

## Supplementary Information

### EsxA and EsxB do not form a complex

We used recombinant EsxA fused to Glutathione S-transferase (GST-EsxA) and asked whether untagged EsxA or EsxB would engage in complex formation. Size exclusion chromatography indicated that GST-EsxA eluted at a distinct exclusion volume as compared to EsxA or EsxB, albeit that all three proteins eluted in volume fractions consistent with formation of homo-oligomers (Suppl. Figure 1S). When GST-EsxA was incubated with EsxA, a new peak containing both proteins was observed. Co-elution was not observed with EsxB (Suppl. Figure 1S). Conversely, GST-EsxB and EsxA did not co-elute and the elution profile of untagged EsxB was not significantly changed upon incubation with GST-EsxB (Suppl. Figure 1S).

Figure S1

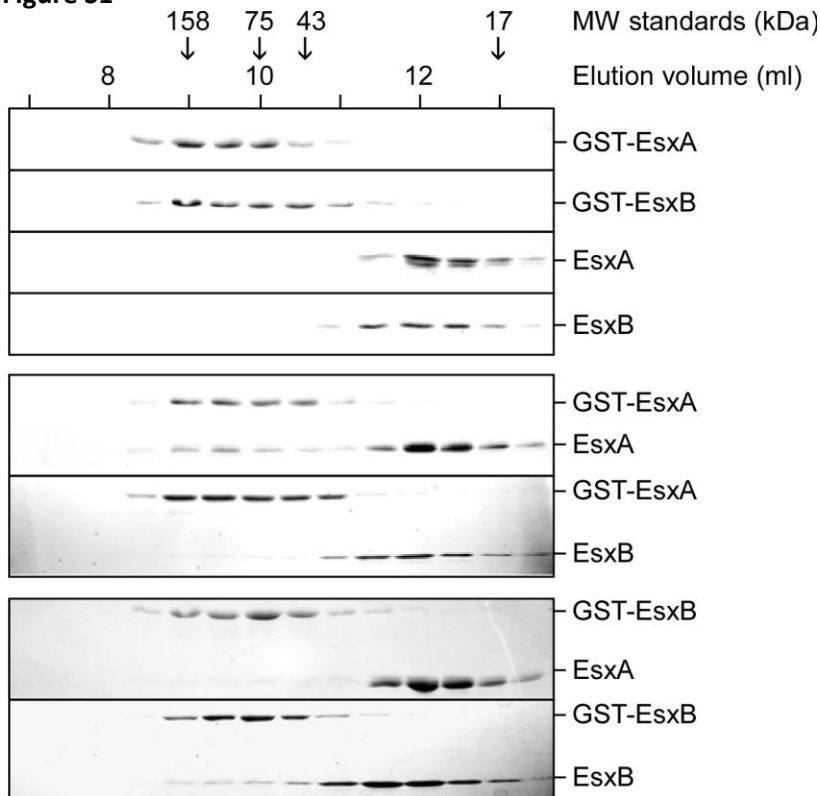


Figure S1. Gel filtration analysis of purified proteins, EsxA, EsxB, GST-EsxA and GST-EsxB, alone or incubated as pairs. The native molecular masses of EsxA and EsxB proteins fused or not to Glutathione S-

transferase (GST) were estimated by gel filtration following separation on a Superdex™ 75 10/300 GL column. For the top four panels, each protein was loaded individually, for the lower four panels, two proteins were pre-incubated for 1 h at room temperature prior to loading on the column. In all cases, aliquots of eluted fractions were subjected to SDS-PAGE and stained by Coomassie Brilliant Blue. Images of the stained gels are shown. Numbers on top indicate elution volumes in ml. The peak positions of molecular weight (MW) standards in kDa are also indicated: Aldolase (158 kDa), Conalbumin (75 kDa), Ovalbumin (43 kDa), and Myoglobin (17 kDa).

**Table S1:** *S. aureus* strains used in this study.

<b>Strains</b>	<b>Description</b>	<b>Source</b>
RN4220	<i>S. aureus sau1 hsdR</i> laboratory strain used for passaging plasmid DNA	(Kreiwirth et al, 1983; Nair et al, 2011)
Newman	Methicillin sensitive <i>S. aureus</i>	(Baba et al, 2008)
USA300	Community-acquired methicillin resistant <i>S. aureus</i>	NARSA repository (Diep et al, 2006)
<i>esxA</i>	USA300 carrying an internal deletion of <i>esxA</i>	(Anderson et al, 2011)
<i>esxB</i>	USA300 carrying an internal deletion of <i>esxB</i>	This study
<i>esxC</i>	USA300 carrying an internal deletion of <i>esxC</i>	This study
<i>esxD</i>	USA300 carrying an internal deletion of <i>esxD</i>	This study
<i>essA</i>	USA300 carrying an internal deletion of <i>essA</i>	This study
<i>essB</i>	USA300 carrying an internal deletion of <i>essB</i>	(Chen et al, 2012)
<i>essC</i>	USA300 carrying an internal deletion of <i>essC</i>	This study
<i>essD</i>	USA300 carrying a <i>bursa aurealis</i> insertion in <i>essD</i>	(Anderson et al, 2011)
<i>saeR</i> (Newman)	Newman carrying a <i>bursa aurealis</i> insertion in <i>saeR</i>	(Bae et al, 2004)
<i>saeS</i> (Newman)	Newman carrying a <i>bursa aurealis</i> insertion in <i>saeS</i>	(Bae et al, 2004)
<i>saeR</i> (USA300)	USA300 carrying a <i>bursa aurealis</i> insertion in <i>saeR</i>	This study
<i>saeS</i> (USA300)	USA300 carrying a <i>bursa aurealis</i> insertion in <i>saeS</i>	This study

