Genome Annotation Submission Cover Sheet

Pre-QC Phage Genome Annotation Checklist

Phage Name:	Adgers
Your Name:	Chris Korey
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Additional emails: (For correspondence)	

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.

Adgers Genome Annotation Notes
Lead Annotators: Ariel McShane and Jared Rice

Genes That Were Deleted

1. Gene 97 of the original phamerator map numbering. Forward orientation in a region of reverse orientation. Has the same start site as another gene in the reverse orientation. Not enough room for a promoter between them. This is in a region that is dissimilar from Monty and Hotorobo.
2. Gene 105 of the original phamerator map numbering. Forward orientation and covers 104 and 106 in original phamerator map

Genes That Were Added

1. 53a (between genes 54 and 55 on the original phamerator map) - coding potential present and the gene was called in Monty and Hotorobo
2. 70a (between genes 71 and 72 on the original phamerator map) - coding potential present and the gene was called in Monty and Hotorobo
3. 101a (between genes 102 and 103) - coding potential present and the gene was called in Hotorobo

Empty Regions - No coding potential and no genes called in these regions in the two closely related phages Monty and Hotorobo. Numbers are referencing the final gene numbers in the dnam5 file

1. Between genes 54 and 55 (102 bp gap)
2. Between genes 60 and 61 (266 bp gap)
3. Between genes 64 and 65 (119 bp gap)
4. Between genes 65 and 66 (106 bp gap)
5. Between genes 80 and 81 (152 bp gap)
6. Between genes 81 and 82 (123 bp gap)