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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 our Editorial Policies and the Editorial Policy Checklist.

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For all statistical analyses, confirm th	at the following items are present in the figure legend, table legend, main text, or Methods section.
n/a Confirmed	
The exact sample size (n) fo	r each experimental group/condition, given as a discrete number and unit of measurement
A statement on whether me	easurements were taken from distinct samples or whether the same sample was measured repeatedly
The statistical test(s) used A Only common tests should be de	ND whether they are one- or two-sided escribed solely by name; describe more complex techniques in the Methods section.
A description of all covariate	es tested
A description of any assump	otions or corrections, such as tests of normality and adjustment for multiple comparisons
	istical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) deviation) or associated estimates of uncertainty (e.g. confidence intervals)
For null hypothesis testing, Give P values as exact values wi	the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted henever suitable.
For Bayesian analysis, inform	nation on the choice of priors and Markov chain Monte Carlo settings
For hierarchical and comple	x designs, identification of the appropriate level for tests and full reporting of outcomes
Estimates of effect sizes (e.g	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 <u>availability</u> of	of computer code
Data collection NA	
Data analysis NA	
	software that are central to the research but not yet described in published literature, software must be made available to editors and tion 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 raw phosphoproteomic data are available at MassIVE, RRID:SCR_013665. The MS raw files are accessible under MassIVE ID: MSV000084813. All other data are available from the corresponding author on reasonable request.

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Lite	sciences	stud	V C	lesi	gn

NA

Wild animals

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All studies must disclos	se on these ¡	points even when the disclosure is negative.	
	Assays were repeated a minimum of 2 independent experiments with technical replicates, statistical analysis was done on independent experiments not technical replicates. A minimum of 3 mice were included in each group.		
Data exclusions No	No data exclusion.		
Replication	l attempts at r	replication were successful.	
Randomization	location of cel	Ils and animals into experimental groups was random.	
Blinding	vestigators we	ere not blinded in this study.	
We require information fr	rom authors a is relevant to y rimental sy tudy lines and archaeolo ther organism ch participants	n/a Involved in the study ChIP-seq Flow cytometry MRI-based neuroimaging Ss	
Antibodies			
Antibodies used	The following antibodies were used for biochemical assays: anti-phosphotyrosine (4G10; Millipore), anti-GFP-agarose (D153; MBL), anti-GFP (118144600; Roche), anti-pERK (9106; Cell Signaling), anti ERK (4695; Cell Signaling), anti-pSRC (2105; Cell Signaling), anti-SRC (2108; Cell Signaling), anti-pZap70 (2701; Cell Signaling), anti-actin (1616; Santa Cruz), anti-PAG (MEM-255, Origene). with anti-CD3 (UCHT1; R&D) for functional stimulation. Slices were stained with anti-CD3 (eBioscience), anti-CD4 (Abcam), anti-CD8 (Cell Signaling Technology), anti-granzyme B (Abcam).		
Validation	Approp	priate controls were included in the study to validate the antibodies.	
Eukaryotic cell	lines		
Policy information abo	out <u>cell lines</u>		
Cell line source(s)		The murine colon adenocarcinoma (MC38) colon carcinoma cells were a gift from Ben Neel of New York University. B16 cells were a gift from Eva Hernandez of New York University. Jurkat cells were purchased from ATCC.	
Authentication		Prior to use, MC38 cells were authenticated by simple sequence length polymorphism (SSLP). B16F10 and Jurkat cell lines were not validated	
Mycoplasma contamina	ation	All cell lines are tested regularly by Lonza mycoplasma detection kit.	
Commonly misidentified lines (See <u>ICLAC</u> register)		NA	
Animals and ot	ther org	ganisms	
Policy information abo	out <u>studies in</u>	nvolving animals; ARRIVE guidelines recommended for reporting animal research	
Laboratory animals			

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April 2020

Field-collected samples

NA

Ethics oversight

nimal studies were approved by the Columbia University Institutional Animal Care and Use Committee.

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