

## Supplemental Figure Legends

**Supplemental Figure S1. ClustalW alignment of translated *sea*-related gene to known *sea* genes.** Using BioEdit software v. 7.0.9.0 (6/27/07) [34], the nucleotide sequence of the *sea*-related gene was translated and aligned using ClustalW to known *sea* genes. Default parameters were used in the ClustalW alignment. The translated sequence predicted 92 amino acids, with 100% similarity to the known *sea* genes over the aligned region of the gene.

**Supplemental Figure S2. Genome browser view of *sea*-related gene BLASTN alignment against annotated *Staphylococcus aureus* genomes from The SEED database.** A BLASTN alignment of the *sea*-related gene was performed against the annotated *S. aureus* genomes from The SEED database ([http://www.theseed.org/wiki/Home\\_of\\_the\\_SEED](http://www.theseed.org/wiki/Home_of_the_SEED)). User defined settings for region size (15,000 bp), number of regions displayed (10), genome selection (collapse close genomes), and coloring algorithm (slow, but exact) were utilized. The default settings were utilized for the remaining options. The focus gene (phage-associated *Staphylococcus enterotoxin*) is boxed in the center of the figure and indicated by the arrow labeled number 1. The arrow of the focus gene always points to the right even if it is located on the minus strand. Similar genes are grouped together by number and shading. Genes with positional conservation in at least four other species are functionally grouped and indicated by gray background boxes. The names of the *S. aureus* organisms are indicated on the left and their FIG identification number is in parentheses.

|                                   | 10     | 20      | 30                        |
|-----------------------------------|--------|---------|---------------------------|
| Air isolate SEA sequence          | .....  | .....   | .....                     |
| <i>S. aureus</i> FRI337           | MKKTAF | TLLLFIA | LTLTTSPLVNGSEKSEEINEKDLRK |
| <i>S. aureus</i> FRI281           | .....  | .....   | .....                     |
| <i>S. aureus</i> strain ATCC13565 | MKKTAF | TLLLFIA | LTLTTSPLVNGSEKSEEINEKDLRK |
| <i>S. aureus</i> strain ATCC25923 | MKKTAF | ILLLFIA | LTTWTSPLVNGSEKSEEINEKDLRK |
| <i>S. aureus</i> phage $\phi$ NM3 | MKKTAF | ILLLFIA | LTTWTSPLVNGSEKSEEINEKDLRK |

|                                   | 60                 | 70              | 80     |
|-----------------------------------|--------------------|-----------------|--------|
| Air isolate SEA sequence          | .....              | .....           | .....  |
| <i>S. aureus</i> FRI337           | KQIYYYNEKAKTENKESH | SDQFLQHTILFKGFF | TNHSWY |
| <i>S. aureus</i> FRI281           | .....              | .....           | .....  |
| <i>S. aureus</i> strain ATCC13565 | KQIYYYNEKAKTENKESH | SDQFLQHTILFKGFF | TNHSWY |
| <i>S. aureus</i> strain ATCC25923 | KQIYYYNEKAKTENKESH | SDQFLQHTILFKGFF | TNHSWY |
| <i>S. aureus</i> phage $\phi$ NM3 | KQIYYYNEKAKTENKESH | SDQFLQHTILFKGFF | TNHSWY |

|                                   | 110                  | 120             | 130   |
|-----------------------------------|----------------------|-----------------|-------|
| Air isolate SEA sequence          | .....                | .....           | ..... |
| <i>S. aureus</i> FRI337           | VDKYKGKKVDLYGAYYGYQC | AGGTPNKTACMYGGV | TLF   |
| <i>S. aureus</i> FRI281           | .....                | .....           | ..... |
| <i>S. aureus</i> strain ATCC13565 | VDKYKGKKVDLYGAYYGYQC | AGGTPNKTACMYGGV | TLF   |
| <i>S. aureus</i> strain ATCC25923 | VDKYKGKKVDLYGAYYGYQC | AGGTPNKTACMYGGV | TLF   |
| <i>S. aureus</i> phage $\phi$ NM3 | VDKYKGKKVDLYGAYYGYQC | AGGTPNKTACMYGGV | TLF   |

|                                   | 160              | 170              | 180    |
|-----------------------------------|------------------|------------------|--------|
| Air isolate SEA sequence          | .....            | .....            | .....  |
| <i>S. aureus</i> FRI337           | INLWLDGKQNTVPLET | VKTNKKNVTVQELDLQ | ARRYLC |
| <i>S. aureus</i> FRI281           | .....            | .....            | .....  |
| <i>S. aureus</i> strain ATCC13565 | INLWLDGKQNTVPLET | VKTNKKNVTVQELDLQ | ARRYLC |
| <i>S. aureus</i> strain ATCC25923 | INLWLDGKQNTVPLET | VKTNKKNVTVQELDLQ | ARRYLC |
| <i>S. aureus</i> phage $\phi$ NM3 | INLWLDGKQNTVPLET | VKTNKKNVTVQELDLQ | ARRYLC |

