## SUPPLEMENTAL MATERIALS

**Table S1. Characteristics of the clinical isolates used in this study**

| Strain | MLST[a] | Enzyme type[b] | Year of isolation | Source[c] | ΦNJS1 sensitivity[d] |
|---|---|---|---|---|---|
| A2312NM | ST-11 | KPC-2 | 2014 | Feces | +++ |
| A1678 | ND | KPC-2 | 2013 | LRS | - |
| A1679 | ST-11 | KPC-2 | 2013 | LRS | - |
| A1705 | ST-449 | KPC-2, NDM-1 | 2013 | Urine | - |
| A1706 | ST-449 | KPC-2, NDM-1 | 2013 | LRS | - |
| A1763 | ST-11 | KPC-2 | 2013 | Feces | - |
| A1806 | ST-1493 | NDM-1 | 2013 | Feces | +++ |
| A1831 | ST-11 | KPC-2 | 2014 | Feces | - |
| A1836 | ST-11 | KPC-2 | 2014 | Feces | ++ |
| A2314 | ST-11 | KPC-2 | 2014 | LRS | +++ |
| A2402 | NEW | KPC-2 | 2014 | Feces | +++ |
| A2440 | ND | NDM-1 | 2014 | Blood | - |
| A1876 | ST-1318 | NDM-1 | 2014 | Feces | - |
| A1838 | ST-17 | IMP | 2014 | Feces | +++ |
| A1682 | ST-17 | ND | 2013 | Blood | ++ |
| A2359 | ST-307 | IMP | 2014 | LRS | - |
| A2368 | ST-307 | IMP | 2014 | LRS | - |
| A1871 | ST-37 | ND | 2014 | Urine | ++ |
| A2612 | ST-395 | KPC | 2015 | Feces | +++ |
| A1851 | ST-395 | ND | 2014 | Feces | - |
| A1824 | ST-65 | KPC-2 | 2014 | Feces | +++ |
| A1749 | ST-709 | ND | 2013 | Feces | - |
| A1860 | ST-846 | IMP | 2014 | Blood | ++ |
| A1683 | ST-86 | ND | 2013 | Blood | - |
| A2366 | ST-875 | ND | 2014 | Feces | - |
| A2369 | NEW | IMP | 2014 | AF | - |
| A2373 | NEW | KPC | 2014 | LRS | +++ |
| A2371 | NEW | KPC | 2014 | LRS | - |
| KP1513 | ND | ND | 2015 | LRS | +++ |
| ATCC BAA-1899 | | KPC, NDM | unknown | Human | ++ |
| ATCC BAA1705 | | ND | 2007 | Urine | - |
| ATCC BAA1706 | | ND | 2007 | Urine | +++ |

[a]MLST type: NEW, new ST types; ND, not determined; [b]Carbapenem antibiotic enzyme type: KPC, carbapenemases; NDM, New Delhi metallo-β-lactamase; IMP, imipenemase metallo-β-lactamase; ND, not determined. [c]Clinical specimens source: AF, ascitic fluid; LRS, lower respiratory secretions; [d] Sensitivity to ΦNJS1: "+++", EOP (Efficiency of Plaques) >0.01, "++", EOP>0.0001, "-" EOP<$10^{-5}$.

**Table S2. *Kp* phages isolated in this study**

| phage | Genbank number | Genome (bps) | GC content | Host range[a] |
|---|---|---|---|---|
| ΦNJS1 | MH445453 | 49,292 | 50.6% | 46.88% |
| ΦNJS2 | MH633485 | 50,132 | 50.8% | 25% |
| ΦNJS3 | MH633486 | 49,387 | 51.1% | 21.88% |
| ΦNJR15 | MH633487 | 49,468 | 51.0% | 21.88% |
| ΦTAH8 | MH633484 | 49,344 | 51.1% | 31.25% |

[a.] 32 Kp clinical isolates were tested. EOP $>10^{-5}$ indicates susceptibility to phage.

