

Table S2. BLASTn alignment of homologs phages sequences (at the GenBank database) with isolated salmophages.

Phage (complete genome)	Genome Length [bp]	G+C Content [%]	No. of Genes / Protein	E-Value	Query Coverage [%]	Percent Identity [%]	Phage Family	Genome	Isolated Country	Isolation Source	Lab Host	GenBank Accession No.
<i>Salmonella</i> phage strain KKP 3829												
<i>Salmonella</i> phage FSL SP-124	59,245	56.5	71/71	0.0	96	96.13	<i>Casjensviridae</i>	Linear DNA	USA	ND	<i>Salmonella enterica</i>	KC139515.1
<i>Salmonella</i> phage FSL SP-088	59,454	56.4	70/70	0.0	96	96.06	<i>Casjensviridae</i>	Linear DNA	USA	ND	<i>Salmonella enterica</i>	NC_021780.1
<i>Salmonella</i> phage SPN19	59,203	56.5	72/72	0.0	95	96.21	<i>Casjensviridae</i>	Circular DNA	South Korea	ND	<i>Salmonella</i> sp.	JN871591.1
<i>Salmonella</i> phage YSD1 strain YSD1_PHAGE	58,916	56.5	71/71	0.0	87	96.28	<i>Casjensviridae</i>	Circular DNA	United Kingdom	ND	<i>S. Typhi</i>	NC_048666.1
<i>Salmonella</i> phage BSPM4	59,097	56.5	78/78	0.0	96	95.69	<i>Casjensviridae</i>	Linear DNA	South Korea	swine intestine	<i>S. Typhimurium</i>	NC_048655.1
<i>Salmonella</i> phage strain KKP 3830												
<i>Salmonella</i> phage YSP2	50,316	42.9	87/87	0.0	98	99.74	<i>Drexelviriidae</i>	Linear DNA	China	sewage	<i>S. Pullorum</i>	NC_047898.1
<i>Salmonella</i> phage GJL01	50,407	42.8	80/80	0.0	97	99.77	<i>Drexelviriidae</i>	Linear DNA	China	sewage	<i>S. Pullorum</i> SP1	KY657202.1
<i>Escherichia</i> phage vB_EcoS_011D2	50,633	42.9	89/89	0.0	93	97.97	<i>Drexelviriidae</i>	Linear DNA	China	sewage	<i>Escherichia coli</i>	MT478992.1
<i>Escherichia</i> phage DanielBernoulli strain Bas08	50,731	43.2	91/91	0.0	86	96.86	<i>Drexelviriidae</i>	Linear DNA	Switzerland	sewage plant inflow	<i>Escherichia coli</i> K-12	MZ501059.1
<i>Citrobacter</i> phage vB_CfrD_Brooksby	50,071	42.8	86/86	0.0	89	96.94	<i>Drexelviriidae</i>	Linear DNA	USA	raw sewage	<i>Citrobacter freundii</i>	OL539443.1

ND – no data