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 Michley. We feel fairly confident in our final review of the genome but greatly appreciate your time and efforts to quality check the annotation.

Please check for a gene at position 39360. We originally added a gene at this location due to a large gap and some coding potential, but in the end removed it due to a lack of BLAST results, high overlap with the preceding gene, and no matches to other phages.

The gene at stop position 40010 should also be checked, as it was not called by GeneMark and had no significant BLAST hits. A gene at stop position 40261 also had no significant BLAST hits.

There are four genes in a row (stops at 13267, 13629, 14024, 14474) that showed some significant similarity to portal protein, but it seemed unusual to have so many of the same function in this manner.

Please check the function of the gene at stop position 32396. Should this be listed just as DNA polymerase?

Please check the gene at stop position 40419. It was not called by GeneMark and does not have many BLAST hits.

Lastly, we had difficulty identifying the start position for the gene at stop position 47759. There seemed to be a small, equal amount of support for multiple start locations.

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

Sincerely,

Dr. Timothy S. Breton and the Michley team (Chelsey Frank, Eli Michaud, Bailey Shevenell, Sarah Stanley, and Jacob Montgomery)