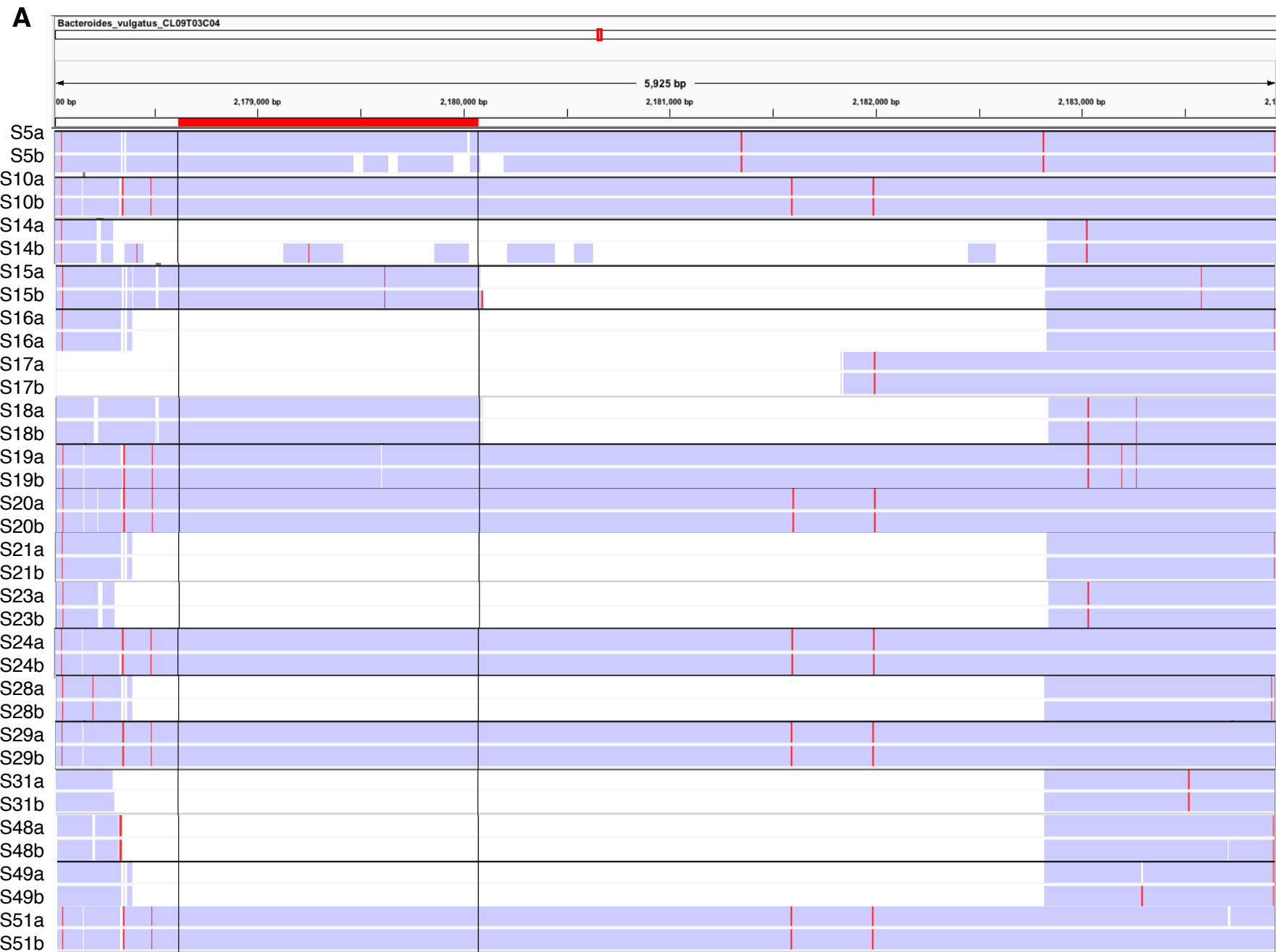
