* Additional Notes section in notes are Blast Results from phagesdb blastp. Phage ‘Shrooms’ seems to be Waltz’s closest homolog. Shrooms was recently QC annotated and was in PhagesDB blast, but was not in NCBI yet. Most of these alignments were 1-to-1 and were listed at the bottom of the notes.

**Gene 4** - Start site was changed from 3443 to 3398 to decrease gap, give best SD score, the longest ORF, and stronger blast results, including a 1-to-1 match of previously QC annotated phage Shrooms\_5. However, this goes against Starterator, Glimmer and GeneMark calls.

**Gene 6** - Blast results also give strong hits to IbrB proteins found in various bacteria.

**Gene 17** - was deleted. Was not called by GeneMark, was the only gene in pham, had no blast, HHPred or phagesdb blast results, and also had a large overlap of previous gene. However, it does show some coding potential.

**Gene 18** - matches to 3 different BlastP superfamilies/conserved domains. RNA ligase, Serine Peptidase, and Aldolase\_Class\_I.

**Gene 19** - called Nuclease w/ Hydrolase Domain based on HHPred and BlastP superfamily hits. Other phage homologs stated “NKF”. An alternative name for the function could be “VRR-NUC domain-containing protein”, which was called in various bacteria towards bottom of Blast list.

**Gene 21** - Start site changed from 16658 to 16514 to decrease gap, increase ORF, give better Blast results, give a 1-to-1 match to previously annotated phage Shrooms, and to agree with Starterator and GeneMark. However, changing the start site gives a worse SD score.

**Gene 24** - HHPred also gives a good hit to a Peptidase\_G2 at 95.99%, but the e-value was 0.057, which is why we chose to leave it out as the function of the gene.

**Gene 29** - called a minor capsid protein based off a few good HHPred results.

**Gene 30** - HHPred gives multiple good hits to phage-related structural proteins including head/capsid proteins. We called the function a portal protein after the top HHPred result.

**Gene 31** - Start site changed from 21867 to 21828 to give better blast results, a better SD score, longer ORF, shorten gap, and to agree with Starterator and GeneMark.

**Gene 35** - was deleted. Although it was called by GeneMark and Glimmer, it was the only gene in its pham, was a very short ORF at 83 bp, did not have any Blast, HHPred or phagesdb blast. However, it does have some coding potential.

**Gene 44** - Start site changed from 26700 to 26652 to give longest ORF, better Blast alignments (1 to 1), to match with Starterator, and to reduce gap. However, it goes against both Glimmer and GeneMark calls.

**Gene 50** - Start site changed from 28637 to 28643 to give better blast results (1-to-1) alignments, a better SD score. However, it shortens the ORF by 6 bp.

**Gene 55** - HHPred gives 3 good hits to Transcription Elongation Factors. Because of this, we considered helix-turn-helix DNA binding domain as a possible function. We did not list as a function because of the high E-value.

**Gene 59** - GeneMark and Starterator suggest start site 32251 instead of 32248. These two start sites have the same SD score, but we chose 32248 to maximize ORF.

**Gene 64** - was deleted. Gene had no blast hits, hhpred results, phagesdb blast results, was the only gene in its pham, and was only 96 bp long.

**Gene 65** - Start site changed from 34808 to 34787 to give a longer ORF, a better SD score, to agree with GeneMark and Starterator, and to obtain better blast alignments (1-to-1).

**Gene 68** - Listed this protein as a minor tail protein because of modest hits/blast results both on BlastP and on PhagesDB. Additionally, the previous 2 genes were minor tail proteins, and this region of the genome includes tail and other structural proteins.

**Gene 69** - Start site changed from 42182 to 42101 to give longest ORF, best SD score, better blast results and alignments (1-to-1) and to agree with Starterator.

**Gene 70** - Although homolog phages listed this gene as a holin, we could not find other evidence (HHPred, blastP) of the holin function. We attempted to find why phage Laroye called this gene a holin, but the CompleteNotes file was not available on phagesdb to review. Therefore, we did not list this gene as a holin.

**Gene 79** - HHpred 47 hits with greater than 96% probability including 5 from Homo sapiens,

**Gene 83** - Phage Shrooms\_84 and LiSara\_82 called this gene a HTH DNA Binding domain. However, upon looking at the Complete Notes file for these phages, we couldn't find other evidence of why this gene was called a HTH binding domain. It would make sense if the function were a HTH DNA Binding domain, because this gene is followed by 3 other genes with the same function.

**Gene 87** - Start site changed from 51081 to 51054 (against GeneMark and Glimmer) to give a 1-to-1 alignment with blast results, decrease the gap from end of previous gene, give better SD score, and increase ORF length. HHPred gives good results to Phage Inhibitor and replisome organizer, but I listed neither as a function for the gene.

**Gene 88** - Start site was changed from 51608 to 51467 to reduce gap, yield best SD score, align 1-to-1 with blast results, and give largest ORF.

**Gene 89** - Start site changed from 51860 to 51815 to match GeneMark's call, give largest ORF, the best SD score, shorten the gap, and give a 1-to-1 alignment to blast results.

**Gene 91** - HHPred gives hit to CRISPR Cas4 Protein.

**Gene 93** - Good blastp hit to a conserved superfamily, but we were unsure if we should call the function of this gene a ligase.

**Gene 95** - Good BlastP superfamily/conserved domains, Phamerator and HHPred hits. Called gamma-glutamylamine cyclotransferase as the function. No other phage homolog called this function, but we believe there is ample evidence. This is a common enzyme in bacteria.

**Gene 98** - Left as a wrap around gene, despite bad blast alignments. The alignments were hardly better at start site 2, but we could not access the SD score for that site.