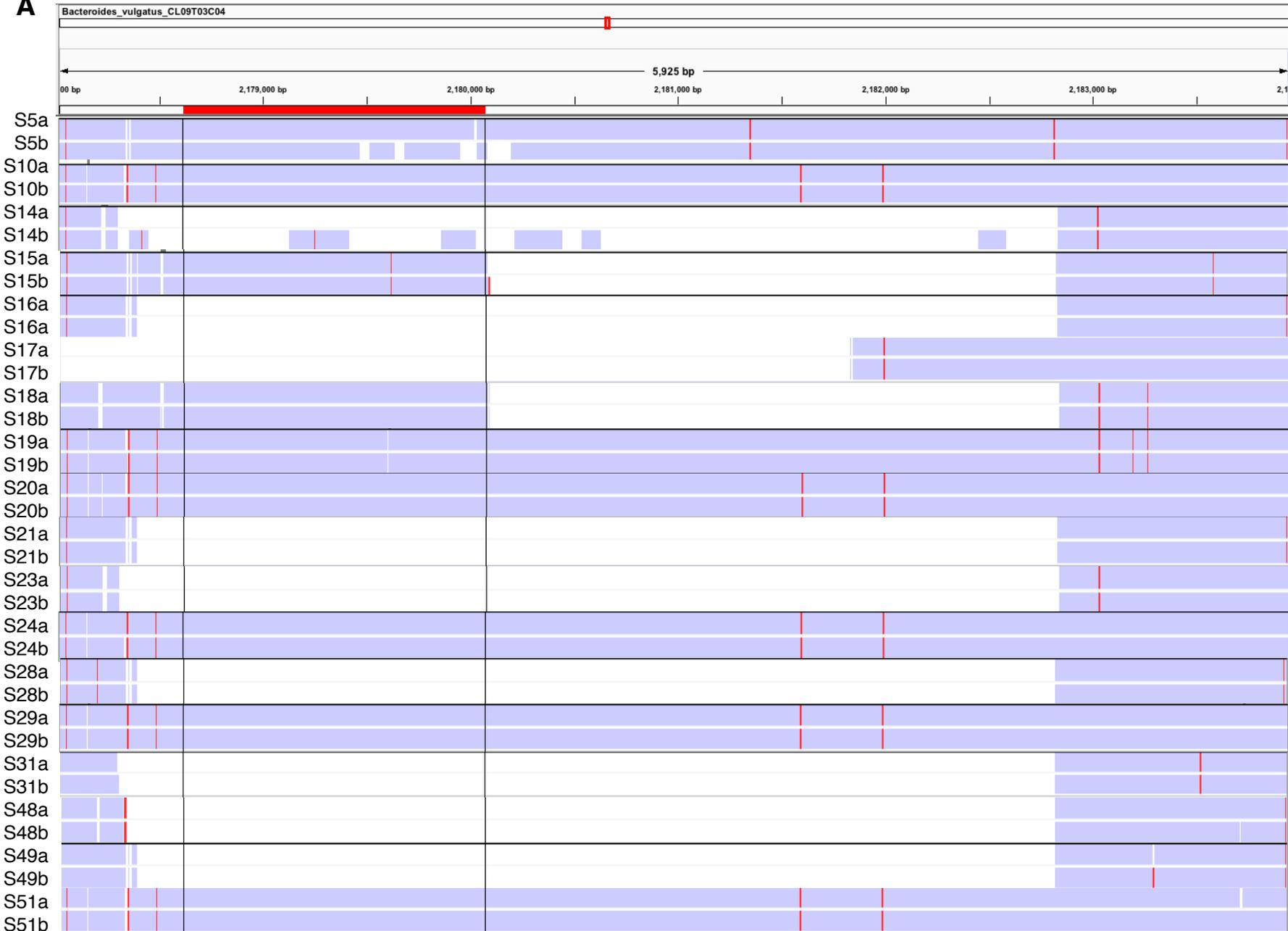


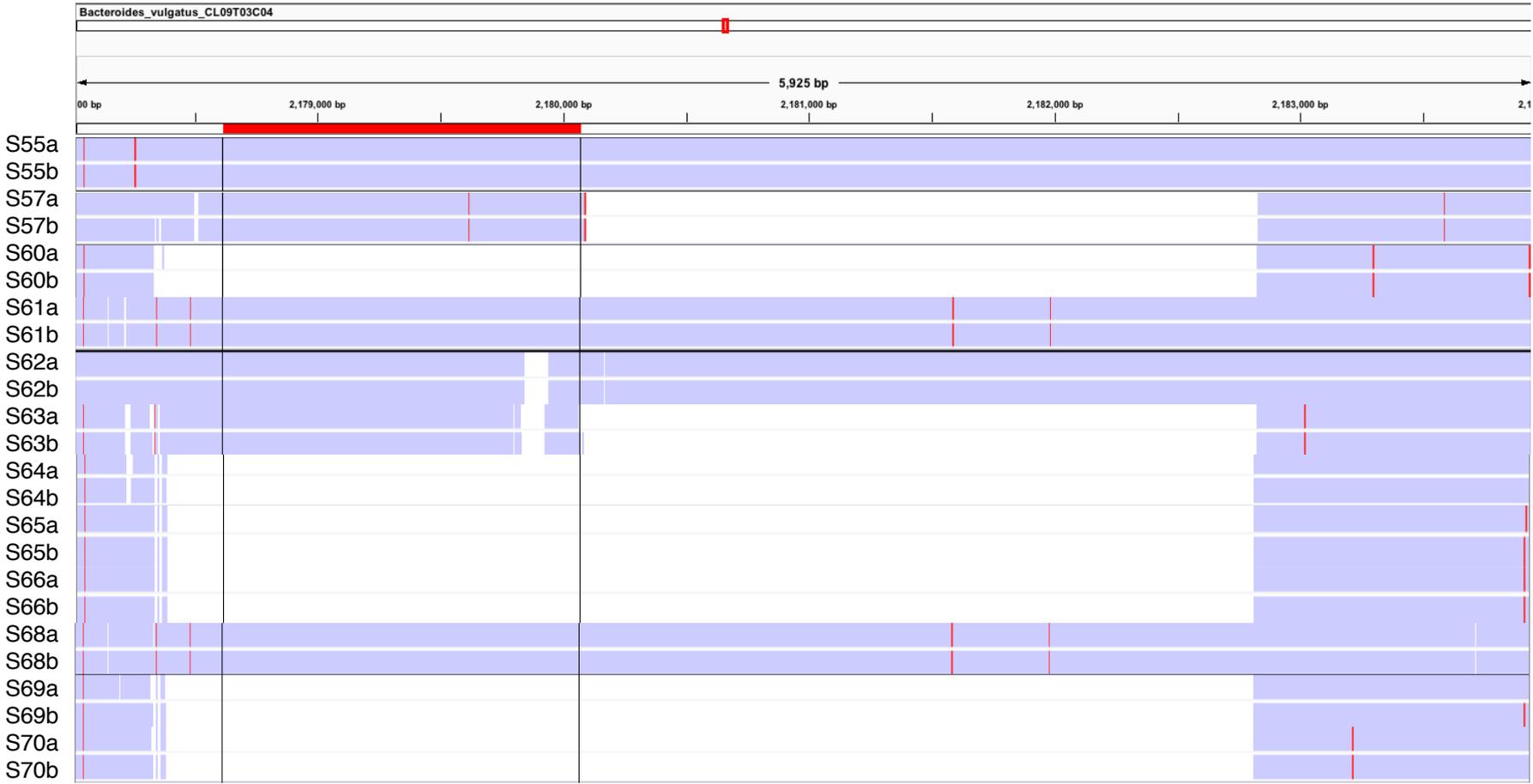
Supplementary Figure S1A

A



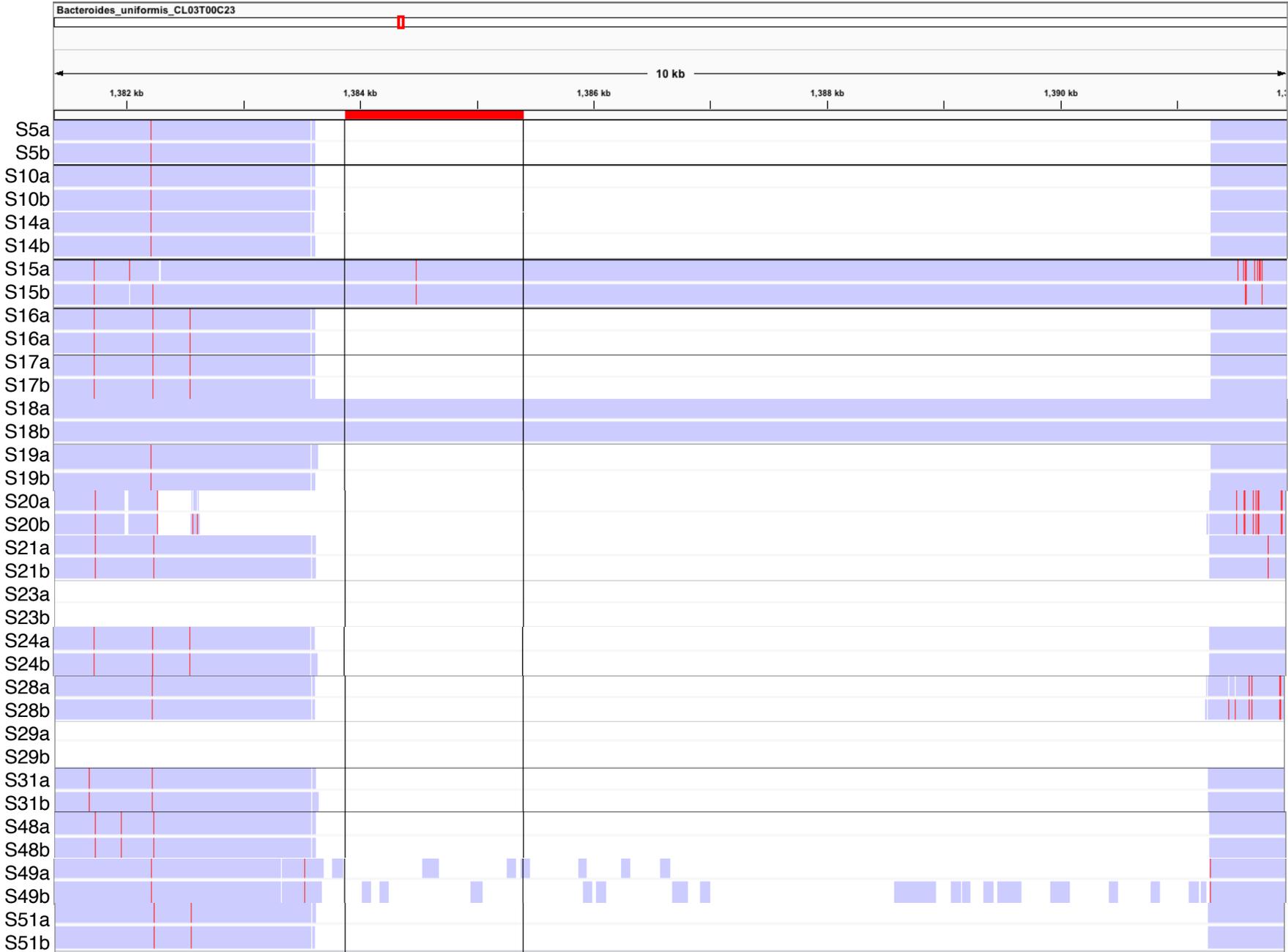
Supplementary Figure S1A Continued

A

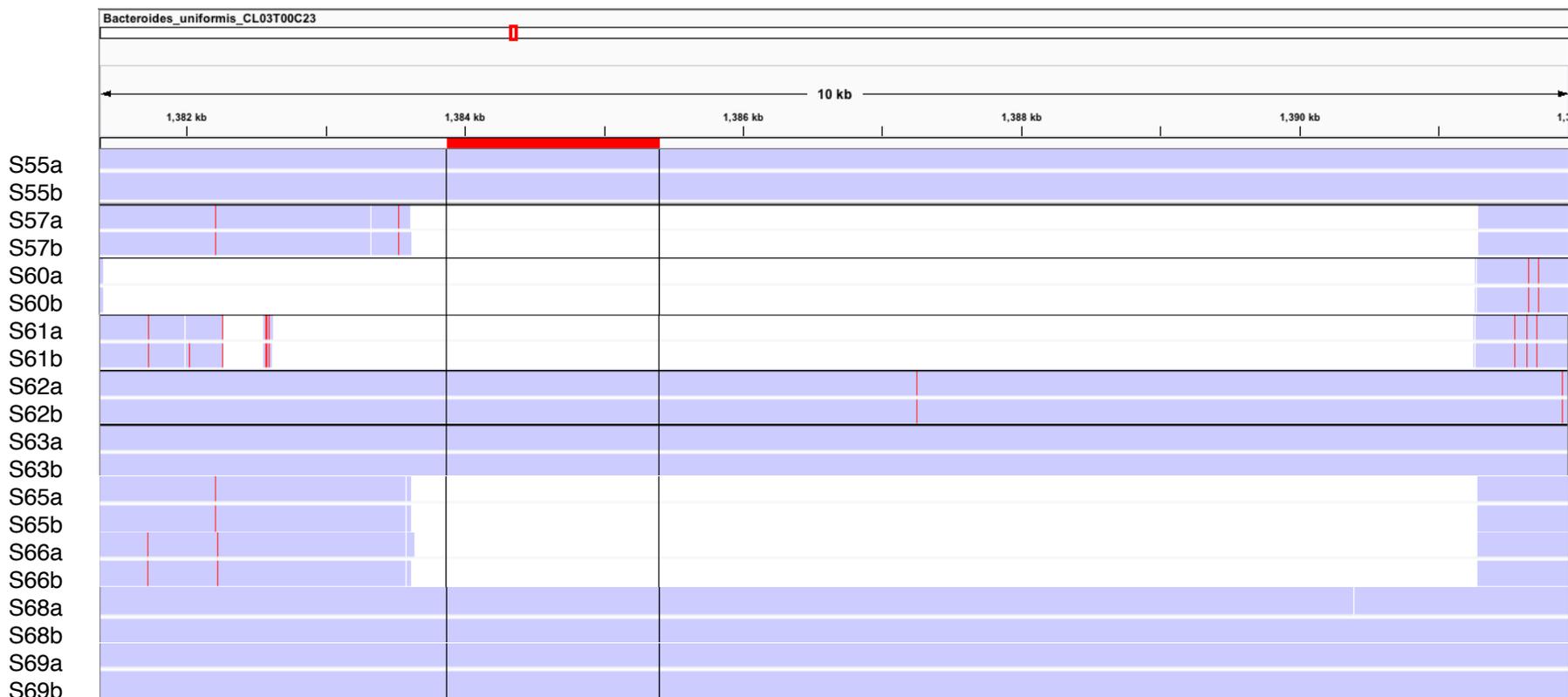


