A Reanalysis of an Existing *Drosophila melanogaster* Dataset Reveals a New Set of Genes Involved in Post-Mating Response

Mapping Commands

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Contents

1 Experiment01_mRNAs

1.1 Experiment01_mRNAs_Bowtie_Commands

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MFAB1.stdout.%j
#SBATCH --error=01_mRNA_MFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MFAB1.fq \
    --al 01_mRNA_MFAB1_bowtie_al-mRNAs.fq \
    --un 01_mRNA_MFAB1_bowtie_un-mRNAs.fq \
    -S 01_mRNA_MFAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MFAB2.stdout.%j
#SBATCH --error=01_mRNA_MFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
```

```
    -a \
    -p 48 \
    -q \
    mRNA_MFAB2.fq \
    --al 01_mRNA_MFAB2_bowtie_al-mRNAs.fq \
    --un 01_mRNA_MFAB2_bowtie_un-mRNAs.fq \
    -S 01_mRNA_MFAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MFHT1.stdout.%j
#SBATCH --error=01_mRNA_MFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MFHT1.fq \
    --al 01_mRNA_MFHT1_bowtie_al-mRNAs.fq \
    --un 01_mRNA_MFHT1_bowtie_un-mRNAs.fq \
    -S 01_mRNA_MFHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MFHT2.stdout.%j
#SBATCH --error=01_mRNA_MFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0
```

```
bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MFHT2.fq \
    --al 01_mRNA_MFHT2_bowtie_al-mRNAs.fq \
    --un 01_mRNA_MFHT2_bowtie_un-mRNAs.fq \
    -S 01_mRNA_MFHT2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MMAB1.stdout.%j
#SBATCH --error=01_mRNA_MMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MMAB1.fq \
    --al 01_mRNA_MMAB1_bowtie_al-mRNAs.fq \
    --un 01_mRNA_MMAB1_bowtie_un-mRNAs.fq \
    -S 01_mRNA_MMAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MMAB2.stdout.%j
#SBATCH --error=01_mRNA_MMAB2.stderr.%j
```

```
module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MMAB2.fq \
    --al 01_mRNA_MMAB2_bowtie_al-mRNAs.fq \
    --un 01_mRNA_MMAB2_bowtie_un-mRNAs.fq \
    -S 01_mRNA_MMAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MMHT1.stdout.%j
#SBATCH --error=01_mRNA_MMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MMHT1.fq \
    --al 01_mRNA_MMHT1_bowtie_al-mRNAs.fq \
    --un 01_mRNA_MMHT1_bowtie_un-mRNAs.fq \
    -S 01_mRNA_MMHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
```

```
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MMHT2.stdout.%j
#SBATCH --error=01_mRNA_MMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MMHT2.fq \
    --al 01_mRNA_MMHT2_bowtie_al-mRNAs.fq \
    --un 01_mRNA_MMHT2_bowtie_un-mRNAs.fq \
    -S 01_mRNA_MMHT2.sam;
```

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#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
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#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VFAB1.stdout.%j
#SBATCH --error=01_mRNA_VFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VFAB1.fq \
    --al 01_mRNA_VFAB1_bowtie_al-mRNAs.fq \
    --un 01_mRNA_VFAB1_bowtie_un-mRNAs.fq \
    -S 01_mRNA_VFAB1.sam;
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#! /bin/bash
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#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VFAB2.stdout.%j
#SBATCH --error=01_mRNA_VFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VFAB2.fq \
    --al 01_mRNA_VFAB2_bowtie_al-mRNAs.fq \
    --un 01_mRNA_VFAB2_bowtie_un-mRNAs.fq \
    -S 01_mRNA_VFAB2.sam;
```

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#! /bin/bash
#SBATCH --export=NONE
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#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VFHT1.stdout.%j
#SBATCH --error=01_mRNA_VFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VFHT1.fq \
```

```
    --al 01_mRNA_VFHT1_bowtie_al-mRNAs.fq \
    --un 01_mRNA_VFHT1_bowtie_un-mRNAs.fq \
    -S 01_mRNA_VFHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VFHT2.stdout.%j
#SBATCH --error=01_mRNA_VFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VFHT2.fq \
    --al 01_mRNA_VFHT2_bowtie_al-mRNAs.fq \
    --un 01_mRNA_VFHT2_bowtie_un-mRNAs.fq \
    -S 01_mRNA_VFHT2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VMAB1.stdout.%j
#SBATCH --error=01_mRNA_VMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
```

```
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VMAB1.fq \
    --al 01_mRNA_VMAB1_bowtie_al-mRNAs.fq \
    --un 01_mRNA_VMAB1_bowtie_un-mRNAs.fq \
    -S 01_mRNA_VMAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VMAB2.stdout.%j
#SBATCH --error=01_mRNA_VMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VMAB2.fq \
    --al 01_mRNA_VMAB2_bowtie_al-mRNAs.fq \
    --un 01_mRNA_VMAB2_bowtie_un-mRNAs.fq \
    -S 01_mRNA_VMAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VMHT1.stdout.%j
#SBATCH --error=01_mRNA_VMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0
```

```
bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VMHT1.fq \
    --al 01_mRNA_VMHT1_bowtie_al-mRNAs.fq \
    --un 01_mRNA_VMHT1_bowtie_un-mRNAs.fq \
    -S 01_mRNA_VMHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VMHT2.stdout.%j
#SBATCH --error=01_mRNA_VMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VMHT2.fq \
    --al 01_mRNA_VMHT2_bowtie_al-mRNAs.fq \
    --un 01_mRNA_VMHT2_bowtie_un-mRNAs.fq \
    -S 01_mRNA_VMHT2.sam;
```

1.2 Experiment01_mRNAs_Salmon_Commands

```
module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    index \
    --transcripts Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --threads 48 \
    --index salmon_index \
    --kmerLen 9;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_mRNA_MFAB1.stdout.%j
#SBATCH --error=02_mRNA_MFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_mRNA_MFAB1_bowtie_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_MFAB1_bowtie_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
```

```
#SBATCH --output=02_mRNA_MFAB2.stdout.%j
#SBATCH --error=02_mRNA_MFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_mRNA_MFAB2_bowtie_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_MFAB2_bowtie_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_mRNA_MFHT1.stdout.%j
#SBATCH --error=02_mRNA_MFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_mRNA_MFHT1_bowtie_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_MFHT1_bowtie_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_mRNA_MFHT2.stdout.%j
#SBATCH --error=02_mRNA_MFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_mRNA_MFHT2_bowtie_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_MFHT2_bowtie_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_mRNA_MMAB1.stdout.%j
#SBATCH --error=02_mRNA_MMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_mRNA_MMAB1_bowtie_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
```

```
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_MMAB1_bowtie_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_mRNA_MMAB2.stdout.%j
#SBATCH --error=02_mRNA_MMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_mRNA_MMAB2_bowtie_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_MMAB2_bowtie_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_mRNA_MMHT1.stdout.%j
#SBATCH --error=02_mRNA_MMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
```

```
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_mRNA_MMHT1_bowtie_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_MMHT1_bowtie_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_mRNA_MMHT2.stdout.%j
#SBATCH --error=02_mRNA_MMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_mRNA_MMHT2_bowtie_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_MMHT2_bowtie_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_mRNA_VFAB1.stdout.%j
#SBATCH --error=02_mRNA_VFAB1.stderr.%j
```

```
module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_mRNA_VFAB1_bowtie_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_VFAB1_bowtie_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_mRNA_VFAB2.stdout.%j
#SBATCH --error=02_mRNA_VFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_mRNA_VFAB2_bowtie_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_VFAB2_bowtie_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
```

```
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_mRNA_VFHT1.stdout.%j
#SBATCH --error=02_mRNA_VFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_mRNA_VFHT1_bowtie_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_VFHT1_bowtie_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_mRNA_VFHT2.stdout.%j
#SBATCH --error=02_mRNA_VFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_mRNA_VFHT2_bowtie_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
```

```
    --numBootstraps 100 \
    --output 02_mRNA_VFHT2_bowtie_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_mRNA_VMAB1.stdout.%j
#SBATCH --error=02_mRNA_VMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_mRNA_VMAB1_bowtie_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_VMAB1_bowtie_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_mRNA_VMAB2.stdout.%j
#SBATCH --error=02_mRNA_VMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
```

```
    --libType U \
    --unmatedReads 01_mRNA_VMAB2_bowtie_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_VMAB2_bowtie_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_mRNA_VMHT1.stdout.%j
#SBATCH --error=02_mRNA_VMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_mRNA_VMHT1_bowtie_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_VMHT1_bowtie_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_mRNA_VMHT2.stdout.%j
#SBATCH --error=02_mRNA_VMHT2.stderr.%j

