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Reporting Summary

Ctatiation

x Life sciences

Behavioural & social sciences

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, seeAuthors & Referees and theEditorial Policy Checklist.

Statistics					
For all statistical analy	ses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.				
n/a Confirmed					
The exact sar	nple 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				
	l test(s) used AND whether they are one- or two-sided 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted Give <i>P</i> values as exact values whenever suitable.					
For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings					
For hierarchi	cal and complex designs, identification of the appropriate level for tests and full reporting of outcomes				
x Estimates of	effect sizes (e.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 abo	out <u>availability of computer code</u>				
Data collection	Data were collected using the corresponding software provided on the commercially available instruments (as stated in the Methods)				
Data analysis	Data were analyzed using GraphPad (v7 or v8) or Genedata Screener				
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					
- Accession codes, ui - A list of figures that	out <u>availability of data</u> include a <u>data availability statement</u> . This statement should provide the following information, where applicable: nique identifiers, or web links for publicly available datasets have associated raw data y restrictions on data availability				
	the data supporting the findings of this study are available within the article and its Supplementary Information files. All the other data of this study are available from the corresponding author upon reasonable request.				
.	ific reporting pelow that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.				
riease select the one i	below that is the best fit for your research, if you are not sure, read the appropriate sections before making your selection.				

Ecological, evolutionary & environmental sciences

Life sciences study design

based on quantitative measurements.

All studies must dis	sclose on these points even when the disclosure is negative.
Sample size	No sample-size calculations were performed. Sample size was determined to be adequate based on the magnitude and consistency of measurable differences between groups.
Data exclusions	No data were excluded
Replication	Replicate experiments were successful. Data included in this manuscript are from two independent laboratories, and were reproducible across both.
Randomization	Rats analyzed were litter mates and sex-matched, and allocated into experimental groups at random.
Blinding	Investigators were not blinded to compounds additions during experiments. Data reported for experiments are not subjective but rather

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		Methods	
n/a	Involved in the study	n/a	Involved in the study
	Antibodies	x	ChIP-seq
	x Eukaryotic cell lines	x	Flow cytometry
×	Palaeontology	x	MRI-based neuroimaging
	🗶 Animals and other organisms		
×	Human research participants		
x	Clinical data		

Antibodies

Antibodies used

Primary antibodies for tryptase (AA1, ab2378, Abcam, Australia), histamine (H7403, Sigma-Aldrich, USA), neutrophil elastase (ab21595, Abcam, Australia) and ED1 (ab31630, Abcam, Australia) were purchased from commercial sources

Validation

Validation from manufacturer's websites:

ab2378 – Validated in WB, ELISA, IHC, ICC, ICC/IF and tested in Mouse, Rat, Human, Cited in 52 publications. H7403 – The product specifically stains histamine-containing cells in paraformaldehyde/carbodiimide-fixed or paraformaldehyde-fixed, paraffin-embedded sections of rat stomach (endocrine cells and mast cells), reacts with a wide range of species, cited in 8 publications. ab21595 – Suitable for: IHC-Fr, ICC/IF, ICC, IHC-P, WB, IP, ELISA, reacts with: Mouse, Rat, Human, cited by 69 publications. ab31630 – Suitable for: Flow Cyt, IHC-Fr, IP, WB, RIA, IHC-FrFI, IHC-P, reacts with: Mouse, Rat, Human, cited by 157 publications. Further information available on manufacturer's websites.

Eukaryotic cell lines

Policy information about <u>cell lines</u>	
Cell line source(s)	1321N1 and HT-29 cells were from ECACC; U2OS-hPAR2 were from DiscoverX; rat KNRK cells were from ATCC. More information in Methods section.
Authentication	Short tandem repeat analysis was used to confirm the identity of the cell lines.
Mycoplasma contamination	All cells used tested negative for mycoplasma.
Commonly misidentified lines (See <u>ICLAC</u> register)	No cell lines used are listed in this database.

Animals and other organisms

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

Laboratory animals Male Wister rats (7–8 weeks old, 250 \pm 30 g)

Wild animals Study did not involve wild animals

Field-collected samples Study did not involve samples collected from the field.

Ethics oversight

All in vivo experimental procedures and animal handling were conducted with approval from the Animal Ethics Committee at the

University of Queensland which follows NHMRC and ARRIVE guidelines.

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