1. Use RNA-seq companion script and RNA-Seq script to generate a PBS scrip for each fastq file.
2. Use the file manipulation script to make a individual directory for each fastq file, then place said fastq file and PBS script along with any other needed files in its corresponding directory. This has to be the case because cufflinks will use intermediate files with the same name, so there would be cross over if one is doing multiple fastq files. This eliminates the crossover.
3. Use output from HT-Seq along with the List\_DESeq2.txt and DESeq2.txt script for DGE analysis.