module purge
```

```
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_mRNA_VMHT2_bowtie_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_VMHT2_bowtie_al-mRNAs.fq_Salmon;
```

2 Experiment01_sRNAs

2.1 Experiment01_sRNAs_Bowtie_Commands

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MFAB1.stdout.%j
#SBATCH --error=01_sRNA_MFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MFAB1.fq \
    --al 01_sRNA_MFAB1_bowtie_al-sRNAs.fq \
    --un 01_sRNA_MFAB1_bowtie_un-sRNAs.fq \
    -S 01_sRNA_MFAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MFAB2.stdout.%j
#SBATCH --error=01_sRNA_MFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
```

```
    -a \
    -p 48 \
    -q \
    sRNA_MFAB2.fq \
    --al 01_sRNA_MFAB2_bowtie_al-sRNAs.fq \
    --un 01_sRNA_MFAB2_bowtie_un-sRNAs.fq \
    -S 01_sRNA_MFAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MFHT1.stdout.%j
#SBATCH --error=01_sRNA_MFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MFHT1.fq \
    --al 01_sRNA_MFHT1_bowtie_al-sRNAs.fq \
    --un 01_sRNA_MFHT1_bowtie_un-sRNAs.fq \
    -S 01_sRNA_MFHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MFHT2.stdout.%j
#SBATCH --error=01_sRNA_MFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0
```

```
bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MFHT2.fq \
    --al 01_sRNA_MFHT2_bowtie_al-sRNAs.fq \
    --un 01_sRNA_MFHT2_bowtie_un-sRNAs.fq \
    -S 01_sRNA_MFHT2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MMAB1.stdout.%j
#SBATCH --error=01_sRNA_MMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MMAB1.fq \
    --al 01_sRNA_MMAB1_bowtie_al-sRNAs.fq \
    --un 01_sRNA_MMAB1_bowtie_un-sRNAs.fq \
    -S 01_sRNA_MMAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MMAB2.stdout.%j
#SBATCH --error=01_sRNA_MMAB2.stderr.%j
```

```
module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MMAB2.fq \
    --al 01_sRNA_MMAB2_bowtie_al-sRNAs.fq \
    --un 01_sRNA_MMAB2_bowtie_un-sRNAs.fq \
    -S 01_sRNA_MMAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MMHT1.stdout.%j
#SBATCH --error=01_sRNA_MMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MMHT1.fq \
    --al 01_sRNA_MMHT1_bowtie_al-sRNAs.fq \
    --un 01_sRNA_MMHT1_bowtie_un-sRNAs.fq \
    -S 01_sRNA_MMHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
```

```
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MMHT2.stdout.%j
#SBATCH --error=01_sRNA_MMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MMHT2.fq \
    --al 01_sRNA_MMHT2_bowtie_al-sRNAs.fq \
    --un 01_sRNA_MMHT2_bowtie_un-sRNAs.fq \
    -S 01_sRNA_MMHT2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VFAB1.stdout.%j
#SBATCH --error=01_sRNA_VFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_VFAB1.fq \
    --al 01_sRNA_VFAB1_bowtie_al-sRNAs.fq \
    --un 01_sRNA_VFAB1_bowtie_un-sRNAs.fq \
    -S 01_sRNA_VFAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VFAB2.stdout.%j
#SBATCH --error=01_sRNA_VFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_VFAB2.fq \
    --al 01_sRNA_VFAB2_bowtie_al-sRNAs.fq \
    --un 01_sRNA_VFAB2_bowtie_un-sRNAs.fq \
    -S 01_sRNA_VFAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VFHT1.stdout.%j
#SBATCH --error=01_sRNA_VFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_VFHT1.fq \
```

```
    --al 01_sRNA_VFHT1_bowtie_al-sRNAs.fq \
    --un 01_sRNA_VFHT1_bowtie_un-sRNAs.fq \
    -S 01_sRNA_VFHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VFHT2.stdout.%j
#SBATCH --error=01_sRNA_VFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_VFHT2.fq \
    --al 01_sRNA_VFHT2_bowtie_al-sRNAs.fq \
    --un 01_sRNA_VFHT2_bowtie_un-sRNAs.fq \
    -S 01_sRNA_VFHT2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VMAB1.stdout.%j
#SBATCH --error=01_sRNA_VMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
```

```
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_VMAB1.fq \
    --al 01_sRNA_VMAB1_bowtie_al-sRNAs.fq \
    --un 01_sRNA_VMAB1_bowtie_un-sRNAs.fq \
    -S 01_sRNA_VMAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VMAB2.stdout.%j
#SBATCH --error=01_sRNA_VMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_VMAB2.fq \
    --al 01_sRNA_VMAB2_bowtie_al-sRNAs.fq \
    --un 01_sRNA_VMAB2_bowtie_un-sRNAs.fq \
    -S 01_sRNA_VMAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VMHT1.stdout.%j
#SBATCH --error=01_sRNA_VMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0
```

```
bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_VMHT1.fq \
    --al 01_sRNA_VMHT1_bowtie_al-sRNAs.fq \
    --un 01_sRNA_VMHT1_bowtie_un-sRNAs.fq \
    -S 01_sRNA_VMHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VMHT2.stdout.%j
#SBATCH --error=01_sRNA_VMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_VMHT2.fq \
    --al 01_sRNA_VMHT2_bowtie_al-sRNAs.fq \
    --un 01_sRNA_VMHT2_bowtie_un-sRNAs.fq \
    -S 01_sRNA_VMHT2.sam;
```

2.2 Experiment01_sRNAs_Salmon_Commands

```
module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    index \
    --transcripts Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --threads 48 \
    --index salmon_index \
    --kmerLen 9;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_sRNA_MFAB1.stdout.%j
#SBATCH --error=02_sRNA_MFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_sRNA_MFAB1_bowtie_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_MFAB1_bowtie_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
```

```
#SBATCH --output=02_sRNA_MFAB2.stdout.%j
#SBATCH --error=02_sRNA_MFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_sRNA_MFAB2_bowtie_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_MFAB2_bowtie_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_sRNA_MFHT1.stdout.%j
#SBATCH --error=02_sRNA_MFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_sRNA_MFHT1_bowtie_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_MFHT1_bowtie_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_sRNA_MFHT2.stdout.%j
#SBATCH --error=02_sRNA_MFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_sRNA_MFHT2_bowtie_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_MFHT2_bowtie_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_sRNA_MMAB1.stdout.%j
#SBATCH --error=02_sRNA_MMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_sRNA_MMAB1_bowtie_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
```

```
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_MMAB1_bowtie_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_sRNA_MMAB2.stdout.%j
#SBATCH --error=02_sRNA_MMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_sRNA_MMAB2_bowtie_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_MMAB2_bowtie_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_sRNA_MMHT1.stdout.%j
#SBATCH --error=02_sRNA_MMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
```

```
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_sRNA_MMHT1_bowtie_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_MMHT1_bowtie_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_sRNA_MMHT2.stdout.%j
#SBATCH --error=02_sRNA_MMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_sRNA_MMHT2_bowtie_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_MMHT2_bowtie_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_sRNA_VFAB1.stdout.%j
#SBATCH --error=02_sRNA_VFAB1.stderr.%j
```

```
module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_sRNA_VFAB1_bowtie_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_VFAB1_bowtie_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_sRNA_VFAB2.stdout.%j
#SBATCH --error=02_sRNA_VFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_sRNA_VFAB2_bowtie_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_VFAB2_bowtie_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
```

```
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_sRNA_VFHT1.stdout.%j
#SBATCH --error=02_sRNA_VFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_sRNA_VFHT1_bowtie_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_VFHT1_bowtie_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_sRNA_VFHT2.stdout.%j
#SBATCH --error=02_sRNA_VFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_sRNA_VFHT2_bowtie_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
```

```
    --numBootstraps 100 \
    --output 02_sRNA_VFHT2_bowtie_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_sRNA_VMAB1.stdout.%j
#SBATCH --error=02_sRNA_VMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_sRNA_VMAB1_bowtie_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_VMAB1_bowtie_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_sRNA_VMAB2.stdout.%j
#SBATCH --error=02_sRNA_VMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
```

```
    --libType U \
    --unmatedReads 01_sRNA_VMAB2_bowtie_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_VMAB2_bowtie_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_sRNA_VMHT1.stdout.%j
#SBATCH --error=02_sRNA_VMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_sRNA_VMHT1_bowtie_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_VMHT1_bowtie_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=02_sRNA_VMHT2.stdout.%j
#SBATCH --error=02_sRNA_VMHT2.stderr.%j

module purge
```

```
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    --unmatedReads 01_sRNA_VMHT2_bowtie_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_VMHT2_bowtie_al-sRNAs.fq_Salmon;
```

3 Experiment02_mRNAs

3.1 Experiment02_mRNAs_Salmon_Commands

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=01_E02.stdout.%j
#SBATCH --error=01_E02.stderr.%j

module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    index \
    --transcripts zzGentrome/Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --threads 20 \
    --index salmon_index \
    --kmerLen 9;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r mRNA_MFAB1.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_MFAB1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r mRNA_MFAB2.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_MFAB2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r mRNA_MFHT1.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_MFHT1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r mRNA_MFHT2.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_MFHT2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r mRNA_MMAB1.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
```

```
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_MMAB1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r mRNA_MMAB2.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_MMAB2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r mRNA_MMHT1.fq \
    --validateMappings \
```

```
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_MMHT1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r mRNA_MMHT2.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_MMHT2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
```

```
    --libType U \
    -r mRNA_VFAB1.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_VFAB1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r mRNA_VFAB2.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_VFAB2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0
```

```
salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r mRNA_VFHT1.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_VFHT1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r mRNA_VFHT2.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_VFHT2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j
```

```
module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r mRNA_VMAB1.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_VMAB1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r mRNA_VMAB2.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_VMAB2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
```

```
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r mRNA_VMHT1.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_VMHT1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r mRNA_VMHT2.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_mRNA_VMHT2;
```

---

4 Experiment02_sRNAs

4.1 Experiment02_sRNAs_Salmon_Commands

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=01_E02.stdout.%j
#SBATCH --error=01_E02.stderr.%j

module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    index \
    --transcripts zzGentrome/Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --threads 20 \
    --index salmon_index \
    --kmerLen 9;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r sRNA_MFAB1.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_MFAB1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r sRNA_MFAB2.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_MFAB2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r sRNA_MFHT1.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_MFHT1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r sRNA_MFHT2.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_MFHT2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r sRNA_MMAB1.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
```

```
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_MMAB1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r sRNA_MMAB2.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_MMAB2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r sRNA_MMHT1.fq \
    --validateMappings \
```

```
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_MMHT1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r sRNA_MMHT2.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_MMHT2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
```

```
    --libType U \
    -r sRNA_VFAB1.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_VFAB1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r sRNA_VFAB2.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_VFAB2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0
```

```
salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r sRNA_VFHT1.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_VFHT1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r sRNA_VFHT2.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_VFHT2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j
```

```
module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r sRNA_VMAB1.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_VMAB1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r sRNA_VMAB2.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_VMAB2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
```

```
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r sRNA_VMHT1.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_VMHT1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=E02
#SBATCH --time=24:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=20
#SBATCH --mem=360G
#SBATCH --output=02_E02.stdout.%j
#SBATCH --error=02_E02.stderr.%j


module load GCC/9.3.0  OpenMPI/4.0.3 Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r sRNA_VMHT2.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 20 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 02_sRNA_VMHT2;
```

---

5 Experiment03_mRNAs

5.1 Experiment03_mRNAs_Bowtie_Commands

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MFAB1.stdout.%j
#SBATCH --error=01_mRNA_MFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MFAB1.fq \
    --al 01_mRNA_MFAB1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MFAB1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MFAB1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MFAB1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MFAB1_bowtie_un-sRNAs_al-mRNAs.fq \
    --un 02_mRNA_MFAB1_bowtie_un-sRNAs_un-mRNAs.fq \
    -S 02_mRNA_MFAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
```

