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 of amino acids	calculated size (kDa)	coverage in MS analysis	number of peptides	Result from BLASTp against Staphylococcus
					(%)		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)
- acid residues showed in *S. aureus* to be important for binding to the cell membrane and pore

Hla protein sequences. Dot; identical amino acid to S. argenteus, bold; a selection of amino

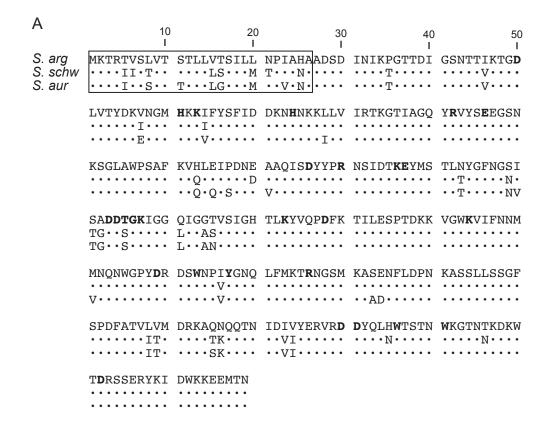
- formation, boxed; cleaved signal peptide. (B) Neighbour-joining phylogenetic tree based on
- 12 alignment of Hla amino acid sequences.

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Figure S1.



В

