

## 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 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

Data analysis

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 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

LC-MS data in mzXML format and molecular networking results are available in the MassIVE repository with the identifier MSV000087335. *S. aureus* short-read sequence data have been deposited in the European Nucleotide Archive/NCBI Sequence Read Archive under BioProjects PRJEB15105, PRJEB21015, PRJEB2655, PRJEB2755, PRJEB2756, PRJEB28206, PRJEB3174, PRJEB32898, PRJNA596428, and PRJEB43456 and the genome accession numbers are provided in Supplementary Table 1. *T. erinacei* type strain IMI 101051 short-read sequence data have been deposited in the European Nucleotide Archive under BioProject PRJEB43453. Tree and genealogy files in Newick format are provided in Supplementary Data 1-10. Source data for Figs. 1-4 and Extended Data Figs. 1, 4, 6, 7, and 9 are provided with the paper.

## 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](https://www.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	Describe how sample size was determined, detailing any statistical methods used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient.
Data exclusions	Describe any data exclusions. If no data were excluded from the analyses, state so OR if data were excluded, describe the exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.
Replication	Describe the measures taken to verify the reproducibility of the experimental findings. If all attempts at replication were successful, confirm this OR if there are any findings that were not replicated or cannot be reproduced, note this and describe why.
Randomization	Describe how samples/organisms/participants were allocated into experimental groups. If allocation was not random, describe how covariates were controlled OR if this is not relevant to your study, explain why.
Blinding	Describe whether the investigators were blinded to group allocation during data collection and/or analysis. If blinding was not possible, describe why OR explain why blinding was not relevant to your study.

## Behavioural & social sciences study design

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

Study description	Briefly describe the study type including whether data are quantitative, qualitative, or mixed-methods (e.g. qualitative cross-sectional, quantitative experimental, mixed-methods case study).
Research sample	State the research sample (e.g. Harvard university undergraduates, villagers in rural India) and provide relevant demographic information (e.g. age, sex) and indicate whether the sample is representative. Provide a rationale for the study sample chosen. For studies involving existing datasets, please describe the dataset and source.
Sampling strategy	Describe the sampling procedure (e.g. random, snowball, stratified, convenience). Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient. For qualitative data, please indicate whether data saturation was considered, and what criteria were used to decide that no further sampling was needed.
Data collection	Provide details about the data collection procedure, including the instruments or devices used to record the data (e.g. pen and paper, computer, eye tracker, video or audio equipment) whether anyone was present besides the participant(s) and the researcher, and whether the researcher was blind to experimental condition and/or the study hypothesis during data collection.
Timing	Indicate the start and stop dates of data collection. If there is a gap between collection periods, state the dates for each sample cohort.
Data exclusions	If no data were excluded from the analyses, state so OR if data were excluded, provide the exact number of exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.

Non-participation

State how many participants dropped out/declined participation and the reason(s) given OR provide response rate OR state that no participants dropped out/declined participation.

Randomization

If participants were not allocated into experimental groups, state so OR describe how participants were allocated to groups, and if allocation was not random, describe how covariates were controlled.

## Ecological, evolutionary & environmental sciences study design

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

Study description

We first examined the distribution of *mecC*-MRSA and other *S. aureus* isolates in hedgehogs in ten European countries and New Zealand. We sequenced 244 isolates to determine the population structure of *S. aureus* in hedgehogs. We also sequenced 913 *S. aureus* isolates from other sources to infer the evolutionary histories, host dynamics, geographical dispersal patterns, and zoonotic potential of the major *mecC*-MRSA clones in Europe. The potential mechanisms for natural selection of *mecC*-MRSA by *T. erinacei* were assessed by sequencing and analysing the genome of *T. erinacei* for penicillin G and cephalosporin C biosynthetic genes and by screening *T. erinacei* for production of beta-lactam antibiotics and antibiotic activity against a panel of *S. aureus* strains.

Research sample

The hedgehog survey was conducted by staff members of the wildlife rescue centres who collected swab samples from the nasal area, skin, and feet of hedgehogs in connection with routine checks. The survey included 828 samples from 276 hedgehogs originating from 16 wildlife rescue centres in ten European countries and two wildlife rescue centres in New Zealand, which represent the geographic distribution of the two European hedgehog species, the west European hedgehog (*Erinaceus europaeus*) present in Western Europe and New Zealand and the northern white-breasted hedgehog (*E. roumanicus*) found in Eastern Europe. Of the 276 hedgehogs included in the survey, 251 belonged to *E. europaeus* and the remaining 25 to *E. roumanicus*. Determination of sex and age was not relevant and therefore not determined. This led to the identification of 244 *S. aureus* isolates. The survey is a convenience sample, because the number and geographic distribution of hedgehog samples were limited by the number of wildlife rescue centres that volunteered to participate in our study and the number of hedgehogs in care at the time of sampling. We also included a collection of 913 *S. aureus* CC130, CC425, and CC1943 isolates from other sources, which represents the known geographic distribution (mainly Western and Central Europe) and host repertoire (mainly humans, cattle, sheep, goats, and wild animals) of each clone.