```
#SBATCH --output=01_mRNA_MFAB2.stdout.%j
#SBATCH --error=01_mRNA_MFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MFAB2.fq \
    --al 01_mRNA_MFAB2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MFAB2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MFAB2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MFAB2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MFAB2_bowtie_un-sRNAs_al-mRNAs.fq \
    --un 02_mRNA_MFAB2_bowtie_un-sRNAs_un-mRNAs.fq \
    -S 02_mRNA_MFAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MFHT1.stdout.%j
#SBATCH --error=01_mRNA_MFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
```

```
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MFHT1.fq \
    --al 01_mRNA_MFHT1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MFHT1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MFHT1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MFHT1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MFHT1_bowtie_un-sRNAs_al-mRNAs.fq \
    --un 02_mRNA_MFHT1_bowtie_un-sRNAs_un-mRNAs.fq \
    -S 02_mRNA_MFHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MFHT2.stdout.%j
#SBATCH --error=01_mRNA_MFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MFHT2.fq \
    --al 01_mRNA_MFHT2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MFHT2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MFHT2.sam;

bowtie \
```

```
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MFHT2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MFHT2_bowtie_un-sRNAs_al-mRNAs.fq \
    --un 02_mRNA_MFHT2_bowtie_un-sRNAs_un-mRNAs.fq \
    -S 02_mRNA_MFHT2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MMAB1.stdout.%j
#SBATCH --error=01_mRNA_MMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MMAB1.fq \
    --al 01_mRNA_MMAB1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MMAB1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MMAB1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MMAB1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MMAB1_bowtie_un-sRNAs_al-mRNAs.fq \
    --un 02_mRNA_MMAB1_bowtie_un-sRNAs_un-mRNAs.fq \
    -S 02_mRNA_MMAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MMAB2.stdout.%j
#SBATCH --error=01_mRNA_MMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MMAB2.fq \
    --al 01_mRNA_MMAB2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MMAB2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MMAB2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MMAB2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MMAB2_bowtie_un-sRNAs_al-mRNAs.fq \
    --un 02_mRNA_MMAB2_bowtie_un-sRNAs_un-mRNAs.fq \
    -S 02_mRNA_MMAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MMHT1.stdout.%j
#SBATCH --error=01_mRNA_MMHT1.stderr.%j
```

```
module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MMHT1.fq \
    --al 01_mRNA_MMHT1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MMHT1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MMHT1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MMHT1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MMHT1_bowtie_un-sRNAs_al-mRNAs.fq \
    --un 02_mRNA_MMHT1_bowtie_un-sRNAs_un-mRNAs.fq \
    -S 02_mRNA_MMHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MMHT2.stdout.%j
#SBATCH --error=01_mRNA_MMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
```

```
    -a \
    -p 48 \
    -q \
    mRNA_MMHT2.fq \
    --al 01_mRNA_MMHT2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MMHT2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MMHT2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MMHT2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MMHT2_bowtie_un-sRNAs_al-mRNAs.fq \
    --un 02_mRNA_MMHT2_bowtie_un-sRNAs_un-mRNAs.fq \
    -S 02_mRNA_MMHT2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VFAB1.stdout.%j
#SBATCH --error=01_mRNA_VFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VFAB1.fq \
    --al 01_mRNA_VFAB1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VFAB1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VFAB1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
```

```
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_VFAB1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VFAB1_bowtie_un-sRNAs_al-mRNAs.fq \
    --un 02_mRNA_VFAB1_bowtie_un-sRNAs_un-mRNAs.fq \
    -S 02_mRNA_VFAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VFAB2.stdout.%j
#SBATCH --error=01_mRNA_VFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VFAB2.fq \
    --al 01_mRNA_VFAB2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VFAB2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VFAB2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_VFAB2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VFAB2_bowtie_un-sRNAs_al-mRNAs.fq \
    --un 02_mRNA_VFAB2_bowtie_un-sRNAs_un-mRNAs.fq \
    -S 02_mRNA_VFAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VFHT1.stdout.%j
#SBATCH --error=01_mRNA_VFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VFHT1.fq \
    --al 01_mRNA_VFHT1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VFHT1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VFHT1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_VFHT1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VFHT1_bowtie_un-sRNAs_al-mRNAs.fq \
    --un 02_mRNA_VFHT1_bowtie_un-sRNAs_un-mRNAs.fq \
    -S 02_mRNA_VFHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VFHT2.stdout.%j
#SBATCH --error=01_mRNA_VFHT2.stderr.%j

module purge
```

```
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VFHT2.fq \
    --al 01_mRNA_VFHT2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VFHT2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VFHT2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_VFHT2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VFHT2_bowtie_un-sRNAs_al-mRNAs.fq \
    --un 02_mRNA_VFHT2_bowtie_un-sRNAs_un-mRNAs.fq \
    -S 02_mRNA_VFHT2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VMAB1.stdout.%j
#SBATCH --error=01_mRNA_VMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
```

```
    -q \
    mRNA_VMAB1.fq \
    --al 01_mRNA_VMAB1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VMAB1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VMAB1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_VMAB1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VMAB1_bowtie_un-sRNAs_al-mRNAs.fq \
    --un 02_mRNA_VMAB1_bowtie_un-sRNAs_un-mRNAs.fq \
    -S 02_mRNA_VMAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VMAB2.stdout.%j
#SBATCH --error=01_mRNA_VMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VMAB2.fq \
    --al 01_mRNA_VMAB2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VMAB2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VMAB2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
```

```
    -a \
    -p 48 \
    -q \
    01_mRNA_VMAB2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VMAB2_bowtie_un-sRNAs_al-mRNAs.fq \
    --un 02_mRNA_VMAB2_bowtie_un-sRNAs_un-mRNAs.fq \
    -S 02_mRNA_VMAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VMHT1.stdout.%j
#SBATCH --error=01_mRNA_VMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VMHT1.fq \
    --al 01_mRNA_VMHT1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VMHT1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VMHT1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_VMHT1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VMHT1_bowtie_un-sRNAs_al-mRNAs.fq \
    --un 02_mRNA_VMHT1_bowtie_un-sRNAs_un-mRNAs.fq \
    -S 02_mRNA_VMHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
```

```
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VMHT2.stdout.%j
#SBATCH --error=01_mRNA_VMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VMHT2.fq \
    --al 01_mRNA_VMHT2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VMHT2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VMHT2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_VMHT2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VMHT2_bowtie_un-sRNAs_al-mRNAs.fq \
    --un 02_mRNA_VMHT2_bowtie_un-sRNAs_un-mRNAs.fq \
    -S 02_mRNA_VMHT2.sam;
```

5.2 Experiment03_mRNAs_Salmon_Commands

```
module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    index \
    --transcripts Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --threads 48 \
    --index salmon_index \
    --kmerLen 9;
```

```
mkdir 03_mRNA_MFAB1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_MFAB2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_MFHT1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_MFHT2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_MMAB1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_MMAB2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_MMHT1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_MMHT2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_VFAB1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_VFAB2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_VFHT1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_VFHT2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_VMAB1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_VMAB2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_VMHT1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_VMHT2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_MFAB1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_MFAB2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_MFHT1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_MFHT2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_MMAB1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_MMAB2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_MMHT1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_MMHT2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_VFAB1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_VFAB2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_VFHT1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_VFHT2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_VMAB1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_VMAB2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_VMHT1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
mkdir 03_mRNA_VMHT2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
```

```
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MFAB1.stdout.%j
#SBATCH --error=04_mRNA_MFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_mRNA_MFAB1_bowtie_un-sRNAs_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_mRNA_MFAB1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MFAB2.stdout.%j
#SBATCH --error=04_mRNA_MFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_mRNA_MFAB2_bowtie_un-sRNAs_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
```

```
    --output 03_mRNA_MFAB2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MFHT1.stdout.%j
#SBATCH --error=04_mRNA_MFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_mRNA_MFHT1_bowtie_un-sRNAs_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_mRNA_MFHT1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MFHT2.stdout.%j
#SBATCH --error=04_mRNA_MFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
```

```
    -r 02_mRNA_MFHT2_bowtie_un-sRNAs_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_mRNA_MFHT2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MMAB1.stdout.%j
#SBATCH --error=04_mRNA_MMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_mRNA_MMAB1_bowtie_un-sRNAs_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_mRNA_MMAB1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MMAB2.stdout.%j
#SBATCH --error=04_mRNA_MMAB2.stderr.%j

module purge
module load GCC/9.3.0
```

```
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_mRNA_MMAB2_bowtie_un-sRNAs_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_mRNA_MMAB2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MMHT1.stdout.%j
#SBATCH --error=04_mRNA_MMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_mRNA_MMHT1_bowtie_un-sRNAs_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_mRNA_MMHT1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
```

```
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MMHT2.stdout.%j
#SBATCH --error=04_mRNA_MMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_mRNA_MMHT2_bowtie_un-sRNAs_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_mRNA_MMHT2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VFAB1.stdout.%j
#SBATCH --error=04_mRNA_VFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_mRNA_VFAB1_bowtie_un-sRNAs_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_mRNA_VFAB1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VFAB2.stdout.%j
#SBATCH --error=04_mRNA_VFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_mRNA_VFAB2_bowtie_un-sRNAs_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_mRNA_VFAB2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VFHT1.stdout.%j
#SBATCH --error=04_mRNA_VFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_mRNA_VFHT1_bowtie_un-sRNAs_al-mRNAs.fq \
    --validateMappings \
```

```
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_mRNA_VFHT1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VFHT2.stdout.%j
#SBATCH --error=04_mRNA_VFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_mRNA_VFHT2_bowtie_un-sRNAs_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_mRNA_VFHT2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VMAB1.stdout.%j
#SBATCH --error=04_mRNA_VMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0
```

```
salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_mRNA_VMAB1_bowtie_un-sRNAs_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_mRNA_VMAB1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VMAB2.stdout.%j
#SBATCH --error=04_mRNA_VMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_mRNA_VMAB2_bowtie_un-sRNAs_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_mRNA_VMAB2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
```

