20230104

Analyze RNA-seq data for N2 and WAN611

export LC\_ALL=en\_US.UTF-8

export LANG=en\_US.UTF-8

export PATH=$PATH:/home/wanlab/apps/FastQC

fastqc:

fastqc -o /public/GW/Y111B2A.3.1\_RNA-seq/results/fastqc /public/GW/Y111B2A.3.1\_RNA-seq/data/N2\_TR\_rep1\_1.fq.gz

fastqc -o /public/GW/Y111B2A.3.1\_RNA-seq/results/fastqc /public/GW/Y111B2A.3.1\_RNA-seq/data/N2\_TR\_rep1\_2.fq.gz

fastqc -o /public/GW/Y111B2A.3.1\_RNA-seq/results/fastqc /public/GW/Y111B2A.3.1\_RNA-seq/data/WAN611\_TR\_rep1\_1.fq.gz

fastqc -o /public/GW/Y111B2A.3.1\_RNA-seq/results/fastqc /public/GW/Y111B2A.3.1\_RNA-seq/data/WAN611\_TR\_rep1\_2.fq.gz

fastqc -o /public/GW/Y111B2A.3.1\_RNA-seq/results/fastqc /public/GW/Y111B2A.3.1\_RNA-seq/data/N2\_TR\_rep2\_1.fq.gz

fastqc -o /public/GW/Y111B2A.3.1\_RNA-seq/results/fastqc /public/GW/Y111B2A.3.1\_RNA-seq/data/N2\_TR\_rep2\_2.fq.gz

fastqc -o /public/GW/Y111B2A.3.1\_RNA-seq/results/fastqc /public/GW/Y111B2A.3.1\_RNA-seq/data/WAN611\_TR\_rep2\_1.fq.gz

fastqc -o /public/GW/Y111B2A.3.1\_RNA-seq/results/fastqc /public/GW/Y111B2A.3.1\_RNA-seq/data/WAN611\_TR\_rep2\_2.fq.gz

**STAR:**

export PATH=$PATH:/home/wanlab/apps/STAR-2.7.10a/source

sh /public/GW/Y111B2A.3.1\_RNA-seq/scripts/STAR\_alignment.sh N2\_TR\_rep1

Graphical user interface, text, chat or text message

Description automatically generated

sh /public/GW/Y111B2A.3.1\_RNA-seq/scripts/STAR\_alignment.sh N2\_TR\_rep2

Graphical user interface, text

Description automatically generated

sh /public/GW/Y111B2A.3.1\_RNA-seq/scripts/STAR\_alignment.sh WAN611\_TR\_rep1

**Graphical user interface, text, application, chat or text message

Description automatically generated**

sh /public/GW/Y111B2A.3.1\_RNA-seq/scripts/STAR\_alignment.sh WAN611\_TR\_rep2

**Graphical user interface, text, application, chat or text message

Description automatically generated**

**STAR\_alignment.sh:**

STAR --genomeDir /home/wanlab/RNA\_seq/celegans\_star\_index/ \

--runThreadN 6 \

--readFilesIn /public/GW/Y111B2A.3.1\_RNA-seq/data/$1/$1\_1.fq /public/GW/Y111B2A.3.1\_RNA-seq/data/$1/$1\_2.fq \

--outFileNamePrefix /public/GW/Y111B2A.3.1\_RNA-seq/results/STAR/$1\_ \

--outSAMtype BAM SortedByCoordinate \

--outSAMunmapped Within \

--outSAMattributes Standard

注意：readfilein 的两个文件与readfilein 必须是一行

Outfilenameprefix也一样

Featurecounts:

Graphical user interface, text

Description automatically generated

Text

Description automatically generated

Counts.sh

/home/wanlab/apps/subread-2.0.0-Linux-x86\_64/bin/featureCounts -T 4 \

-a /home/wanlab/RNA\_seq/Caenorhabditis\_elegans.WBcel235.106.gtf \

-o /public/GW/Y111B2A.3.1\_RNA-seq/results/featurecounts/N2\_WAN611\_TR\_featurecounts.txt \

