Genome Annotation Submission Cover Sheet

Pre-QC Phage Genome Annotation Checklist

Phage Name:	SnapTap
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Please check each box indicating completion of each task. Annotation Guide section #'s indicated

- [x] 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?
- [x] 2. Are all the genes "valid" when you click the "validate" button? *Section 9.3.2*
- [x] 3. Have the genes been renumbered such that they go sequentially from 1 to the highest number? *Section 9.3.3*
- [x] 4. Have all old BLAST hits been cleared, and all gene features reBLASTed? *Section 9.3.4*
- [x] 5. Are the locus tags the phage name? *Section 9.3.3*
- [x] 6. Has the Documentation been recreated to match the information in the feature table? *Section 1.4*
- [x] 7. Have tRNA ends been adjusted with web-based Aragorn and/or tRNAscan SE? *Section 9.5.3-4*

8. For the items below, generate a genome profile, and review the following. *Section 11.3*

   For the YourPhageName_CompleteNotes.dnam5 file:

   - [x] a. Have any duplicate genes (or any with the same stop coordinate?) been removed?
   - [x] b. Does every gene have **one and only one** complete set of Notes (see fig 12.2 in the Annotation Guide)?
   - [x] c. Do the functions in the Notes match the official function list?
   - [x] d. Is the function field EMPTY for all features?
   - [x] e. Do the notes contain the initial Glimmer/GeneMark data from the autoannotation?

   For the YourPhageName .dnam5 file:

   - [x] a. Have any duplicate genes (or any with the same stop coordinate?) been removed?
   - [x] b. Is the Notes field empty for all the features with no known function?
   - [x] c. Do the function names in the Notes match the official function list, when applicable?
   - [x] d. Is the function field EMPTY for all features?

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