**Texage. Notes on genes, sequences of interest:**

Texage is nearly identical to another phage, QuinnKiro, whose genome is fully annotated. Mycobacterium phage QuinnKiro, complete genome GenBank: KM592966.1

There are 108 changes, mostly substitutions.

There is a 20 nucleotide insertion at the end of the genome, after nt#49740, that contains a stretch of 12 C residues in tandem.

In determining start site strength, we used the Final SD score with the Kibler 6/Larlin Medium algorithm

Genes 6 and 7 are Asn(gtt) and Trp(caa) tRNAs. The second does not have a conventional CCA at the 3’ end. It has CAA instead. The QuinnKiro annotation for the Trp tRNA end at the “C”, two nucleotides short of the Texaage annotation. That C is followed by AA in the sequence which is the same as Texage.

Genes 24 and 25 annotated as a programmed translational frame shift.

Gene 33, an integrase, is followed by a gap of 158 which might be the attP site. Texage is a temperate phage.

Gene 41. Two starts, one codon apart. QuinnKiro used the TTG with lower SD score. We chose the ATG with the better SD score.

Gene 51 is very short to be a gene on its own and has 18 bp overlap with 52 in a different frame. There is GGGGA sequence – another programmed translational frame shift? There is no reporting of this.

Gene 57 was an added gene. There was a large gap and ORF with some clear coding potential on GeneMark. Our annotation has a large overlap of gene 56 with 57, which is the same in the QuinnKiro annotation.

Gene (?) 88. Not sure it is a gene. Was called in QuinnKiro but is very short and has no coding potential on GeneMark.