Actinobacteriophage Genome Annotation Submission Cover Sheet

This Cover Sheet will accompany each genome's annotation file(s) submission and succinctly describe the work that your students and you have done. This document ensures that the work done was as complete and thorough as it could be. Most important to the QC reviewer, denote where the trouble spots were in your annotation and how they were resolved.

Phage Name. HamCheese
Your Name. Stephanie Mathews
Your Institution. North Carolina State University
Your email. sklambet@ncsu.edu
Additional emails. (for correspondence).

Describe any issues or specific genes that you would like to highlight for the QC reviewer. This includes any genes that you had questions about or received help with or that warrant further inspection in the QC review process. Include those genes that you deliberated on and/or want to strongly advocate for. If you contacted SMART, workshop facilitator, or a buddy school for help, please document.

1. There was a gene added start 18605 because of coding potential but the other values for BLAST NCBI, BLAST phages DB, and HHPred are not strong. Z score was not strong but ok.
2. Gene 41 (start site 26,795) and the following genes 42 (start site 27,156) have a large overlap of 238 bp. The predicted function for both genes is DNA methylase (based on the Pham in phagesDB) Within AS3 subcluster some of the annotated phage show this overlap: Andrew, Leona, Juno. Others do not have this overlap: KHumprhy, RedFox, and Renna12. It appears the genes are in different coding frames. There is not a documented frameshift for this protein function, so it was not called.
3. There are also gaps at the end of the genome, but it reflects the lack of coding potential. (37411-37527, 37845-38089).

Please record yes/no for each of the questions below. If further explanation is needed, please add this item to the above box.

In the submitted DNA Master file (Yes/No):

Yes 1. Does the genome sequence in your submitted DNA Master file match the nucleotide fasta file posted on phagesDB (same number of bases, no N bases, etc.)?
Yes 2. Are all the genes 'Valid" when you click the Validation button? *(frameshift shows two ORFs with same 5' as they should be)*
Yes 3. Are the genes (and matching LocusTag numbers) sequential, starting with #1, counting by 1s.
Yes 4. Are the Locus Tags the "SEA_PHAGE NAME" format?
Yes 5. Has the documentation been recreated from the Feature Table to match the latest file version?
Yes 6. Have tRNAs followed the tRNA protocol, **COPYING** tRNA-AMINOACID type (DNA equivalent of the anti-codon) from Aragorn output - tRNA-Gln(ctg) - AND the ends been adjusted to match the Aragorn output? *(there are no tRNAs)*
Yes 7. Has the frameshift in the tail assembly chaperone been annotated correctly (if applicable)?
Yes 8. Have you cleared your Draft_Blast data and have you re-Blasted the submitted DNA Master file?
Yes 9. Has every gene been described and supported in your Supporting Data file?
Yes 10. Did you investigate 'gaps'?
Yes 11. Did you delete the genes that you meant to delete?

Now, make a profile of the file you plan to send. (And you can save this file for Review to Improve!)

Yes 1. Have any duplicate genes been deleted?

Yes 2. Has the Notes field been cleared (using the automated buttons)?
Yes 3. Do the gene numbers and locus tags match?
Yes 4. Are the correct Feature Types correctly selected (most will be ORFs, but check that tRNAs and tmRNAs are correctly labeled)?
Yes 5. Do the function names in the Product field either match the official function list or say "Hypothetical Protein"?
Yes 6. Has the Function field been cleared (using the automated buttons)?
xxf

How are you documenting your gene calls in class? Choose any/all that apply:

* PECAAN output
DNA Master shorthand (previously used format)

* Spreadsheet
Powerpoint
Word document (must be easily searchable)
Other: Describe.

What is the file type (sort) submitted for QC to document your gene calls? Choose only one.:
PECAAN output
DNA Master shorthand (previously used format)

* Spreadsheet
Powerpoint
Word document (must be easily searchable)
Other: Describe.