

Materials to be published online as a supplement to

## **Diversity of active viral infections within the *Sphagnum* microbiome**

**Joshua M.A. Stough<sup>1\*</sup>, Max Kolton<sup>2</sup>, Joel E. Kostka<sup>2</sup>, David J. Weston<sup>3,4</sup>, Dale A. Pelletier<sup>3</sup>,  
and Steven W. Wilhelm<sup>1#</sup>**

Addresses:

<sup>1</sup> Department of Microbiology, University of Tennessee, Knoxville, Tennessee, United States of America 37996

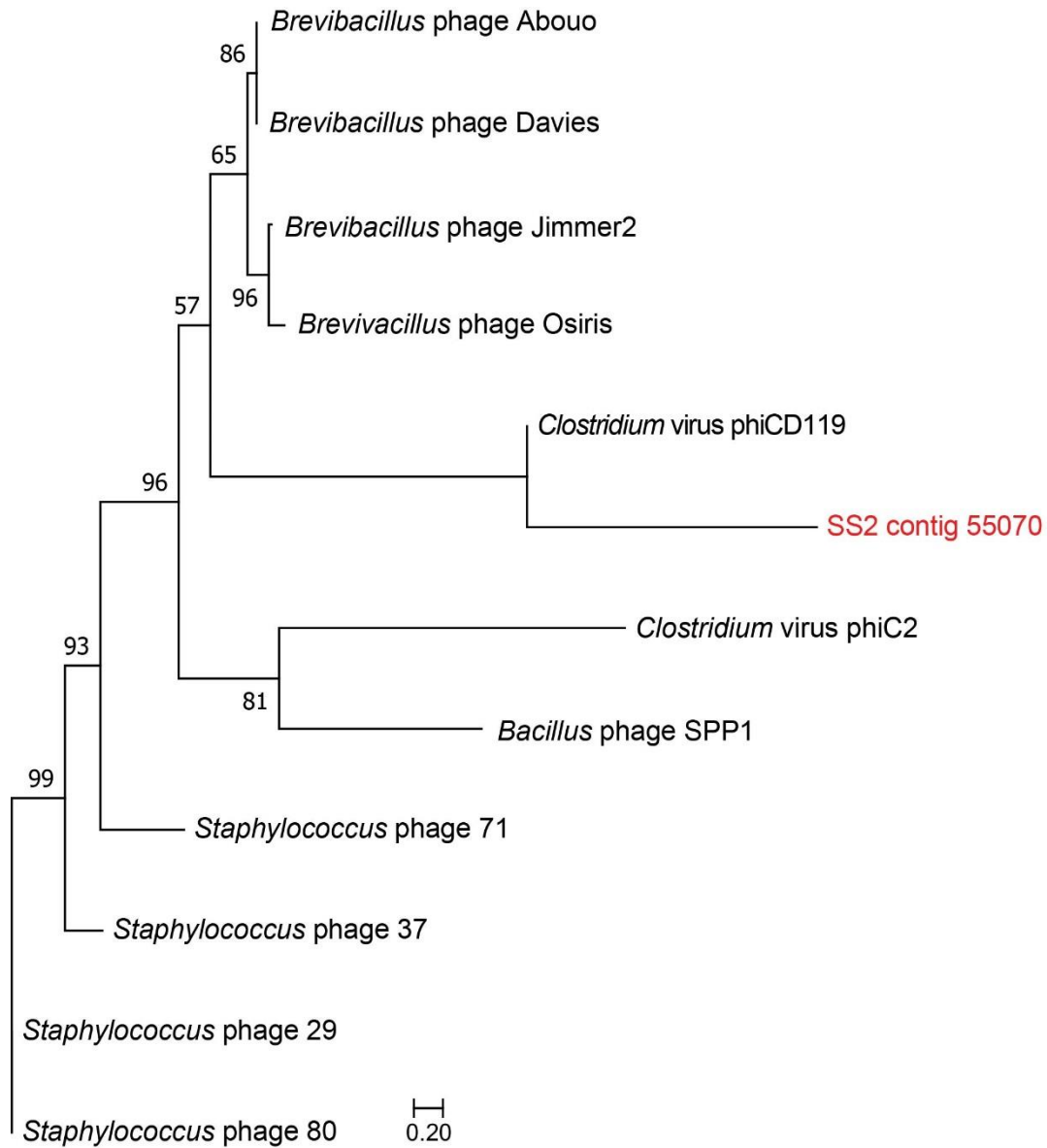
<sup>2</sup> School of Biology and School of Earth and Atmospheric Sciences, Georgia Institute of Technology, Atlanta, GA, USA