Sampling strategy

We did not use statistical methods to predetermine sample size, because the number and geographic distribution of hedgehog samples were limited by the number of wildlife rescue centres that volunteered to participate in our study and the number of hedgehogs in care at the time of sampling. *S. aureus* CC130, CC425, and CC1943 isolates from other sources were selected to represent the known geographic distribution (mainly Western and Central Europe) and host repertoire (mainly humans, cattle, sheep, goats, and wild animals) of each clone.

Data collection

Personnel at the different wildlife rescue centres were instructed to obtain samples from the nasal area, skin, and feet of hedgehogs kept in separate enclosures using FLOQSwabs (Copan). Swabs were stored in liquid Amies medium at ambient temperature and sent to the National Reference Laboratory for Antimicrobial Resistance at Statens Serum Institut in Denmark or the Department of Veterinary Medicine at University of Cambridge in the United Kingdom immediately after sample collection.

Timing and spatial scale

The hedgehog survey was conducted between 12th April and 21st November 2018 and included 16 wildlife rescue centres in ten European countries and two wildlife rescue centres in New Zealand, which represent the geographic distribution of the two European hedgehog species: Attica, Greece, Județul Cluj, Romania, Treviso, Italy, Prague, Czech Republic, Jutland, Denmark, Zealand, Denmark, Valencia, Spain, Catalunya, Spain, Norte Region, Portugal, Loire-sur-Rhône, France, Fouencamps, France, Cornwall, England, Berkshire, England, Cambridgeshire, England, Northumberland, England, Powys, Wales, South Island, New Zealand, and North Island, New Zealand. Swab samples were typically collected within 24 to 48 hours at each wildlife rescue centre. There were no specific instructions on when to collect swab samples, because *S. aureus* colonisation is not expected to display substantial seasonal fluctuations. The 913 *S. aureus* CC130, CC425, and CC1943 isolates from other sources were collected between 1975 and 2018 and originated from 16 European countries, which represent the geographic distribution of each clone: Denmark, England, Germany, Spain, Scotland, Sweden, France, Norway, Italy, Austria, Wales, Belgium, Switzerland, Finland, Greenland, and the Netherlands.

Data exclusions

No animals, samples, or isolates were excluded from our analyses.

Reproducibility

Each sequenced *S. aureus* genome was subjected to multilocus sequence typing and the derived clonal complex was compared to the *spa* type of the original isolate when available, including 63% (154/244) of the isolates from the hedgehog survey and 63% (576/913) of the isolates from other sources. The analysis showed that the two methods assigned 100% (730/730) of the isolates to the same clonal complex. Determination of *T. erinacei* inhibition zones against the panel of *S. aureus* strains was repeated four times for each strain. The dates of the most recent common ancestors of the major *mecC*-MRSA lineages were analysed by two different approaches (*BactDating* and *Treedater*), which produced very similar estimates.

Randomization

We did not perform randomization as our study was observational rather than experimental.

Blinding

We did not perform blinding as our study was observational rather than experimental.

Did the study involve field work?  Yes  No

## Field work, collection and transport

Field conditions

Describe the study conditions for field work, providing relevant parameters (e.g. temperature, rainfall).

Location

State the location of the sampling or experiment, providing relevant parameters (e.g. latitude and longitude, elevation, water depth).

## Access &amp; import/export

Describe the efforts you have made to access habitats and to collect and import/export your samples in a responsible manner and in compliance with local, national and international laws, noting any permits that were obtained (give the name of the issuing authority, the date of issue, and any identifying information).

## Disturbance

Describe any disturbance caused by the study and how it was minimized.

## 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
- Antibodies
- Eukaryotic cell lines
- Palaeontology and archaeology
- Animals and other organisms
- Human research participants
- Clinical data
- Dual use research of concern

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

### Antibodies

## Antibodies used

Describe all antibodies used in the study; as applicable, provide supplier name, catalog number, clone name, and lot number.

## Validation

Describe the validation of each primary antibody for the species and application, noting any validation statements on the manufacturer's website, relevant citations, antibody profiles in online databases, or data provided in the manuscript.

### Eukaryotic cell lines

Policy information about [cell lines](#)

## Cell line source(s)

State the source of each cell line used.

