1. Quality control check of the reads was done using FastQC uninteractive mode release version 0.11.5
2. Copy kallisto file to my own home directory: cp -avr /local/prog/Kallisto\_version\_43.1/ /mnt/scratch/adam013/
3. command for creating the index: kallisto index -i transcripts.idx transcripts.fasta.gz
4. command for doing the count: kallisto quant -i transcripts.idx -o output -b 100 reads\_1.fastq.gz reads\_2.fastq.gz

**code used foor building the index and the quantification**

parameter for building the index from Trinity de novo assembled transcriptome

./Kallisto\_version\_43.1/kallisto\_linux-v0.43.1/kallisto index -i S\_exigua\_transcriptome.idx Trinity.fasta

parameter for running Quant command for quantification of the reads abundance

./Kallisto\_version\_43.1/kallisto\_linux-v0.43.1/kallisto quant -i S\_exigua\_transcriptome.idx -o run0205\_1-1\_count -b 100 ./Hi1622\_caterpillar\_transcriptomics/for\_customer/run0205\_1-1/run0205\_1-1\_S1\_L001\_R1\_001.nophix.fastq.gz ./Hi1622\_caterpillar\_transcriptomics/for\_customer/run0205\_1-1/run0205\_1-1\_S1\_L001\_R2\_001.nophix.fastq.gz && ./Kallisto\_version\_43.1/kallisto\_linux-v0.43.1/kallisto quant -i S\_exigua\_transcriptome.idx -o run0205\_1-2\_count -b 100 ./Hi1622\_caterpillar\_transcriptomics/for\_customer/run0205\_1-2/run0205\_1-2\_S2\_L001\_R1\_001.nophix.fastq.gz ./Hi1622\_caterpillar\_transcriptomics/for\_customer/run0205\_1-2/run0205\_1-2\_S2\_L001\_R2\_001.nophix.fastq.gz && ………………..etc