<sup>3</sup> Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, Tennessee, USA

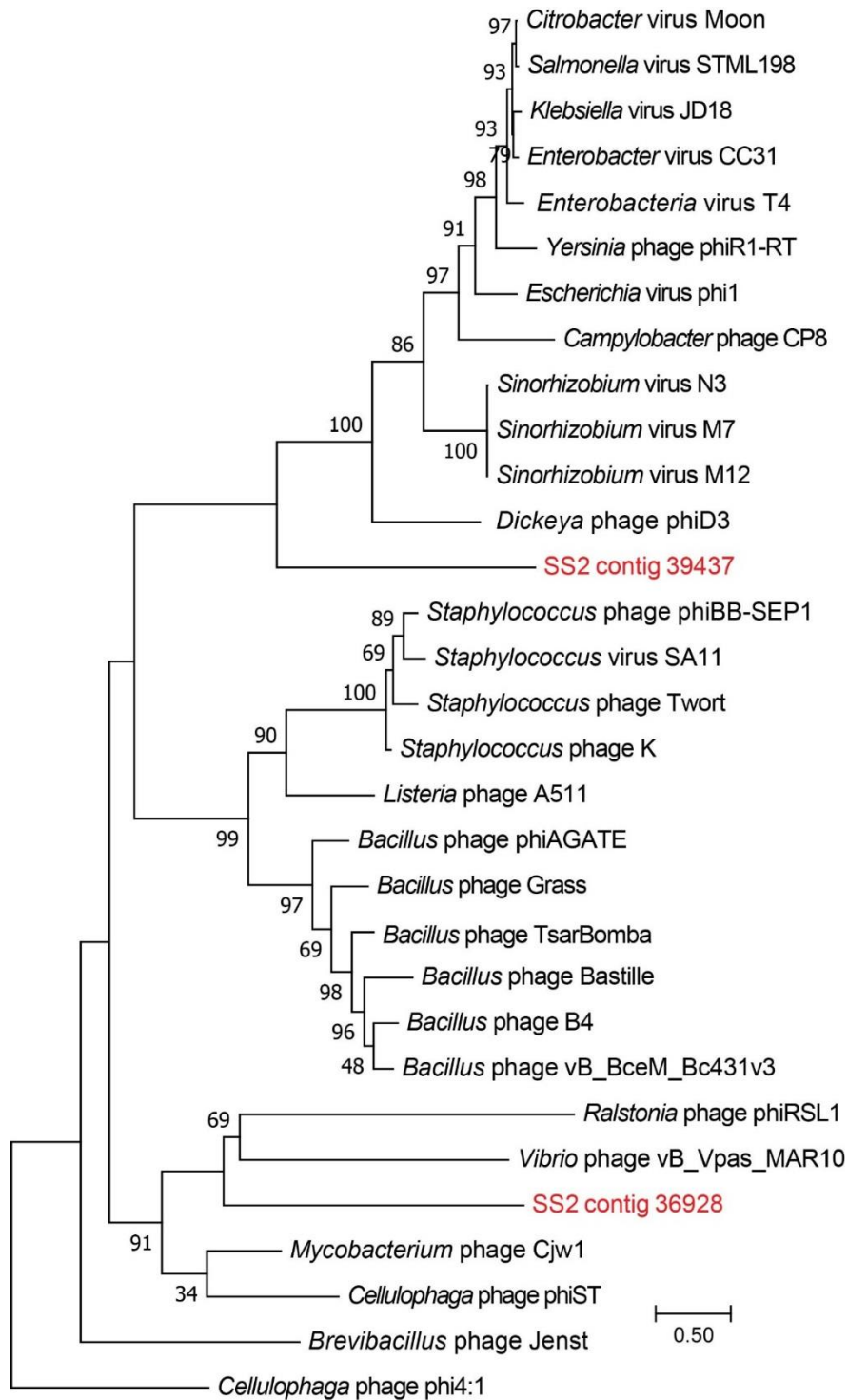
<sup>4</sup> Climate Change Science Institute, Oak Ridge National Laboratory, Oak Ridge, Tennessee, USA

#Address correspondence to Steven W. Wilhelm: [wilhelm@utk.edu](mailto:wilhelm@utk.edu)