```
#SBATCH --output=04_mRNA_VMHT1.stdout.%j
#SBATCH --error=04_mRNA_VMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_mRNA_VMHT1_bowtie_un-sRNAs_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_mRNA_VMHT1_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VMHT2.stdout.%j
#SBATCH --error=04_mRNA_VMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_mRNA_VMHT2_bowtie_un-sRNAs_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_mRNA_VMHT2_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
```

---

6 Experiment03_mRNAs_all

6.1 Experiment03_mRNAs_Bowtie_Commands

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MVABHT.stdout.%j
#SBATCH --error=01_mRNA_MVABHT.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MVABHT.fq \
    --al 01_mRNA_MVABHT_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MVABHT_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MVABHT.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MVABHT_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MVABHT_bowtie_un-sRNAs_al-mRNAs.fq \
    --un 02_mRNA_MVABHT_bowtie_un-sRNAs_un-mRNAs.fq \
    -S 02_mRNA_MVABHT.sam;
```

6.2 Experiment03_mRNAs_Salmon_Commands

```
module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    index \
    --transcripts Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --threads 48 \
    --index salmon_index \
    --kmerLen 9;
```

```
mkdir 03_mRNA_MVABHT_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MVABHT.stdout.%j
#SBATCH --error=04_mRNA_MVABHT.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_mRNA_MVABHT_bowtie_un-sRNAs_al-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_mRNA_MVABHT_bowtie_un-sRNAs_al-mRNAs.fq_Salmon;
```

---

7 Experiment03_sRNAs

7.1 Experiment03_sRNAs_Bowtie_Commands

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MFAB1.stdout.%j
#SBATCH --error=01_sRNA_MFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MFAB1.fq \
    --al 01_sRNA_MFAB1_bowtie_al-mRNAs.fq \
    --un 01_sRNA_MFAB1_bowtie_un-mRNAs.fq \
    -S 01_sRNA_MFAB1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_MFAB1_bowtie_un-mRNAs.fq \
    --al 02_sRNA_MFAB1_bowtie_un-mRNAs_al-sRNAs.fq \
    --un 02_sRNA_MFAB1_bowtie_un-mRNAs_un-sRNAs.fq \
    -S 02_sRNA_MFAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
```

```
#SBATCH --output=01_sRNA_MFAB2.stdout.%j
#SBATCH --error=01_sRNA_MFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MFAB2.fq \
    --al 01_sRNA_MFAB2_bowtie_al-mRNAs.fq \
    --un 01_sRNA_MFAB2_bowtie_un-mRNAs.fq \
    -S 01_sRNA_MFAB2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_MFAB2_bowtie_un-mRNAs.fq \
    --al 02_sRNA_MFAB2_bowtie_un-mRNAs_al-sRNAs.fq \
    --un 02_sRNA_MFAB2_bowtie_un-mRNAs_un-sRNAs.fq \
    -S 02_sRNA_MFAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MFHT1.stdout.%j
#SBATCH --error=01_sRNA_MFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
```

```
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MFHT1.fq \
    --al 01_sRNA_MFHT1_bowtie_al-mRNAs.fq \
    --un 01_sRNA_MFHT1_bowtie_un-mRNAs.fq \
    -S 01_sRNA_MFHT1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_MFHT1_bowtie_un-mRNAs.fq \
    --al 02_sRNA_MFHT1_bowtie_un-mRNAs_al-sRNAs.fq \
    --un 02_sRNA_MFHT1_bowtie_un-mRNAs_un-sRNAs.fq \
    -S 02_sRNA_MFHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MFHT2.stdout.%j
#SBATCH --error=01_sRNA_MFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MFHT2.fq \
    --al 01_sRNA_MFHT2_bowtie_al-mRNAs.fq \
    --un 01_sRNA_MFHT2_bowtie_un-mRNAs.fq \
    -S 01_sRNA_MFHT2.sam;

bowtie \
```

```
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_MFHT2_bowtie_un-mRNAs.fq \
    --al 02_sRNA_MFHT2_bowtie_un-mRNAs_al-sRNAs.fq \
    --un 02_sRNA_MFHT2_bowtie_un-mRNAs_un-sRNAs.fq \
    -S 02_sRNA_MFHT2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MMAB1.stdout.%j
#SBATCH --error=01_sRNA_MMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MMAB1.fq \
    --al 01_sRNA_MMAB1_bowtie_al-mRNAs.fq \
    --un 01_sRNA_MMAB1_bowtie_un-mRNAs.fq \
    -S 01_sRNA_MMAB1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_MMAB1_bowtie_un-mRNAs.fq \
    --al 02_sRNA_MMAB1_bowtie_un-mRNAs_al-sRNAs.fq \
    --un 02_sRNA_MMAB1_bowtie_un-mRNAs_un-sRNAs.fq \
    -S 02_sRNA_MMAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MMAB2.stdout.%j
#SBATCH --error=01_sRNA_MMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MMAB2.fq \
    --al 01_sRNA_MMAB2_bowtie_al-mRNAs.fq \
    --un 01_sRNA_MMAB2_bowtie_un-mRNAs.fq \
    -S 01_sRNA_MMAB2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_MMAB2_bowtie_un-mRNAs.fq \
    --al 02_sRNA_MMAB2_bowtie_un-mRNAs_al-sRNAs.fq \
    --un 02_sRNA_MMAB2_bowtie_un-mRNAs_un-sRNAs.fq \
    -S 02_sRNA_MMAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MMHT1.stdout.%j
#SBATCH --error=01_sRNA_MMHT1.stderr.%j
```

```
module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MMHT1.fq \
    --al 01_sRNA_MMHT1_bowtie_al-mRNAs.fq \
    --un 01_sRNA_MMHT1_bowtie_un-mRNAs.fq \
    -S 01_sRNA_MMHT1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_MMHT1_bowtie_un-mRNAs.fq \
    --al 02_sRNA_MMHT1_bowtie_un-mRNAs_al-sRNAs.fq \
    --un 02_sRNA_MMHT1_bowtie_un-mRNAs_un-sRNAs.fq \
    -S 02_sRNA_MMHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MMHT2.stdout.%j
#SBATCH --error=01_sRNA_MMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
```

```
    -a \
    -p 48 \
    -q \
    sRNA_MMHT2.fq \
    --al 01_sRNA_MMHT2_bowtie_al-mRNAs.fq \
    --un 01_sRNA_MMHT2_bowtie_un-mRNAs.fq \
    -S 01_sRNA_MMHT2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_MMHT2_bowtie_un-mRNAs.fq \
    --al 02_sRNA_MMHT2_bowtie_un-mRNAs_al-sRNAs.fq \
    --un 02_sRNA_MMHT2_bowtie_un-mRNAs_un-sRNAs.fq \
    -S 02_sRNA_MMHT2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VFAB1.stdout.%j
#SBATCH --error=01_sRNA_VFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_VFAB1.fq \
    --al 01_sRNA_VFAB1_bowtie_al-mRNAs.fq \
    --un 01_sRNA_VFAB1_bowtie_un-mRNAs.fq \
    -S 01_sRNA_VFAB1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
```

```
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_VFAB1_bowtie_un-mRNAs.fq \
    --al 02_sRNA_VFAB1_bowtie_un-mRNAs_al-sRNAs.fq \
    --un 02_sRNA_VFAB1_bowtie_un-mRNAs_un-sRNAs.fq \
    -S 02_sRNA_VFAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VFAB2.stdout.%j
#SBATCH --error=01_sRNA_VFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_VFAB2.fq \
    --al 01_sRNA_VFAB2_bowtie_al-mRNAs.fq \
    --un 01_sRNA_VFAB2_bowtie_un-mRNAs.fq \
    -S 01_sRNA_VFAB2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_VFAB2_bowtie_un-mRNAs.fq \
    --al 02_sRNA_VFAB2_bowtie_un-mRNAs_al-sRNAs.fq \
    --un 02_sRNA_VFAB2_bowtie_un-mRNAs_un-sRNAs.fq \
    -S 02_sRNA_VFAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VFHT1.stdout.%j
#SBATCH --error=01_sRNA_VFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_VFHT1.fq \
    --al 01_sRNA_VFHT1_bowtie_al-mRNAs.fq \
    --un 01_sRNA_VFHT1_bowtie_un-mRNAs.fq \
    -S 01_sRNA_VFHT1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_VFHT1_bowtie_un-mRNAs.fq \
    --al 02_sRNA_VFHT1_bowtie_un-mRNAs_al-sRNAs.fq \
    --un 02_sRNA_VFHT1_bowtie_un-mRNAs_un-sRNAs.fq \
    -S 02_sRNA_VFHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VFHT2.stdout.%j
#SBATCH --error=01_sRNA_VFHT2.stderr.%j

module purge
```

```
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_VFHT2.fq \
    --al 01_sRNA_VFHT2_bowtie_al-mRNAs.fq \
    --un 01_sRNA_VFHT2_bowtie_un-mRNAs.fq \
    -S 01_sRNA_VFHT2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_VFHT2_bowtie_un-mRNAs.fq \
    --al 02_sRNA_VFHT2_bowtie_un-mRNAs_al-sRNAs.fq \
    --un 02_sRNA_VFHT2_bowtie_un-mRNAs_un-sRNAs.fq \
    -S 02_sRNA_VFHT2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VMAB1.stdout.%j
#SBATCH --error=01_sRNA_VMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
```

```
    -q \
    sRNA_VMAB1.fq \
    --al 01_sRNA_VMAB1_bowtie_al-mRNAs.fq \
    --un 01_sRNA_VMAB1_bowtie_un-mRNAs.fq \
    -S 01_sRNA_VMAB1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_VMAB1_bowtie_un-mRNAs.fq \
    --al 02_sRNA_VMAB1_bowtie_un-mRNAs_al-sRNAs.fq \
    --un 02_sRNA_VMAB1_bowtie_un-mRNAs_un-sRNAs.fq \
    -S 02_sRNA_VMAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VMAB2.stdout.%j
#SBATCH --error=01_sRNA_VMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_VMAB2.fq \
    --al 01_sRNA_VMAB2_bowtie_al-mRNAs.fq \
    --un 01_sRNA_VMAB2_bowtie_un-mRNAs.fq \
    -S 01_sRNA_VMAB2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
```

