

1 **Supplemental information**

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3 **Table S1. Results from MS analyses**

Gel bands from		Match in RK308 ORF collection					
Fig. 2A							
#	Estimated size (kDa)	Contig number	number of amino acids	calculated size (kDa)	coverage in MS analysis (%)	number of peptides	Result from BLASTp against <i>Staphylococcus</i> proteins
1	45	8	395	45	41	17	Cysteine protease
2	35	8	319	36	66	27	Beta-channel forming cytolysin
3	20	17	189	21	56	11	DUF4888 domain-containing protein (domain of unknown function)

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6 **Figure S1.**

7 **Hla protein sequence analyses.** (A) Alignment of *S. argenteus* RK308 and MSHR1132T,
8 which are identical (*S. arg*), *S. schweitzeri* FSA084T (*S. schw*) and *S. aureus* 1800T (*S. aur*)
9 Hla protein sequences. Dot; identical amino acid to *S. argenteus*, bold; a selection of amino
10 acid residues showed in *S. aureus* to be important for binding to the cell membrane and pore
11 formation, boxed; cleaved signal peptide. (B) Neighbour-joining phylogenetic tree based on
12 alignment of Hla amino acid sequences.

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Figure S1.