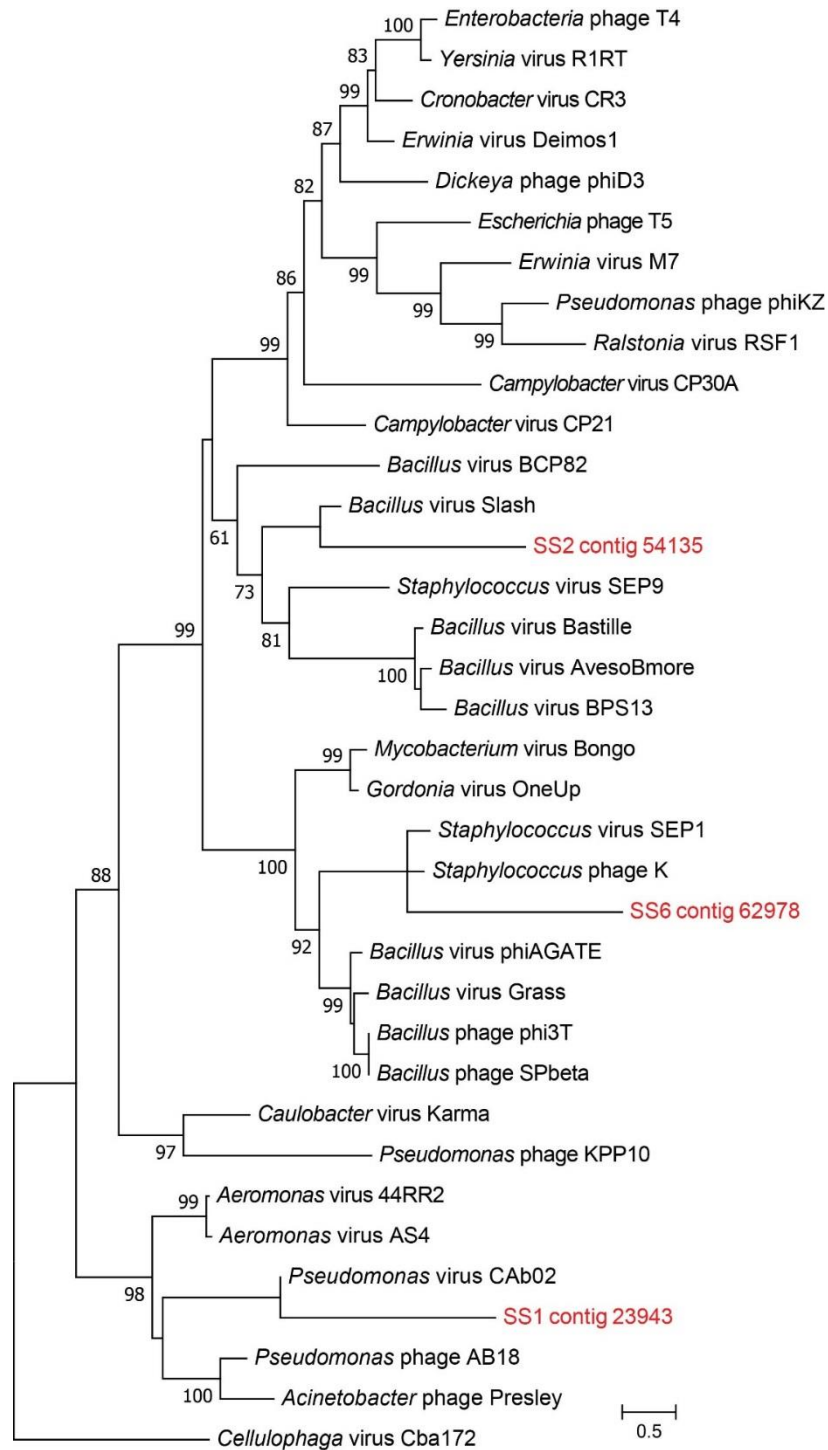
\*present address: Department of Microbiology & Immunology, University of Michigan, Ann Arbor 48109