```
    -a \
    -p 48 \
    -q \
    01_sRNA_VMAB2_bowtie_un-mRNAs.fq \
    --al 02_sRNA_VMAB2_bowtie_un-mRNAs_al-sRNAs.fq \
    --un 02_sRNA_VMAB2_bowtie_un-mRNAs_un-sRNAs.fq \
    -S 02_sRNA_VMAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VMHT1.stdout.%j
#SBATCH --error=01_sRNA_VMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_VMHT1.fq \
    --al 01_sRNA_VMHT1_bowtie_al-mRNAs.fq \
    --un 01_sRNA_VMHT1_bowtie_un-mRNAs.fq \
    -S 01_sRNA_VMHT1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_VMHT1_bowtie_un-mRNAs.fq \
    --al 02_sRNA_VMHT1_bowtie_un-mRNAs_al-sRNAs.fq \
    --un 02_sRNA_VMHT1_bowtie_un-mRNAs_un-sRNAs.fq \
    -S 02_sRNA_VMHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
```

```
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VMHT2.stdout.%j
#SBATCH --error=01_sRNA_VMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_VMHT2.fq \
    --al 01_sRNA_VMHT2_bowtie_al-mRNAs.fq \
    --un 01_sRNA_VMHT2_bowtie_un-mRNAs.fq \
    -S 01_sRNA_VMHT2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_VMHT2_bowtie_un-mRNAs.fq \
    --al 02_sRNA_VMHT2_bowtie_un-mRNAs_al-sRNAs.fq \
    --un 02_sRNA_VMHT2_bowtie_un-mRNAs_un-sRNAs.fq \
    -S 02_sRNA_VMHT2.sam;
```

7.2 Experiment03_sRNAs_Salmon_Commands

```
module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    index \
    --transcripts Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --threads 48 \
    --index salmon_index \
    --kmerLen 9;
```

```
mkdir 03_sRNA_MFAB1_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
mkdir 03_sRNA_MFAB2_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
mkdir 03_sRNA_MFHT1_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
mkdir 03_sRNA_MFHT2_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
mkdir 03_sRNA_MMAB1_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
mkdir 03_sRNA_MMAB2_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
mkdir 03_sRNA_MMHT1_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
mkdir 03_sRNA_MMHT2_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
mkdir 03_sRNA_VFAB1_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
mkdir 03_sRNA_VFAB2_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
mkdir 03_sRNA_VFHT1_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
mkdir 03_sRNA_VFHT2_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
mkdir 03_sRNA_VMAB1_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
mkdir 03_sRNA_VMAB2_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
mkdir 03_sRNA_VMHT1_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
mkdir 03_sRNA_VMHT2_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_MFAB1.stdout.%j
#SBATCH --error=04_sRNA_MFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
```

```
    -r 02_sRNA_MFAB1_bowtie_un-mRNAs_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_sRNA_MFAB1_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_MFAB2.stdout.%j
#SBATCH --error=04_sRNA_MFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_sRNA_MFAB2_bowtie_un-mRNAs_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_sRNA_MFAB2_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_MFHT1.stdout.%j
#SBATCH --error=04_sRNA_MFHT1.stderr.%j

module purge
module load GCC/9.3.0
```

```
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_sRNA_MFHT1_bowtie_un-mRNAs_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_sRNA_MFHT1_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_MFHT2.stdout.%j
#SBATCH --error=04_sRNA_MFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_sRNA_MFHT2_bowtie_un-mRNAs_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_sRNA_MFHT2_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
```

```
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_MMAB1.stdout.%j
#SBATCH --error=04_sRNA_MMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_sRNA_MMAB1_bowtie_un-mRNAs_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_sRNA_MMAB1_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_MMAB2.stdout.%j
#SBATCH --error=04_sRNA_MMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_sRNA_MMAB2_bowtie_un-mRNAs_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_sRNA_MMAB2_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_MMHT1.stdout.%j
#SBATCH --error=04_sRNA_MMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_sRNA_MMHT1_bowtie_un-mRNAs_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_sRNA_MMHT1_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_MMHT2.stdout.%j
#SBATCH --error=04_sRNA_MMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_sRNA_MMHT2_bowtie_un-mRNAs_al-sRNAs.fq \
    --validateMappings \
```

```
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_sRNA_MMHT2_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_VFAB1.stdout.%j
#SBATCH --error=04_sRNA_VFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_sRNA_VFAB1_bowtie_un-mRNAs_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_sRNA_VFAB1_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_VFAB2.stdout.%j
#SBATCH --error=04_sRNA_VFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0
```

```
salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_sRNA_VFAB2_bowtie_un-mRNAs_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_sRNA_VFAB2_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_VFHT1.stdout.%j
#SBATCH --error=04_sRNA_VFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_sRNA_VFHT1_bowtie_un-mRNAs_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_sRNA_VFHT1_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
```

```
#SBATCH --output=04_sRNA_VFHT2.stdout.%j
#SBATCH --error=04_sRNA_VFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_sRNA_VFHT2_bowtie_un-mRNAs_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_sRNA_VFHT2_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_VMAB1.stdout.%j
#SBATCH --error=04_sRNA_VMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_sRNA_VMAB1_bowtie_un-mRNAs_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_sRNA_VMAB1_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_VMAB2.stdout.%j
#SBATCH --error=04_sRNA_VMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_sRNA_VMAB2_bowtie_un-mRNAs_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_sRNA_VMAB2_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_VMHT1.stdout.%j
#SBATCH --error=04_sRNA_VMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_sRNA_VMHT1_bowtie_un-mRNAs_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
```

```
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_sRNA_VMHT1_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_VMHT2.stdout.%j
#SBATCH --error=04_sRNA_VMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_sRNA_VMHT2_bowtie_un-mRNAs_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_sRNA_VMHT2_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
```

---

8 Experiment03_sRNAs_all

8.1 Experiment03_sRNAs_Bowtie_Commands

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MVABHT.stdout.%j
#SBATCH --error=01_sRNA_MVABHT.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MVABHT.fq \
    --al 01_sRNA_MVABHT_bowtie_al-mRNAs.fq \
    --un 01_sRNA_MVABHT_bowtie_un-mRNAs.fq \
    -S 01_sRNA_MVABHT.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_MVABHT_bowtie_un-mRNAs.fq \
    --al 02_sRNA_MVABHT_bowtie_un-mRNAs_al-sRNAs.fq \
    --un 02_sRNA_MVABHT_bowtie_un-mRNAs_un-sRNAs.fq \
    -S 02_sRNA_MVABHT.sam;
```

8.2 Experiment03_sRNAs_Salmon_Commands

```
module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    index \
    --transcripts Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --threads 48 \
    --index salmon_index \
    --kmerLen 9;
```

```
mkdir 03_sRNA_MVABHT_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_MVABHT.stdout.%j
#SBATCH --error=04_sRNA_MVABHT.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 02_sRNA_MVABHT_bowtie_un-mRNAs_al-sRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 03_sRNA_MVABHT_bowtie_un-mRNAs_al-sRNAs.fq_Salmon;
```

---

9 Experiment04_mRNAs

9.1 Experiment04_mRNAs_Bowtie_Commands

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MFAB1.stdout.%j
#SBATCH --error=01_mRNA_MFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MFAB1.fq \
    --al 01_mRNA_MFAB1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MFAB1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MFAB1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MFAB1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MFAB1_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_MFAB1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_MFAB1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.all.cd-hit-est.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
```

```
    02_mRNA_MFAB1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_MFAB1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_MFAB1_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_MFAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MFAB2.stdout.%j
#SBATCH --error=01_mRNA_MFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MFAB2.fq \
    --al 01_mRNA_MFAB2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MFAB2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MFAB2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MFAB2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MFAB2_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_MFAB2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_MFAB2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.all.cd-hit-est.fa \
    --best \
    --strata \
    -t \
    -a \
```

```
    -p 48 \
    -q \
    02_mRNA_MFAB2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_MFAB2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_MFAB2_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_MFAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MFHT1.stdout.%j
#SBATCH --error=01_mRNA_MFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MFHT1.fq \
    --al 01_mRNA_MFHT1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MFHT1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MFHT1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MFHT1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MFHT1_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_MFHT1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_MFHT1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.all.cd-hit-est.fa \
    --best \
    --strata \
```

```
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_MFHT1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_MFHT1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_MFHT1_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_MFHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MFHT2.stdout.%j
#SBATCH --error=01_mRNA_MFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MFHT2.fq \
    --al 01_mRNA_MFHT2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MFHT2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MFHT2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MFHT2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MFHT2_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_MFHT2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_MFHT2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.all.cd-hit-est.fa \
```

```
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_MFHT2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_MFHT2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_MFHT2_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_MFHT2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MMAB1.stdout.%j
#SBATCH --error=01_mRNA_MMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MMAB1.fq \
    --al 01_mRNA_MMAB1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MMAB1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MMAB1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MMAB1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MMAB1_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_MMAB1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_MMAB1.sam;
```

```
bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.all.cd-hit-est.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_MMAB1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_MMAB1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_MMAB1_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_MMAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MMAB2.stdout.%j
#SBATCH --error=01_mRNA_MMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MMAB2.fq \
    --al 01_mRNA_MMAB2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MMAB2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MMAB2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MMAB2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MMAB2_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_MMAB2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
```

```
    -S 02_mRNA_MMAB2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.all.cd-hit-est.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_MMAB2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_MMAB2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_MMAB2_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_MMAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MMHT1.stdout.%j
#SBATCH --error=01_mRNA_MMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MMHT1.fq \
    --al 01_mRNA_MMHT1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MMHT1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MMHT1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MMHT1_bowtie_un-sRNAs.fq \
```

```
    --al 02_mRNA_MMHT1_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_MMHT1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_MMHT1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.all.cd-hit-est.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_MMHT1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_MMHT1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_MMHT1_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_MMHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MMHT2.stdout.%j
#SBATCH --error=01_mRNA_MMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MMHT2.fq \
    --al 01_mRNA_MMHT2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MMHT2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MMHT2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
```

```
    -q \
    01_mRNA_MMHT2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MMHT2_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_MMHT2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_MMHT2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.all.cd-hit-est.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_MMHT2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_MMHT2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_MMHT2_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_MMHT2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VFAB1.stdout.%j
#SBATCH --error=01_mRNA_VFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VFAB1.fq \
    --al 01_mRNA_VFAB1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VFAB1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VFAB1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
```

```
    -a \
    -p 48 \
    -q \
    01_mRNA_VFAB1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VFAB1_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_VFAB1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_VFAB1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.all.cd-hit-est.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_VFAB1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_VFAB1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_VFAB1_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_VFAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VFAB2.stdout.%j
#SBATCH --error=01_mRNA_VFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VFAB2.fq \
    --al 01_mRNA_VFAB2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VFAB2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VFAB2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
```

