Genome Annotation Submission Cover Sheet

Pre-QC Phage Genome Annotation Checklist

Phage Name:	LouisV14
Your Name:	Nancy L. Jones
Your Institution:	La Salle University
Your email:	jones@lasalle.edu
Additional emails: (For correspondence)	timmerma@lasalle.edu

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.

LouisV14 Annotation Summary

The first 30 genes were straight forward with most of them being accepted as called. Four genes were extended slightly in order to give better Blast and SD scores.

Genes 31 to 39 were modified to include more of the genome. In this region there were 3 reverse genes; we adjusted the annotation to include more DNA while still leaving enough space for the RNA polymerase to attach to the strand. A -1 frameshift occurs at Gene 15.

The rest of the genome was not quite as straight forward. It seemed appropriate to add a gene between genes 48 and 49 (37782 – 38171). Gene 53 was deleted and gene 54 was significantly changed to cover the DNA from the deleted gene. Gene 59 (a reverse gene) was deleted and replaced with a forward gene (42118 – 42489). Other genes in this region were