**Mycobacteriophage Farber Annotation Cover Sheet**

Gp39 (incusion/exclusion): very short ORF; 129 bp. Aligns 1:1 with gp38 of Jobu08 and 8:1 with gp36 of Bxz2. No other upstream start sites are possible. Coding potential is shown in GeneMark-Smeg output.

Gp56 (inclusion/exclusion): very short ORF, 114 bp. Aligns 1:1 with gp56 of JHC117, 1:1 with gp55 of Jobu08, and 1:24 with gp52 of Bxz2. Coding potential is shown in GeneMark-Smeg output.

Gp60 (start site choice): (38143) SD score of 189 yields longest ORF and 1:1 Blast match 1:1 gp60 JHC117 but 6:1 with gp56 of Bxz2; (38128) SD score of 441 yields shorter ORF

Gp63 (inclusion/exclusion): very short ORF, 105 bp but has 1:1 Blast matches with gp63 of Jobu08 and gp60 of Bxz2

Note: a 359 bp gap exists between gp75 and 76. Neither Glimmer nor GeneMark predicted any genes in this region, and this region does not contain any coding potential as shown on GeneMark-Smeg output. Highly similar phage Microwolf does also not call any genes in this region; we believe it should remain a gap.

Unusual finding: gp80 appears to be a fusion of two separate genes in related phages.