1.

unitigs	
contigs	167
scaffolds	58
N50	193741
Genome length	5431836

2. Abyss-pe: assemble pair end data sets from unitigs into contigs.
   K: size of k-mera length within a sequence, we use K-mer as a parameter and want to make sure it is able to account for the genome
   B: B is the bloom size so we used B=2G

3. Klebsiella pneumoniae
4. I was only able to use SPAdes unfortunately so the QUAST was only ran based on the SPAdes output. Although speaking to other people in my class many of them said that SPAdes gave them a higher quality output.
5. BUSCO is used to search for genes that we may expect to see in the genome by copy of orthologs. My report did not have a BUSCO % on it.
6. recA, 16s rRNA, rpsB,
7. In our line of code we start by putting prokka to tell the system to use prokka to follow the commands. We then put –outdir which tells it what the title of the folder will be, –prefix tells it what the file name will be.
8. The function of recA plays a part in recombination and repair of chromosomes. 16s rRNA is an internal transcribed spacer sequence (ITS) it is also important way of identification. rpsB is used for DNA binding during transcription.
9.