

**Table S1:** Sequences and coordinates of the boundaries of highly covered regions of the six bacteriophage genomes reported.

Highly covered regions		Start	End	Size
PAK_P1	sequence	AGCGA	CGTGGTT	1170
	coordinates	67966	69139	
PAK_P2	sequence	AGCGA	CGTGGTT	1170
	coordinates	66530	67695	
PAK_P4	sequence	AGCGA	CGTGGTT	1180
	coordinates	67395	68569	
CHA_P1	sequence	AGCCATT	CTTGTT	756
	coordinates	62708	63463	
PAK_P3	sequence	AGCCATT	CTTGTT	746
	coordinates	62771	63516	
PAK_P5	sequence	AGCCATT	CTTGTT	760
	coordinates	62171	62930	