Lehigh University has investigated the genome of Mycobacteriophage James. We would like the following areas examined further. gp12 and gp13 are a tail assembly chaperone created by a translational frameshift. gp19 is called in both phamerator and DNAmaster as a minor tail protein and D-ala-D-ala carboxypeptidase. We feel this call is valid but would like examined further to ensure the correct functional annotation was called. gp35 is called in blast and phamerator as a DnaQ-like exonuclease, however HHpred has strong evidence that it is the DNA polymerase III epsilon subunit. This is the proofreading domain of this DNA polymerase. We currently have this called as DnaQ-like protein, however both functions potentially could be called.

Two other areas of interest were gp56 was deleted. Also gp58 does not have good alignment with other mycobacteriophage, however all start sites were examined and this is the best choice.

All large gaps and overlaps are valid based on homology with other F1 phages.