for immunofluorescence:
rabbit anti-SDC4 antibody (5 µg/ml; 3644, BioVision); rat anti-mouse alpha5 integrin/CD49e antibody (10 µg/ml; 5H10-27 (MFR5); BD Biosciences); anti-human alpha5 integrin antibody (10 µg/ml; mab11, purified in-house from hybridoma); mouse anti-CYTH2 mAb (5 µg/ml; MA1-061, Pierce); mouse anti-ARF6 mAb (10 µg/ml; 3A-1, Santa Cruz sc-7971); rabbit anti-IQSEC1 pAb (5 µg/ml; PA5-38019, Invitrogen); rabbit anti-ARF6 (10 µg/ml; PA1-093, Invitrogen); mouse anti-tubulin (DM1A; Sigma-Aldrich/Merck); rabbit anti-ARF6 (#5740, Cell Signalling Technologies); mouse anti-CYTH2 (6H5, Abnova).

Secondary antibodies: horseradish peroxidase (HRP) conjugated anti-rat Histofine (414311F, undiluted, Nichirei Bio, Tokyo, Japan) for CD31, syndecan-4 and F4/80, goat anti-rabbit (P0448, 1:200, DakoCytomation, Glostrup, Denmark) for Ki-67, cytohesin-2, fibronectin, fluorescein, Arf6 and rabbit on Rodent HRP Polymer (RMR622H, undiluted, Biocare Medical, Pacheco, CA) for α-SMA.
AlexaFluor-488-conjugated AffiniPure Donkey anti-Rat (1:400, 3.75 µg/ml; 712-545-153, Jackson ImmunoResearch)
AlexaFluor-647-conjugated AffiniPure Donkey anti-Rabbit (1:400, 3.75 µg/ml; 711-605-152, Jackson ImmunoResearch
AlexaFluor-488-conjugated AffiniPure Donkey anti-Rabbit (1:400, 3.75µg/ml; 711-545-152, Jackson ImmunoResearch)
AlexaFluor-647-conjugated AffiniPure Donkey anti-Mouse (1:400, 3.75 µg/ml; 715-605-151, Jackson ImmunoResearch)
AlexaFluor-488-conjugated AffiniPure Donkey anti-Mouse (1:400, 3.75 µg/ml; 715-545-151, Jackson ImmunoResearch)
AlexaFluor-647-conjugated AffiniPure Donkey anti-Rabbit (1:400, 3.75µg/ml; 711-605-152, Jackson ImmunoResearch)
AlexaFluor-647-conjugated AffiniPure Donkey anti-Rat (1:400, 3.75µg/ml; 712-605-153, Jackson ImmunoResearch)
AlexaFluor-594-conjugated AffiniPure Donkey anti-Mouse (1:400, 3.75µg/ml; 715-585-151, Jackson ImmunoResearch)
AlexaFluor-594-conjugated phalloidin (1:400; A12381, Invitrogen)

Antibodies for Flow Cytometry:
10µg/mL mouse anti-Human SDC4 primary antibody (5G9; sc-12766, Santa Cruz). AlexaFluor-488-conjugated AffiniPure Donkey anti-Mouse secondary antibody (1:400, 3.75µg/ml; #715-545-151, Jackson ImmunoResearch)

ARF6 Effector Pulldown Assay - Primary antibodies:
1µg/ml mouse anti-ARF6 monoclonal antibody (ARFAG; #A5230, Merck)
1µg/ml mouse anti-Tubulin monoclonal antibody (DM1A; #T9026, Merck).

ARF6 Effector Pulldown Assay - Secondary antibodies:
AlexaFluor-680-conjugated Goat anti-Mouse IgG (H+L) highly cross-adsorbed secondary antibody (1/5000, 0.4µg/ml; #A21058, Invitrogen).

Co-immunoprecipitation Blots - Primary antibodies:
1µg/ml mouse anti-ARF6 (ARFAG; #A5230, Merck)
1µg/ml mouse anti-CYTH2 (6H5; #H00009266-M02, Abnova)
0.2µg/ml mouse anti-actin (AC-40; #A3853, Merck).
1µg/ml rabbit anti-ARF6 (D12G6; #5740, Cell Signalling Technologies) –in total cell lysates

Co-immunoprecipitation Blots - Secondary antibodies
HRP-linked goat anti-mouse (0.2µg/ml, 1:5000; #31160, Pierce)
HRP-linked goat anti-rabbit (0.2µg/ml, 1:5000; #31210, Pierce)
AlexaFluor-790-conjugated Goat anti-Mouse IgG (H+L) highly cross-adsorbed secondary antibody (1/10000, 0.2µg/ml; A11357, Invitrogen).

