Figure S1. Rectangular phylogenetic tree based on proteomic analysis generated by VIPTree.

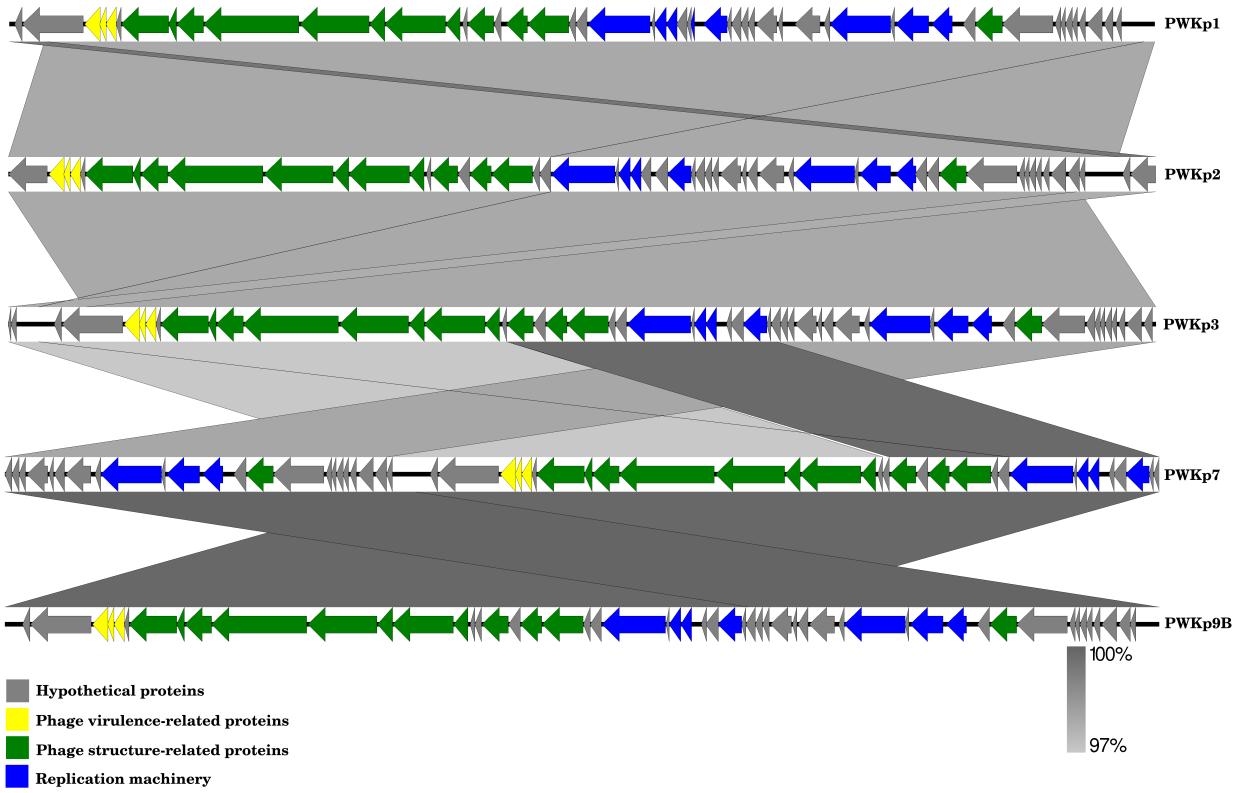

Figure S2. Genetic structure and collinear analysis of viruses belonged to *Autographiviridae* family. Arrows, transcription direction of genes and ORFs. Genes were grouped according to their predictive functions, indicated by colour.

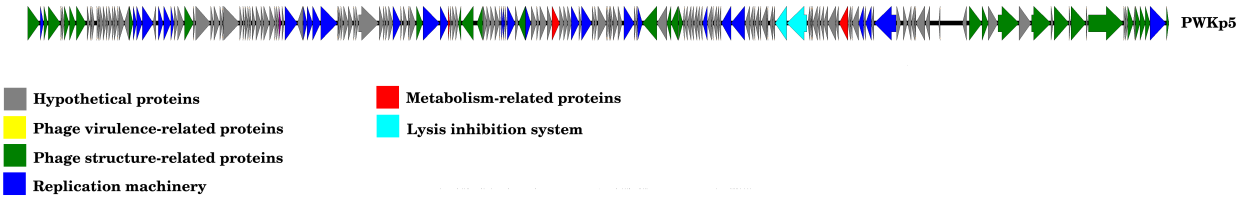

Figure S3. Genetic structure of PWKp5, a virus belonging to *Ackermannviridae* family. Arrows, transcription direction of genes and ORFs. Genes were grouped according to their predictive functions, indicated by colour.

