Genome Annotation Submission Cover Sheet

Pre-QC Phage Genome Annotation Checklist

Phage Name:	PhrodoBaggins
Your Name:	Susan Gurney
Your Institution:	Drexel University
Your email:	smg366@drexel.edu
Additional emails: (For correspondence)	rrd62@drexel.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.

-The following genes have functions not listed on the official function list:
Gene 13 - Sap Domain Protein, Gene 19 - Queuine tRNA ribosyltransferase, Gene 62 - DNA Polymerase I, Gene 72 RNase E.
- In Phamerator Phage Vista has a Gene "84" which could be in PhrodoBaggins between genes 86 and 87, but there is no coding potential evident in this regions on the GeneMark Reports.
- There are very large gaps (over 350pb) between genes 9 and 10, 53-54 and 66-67, but there is no evidence that there should be genes added to these regions.
- There are gaps of over 100bp between genes 5-6, 7-8, 10-11, 11-12, 20-21, 26-27, 50-51, 65-66, 67-68, 92-93, 94-95, 97-98. There is no evidence that genes should be added, but we