|                                   | 210              | 220             | 230      |
|-----------------------------------|------------------|-----------------|----------|
| Air isolate SEA sequence          | .....            | .....           | .....    |
| <i>S. aureus</i> FRI337           | GKVQRGLIVFHTSTEP | SVNYDLFGAQQGQNS | NTLLRIYF |
| <i>S. aureus</i> FRI281           | .....            | .....           | .....    |
| <i>S. aureus</i> strain ATCC13565 | GKVQRGLIVFHTSTEP | SVNYDLFGAQQGQNS | NTLLRIYF |
| <i>S. aureus</i> strain ATCC25923 | GKVQRGLIVFHTSTEP | SVNYDLFGAQQGQNS | NTLLRIYF |
| <i>S. aureus</i> phage $\phi$ NM3 | GKVQRGLIVFHTSTEP | SVNYDLFGAQQGQNS | NTLLRIYF |

|                                   | 260       | 270              | 280          |
|-----------------------------------|-----------|------------------|--------------|
| Air isolate SEA sequence          | .....     | .....            | .....        |
| <i>S. aureus</i> FRI337           | DIYLYTS   | .....            | .....        |
| <i>S. aureus</i> FRI281           | DIYLYTSTW | FTRNVIIMNRESESLQ | AVKKVYVLYALS |
| <i>S. aureus</i> strain ATCC13565 | DIYLYTSTY | .....            | .....        |
| <i>S. aureus</i> strain ATCC25923 | DIYLYTST  | .....            | .....        |
| <i>S. aureus</i> phage $\phi$ NM3 | DIYLYTST  | .....            | .....        |

Figure S1.

Casas et al., 2010

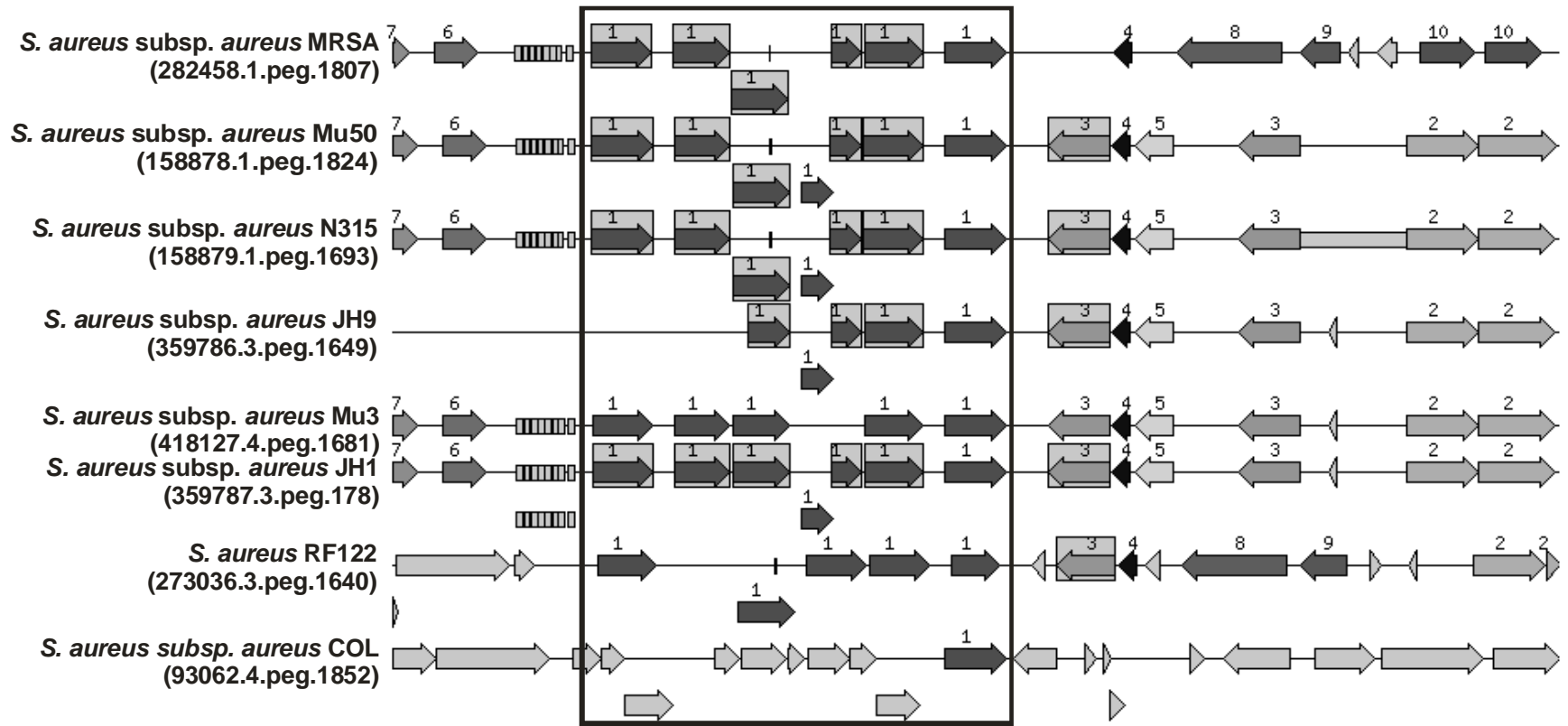


Figure S2.

Casas et al., 2010