Dear SEA-PHAGES SMART QC Team,

The students in the Spring 2017 SEA-PHAGES bioinformatics class at the University of Maine at Farmington have finished their review and annotation of phage Miley16. We feel fairly confident in our final review of the genome but greatly appreciate your time and efforts to quality check the annotation.

We would like you to evaluate the start sites for gene positions 21465-21587, 43082-43258, 46324-46316, and 72841-73020.

In addition, gene position 21465-21587 was removed because of 1) not being called by GeneMark, 2) a lack of BLASTP hits on NCBI, and 3) similar phages (Breezona and Winky) do not have this gene. This likely warrants further consideration, however, before being completely removed.

There are large gaps without genes in positions 36246-36611 and 42319-42450, but Phamerator indicates that they are conserved across closely related genomes, so we are relatively confident in their calls.

Lastly, there was a translational frameshift we corrected in gene 9991-10814. Please review this, as we are not completely confident in our ability to identify the exact frameshift location.

Thank you again for your efforts in ensuring a properly annotated Miley16 genome.

Sincerely,

Dr. Timothy S. Breton and the Miley16 team (Liesel Krout, Mia Comis, Madison Davick, Kaleb Fletcher, Carlos Berdeja, Eli Michaud, Bailey Shevenell, Chelsey Frank, and Jacob Montgomery)