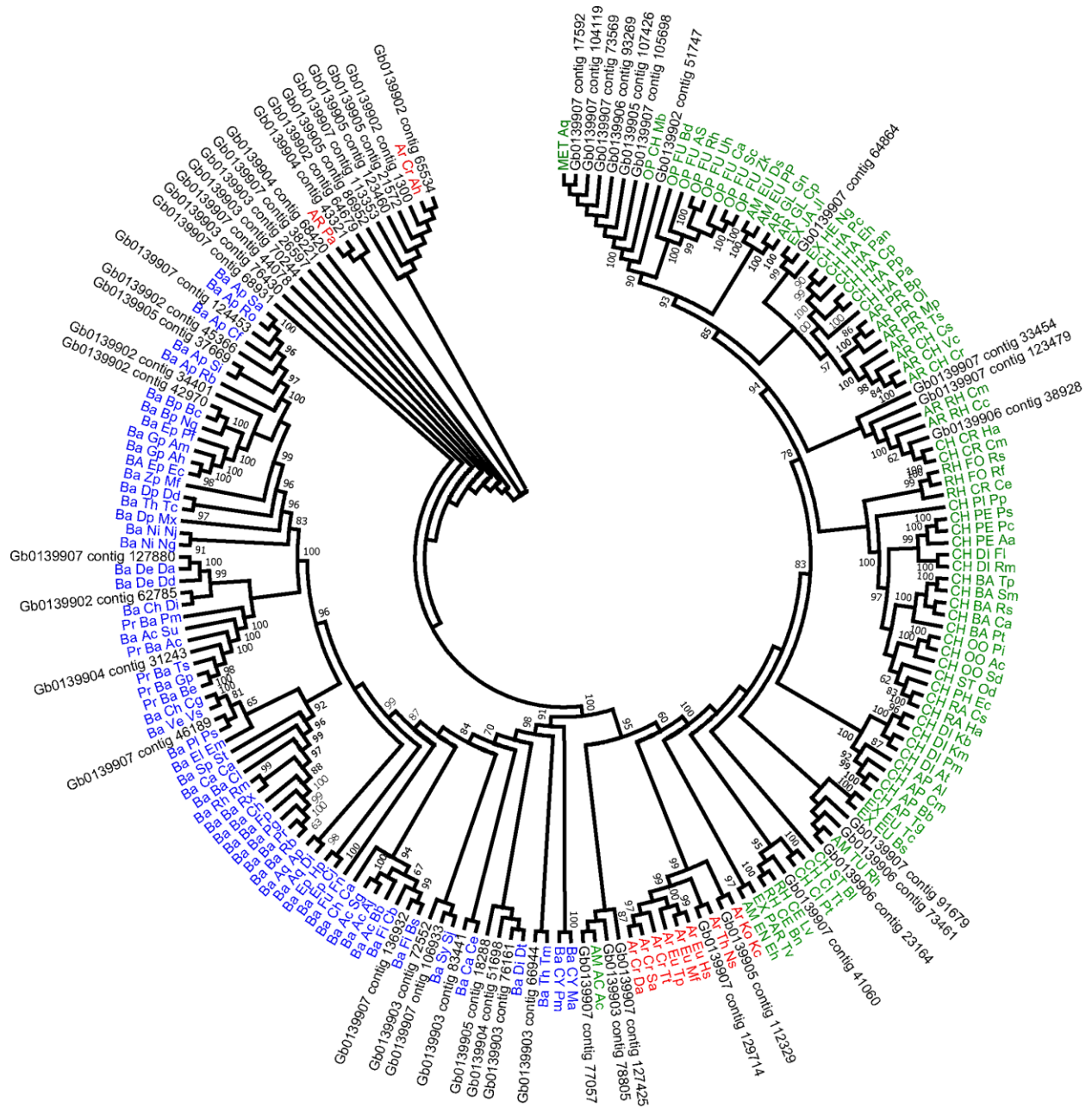
SFig 1: Phylogenetic placement of identified phage portal protein contigs (red) on a *gp20* maximum likelihood reference tree (references in black). Full alignment length 197 amino acids. Node support (aLRT-SH statistic) >50% are shown.



SFig 2: Phylogenetic placement of identified RecA contigs (red) on a maximum likelihood reference tree (references in black). Final alignment length 351 amino acids. Node support (aLRT-SH statistic) >50% are shown.



SFig 3: Phylogenetic placement of identified phage ribonucleotide reductase contigs (red) on a maximum likelihood reference tree (references in black). Final alignment length 318 amino acids. Node support (aLRT-SH statistic) >50% are shown.



SFig 4: Phylogenetic placement of identified Rpb1 contigs on a maximum likelihood reference tree (Eukaryotes – Green, Bacteria – Blue, Archaea – Red, Contigs – Black). Full alignment length 1726 bases. Node support (aLRT-SH statistic) > 50% are shown.