**Mattes**

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

2. Start choice change made for 30477-30698 that was ***not*** supported by Glimmer or Genemark, but this longer ORF was supported by a 1:1 Blast, and within Starterator

3. Two genes were deleted from the original:

2631-2326 (in reverse direction amidst others in the forward direction and completely overlapped with the next gene (2276-3598), which had a supported function.

33621-33238 (in reverse direction amidst others in the forward direction and overlapped with the next gene, which had a supported function

4. Unsure about the regions 8529-9080 and 9139-9465. They belong to the same pham, and 9139-9465 does not have a 1:1 Blast alignment.

5. This phage was one that crashed Starterator. As a result, we searched phams on <http://phages.wustl.edu/starterator/> . We do have “percentage support” for each, but did not include it in the annotation. (As a side note, I do like this method rather than the starterator maps)