**Phage Gorgeous Cover Sheet (updated 9/4/15)**

The DNA Master Complete Notes section was updated on 9/4/15 to include COVE scores for all annotated tRNA genes. The SD scores were reported inaccurately with initial Complete Notes file. This aspect has now been corrected. The Complete Notes file was also updated to include more accurate predictions of gene coding potential according to GeneMark Smeg. The reverse genes are in a different reading frame in DNA Master then reported by the GeneMark Smeg output. When this aspect was taken into consideration, many of the reverse genes did have coding potential according to GeneMark Smeg.

Finally, gp22 was reannotated as being the Terminase gene. This is due to the fact that the gp22 gene product gave hits with good E values to phage annotated terminase genes. This piece of information has been included in the Gorgeous Final DNA Master File.

**Feature 2** (prior to renumbering) was deleted because it was a reverse gene that completely overlapped (and was surrounded by) forward genes. Additionally, there were no Blast, BlastP or HHpred results for that gene.

**Feature 2** (after renumbering -- originally gene 3) shows a potential start site change. Both Glimmer and GeneMark listed the start site at 620. However, a start site at 590 yields the largest ORF and shortens the gap between the previous gene, but has a worse SD score. Blast results showed similarly distant alignments at both start sites.

**Feature 13, 14, 15, 16, 57, 58 (all tRNAs)** 5’ end were changed to match Aragorn’s listing. Also, many of the 5’ ends on these features varied among ARAGorn, LoweLab, and DNAMaster.

**Feature 51** start site was changed from 33936 to 33939 because it gives a longer ORF and a better alignment. Also, GeneMark listed the start site at 33939, while Glimmer called the site at 33936.

**Feature 68** showed different start sites according to Glimmer and GeneMark, however the results weren’t convincing enough to make the change.

**Feature 71 and 87** (prior to renumbering) was deleted.

Also, **gp19** has potential as a tail fiber protein with a hydrolase domain.

We currently list **gp42** as a lysis gene since it gives strong homology to lysis genes. However, we cannot find another lysis gene (B) next to gp42 if in fact gp42 is one of the lysis genes in a lysis cassette.

We list **gp55** as a DNA binding protein as its function. The gene does show strong hits to transposase genes as well.

**Gp61** has a CRISPR-like domain.

Finally, based on synteny alone, we are calling the functions of the **gp34 & gp35** the tail assembly chaperones since they are located next to the TMP. We annotated gp35 as a frameshift protein. There is a string of 6 T’s close to the end of **gp34**. We called the frameshift a -1 frameshift that involves the first T in the string of T’s.