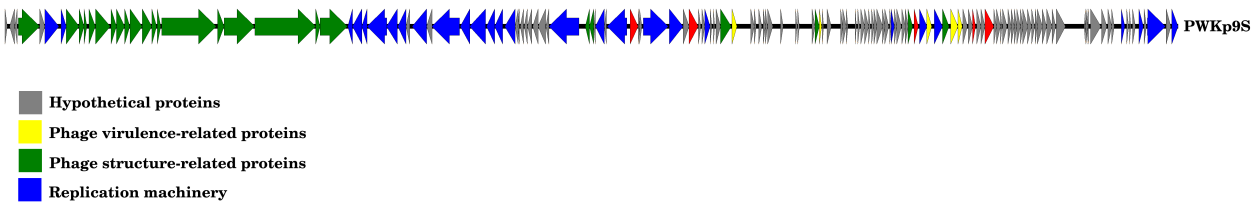

Figure S4. Genetic structure of PWKp9S, a virus belonging to *Demerecviridae* family. Arrows, transcription direction of genes and ORFs. Genes were grouped according to their predictive functions, indicated by colour.

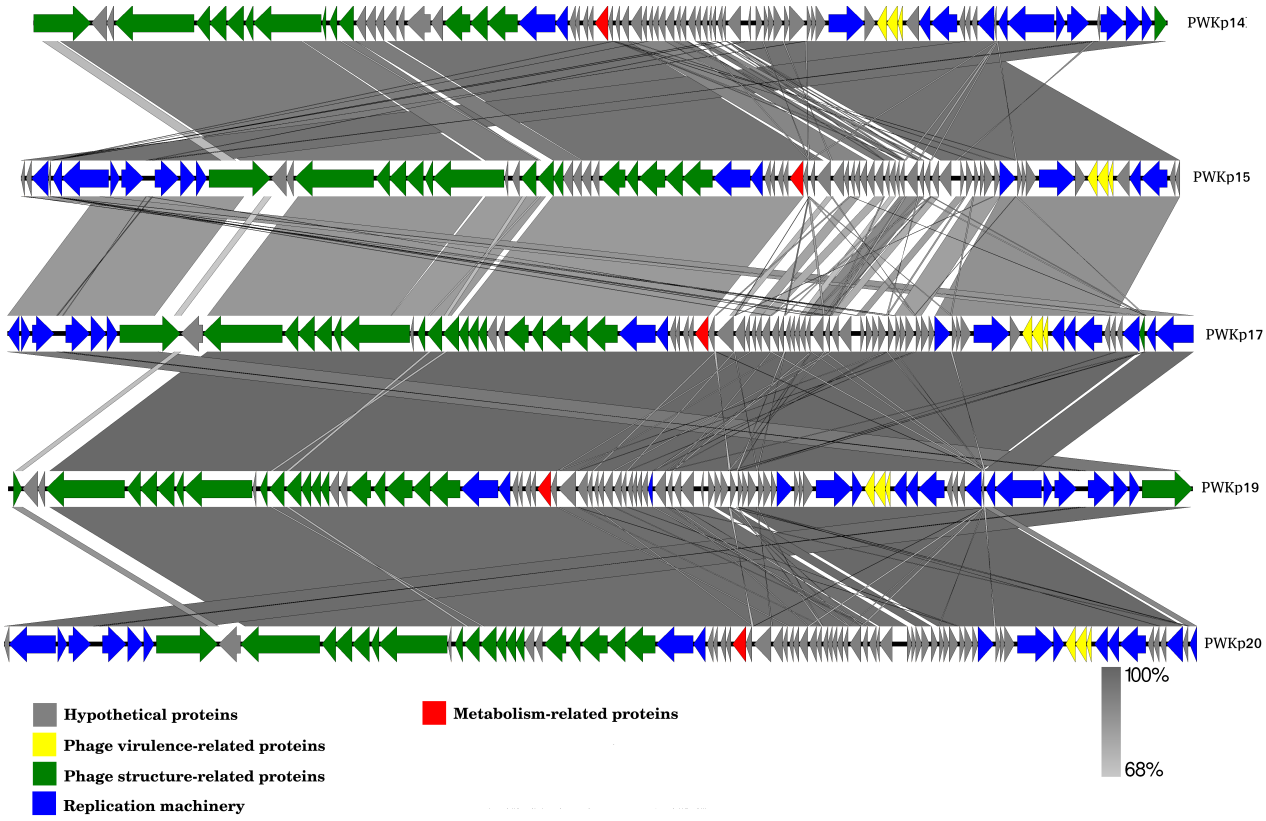

Figure S5. Genetic structure and collinear analysis of viruses belonged to *Drexlerviridae* family. Arrows, transcription direction of genes and ORFs. Genes were grouped according to their predictive functions, indicated by colour.