ECL Detection: SuperSignal™ West Femto Maximum Sensitivity Substrate. Catalog number: 34094

Validation

Immunohistochemistry: The specificity of the secondary antibodies was ensured with stainings lacking the primary antibody. Each staining patch also included untreated samples and a positive control sample. All immunohistochemical stainings were performed by standard protocols established by testing different dilutions of primary antibody.
Flow cytometry and immunoblotting: Confirmation via siRNA knockdown
Immunofluorescence: 5 1 integrin & paxillin subcellular distribution in focal adhesions; huSDC4 - lack of detection in SDC4-/- cells and elevated detection following over-expression of human SDC4; ARF6, CYTH2 & IQSEC1 specificity and level of autofluorescence tested using secondary antibody-only and primary antibody-only conditions.

Additional detailed information on the antibodies used in this study, including validation and relevant citations, are available via the following manufacturer's webpages and other online resources:

Primary antibodies:

Actin:
Mouse anti-actin (AC-40; #A3853, Merck): https://www.sigmaaldrich.com/GB/en/product/sigma/a3853

α-SMA:
Rabbit anti-α-smooth muscle actin (α-SMA) (ab5694, Abcam): https://www.abcam.com/products/primary-antibodies/alpha-smooth-muscle-actin-antibody-ab5694.html

ARF6:
Mouse anti-ARF6 monoclonal antibody (ARFAG; #A5230, Merck): https://www.sigmaaldrich.com/GB/en/product/sigma/a5230
Rabbit anti-Arf6 (PA1-093, Invitrogen): https://www.thermofisher.com/antibody/product/ARF6-Antibody-Polyclonal/PA1-093
Rabbit anti-ARF6 (D12G6; #5740, Cell Signalling Technologies): https://www.cellsignal.com/products/primary-antibodies/arf6-d12g6-rabbit-mab/5740#:~:text=Arf6%20is%20localized%20mainly%20to,factors%20(3%2C4)
Mouse anti-ARF6 mAb (3A-1, Santa Cruz sc-7971): https://www.scbt.com/p/arf6-antibody-3a-1

CD31/PECAM1:
Rat anti-CD31 (550274, BD Biosciences): https://www.bdbiosciences.com/en-gb/products/reagents/flow-cytometry-reagents/research-reagents/single-color-antibodies-ruo/purified-rat-anti-mouse-cd31.550274

CYTH2:
Mouse anti-CYTH2 (6H5, Abnova): https://www.novusbio.com/products/cytohesin-2-antibody-6h5_h00009266-m02; https://www.thermofisher.com/antibody/product/CYTH2-Antibody-clone-6H5-Monoclonal/H00009266-M02
Mouse anti-CYTH2 mAb (10A12; MA1-061, Pierce): https://www.thermofisher.com/antibody/product/Cytohesin-2-Antibody-clone-10A12-Monoclonal/MA1-061
Rabbit anti-cytohesin-2 (N7, generous gift from Hiroyuki Sakagami):
https://www.sciencedirect.com/science/article/pii/S0969996121002151

F4/80:
Rat anti-F4/80 (MF48000 BM8, Invitrogen): https://www.thermofisher.com/antibody/product/F4-80-Antibody-clone-BM8-Monoclonal/MF48000

Ki67:
Rabbit anti-mouse Ki67 (M7249 TEC-3, Bethyl Labs): https://www.alzforum.org/antibodies/ki-67-tec-3

Cytokeratin-17:
Rabbit anti-cytokeratin 17 (ab53707, Abcam): https://www.abcam.com/products/primary-antibodies/cytokeratin-17-antibody-cytoskeleton-marker-ab53707.html

Fibronectin:
Rabbit anti-fibronectin (ab2413, Abcam); https://www.abcam.com/products/primary-antibodies/fibronectin-antibody-ab2413.html

Fluorescein:
Rabbit anti-fluorescein (71-1900, Invitrogen): https://www.thermofisher.com/antibody/product/FITC-Antibody-Polyclonal/71-1900