**Table S2:** Sequence and use of oligonucleotides designed for this study.

Name	Nucleotide Sequence	Usage
<i>essA-attB1-F</i>	GGGGACAAGTTTGTACAAAAAAGCAGGCTCTTTTG CTGAAGAGCCACAAGAACC	Cloning of the <i>essA</i> deletion mutant in pKOR1 for allelic replacement
<i>essA-15codons-R</i>	AAAGATCTAGATGCTGTTAAAAAAGTTAAAGC	Same as above
<i>essA-15codons-F</i>	AAAGATCTGGGAGACGAACGAAAAATGAATCAG	Same as above
<i>essA-attB2-R</i>	GGGGACCACTTTGTACAAGAAAGCTGGGTGCGCTC ATTATGCTTCATTACTG	Same as above
<i>essC-attB1-F</i>	GGGGACAAGTTTGTACAAAAAAGCAGGCTGTTGAT CCATTACCTGTGCAGAAG	Cloning of the <i>essC</i> deletion mutant in pKOR1 for allelic replacement
<i>essC-15codons-R</i>	AAAGATCTGAGCATCTTCAATTGTTTGTATAT	Same as above
<i>essC-15codons-F</i>	AAAGATCTGAACTTGGCTTGAACATTTTATTG	Same as above
<i>essC-attB2-R</i>	GGGGACCACTTTGTACAAGAAAGCTGGGTCTATT GCTTAACATCTTTCATC	Same as above
<i>esxB-attB1-F</i>	GGGGACAAGTTTGTACAAAAAAGCAGGCTCCGAG AGAAATTGCCATATTGCTG	Cloning of the <i>esxB</i> deletion mutant in pKOR1 for allelic replacement
<i>esxB-15codons-R</i>	AAAGATCTATCAACCTTGCCACCATCTGCTTAA	Same as above
<i>esxB-15codons-F</i>	AAAGATCTGATACATTATCAATTAAGCAAGGGC	Same as above
<i>esxB-attB2-R</i>	GGGGACCACTTTGTACAAGAAAGCTGGGTCTAATG ACTGTTGCAGCACTACTATAG	Same as above
<i>esxC-attB1-F</i>	GGGGACAAGTTTGTACAAAAAAGCAGGCT GCAATGTTTTATATGATAAATCAG	Cloning of the <i>esxC</i> deletion mutant in pKOR1 for allelic replacement
<i>esxC-15codons-R</i>	AAAGATCTTTAAATTCGACTTAACCATTGTTTC	Same as above
<i>esxC-15codons-F</i>	AAAGATCTGCTGGCGAAAAGGCAAGTGAATATTTT	Same as above
<i>esxC-attB2-R</i>	GGGGACCACTTTGTACAAGAAAGCTGGGTCTCGTA TAAATGTATTAATGACACC	Same as above
<i>esxD-attB1-F</i>	GGGGACAAGTTTGTACAAAAAAGCAGGCTGGCAA GGTTGATCAAGCGAAAC	Cloning of the <i>esxD</i> deletion mutant in pKOR1 for allelic replacement
<i>esxD-15codons-R</i>	AAAGATCT TGCAATCGTTTCAGCTTTAACAC	Same as above
<i>esxD-15codons-F</i>	AAAGATCTTGGGGTACGGAATTTGCCAAGC	Same as above
<i>esxD-attB2-R</i>	GGGGACCACTTTGTACAAGAAAGCTGGGTGTGAAA TACGACTAAGCTGCTTG	Same as above
<i>esxA-NdeI-F</i>	AAACATATGGCAATGATTAAGATGAGTCCAGAGGA A	For purification of his-EsxA in <i>E. coli</i> using pET15b
<i>esxA-XhoI-R</i>	AAACTCGAGTTATTGCAAACCGAAATTATTAGAAA GTTG	Same as above
<i>esxA-BamHI-F</i>	AAAGGATCCATGGCAATGATTAAGATGAGTCCAGA GGAA	For purification of GST-EsxA in <i>E. coli</i> using pGEX-2TK
<i>esxA-EcoRI-R</i>	AAAGAATTCTTATTGCAAACCGAAATTATTAGAAA TTG	Same as above
<i>esxB-NdeI-F</i>	AAACATATGGGTGGATATAAAGGTATTAAGCAGA T	For purification of his-EsxB in <i>E. coli</i> using pET15b
<i>esxB-XhoI-R</i>	AAACTCGAGTCATGGGTTCCACCTATCAAGCCCTTG CTT	Same as above
<i>esxB-BamHI-F</i>	AAAGGATCCATGGGTGGATATAAAGGTATTAAGC AGAT	For purification of GST-EsxB in <i>E. coli</i>