Supplementary Figure S1B

B



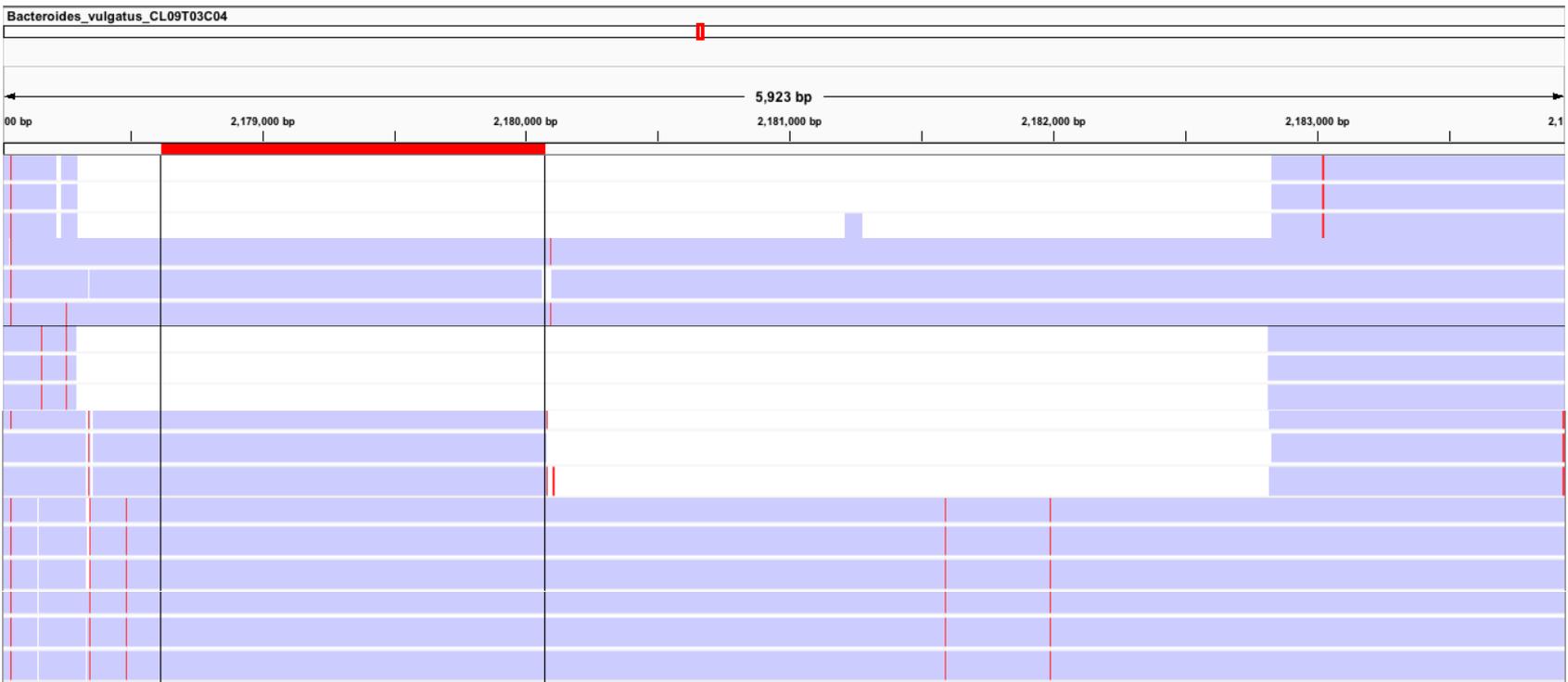
Supplementary Figure S1B Continued



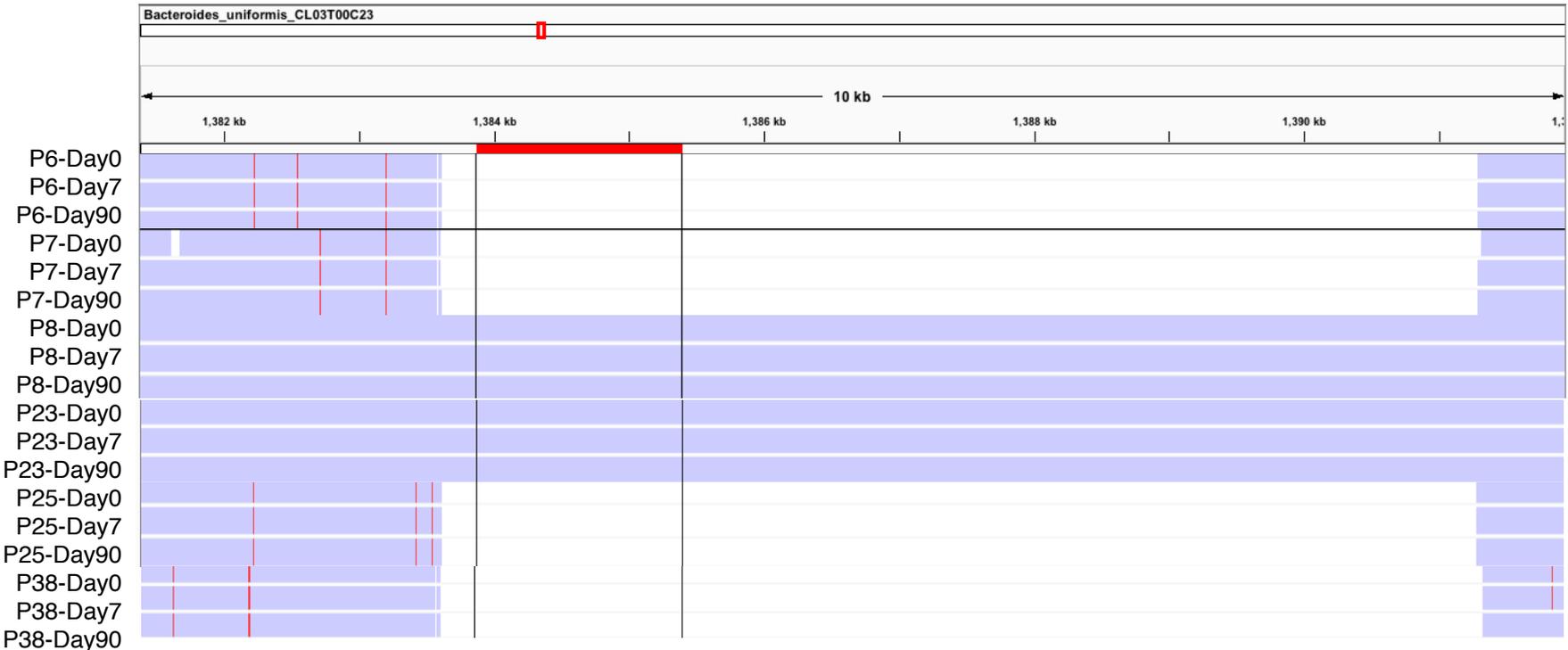
Supplementary Figure S1: IGV analysis for the HMP data set.

Aligned Bacteriocin genes, (A) BSAP-3 and (B) BSAP-2, were visualized using IGV for the HMP data set. For the BSAP-3, 2,178,016 to 2,183,973 regions of *B. vulgatus* were selected to display 5' and 3' sequences and BSAP-3 gene (red colored box: 2,178,616 to 2,180,073). For the BSAP-2, 1,381,372 to 1,392,000 regions of *B. uniformis* were selected to show 5' and 3' sequences and BSAP-2 gene (red colored box: 1,383,872-1,385,398).