Integrin alpha5beta1:
Rat anti-mouse alpha5 integrin/CD49e antibody (5H10-27 (MFR5); BD Biosciences): https://www.bdbiosciences.com/en-us/products/reagents/flow-cytometry-reagents/research-reagents/single-color-antibodies-ruo/purified-rat-anti-mouse-cd49e.553319
Rat anti-human alpha5 integrin antibody (mab11, purified in-house from hybridoma):
https://www.science.org/doi/10.1126/science.7846531?url_ver=Z39.88-2003&rfr_id=ori:rid:crossref.org&rfr_dat=cr_pub%20%200pubmed
https://rupress.org/jcb/article-pdf/131/3/791/1479424/791.pdf
https://www.merckmillipore.com/GB/en/product/Anti-Integrin-alpha-5-CD49e-Antibody-clone-mAb11,MM_NF-MABT822?ReferrerURL=https%3A%2F%2Fwww.google.com%2F

IQSEC1:
Rabbit anti-IQSEC1 pAb (PA5-38019, Invitrogen): https://www.thermofisher.com/antibody/product/IQSEC1-Antibody-Polyclonal/PA5-38019

SDC4:
Rabbit anti-SDC4 antibody (3644, BioVision): https://www.biovision.com/syndecan-4-antibody.html; https://www.abcam.com/products/primary-antibodies/syndecan-4-antibody-ab286154.html

Rat anti-mouse-Syndecan-4 (KY/8.2, BD Biosciences): https://www.fishersci.com/shop/products/anti-syndecan-4-clone-ky-8-2-bd/BDB550350
Mouse anti-Human SDC4 primary antibody (5G9; sc-12766, Santa Cruz): https://www.scbt.com/p/syndecan-4-antibody-5g9?gclid=EAIaIQobChMIu82_iOudggMVxPrtCh2OtAtEEAAYBCAAEgIiVvD_BwE

Tubulin:
mouse anti-tubulin (DM1A; Sigma-Aldrich/Merck); https://www.sigmaaldrich.com/GB/en/product/mm/mabt205; https://www.thermofisher.com/antibody/product/alpha-Tubulin-Antibody-clone-DM1A-Monoclonal/14-4502-82#:~:text=The%20DM1a%20antibody%20recognizes%20the,fixed%20paraffin%20embedded%20tissue%20sections.

HRP-conjugated Secondary antibodies:

Horseradish peroxidase (HRP) conjugated anti-rat Histofine (414311F, Nichirei Bio)
https://nichireibiosciences.com/wp-content/themes/nichirei/pdf/Simple%20Stain%20MAX.pdf
https://www.cosmobiousa.com/content/document/cosmo-bio-ltd/nic-414311f_n-histofine-simple-stain-mouse-max-po-rat_datasheet.pdf
Horseradish peroxidase (HRP) conjugated goat anti-rabbit (P0448, DakoCytomation):
https://www.agilent.com/en/product/specific-proteins/elisa-kits-accessories/goat-anti-rabbit-immunoglobulins-hrp-affinity-isolated-2717113
Rabbit on Rodent HRP Polymer (RMR622H, undiluted, Biocare Medical, Pacheco, CA):
https://bio-optica.it/ftp/Sito/technical_datasheet/RMR622.pdf

Fluorophore-conjugated Secondary antibodies:

AlexaFluor-488-conjugated AffiniPure Donkey anti-Rat (712-545-153, Jackson ImmunoResearch): https://www.jacksonimmuno.com/catalog/products/712-545-153
AlexaFluor-647-conjugated AffiniPure Donkey anti-Rabbit (711-605-152, Jackson ImmunoResearch: https://www.jacksonimmuno.com/catalog/products/711-605-152
AlexaFluor-488-conjugated AffiniPure Donkey anti-Rabbit (711-545-152, Jackson ImmunoResearch): https://www.jacksonimmuno.com/catalog/products/711-545-152
AlexaFluor-647-conjugated AffiniPure Donkey anti-Mouse (715-605-151, Jackson ImmunoResearch): https://www.jacksonimmuno.com/catalog/products/715-605-151
AlexaFluor-488-conjugated AffiniPure Donkey anti-Mouse (715-545-151, Jackson ImmunoResearch): https://www.jacksonimmuno.com/catalog/products/715-545-151
AlexaFluor-647-conjugated AffiniPure Donkey anti-Rabbit (711-605-152, Jackson ImmunoResearch): https://www.jacksonimmuno.com/catalog/products/711-605-152
AlexaFluor-647-conjugated AffiniPure Donkey anti-Rat (712-605-153, Jackson ImmunoResearch): https://www.jacksonimmuno.com/catalog/products/712-605-153
AlexaFluor-594-conjugated AffiniPure Donkey anti-Mouse (715-585-151, Jackson ImmunoResearch): https://www.jacksonimmuno.com/catalog/products/715-585-151