<i>esxB-EcoRI-R</i>	AAAGAATTCTCATGGGTTACCCTATCAAGCCCTGCTT	using pGEX-2TK Same as above
<i>esxD-NdeI-F</i>	AACATATGACGTTGAGTGGAAAAATTAG	For purification of his-EsxD in <i>E.coli</i> using pET15b and complementation.
<i>esxD-BamHI-R</i>	AAGGATCCCTATCCCTCAATATTATAG	Same as above
<i>EsxD-6xHis-BamHI-R</i>	AAGGATCCCTTAGTGATGGTGATGGTGATGTCCTCAATATTATAGTAAAGC	His complementation
<i>esxA-FBTH-5'</i>	CGCAGTCTAGACATGGCAATGATTAAGATGAGTCCAGAG	Bacterial 2-Hybrid cloning EsxA
<i>esxA-RBTH-3'</i>	CGCAGGGTACCTTATTGCAAACCGAAATTATTAGAAAGT	Same as above
<i>esxB-FBTH-5'</i>	CGCAGTCTAGACATGGGTGGATATAAAGGTATTAAGCA	Bacterial 2-Hybrid cloning EsxB
<i>esxB-RBTH-3'</i>	CGCAGGGTACCTCATGGGTTACCCTATCAAGCCCTTGC	Same as above
<i>esxC-FBTH-5'</i>	CGCAGTCTAGACATGAATTTAATGATATTGAAACAATG	Bacterial 2-Hybrid cloning EsxC
<i>esxC-RBTH-3'</i>	CGCAGGAATTCCTAATTCATTGCTTTATAAAATATTCA	Same as above
<i>esxD-FBTH-5'</i>	CGCAGTCTAGACATGACGTTGAGTGGAAAAATTAGTGTT	Bacterial 2-Hybrid cloning EsxD
<i>esxD-RBTH-3'</i>	CGCAGGGTACCTATCCCTCAATATTATAGTAAAGCTTG	Same as above
<i>EsxD1-99BamHI-R</i>	AAAAGGATCCCTAAAGCTTGGCAAATTCGTACCCC	EsxD YxxxE motif mutation
<i>EsxD-Y100A-BamHI-R</i>	AAAAGGATCCCTATCCCTCAATATTATAGGCAAGCTTGGCAAATCCG	Same as above
<i>EsxD-E104A-BamHI-R</i>	AAAAGGATCCCTATCCCGCAATATTATAGTAAAGC	Same as above
<i>EsxD-Y100A-E104A-BHIR</i>	AAAAGGATCCCTATCCCGCAATATTATAGGCAAGCTTGGCAAATTC	Same as above

## REFERENCES

Anderson M, Chen YH, Butler EK, Missiakas DM (2011) EsaD, a secretion factor for the Ess pathway in *Staphylococcus aureus*. *J Bacteriol* 193: 1583-1589

Baba T, Bae T, Schneewind O, Takeuchi F, Hiramatsu K (2008) Genome sequence of *Staphylococcus aureus* strain Newman and comparative analysis of staphylococcal genomes: polymorphism and evolution of two major pathogenicity islands. *J Bacteriol* 190: 300-310

Bae T, Banger AK, Wallace A, Glass EM, Aslund F, Schneewind O, Missiakas DM (2004) *Staphylococcus aureus* virulence genes identified by bursa aurealis mutagenesis and nematode killing. *Proc Natl Acad Sci U S A* 101: 12312-12317

Chen YH, Anderson M, Hendrickx AP, Missiakas D (2012) Characterization of EssB, a protein required for secretion of ESAT-6 like proteins in *Staphylococcus aureus*. *BMC Microbiol* 12: 219

Diep BA, Gill SR, Chang RF, Phan TH, Chen JH, Davidson MG, Lin F, Lin J, Carleton HA, Mongodin EF, Sensabaugh GF, Perdreau-Remington F (2006) Complete genome sequence of USA300, an epidemic clone of community-acquired methicillin-resistant *Staphylococcus aureus*. *Lancet* 367: 731-739

Kreiswirth BN, Lofdahl S, Betley MJ, O'Reilly M, Schlievert PM, Bergdoll MS, Novick RP (1983) The toxic shock syndrome exotoxin structural gene is not detectably transmitted by a prophage. *Nature* 305: 709-712

Nair D, Memmi G, Hernandez D, Bard J, Beaume M, Gill S, Francois P, Cheung AL (2011) Whole-genome sequencing of *Staphylococcus aureus* strain RN4220, a key laboratory strain used in virulence research, identifies mutations that affect not only virulence factors but also the fitness of the strain. *J Bacteriol* 193: 2332-2335