## Authentication

Describe the authentication procedures for each cell line used OR declare that none of the cell lines used were authenticated.

## Mycoplasma contamination

Confirm that all cell lines tested negative for mycoplasma contamination OR describe the results of the testing for mycoplasma contamination OR declare that the cell lines were not tested 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.

### Palaeontology and Archaeology

## Specimen provenance

Provide provenance information for specimens and describe permits that were obtained for the work (including the name of the issuing authority, the date of issue, and any identifying information).

## Specimen deposition

Indicate where the specimens have been deposited to permit free access by other researchers.

## Dating methods

If new dates are provided, describe how they were obtained (e.g. collection, storage, sample pretreatment and measurement), where they were obtained (i.e. lab name), the calibration program and the protocol for quality assurance OR state that no new dates are provided.

Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

## Ethics oversight

Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.

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

### Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

## Laboratory animals

The study did not involve laboratory animals.

**Wild animals**

*The hedgehog survey involved 251 west European hedgehogs (*Erinaceus europaeus*) and 25 northern white-breasted hedgehogs (*E. roumanicus*) that had been admitted to wildlife rescue centres for treatment of a diverse range of conditions. Determination of sex and age was not relevant and therefore not determined. The sampling procedure did not cause pain, suffering, distress or lasting harm, deprived the animal of usual care, or affected the fate of the animals. The survey did not involve wild hedgehogs captured for scientific purposes.*

**Field-collected samples**

*The study did not involve samples collected from the field.*

**Ethics oversight**

*The hedgehog survey was conducted by staff members of the wildlife rescue centres who collected swab samples in connection with routine checks. In accordance with the Animal Welfare Act 1999 administered by the New Zealand Ministry for Primary Industries and Directive 2010/63/EU of the European Parliament and of the Council of 22 September 2010 on the protection of animals used for scientific purposes, no ethical approval was required as sample collection did not cause pain, suffering, distress or lasting harm equivalent to, or higher than, that caused by the introduction of a needle in accordance with good veterinary practice or deprived the animal of usual care. Ethical review was undertaken at the Department of Veterinary Medicine, University of Cambridge (ref. CR76).*

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

## Human research participants

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Policy information about [studies involving human research participants](#)

**Population characteristics**

*Describe the covariate-relevant population characteristics of the human research participants (e.g. age, gender, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."*

**Recruitment**

*Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.*

**Ethics oversight**

*Identify the organization(s) that approved the study protocol.*

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

## Clinical data

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Policy information about [clinical studies](#)

All manuscripts should comply with the ICMJE [guidelines for publication of clinical research](#) and a completed [CONSORT checklist](#) must be included with all submissions.

**Clinical trial registration**

*Provide the trial registration number from ClinicalTrials.gov or an equivalent agency.*

**Study protocol**

*Note where the full trial protocol can be accessed OR if not available, explain why.*

**Data collection**

*Describe the settings and locales of data collection, noting the time periods of recruitment and data collection.*

**Outcomes**

*Describe how you pre-defined primary and secondary outcome measures and how you assessed these measures.*

## Dual use research of concern

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Policy information about [dual use research of concern](#)

**Hazards**

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

- | No                       | Yes                      |                            |
|--------------------------|--------------------------|----------------------------|
| <input type="checkbox"/> | <input type="checkbox"/> | Public health              |
| <input type="checkbox"/> | <input type="checkbox"/> | National security          |
| <input type="checkbox"/> | <input type="checkbox"/> | Crops and/or livestock     |
| <input type="checkbox"/> | <input type="checkbox"/> | Ecosystems                 |
| <input type="checkbox"/> | <input type="checkbox"/> | Any other significant area |

## Experiments of concern

Does the work involve any of these experiments of concern:

- | No                       | Yes                      |   |
|--------------------------|--------------------------|---|
| <input type="checkbox"/> | <input type="checkbox"/> | Demonstrate how to render a vaccine ineffective                             |
| <input type="checkbox"/> | <input type="checkbox"/> | Confer resistance to therapeutically useful antibiotics or antiviral agents |
| <input type="checkbox"/> | <input type="checkbox"/> | Enhance the virulence of a pathogen or render a nonpathogen virulent        |
| <input type="checkbox"/> | <input type="checkbox"/> | Increase transmissibility of a pathogen                                     |
| <input type="checkbox"/> | <input type="checkbox"/> | Alter the host range of a pathogen  |
| <input type="checkbox"/> | <input type="checkbox"/> | Enable evasion of diagnostic/detection modalities                           |
| <input type="checkbox"/> | <input type="checkbox"/> | Enable the weaponization of a biological agent or toxin                     |
| <input type="checkbox"/> | <input type="checkbox"/> | Any other potentially harmful combination of experiments and agents         |

## ChIP-seq

### Data deposition

- Confirm that both raw and final processed data have been deposited in a public database such as [GEO](#).
- Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

#### Data access links

May remain private before publication.

