Dear QC,

It is a pleasure to provide you with our complete annotation of Pipsqueaks. We have a few places for you to look during your quality control check.

1. We had trouble getting the translational frame shift to annotate correctly for genes 14 and 15. We came close, but we can’t get rid of this error message during the validation – “join(9036. .9566)
   Incorrect region counts”
2. We inserted two genes – gp70 and gp73. The gp70 region originally had one gene called in the reverse orientation in the middle of a sea of forward orientation ORFs. We deleted that ORF and inserted gp70. There was a large open space on the 3’end of the genome after gp72 (the last one called by DNA Master). Looking at other N cluster phage and using BLASTX we identified a final gene that we think is worth annotating. We inserted gp73 here.
3. There is a gap between 30 and 31 that is large. This region is ~25400 to 26300. In the closest phage, Carcharodon, gp31 is much longer than our gene 31, but there is no way to expand our ORF to extend it. There is another open reading frame in a different frame in Pipsqueaks in that gap, but it would have a significant overlap with our gp31. We decided to not call the gene and let the QC team look at it. When we look at the Phamerator alignment between Carcharodon (top) and Pipsqueaks (bottom) you can see a small region that is missing from Pipsqueaks right in the middle of gp31. It may be that this deletion threw off the frame and split the ORF?



These were our major concerns. Thanks for looking at the annotation. We had a great time completing the project.