Hi Megan:

I believe the following script is related to the analysis you are looking at.

Best,

Fan

########## march 12, 2013, tophat2 analysis #############

#### tophat2: use default tophat2 parameters with the standard sequence read output requiring unique genomic hit with suppliing transcriptome: output in bob\_mm10\_th2out\_${sample}\_g1tx

1190\_1  AdL01HC

1190\_2  AdL02HC

1190\_3  AdH02HC

1190\_4  AdH03HC

1190\_5  P14L01HC

1190\_6  P14L03HC

1190\_7  P14H01HC

1190\_8  P14H02HC

pwd

/home/mengf\_lab/club\_house/LRHR/tophat2

mkdir logs

1. tophat2: output in LRHR\_rgsc34\_th2out\_1190\_${sample}\_g1tx

for sample in 1 2 3 4 5 6 7 8

do

fqpath=/home/mengf\_lab/club\_house/archive\_from\_old\_cluster/akillab/Manhong/tophat/INPUT/SOLEXA/

bt2indexpath=/home/mengf\_lab/mengf/illumina/Rattus\_norvegicus/NCBI/RGSC\_v3.4/Sequence/Bowtie2Index/genome

gtfpath=/home/mengf\_lab/mengf/illumina/Rattus\_norvegicus/NCBI/RGSC\_v3.4/Annotation/Genes/genes.gtf

jobname=LRHR\_${sample}\_g1tx

qsub -pe smp 8 -cwd -b y -N $jobname -o logs/$jobname.o -e logs/$jobname.e "tophat2 -p 8  -g 1 -G $gtfpath  -o LRHR\_rgsc34\_th2out\_1190\_${sample}\_g1tx $bt2indexpath ${fqpath}1190\_${sample}.txt"

done

2. cufflink: output in LRHR\_rgsc34\_th2clout\_1190\_${sample}\_g1tx

for sample in 1 2 3 4 5 6 7 8

do

jobname=LRHR\_cl${sample}\_g1tx

qsub -pe smp 8 -cwd -b y -N $jobname -o logs/cl${sample}\_g1tx.o -e logs/cl$sample\_g1tx.e "cufflinks -p 8 -o LRHR\_rgsc34\_th2clout\_1190\_${sample}\_g1tx LRHR\_rgsc34\_th2out\_1190\_${sample}\_g1tx/accepted\_hits.bam"

done

3.  cuffmerge: output in LRHR\_rgsc34\_th2cl\_cmerge\_1190\_g1tx

for d in $(ls -d LRHR\_rgsc34\_th2clout\_1190\_\*\_g1tx)

do

ls ${d}/transcripts.gtf

done

vi LRHR\_th2cl\_g1tx\_assemblies.txt

LRHR\_rgsc34\_th2clout\_1190\_1\_g1tx/transcripts.gtf

LRHR\_rgsc34\_th2clout\_1190\_2\_g1tx/transcripts.gtf

LRHR\_rgsc34\_th2clout\_1190\_3\_g1tx/transcripts.gtf

LRHR\_rgsc34\_th2clout\_1190\_4\_g1tx/transcripts.gtf

LRHR\_rgsc34\_th2clout\_1190\_5\_g1tx/transcripts.gtf

LRHR\_rgsc34\_th2clout\_1190\_6\_g1tx/transcripts.gtf

LRHR\_rgsc34\_th2clout\_1190\_7\_g1tx/transcripts.gtf

LRHR\_rgsc34\_th2clout\_1190\_8\_g1tx/transcripts.gtf

gtfpath=/home/mengf\_lab/mengf/illumina/Rattus\_norvegicus/NCBI/RGSC\_v3.4/Annotation/Genes/genes.gtf

fapath=/home/mengf\_lab/mengf/illumina/Rattus\_norvegicus/NCBI/RGSC\_v3.4/Sequence/WholeGenomeFasta/genome.fa

for parameter in g1tx

do

qsub -pe smp 8 -cwd -b y -N cmg\_${parameter} -o logs/cmg\_${parameter}.o -e logs/cmg\_${parameter}.e "cuffmerge -o LRHR\_rgsc34\_th2cl\_cmerge\_1190\_${parameter} -g $gtfpath -s $fapath -p 8 LRHR\_th2cl\_${parameter}\_assemblies.txt"

done

## cuffdiff: need to know the sample grouping information

1190\_1  AdL01HC

1190\_2  AdL02HC

1190\_3  AdH02HC

1190\_4  AdH03HC

1190\_5  P14L01HC

1190\_6  P14L03HC

1190\_7  P14H01HC

1190\_8  P14H02HC

gtfpath=/home/mengf\_lab/mengf/illumina/Rattus\_norvegicus/NCBI/RGSC\_v3.4/Annotation/Genes/genes.gtf

fapath=/home/mengf\_lab/mengf/illumina/Rattus\_norvegicus/NCBI/RGSC\_v3.4/Sequence/WholeGenomeFasta/genome.fa

pre=LRHR\_rgsc34\_th2out

hit=/accepted\_hits.bam

for parameter in g1tx

do

qsub -pe smp 8 -cwd -b y -N  AdLvsAdH${parameter} -o logs/AdLvsAdH${parameter}.o -e logs/AdLvsAdH${parameter}.e \

"cuffdiff -o ${pre}\_${parameter}\_diff\_AdLvsAdH\_out -b $fapath -p 8 -u LRHR\_rgsc34\_th2cl\_cmerge\_1190\_${parameter}/merged.gtf ${pre}\_1190\_1\_${parameter}${hit},${pre}\_1190\_2\_${parameter}${hit} ${pre}\_1190\_3\_${parameter}${hit},${pre}\_1190\_4\_${parameter}${hit}"

qsub -pe smp 8 -cwd -b y -N  P14LvsP14H${parameter} -o logs/P14LvsP14H${parameter}.o -e logs/P14LvsP14H${parameter}.e \

"cuffdiff -o ${pre}\_${parameter}\_diff\_P14LvsP14H\_out -b $fapath -p 8 -u LRHR\_rgsc34\_th2cl\_cmerge\_1190\_${parameter}/merged.gtf ${pre}\_1190\_5\_${parameter}${hit},${pre}\_1190\_6\_${parameter}${hit} ${pre}\_1190\_7\_${parameter}${hit},${pre}\_1190\_8\_${parameter}${hit}"

qsub -pe smp 8 -cwd -b y -N  P14LvsAdL${parameter} -o logs/P14LvsAdL${parameter}.o -e logs/P14LvsAdL${parameter}.e \

"cuffdiff -o ${pre}\_${parameter}\_diff\_P14LvsAdL\_out -b $fapath -p 8 -u LRHR\_rgsc34\_th2cl\_cmerge\_1190\_${parameter}/merged.gtf ${pre}\_1190\_5\_${parameter}${hit},${pre}\_1190\_6\_${parameter}${hit} ${pre}\_1190\_1\_${parameter}${hit},${pre}\_1190\_2\_${parameter}${hit}"

qsub -pe smp 8 -cwd -b y -N  P14HvsAdH${parameter} -o logs/P14HvsAdH${parameter}.o -e logs/P14HvsAdH${parameter}.e \

"cuffdiff -o ${pre}\_${parameter}\_diff\_P14HvsAdH\_out -b $fapath -p 8 -u LRHR\_rgsc34\_th2cl\_cmerge\_1190\_${parameter}/merged.gtf ${pre}\_1190\_7\_${parameter}${hit},${pre}\_1190\_8\_${parameter}${hit} ${pre}\_1190\_3\_${parameter}${hit},${pre}\_1190\_4\_${parameter}${hit}"

done