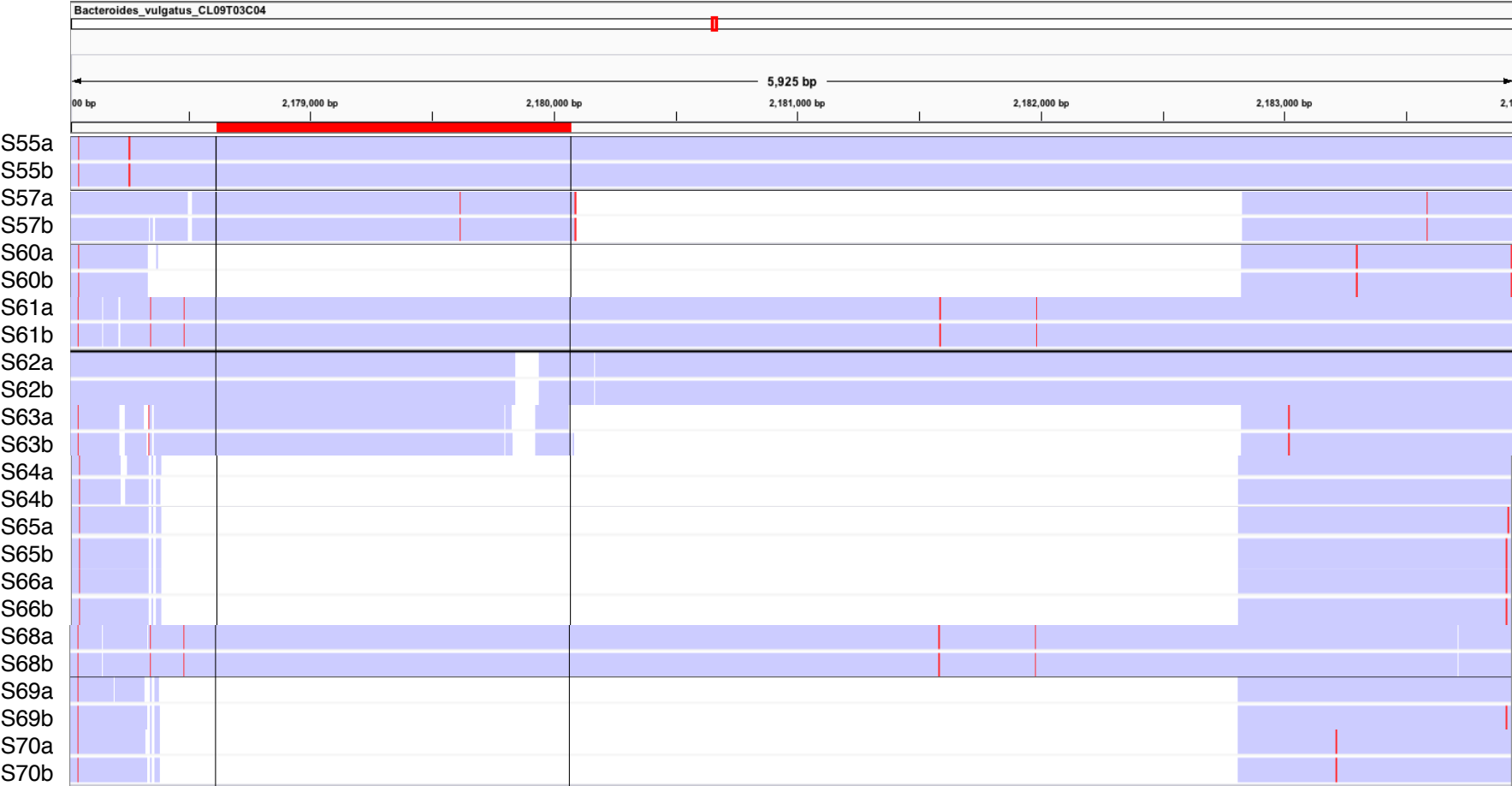


