BrownCNA

Thank you with the QC checking of this genome. It was pretty straightforward and we had 2 different class sections work on the annotations that were compared for the final file.

We had 2 genes that I would like help another opinion on. Larry’s class added one ORF, but it was not added by mine; both Larry’s class and mine deleted the other, but that ORF has a match to Bane2 (which is not on phamerator). If they need to be added, I have tried to be as thorough as possible with the notes below.

* Larry added a gene between ORF # 82 and 83. But same gene product as gene 82… and 95bp overlap. I am skeptical that it should be added and have not included it in the DNAmaster file.

Gene information:

SSC: Start 64288 Stop 64085 (REV)

CP: all coding potential captured

SD: 375 not highest score

SCS: not called by Glimmer or GeneMark

Gap: 95bp overlap with ORF 82

Blast: match to gp 79 Jamal, aa1 of Jamal aligned to aa6 of query

LO: 204bp not longest possible

F: NKF

FS: checked phamerator/blastP/HHpred

This ORF and the previous ORF 82 both match to the same gene product in other phages. Alignments are better with this gene (gp 79 of Adawi aligned aa1 to aa1 of query) but the E values are much smaller with the products of ORF 82.

* Deleted gene 87 (original numbering), would be gene after gene 89 in new numbering – only 84/102 nucleotides, only matches on blast is to Bane2 – better match with the 102 length. It is an orpham. It would be a 1bp overlap with the prior ORF, and would now make the ORF after it have a 19 bp overlap instead of an 82 bp gap.

If added, the information should be:

Original GeneMark call @bp 66626

SSC: Start:66626 Stop: 66543 Rev

CP: 66626 Does not inlcude all coding potential

SD:-5.834, not the best SD score

SCS:Does not agree with genemark, not called by Glimmer

Gap: 1 bp overlap with previous ORF

Blast:1:1 aa match to Bane 2

LO:102 is the longest possible ORF

ST: conserved start

F: NKF

FS checked phamerator/blastP/HHpred

* My other concern is with the calling of HNH endonucleases towards the end of the genome. I have added the function to ORF 77 – it was called in several genomes. The concern is that it is also called for ORF 79, 81 and 89 in Zemanar, but not in others. I have not included it as a function for these 3 ORFs.