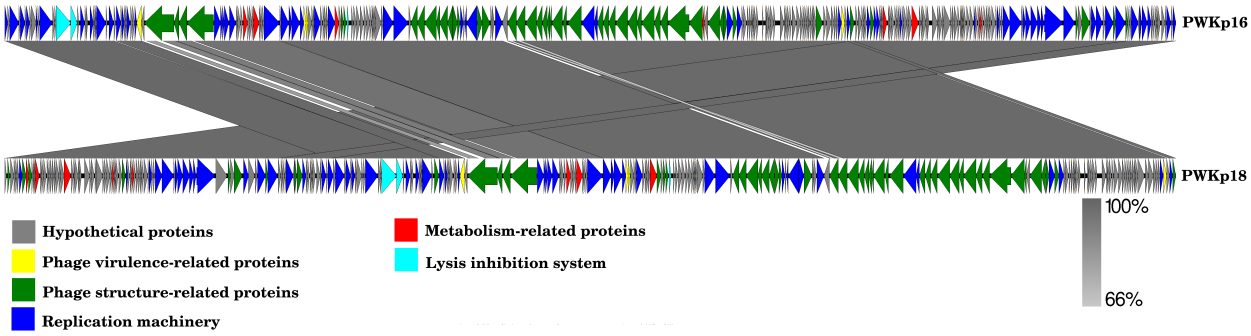

Figure S6. Genetic structure and collinear analysis of viruses belonged to *Myoviridae* family. Arrows, transcription direction of genes and ORFs. Genes were grouped according to their predictive functions, indicated by colour.

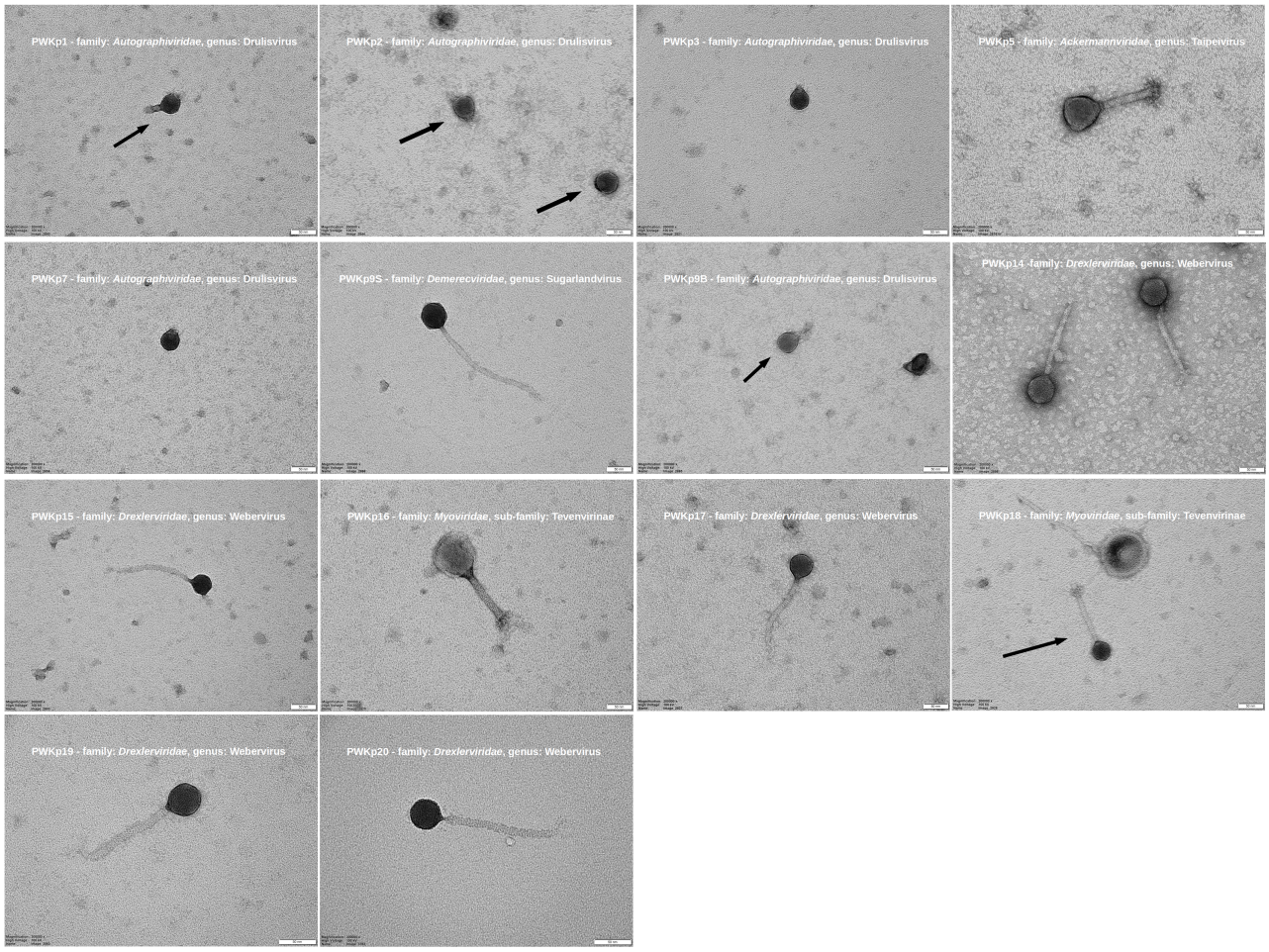

Figure S7. Electron microscope pictures from the bacteriophages isolated and characterised in this study. Black arrows indicate the location of some phages.

