

**Supplementary Table 1: Genome and prophage analysis of *Entelli-02***

<b>Total # of reads</b>	<b># Matched with cocktail phages</b>	<b># Matched with host bacterial genome</b>	<b># Matched with predicted prophage region</b>
14,623,072	14,508,309 (99.21%)	39,992 (0.27%)	12,996 (0.09%)