**DuchessDung**

I feel rather confident on my work with the bacteriophage known as DuchessDung. I made a few changes to start codons, as well as the deletion of certain genes.

* **GENE NUMBER 1 STARTS AT THE FIRST BASE PAIR OF THE GENOME. SO THERE IS NO SD, OR ANY PROMOTOR OR ENHANCER REGIONS. I DID GET THE LONGEST POSSIBLE ORF, GOOD CODING POTENTIAL AND A KNOWN FUNCTION FROM BOTH BLAST, PHAMERATOR, AND NCBI DATABASE. THIS ONE NEEDS ATTENTION I WAS HESITANT TO DELETE IT DUE TO ITS LENGTH AND FUNCTION, BUT I AM UNSURE IF IT CAN ACTUALLY BE CONSIDERED A GENE OR NOT AT THE FIRST BASE PAIR.**
* **Gene 44:** Was deleted since it was in the wrong direction, did not have coding potential with GeneMark. It also had long overlap when the Glimmer starting point was chosen.
* **Gene 48**: Was only called by genemark, no coding potential with glimmer. Was only 78bp long, so it was deleted. Also did not have any blast or NCBI results.
* **Gene 58**: The starting point was changed to 47,883 in order to reduce the overlap with the next gene, still has coding potential.
* **Gene 66**: The start codon was changed in order to reduce the amount of gap and make it the longest possible open reading frame. It also now has an ATG start codon.
* **Gene 74**: Starting location was changed to 57,639 bp, in order to in order to give it a longer reading frame. **This gene does have a 7 base pair overlap so I would like it reviewed. The reason this overlap was chosen was very unique. The starting sequence of this gene was ATGATGAT this allowed for the proper sequence to work and be read accordingly. I would like someone to double check this, but I do believe it is possible due to the unique arrangement of the sequence of the two genes.**
* **Gene 82:** I changed the start from 61,819 to 61,801 which gave it less overlap and also gave it a starting codon of ATG. **Please review this one, has too much overlap, (7bp).**
* **Gene 84:**  The start codon was changed in order to give it the longest possible open reading frame, since gene number 85 was deleted.
* **Gene 85:** was deleted having no coding potential with glimmer, it was also a rather short suspected gene at 111bp.