/public/GW/Y111B2A.3.1\_RNA-seq/results/STAR/\*\_Aligned.sortedByCoord.out.bams

Analyze small RNA-seq data for N2 and WAN611:

export LC\_ALL=en\_US.UTF-8

export LANG=en\_US.UTF-8

export PATH=$PATH:/home/wanlab/apps/FastQC

export PATH=$PATH:/home/wanlab/apps/subread-2.0.3-Linux-x86\_64/bin

fastqc:

fastqc -o /public/GW/Y111B2A.3.1\_small\_RNA\_seq/results/fastqc /public/GW/Y111B2A.3.1\_small\_RNA\_seq/data/N2\_SR\_rep1.fq

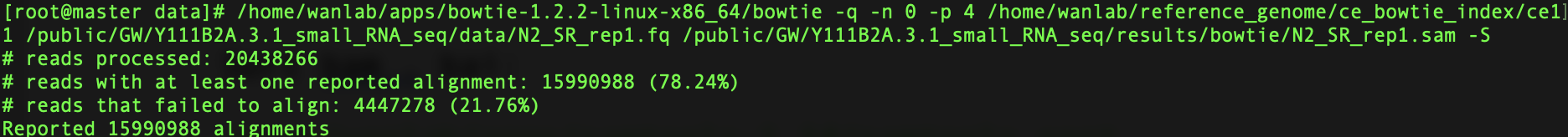
fastqc -o /public/GW/Y111B2A.3.1\_small\_RNA\_seq/results/fastqc /public/GW/Y111B2A.3.1\_small\_RNA\_seq/data/N2\_SR\_rep2.fq

fastqc -o /public/GW/Y111B2A.3.1\_small\_RNA\_seq/results/fastqc /public/GW/Y111B2A.3.1\_small\_RNA\_seq/data/WAN611\_SR\_rep1.fq

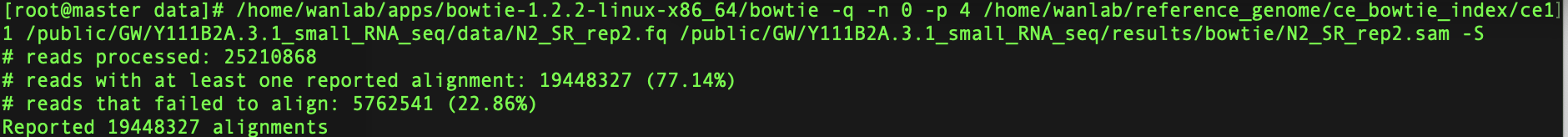
fastqc -o /public/GW/Y111B2A.3.1\_small\_RNA\_seq/results/fastqc /public/GW/Y111B2A.3.1\_small\_RNA\_seq/data/WAN611\_SR\_rep2.fq

Bowtie:

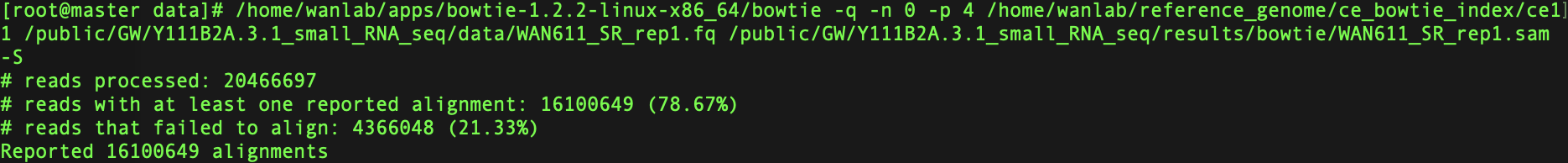
/home/wanlab/apps/bowtie-1.2.2-linux-x86\_64/bowtie -q -n 0 -p 4 /home/wanlab/reference\_genome/ce\_bowtie\_index/ce11 /public/GW/Y111B2A.3.1\_small\_RNA\_seq/data/N2\_SR\_rep1.fq /public/GW/Y111B2A.3.1\_small\_RNA\_seq/results/bowtie/N2\_SR\_rep1.sam -S