Supplementary Figure 1A

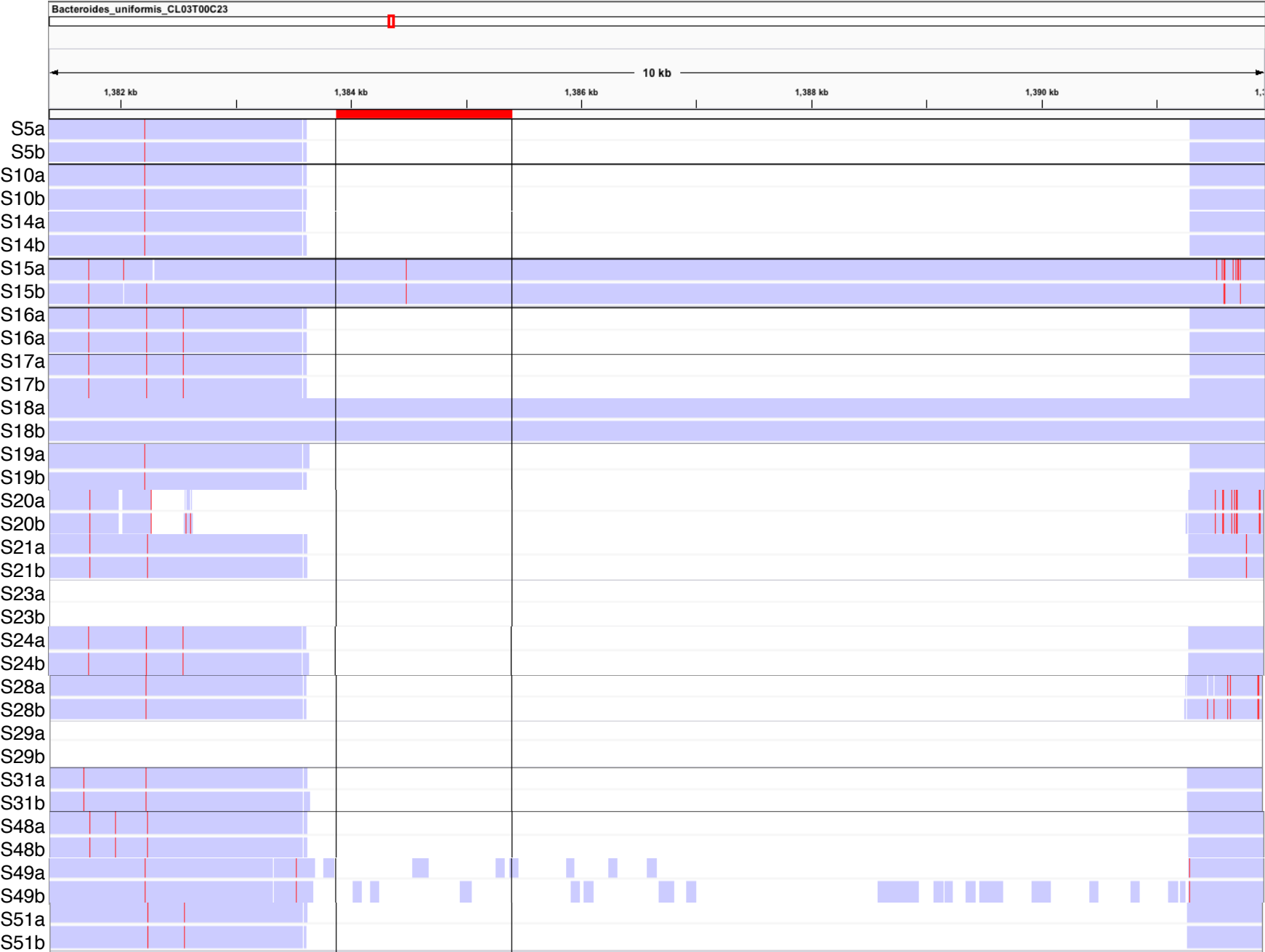


A

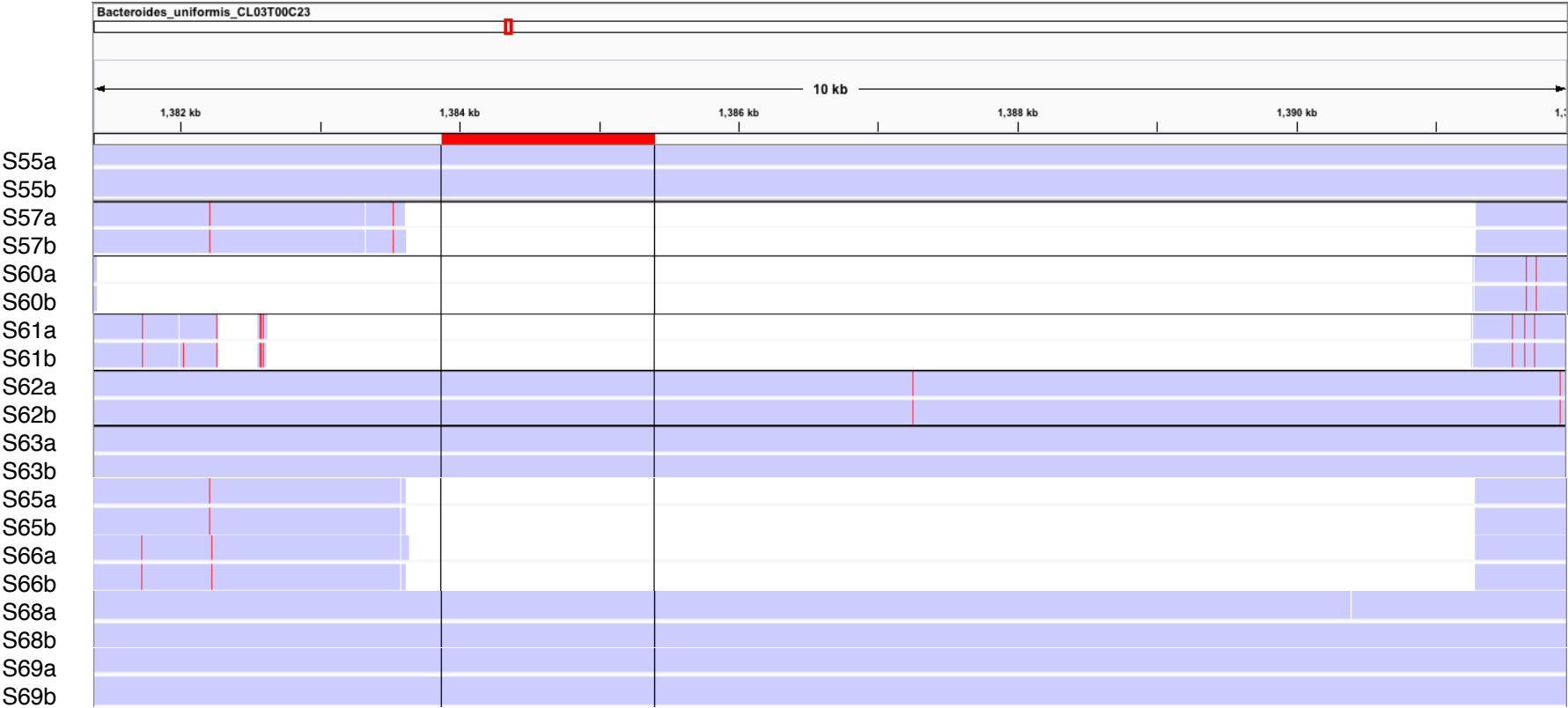


Supplementary Figure 1B

