**Joselito**

1. SD scoring matrix Kibler6 and Spacing weight matrix Karlin medium were used

2. Five genes were deleted from the original:

40305-40385: forward call in the midst of reverse, 81nt in length with no significant similarity

43077-43322: forward in the midst of reverse genes with no significant similarity

47569-47625: 57nt in length with no significant similarity

47622-47720: 99nt in length with no significant similarity

51560-31: no significant similarity **(please investigate as this seems to be the site where the genome circularizes)**

3. We searched phams on <http://phages.wustl.edu/starterator/> . We do have “percentage support” for each, but did not include it in the annotation.

4. On phamerator.org, we used Mulciber, Jabith, and Et2Brutus to compare.

5. Joselito\_26: 6.5% of phage call the start at 17613. This start is a candidate start in Joselito, and gives a 1:1 with other tape measure proteins. Neither Glimmer or Genemark called it at this start site.

6. Joselito\_ 45 matches what is called DNA polymerase 1 with good identity, but has similarity to DnaQ-like (or DEDD) 3'-5' exonuclease domain superfamily. Unsure to call it DnaQ exonuclease (DNA polymerase III subunit) or DNA polymerase 1.

7. Joselito\_4 not called initially, so it was inserted. Starterator supports this start site for other A11s (such as Jabith and Mulciber)

8. Regions 25791-26120 and 45102-45300 were investigated because of the gap size, but nothing of note was discovered.