**Romney2012 Cover Sheet**

Gp25 (15885-18485): start choice site. We did not choose the suggested start of 16026 bp on Starterator, but there are many conserved starts for this gene. Start site has significant overlap with previous gene, which is a part of the tail assembly chaperone programmed frameshift.

Gp35 (27804-27208): start choice site disagrees with Glimmer and GeneMark predictions. Gene was manually altered to minimize gap and improve Blast matches. Starterator was not informative.

Gp36 (27959-27801): gene not originally called by Glimmer or GeneMark; manually added using Phamerator maps as a guide. Starterator not informative because gene not called.

Gp39 (28457-28371): gene is 87 bp long; very suspicious. However, students argued for inclusion, as it minimizes gaps, has a 4 bp overlap with previous gene, includes coding potential, and has Blast matches to non-draft genomes.

Gp51 (36388-35442): functional assignment is questionable. This was only chosen due to the function source coming from a hit in HHPRed matching *Mycobacterium tuberculosis*. BlastP search on phagesdb yielded "function unknown" for all matches listed. BlastP (NCBI) best hit was gp51 of Peaches (unknown function) with an E-value of 0.00

Gp58 (39042-38956): gene is 87 bp long; very suspicious. Students argued for inclusion and was only kept in the annotation due to the presence of Blast matches to non-draft genomes, minimizing gaps in the genome sequence, and having a 4 bp overlap with the previous gene

Gp64 (41969-41889): gene is 81 bp long; very suspicious. Students argued for inclusion due to the presence of Blast matches to non-draft genomes, minimizing gaps in sequence, and having a 4 bp overlap with the previous gene.

Gp70 (44606-44379): start choice site. Starterator suggests start site of 44507 bp; many other conserved starts are present in the Starterator results. The 44606 bp start is the longer of two possible TTG starts and has the third best RBS score (top three are relatively close).