Jamemuya19

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

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 ? 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? YES
7. Has the frameshift in the tail assembly chaperone been annotated correctly (if applicable)? NOT APPLICABLE
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? YES
12. Have any duplicate genes been deleted? THERE WERE NO DUPLICATES.
13. Has the Notes field been cleared (using the automated buttons)? YES
14. Do the gene numbers and locus tags match? YES
15. Are the correct Feature\_Types correctly selected (most will be ORFs, but check that tRNAs and tmRNAs are correctly labeled)? YES
16. Do the function names in the Product field either match the official function list or say “Hypothetical Protein”? YES
17. Has the Function field been cleared (using the automated buttons)? YES

How are you documenting your gene calls in class?

* Spreadsheet

What is the file type (sort) submitted for QC to document your gene calls?

* Spreadsheet