

Supplementary material for the manuscript:

**Methicillin-sensitive *Staphylococcus aureus* lineages contribute towards poor patient outcomes in orthopaedic device-related infections**

*Virginia Post*<sup>1\*</sup>, *Ben Pascoe*<sup>2,3\*</sup>, *Matthew D. Hitchings*<sup>4</sup>, *Christoph Erichsen*<sup>5</sup>, *Julian Fischer*<sup>6</sup>, *Mario Morgenstern*<sup>7</sup>, *R. Geoff Richards*<sup>1</sup>, *Samuel K. Sheppard*<sup>2#</sup> & *T. Fintan Moriarty*<sup>1,7#</sup>

<sup>1</sup>AO Research Institute Davos, Davos, Switzerland

<sup>2</sup>Ineos Oxford Institute of Antimicrobial Research, Department of Biology, University of Oxford, Oxford, United Kingdom

<sup>3</sup>Faculty of Veterinary Medicine, Chiang Mai University, Chiang Mai, Thailand

<sup>4</sup>Swansea University Medical School, Swansea University, Swansea, United Kingdom

<sup>5</sup>Department of Trauma Surgery, Trauma Centre Murnau, Murnau, Germany

<sup>6</sup>Centrum of Orthopedic Isartal, Pullach im Isartal, Germany

<sup>7</sup>Department of Orthopedic and Trauma Surgery, University Hospital Basel, Switzerland

**Running title:** Orthopaedic device related *S. aureus* infections

**#Address correspondence to:** T. Fintan Moriarty, [fintan.moriarty@aofoundation.org](mailto:fintan.moriarty@aofoundation.org) or Samuel K. Sheppard, [samuel.sheppard@biology.ox.ac.uk](mailto:samuel.sheppard@biology.ox.ac.uk)

*\*VP and BP contributed equally to this work. SKS and TFM contributed equally to this work.*

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[separate .xlsx file]

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**Table S2:**     Genome quality control and extended typing results.

**Table S3:**     Summary of core and accessory genome characterization with PIRATE.

**Table S4:**     Summary of genes identified by screening known virulence genes with the VfDB.

**Table S5:**     Summary of IEC genes and typing.

**Table S6:**     Summary of genes identified by screening antibiotic resistance genes with the AMRfinder (NCBI) and CARD databases.

**Table S7:**     Summary of OD values of biofilm assay.

**Table S8:**     Summary of virulence phenotype data.

**Table S9:**     Summary of genes associated with virulence phenotypes (SCOARY).

**Table S10:**   Per isolate recombination statistics using Gubbins.

## Additional materials and files

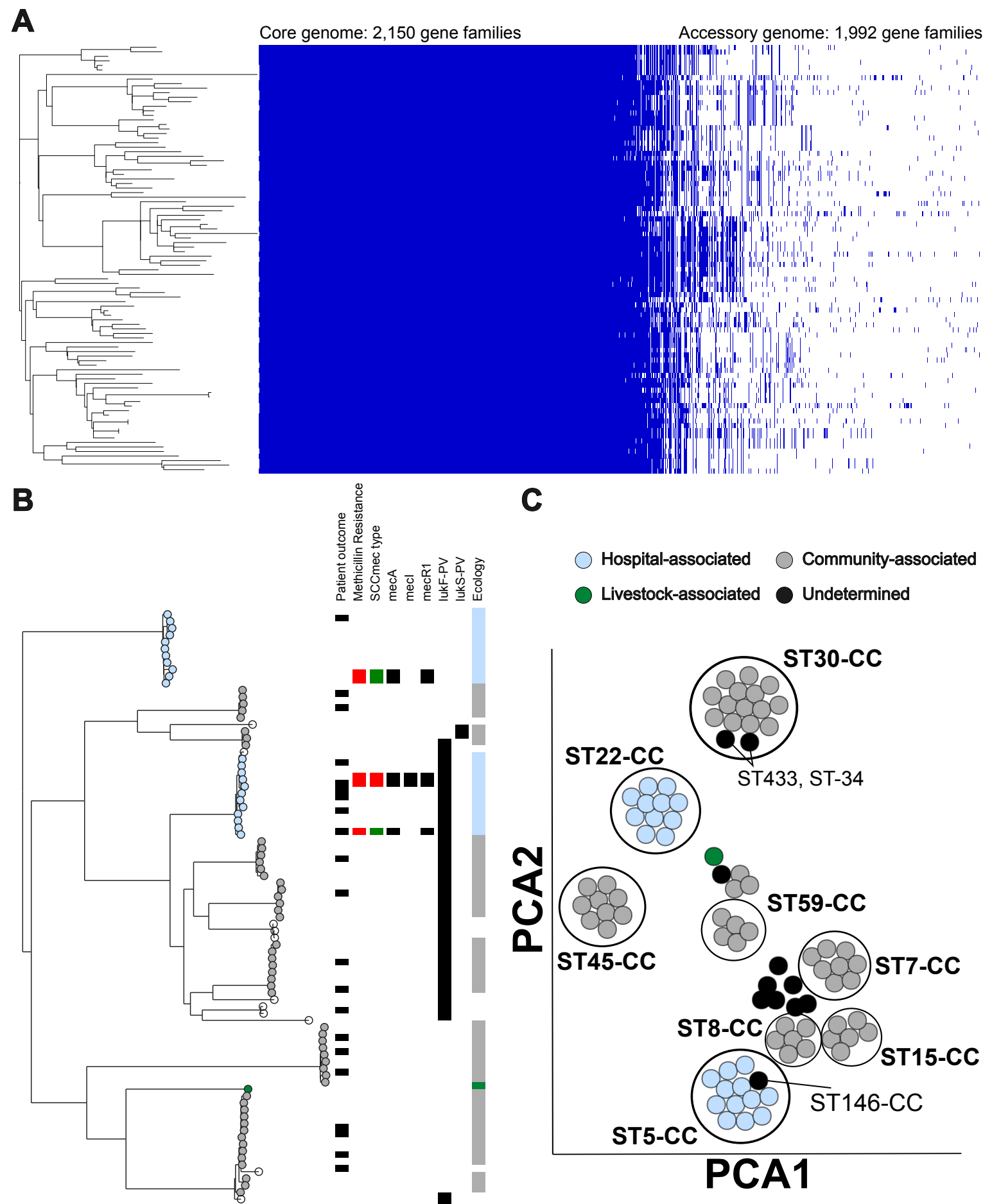
**Figshare:**     All supplementary files can also be found on FigShare doi:  
10.6084/m9.figshare.7926866