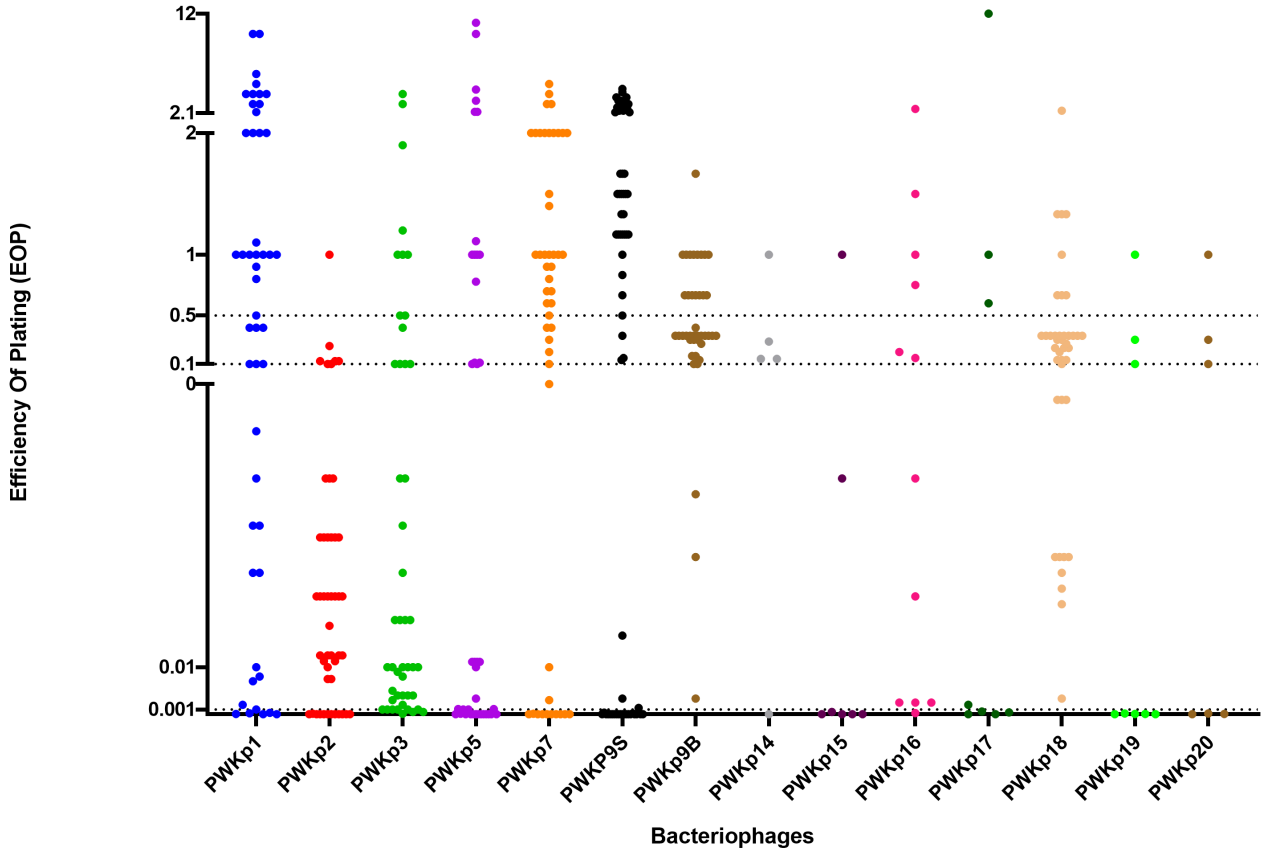

Figure S8. Distribution of Efficiency of Plating (EOP) values obtained for the fourteen phages against their respective susceptible *K. pneumoniae* ST16 isolates. Each EOP value was estimated by the ratio between the number of plaques obtained in each tested *K. pneumoniae* isolate relative to the original host. For interpretative purposes, EOP≥0.5 indicated high productive infection, 0.1≤EOP<0.5 indicated moderate productive infection, 0.001<EOP<0.1 indicated low productive infection, and EOP≤0.001 inefficient infection[60].

