S7 Figure: Clustering of Samy with PhiC31 and other actinophages

A. Local view of the proteomic tree of viruses grouping with Samy using VIPTree. This analysis was conducted via the VIPTree (1) web server, comparing Samy (red star) against all reference viral genomes of the GenomeNet/Virus-Host DB (2). Here, only the relevant region of the tree with the clusters of phages closest to Samy are displayed. Branch lengths (similarity scores, $S_G$) are log-scaled and indicated above dashed grey lines.

B. Viral clustering outputted by VirClust. The genome clustering of all genomes presented in the panel A was performed via the VirClust web server (3) and based on protein super clusters (PSCs). The resulting tree was split into viral genome clusters (VGCs) using a 0.9 intergenomic distance threshold. The heat map represents the PSC distribution in the viral genome.
genomes. The color scale indicates the number of copies per genome (from 0 to 2). The percentage of PSCs shared with other genomes are indicated in dark grey.

**References:**

