Quinnkiro Cover Sheet

The College of St. Scholastica

Please accept our fully annotated genome of the Mycobacteriophage *QuinnKiro*, annotated by students at The College of St. Scholastica. We feel confident with our gene selection and gene functions; however, we would like you to pay special attention to the following genes due to the reasons outlined below. Deleted gene numbers reflect the original auto-annotated position:

* Multiple attempts to complete the full genome BLAST were unsuccessful. For genes without BLAST results, BLASTp was run from the NCBI and phagesdb.org sites and results were recorded in the notes section.
* Gene 1 - We deleted the gene due to no coding potential present and no blast matches.
* Gene 7 - We deleted the gene because there was no coding potential within the called area.
* Gene 24 - We identified that this gene is where the frameshift happened. We followed the SEA Phages manual when splitting the gene in the “Regions” tab of DNA Master.
* Gene 34 - We deleted the gene because there was no coding potential for it.
* Gene 36 - There was no 1:1 blast matches. The best one we could find was 3:1.
* Gene 48 - We changed our start site to cover all the coding potential but neither Genemark nor Glimmer agree with our call. There is no blast matches to our modified gene.
* Gene 52 - There was no blast matches on either phagesdb or NCBI.
* Gene 53 - The start site does not appear to be present in our coding potential .pdf file. Both Genemark and Glimmer agree with our start site.
* Gene 65 - The only blast match was 4:3.
* Gene 78 - Even though our start site agrees with both Genemark and Glimmer, and we did get a 1:1 blast match, our range does not appear to capture all the coding potential. Please look into it.
* Gene 79 - We could not find any blast matches on phagesdb or NCBI, but there is still significant coding potential that was called by both Genemark and Glimmer.
* Genes 81 and 82 have a gap of 80. Although there is no coding potential in this area, the gap might be too big.
* Gene 82 - The only blast match was 5:4.
* Gene 84 - The only blast match was 3:4.
* Gene 85 - The only possibility that has a 1:1 blast match appears not to capture all coding potential. The possibilities that include all coding potential do not have blast matches.
* Gene 89 - Although there is no coding potential in this area, both Glimmer and Genemark called the gene and there is a 1:1 blast match. We deleted.