B



Supplementary Figure 1B Continued



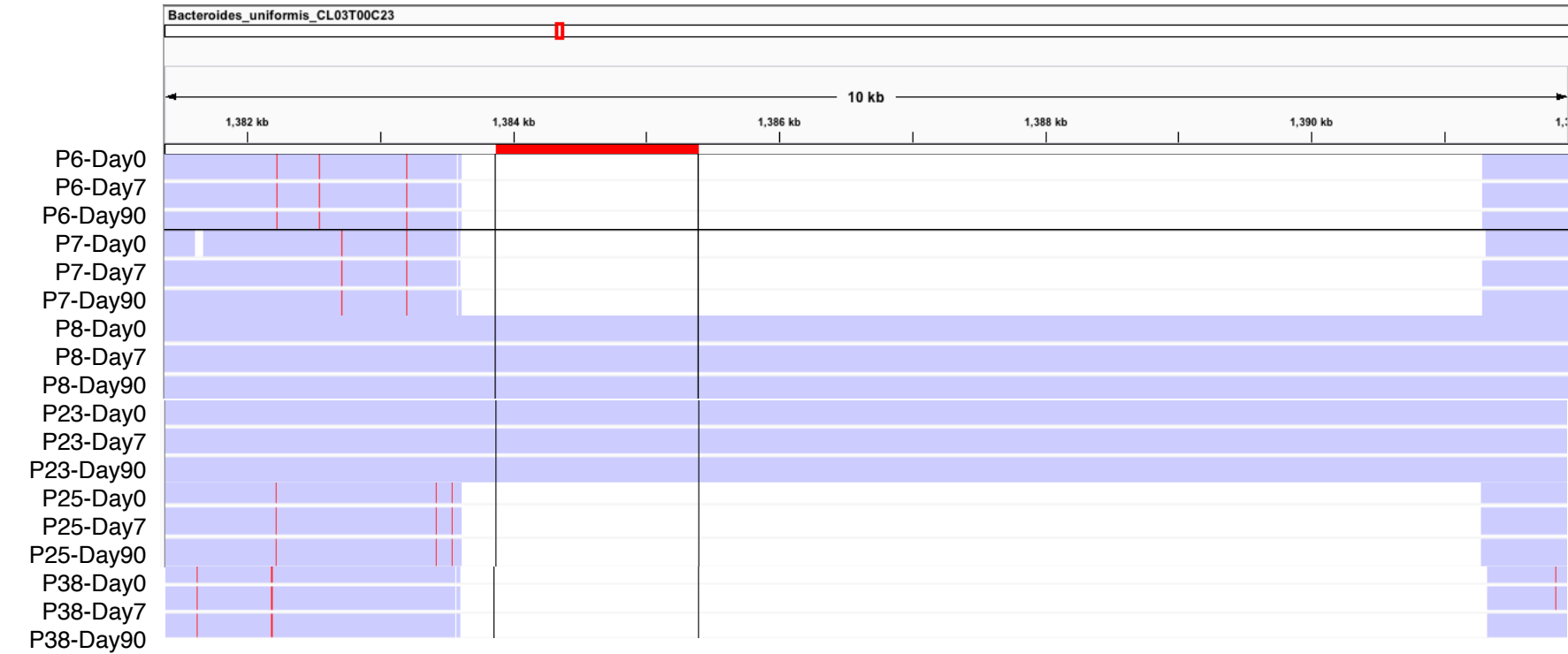
Supplementary Figure 1: IGV analysis for the HMP data set.