```
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_VFAB2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VFAB2_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_VFAB2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_VFAB2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.all.cd-hit-est.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_VFAB2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_VFAB2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_VFAB2_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_VFAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VFHT1.stdout.%j
#SBATCH --error=01_mRNA_VFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VFHT1.fq \
    --al 01_mRNA_VFHT1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VFHT1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VFHT1.sam;

bowtie \
```

```
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_VFHT1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VFHT1_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_VFHT1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_VFHT1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.all.cd-hit-est.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_VFHT1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_VFHT1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_VFHT1_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_VFHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VFHT2.stdout.%j
#SBATCH --error=01_mRNA_VFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VFHT2.fq \
    --al 01_mRNA_VFHT2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VFHT2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VFHT2.sam;
```

```
bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_VFHT2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VFHT2_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_VFHT2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_VFHT2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.all.cd-hit-est.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_VFHT2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_VFHT2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_VFHT2_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_VFHT2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VMAB1.stdout.%j
#SBATCH --error=01_mRNA_VMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VMAB1.fq \
    --al 01_mRNA_VMAB1_bowtie_al-sRNAs.fq \
```

```
    --un 01_mRNA_VMAB1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VMAB1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_VMAB1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VMAB1_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_VMAB1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_VMAB1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.all.cd-hit-est.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_VMAB1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_VMAB1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_VMAB1_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_VMAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VMAB2.stdout.%j
#SBATCH --error=01_mRNA_VMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
```

```
    mRNA_VMAB2.fq \
    --al 01_mRNA_VMAB2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VMAB2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VMAB2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_VMAB2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VMAB2_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_VMAB2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_VMAB2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.all.cd-hit-est.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_VMAB2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_VMAB2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_VMAB2_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_VMAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VMHT1.stdout.%j
#SBATCH --error=01_mRNA_VMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
```

```
    -p 48 \
    -q \
    mRNA_VMHT1.fq \
    --al 01_mRNA_VMHT1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VMHT1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VMHT1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_VMHT1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VMHT1_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_VMHT1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_VMHT1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.all.cd-hit-est.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_VMHT1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_VMHT1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_VMHT1_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_VMHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VMHT2.stdout.%j
#SBATCH --error=01_mRNA_VMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
```

```
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VMHT2.fq \
    --al 01_mRNA_VMHT2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VMHT2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VMHT2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_VMHT2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VMHT2_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_VMHT2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_VMHT2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.all.cd-hit-est.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_VMHT2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_VMHT2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_VMHT2_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_VMHT2.sam;
```

9.2 Experiment04_mRNAs_Salmon_Commands

```
module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    index \
    --transcripts Drosophila_melanogaster.BDGP6.28.cdna.all.cd-hit-est.fa \
    --threads 48 \
    --index salmon_index \
    --kmerLen 9;
```

```
mkdir 04_mRNA_MFAB1;
mkdir 04_mRNA_MFAB2;
mkdir 04_mRNA_MFHT1;
mkdir 04_mRNA_MFHT2;
mkdir 04_mRNA_MMAB1;
mkdir 04_mRNA_MMAB2;
mkdir 04_mRNA_MMHT1;
mkdir 04_mRNA_MMHT2;
mkdir 04_mRNA_VFAB1;
mkdir 04_mRNA_VFAB2;
mkdir 04_mRNA_VFHT1;
mkdir 04_mRNA_VFHT2;
mkdir 04_mRNA_VMAB1;
mkdir 04_mRNA_VMAB2;
mkdir 04_mRNA_VMHT1;
mkdir 04_mRNA_VMHT2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MFAB1.stdout.%j
#SBATCH --error=04_mRNA_MFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
```

```
    -r 03_mRNA_MFAB1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_MFAB1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MFAB2.stdout.%j
#SBATCH --error=04_mRNA_MFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_MFAB2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_MFAB2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MFHT1.stdout.%j
#SBATCH --error=04_mRNA_MFHT1.stderr.%j

module purge
module load GCC/9.3.0
```

```
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_MFHT1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_MFHT1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MFHT2.stdout.%j
#SBATCH --error=04_mRNA_MFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_MFHT2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_MFHT2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
```

```
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MMAB1.stdout.%j
#SBATCH --error=04_mRNA_MMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_MMAB1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_MMAB1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MMAB2.stdout.%j
#SBATCH --error=04_mRNA_MMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_MMAB2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_MMAB2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MMHT1.stdout.%j
#SBATCH --error=04_mRNA_MMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_MMHT1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_MMHT1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MMHT2.stdout.%j
#SBATCH --error=04_mRNA_MMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_MMHT2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
```

```
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_MMHT2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VFAB1.stdout.%j
#SBATCH --error=04_mRNA_VFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_VFAB1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_VFAB1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VFAB2.stdout.%j
#SBATCH --error=04_mRNA_VFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0
```

```
salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_VFAB2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_VFAB2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VFHT1.stdout.%j
#SBATCH --error=04_mRNA_VFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_VFHT1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_VFHT1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
```

```
#SBATCH --output=04_mRNA_VFHT2.stdout.%j
#SBATCH --error=04_mRNA_VFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_VFHT2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_VFHT2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VMAB1.stdout.%j
#SBATCH --error=04_mRNA_VMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_VMAB1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_VMAB1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VMAB2.stdout.%j
#SBATCH --error=04_mRNA_VMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_VMAB2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_VMAB2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VMHT1.stdout.%j
#SBATCH --error=04_mRNA_VMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_VMHT1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
```

