#!/bin/bash

#Readcounting by FeatureCounts

GNM=/groups/songli\_lab/RegNetRNAseq/data/TAIR10\_Chr.all.fasta;

GTF=/groups/songli\_lab/RegNetRNAseq/data/Araport11\_GFF3\_genes\_transposons.201606.gtf

GnmDir=/groups/songli\_lab/RegNetRNAseq/data/Gnmdir;

# setting out the directories;

dir1=/groups/songli\_lab/RegNetRNAseq/

cd $dir1/data/SRA

for f1 in \*.sra

do

f2=${f1%.sra}

echo "$f1"

echo "$f2"

cd $dir1/data/rc1

mkdir $f2

cd $dir1/data/fastq

if [ -d $f2"\_2" ]

then

bamsuffix=Aligned.sortedByCoord.out.bam;

outdir=$dir1/data/rc1

file1=$f2$bamsuffix

aligndir=$dir1/data/bam/$f2

featureCounts -T 8 \ -t exon \ -g gene\_id \ -p \ -a $GTF \ -o $outdir/$f2/$f2.readcount.txt \ $aligndir/$file1

else

bamsuffix=Aligned.sortedByCoord.out.bam;

outdir=$dir1/data/rc1

file1=$f2$bamsuffix

aligndir=$dir1/data/bam/$f2

featureCounts -T 8 \ -t exon \ -g gene\_id \ -a $GTF \ -o $outdir/$f2/$f2.readcount.txt \

$aligndir/$file1

fi

done