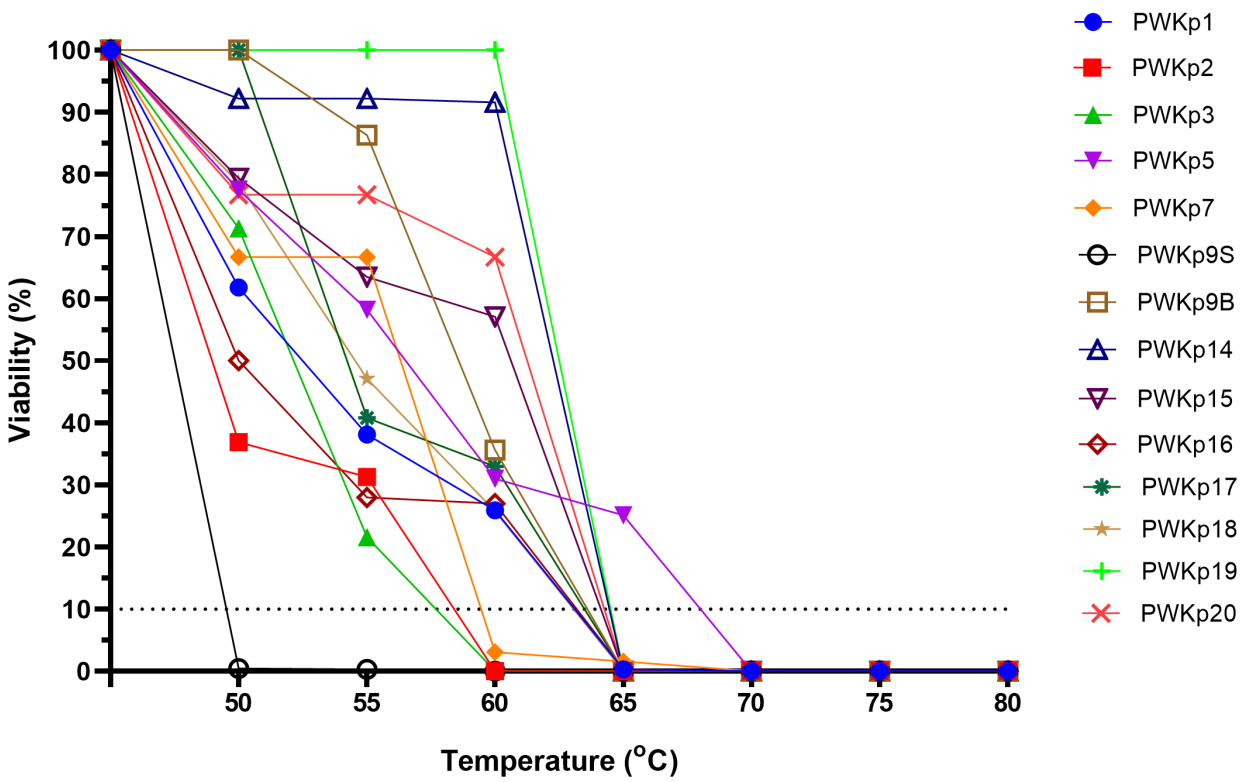

Figure S9. Temperature susceptibility of *Klebsiella* phages over one-hour incubation at different temperatures. The plotted values represent a median of three independent experiments. We stipulated 10% viability as a critical point as this would mean an one logarithm (1 log) reduction in the bacteriophage concentration.

