### Quality control of raw data using FastQC

Command:

fastqc --extract -f fastq {input.r1} {input.r2} -o {out\_dir}

Soft version:

0.11.6

#--------------------

### Trimmomatics to remove the adaptors and cutoff the low-quality bases

Command:

trimmomatic-0.36.jar PE -threads 10 -phred33 {input.r1} {input.r2} {op.r1} {oup.r1} {op.r2} {oupr2} ILLUMINACLIP:{adaptor\_file}:2:30:5 LEADING:3 TRAILING:3 SLIDINGWINDOW:4:15 HEADCROP:0 MINLEN:36

Soft version:

0.36-5

#--------------------

### Aligning clean reads to the reference genome using STAR

#for one read file, run

STAR --runThreadN 8 --genomeDir {star\_idx} --readFilesIn {input.r1} {input.r2} --outSAMtype BAM SortedByCoordinate --outFileNamePrefix {out\_prefix}

#------------------

### Run featureCounts to get the amount of the unique aligments of a feature

featureCounts -p -T 10 -d 30 -D 1000 -C -s 1 -t exon -g GENE --primary -O -a {genome.gff} -o {readscount} {\*\_Aligned.sortedByCoord.out.bam}

#------------------