September 1, 2016

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Dear Annotation Quality Control Team,

We are submitting a completed annotation for the phage Findley. It belongs to Subcluster K2, has a genome length of 58,150 bp, and is Siphoviridae morphotype. This phage was sequenced in Pittsburgh Bacteriophage Institute. Upon completion of annotation, we documented 94 genes.

We used the Function Assignments (2015-16 SEA PHAGES) pdf to finalize gene names. However, the following genes did not have an exact name fit and thus may require additional attention: genes 31, 36, 40, 47, 53, 55, 60, 72, 77, and 82.

 Thank you for your time and consideration of our completed annotation of Findley. Please feel free to contact Peter Park (peter.park@nyack.edu) regarding any comments or concerns.

 Sincerely,

 Peter J. Park, PhD