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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, seeAuthors & Referees and theEditorial Policy Checklist.

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			
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			
	test(s) used AND whether they are one- or two-sided ests 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)			
	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	nalysis, 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 e	ffect 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 c	ode		
Policy information abou	ut <u>availability of computer code</u>		
Data collection	N/A		
Data analysis	N/A		
	m algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.		
Data			
- Accession codes, uni - A list of figures that	nt <u>availability of data</u> nclude a <u>data availability statement</u> . This statement should provide the following information, where applicable: que identifiers, or web links for publicly available datasets have associated raw data restrictions on data availability		
	ndings are included in this published article (and its Supplementary files), and all relevant materials are available from the authors. No its were generated in this study.		
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.		
x Life sciences	Behavioural & social sciences Ecological, evolutionary & environmental sciences		

Lite scien	ces sti	udy design		
All studies must disc	lose on these	points even when the disclosure is negative.		
·	Wound healing	or cell-based assays, three wells or three independently-treated samples were used. Vound healing model was conducted in 5 animals/treatment group. ermeability model was conducted on two animals, as published in Cell. 2016, 167(1):275-284		
Data exclusions	N/A			
Replication	2-3			
Randomization	Mice were allocated randomly to different groups.			
Blinding	Some key obse	me key observations were conducted by more than one person in the lab.		
We require information	n from authors	pecific materials, systems and methods about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material,		
,		your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.		
Materials & exp		·		
n/a Involved in the Antibodies	e study	n/a Involved in the study X ChIP-seq		
X Eukaryotic c	ell lines	Flow cytometry		
× Palaeontolog		MRI-based neuroimaging		
	other organisr arch participan			
Antibodies				
Antibodies used	A	ntibodies were from Cell Signaling and Sigma.		
Validation		Il antibodies were from reputable sources and have been extensively validated in the literatures. In our hands, they all interacted with proteins of the expected molecular mass and functional activation.		
Eukaryotic ce	ell lines			
Policy information al	bout <u>cell lines</u>	<u> </u>		
Cell line source(s)		Bovine retinal microvascular endothelial cells (BRECs) and bovine choroidal microvascular endothelial cells (BCECs) were from VEC technologies; Human retinal microvascular endothelial cells (passage <15) was from Cell Systems Corporation; Normal human retinal pigment epithelial cells were obtained from Lonza; alll other cell lines were obtained from ATCC.		
Authentication		All cell lines are from Lonza, ATCC or VEC technologies		
Mycoplasma conta	amination	No contamination of mycoplasma in any of the cell line we used.		
Commonly misider (See <u>ICLAC</u> register)	ntified lines	N/A		
Animals and	other org	ganisms		
Policy information al	bout <u>studies i</u>	involving animals; ARRIVE guidelines recommended for reporting animal research		
Laboratory animal	s C	57BL/6 male or female mice 6–10 week of age and HA-Hrhr/IAF male guinea pigs 450-500g		
Wild animals	N	N/A		
Field-collected san	mples A	Il mouse procedures were approved by the University of California, San Diego Institutional Animal Care and Use Committee.		

Ethics oversight

All mouse procedures were approved by the University of California, San Diego Institutional Animal Care and Use Committee.

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