**Glexan genes requiring additional attention**

**SD score** for all genes used Kibler6/Karlin Medium settings

**Genes added**  
Gene 44 - SSC:35936-36505 (REV): Original gene call by autoannotation was a forward gene that was not present in related phages according to Phamerator. Gene was added using the largest ORF, however, the BLASTp results do not show any 1:1 alignments.

Gene 96 - SSC: 59099-59662: Original autoannotation left a large gap that was not conserved in related phages according to Phamerator. Newly added gene shows some alignment in BLASTp. Function was designated as NKF since BLASTp, HHPred, and Phamerator gave conflicting results for function.

Gene 120 - SSC: 67543-67755 and Gene 121 - SSC: 67736-67990: Original autoannotation called two genes in the reverse direction that were not present in related phages according to Phamerator. Gene 120 shows some 1:1 alignment in BLASTp, whereas Gene 121 shows good alignment in BLASTp.

**Gap**

A large gap of 544bp upstream of Gene 58 appears to be conserved in related phages according to Phamerator. There was no coding potential in this region according to GeneMark.

**Programmed Translational Frameshift?**

Genes 18 (SSC:12014-12547) and 19 (SSC: 12679-12957) encode tail assembly chaperone proteins just upstream to the gene for the tape measure protein. Gene 19 shows 1:1 alignment with related phages (Kostya and 244), however, not with other related phages. In Phamerator, the suggested start site for gene 19 is the start site that Glimmer called for gene 18 (@bp 12086). I’m not sure if that is strong enough evidence for a programmed translational frameshift.