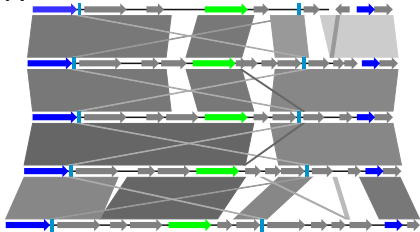


A



B

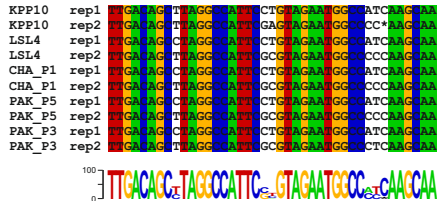


Figure S1: Identification of repeated promoter-like regions of the KPP10-like clade

A. Representation of the homology (Blastn) between the five KPP10-like bacteriophages in which 41-nt

repeats were identified (represented as light blue boxes). B. Alignment of the total of 10 repeats identified

in the five genomes, with colors indicating strictly conserved bases, with a WebLogo representation of the

consensus (the height of the letters represents their frequency at each position) shown underneath.