Lehigh University would like submit Mycobacteriophage Mitti for QC and Genbank submission. We have reviewed all gaps present and they are valid based on homology with other K4 phages. Some genes that warrant additional attention are listed below.

gp3 (478-645) has incorrect BLAST data saved in DNA master, however using online BLAST gives alignment of Q1:S1 with Mycobacteriophage Cheetobro gp3.

gps20-21 (12354-13234) is a translational frameshift.

gp48 is not present in original Mitti phamerator maps but was added based on homology with other K4 mycobacteriophage as the CRO (control of repressor’s operator) protein.

gp50 (36824-36952) has an altered start site compared to other K4 phages. We have investigated the region, there are no other start site choices prior to the selected start site. This is not the result of a second translational frameshift because it is lacking a slippery sequence. We feel the gene is valid as called.

gp53 (37483-37794) was called an endonuclease in Cheetobro and Fionnbharth, but not in more recently annotated phages (Taquito). There is no HHpred data to call this an endonuclease. This gene does not have a functional call in Mitti because it lacks proper evidence for an endonuclease.

gp87 (53399-53707) is homologous to Fionnbharth gp87, functionally annotated as a pyrophosphatase. More recently annotated phages (Taquito) do not call this function, there is no HHPred data to support this function. We did not call gp87 as a pyrophosphatase in Mitti.

The Aragorn web based program calls two tRNAs. One is indicated in the final DNA master file (gp38) tRNA-Lys. The second Aragorn call is (14120-14213) calling a tRNA-Arg. We chose not to call this a true tRNA based on the following reasons. None of the other K4 phages have this tRNA. There is a protein coding gene for the tape measure in the same region.