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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 <u>Authors & Referees</u> and the <u>Editorial Policy Checklist</u>.

### Statistical parameters

		Methods section).
n/a	Cor	nfirmed
	$\boxtimes$	The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
		An indication of whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
$\boxtimes$		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.
$\boxtimes$		A description of all covariates tested
$\boxtimes$		A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
	$\boxtimes$	A full description of the statistics including <u>central tendency</u> (e.g. means) or other basic estimates (e.g. regression coefficient) AND <u>variation</u> (e.g. standard deviation) or associated <u>estimates of uncertainty</u> (e.g. confidence intervals)
$\boxtimes$		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 <i>Give P values as exact values whenever suitable.</i>
$\boxtimes$		For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
$\boxtimes$		For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
$\boxtimes$		Estimates of effect sizes (e.g. Cohen's d, Pearson's r), indicating how they were calculated
	$\boxtimes$	Clearly defined error bars  State explicitly what error bars represent (e.g. SD, SE, CI)

Our web collection on <u>statistics for biologists</u> may be useful.

#### Software and code

Policy information about availability of computer code

Data collection V

We only used commercially/publicly available software and we describe and reference it thoroughly in the Methods. Include FEI's EPU, Relion2.1, Coot, Phenix, Graphpad Prism, UCSF Chimera.

Data analysis

We only used commercially/publicly available software and we describe and reference it thoroughly in the Methods. Include FEI's EPU, Relion2.1, Coot, Phenix, Graphpad Prism, UCSF Chimera.

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 upon request. 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

Provide your data availability statement here.

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riela-specific reporting					
Please select the best fit for your research. If you are not sure, read the appropriate sections before making your selection.					
Life sciences		Behavioural & social sciences			
For a reference copy of t	he document with	h all sections, see <u>nature.com/authors/policies/ReportingSummary-flat.pdf</u>			
Life scien	ices				
Study design	1				
All studies must dis	close on these	e points even when the disclosure is negative.			
Sample size	No statistical methods were used to predetermine sample size. The experiments were not randomized and the investigators were not blinded to allocation during experiments and outcome assessments.				
Data exclusions	No data were	excluded.			
Replication	Experiments w	were repeated with independent samples as described in Methods and EF Fig. legends.			
Randomization	No statistical methods were used to predetermine sample size. The experiments were not randomized and the investigators were not blinded to allocation during experiments and outcome assessments.				
Blinding	No statistical methods were used to predetermine sample size. The experiments were not randomized and the investigators were not blinded to allocation during experiments and outcome assessments.				
		ental systems			
Policy information a		lity of materials			
n/a Involved in t					
Unique m					
Antibodies  Eukaryotic cell lines					
	Research animals				
Human research participants					
Unique materials					
Obtaining unique	materials N	No restrictions.			
Antibodies					
Antibodies used We		e generated a new monoclonal IgG antibody as described in the Methods section.			
Validation		e thoroughly described validation of this antibody in the Methods section.			
Eukaryotic cell lines					
Policy information about <u>cell lines</u>					
Cell line source(s)		ATCC CRL-3022 and Sf9 insect cells			
Authentication		The cells lines were purchased directly from the manufacturer			
Mycoplasma cont	tamination	Not tested.			
Commonly misidentified lines (See ICLAC register)					

# Method-specific reporting

n/a Involved in the study

ChIP-seq

Flow cytometry

Magnetic resonance imaging