Genome Annotation Submission Cover Sheet

Preliminary Annotation Review Checklist 5-15-2018

Phage Name:	Rutherferd
Your Name:	Zachary Stone
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Please check each box indicating completion of each task. If you are not sure how to do something, please see the Online Bioinformatics manual page "How to Pass Preliminary Review".

- ☑ 1. Does the genome sequence in your final contain the same number of bases and is it the same as the posted sequence on phagesdb.org?
- ☑ 2. Are all the genes "valid" when you click the "validate" button?
- ☑ 3. Have the genes been renumbered such that they go sequentially from 1 to the highest number?
- ☑ 4. Have all old BLAST hits been cleared, and all gene features reBLASTed?
- ☑ 5. Are the locus tags the"SEA_ PHAGENAME"?
- ☑ 6. Has the Documentation been recreated to match the information in the feature table?
- ☑ 7. Have tRNA ends been adjusted with web-based Aragorn and/or tRNAscan SE?
- ☑ 8. Has the frameshift in the tail assembly chaperone been annotated (where applicable?)

9. For the items below, generate a genome profile, and review the following. For the

YourPhageName_CompleteNotes.dnam5 file:

- ☑ a. Have any duplicate genes (or any with the same stop coordinate?) been removed?
- ☑ b. Does every gene have **one and only one** complete set of Notes
- ☑ c. Do the functions in the Notes match the official function list?
- ☑ d. Are all three lines of functional evidence described for EVERY gene?
- ☑ e. Do the notes contain the initial Glimmer/GeneMark data from the autoannotation?

For the YourPhageName .dnam5 file:

- ☑ a. Have any duplicate genes (or any with the same stop coordinate?) been removed?
- ☑ b. Is the Notes field empty (including hidden marks?)
- ☑ c. Do the function names in the Product field either match the official function list or say "Hypothetical Protein"?
- ☑ d. Is the Function field empty (including hidden marks?)

☑ 10. Did you use PECAAN to annotate your phage?

If, so please describe how in the text field after question 11.

11. Describe any issues or specific genes that you were unable to satisfactorily resolve, and warrant further inspection in the Quality Control review.

1) There is a 340 bp gap between genes 55 and 56 that has no favorable RBS scores
2) Gap (352 bps) between genes 59 and 60 as a result of changes made to original gene 58 call. There is a conserved Methylase domain within this frame, but no favorable RBS scores.
3) Gap (141 bps) between genes 62 and 63 has favorable RBS scores with a poor potential gene length. Coding potential called by GeneMark but not enough to call a gene.
4) Gap (261 bps) between 75 and 76 is 94% identical to a known gene in a closely related phage (Bigfoot) with no favorable RBS scores or any other evidence.
5) Gap (266 bps) between genes 84 and 85 has poor RBS scores and no call by glimmer. GeneMark shows coding potential.
6) Gap (131 bps) between genes 87 and 88 is 100% identical to a closely related phage (Trouble) with no favorable RBS scores or coding potential.
7) change made to gene 58: original length of 1578 bps which overlaps with gene 59 in a different frame. Gene 58 became a ~500 bp gene (58) and a ~500 bp gene (60) with a large gap as well. genes 58, 59 and 60 each have