Supplementary Figure S2A



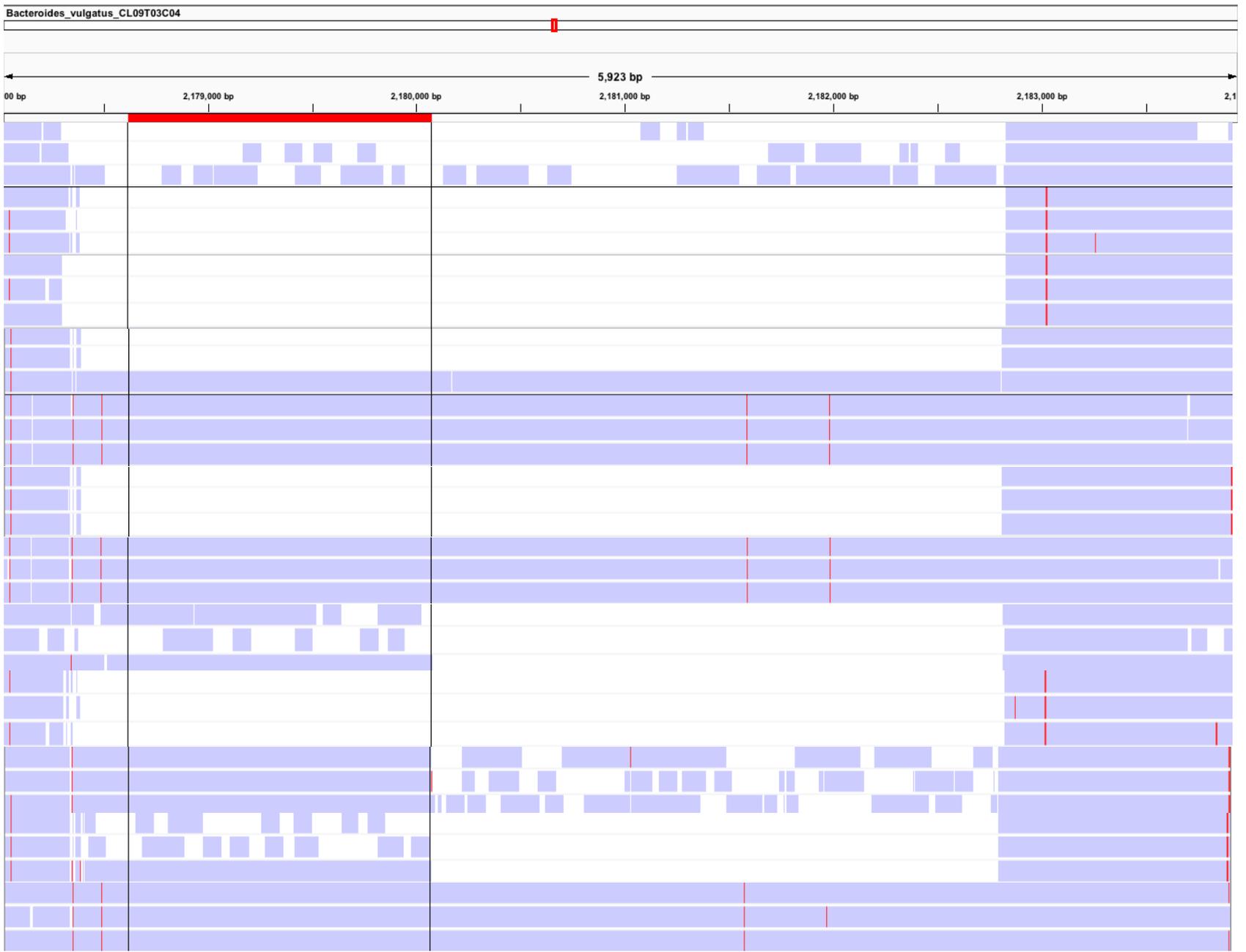
Supplementary Figure S2B



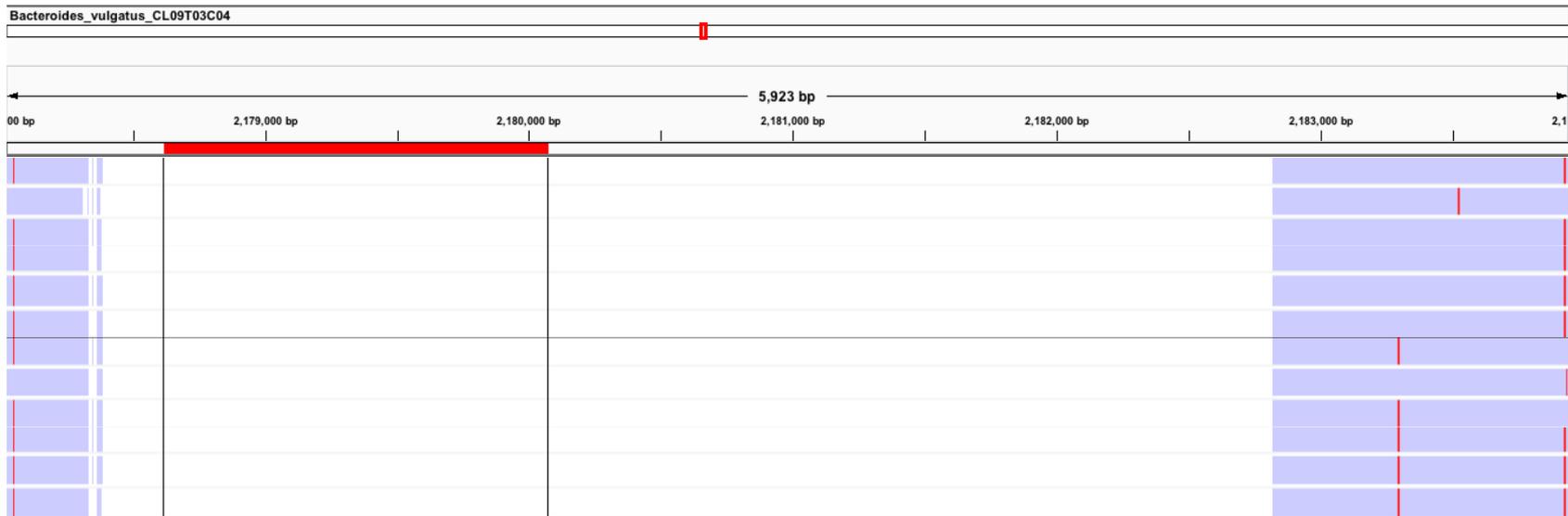
Supplementary Figure S2: IGV analysis for the control samples from Raymond et al. [18].