**Table S3. Primers used in this study**

| **Primer** | **Sequence** |
|---|---|
| mcr1_IS_LRed_u1 | 5’ GTAACCGTCTCATTTAAACCGTCTTTCGCCTCCCTTTCCTGTTTCCGATACCGTTGCACTTGGTTTGACAATTC 3’ |
| mcr1_IS_LRed_l1 | 5’ CTTGAAAATACATGGTATTGCGTAAAGGGCGGTAAAAGTCTATCCTGGTGTGTGCGGTGGGTTTGGAAAAAATAC 3’ |
| mcr1_LRed_u1 | 5’ GCAGTATAATTGCCGTAATTATCCCACCGTTTATTTTTTGAGTAGTTTCTCGTGTAGGCTGGAGCTGCTTC 3’ |
| mcr1_LRed_l1 | 5’ GACAAGAGCGATACTCATCTCAGCAAGTAGGCGTTTATTTGATAAATACGCATATGAATATCCTCCTTAG 3’ |
| oriR6kseqprim1 | 5’ GACACAGGAACACTTAACGGC 3’ |
| psyn-u1 | 5’ CCTGACGGATGGCCTTTTTG 3’ |

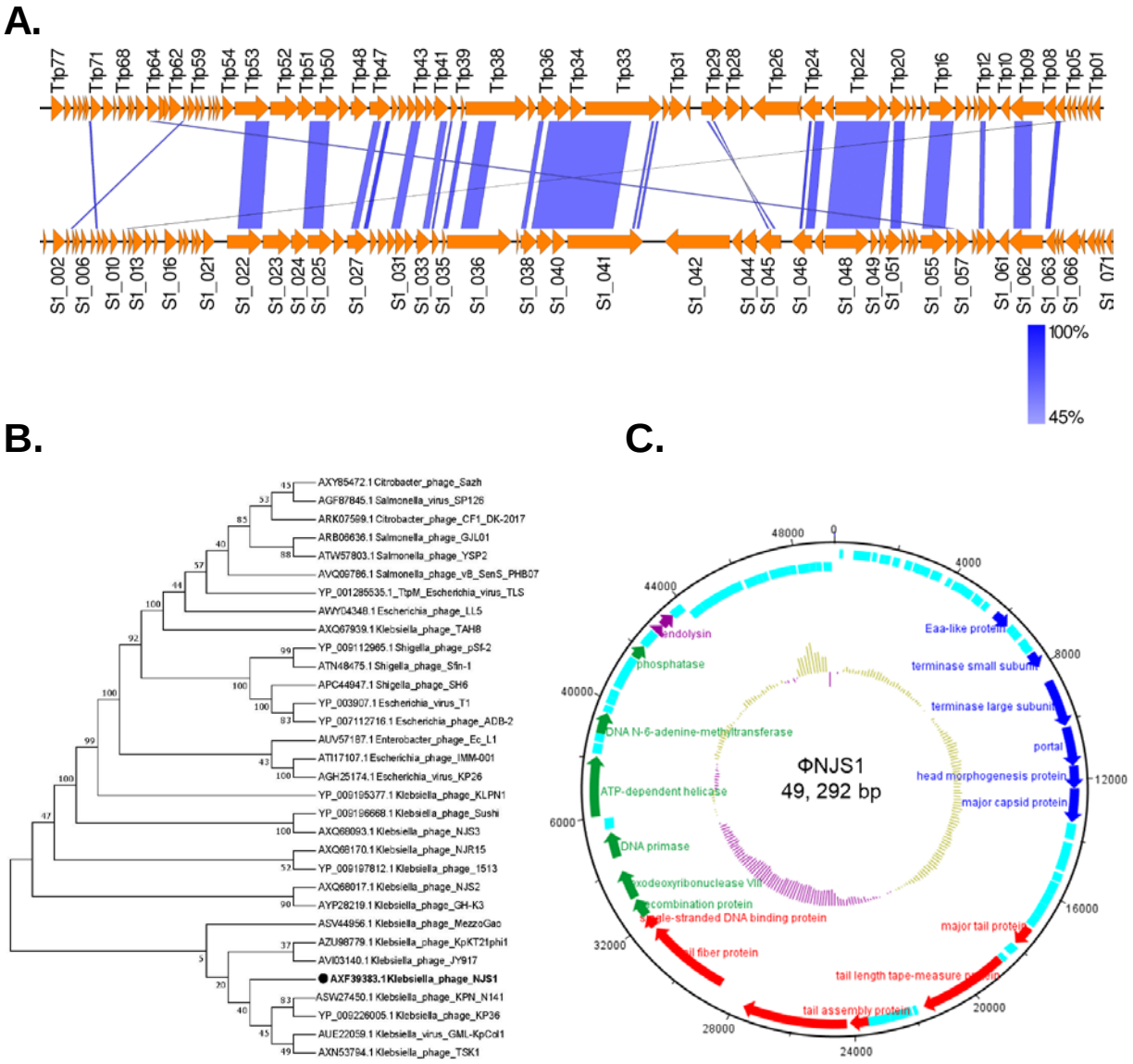


**Fig. S1.** Genome map and comparison of ΦNJS1 with other phages. **A.** Direct comparison of the genomic structures of NJS1 (accession no. MH445453) and close-related Enterobacteria phage T1 genome (NC_005833) by GATU software, RAST and PHASTER programs. Shaded boxes represent the sequence identity levels between these two genomes. **B**. Phylogenetic tree based on the tape measure proteins (TMP) by using the Neighbor-Joining method. **C.** Genome map. The inner circle indicates the GC content. The color of each gene refers to the functional category: phage structure (blue and red), replication/recombination/repair (green), lysis (purple). The scale units are base pairs.

