**Initial Mapping of the reads to the CF39S Genome (2018/11/28-30)**

For these data sets, the entirety of the RNA-Seq reads were processed using Xpression to give the associated counts table (and statisitcs files) that are present in each folder. Note that the following Parameters were used when generating these files (using the instance of Xpression that is installed on Joe’s computer):

* CPU cores = 6
* Allowed Mismatches = 2 nucleotides
* Strand Specificity = Yes
* Native Direction = Yes
* Read Position = 1
* Input Format = FastQ
* Package results

These results were then looked at to 1) Ensure that I have enough reads for each library, and 2) See how many reads I do have to work with.