Genome Annotation Submission Cover Sheet

Pre-QC Phage Genome Annotation Checklist

Phage Name:	Porcelain
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Please check each box indicating completion of each task. Annotation Guide section #'s indicated

- ☑ 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?
- ☑ 2. Are all the genes "valid" when you click the "validate" button? *Section 9.3.2*
- ☑ 3. Have the genes been renumbered such that they go sequentially from 1 to the highest number? *Section 9.3.3*
- ☑ 4. Have all old BLAST hits been cleared, and all gene features reBLASTed? *Section 9.3.4*
- ☑ 5. Are the locus tags the phage name? *Section 9.3.3*
- ☑ 6. Has the Documentation been recreated to match the information in the feature table? *Section 1.4*
- ☑ 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:

- ☑ a. Have any duplicate genes (or any with the same stop coordinate?) been removed?
- ☑ b. Does every gene have **one and only one** complete set of Notes (see fig 12.2 in the Annotation Guide)?
- ☑ c. Do the functions in the Notes match the official function list?
- ☑ d. Is the function field EMPTY for all features?
- ☑ e. Do the notes contain the initial Glimmer/GeneMark data from the autoannotation?

For the YourPhageName .dnam5 file:

- ☑ a. Have any duplicate genes (or any with the same stop coordinate?) been removed?
- ☑ b. Is the Notes field empty for all the features with no known function?
- ☑ c. Do the function names in the Notes match the official function list, when applicable?
- ☑ 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.

For the gene at 30058 – 32904, there were a couple of possible functions listed. We decided to use D-ala-D carboxypeptidase, but B-lactamase was also another option.
Please note we reorganized some genes between 63500 and 65300. Three autoannotated genes were deleted and new genes were inserted. The deleted genes were auto-annotated in the reverse direction amid a section of genes in the forward direction. Both forward and reverse genes had coding potential, but we made the decision to call the forward genes as they were more in line with other phages, and had functions.
Gene at 68233 – 68331 is very small (99bp) and we were uncertain whether or not to keep it as a gene. It has very little coding potential, but is called by Omega and MiaZeal.
Gene at 70978 – 71046 is very small (69 bp), so it may not be a gene; however, Courthouse