

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

| Phage (complete genome) | Genome Length [bp] | G+C Content [%] | No. of Genes / Protein | E-Value | Query Coverage [%] | Percent Identity [%] | Phage Family / Genus | Genome | Isolated Country | Isolation Source | Lab Host | GenBank Accession No. |
|------------------------------------|--------------------|-----------------|------------------------|---------|--------------------|----------------------|-----------------------------------------|--------------|------------------|-----------------------------------|--------------------------------------------|-----------------------|
| Serratia phage KKP_3708 | | | | | | | | | | | | |
| Klebsiella phage Amrap | 41,209 | 52.5 | 57 / 57 | 0.0 | 90 | 89.85 | <i>Autographiviridae / Przondovirus</i> | Linear DNA | United Kingdom | wastewater | <i>Klebsiella oxytoca</i> | OQ579031.1 |
| Klebsiella phage vB_Ko_K26PH128 C1 | 41,030 | 52.6 | 51 / 51 | 0.0 | 88 | 92.36 | <i>Autographiviridae / Przondovirus</i> | Circular DNA | ND | ND | ND | OY978813.1 |
| Klebsiella phage VLCpiA3b | 40,231 | 53.1 | 48 / 48 | 0.0 | 85 | 92.79 | <i>Autographiviridae / Przondovirus</i> | Circular DNA | Spain | soil and water | <i>Klebsiella pneumoniae</i> | ON602742.1 |
| Klebsiella phage P79_1 | 40,510 | 53.1 | 43 / 43 | 0.0 | 85 | 92.47 | <i>Autographiviridae / Przondovirus</i> | Linear DNA | China | wastewater | <i>Klebsiella pneumoniae</i> strain Kp2245 | OR256027.1 |
| Klebsiella phage KP32_isolate 194 | 41,161 | 52.8 | 44 / 43 | 0.0 | 85 | 92.45 | <i>Autographiviridae / Przondovirus</i> | Linear DNA | Russia | clinical isolate | <i>Klebsiella pneumoniae</i> | NC_047969.1 |
| Serratia phage KKP_3709 | | | | | | | | | | | | |
| Serratia phage vB_SmaM_Hera | 67,493 | 49.9 | 100 / 100 | 0.0 | 97 | 98.36 | <i>- / Myosmarovirus</i> | Linear DNA | USA | raw sewage | <i>Serratia marcescens</i> | MW021759.1 |
| Serratia phage MTx | 68,621 | 49.9 | 103 / 103 | 0.0 | 95 | 97.32 | <i>- / Myosmarovirus</i> | Linear DNA | USA | wastewater treatment plant sample | <i>Serratia marcescens</i> | NC_048759.1 |
| Erwinia phage vB_EamM_TropicalSun | 68,439 | 49.1 | 105 / 105 | 0.0 | 83 | 82.25 | <i>- / Myosmarovirus</i> | Linear DNA | Indonesia | ND | <i>Erwinia amylovora</i> | MN013090.1 |
| Serratia phage MyoSmar | 68,745 | 49.2 | 105 / 105 | 0.0 | 81 | 83.18 | <i>- / Myosmarovirus</i> | Linear DNA | USA | pond water | <i>Serratia marcescens</i> | NC_048800.1 |
| Serratia phage SMP | 68,405 | 49.2 | 99 / 99 | 0.0 | 79 | 82.13 | <i>- / Myosmarovirus</i> | Linear DNA | China | sewage | <i>Serratia marcescens</i> | OP490597.1 |

| Enterobacter phage KKP_3711 | | | | | | | | | | | | |
|-----------------------------|---------|------|-----------|-----|----|-------|-----------------------------------------|------------|---------|--------------------------------|---------------------------------------|------------|
| Salmonella phage SP33 | 110,293 | 39.2 | 157 / 157 | 0.0 | 11 | 71.54 | <i>Demereciviridae / Tequintavirus</i> | Linear DNA | China | pig farm | <i>Salmonella Typhimurium</i> | OR862218.1 |
| Klebsiella phage vB_Kpn_3 | 112,003 | 42.1 | 183 / 183 | 0.0 | 9 | 72.05 | <i>Demereciviridae / Sugarlandvirus</i> | Linear DNA | Iran | wastewater from Qaem hospitals | MDR <i>Klebsiella pneumoniae</i> | MZ079855.1 |
| Escherichia phage EC142 | 108,723 | 39.0 | 155 / 155 | 0.0 | 9 | 71.75 | <i>Demereciviridae / Tequintavirus</i> | Linear DNA | Denmark | bird feces | <i>Escherichia coli</i> strain ECOR4 | ON185584.1 |
| Escherichia phage EC104 | 108,711 | 39.0 | 155 / 155 | 0.0 | 9 | 71.75 | <i>Demereciviridae / Tequintavirus</i> | Linear DNA | Denmark | bird feces | <i>Escherichia coli</i> strain ECOR19 | ON185581.1 |
| Escherichia phage EC122 | 108,723 | 39.0 | 156 / 156 | 0.0 | 9 | 71.75 | <i>Demereciviridae / Tequintavirus</i> | Linear DNA | Denmark | bird feces | <i>Escherichia coli</i> strain ECOR20 | ON185583.1 |

ND – no data