Journey13

Coversheet

Gp2 (1187-2110) – although A2 phages in general have a large gap between gp1 and gp2, we opted to choose 1187 after much deliberation as the start, although it results in an unusual 145bp overlap for the following reasons:

-it captures the entire coding potential

-has best SD score

-best start from analysis of Starterator data

Gp 32(25973-26401) – This putative gene is a 1:1 match to *M. hassiacum* excisionase and is listed as the putative excisionase for D29\_34.1. There was no supporting evidence for this function in HHpred and CD. There is another gene (gp34, 26771-26962) which was putatively identified as the excisionase, supported by evidence from HHpred and CD. Consequently, gp32 was listed as NKF and gp 35, Xis.

Between gp58 and 59, there is an open reading frame(38546-38587) which if included would result in 4bp overlap of both flanking genes, but it’s very small (42bp). It was interesting that Odin (a closely related phage to Journey13) has a similar uncalled open reading frame (slightly bigger at 93bp) which has the same 4bp overlaps.

Gp73 (44249-44569) – in HHpred there are several organisms with Prob >80 (80-93), that suggest this gene is MazG, but none were phage or mycobacteria. Gp32 was identified as MazG. Consequently, gp73 was listed as NKF.