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Reporting Summary

Nature Research 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 Research policies, see Authors & Referees 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	Binding experiments data were collected with Biacore X Control Software from Biacore (GE Healthcare), fluorescence and absorbance data were obtained with Gen5 version 1.07 from Biotek and flow cytometry data with INSPIRE Software from Amnis Corporation (Merck Millipore).
Data analysis	Binding experiments were analyzed with BIAevaluation software version 3.0 from Biacore, flow cytometry data were analyzed with IDEAS Application version 6.0 from Amnis Corporation (Merck Millipore). Fluorescence and absorbance data (MTT, ROS, TMRM, GSH, IL-2 release and CypD and A inhibition assays) were analyzed with GraphPad Prism software version 6.0.

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/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research 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 list of figures that have associated raw data
- A description of any restrictions on data availability

The datasets generated during and/or analysed during the current study are available from the corresponding author on reasonable request

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	All experiments were repeated a minimum of three times independently (with each condition performed by duplicate). Sample size was chosen based on prior experience of the investigators with similar experiments previously published. The authors have published numerous peer reviewed papers demonstrating clear positive findings with similar sample sizes for the types of experiments included.
Data exclusions	Positive controls were added in each experiment, if the positive control did not work, the assay was eliminated. No data points were excluded from analysis in any experiment depicted in this manuscript.
Replication	All attempts and replications were successful.
Randomization	Randomization is not relevant for cell culture experiments. In the case of human T lymphocytes results, randomization was performed by randomly choosing healthy donors and blinding subject identities to investigators
Blinding	Healthy blood donors (human T lymphocytes) were chosen by the medical service of the Universidad de Santiago de Compostela blinding to investigators any information about them. All the data are quantitative, measurements were made using different laboratory instruments such as imagine flow cytometer, biosensor, spectrophotometers, which are not subjected to operator bias.

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
☒	☐ Animals and other organisms
☐	☒ Human research participants
☒	☐ Clinical data

Methods

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

Antibodies

Antibodies used	Pan T Cell Isolation KIT (Miltenyi Biotec, Catalog number 130-096-535) includes: Pan T Cell Biotin-Antibody Cocktail, human (Cocktail of biotin-conjugated monoclonal antibodies against CD14, CD15, CD16, CD19, CD34, CD36, CD56, CD123, and CD235a (GlycophorinA)) and Pan T Cell MicroBead Cocktail, human (MicroBeads conjugated to monoclonal anti- biotin antibody (isotype: mouse IgG1) and monoclonal anti-CD61 antibody (isotype: mouse IgG1)). Lots: 5150327501 and 5180308452.
Validation	Non-target cells, i.e., monocytes, neutrophils, eosinophils, B cells, stem cells, dendritic cells, NK cells, granulocytes, or erythroid cells are labeled by using a cocktail of biotin-conjugated antibodies. The cocktail contains antibodies against CD14, CD15, CD16, CD19, CD34, CD36, CD56, CD123, and CD235a (Glycophorin A). Subsequently, non-target cells are magnetically labelled with the Pan T Cell MicroBead Cocktail. Isolation of highly pure T cells is achieved by depletion of magnetically labelled cells.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	Human neuroblastoma SH-SY5Y cell line was obtained from American Type Culture Collection, number CRL 2266
Authentication	Cell line was not authenticated aside from authentication provided by ATCC

Mycoplasma contamination	All cell lines were tested negative for mycoplasma contamination
Commonly misidentified lines (See ICLAC register)	N/A

Human research participants

Policy information about studies involving human research participants

Population characteristics	Fresh blood for T lymphocyte isolation was obtained from healthy volunteers. Gender: man and woman. Age: 20 to 40 years old.
Recruitment	Participants were recruited in the medical service of the Universidad de Santiago de Compostela after written consent.
Ethics oversight	The institutional and regional ethical board (Comité Autonómico de Ética da Investigación de Galicia, Comité Territorial de Ética da Investigación de Santiago-Lugo, Secretaria Xeral, Consellería de Sanidade, Xunta de Galicia) approved the study (Reference: 2016/508, Approved date: December 19, 2016, according to the principles outlined in the Declaration of Helsinki).

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

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	Samples were obtained from human neuroblastoma SH-SY5Y cell line. Cells were resuspended in PBS with calcium and loaded with 0.01 µM Calcein-AM and incubated at 37ºC for 15 min. Then, 0.4 mM CoCl2 and compounds at selected concentrations were added and incubated for 15 min at 37ºC.
Instrument	Image Stream MKII (Amnis Corporation, Merck-Millipore)
Software	Data were collected with INSPIRE Software and analyzed with IDEAS Application version6.0 (Amnis Corporation, Merck-Millipore)
Cell population abundance	One million SH-SY5Y cells were used for each condition. Cell populations were not sorted by primary antibodies, so purity assessment is not relevant
Gating strategy	At first, a scatter plot of the brightfield Area versus Aspect Ratio of the population was performed in order to select single cells and eliminate debris and doublets. Then, a histogram of the brightfield channel Gradient RMS for the population chosen was made to determine focused cells. Cells with a Gradient RMS lower than 40 were excluded from the analysis. Finally, a histogram with the fluorescence intensity of Calcein-AM was performed, all positive cells were selected and the mean was calculated.

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