**Genome Annotation Submission for PeteyPab, PotatoChip, and Zion**

These 3 Corynebacterium genomes were isolated in Fall 2016. All three share significant sequence similarity such that changes (insertion/deletion) of genes in one genome should likely be mirrored in the other 2 genomes.

The following items were of particular concern during annotation and warrant second review:

* A very small reverse gene (72bp) was called in the region 50311-50382. The gene has a blip of coding potential support and fills the gap but there is concern about the very small ORF size. Leaving it out would leave a gap. With this gene in place, there is tight packing with the genes on either side.
* A second small reverse gene (144bp) was called in the region 59984-60127. This gene was not called by any of the standard algorithms, but does have coding potential support and decent SD scores.
* A third small forward gene (87bp) was called in the region 60913-60999. Decent SD scores and would be the first gene in the string of forward genes after a region of reverse genes. Leaving it out increases the gap between R and F genes. There is coding potential support for this putative gene call.