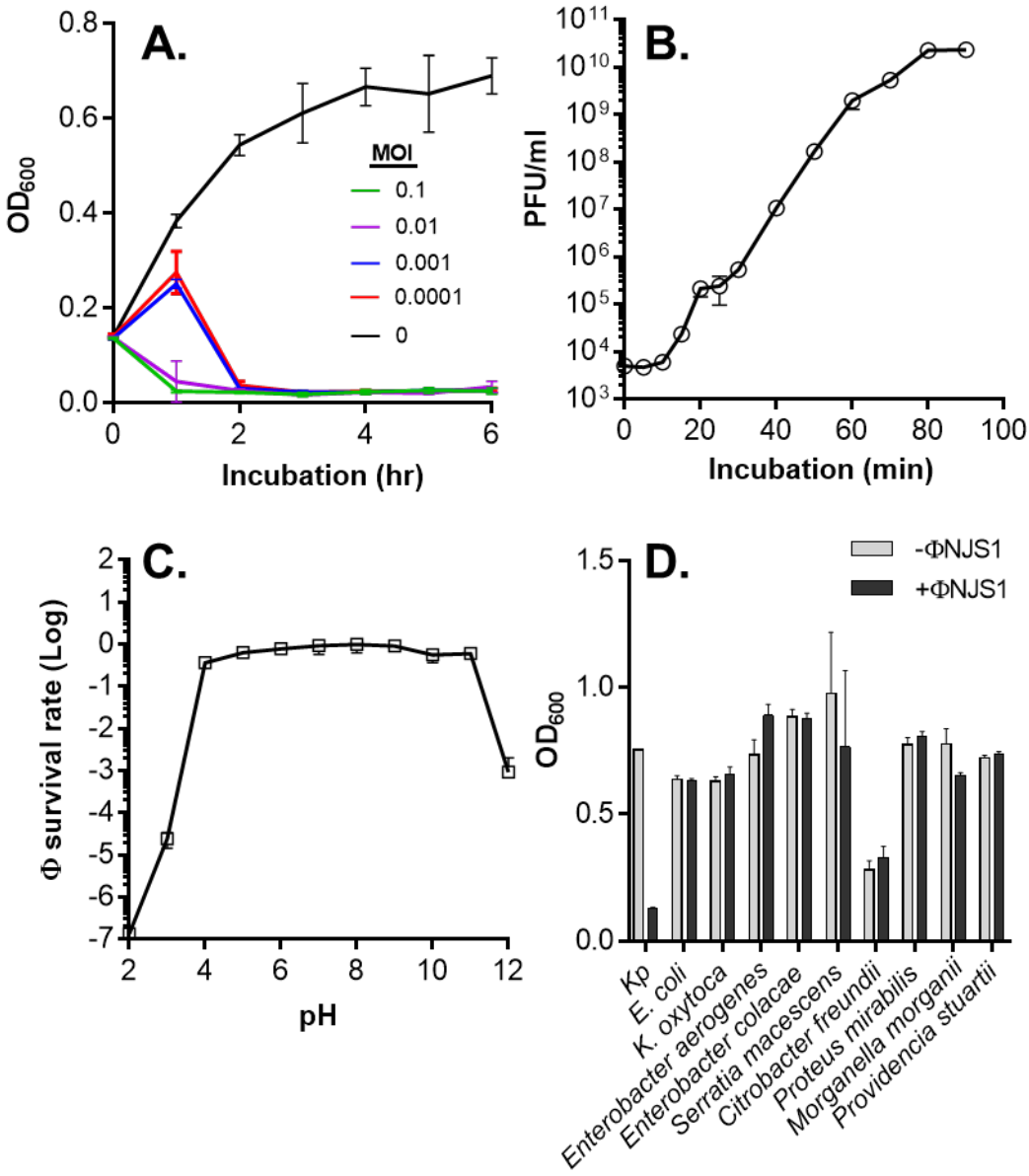


**Fig. S2.** The characteristics of ΦNJS1. **A.** Infectious dose. Approximately $10^8$ CFU/ml mid-log *Kp* cells were incubated with the phage at a multiplicity of infection (MOI) of 0.0001, 0.001, 0.01, or 0.1. Phage infection dynamics ($OD_{600}$) was measured at 1 hr intervals for 6 hr standing incubation at 37°C. The mean of 3 independent assays is shown and error bars represent the standard deviation. **B**. One-step growth curve of the ΦNJS1with *Kp*. Approximately $3\times10^8$ CFU/ml mid-log *Kp* cells were incubated with the phage at a MOI of 0.0001. After 10 mins of phage adsorption, unadsorbed phages were removed by centrifugation and bacterial cells were resuspended in fresh LB and incubated at 37°C under constant shaking. Samples were taken at 5-min intervals for titration immediately. The mean of 3 independent assays is shown, and error bars represent the standard deviation. **C.