AlexaFluor-680-conjugated Goat anti-Mouse IgG (H+L) highly cross-adsorbed secondary antibody (#A21058, Invitrogen):
https://www.thermofisher.com/antibody/product/Goat-anti-Mouse-IgG-H-L-Highly-Cross-Adsorbed-Secondary-Antibody-Polyclonal/A-21058
AlexaFluor-790-conjugated Goat anti-Mouse IgG (H+L) highly cross-adsorbed secondary antibody (#A11357, Invitrogen): https://www.thermofisher.com/antibody/product/Goat-anti-Mouse-IgG-H-L-Highly-Cross-Adsorbed-Secondary-Antibody-Polyclonal/A11357

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	HaCaT: Spontaneously immortalized keratinocyte cell line from the adult human skin of a 62-year-old male. Im+/+ and Syn4 -/- (SDC4-/-) MEFs: Mouse embryonic fibroblasts isolated in Martin Humphries' lab Syn4WT, Syn4Y180L & Syn4Y180E: Syn4-/- MEFs retrovirally-transduced with HA-tagged wild type human SDC4, or Y180L or Y180E point mutations in HA-tagged human SDC4 gereated in Martin Humphries' Lab TIF: Telomerase-immortalised foreskin fibroblasts. Male. Obtained from Patrick Caswell's lab
Authentication	HaCaT: Authentication method - 10-Locus STR Profiling : GenePrint® 10, Promega; Database/s used for comparison: Cellosaurus /ATCC TIFs & MEFs were not authenticated
Mycoplasma contamination	HaCaT and TIF cells tested negative for mycoplamsa MEFs were not routinely tested
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used in this study

Palaeontology and Archaeology

Specimen provenance	*Provide provenance information for specimens and describe permits that were obtained for the work (including the name of the issuing authority, the date of issue, and any identifying information). Permits should encompass collection and, where applicable, export.*

Specimen deposition | *Indicate where the specimens have been deposited to permit free access by other researchers.*

Dating methods | *If new dates are provided, describe how they were obtained (e.g. collection, storage, sample pretreatment and measurement), where they were obtained (i.e. lab name), the calibration program and the protocol for quality assurance OR state that no new dates are provided.*

☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

Ethics oversight | *Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.*

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

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 | 8-10 week old BALB/c and C57BL/6 mice (Janvier Labs, Le-Genest-Saint-Isle, France and Harlan; Indianapolis, Indiana, USA), or SDC4 KO C57BL/6 (obtained from Dr. Mark Bass, University of Sheffield, Sheffield, UK. SDC4 KO C57BL/6 was originally generated in the Centre for Animal Resources and Development, Kumamoto University, Japan and obtained with the kind permission of professor Tetsuhito Kojima, Nagoya University, Japan) and SDC4 WT C57BL/6 mice were used in the study.

Wild animals | No wild animals were used in the study.

Reporting on sex | Male mice were used.

Field-collected samples | No field-collected samples were used in the study

Ethics oversight | All animal experiments were performed in accordance with protocols approved by the National Animal Ethics Committee of Finland, the institutional animal care and use committees of the Sanford Burnham Prebys Medical Discovery Institute (La Jolla, CA, USA) and the University of California at Santa Barbara (Santa Barbara, CA, USA).

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

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration | *Provide the trial registration number from ClinicalTrials.gov or an equivalent agency.*

Study protocol | *Note where the full trial protocol can be accessed OR if not available, explain why.*

Data collection | *Describe the settings and locales of data collection, noting the time periods of recruitment and data collection.*

Outcomes | *Describe how you pre-defined primary and secondary outcome measures and how you assessed these measures.*

Dual use research of concern

Policy information about dual use research of concern

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes	
☒	☐	Public health
☒	☐	National security
☒	☐	Crops and/or livestock
☒	☐	Ecosystems
☒	☐	Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes	
☒	☐	Demonstrate how to render a vaccine ineffective
☒	☐	Confer resistance to therapeutically useful antibiotics or antiviral agents
☒	☐	Enhance the virulence of a pathogen or render a nonpathogen virulent
☒	☐	Increase transmissibility of a pathogen
☒	☐	Alter the host range of a pathogen
☒	☐	Enable evasion of diagnostic/detection modalities
☒	☐	Enable the weaponization of a biological agent or toxin
☒	☐	Any other potentially harmful combination of experiments and agents

Plants

Seed stocks	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*

ChIP-seq

Data deposition

☐ Confirm that both raw and final processed data have been deposited in a public database such as GEO.

