This is the script to run the pipeline

#!/bin/bash

#SBATCH --partition=amilan

#SBATCH --job-name=alc\_ex\_rna

#SBATCH --mail-type=END,FAIL when job is done or fails, will notify e mail

#SBATCH --output=nextflow.out

#SBATCH --error=nextflow.err

#SBATCH --nodes=2 how many resources you need

#SBATCH --ntasks=4

#SBATCH --mem=16gb memory

#SBATCH --time=23:00:00

pwd; hostname; date tells you what was done, who did it and echo

**echo** **"Alcohol Exercise RNA-Seq"**

module load anaconda

conda activate /home/erme3555/.conda/envs/myenv file path to Erika’s

conda env

nextflow run nf-core/rnaseq \

-with-conda true \

-profile conda \

--input /projects/erme3555/alc\_ex\_rna/design.csv \

--outdir /scratch/alpine/erme3555/alc\_exer\_rna/results3/ \ output directory

--genome Rnor\_6.0 \

--aligner star\_rsem \

--email jlleasure@uh.edu \

-resume

conda deactivate

sample,fastq\_1,fastq\_2,strandedness (these are like column titles for excel file)

A2042,/pl/active/IBG/erika/alc\_exer\_rna/01.RawData/A2042/A2042\_1.fq.gz,/pl/active/IBG/erika/alc\_exer\_rna/01.RawData/A2042/A2042\_2.fq.gz,auto

A2059,/pl/active/IBG/erika/alc\_exer\_rna/01.RawData/A2059/A2059\_1.fq.gz,/pl/active/IBG/erika/alc\_exer\_rna/01.RawData/A2059/A2059\_2.fq.gz,auto

A2060,/pl/active/IBG/erika/alc\_exer\_rna/01.RawData/A2060/A2060\_1.fq.gz,/pl/active/IBG/erika/alc\_exer\_rna/01.RawData/A2060/A2060\_2.fq.gz,auto

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#SBATCH --mem=16gb

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pwd; hostname; date

**echo** **"Alcohol Exercise RNA-Seq"**

module load anaconda

conda activate /home/leasure/.conda/envs/myenv

nextflow run nf-core/rnaseq \

-with-conda true \

-profile conda \

--input /projects/leasure/RNAseq\_data/test/testA2042.fq.gz \

--outdir /projects/leasure/RNAseq\_data/results \

--genome Rnor\_6.0 \

--aligner star\_rsem \

--email jlleasure@uh.edu \

-resume

conda deactivate