



**Supplementary Figure 6.** Coverage of the accessory genome across the species. The left panel shows the ML tree, with BAPs cluster in a column to the right, as 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. For each isolate in the tree, regions are colored gray if they were present in single copy, and black if they were in multiple copy. i.e. duplications. Missing regions are in white.