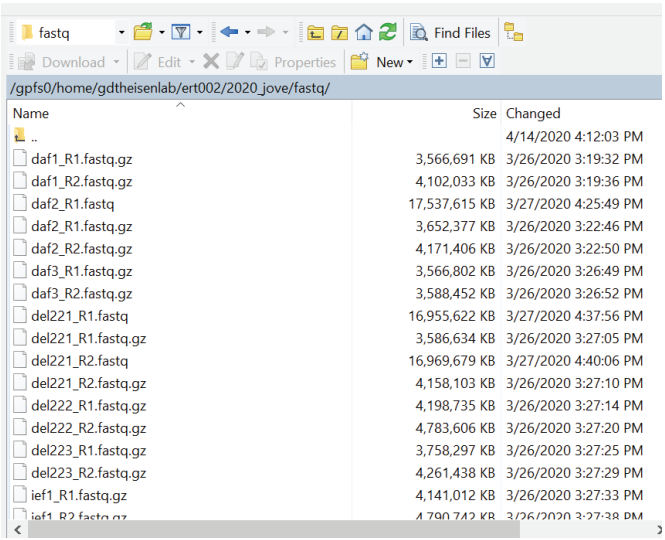
A

```
cd project
mkdir fastq
```

B



C

```
mkdir trimmed
cd fastq
trim_galore -o path_to/project/trimmed --paired sample1_R1.fastq.gz sample1_R2.fastq.gz
```

D

```
cd ..
mkdir STAR_output
cd trimmed
STAR --runThreadN [N] --genomeDir path_to/STAR_index --readFilesIn sample1_R1_val_1.fq.gz sample1_R2_val_2.fq.gz
--readFilesCommand zcat --outFileNamePrefix path_to/project/STAR_output/sample1_ --quantMode GeneCounts
--twopassMode Basic --outSAMunmapped Within
```