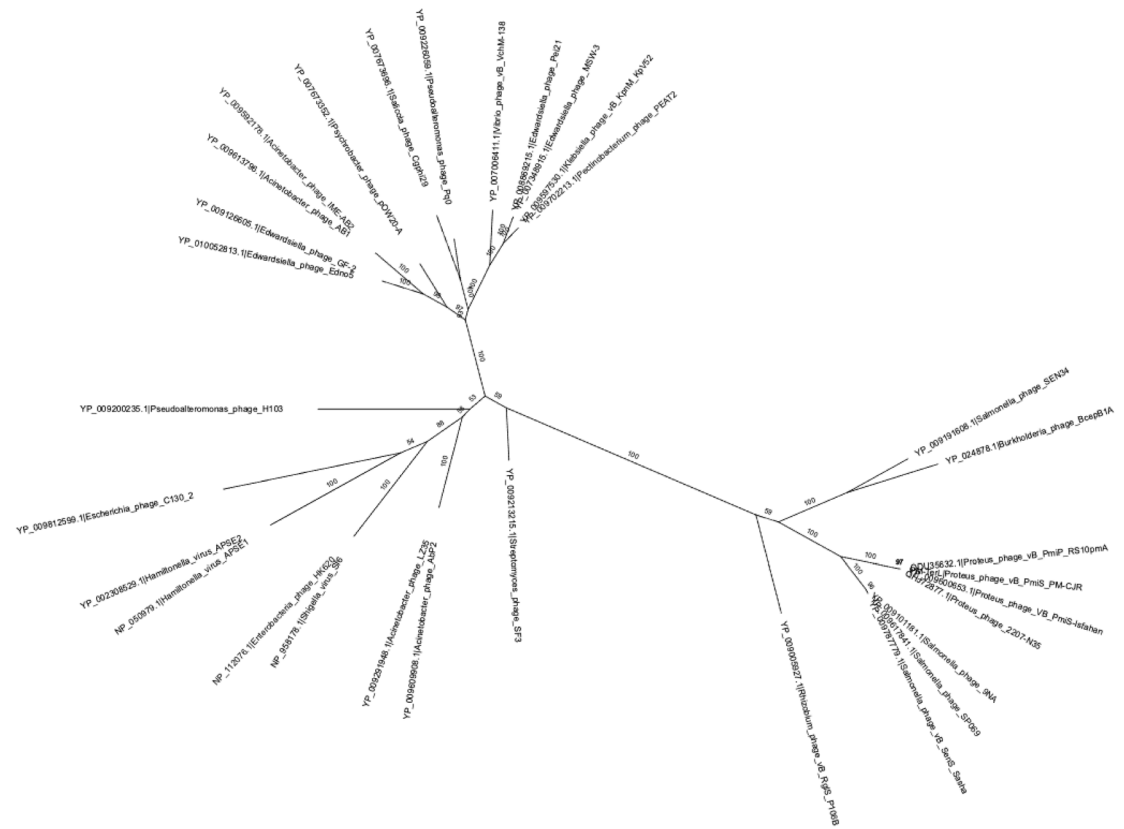


(a)



(b)

Figure S1. Phylogenetic trees based on amino acid sequences of conserved proteins of phage vB_PmiS_PM-CJR and related bacteriophages. (a) Phylogenetic analysis of terminase large subunits. (b) Phylogenetic analysis of major capsid proteins. Multiple sequence alignments were generated by MAFFT in L-INS-I mode and trimmed with TrimAl. Phylogenetic trees were reconstructed with IQ-TREE 2 and visualized with FigTree, with bootstrap support values reported over tree branches. As the analysis was used to understand phylogenetic relationships of phages rather than reconstruct their evolutionary history, no rooting was applied.

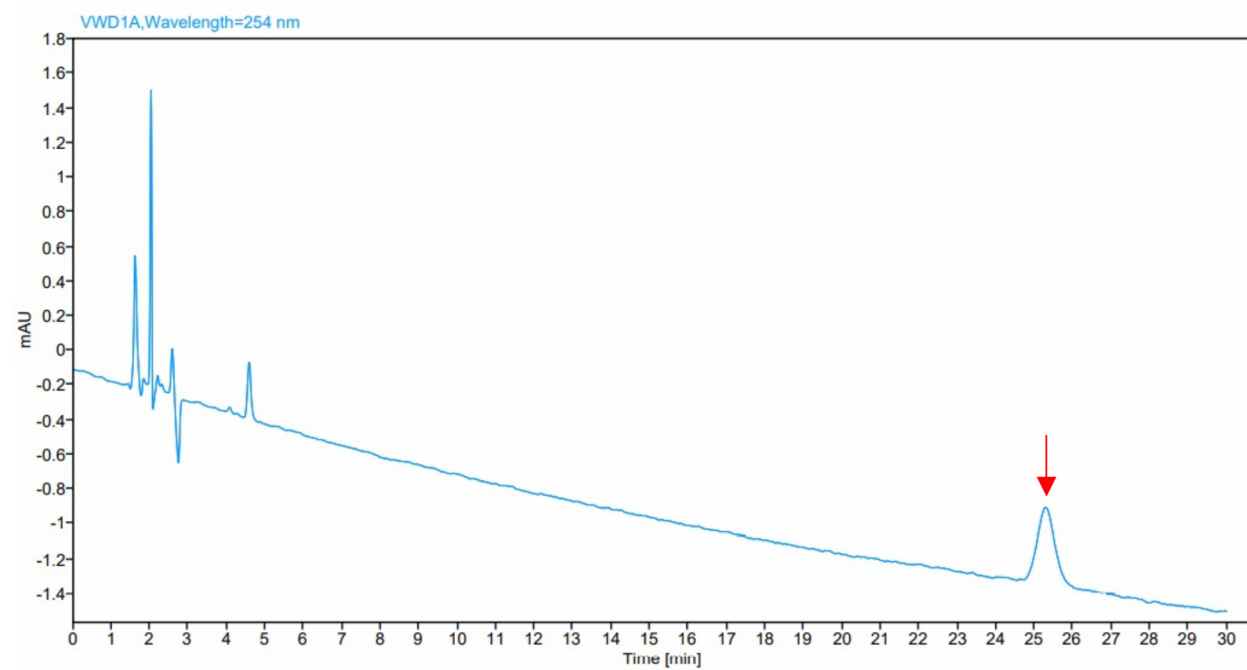


Figure S3. Purified tail spike purity analysis using reverse phase HPLC. A single peak (indicated with a red arrow) is visible at 25–26 min time mark.