To do:

1. Focus on cox1
   1. Record exon boundaries
   2. Intron boundaries
   3. Use ORF finder to record number and location of retrotransposable elements
   4. Compare sequences of retrotransposable elements (are they all the same, different…)
2. Record gene order for all species starting with cox1. I think we will focus on just the genes and rRNA not the tRNAs
3. Record bps for exons, introns, intergenic space for all species