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In the data availability statement, information about access to primary datasets (generated during the study) and referenced datasets (datasets analyzed in the study) must be provided. Where data are publicly available, accession codes or other unique identifiers if relevant must be provided.

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The data availability statement should include the following information: reasons for controlled access (e.g., privacy, ethical/legal issues), conditions of access must be described precisely including contact details for access requests, timeframe for response to requests, restrictions imposed on data use via data use agreements. A copy or link to the data use agreement should be provided if requested by editors. Restrictions on controlled access datasets including restrictions on downstream data reuse or authorship requirements must be clearly described in manuscript and to editors at the time of submission. Editors may decline further consideration of the manuscript after evaluation if restrictions are found to be unduly prohibitive.

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Researchers should provide information in the manuscript on their data collection methods sufficient to support peer review. If data processing steps were performed by the third-party, out of the control of the authors, this should be clearly stated in the methods. Editors reserve the right to decline consideration if a manuscript fails to provide sufficient information regarding data collection approach.

Mandates for specific datasets

For the following types of dataset, submission to a community-endorsed, public repository is **mandatory**. Accession numbers must be provided in the paper. Examples of appropriate public repositories are listed below and here.

DNA, RNA and protein sequences
Protein sequences: UniProt

DNA and RNA sequences: Genbank/European Nucleotide Archive (ENA)/DNA DataBank of Japan (DDBJ), Protein DataBank, UniProt.

DNA and RNA sequencing data (traces for capillary electrophoresis and short reads for next-generation sequencing): NCBI trace and short-read archive, ENA's Sequence Read Archive.

Genetic polymorphisms: dbSNP, dbVar, European Variation Archive (EVA).

Linked genotype and phenotype data: dbGAP, European Genome-Phenome Archive (EGA).

Data for human subjects should be submitted to a public repository with appropriate access control (see above). Any restrictions on data access for sensitive data (e.g. electronic medical records, forensic data, and personal data from vulnerable populations) require an explanation of the nature of and reasons for the restrictions, and details of the conditions under which the data can be accessed or reused.

Deep sequencing data: deposit in Gene Expression Omnibus (GEO) or ArrayExpress upon submission to the journal. Accession numbers must be provided in the published manuscript.

This policy includes even short stretches of novel sequence information such as epitopes, functional domains, genetic markers, or haplotypes. Short novel sequences must include surrounding sequence information to provide context.

The sequences of all RNAi, antisense and morpholino probes must be included in the paper or deposited in a public database, with the accession number quoted. When an unpublished library is included in the paper, at minimum the sequences of the probes central to the conclusions of the paper must be presented.

Macromolecular structures

Authors of papers describing structures of biological macromolecules must provide an official validation report from the Worldwide Protein Data Bank (wwPDB). Atomic coordinates and related experimental data (structure factor amplitudes/intensities for crystal structures, or restraints for NMR structures) must be provided when requested by Editorial Board Members for the purposes of evaluating the manuscript, if they are not already freely accessible in a publicly available and recognized database (e.g. Protein DataBank, UniProt, Nucleic Acid

Database or Biological Magnetic Resonance Data Bank). Electron microscopy-derived density maps and coordinate data must be deposited in the Electron Microscopy Data Bank (EMDB). Accessibility in repositories must be designated 'for immediate release on publication'.

Microarray data

MIAME-compliant microarray data: deposit in GEO or ArrayExpress upon submission to *Scientific Reports*.

Data must be MIAME-compliant, as described at the FGED website specifying microarray standards.

Crystallographic data for small molecules

Manuscripts reporting new three-dimensional structures of small molecules from crystallographic analysis should include a .cif file and a structural figure with probability ellipsoids for publication as Supplementary Information. These files must have been checked using the IUCR's CheckCIF routine, and a PDF copy of the output must be included at submission, together with a justification for any alerts reported. Crystallographic data for small molecules should be submitted to the Cambridge Structural Database and the deposition number referenced appropriately in the manuscript. Full access must be provided on publication.

Proteomics data

For proteomics data: PRIDE, PeptideAtlas, Tranche

Authors reporting results generated using the technique of mass spectrometry-based proteomics should deposit the raw MS/MS data supporting the conclusions in their paper in a public repository.

