



Supplementary Figure 8. Accessory genome insertions, duplications and IS elements in persistent, acute and other isolates. Three ML phylogenetic trees are shown in the left panel, created from only persistent isolates (top), only acute isolates (middle) and other isolates (bottom). For each, the column to the right of the tree indicates the BAPs cluster of the isolates in the species phylogeny in Figure 1. In all cases, the topologies of the individual trees are consistent with the tree in Figure 1. The right-hand panel shows coverage of the accessory genome in each isolate. To the top and bottom of the right panel are representations of the assembled accessory contigs from isolates in the study. The contig color gives an indication of the content of the contig. Pink = bacteriophage, green = integrative and conjugative element (ICE), blue = transposon, red = IS element. Contigs present in the reference genome are labeled in bold above the panel, along with the location of some important virulence genes. Regions of single copy coverage are colored green in persistent isolates, red in acute isolates and gray in others. Regions of duplication are colored black, and deletions are white. IS element insertion locations are shown in blue.