```
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_VMHT1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VMHT2.stdout.%j
#SBATCH --error=04_mRNA_VMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_VMHT2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_VMHT2;
```

---

10 Experiment04_mRNAs_r28_Canonical

10.1 Experiment04_mRNAs_r28_Canonical_Bowtie_Commands

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MFAB1.stdout.%j
#SBATCH --error=01_mRNA_MFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0
module load SAMtools/1.10

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MFAB1.fq \
    --al 01_mRNA_MFAB1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MFAB1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MFAB1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MFAB1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MFAB1_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_MFAB1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_MFAB1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
```

```
    -q \
    02_mRNA_MFAB1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_MFAB1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_MFAB1_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_MFAB1.sam;

samtools \
    view \
    -bS \
    03_mRNA_MFAB1.sam \
    | \
    samtools \
sort \
-m 2G \
-@ 48 - \
-T mRNA_MFAB1.fq \
-o 03_mRNA_MFAB1.bam;

samtools \
    index \
    03_mRNA_MFAB1.bam
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MFAB2.stdout.%j
#SBATCH --error=01_mRNA_MFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0
module load SAMtools/1.10

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MFAB2.fq \
    --al 01_mRNA_MFAB2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MFAB2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MFAB2.sam;

bowtie \
```

```
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MFAB2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MFAB2_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_MFAB2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_MFAB2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_MFAB2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_MFAB2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_MFAB2_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_MFAB2.sam;

samtools \
    view \
    -bS \
    03_mRNA_MFAB2.sam \
    | \
    samtools \
sort \
-m 2G \
-@ 48 - \
-T mRNA_MFAB2.fq \
-o 03_mRNA_MFAB2.bam;

samtools \
    index \
    03_mRNA_MFAB2.bam
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MFHT1.stdout.%j
#SBATCH --error=01_mRNA_MFHT1.stderr.%j

module purge
```

```
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0
module load SAMtools/1.10

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MFHT1.fq \
    --al 01_mRNA_MFHT1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MFHT1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MFHT1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MFHT1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MFHT1_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_MFHT1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_MFHT1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_MFHT1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_MFHT1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_MFHT1_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_MFHT1.sam;

samtools \
    view \
    -bS \
    03_mRNA_MFHT1.sam \
    | \
    samtools \
sort \
-m 2G \
-@ 48 - \
```

```
-T mRNA_MFHT1.fq \
-o 03_mRNA_MFHT1.bam;

samtools \
    index \
    03_mRNA_MFHT1.bam
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MFHT2.stdout.%j
#SBATCH --error=01_mRNA_MFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0
module load SAMtools/1.10

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MFHT2.fq \
    --al 01_mRNA_MFHT2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MFHT2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MFHT2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MFHT2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MFHT2_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_MFHT2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_MFHT2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fa \
    --best \
```

```
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_MFHT2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_MFHT2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_MFHT2_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_MFHT2.sam;

samtools \
    view \
    -bS \
    03_mRNA_MFHT2.sam \
    | \
    samtools \
sort \
-m 2G \
-@ 48 - \
-T mRNA_MFHT2.fq \
-o 03_mRNA_MFHT2.bam;

samtools \
    index \
    03_mRNA_MFHT2.bam
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MMAB1.stdout.%j
#SBATCH --error=01_mRNA_MMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0
module load SAMtools/1.10

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MMAB1.fq \
    --al 01_mRNA_MMAB1_bowtie_al-sRNAs.fq \
```

```
    --un 01_mRNA_MMAB1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MMAB1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MMAB1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MMAB1_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_MMAB1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_MMAB1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_MMAB1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_MMAB1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_MMAB1_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_MMAB1.sam;

samtools \
    view \
    -bS \
    03_mRNA_MMAB1.sam \
    | \
    samtools \
sort \
-m 2G \
-@ 48 - \
-T mRNA_MMAB1.fq \
-o 03_mRNA_MMAB1.bam;

samtools \
    index \
    03_mRNA_MMAB1.bam
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
```

```
#SBATCH --output=01_mRNA_MMAB2.stdout.%j
#SBATCH --error=01_mRNA_MMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0
module load SAMtools/1.10

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MMAB2.fq \
    --al 01_mRNA_MMAB2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MMAB2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MMAB2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MMAB2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MMAB2_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_MMAB2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_MMAB2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_MMAB2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_MMAB2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_MMAB2_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_MMAB2.sam;

samtools \
    view \
    -bS \
    03_mRNA_MMAB2.sam \
    | \
```

```
    samtools \
sort \
-m 2G \
-@ 48 - \
-T mRNA_MMAB2.fq \
-o 03_mRNA_MMAB2.bam;

samtools \
    index \
    03_mRNA_MMAB2.bam
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MMHT1.stdout.%j
#SBATCH --error=01_mRNA_MMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0
module load SAMtools/1.10

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MMHT1.fq \
    --al 01_mRNA_MMHT1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MMHT1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MMHT1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MMHT1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MMHT1_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_MMHT1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_MMHT1.sam;
```

```
bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_MMHT1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_MMHT1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_MMHT1_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_MMHT1.sam;

samtools \
    view \
    -bS \
    03_mRNA_MMHT1.sam \
    | \
    samtools \
sort \
-m 2G \
-@ 48 - \
-T mRNA_MMHT1.fq \
-o 03_mRNA_MMHT1.bam;

samtools \
    index \
    03_mRNA_MMHT1.bam
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MMHT2.stdout.%j
#SBATCH --error=01_mRNA_MMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0
module load SAMtools/1.10

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
```

```
    -p 48 \
    -q \
    mRNA_MMHT2.fq \
    --al 01_mRNA_MMHT2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MMHT2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MMHT2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MMHT2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MMHT2_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_MMHT2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_MMHT2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_MMHT2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_MMHT2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_MMHT2_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_MMHT2.sam;

samtools \
    view \
    -bS \
    03_mRNA_MMHT2.sam \
    | \
    samtools \
sort \
-m 2G \
-@ 48 - \
-T mRNA_MMHT2.fq \
-o 03_mRNA_MMHT2.bam;

samtools \
    index \
    03_mRNA_MMHT2.bam
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
```

```
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VFAB1.stdout.%j
#SBATCH --error=01_mRNA_VFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0
module load SAMtools/1.10

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VFAB1.fq \
    --al 01_mRNA_VFAB1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VFAB1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VFAB1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_VFAB1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VFAB1_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_VFAB1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_VFAB1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_VFAB1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_VFAB1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_VFAB1_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_VFAB1.sam;

samtools \
```

```
    view \
    -bS \
    03_mRNA_VFAB1.sam \
    | \
    samtools \
sort \
-m 2G \
-@ 48 - \
-T mRNA_VFAB1.fq \
-o 03_mRNA_VFAB1.bam;

samtools \
    index \
    03_mRNA_VFAB1.bam
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VFAB2.stdout.%j
#SBATCH --error=01_mRNA_VFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0
module load SAMtools/1.10

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VFAB2.fq \
    --al 01_mRNA_VFAB2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VFAB2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VFAB2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
```

```
    01_mRNA_VFAB2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VFAB2_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_VFAB2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_VFAB2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_VFAB2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_VFAB2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_VFAB2_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_VFAB2.sam;

samtools \
    view \
    -bS \
    03_mRNA_VFAB2.sam \
    | \
    samtools \
sort \
-m 2G \
-@ 48 - \
-T mRNA_VFAB2.fq \
-o 03_mRNA_VFAB2.bam;

samtools \
    index \
    03_mRNA_VFAB2.bam
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VFHT1.stdout.%j
#SBATCH --error=01_mRNA_VFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0
module load SAMtools/1.10

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
```

```
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VFHT1.fq \
    --al 01_mRNA_VFHT1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VFHT1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VFHT1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_VFHT1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VFHT1_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_VFHT1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_VFHT1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_VFHT1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_VFHT1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_VFHT1_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_VFHT1.sam;

samtools \
    view \
    -bS \
    03_mRNA_VFHT1.sam \
    | \
    samtools \
sort \
-m 2G \
-@ 48 - \
-T mRNA_VFHT1.fq \
-o 03_mRNA_VFHT1.bam;

samtools \
    index \
    03_mRNA_VFHT1.bam
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VFHT2.stdout.%j
#SBATCH --error=01_mRNA_VFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0
module load SAMtools/1.10

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VFHT2.fq \
    --al 01_mRNA_VFHT2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VFHT2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VFHT2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_VFHT2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VFHT2_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_VFHT2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_VFHT2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_VFHT2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_VFHT2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_VFHT2_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
```

```
    -S 03_mRNA_VFHT2.sam;

samtools \
    view \
    -bS \
    03_mRNA_VFHT2.sam \
    | \
    samtools \
sort \
-m 2G \
-@ 48 - \
-T mRNA_VFHT2.fq \
-o 03_mRNA_VFHT2.bam;

samtools \
    index \
    03_mRNA_VFHT2.bam
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VMAB1.stdout.%j
#SBATCH --error=01_mRNA_VMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0
module load SAMtools/1.10

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VMAB1.fq \
    --al 01_mRNA_VMAB1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VMAB1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VMAB1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
```

```
    -a \
    -p 48 \
    -q \
    01_mRNA_VMAB1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VMAB1_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_VMAB1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_VMAB1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_VMAB1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_VMAB1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_VMAB1_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_VMAB1.sam;

samtools \
    view \
    -bS \
    03_mRNA_VMAB1.sam \
    | \
    samtools \
sort \
-m 2G \
-@ 48 - \
-T mRNA_VMAB1.fq \
-o 03_mRNA_VMAB1.bam;

samtools \
    index \
    03_mRNA_VMAB1.bam
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VMAB2.stdout.%j
#SBATCH --error=01_mRNA_VMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0
module load SAMtools/1.10
```

```
bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VMAB2.fq \
    --al 01_mRNA_VMAB2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VMAB2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VMAB2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_VMAB2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VMAB2_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_VMAB2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_VMAB2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_VMAB2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_VMAB2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_VMAB2_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_VMAB2.sam;

samtools \
    view \
    -bS \
    03_mRNA_VMAB2.sam \
    | \
    samtools \
sort \
-m 2G \
-@ 48 - \
-T mRNA_VMAB2.fq \
-o 03_mRNA_VMAB2.bam;

samtools \
```

```
    index \
    03_mRNA_VMAB2.bam
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VMHT1.stdout.%j
#SBATCH --error=01_mRNA_VMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0
module load SAMtools/1.10

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VMHT1.fq \
    --al 01_mRNA_VMHT1_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VMHT1_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VMHT1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_VMHT1_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VMHT1_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_VMHT1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_VMHT1.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
```

```
    -q \
    02_mRNA_VMHT1_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_VMHT1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_VMHT1_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_VMHT1.sam;

samtools \
    view \
    -bS \
    03_mRNA_VMHT1.sam \
    | \
    samtools \
sort \
-m 2G \
-@ 48 - \
-T mRNA_VMHT1.fq \
-o 03_mRNA_VMHT1.bam;

samtools \
    index \
    03_mRNA_VMHT1.bam
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_VMHT2.stdout.%j
#SBATCH --error=01_mRNA_VMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0
module load SAMtools/1.10

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_VMHT2.fq \
    --al 01_mRNA_VMHT2_bowtie_al-sRNAs.fq \
    --un 01_mRNA_VMHT2_bowtie_un-sRNAs.fq \
    -S 01_mRNA_VMHT2.sam;

bowtie \
```

```
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_VMHT2_bowtie_un-sRNAs.fq \
    --al 02_mRNA_VMHT2_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_VMHT2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_VMHT2.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_mRNA_VMHT2_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    --al 03_mRNA_VMHT2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --un 03_mRNA_VMHT2_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
    -S 03_mRNA_VMHT2.sam;

samtools \
    view \
    -bS \
    03_mRNA_VMHT2.sam \
    | \
    samtools \
sort \
-m 2G \
-@ 48 - \
-T mRNA_VMHT2.fq \
-o 03_mRNA_VMHT2.bam;

samtools \
    index \
    03_mRNA_VMHT2.bam
```

10.2 Experiment04_mRNAs_r28_Canonical_Salmon_Commands

```
module purge
module load GCC/11.2.0
module load OpenMPI/4.1.1
module load Salmon/1.9.0

salmon \
    index \
    --transcripts Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fa \
    --threads 48 \
    --index salmon_index \
    --kmerLen 9;
```

```
mkdir 04_mRNA_MFAB1;
mkdir 04_mRNA_MFAB2;
mkdir 04_mRNA_MFHT1;
mkdir 04_mRNA_MFHT2;
mkdir 04_mRNA_MMAB1;
mkdir 04_mRNA_MMAB2;
mkdir 04_mRNA_MMHT1;
mkdir 04_mRNA_MMHT2;
mkdir 04_mRNA_VFAB1;
mkdir 04_mRNA_VFAB2;
mkdir 04_mRNA_VFHT1;
mkdir 04_mRNA_VFHT2;
mkdir 04_mRNA_VMAB1;
mkdir 04_mRNA_VMAB2;
mkdir 04_mRNA_VMHT1;
mkdir 04_mRNA_VMHT2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MFAB1.stdout.%j
#SBATCH --error=04_mRNA_MFAB1.stderr.%j

module purge
module load GCC/11.2.0
module load OpenMPI/4.1.1
module load Salmon/1.9.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
```

```
    -r 03_mRNA_MFAB1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_MFAB1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MFAB2.stdout.%j
#SBATCH --error=04_mRNA_MFAB2.stderr.%j

module purge
module load GCC/11.2.0
module load OpenMPI/4.1.1
module load Salmon/1.9.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_MFAB2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_MFAB2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MFHT1.stdout.%j
#SBATCH --error=04_mRNA_MFHT1.stderr.%j

module purge
module load GCC/11.2.0
module load OpenMPI/4.1.1
module load Salmon/1.9.0
```

```
salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_MFHT1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_MFHT1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MFHT2.stdout.%j
#SBATCH --error=04_mRNA_MFHT2.stderr.%j

module purge
module load GCC/11.2.0
module load OpenMPI/4.1.1
module load Salmon/1.9.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_MFHT2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_MFHT2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MMAB1.stdout.%j
#SBATCH --error=04_mRNA_MMAB1.stderr.%j
```

```
module purge
module load GCC/11.2.0
module load OpenMPI/4.1.1
module load Salmon/1.9.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_MMAB1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_MMAB1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MMAB2.stdout.%j
#SBATCH --error=04_mRNA_MMAB2.stderr.%j

module purge
module load GCC/11.2.0
module load OpenMPI/4.1.1
module load Salmon/1.9.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_MMAB2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_MMAB2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
```

```
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MMHT1.stdout.%j
#SBATCH --error=04_mRNA_MMHT1.stderr.%j

module purge
module load GCC/11.2.0
module load OpenMPI/4.1.1
module load Salmon/1.9.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_MMHT1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_MMHT1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MMHT2.stdout.%j
#SBATCH --error=04_mRNA_MMHT2.stderr.%j

module purge
module load GCC/11.2.0
module load OpenMPI/4.1.1
module load Salmon/1.9.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_MMHT2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_MMHT2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VFAB1.stdout.%j
#SBATCH --error=04_mRNA_VFAB1.stderr.%j

module purge
module load GCC/11.2.0
module load OpenMPI/4.1.1
module load Salmon/1.9.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_VFAB1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_VFAB1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VFAB2.stdout.%j
#SBATCH --error=04_mRNA_VFAB2.stderr.%j

module purge
module load GCC/11.2.0
module load OpenMPI/4.1.1
module load Salmon/1.9.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_VFAB2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
```

```
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_VFAB2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VFHT1.stdout.%j
#SBATCH --error=04_mRNA_VFHT1.stderr.%j

module purge
module load GCC/11.2.0
module load OpenMPI/4.1.1
module load Salmon/1.9.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_VFHT1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_VFHT1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VFHT2.stdout.%j
#SBATCH --error=04_mRNA_VFHT2.stderr.%j

module purge
module load GCC/11.2.0
module load OpenMPI/4.1.1
module load Salmon/1.9.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
```

```
    -r 03_mRNA_VFHT2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_VFHT2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VMAB1.stdout.%j
#SBATCH --error=04_mRNA_VMAB1.stderr.%j

module purge
module load GCC/11.2.0
module load OpenMPI/4.1.1
module load Salmon/1.9.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_VMAB1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_VMAB1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VMAB2.stdout.%j
#SBATCH --error=04_mRNA_VMAB2.stderr.%j

module purge
module load GCC/11.2.0
module load OpenMPI/4.1.1
module load Salmon/1.9.0
```

```
salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_VMAB2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_VMAB2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VMHT1.stdout.%j
#SBATCH --error=04_mRNA_VMHT1.stderr.%j

module purge
module load GCC/11.2.0
module load OpenMPI/4.1.1
module load Salmon/1.9.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_VMHT1_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_VMHT1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_VMHT2.stdout.%j
#SBATCH --error=04_mRNA_VMHT2.stderr.%j
```

```
module purge
module load GCC/11.2.0
module load OpenMPI/4.1.1
module load Salmon/1.9.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_VMHT2_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_VMHT2;
```