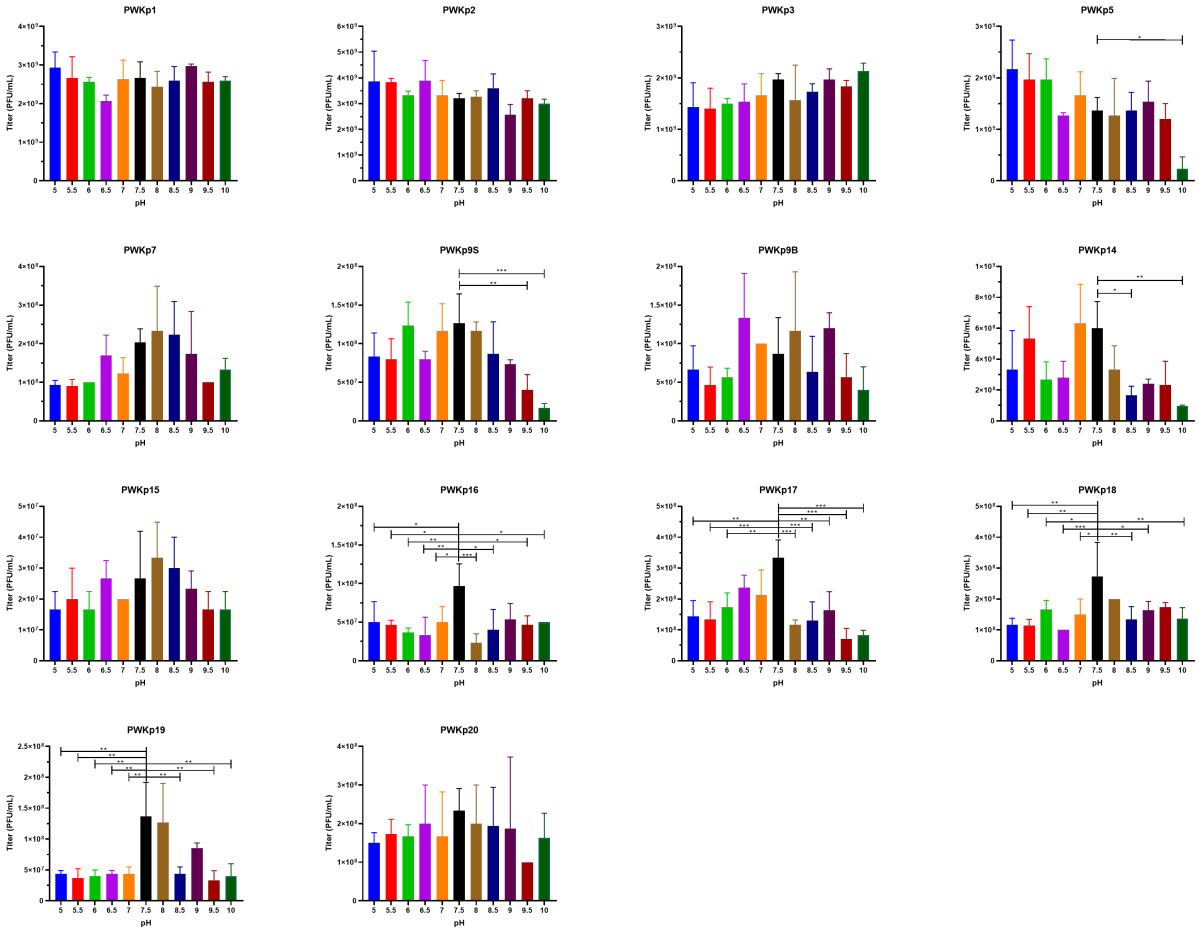

Figure S10. Bar charts demonstrating the pH susceptibility of the studied *Klebsiella* phages over one-hour incubation at different SM Buffer pHs. Error bars represent the SD (n=3). One-way ANOVA tests were used to evaluated possibles statistical difference among the different tested pHs followed by Dunnett's multiple comparisons tests.* indicates 0.01< *p* value <0.05, ** indicates 0.001< *p* value < 0.01, *** indicates 0.0001< *p* value < 0.001.

