Tnguyen7 Cover Sheet

The College of St. Scholastica

Please accept our fully annotated genome of the Mycobacteriophage *Tnguyen7*, 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 attention to the following genes due to the reasons outlined below. Deleted gene numbers reflect the original auto-annotated position:

* Gene 7 - No 1:1 blast matches, we had to stay with the match of 3:2.
* Gene 17 - The called site does not contain all the coding potential; however, it does have a 1:1 blast match.
* Gene 23 - We identified the frameshift occurred at this particular gene. We followed the SEA Phages manual when splitting the gene in the “Regions” tab of DNA Master.
* Gene 24 - Best blast match for called start site was 9:9.
* Gene 28 - Glimmer and Genemark called for different start sites. We agreed to follow Glimmer, which had a 1:1 blast match.
* Gene 31 - Best blast match for called site was 34:34.
* Gene 42 - Best blast match for called site was 17:17.
* Gene 60 - We deleted the gene because it was a forward gene overlapped by two reverse genes.
* Gene 62 - We kept this gene, but it could potentially be deleted. It was only called by GeneMark and the blast match was 1:1 with a hypothetical protein. It is also only 84 bp long.
* Gene 64 - The blast starts with 1:1 but eventually turns to 50:51 further down the sequence.
* Gene 67 - This gene was deleted, due to no blast matches, being called only by GeneMark, and containing only 72 bp.
* Gene 68 - We changed the start site to obtain a 1:1 blast match as well as to become the longest ORF. In addition, we were able to go from a large gap to only a slight overlap of 3 bp.
* Gene 70 - Best blast match for called site was 2:5.
* Gene 78 - The coding potential is not all contained in the region.
* Gene 82 - We deleted due to no blast matches, along with it being a lone forward gene among many reverse genes.
* Gene 83 - Best blast match for called site was 6:1.
* Gene 85 - We changed the start site to obtain a 1:1 blast match.
* Gene 86 - We changed the start site to be called by GeneMark.
* Gene 87 - We changed the start site to obtain a 1:1 blast match as well as to go from a huge gap to an overlap of 17 bp.
* Gene 89 - Best blast match for called site was 35:26.
* Gene 93 - There was no coding potential present for this gene.