Recommendations for other datasets

In addition to these mandates, the preferred way to share any data sets is via public repositories. A list of approved and recommended data repositories, organized by discipline, is maintained here. Please consult this list to identify an appropriate repository for your data sets.

When repositories do not exist for a particular data type, authors can deposit and share data via figshare or Dryad, two general-purpose scientific data repositories.

Sharing biological materials

A condition of publication in *Scientific Reports* is that authors are required to make materials, data and associated protocols promptly available to others without preconditions.

For materials such as mutant strains and cell lines, *Scientific Reports* require authors to use established public repositories when one exists (for example, Jackson Laboratory, the European Mouse Mutant Archive (EMMA), the European Conditional Mouse Mutagenesis Program (EUCOMM), the Knockout Mouse Project (KOMP), Addgene, RIKEN Bioresource Centre, the Mutant Mouse Regional Resource Centers, American Type Culture Collection (Americas), American Type Culture Collection (Asia/Europe), UK Stem Cell Bank), and provide accession numbers in the manuscript.

Cell lines

The distribution of human cell lines used in research should not be hindered by restrictions from donors. Researchers developing cell lines must investigate and disclose any restrictions associated with the human or other tissue they are using, particularly if someone else collected the samples, if the samples come from multiple clinical sources or if they come from several legal jurisdictions. If a scientist needs to create cell lines that might be used for as-yet-unforeseen purposes, only tissue with no restrictions should be used. Authors of papers that involve consent forms must, at the time of submitting the manuscript, make *Scientific Reports* aware of any limits that result from those forms.

Flow cytometry

Every manuscript that contains flow cytometry experiments should identify in the methods section all antibody reagents by clone identifier, vendor and fluorochrome. Authors should identify the instrument and software used to collect and analyse experimental data. Axes labels for plots or graphs depicting flow cytometry data should state the marker (for example, CD4) and the axes scales (log or linear) should be clearly visible. Authors should provide numerical analysis for the number of cells analysed and the absolute numbers or percentages (with statistics stated in either the text, legend or in a supplementary table) of the relevant cell population(s) within post-sort fractions. Hints for good general practice in the description of flow cytometry experiments can be found in the MIFlowCyt Standards section of SourceForge.

For papers describing a new cell population or for which a given sorted cell population is critical to the main message imparted by the new work, authors should describe in a supplementary figure or two the full gating strategy used for

the experiments described in the manuscript. A figure depicting the 'gates' used to identify sorted subsets is useful and should be provided to the referees on request. These data would include preliminary forward and side scatter gates of the starting cell population, indicating where boundaries between 'positive' and 'negative' staining cell populations are defined. For preliminary sorts that use 'cocktails' of antibodies to exclude certain cell populations, for example, lineage-minus (Lin-), the antibodies and fluorochromes that are contained in the 'cocktail' need to be specified for the 'dump' channel.

Data citation

Authors should cite any datasets stored in external repositories that are mentioned within their manuscript. For previously published datasets, we ask authors to cite both the related research articles and the datasets themselves. For more information on how to cite datasets in submitted manuscripts, please see our submission guidelines.

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Scientific Reports follows the Nature Portfolio policies for the sharing of computer code and algorithm (read these policies in full).

For all studies using custom code or mathematical algorithm that is central to the conclusions, authors must provide any previously unreported custom computer code or algorithm used to generate results upon editor or reviewer request. We reserve the right to decline the manuscript if important code is unavailable. The Methods section must include a statement with the heading 'Code availability' that describes how readers can access the code or algorithm, including any restrictions to access. To ensure that the version of custom code, software or algorithm described in the publication is maintained, we will publish it as a Supplementary document or, when applicable, request that authors maintain it in an established software version control repository.

Digital image integrity and standards

High-resolution images are not required at initial submission. When a paper is accepted, the publishing team will request high-resolution files suitable for publication.

All digitized images submitted with the final revision of the manuscript should be 300 DPI if possible.

A certain degree of image processing is acceptable for publication (and for some experiments, fields and techniques is unavoidable), but the final image must correctly represent the original data and conform to community standards. The guidelines below will aid in accurate data presentation at the image processing level; authors must also take care to exercise prudence during data acquisition, where misrepresentation must equally be avoided. Manuscripts should include an 'equipment and settings' section with their methods that describes for each figure the pertinent instrument settings, acquisition conditions and processing changes, as described in this guide.

