Lehigh University would like Mycobacteriophage Tyke’s genome investigated further for the following features. We would like the QC team to evaluate features 129 and 130 to ensure that these were called correctly. These features are a tail assembly chaperone caused by a translational frame shift.

We have investigated all gaps and they are valid based on Phamerator homology to comparable C1 phages. Tyke contains 232 ORF, 32 tRNAs, and 1tmRNA (feature 182).