Genome Annotation Submission Cover Sheet

Pre-QC Phage Genome Annotation Checklist

Phage Name:

Your Name:

Your Institution:

Your email:

Additional emails: (For correspondence)

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

- 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? Section 9.3.2
- 3. Have the genes been renumbered such that they go sequentially from 1 to the highest number? Section 9.3.3
- 4. Have all old BLAST hits been cleared, and all gene features reBLASTed? Section 9.3.4
- 5. Are the locus tags the phage name? Section 9.3.3
- 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? 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:

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 (see fig 12.2 in the Annotation Guide)?

- c. Do the functions in the Notes match the official function list?
- d. Is the function field EMPTY for all features?
- 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 for all the features with no known function?
- c. Do the function names in the Notes match the official function list, when applicable?
- 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.