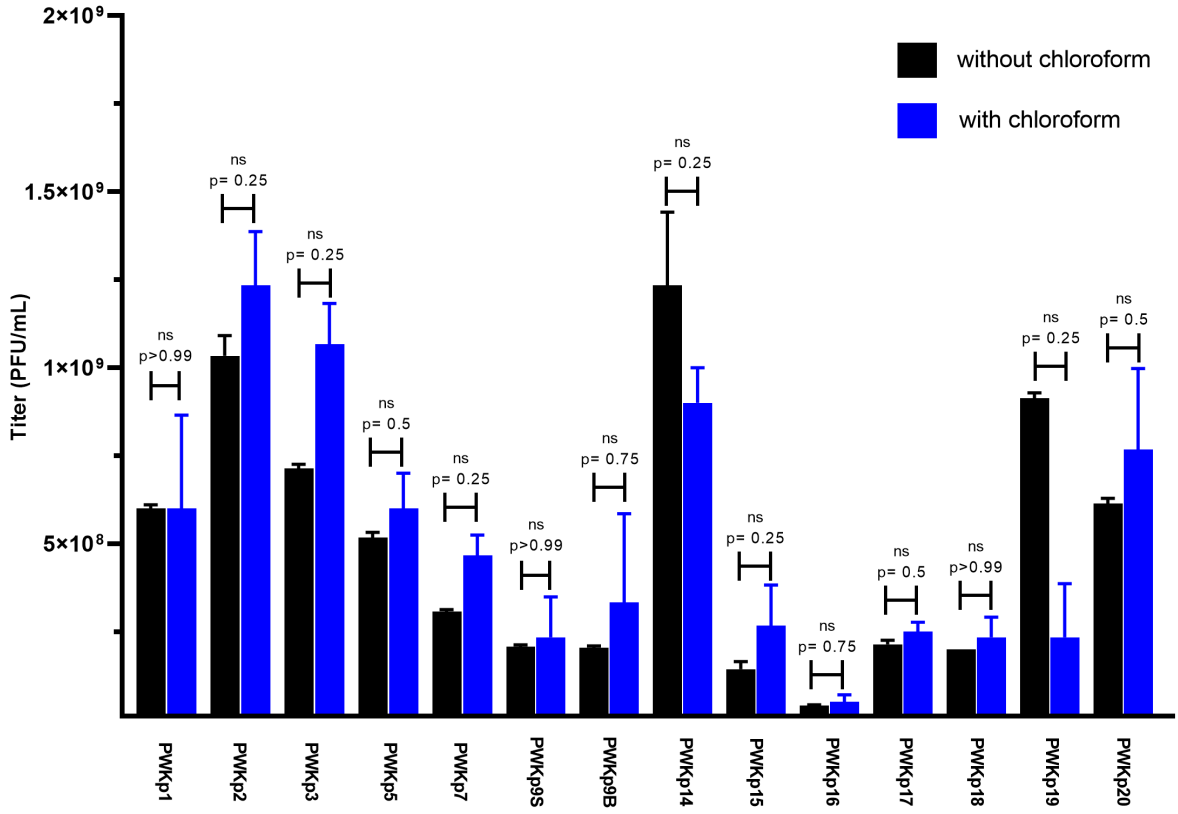

Figure S11. Bar charts demonstrating the chloroform susceptibility of the studied *Klebsiella* phages over one-hour incubation. Error bars represent the SD (n=3). Two-tailed t-test (Wilcoxon matched-pairs signed rank test) was used to evaluated possibles statistical difference between the presence/absence of chloroform. ns, not significant.

