

## Genomic and Proteomic Analysis of SixVi01-like Phages Reveals Wide Host Range and Multiple Tail Spike Proteins

**The following supplementary tables are supplied as excel files:**

**Supplementary Table S1.** 150 Vi01-like *Enterobacteriaceae Ackermannviridae*. The 150 phages utilized in this study organized by subcluster and genera, and are listed with a link to NCBI, their GenBank accession number, associated reference, and MCP family (if they share identical major capsid proteins (MCP)).

**Supplementary Table S2:** Use of Structural Homology and Operons to Identify Putative Functions of Vi01-like proteins. Tables are provided for phages FrontPhageNews and ChubbyThor of retrieved structural hits having greater than 60% confidence from Phyre2 analysis of hypothetical proteins. The HHPRED values greater than 50% confidence are given for the same proteins. In addition, predicted tables are provided for predicted operons for each phage.

**Supplementary Table S3:** Mass spectrometry of Sajous1 virions. Note the gp number conversion due to subsequent rearrangement of bp1 in this genome.

**Supplementary Table S4:** Strain information for *Salmonella*, *Shigella*, *Citrobacter* and *E. coli* clinical isolates utilized in this study. Strain information for clinical isolates utilized in this study. *Salmonella*, *Shigella* and *Citrobacter* clinical isolates were obtained from the CDC while *E. coli* isolates were obtained from Intermountain Healthcare.