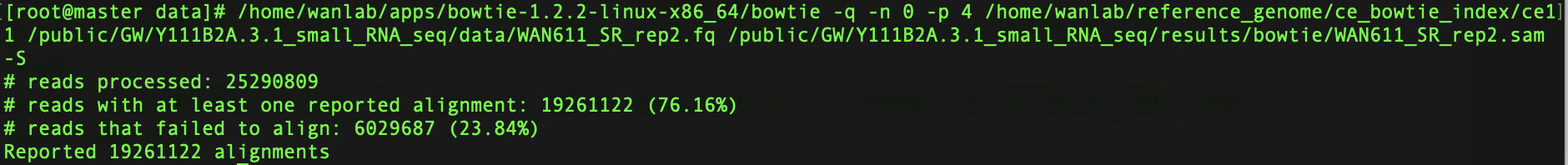
/home/wanlab/apps/bowtie-1.2.2-linux-x86\_64/bowtie -q -n 0 -p 4 /home/wanlab/reference\_genome/ce\_bowtie\_index/ce11 /public/GW/Y111B2A.3.1\_small\_RNA\_seq/data/N2\_SR\_rep2.fq /public/GW/Y111B2A.3.1\_small\_RNA\_seq/results/bowtie/N2\_SR\_rep2.sam -S



/home/wanlab/apps/bowtie-1.2.2-linux-x86\_64/bowtie -q -n 0 -p 4 /home/wanlab/reference\_genome/ce\_bowtie\_index/ce11 /public/GW/Y111B2A.3.1\_small\_RNA\_seq/data/WAN611\_SR\_rep1.fq /public/GW/Y111B2A.3.1\_small\_RNA\_seq/results/bowtie/WAN611\_SR\_rep1.sam -S



/home/wanlab/apps/bowtie-1.2.2-linux-x86\_64/bowtie -q -n 0 -p 4 /home/wanlab/reference\_genome/ce\_bowtie\_index/ce11 /public/GW/Y111B2A.3.1\_small\_RNA\_seq/data/WAN611\_SR\_rep2.fq /public/GW/Y111B2A.3.1\_small\_RNA\_seq/results/bowtie/WAN611\_SR\_rep2.sam -S



Sam to bam:

/home/wanlab/apps/samtools-1.14/samtools view -bS /public/GW/Y111B2A.3.1\_small\_RNA\_seq/results/bowtie/N2\_SR\_rep1.sam >/public/GW/Y111B2A.3.1\_small\_RNA\_seq/results/bowtie/N2\_SR\_rep1.bam

/home/wanlab/apps/samtools-1.14/samtools view -bS /public/GW/Y111B2A.3.1\_small\_RNA\_seq/results/bowtie/N2\_SR\_rep2.sam > /public/GW/Y111B2A.3.1\_small\_RNA\_seq/results/bowtie/N2\_SR\_rep2.bam

/home/wanlab/apps/samtools-1.14/samtools view -bS /public/GW/Y111B2A.3.1\_small\_RNA\_seq/results/bowtie/WAN611\_SR\_rep1.sam > /public/GW/Y111B2A.3.1\_small\_RNA\_seq/results/bowtie/WAN611\_SR\_rep1.bam

/home/wanlab/apps/samtools-1.14/samtools view -bS /public/GW/Y111B2A.3.1\_small\_RNA\_seq/results/bowtie/WAN611\_SR\_rep2.sam > /public/GW/Y111B2A.3.1\_small\_RNA\_seq/results/bowtie/WAN611\_SR\_rep2.bam

Featurecounts:

sh /public/GW/Y111B2A.3.1\_small\_RNA\_seq/scripts/featurecounts.sh

featurecounts.sh:

/home/wanlab/apps/subread-2.0.0-Linux-x86\_64/bin/featureCounts -T 4 -s 2 \

-a /home/wanlab/RNA\_seq/Caenorhabditis\_elegans.WBcel235.106.gtf \

-o /public/GW/Y111B2A.3.1\_small\_RNA\_seq/results/counts/N2\_WAN611\_SR\_featurecounts.txt \

/public/GW/Y111B2A.3.1\_small\_RNA\_seq/results/bowtie/\*.bam

Text

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