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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.

Please do not complete any field with "not applicable" or n/a. Refer to the help text for what text to use if an item is not relevant to your study. For final submission: please carefully check your responses for accuracy; you will not be able to make changes later.

Statistics			
For all statistical analys	es, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.		
n/a Confirmed	Confirmed		
☐ The exact sam	The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement		
A statement of	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		
	ion of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)		
V	hesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted exact values whenever suitable.		
For Bayesian a	analysis, information on the choice of priors and Markov chain Monte Carlo settings		
For hierarchic	al and complex designs, identification of the appropriate level for tests and full reporting of outcomes		
Estimates of e	ffect sizes (e.g. Cohen's d, Pearson's r), indicating how they were calculated		
ı	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.		
Software and c	ode		
Policy information abou	ut <u>availability of computer code</u>		
Data collection	Symplur Transcript and Analytics tool for extraction of tweets.		
Data analysis Microsoft Excel.			
	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 <u>availability of data</u> 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 list of figures that have associated raw data - A description of any restrictions on data availability			
The data used in this study is publicly available on Twitter, Facebook and Macmillan.org.uk.			
Field-speci	fic reporting		
Please select the one b	elow 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		

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.			
Sample size	Not applicable		
Data exclusions	Not applicable		
Replication	Not applicable		
Randomization	Not applicable		
Blinding	Not applicable		

Behavioural & social sciences study design

All studies must disclo	se on these points even when the disclosure is negative.
Study description	Collection, classification and frequency analysis of qualitative data posted about lung cancer on three different social media platforms.
Research sample	Posts made by registered users of three social media platforms i.e. Twitter, Lung Cancer Support Group on Facebook and lung cancer discussion forum on Macmillan.org.uk.
Sampling strategy	Sampling of posts on the social media platforms: For the sample of posts from Twitter, the sampling was done through the use of hashtags and use of Symplur's Transcript and Analytics tool, for which the sampling procedure is unknown. For the Lung Cancer Support Group on Facebook and lung cancer discussion forum on Macmillan.org.uk, all posts were included in the sample from the one month period.
Data collection	Data was collected manually by one researcher using a computer. The researcher was not blind to the experimental condition that was being investigated.
Timing	Data posted during October 2017, was collected from all three social media platforms in December 2017.
Data exclusions	No data was excluded during the collection stage. Non English language posts were excluded during the categorisation stage.
Non-participation	No participants dropped out or declined to participate.
Randomization	Participants were not allocated to experimental groups other than social media platform from which the data was sourced.

Ecological, evolutionary & environmental sciences study design

Study description	Not applicable
Research sample	Not applicable
Sampling strategy	Not applicable

Data collection	Not applicable		
Timing and spatial scale	Not applicable		
Data exclusions	Not applicable		
Reproducibility	Not applicable		
Randomization	Not applicable		
Blinding	Not applicable		
Did the study involve field			
Field work, collect	ion and transport		
Field conditions	Not applicable		
Location	Not applicable		
Access and import/export	Not applicable		
Disturbance	Not applicable		
We require information from a	n/a Involved in the study ChIP-seq Flow cytometry MRI-based neuroimaging		
Antibodies used	Not applicable		
Validation	Not applicable		
Eukaryotic cell lin	es		
Policy information about <u>ce</u>			
Cell line source(s)	Not applicable		
Authentication	Not applicable.		
Mycoplasma contaminati	on Not applicable		

Commonly misidentified lines (See <u>ICLAC</u> register)	S Not applicable		
Palaeontology			
Specimen provenance Not applicable			
Specimen deposition	Not applicable		
Dating methods	Not applicable		
Tick this box to confirm th	nat the raw and calibrated dates are available in the paper or in Supplementary Information.		
Animals and other o	organisms		
Policy information about studie	es involving animals; ARRIVE guidelines recommended for reporting animal research		
Laboratory animals	Study did not involve laboratory animals.		
Wild animals	Not applicable		
Field-collected samples	Not applicable		
Ethics oversight	Not applicable		
Note that full information on the a	pproval of the study protocol must also be provided in the manuscript.		
Human research pai	rticipants		
Policy information about studie	es involving human research participants		
Population characteristics	See above		
Recruitment	Participants have a user account for the social media platforms included in the study.		
Ethics oversight	Relevant ethical guidelines were applied and approval was provided by the University of Edinburgh IRB.		
Note that full information on the a	pproval of the study protocol must also be provided in the manuscript.		
Clinical data			
Policy information about clinical	al studies The ICMJE guidelines for publication of clinical research and a completed <u>CONSORT checklist</u> must be included with all submissions.		
Clinical trial registration	Not applicable		
Study protocol	Not applicable		
Data collection	Not applicable		
Outcomes	Not applicable		
ChIP-seq			
Data deposition			
Confirm that both raw an	d final processed data have been deposited in a public database such as <u>GEO</u> .		
Confirm that you have de	posited or provided access to graph files (e.g. BED files) for the called peaks.		

Data access links May remain private before publication	Not applicable	
Files in database submission	Not applicable	
Genome browser session (e.g. <u>UCSC</u>)		applicable
Methodology		
Replicates	Not applicable	
Sequencing depth	Not	applicable
Antibodies	Not	applicable
Peak calling parameters	Not	applicable
Data quality	Not	applicable applicable
Software	Not	applicable applicable
Flow Cytometry		
Plots		
Confirm that:	narkar a	nd fluorochrome used (e.g. CD4-FITC).
		Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).
		itliers or pseudocolor plots.
A numerical value for nun	mber of o	cells or percentage (with statistics) is provided.
Methodology		
Sample preparation	Not app	licable
Instrument	Not app	licable
Software	Not app	licable
Cell population abundance	Not applicable	
Gating strategy	ating strategy Not applicable	
Tick this box to confirm the	nat a figu	are exemplifying the gating strategy is provided in the Supplementary Information.
Magnetic resonance	e imag	ging
Experimental design		
Design type		
Design specifications		Not applicable
Behavioral performance measures		Not applicable

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Acquisition		
Imaging type(s)	Not applicable	
Field strength	Not applicable	
Sequence & imaging parameters	Not applicable	
Area of acquisition	Not applicable	
Diffusion MRI Used	✓ Not used	
Parameters Not applica	ble.	
Preprocessing		
Preprocessing software	Not applicable	
Normalization	Not applicable	
Normalization template	Not applicable	
Noise and artifact removal	Not applicable	
Volume censoring	Not applicable	
Statistical modeling & inferenc	e	
Model type and settings	Not applicable	
Effect(s) tested	Not applicable	
Specify type of analysis: Whol	e brain ROI-based Both	
Anatomi	ical location(s) Not applicable	
Statistic type for inference (See <u>Eklund et al. 2016</u>)	Not applicable.	
Correction	Not applicable	
Models & analysis		
n/a Involved in the study Involved in the study Functional and/or effective connectivity Graph analysis Multivariate modeling or predictive analysis Multivariate modeling or predictive analysis Involved in the study Involved in the		
Functional and/or effective connect		
Graph analysis	Not applicable	
Multivariate modeling and predictiv	ve analysis Not applicable	

