Supplemental Table S1: To determine diversity of the phages used in this study, we calculated average nucleotide identities (ANIs) with fastANI 1.31. The phages were sequenced with Oxford Nanopore or Oxford Nanopore and Illumina technologies. p0017 and pyo genomes were assembled from nanopore reads with canu 2.0 while p0045, p0017S, p002y, p003p, p0040, and p0006 genomes were assembled from Illumina and nanopore reads with Unicycler 0.4.8.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| p0045 |  |  |  |  |  |  |  |  |
| p0017S | 99.59 |  |  |  |  |  |  |  |
| p002y | 99.59 | 99.98 |  |  |  |  |  |  |
| p003p | 97.83 | 97.80 | 97.81 |  |  |  |  |  |
| p0040 | 99.47 | 99.85 | 99.72 | 97.75 |  |  |  |  |
| p0006 | NA | NA | NA | NA | NA |  |  |  |
| pyo (ONT) | NA | NA | NA | NA | NA | 98.88 |  |  |
| p0017 (ONT) | NA | NA | NA | NA | NA | NA | NA |  |
|  | p0045 | p0017S | p002y | p003p | p0040 | p0006 | pyo (ONT) | p0017 (ONT) |