- Authors should list all image acquisition tools and image processing software packages used. Authors should document key image-gathering settings and processing manipulations in the methods.
- Images gathered at different times or from different locations should not be combined into a single image, unless it is stated that the resultant image is a product of time-averaged data or a time-lapse sequence. If juxtaposing images is essential, the borders should be clearly demarcated in the figure and described in the legend.
- The use of touch-up tools, such as cloning and healing tools in Photoshop, or any feature that deliberately obscures manipulations, is to be avoided.
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When submitting revised final figures upon conditional acceptance, authors may be asked to submit original, unprocessed images.

Electrophoretic gels and els

Positive and negative controls, as well as molecular size markers, should be included on each gel and blot – either in the main figure or an expanded data supplementary figure. For previously characterized antibodies, a citation must be provided. For antibodies less well characterized in the system under study, a detailed characterization that demonstrates not only the specificity of the

antibody but also the range of reactivity of the reagent in the assay should be published as Supplementary Information.

The display of cropped gels and blots in the main paper is encouraged if it improves the clarity and conciseness of the presentation. In such cases, the cropping must be mentioned in the figure legend and the supplementary information must include original gels and blots, with gel/membrane edges visible. These uncropped images should be labelled as in the main text and placed in a single supplementary figure. The manuscript's figure legends should state that 'original blots/gels are presented in Supplementary Figure X.'

- Quantitative comparisons between samples on different gels/blots are discouraged; if this is unavoidable, the figure legend must state that the samples derive from the same experiment and that gels/blots were processed in parallel. Vertically sliced images that juxtapose lanes that were non-adjacent in the gel must have a clear separation or a black line delineating the boundary between the gels. Loading controls must be run on the same blot.
- Cropped gels in the paper must retain important bands.
- Cropped blots in the body of the paper should retain at least six band widths above and below the band.
- High-contrast gels and blots are discouraged, as overexposure may mask additional bands. Authors should strive for exposures with grey backgrounds. Multiple exposures should be presented in Supplementary Information if high contrast is unavoidable. Immunoblots should be surrounded by a black line to indicate the borders of the blot if the background is faint.
- For quantitative comparisons, appropriate reagents, controls and imaging methods with linear signal ranges should be used.

Microscopy

Authors should be prepared to supply *Scientific Reports* with original data on request, at the resolution collected, from which their images were generated. Cells from multiple fields should not be juxtaposed in a single field; instead, multiple supporting fields of cells should be shown as Supplementary Information.

Adjustments should be applied to the entire image. Threshold manipulation, expansion or contraction of signal ranges and the altering of high signals should be avoided. If 'pseudo-colouring' and nonlinear adjustment (e.g. 'gamma changes') are used, this must be disclosed. Adjustments of individual colour

channels are sometimes necessary on 'merged' images, but this should be noted in the figure legend.

We encourage the inclusion of the following with the final revised version of the manuscript for publication:

- In the methods, specify the type of equipment (microscopes/objective lenses, cameras, detectors, filter model and batch number) and acquisition software used. Although we appreciate that there is some variation between instruments, equipment settings for critical measurements should also be listed.
- An 'equipment and settings' section within the methods should list for each image: acquisition information, including time and space resolution data (xyzt and pixel dimensions); image bit depth; experimental conditions such as temperature and imaging medium; and fluorochromes (excitation and emission wavelengths or ranges, filters, dichroic beamsplitters, if any).
- The display lookup table (LUT) and the quantitative map between the LUT and the bitmap should be provided, especially when rainbow pseudocolour is used. If the LUT is linear and covers the full range of the data, that should be stated.
- Processing software should be named and manipulations indicated (such as type of deconvolution, three-dimensional reconstructions, surface and volume rendering, 'gamma changes', filtering, thresholding and projection).
- Authors should state the measured resolution at which an image was acquired and any downstream processing or averaging that enhances the resolution of the image.

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The threat posed by bioweapons raises the unusual need to assess the balance of risk and benefit in publication. Editorial Board Members may not be best qualified to make such judgments unassisted, and so we reserve the right to take expert

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