Lehigh has investigated the genome of mycobacteriophage Yahalom. We feel all gaps are valid based on homology with other B3 phages. A few regions we would like investigated further. gp26 and gp27 are both tail assembly chaperones but are not called as a frameshift. This is called as two genes in phamerator in other B3 phages as well. gp49 has strong evidence that it is a exonuclease in HHPRED but not on phamerator or BLAST. gp77 and gp78 are in the same family but only gp78 is called as HNH endonuclease. I am not sure if both should be called as a HNH exonuclease or if this is mislabeled in phamerator. Based on homology gp87 could begin at 63111 or 63093 but was called for the longer ORF based on the gap and coding potential.

Other features of interest are gp5 has homology with other phages as a ParB, however due to the functional naming document is not called as such because there is no ParA present. Also Yahalom was no longer in phamerator so starterator could not run.