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 2A



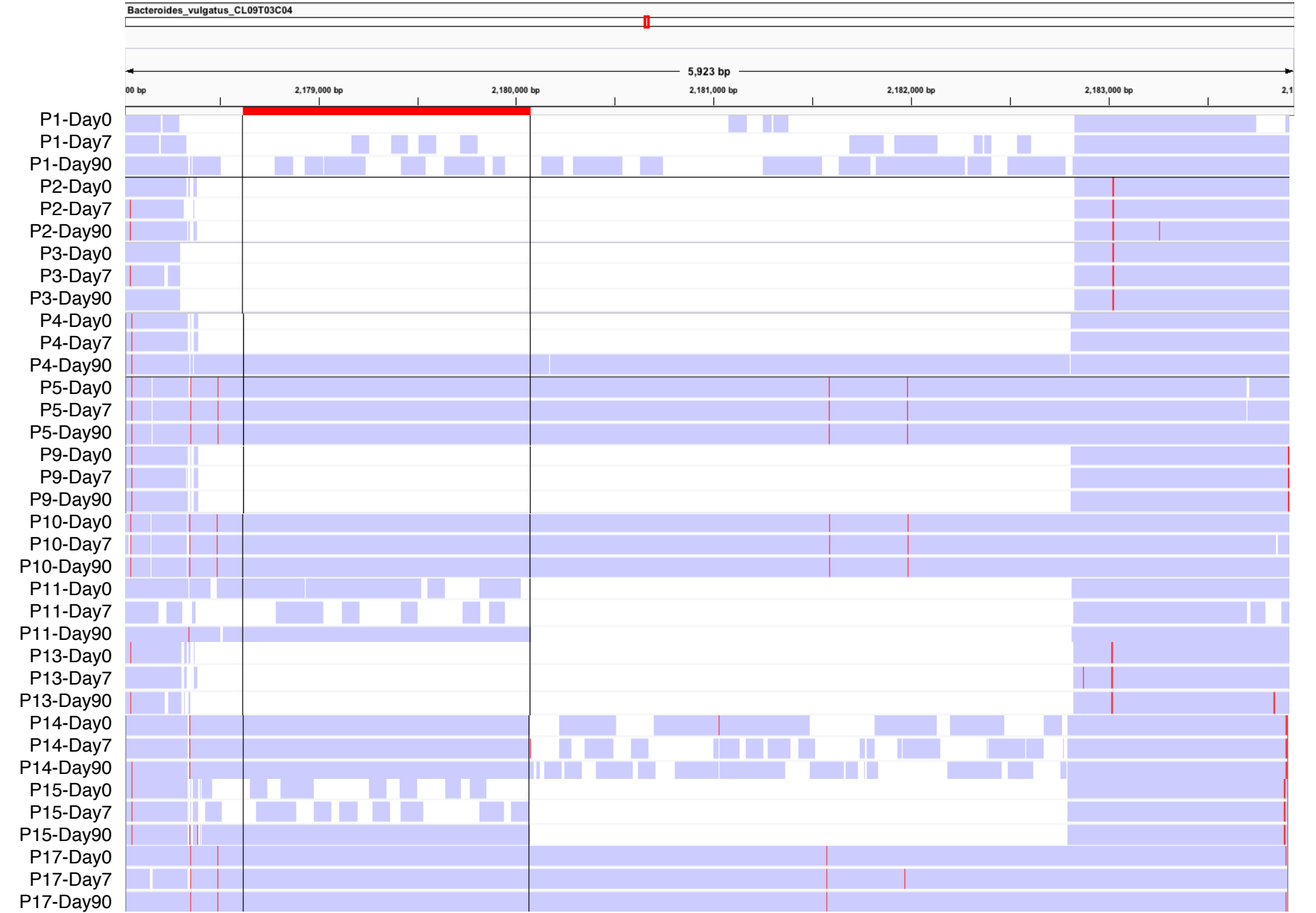
Supplementary Figure 2B



Supplementary Figure 2: IGV analysis for the control samples from Raymond et al.

For control samples from Raymond et al., aligned Bacteriocin genes, (B) 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).