☐ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links *May remain private before publication.*	*For "Initial submission" or "Revised version" documents, provide reviewer access links. For your "Final submission" document, provide a link to the deposited data.*
Files in database submission	*Provide a list of all files available in the database submission.*
Genome browser session (e.g. UCSC)	*Provide a link to an anonymized genome browser session for "Initial submission" and "Revised version" documents only, to enable peer review. Write "no longer applicable" for "Final submission" documents.*

Methodology

Replicates	*Describe the experimental replicates, specifying number, type and replicate agreement.*
Sequencing depth	*Describe the sequencing depth for each experiment, providing the total number of reads, uniquely mapped reads, length of reads and whether they were paired- or single-end.*
Antibodies	*Describe the antibodies used for the ChIP-seq experiments; as applicable, provide supplier name, catalog number, clone name, and lot number.*
Peak calling parameters	*Specify the command line program and parameters used for read mapping and peak calling, including the ChIP, control and index files used.*
Data quality	*Describe the methods used to ensure data quality in full detail, including how many peaks are at FDR 5% and above 5-fold enrichment.*
Software	*Describe the software used to collect and analyze the ChIP-seq data. For custom code that has been deposited into a community repository, provide accession details.*

Flow Cytometry

Plots

Confirm that:

☐ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☐ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☐ All plots are contour plots with outliers or pseudocolor plots.

☐ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	*Describe the sample preparation, detailing the biological source of the cells and any tissue processing steps used.*
Instrument	*Identify the instrument used for data collection, specifying make and model number.*
Software	*Describe the software used to collect and analyze the flow cytometry data. For custom code that has been deposited into a community repository, provide accession details.*
Cell population abundance	*Describe the abundance of the relevant cell populations within post-sort fractions, providing details on the purity of the samples and how it was determined.*
Gating strategy	*Describe the gating strategy used for all relevant experiments, specifying the preliminary FSC/SSC gates of the starting cell population, indicating where boundaries between "positive" and "negative" staining cell populations are defined.*

☐ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.

Magnetic resonance imaging

Experimental design

Design type	*Indicate task or resting state; event-related or block design.*
Design specifications	*Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.*
Behavioral performance measures	*State number and/or type of variables recorded (e.g. correct button press, response time) and what statistics were used to establish that the subjects were performing the task as expected (e.g. mean, range, and/or standard deviation across subjects).*

Acquisition

Imaging type(s)	*Specify: functional, structural, diffusion, perfusion.*
Field strength	*Specify in Tesla*
Sequence & imaging parameters	*Specify the pulse sequence type (gradient echo, spin echo, etc.), imaging type (EPI, spiral, etc.), field of view, matrix size, slice thickness, orientation and TE/TR/flip angle.*
Area of acquisition	*State whether a whole brain scan was used OR define the area of acquisition, describing how the region was determined.*

Diffusion MRI ☐ Used ☐ Not used

Preprocessing

Preprocessing software	*Provide detail on software version and revision number and on specific parameters (model/functions, brain extraction, segmentation, smoothing kernel size, etc.).*
Normalization	*If data were normalized/standardized, describe the approach(es): specify linear or non-linear and define image types used for transformation OR indicate that data were not normalized and explain rationale for lack of normalization.*
Normalization template	*Describe the template used for normalization/transformation, specifying subject space or group standardized space (e.g. original Talairach, MNI305, ICBM152) OR indicate that the data were not normalized.*
Noise and artifact removal	*Describe your procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and physiological signals (heart rate, respiration).*

Volume censoring | *Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.*

Statistical modeling & inference

Model type and settings | *Specify type (mass univariate, multivariate, RSA, predictive, etc.) and describe essential details of the model at the first and second levels (e.g. fixed, random or mixed effects; drift or auto-correlation).*

Effect(s) tested | *Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA or factorial designs were used.*

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☐ Both

Statistic type for inference | *Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.*

(See Eklund et al. 2016)

Correction | *Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).*

Models & analysis

n/a	Involved in the study
☐	☐ Functional and/or effective connectivity
☐	☐ Graph analysis
☐	☐ Multivariate modeling or predictive analysis

Functional and/or effective connectivity | *Report the measures of dependence used and the model details (e.g. Pearson correlation, partial correlation, mutual information).*

Graph analysis | *Report the dependent variable and connectivity measure, specifying weighted graph or binarized graph, subject- or group-level, and the global and/or node summaries used (e.g. clustering coefficient, efficiency, etc.).*

Multivariate modeling and predictive analysis | *Specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.*