For control samples from Raymond et al., aligned Bacteriocin genes, (A) BSAP-3 and (B) BSAP-2, were visualized using IGV. For the BSAP-3, 2,178,016 to 2,183,973 regions of *B. vulgatus* were selected to display 5' and 3' sequences and BSAP-3 gene (red colored box: 2,178,616 to 2,180,073). For the BSAP-2, 1,381,372 to 1,392,000 regions of *B. uniformis* were selected to show 5' and 3' sequences and BSAP-2 gene (red colored box: 1,383,872-1,385,398).

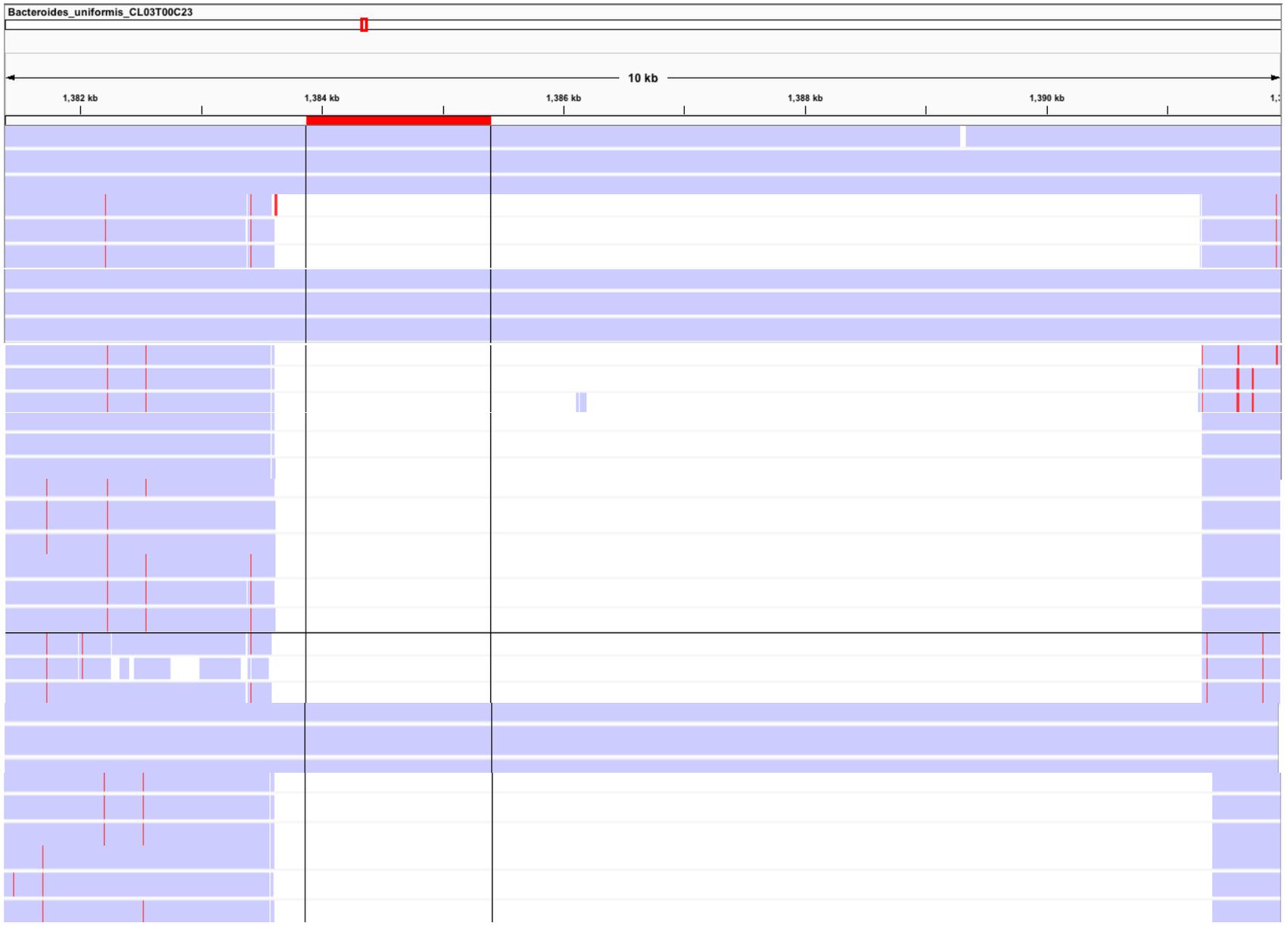
Supplementary Figure S3A



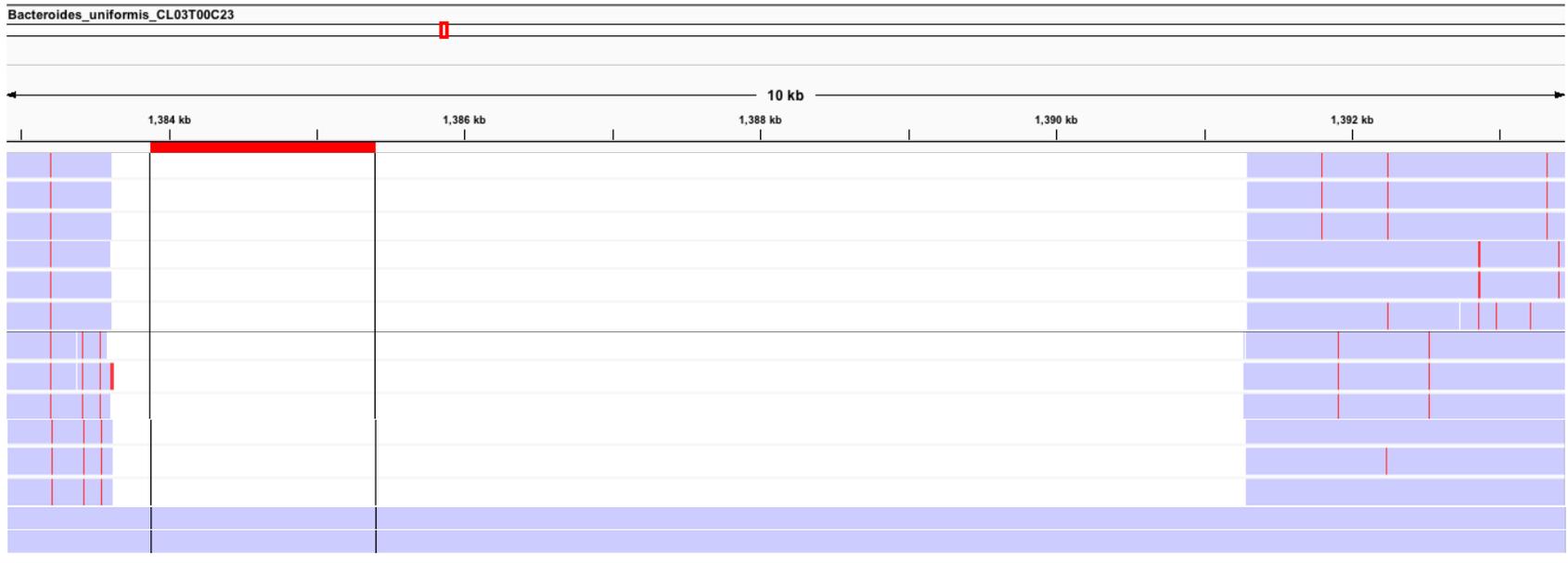
Supplementary Figure S3A - Continued



Supplementary Figure S3B