For "Initial submission" or "Revised version" documents, provide reviewer access links. For your "Final submission" document, provide a link to the deposited data.

#### Files in database submission

Provide a list of all files available in the database submission.

#### Genome browser session

(e.g. [UCSC](#))

Provide a link to an anonymized genome browser session for "Initial submission" and "Revised version" documents only, to enable peer review. Write "no longer applicable" for "Final submission" documents.

## Methodology

### Replicates

Describe the experimental replicates, specifying number, type and replicate agreement.

### Sequencing depth

Describe the sequencing depth for each experiment, providing the total number of reads, uniquely mapped reads, length of reads and whether they were paired- or single-end.

### Antibodies

Describe the antibodies used for the ChIP-seq experiments; as applicable, provide supplier name, catalog number, clone name, and lot number.

### Peak calling parameters

Specify the command line program and parameters used for read mapping and peak calling, including the ChIP, control and index files used.

### Data quality

Describe the methods used to ensure data quality in full detail, including how many peaks are at FDR 5% and above 5-fold enrichment.

### Software

Describe the software used to collect and analyze the ChIP-seq data. For custom code that has been deposited into a community repository, provide accession details.

## 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

Describe the sample preparation, detailing the biological source of the cells and any tissue processing steps used.

### Instrument

Identify the instrument used for data collection, specifying make and model number.

- Software *Describe the software used to collect and analyze the flow cytometry data. For custom code that has been deposited into a community repository, provide accession details.*
- Cell population abundance *Describe the abundance of the relevant cell populations within post-sort fractions, providing details on the purity of the samples and how it was determined.*
- Gating strategy *Describe the gating strategy used for all relevant experiments, specifying the preliminary FSC/SSC gates of the starting cell population, indicating where boundaries between "positive" and "negative" staining cell populations are defined.*
- Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.

## Magnetic resonance imaging

### Experimental design

- Design type *Indicate task or resting state; event-related or block design.*
- Design specifications *Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.*
- Behavioral performance measures *State number and/or type of variables recorded (e.g. correct button press, response time) and what statistics were used to establish that the subjects were performing the task as expected (e.g. mean, range, and/or standard deviation across subjects).*

### Acquisition

- Imaging type(s) *Specify: functional, structural, diffusion, perfusion.*
- Field strength *Specify in Tesla*
- Sequence & imaging parameters *Specify the pulse sequence type (gradient echo, spin echo, etc.), imaging type (EPI, spiral, etc.), field of view, matrix size, slice thickness, orientation and TE/TR/flip angle.*
- Area of acquisition *State whether a whole brain scan was used OR define the area of acquisition, describing how the region was determined.*
- Diffusion MRI  Used  Not used

### Preprocessing

- Preprocessing software *Provide detail on software version and revision number and on specific parameters (model/functions, brain extraction, segmentation, smoothing kernel size, etc.).*
- Normalization *If data were normalized/standardized, describe the approach(es): specify linear or non-linear and define image types used for transformation OR indicate that data were not normalized and explain rationale for lack of normalization.*
- Normalization template *Describe the template used for normalization/transformation, specifying subject space or group standardized space (e.g. original Talairach, MNI305, ICBM152) OR indicate that the data were not normalized.*
- Noise and artifact removal *Describe your procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and physiological signals (heart rate, respiration).*
- Volume censoring *Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.*

### Statistical modeling & inference

- Model type and settings *Specify type (mass univariate, multivariate, RSA, predictive, etc.) and describe essential details of the model at the first and second levels (e.g. fixed, random or mixed effects; drift or auto-correlation).*
- Effect(s) tested *Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA or factorial designs were used.*
- Specify type of analysis:  Whole brain  ROI-based  Both
- Statistic type for inference (See [Eklund et al. 2016](#)) *Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.*
- Correction *Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).*

## Models & analysis

- n/a | Involved in the study
- Functional and/or effective connectivity
  - Graph analysis
  - Multivariate modeling or predictive analysis

Functional and/or effective connectivity

*Report the measures of dependence used and the model details (e.g. Pearson correlation, partial correlation, mutual information).*

Graph analysis

*Report the dependent variable and connectivity measure, specifying weighted graph or binarized graph, subject- or group-level, and the global and/or node summaries used (e.g. clustering coefficient, efficiency, etc.).*

Multivariate modeling and predictive analysis

*Specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.*