**HokkenD Annotation Cover Letter**

This phage gave us a great deal of difficulty. The *M. smeg* GeneMark data was useless during annotation so we used the heuristic model.

We chose 150 for the start site of **Gene 1** because it had the best RBS score and was the closest start to the beginning of the coding potential. We were concerned because this gene had very odd BLAST matches. Only gp1 from Courthouse was a 1:1 match.

We had difficulty annotating multiple gene between **gene 114** and **gene 119**. These genes showed abnormal coding potential in the GeneMark heuristic data. Glimmer and GeneMark did not agree on any of these genes and the BLAST data was not helpful.

**Gene 127** is a small gene with abnormal coding potential in the GeneMark heuristic data. The start site we chose 71161 included the most coding potential but it didn’t have any BLAST 1:1 matches.

We noticed large gaps in multiple spots throughout the genome (18->19, 76->77, 87->88, 96->97, 117->118, 177->178, 179->180, 180->181, 230->231). These sections were searched for uncalled genes but none were discovered.