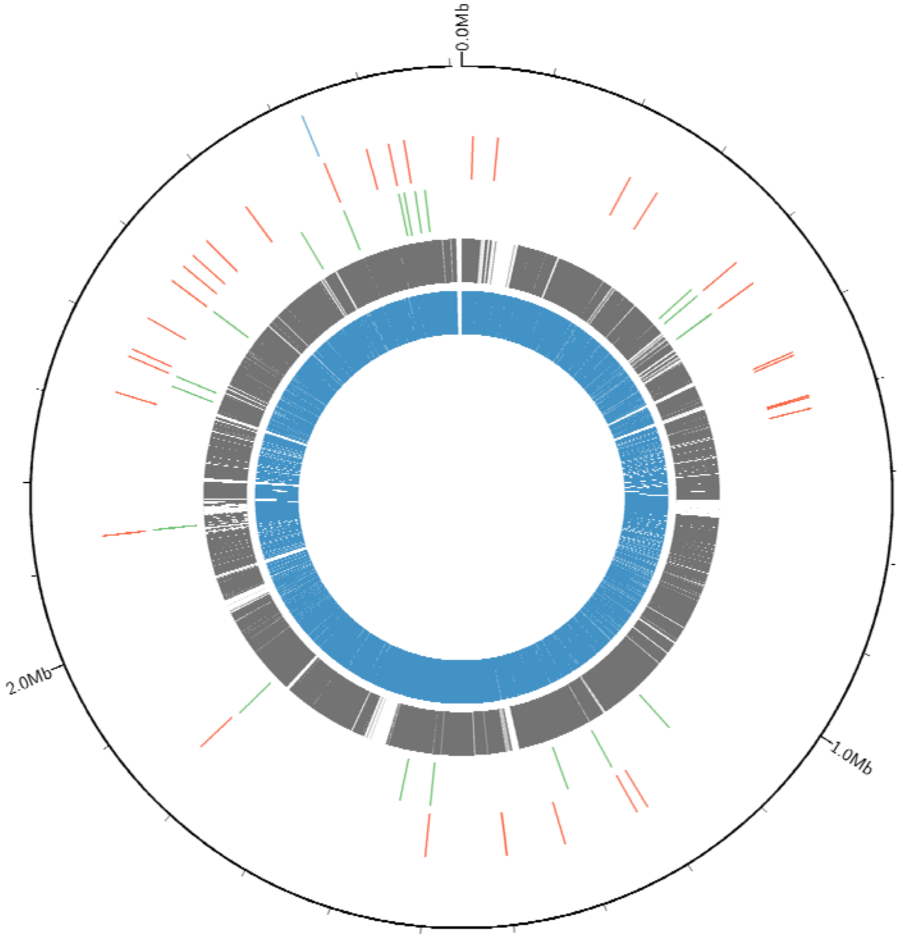
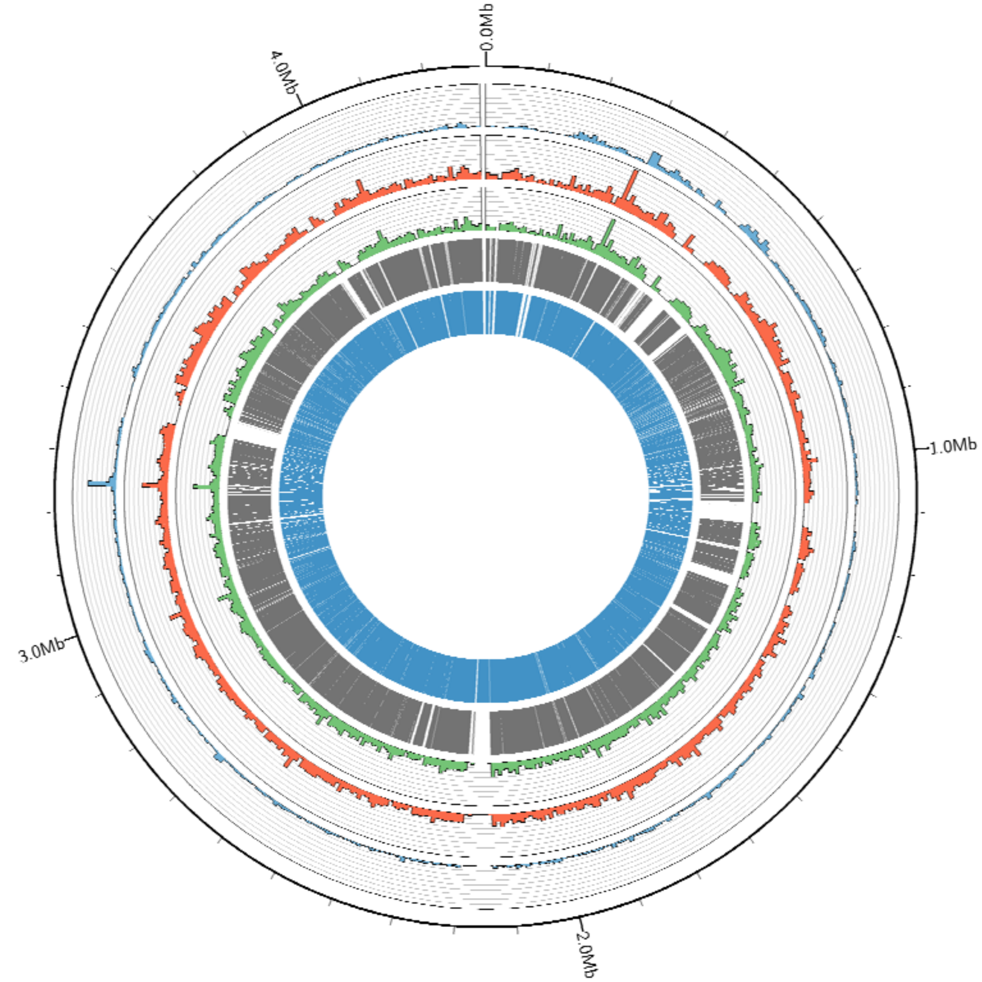
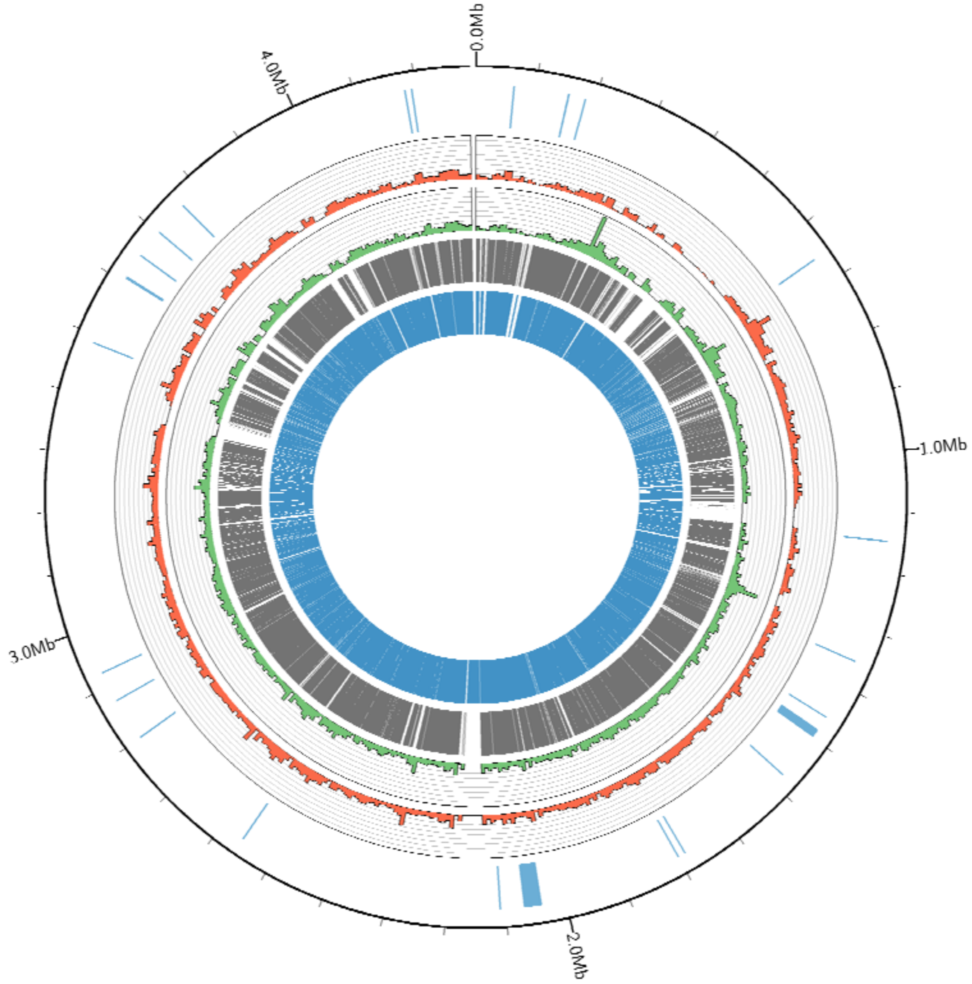


