Files Included in folder:

1. Bioinformatic analyses.docx – written methods of data processing
2. Compiled Fastqc Summary.pptx – representative FastQC plots (from representative runs)
3. STARAlignedReads\_scrubbed.xlsx – STAR aligned read statistics based on run and total number of reads
4. Count QC.docx – correlations using read counts between sequencing runs
5. Count\_Matrix\_Genes.rda - read count matrices on R based on each HiSeq 2000 run
6. Count\_Matrix\_Genes.R – counting script