**Microreact:** Interactive phylogenies are hosted with

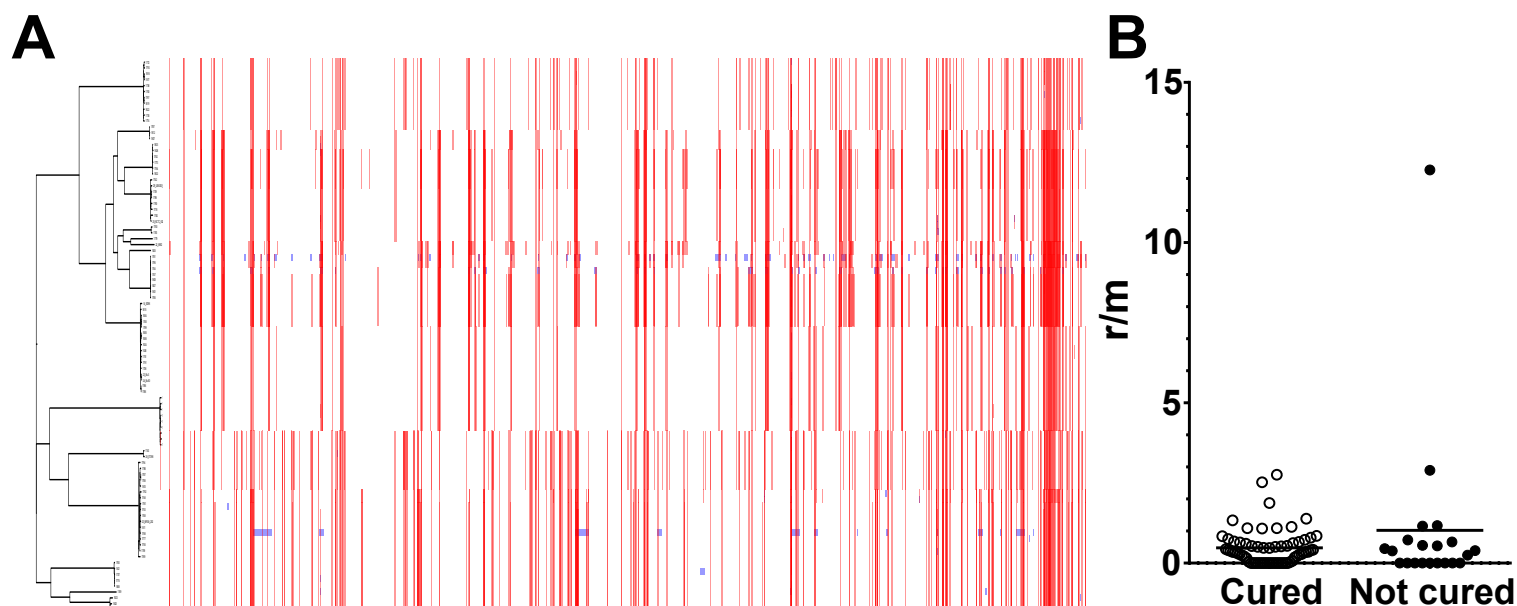
[<https://microreact.org/project/1KsjRuuiKzsuioCxQM1HF-davos-odri-s-aureus-virulence>]

and without AMR and virulence determinants

[<https://microreact.org/project/u7RjbMpReHLikTWN8Angxf-postpascoeetal-saureus-odri>]



**Supplementary figure S1:** (A) Pangenome matrix from PIRATE visualised in phandango. Blue blocks represent shared gene families between isolates. (B) Alternative visualisation of the same maximum likelihood phylogeny of our 86 isolates. Isolates are coloured by their predicted clonal lineage origins; hospital-, community-, livestock-, and undetermined lineages are coloured in blue, grey, green and black, respectively. (C) Accessory genome clustering of isolates with PopPunk groups isolates similarly to their position in the core genome phylogeny.



**Supplementary figure S2: (A)** The same maximum likelihood phylogeny of our 86 isolates as Figure 1 is visualised in phandango alongside output from Gubbins. Red lines represent areas of putative recombination events that are common in multiple isolates, and blue areas are those identified only in a single isolate. The effective rate of recombination ( $r/m$ ) for each isolate, grouped by infection outcome ("cured" / "not cured") is summarised **(B)**. Each circle represents an isolate and the average rate is designated by a black line. The effective rate of recombination ( $r/m$ ) is measured by the frequency at which recombination ( $r$ ) occurs relative to mutation ( $m$ ).