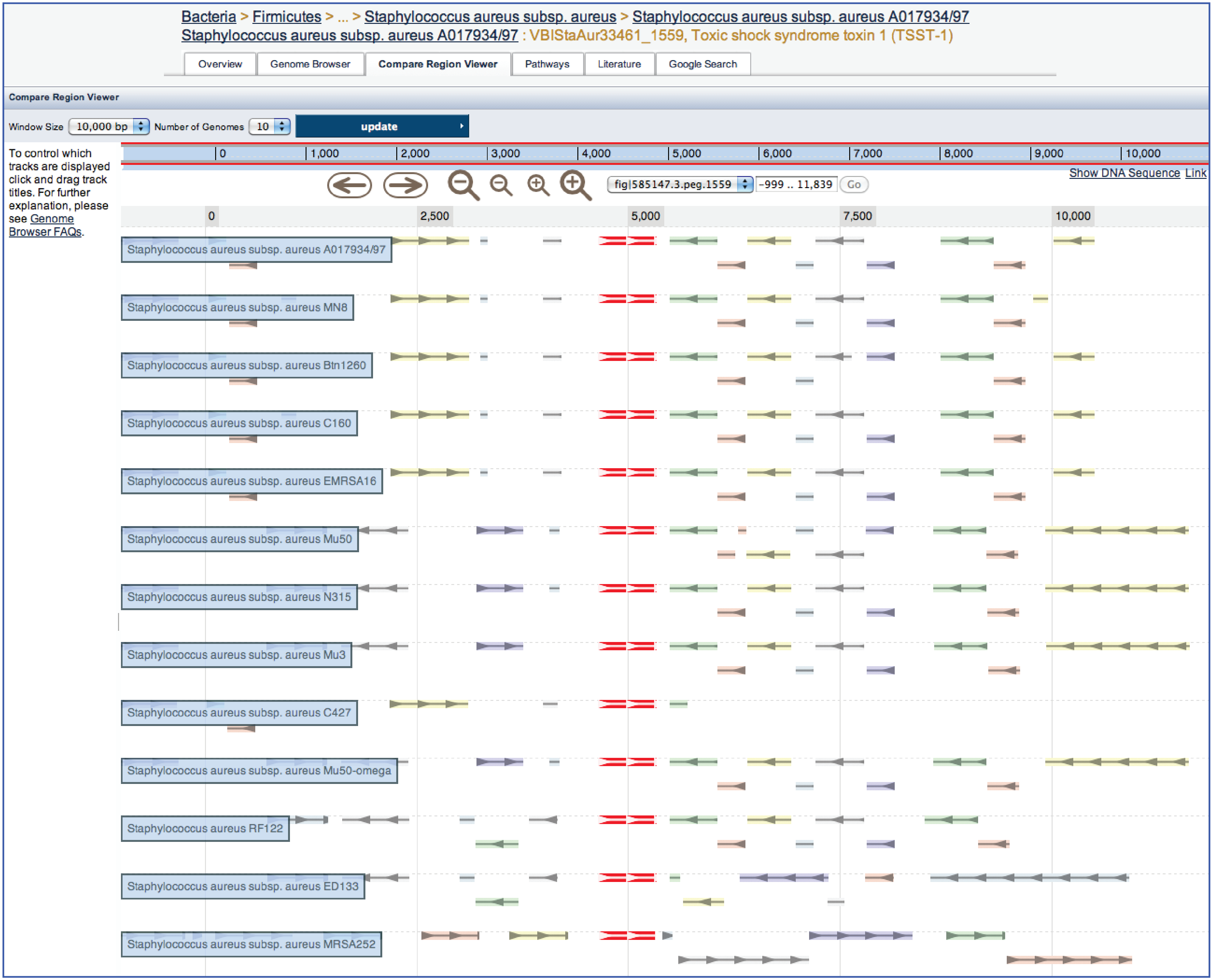
Fig. S1. Application of the Compare Region Viewer tool to evaluate synteny in the region flanking the gene encoding the toxic shock syndrome toxin 1 (TSST-1) across 13 *Staphylococcus aureus* genomes. The image is a screen capture from the 'Compare Region Viewer' page, which was accessed from the *Staphylococcus aureus* subsp. aureus A017934/97 'Feature Table'. By default, the selected CDS (TSST-1) is oriented in the center of the synteny plot (red), allowing for the comparison of flanking genomic regions across closely related genomes (38 total genomes were displayed, with 13 genomes retained in the screen capture). Additional CDS coloring is based on common protein functions. Arrows depict transcription orientation, and leading (above) and lagging (below) strand-encoded CDS are distinguished. For more information regarding the Compare Region Viewer tool, see the "Genome Browser FAQs" (http://enews.patricbrc.org/faqs/).



Bacteria > Firmicutes > ... > Staphylococcus aureus subsp. aureus > Staphylococcus aureus subsp. aureus A017934/97

Staphylococcus aureus subsp. aureus A017934/97 : VBIStaAur33461_1559, Toxic shock syndrome toxin 1 (TSST-1)

Compare Region Viewer

Window Size 10,000 bp

Number of Genomes 10

To control which tracks are displayed click and drag track titles. For further explanation, please see Genome Browser FAQs.

fig|585147.3.peg.1559

-999 .. 11,839