nature portfolio

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Reporting Summary

Nature Portfolio 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 Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, 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
☐	☒	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
☐	☒	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. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	For Bayesian analysis, 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 effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	N/A
Data analysis	N/A

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 and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio 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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

Data of this study are available from the corresponding authors upon reasonable request. Source data for Figure 7 are available in Supplementary Data 1

Human research participants

Policy information about studies involving human research participants and Sex and Gender in Research.

Reporting on sex and gender	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

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

Field-specific reporting

Please select the one below 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

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	We used the sample size because the experiments re-produced clear results.
Data exclusions	No data were excluded from the analysis.
Replication	We performed adequate experiments for confirming the reproducibility results in addition to preliminary tests.
Randomization	The mice were randomly assigned to the test.
Blinding	The tests were not blinded as the tumours in the control groups grew to an apparently visible size.

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

n/a	Involved in the study
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☐	☒ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	· mAbs against the SA peptidoglycan epitope (clone Staph12-569.3, murine IgG3, https://scicrunch.org/resolver/RRID:AB_129994) purchased from QED Bioscience Inc. (San Diego, CA, USA). · mAb against SC, including the anti-SC spike mAb (GTX632604, https://scicrunch.org/resolver/RRID:AB_2864418) purchased from GeneTex (Irvine, CA, USA). · Therapeutic mAb against human EGFR, (HER1) panitumumab (Vectibix, humanised IgG2) purchased from Amgen (Thousand Oaks, CA, USA).

Validation	All antibodies used in our studies were commercially available or in clinical use.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	· VeroE6/TMPRSS2 cells (JCRB #1819) · EGFR-overexpressed A431 cells for in vitro PIT
Authentication	· VeroE6/TMPRSS2 cells were obtained from JCRB Cell Bank in Japan. · EGFR-overexpressed A431 cells have been used in different studies to date.
Mycoplasma contamination	We confirmed all cell lines tested negative for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	*Name any commonly misidentified cell lines used in the study and provide a rationale for their use.*

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	· Cotton rats are used in SA-targeting PIAS on MRSA-colonised rats; the rats are used for investigating SA colonisation because cotton rats are well carrier for SA. · Athymic nude mice are used as a tumor bearing mouse model to evaluate the anti-cancer effect of PIT.
Wild animals	N/A
Reporting on sex	female
Field-collected samples	N/A
Ethics oversight	The animal experiment was performed after approval by a local ethical review and followed ARRIVE guidelines.

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

Flow Cytometry

Plots

Confirm that:

☒ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☒ All plots are contour plots with outliers or pseudocolor plots.

☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	mAb–IR700 conjugate (1 μg) was added to 100 μL of a microbial suspension containing approximately 1 × 10^5 colony-forming units (c.f.u.) and incubated for 1 h at 4°C, followed by washing the cells with 3 mL of RPMI twice. The fluorescence of IR700 was measured with a flow cytometry analyser (MACSQant analyser; Miltenyi Biotec, Bergisch Gladbach, Germany) and fluorescence microscopy (IX73; Olympus, Tokyo, Japan) with the following filter settings: 608–648-nm excitation filter and 672–712-nm emission filter. To confirm the target specificity of mAb–IR700 conjugate, unconjugated mAb was added before mAb–IR700 treatments.
Instrument	MACSQant analyser; Miltenyi Biotec, Bergisch Gladbach, Germany
Software	Software for MACSQant analyser; Miltenyi Biotec, Bergisch Gladbach, Germany
Cell population abundance	Used for the analysis of bacterial cells according to the manufacturer's instructions.
Gating strategy	Gatedbacterial cells according to manufacturer's instructions.

☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.