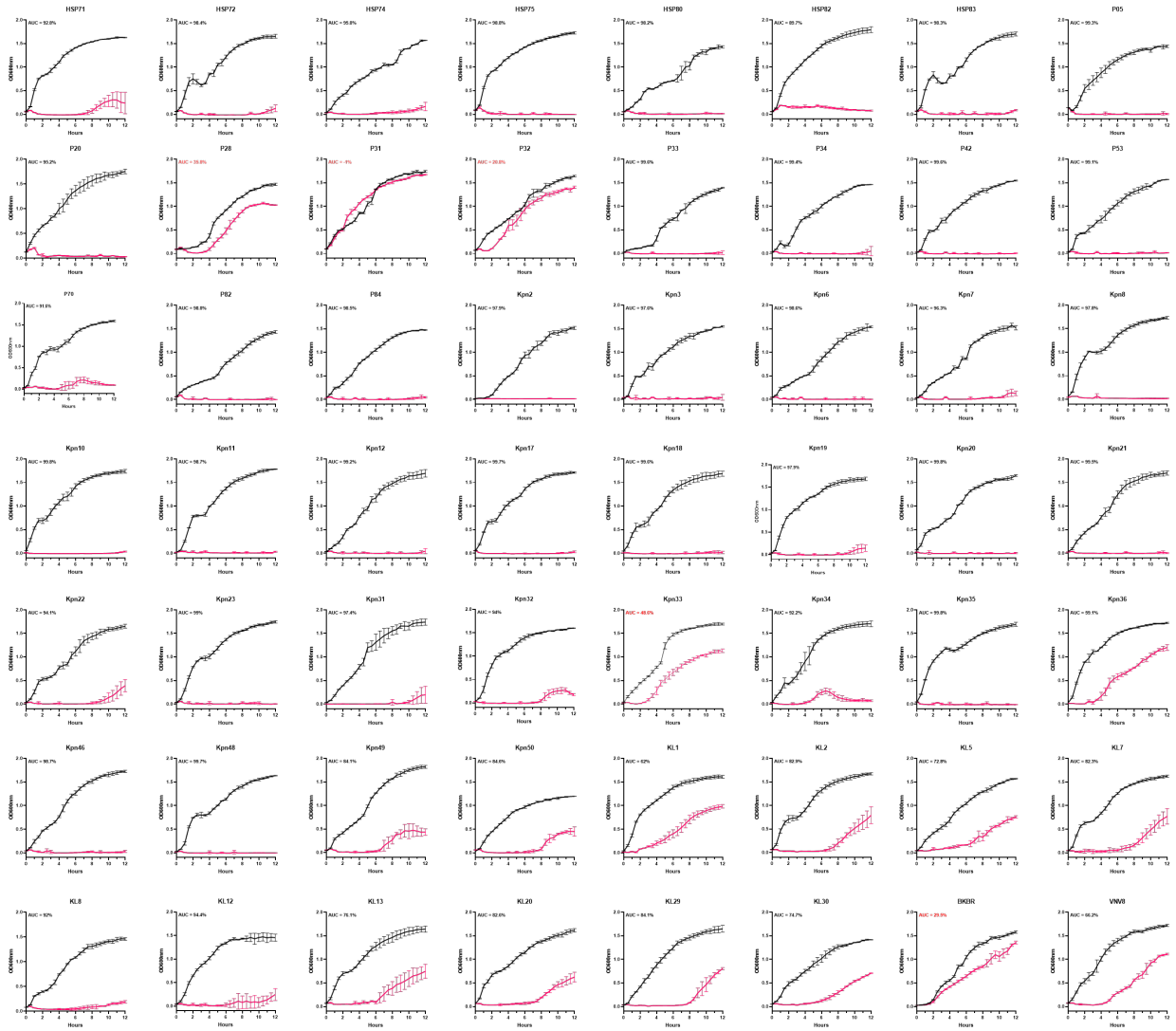

Figure S12. Broth inhibition assays performed in the presence of Katrice-16 against our *Klebsiella pneumoniae* ST16 collection (n=56). Black lines represent each bacteria's growth curve without bacteriophage and the pink lines in the presence of Katrice-16. We started the experiment using 10^7 CFU/mL of each bacterial isolate and 10^8 PFU/mL of our phage cocktail, resulting in a Multiplicity of Infection (MOI) = 10. The area under the curve was calculated using GraphPrism version 8.4.3.

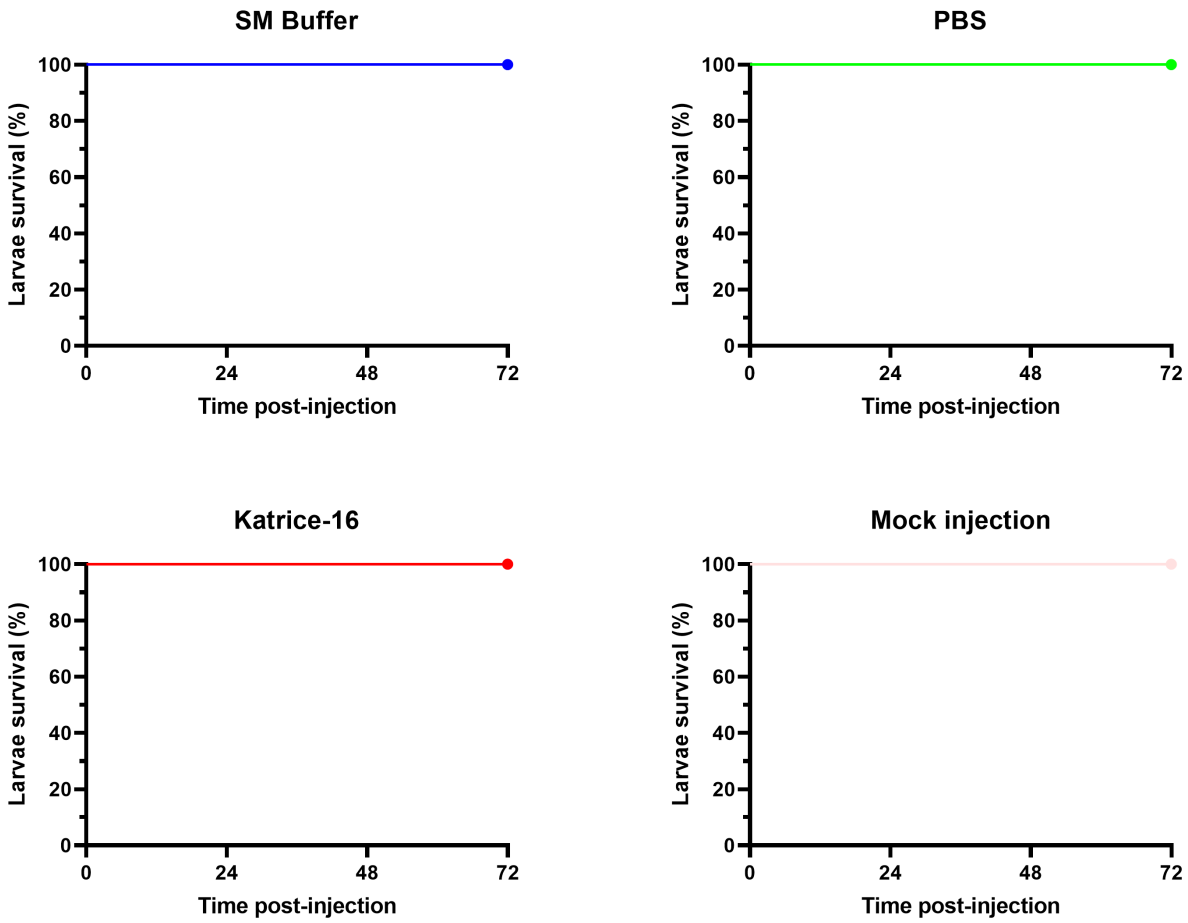

Figure S13. Survival curves of the controls used in the *Galleria mellonella* assays.