RNA-seq pipeline code:

cutadapt -a AGATCGGAAGAGC -O 7 -m20 -q5 -p result/tophat\_out/Sample\_T1/tmp.R2.fastq -o result/tophat\_out/Sample\_T1/tmp.R1.fastq ./fastq/Sample\_T1/T1\_ACAGTG\_L001\_R1.fastq.gz ./fastq/Sample\_T1/T1\_ACAGTG\_L001\_R2.fastq.gz > result/tophat\_out/Sample\_T1/T1.trimmed.stat 2>&1                                                                              
cutadapt -a AGATCGGAAGAGC -O 7 -m20 -q5 -o result/tophat\_out/Sample\_T1/T1\_R2\_trimmed.fastq -p result/tophat\_out/Sample\_T1/T1\_R1\_trimmed.fastq result/tophat\_out/Sample\_T1/tmp.R2.fastq result/tophat\_out/Sample\_T1/tmp.R1.fastq >> result/tophat\_out/Sample\_T1/T1.trimmed.stat 2>&1           
  
tophat --library-type fr-unstranded --no-coverage-search --keep-fasta-order --rg-id 1 --rg-sample T1 --rg-library 150224\_liu --rg-platform-unit CAGATC.L006 --rg-center PMgenomics --rg-platform Illumina -p6 -r 35 -G /mnt/work1/data/genomes/mouse/mm10/iGenomes/Annotation/Genes/genes.gtf -o tophat\_out/Sample\_T1 /mnt/work1/data/genomes/mouse/mm10/iGenomes/Sequence/Bowtie2Index/genome tophat\_out/Sample\_T1/T1\_R1\_trimmed.fastq tophat\_out/Sample\_T1/T1\_R2\_trimmed.fastq  
  
cufflinks --no-update-check -N -p 6 -o result/cufflinks\_out/Sample\_T1 -G /mnt/work1/data/genomes/mouse/mm10/iGenomes/Annotation/Genes/genes.gtf result/tophat\_out/Sample\_T1/accepted\_hits.bam  
  
cuffquant --no-update-check -u -p 6 -o result/cuffquant\_out/Sample\_T1 -b /mnt/work1/data/genomes/mouse/mm10/iGenomes/Sequence/WholeGenomeFasta/genome.fa /mnt/work1/data/genomes/mouse/mm10/iGenomes/Annotation/Genes/genes.gtf  result/tophat\_out/Sample\_T1/accepted\_hits.bam    
  
cuffdiff --no-update-check -p6 -b /mnt/work1/data/genomes/mouse/mm10/iGenomes/Sequence/WholeGenomeFasta/genome.f  
a -u --library-norm-method quartile --use-sample-sheet /mnt/work1/data/genomes/mouse/mm10/iGenomes/Annotation/Genes/genes.gtf sa  
mple\_sheet.txt