

**Table S4. The top 7 forward and reverse sequences in the phage IME-EC2 genome**

Orientation	Frequency	Position <sup>1</sup>	Read sequence
Reverse	695	<b>38179</b>	AAATCAGGCGTCGCGGATATCTCGCGTATG
	99	38177	ATCAGGCGTCGCGGATATCTCGCGTATGTA
	79	38180	GAAATCAGGCGTCGCGGATATCTCGCGTAT
	77	38181	AGAAATCAGGCGTCGCGGATATCTCGCGTA
Forward	66	<b>37880</b>	ATCAGCTTGATCTCCTCGGTGGTCATTGGC
	63	37873	CTCCGCCATCAGCTTGATCTCCTCGGTGGT
	62	37879	CATCAGCTTGATCTCCTCGGTGGTCATTGG

<sup>1</sup>Reverse has definite HFSs with several base variation, while the HFSs on forward were not evident as reverse, which was 10 times with the forward, that indicating the reverse fixed while the forward was slightly random.

The direct repeat length = 38179 (R) – 37880 (F) = 299bp