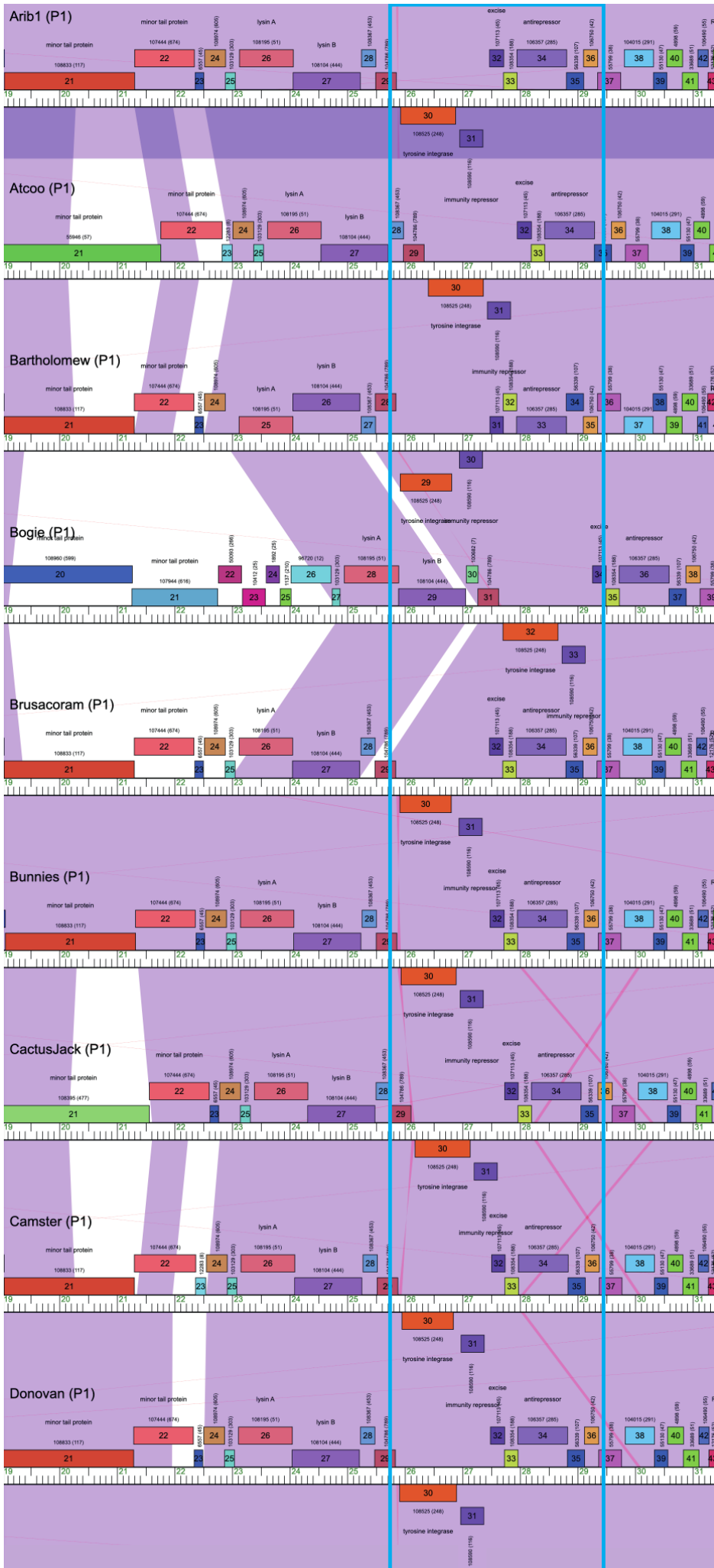
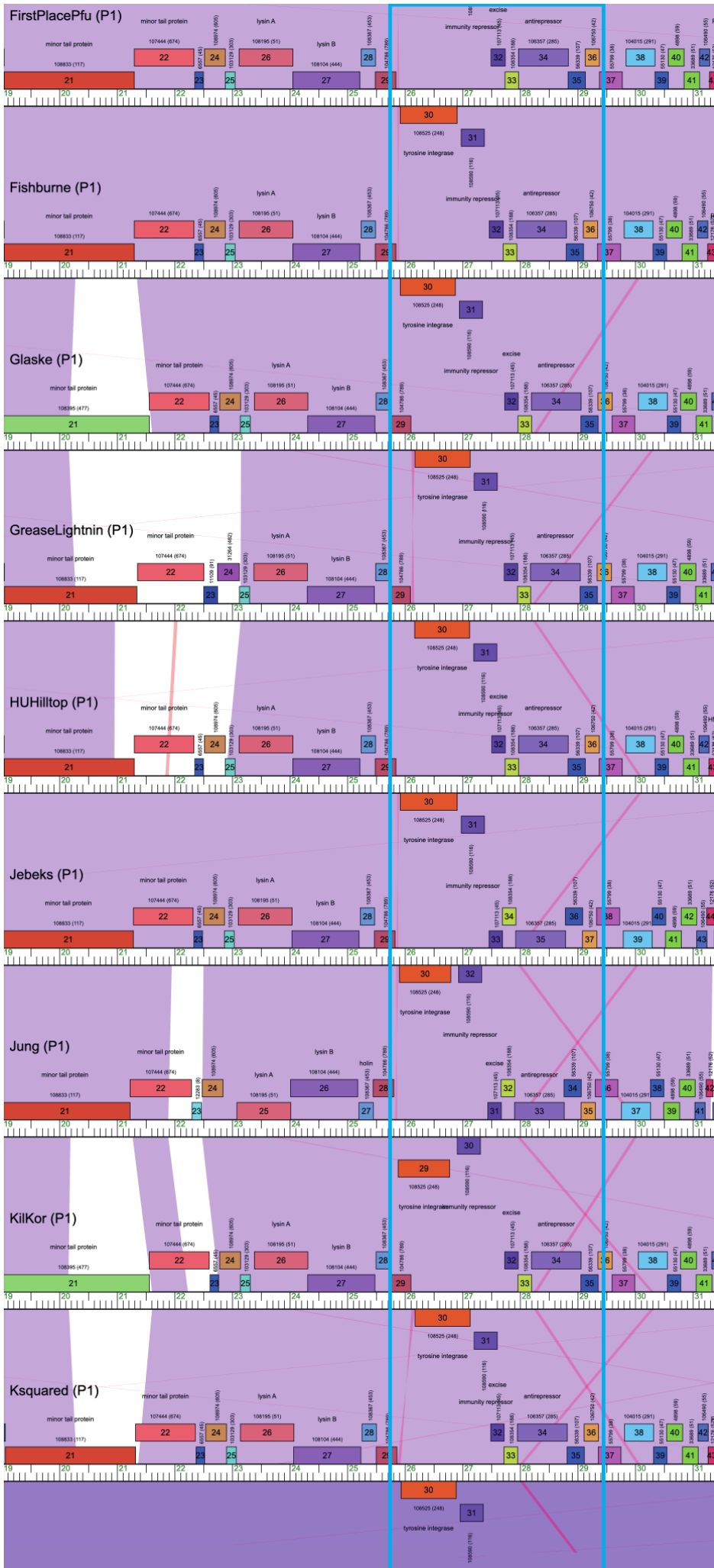
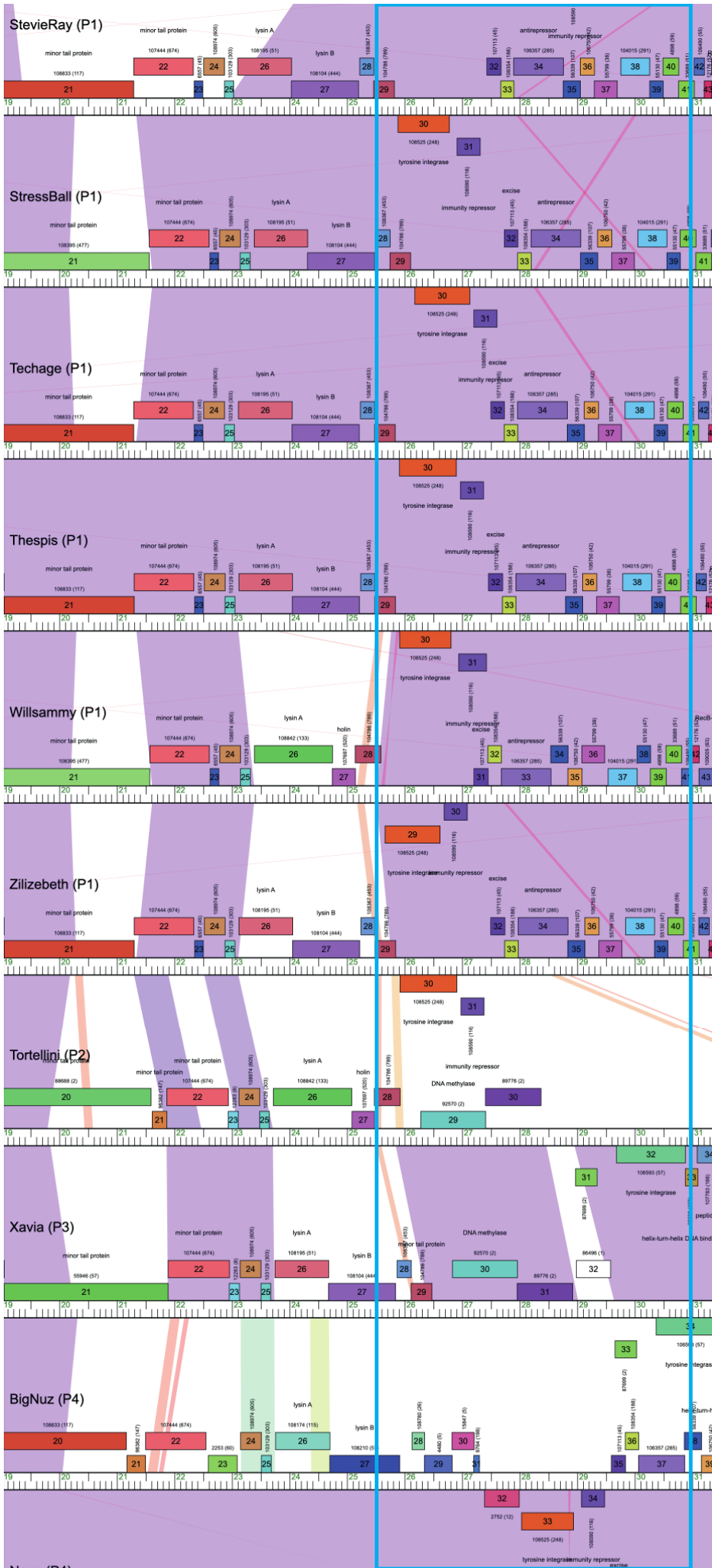


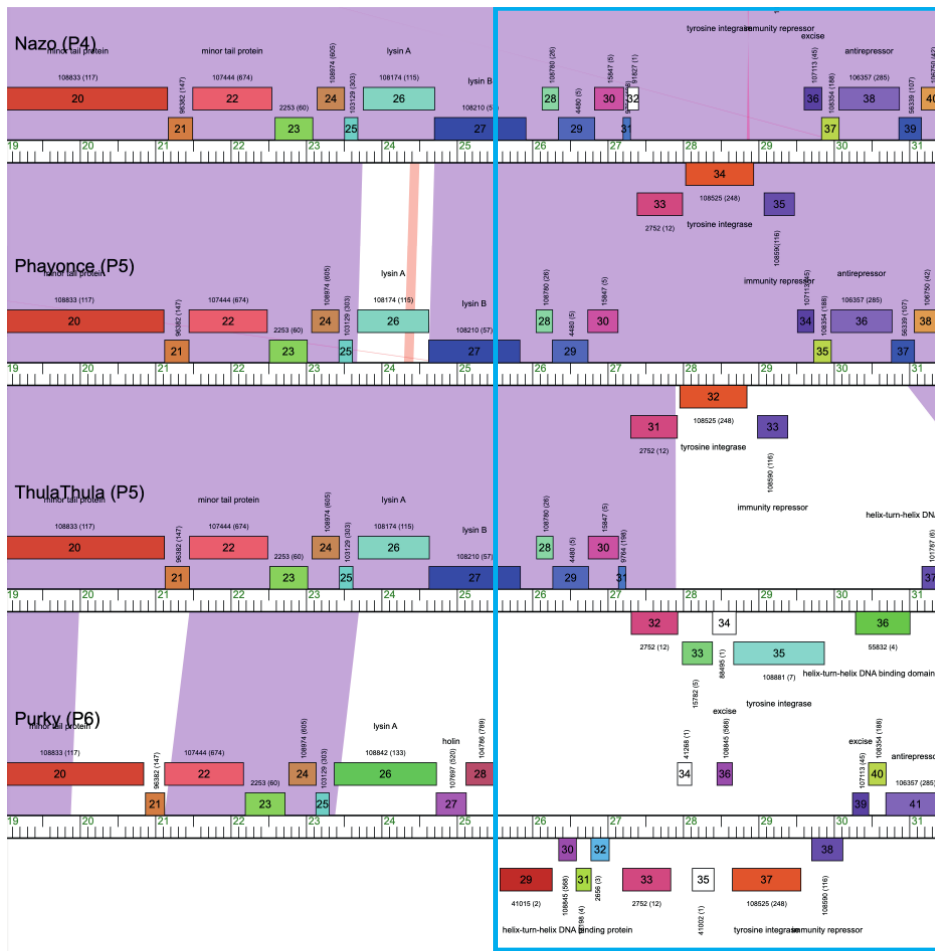
**Figure S1.** Heatmap of average nucleotide identity (ANI) values of 40 cluster P mycobacteriophage genomes (Table S1). Colors highlight membership in sub-clusters P1 to P6.











**Figure S2.** Phamerator map of regions encoding a tyrosine integrase, immunity repressor, and excise gene in cluster P mycobacteriophages (Table S2). All but three cluster P mycobacteriophages – Tortellini (P2), Xavia (P3), and ThulaThula (P5) – exhibit a conserved integration-dependent immunity system. In this Phamerator map, protein-coding genes with their putative functional assignments (if available) are displayed above or below a ruler, signifying genes on forward or reverse strands, respectively. The numbers shown above each gene indicate the protein family (pham) and, in parenthesis, the number of members in the pham family. Coloring between genomes represents nucleotide similarity with areas of highest similarity shown in purple (BLAST e-value = 0), followed by red (BLAST e-value of  $\sim 10^{-4}$ ) and white (no significant similarity). The location of the genes of interest is indicated by a blue box.