Figure S2: Phylogenetic tree for the primase of PAK_P1-like and KPP10-like bacteriophages and their closest relatives.
The maximum likelihood tree was built from a protein alignment for the primase common to 19 bacteriophages. The primase was not identified in the PVP-SE1 and GAP31 genomes. Bootstrap values are indicated on the tree. The tree was rooted on the midpoint root. The tree is based on the sequence of the primase, a nonstructural protein, and confirms the topology of the tree based on the three concatenated structural proteins.