** Phage stability in different pHs. $10^8$ PFU/mL phage

particles were incubated in 0.8% NaCl buffered to different pH for 24 hr at 37℃. The survival rate of the phage was compared to that of the control samples (4°C, pH 7). The mean of 3 independent assays is shown and error bars represent the standard deviation. D. Host range specificity. All *Enterobacteriaceae* strains were cocultured without or with phage at MOI=1 under shaking condition at 37℃. At the 6-hr time point, $OD_{600}$ was measured.

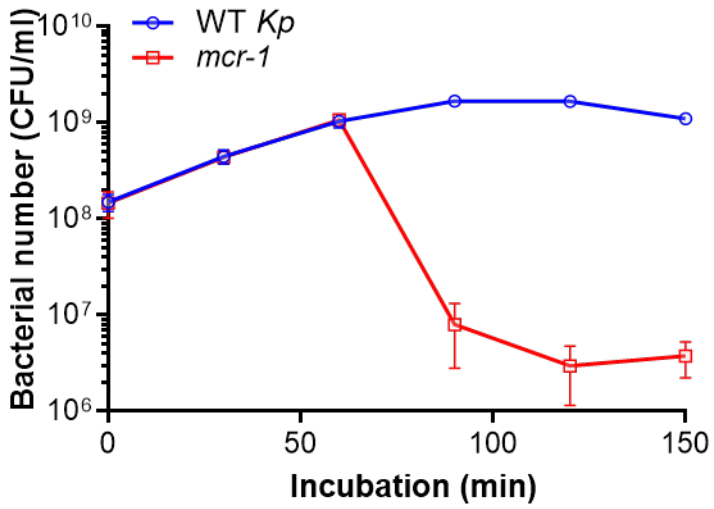


**Fig. S3.** *Kp* CFU during phage infection. $2\times10^8$ CFU/ml WT *Kp* and *Kp* (*mcr-1*) were mixed with ΦNJS1at MOI=$10^{-4}$ and incubated at 37°C. Viable bacteria were then counted by serial dilution and plating on LB agar. The mean of three independent assays is shown and error bars represent the standard deviation.

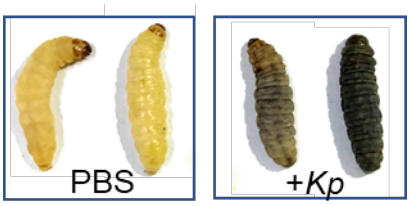


**Fig. S4.** *G. mellonella* responses to *Kp* infection. Larvae were injected with 10 μl of *Kp* cells ($10^6$ CFU) or PBS in parallel. Infected larva became pigmented progressively darker over the course of the infection. Photography was taken after 24 hrs of infection.