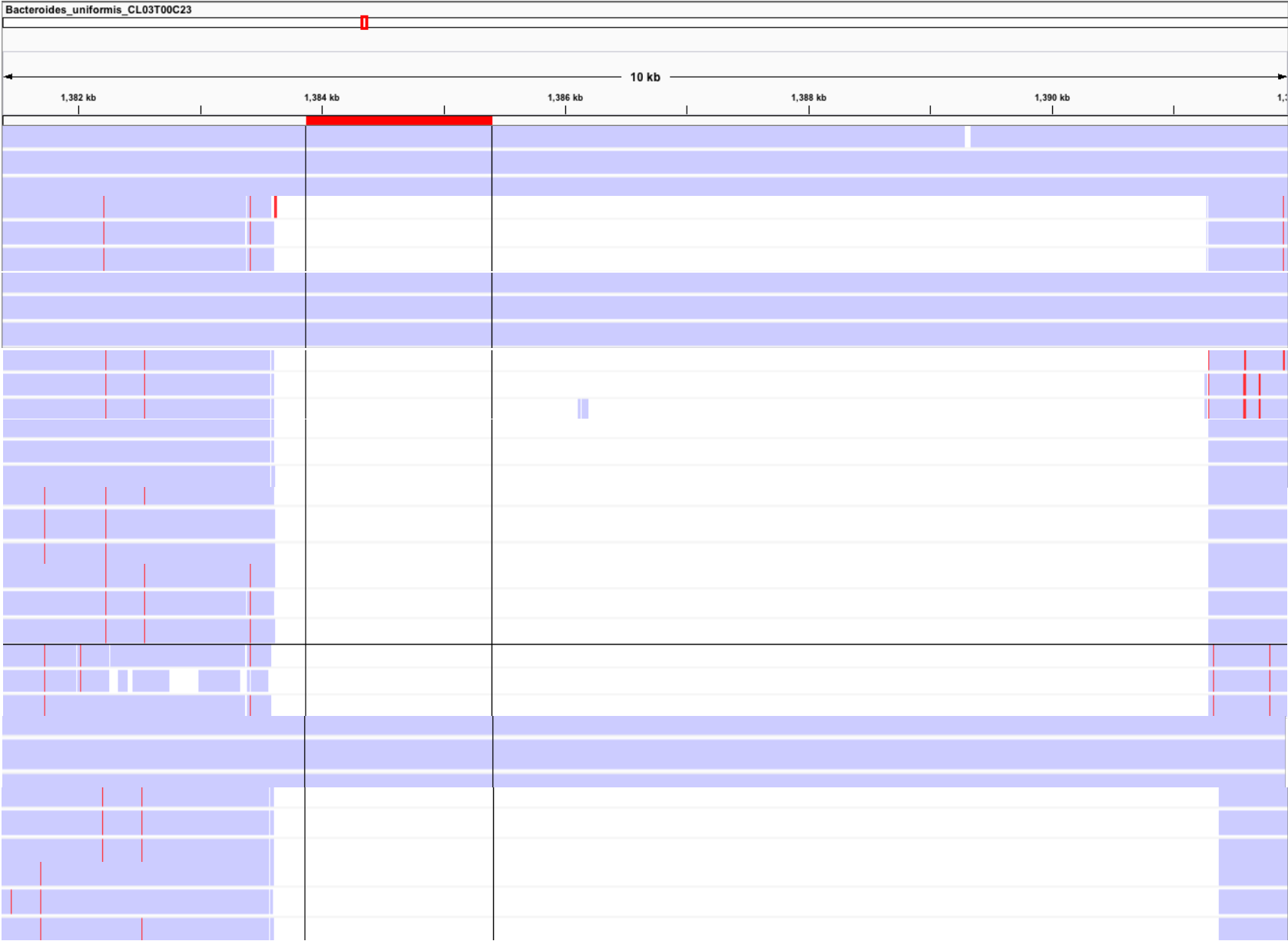
Supplementary Figure 3A



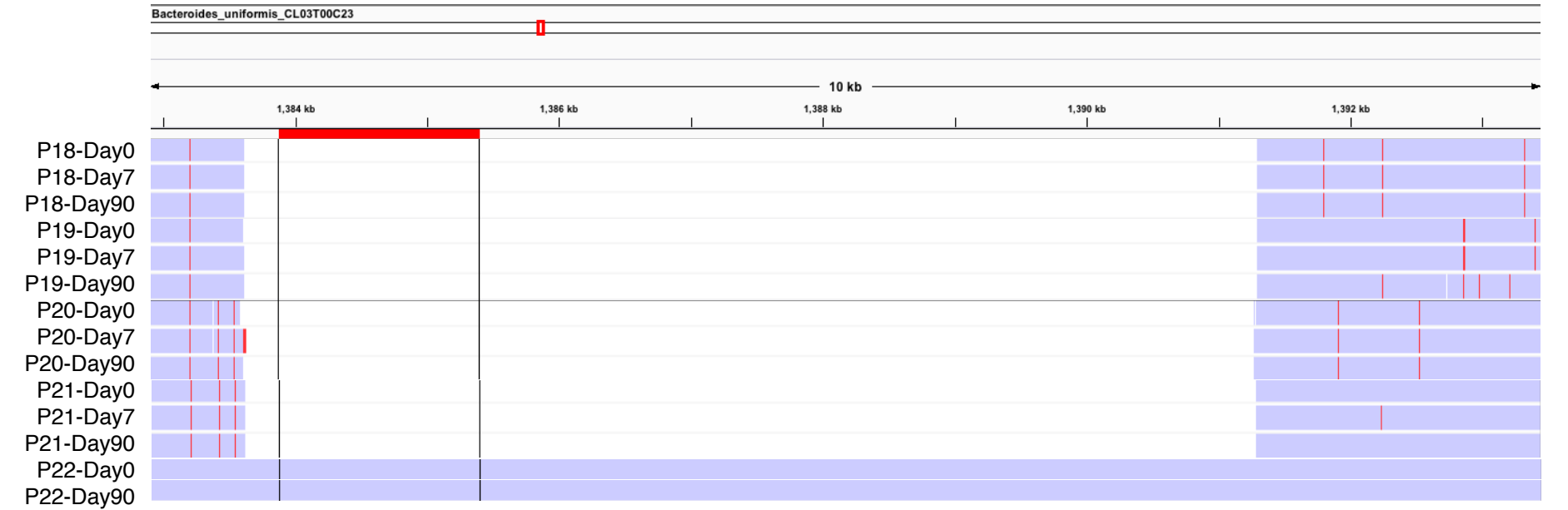
Supplementary Figure 3A - Continued



Supplementary Figure 3B

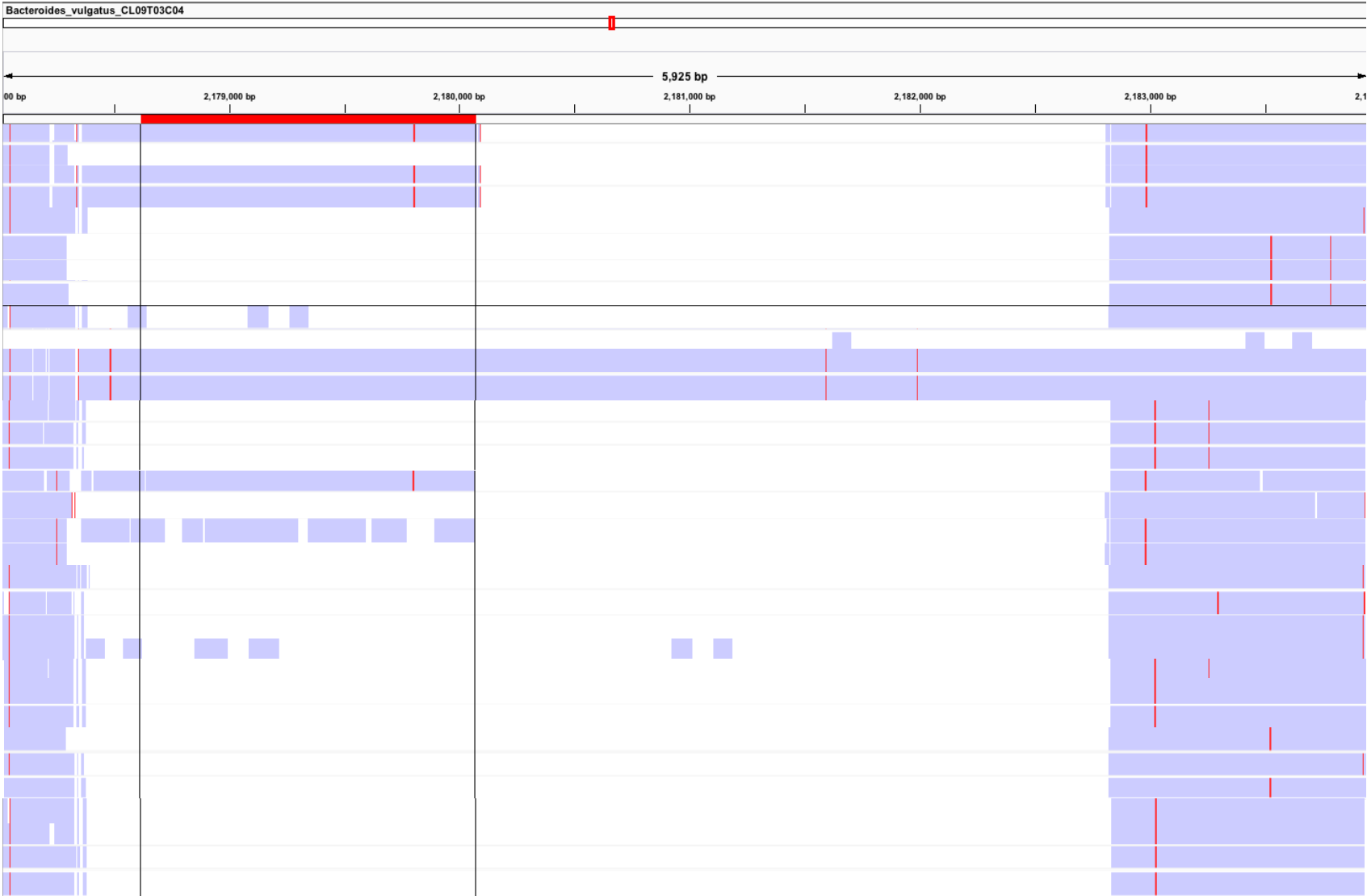


Supplementary Figure 3B - Continued

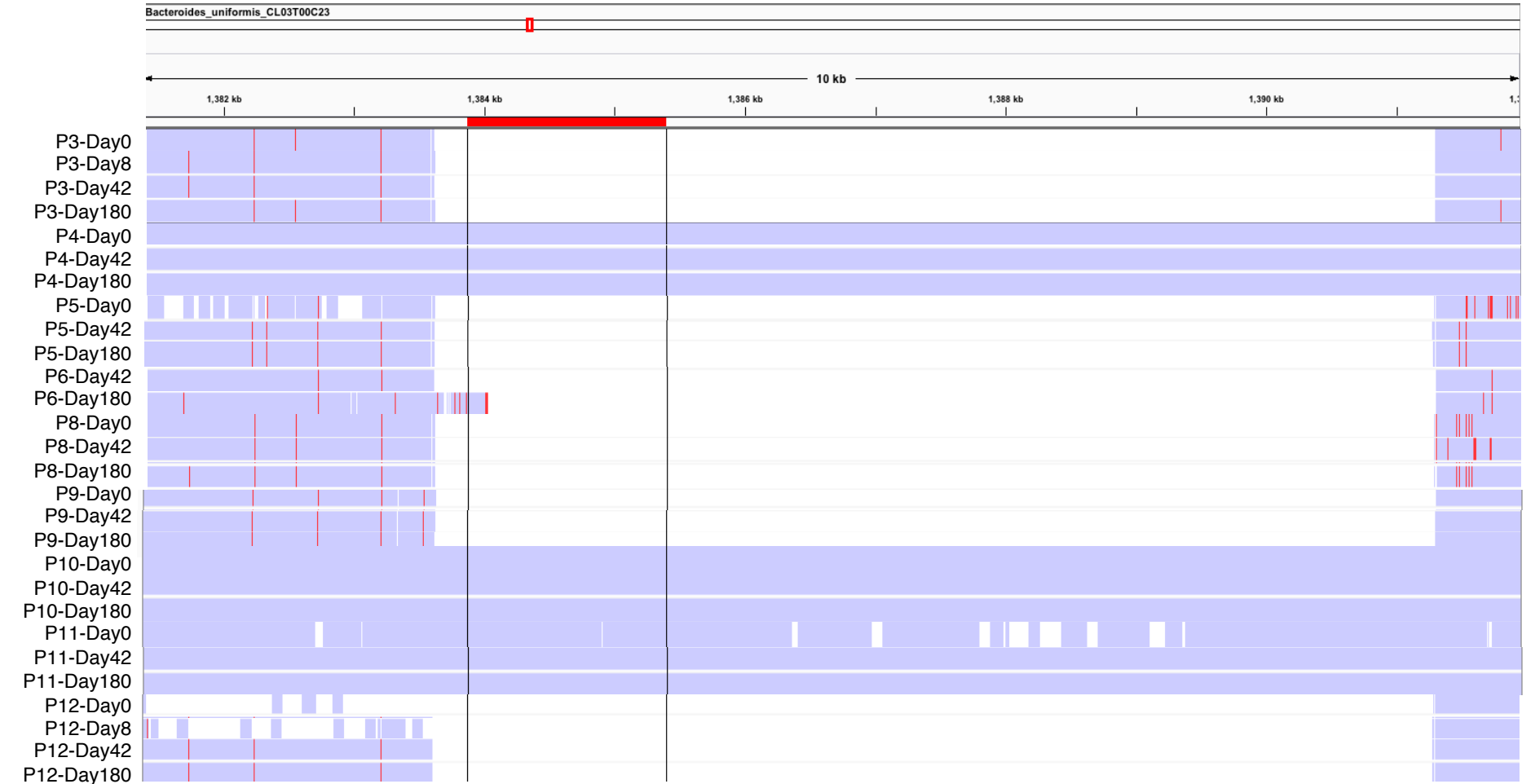


Supplementary Figure 3: IGV analysis for the antibiotic treated samples from Raymond et al.
For antibiotic treated samples from Raymond et al., aligned Bacteriocin genes, (A) BSAP-3 and (B) BSAP-2, were visualized using IGV. For the BSAP-3, 2,178,016 to 2,183,973 regions of *B. vulgatus* were selected 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 4A



Supplementary Figure 4B



Supplementary Figure 4: IGV analysis for the antibiotic treated samples from Pallega et al.

For antibiotic treated samples from Pallega 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).