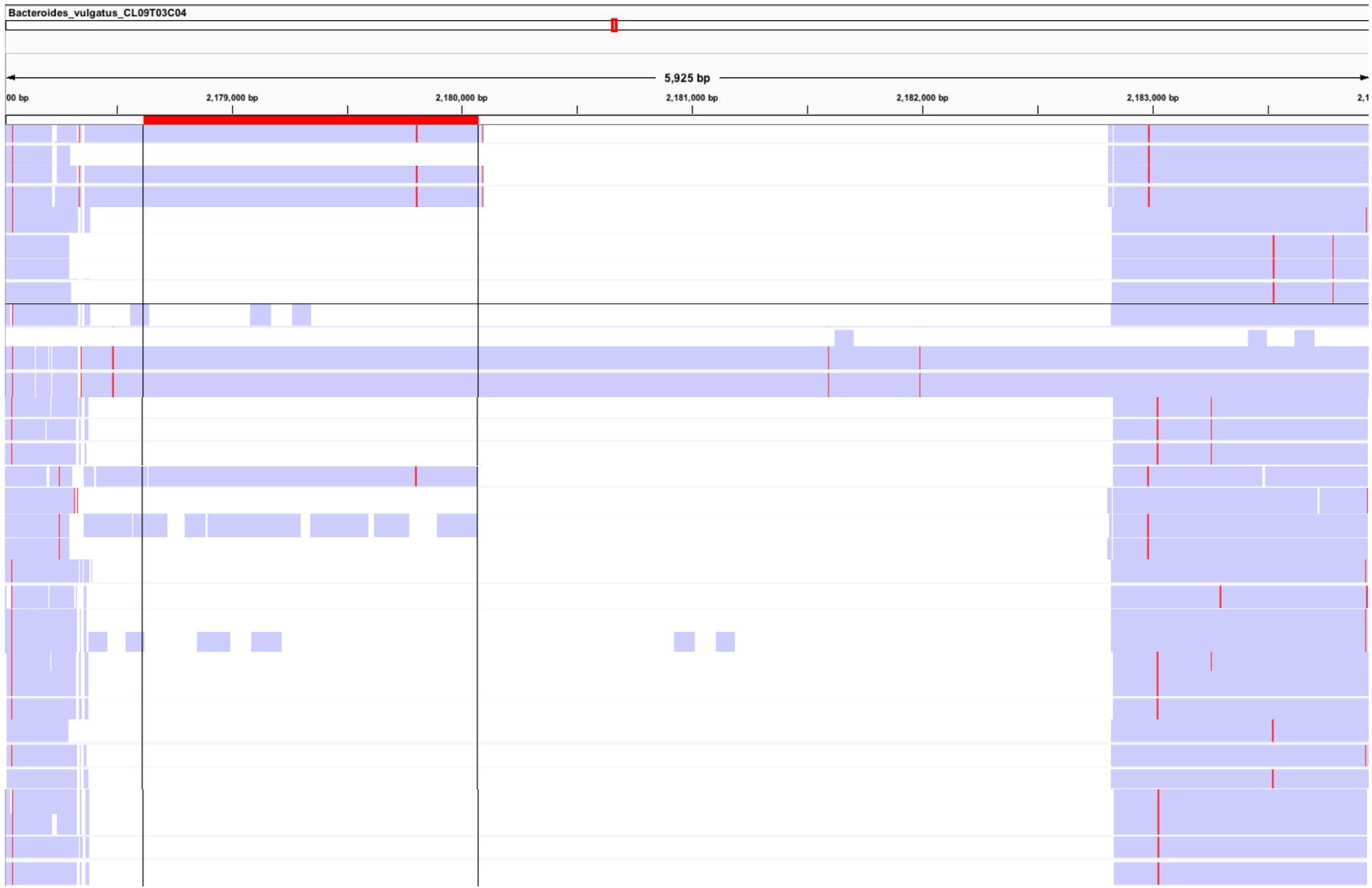


Supplementary Figure S3B - Continued

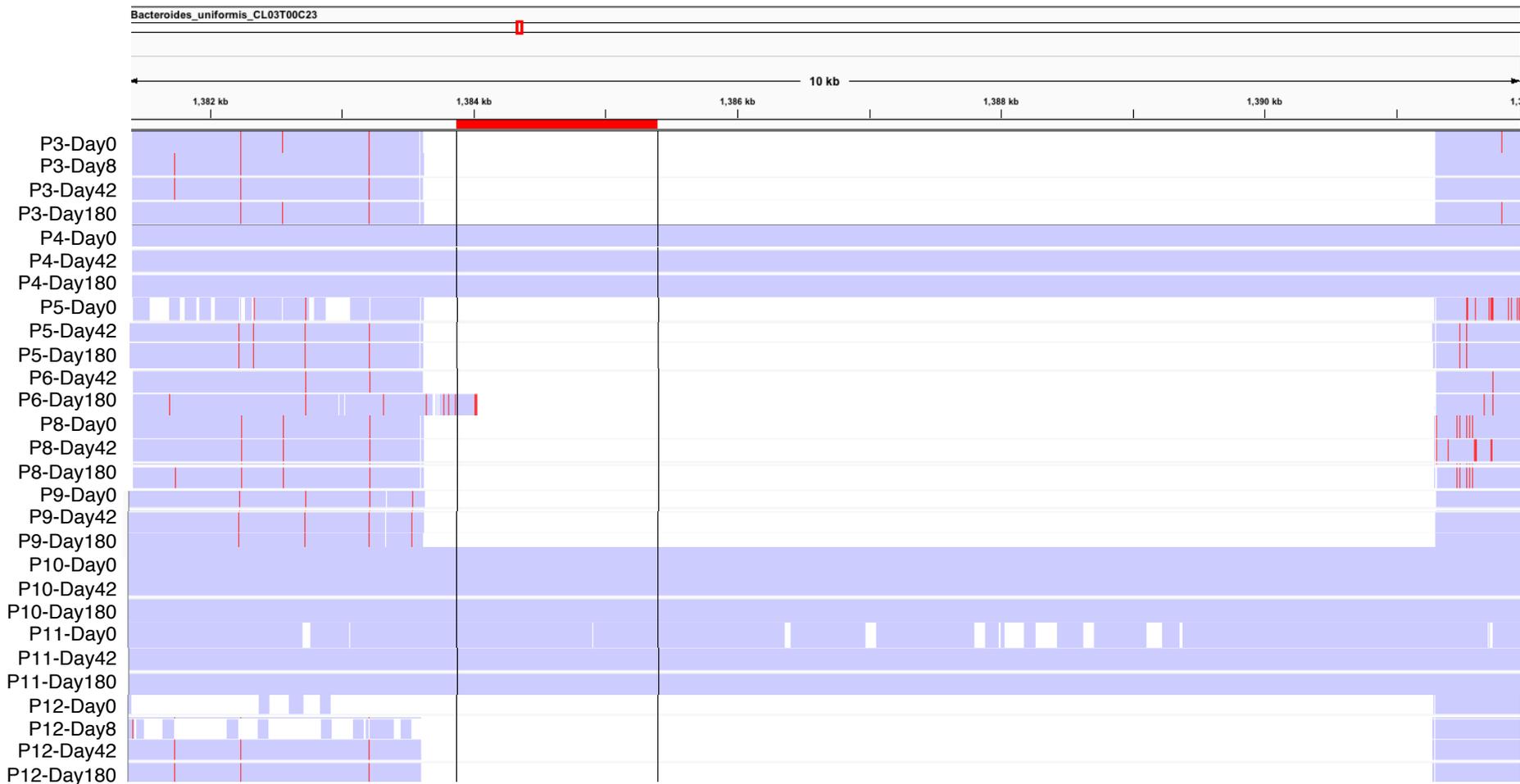


Supplementary Figure S3: IGV analysis for the antibiotic treated samples from Raymond et al. [18]. For antibiotic treated samples from Raymond et al., aligned Bacteriocin genes, (A) BSAP-3 and (B) BSAP-2, were visualized using IGV. For the BSAP-3, 2,178,016 to 2,183,973 regions of *B. vulgatus* were selected to display 5' and 3' sequences and BSAP-3 gene (red colored box: 2,178,616 to 2,180,073). For the BSAP-2, 1,381,372 to 1,392,000 regions of *B. uniformis* were selected to show 5' and 3' sequences and BSAP-2 gene (red colored box: 1,383,872-1,385,398).

Supplementary Figure S4A



Supplementary Figure S4B



Supplementary Figure S4: IGV analysis for the antibiotic treated samples from Palleja et al. [19]. For antibiotic treated samples from Palleja et al., aligned Bacteriocin genes, (A) BSAP-3 and (B) BSAP-2, were visualized using IGV. For the BSAP-3, 2,178,016 to 2,183,973 regions of *B. vulgatus* were selected to display 5' and 3' sequences and BSAP-3 gene (red colored box: 2,178,616 to 2,180,073). For the BSAP-2, 1,381,372 to 1,392,000 regions of *B. uniformis* were selected to show 5' and 3' sequences and BSAP-2 gene (red colored box: 1,383,872-1,385,398).