Supplementary Figure 1. Location of variable sites in MRSA cluster 2. Circular plot of *S. aureus* genome. From inner ring to outer: inner ring (blue) showing coding regions of the MRSA252 reference genome; (grey) regions of MRSA252 called in case Q; (green) location of observed variable sites in case W relative to case Q, each variable site shown as a line; (red) location of variable sites in case X relative to case Q; outer ring (blue) location of the variable site in case U relative to case Q.



Supplementary Figure 2. Location of variable sites in *C. difficile* cluster 1. Circular plot of *C. difficile* genome. From inner ring to outer: inner ring (blue) showing coding regions of the 630 reference genome; (grey) regions of 630 called in case D; (green) frequency histogram of location of observed variable sites in case A relative to case D; (red) frequency histogram of location of variable sites in case B relative to case D; outer ring (blue) frequency histogram of location of variable sites in case C relative to case D.



Supplementary Figure 3. Location of variable sites in *C. difficile* cluster 2. Circular plot of *C. difficile* genome. From inner ring to outer: inner ring (blue) showing coding regions of the 630 reference genome; (grey) regions of 630 called in case F; (green) frequency histogram of location of observed variable sites in case H relative to case F; (red) frequency histogram of location of variable sites in case E relative to case F; outer ring (blue) location of variable sites in case G relative to case F, each variable site shown as a line.