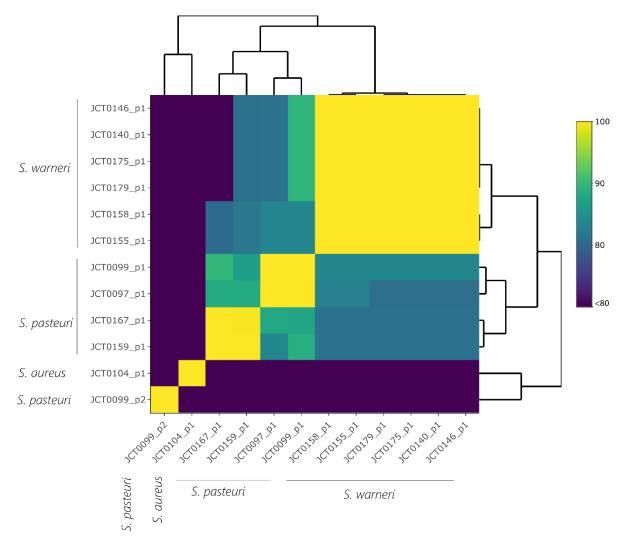


Supplementary Figure 1: Phylogenetic analysis of the *Staphylococcus* isolates. Maximum likelihood tree generated by concatenating the nucleotide sequences of 7 orthologous group genes (*mutS*, *recD2*, *pepA*, *yheS*, *pheT*, *pbp3* and *rpoC*) and aligning the concatenated sequences across the 14 strains, as proposed by Graña-Miraglia et al., 2018. Bootstraps are presented as a percentage of 1000 replicates, values over 80% are displayed as purple circles in the centre of branches. Scale bar refers to the nucleotide substitutions per site.



Supplementary Figure 2: Dendrogram and heatmap of hierarchical clustering of average nucleotide identity (ANI) between 12 *Staphylococcus* JCT prophages (query and references) using FastANI. Where FastANI could not calculate a score due to similarity falling below the threshold, a value <80 has been presented.



- 15 Supplementary Figure 3: Gene cluster comparisons between Staphylococcus JCT
- prophages and ViPTree-predicted closest phage relatives visualised using LoVis4u.
- 17 Genomes have been reorientated to start with the integrase gene when present. The colour
- of arrows indicates homologous genes with connecting lines in grey further indicating
- 19 regions of homology. Predicted phage modules are indicated by solid-coloured lines under
- 20 corresponding regions of each genome.
- 21 (a) Comparison of JCT0159_p1 and JCT0167_p1 with the closest
- 22 relative Staphylococcus phage vBSpsSQT1. (b) Comparison of JCT0099 p1 and
- JCT0097 p1 with the closest relative Staphylococcus phage IME-SA4. (c) Comparison of
- 24 JCT0158_p1, JCT0155_p1, JCT0140_p1, JCT0179_p1, JCT0175_p1, and JCT0146_p1
- with the closest relative Staphylococcus virus IME1354_01. (d) Comparison of JCT0104_p1
- with the closest relative *Staphylococcus* phage JS01. (e) Comparison of JCT0099_p2 with
- the closest relative *Staphylococcus* phage IME-1348.