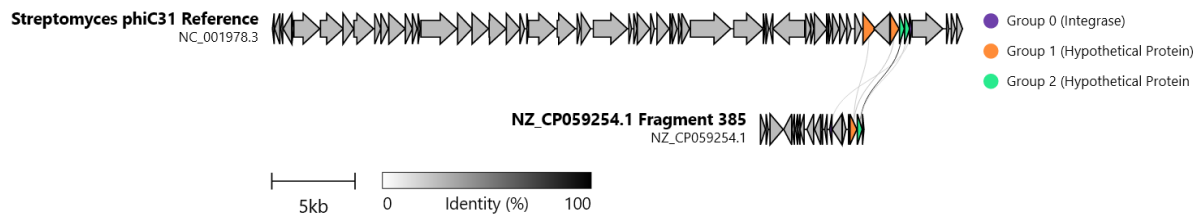
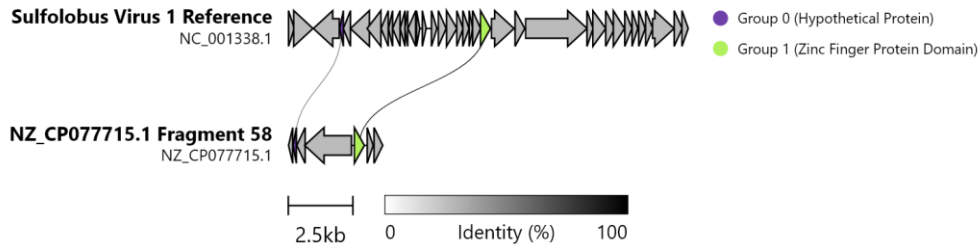


A**B**

Supplementary Figure 3: Comparison of artificial RefSeq contigs with reference genomes.

Panel (A). Comparison of artificial RefSeq contig NZ_CP059254.1 fragment 385 to *Streptomyces phiC31* phage reference genome (NC_001978.3). The 6217-bp contig NZ_CP059254.1 fragment 385 was identified as *Streptomyces virus phiC31* by Kraken2. The contig originally belonged to the complete chromosomal sequence of *Streptomyces albidoflavus* strain J1074/R2. Panel (B). Comparison of artificial RefSeq contig NZ_CP077715.1 fragment 358 to *Sulfolobus virus 1* reference genome (NC_001338.1). The 3647-bp contig NZ_CP077715.1 fragment 58 was identified as *Sulfolobus virus 1* by Kraken2. The contig originally belonged to the complete chromosomal sequence of *Saccharolobus shibatae* strain BEU9. Contigs and reference genomes were annotated with pharokka and the genes were globally aligned and visualised with clinker. Homologous genes between the two sequences are coloured by homology and annotated with their function, as predicted by pharokka.