I. Intro
   A. Bac. of interest chosen because it produces one of the most poisonous substances known, botulinum toxin.
   B. Given forward and reverse reads of *Clostridium botulinum* genetic material. I want to use a high-quality assembly so that I can annotate the genome.

II. Methods
   A. Assemble genome with two different assemblers
      1. Abyss and Spades
      2. Take the reads and try to put them together into one big piece
   B. Assess quality using Quast
      1. Run scaffold output from Abyss and Spades
   C. Annotate the genome using two different annotators
      1. Use scaffold output from Abyss and Spades

III. Results/Conclusions
   A. Compare quality of our two different assemblers

	Quality assessment using QUAST					**Genome Annotation**	
	N50	**L50**	**Largest contig**	**# contigs**	**GC%**	**CDS Prokka**	**CDS Rast**
Abyss	550,747	3	1,095,256	24	27.78	4,100	4,242
Spades	467,820	4	993,415	26	27.75	4,096	4,258

   B. Even though Abyss had slightly better metrics for alignment completeness and contiguity, Spades had about the same number of coding sequences (CDS). Additionally, we see that Rast was able to identify slightly more CDS than Prokka, regardless of data input.