11 Experiment04_mRNAs_all

11.1 Experiment04_mRNAs_All_Bowtie_Commands

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_mRNA_MVABHT.stdout.%j
#SBATCH --error=01_mRNA_MVABHT.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    mRNA_MVABHT.fq \
    --al 01_mRNA_MVABHT_bowtie_al-sRNAs.fq \
    --un 01_mRNA_MVABHT_bowtie_un-sRNAs.fq \
    -S 01_mRNA_MVABHT.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_mRNA_MVABHT_bowtie_un-sRNAs.fq \
    --al 02_mRNA_MVABHT_bowtie_un-sRNAs_al-rRNA-biotypes.fq \
    --un 02_mRNA_MVABHT_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
    -S 02_mRNA_MVABHT.sam;

bowtie \
    -x Drosophila_melanogaster.BDGP6.28.cdna.all.cd-hit-est.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
```

```
02_mRNA_MVABHT_bowtie_un-sRNAs_un-rRNA-biotypes.fq \
--al 03_mRNA_MVABHT_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
--un 03_mRNA_MVABHT_bowtie_un-sRNAs_un-rRNA-biotypes_un-clust-filtered-mRNAs.fq  \
-S 03_mRNA_MVABHT.sam;
```

11.2 Experiment04_mRNAs_All_Salmon_Commands

```
module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    index \
    --transcripts Drosophila_melanogaster.BDGP6.28.cdna.all.cd-hit-est.fa \
    --threads 48 \
    --index salmon_index \
    --kmerLen 9;
```

```
mkdir 04_mRNA_MVABHT;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_mRNA_MVABHT.stdout.%j
#SBATCH --error=04_mRNA_MVABHT.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_mRNA_MVABHT_bowtie_un-sRNAs_un-rRNA-biotypes_al-clust-filtered-mRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_mRNA_MVABHT;
```

---

12 Experiment04_sRNAs

12.1 Experiment04_sRNAs_Bowtie_Commands

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MFAB1.stdout.%j
#SBATCH --error=01_sRNA_MFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MFAB1.fq \
    --al 01_sRNA_MFAB1_bowtie_al-mRNAs.fq \
    --un 01_sRNA_MFAB1_bowtie_un-mRNAs.fq \
    -S 01_sRNA_MFAB1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_MFAB1_bowtie_un-mRNAs.fq \
    --al 02_sRNA_MFAB1_bowtie_un-mRNAs_al-rRNA-biotypes.fq \
    --un 02_sRNA_MFAB1_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    -S 02_sRNA_MFAB1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.filtered-biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
```

```
    02_sRNA_MFAB1_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    --al 03_sRNA_MFAB1_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --un 03_sRNA_MFAB1_bowtie_un-mRNAs_un-rRNA-biotypes_un-clust-filtered-ncRNAs.fq  \
    -S 03_sRNA_MFAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MFAB2.stdout.%j
#SBATCH --error=01_sRNA_MFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MFAB2.fq \
    --al 01_sRNA_MFAB2_bowtie_al-mRNAs.fq \
    --un 01_sRNA_MFAB2_bowtie_un-mRNAs.fq \
    -S 01_sRNA_MFAB2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_MFAB2_bowtie_un-mRNAs.fq \
    --al 02_sRNA_MFAB2_bowtie_un-mRNAs_al-rRNA-biotypes.fq \
    --un 02_sRNA_MFAB2_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    -S 02_sRNA_MFAB2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.filtered-biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
```

```
    -p 48 \
    -q \
    02_sRNA_MFAB2_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    --al 03_sRNA_MFAB2_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --un 03_sRNA_MFAB2_bowtie_un-mRNAs_un-rRNA-biotypes_un-clust-filtered-ncRNAs.fq  \
    -S 03_sRNA_MFAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MFHT1.stdout.%j
#SBATCH --error=01_sRNA_MFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MFHT1.fq \
    --al 01_sRNA_MFHT1_bowtie_al-mRNAs.fq \
    --un 01_sRNA_MFHT1_bowtie_un-mRNAs.fq \
    -S 01_sRNA_MFHT1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_MFHT1_bowtie_un-mRNAs.fq \
    --al 02_sRNA_MFHT1_bowtie_un-mRNAs_al-rRNA-biotypes.fq \
    --un 02_sRNA_MFHT1_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    -S 02_sRNA_MFHT1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.filtered-biotype-rRNA.fa \
    --best \
    --strata \
```

```
    -t \
    -a \
    -p 48 \
    -q \
    02_sRNA_MFHT1_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    --al 03_sRNA_MFHT1_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --un 03_sRNA_MFHT1_bowtie_un-mRNAs_un-rRNA-biotypes_un-clust-filtered-ncRNAs.fq  \
    -S 03_sRNA_MFHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MFHT2.stdout.%j
#SBATCH --error=01_sRNA_MFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MFHT2.fq \
    --al 01_sRNA_MFHT2_bowtie_al-mRNAs.fq \
    --un 01_sRNA_MFHT2_bowtie_un-mRNAs.fq \
    -S 01_sRNA_MFHT2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_MFHT2_bowtie_un-mRNAs.fq \
    --al 02_sRNA_MFHT2_bowtie_un-mRNAs_al-rRNA-biotypes.fq \
    --un 02_sRNA_MFHT2_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    -S 02_sRNA_MFHT2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.filtered-biotype-rRNA.fa \
```

```
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_sRNA_MFHT2_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    --al 03_sRNA_MFHT2_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --un 03_sRNA_MFHT2_bowtie_un-mRNAs_un-rRNA-biotypes_un-clust-filtered-ncRNAs.fq  \
    -S 03_sRNA_MFHT2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MMAB1.stdout.%j
#SBATCH --error=01_sRNA_MMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MMAB1.fq \
    --al 01_sRNA_MMAB1_bowtie_al-mRNAs.fq \
    --un 01_sRNA_MMAB1_bowtie_un-mRNAs.fq \
    -S 01_sRNA_MMAB1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_MMAB1_bowtie_un-mRNAs.fq \
    --al 02_sRNA_MMAB1_bowtie_un-mRNAs_al-rRNA-biotypes.fq \
    --un 02_sRNA_MMAB1_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    -S 02_sRNA_MMAB1.sam;
```

```
bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.filtered-biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_sRNA_MMAB1_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    --al 03_sRNA_MMAB1_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --un 03_sRNA_MMAB1_bowtie_un-mRNAs_un-rRNA-biotypes_un-clust-filtered-ncRNAs.fq  \
    -S 03_sRNA_MMAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MMAB2.stdout.%j
#SBATCH --error=01_sRNA_MMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MMAB2.fq \
    --al 01_sRNA_MMAB2_bowtie_al-mRNAs.fq \
    --un 01_sRNA_MMAB2_bowtie_un-mRNAs.fq \
    -S 01_sRNA_MMAB2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_MMAB2_bowtie_un-mRNAs.fq \
    --al 02_sRNA_MMAB2_bowtie_un-mRNAs_al-rRNA-biotypes.fq \
    --un 02_sRNA_MMAB2_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
```

```
    -S 02_sRNA_MMAB2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.filtered-biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_sRNA_MMAB2_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    --al 03_sRNA_MMAB2_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --un 03_sRNA_MMAB2_bowtie_un-mRNAs_un-rRNA-biotypes_un-clust-filtered-ncRNAs.fq  \
    -S 03_sRNA_MMAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MMHT1.stdout.%j
#SBATCH --error=01_sRNA_MMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MMHT1.fq \
    --al 01_sRNA_MMHT1_bowtie_al-mRNAs.fq \
    --un 01_sRNA_MMHT1_bowtie_un-mRNAs.fq \
    -S 01_sRNA_MMHT1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_MMHT1_bowtie_un-mRNAs.fq \
```

```
    --al 02_sRNA_MMHT1_bowtie_un-mRNAs_al-rRNA-biotypes.fq \
    --un 02_sRNA_MMHT1_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    -S 02_sRNA_MMHT1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.filtered-biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_sRNA_MMHT1_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    --al 03_sRNA_MMHT1_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --un 03_sRNA_MMHT1_bowtie_un-mRNAs_un-rRNA-biotypes_un-clust-filtered-ncRNAs.fq  \
    -S 03_sRNA_MMHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MMHT2.stdout.%j
#SBATCH --error=01_sRNA_MMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MMHT2.fq \
    --al 01_sRNA_MMHT2_bowtie_al-mRNAs.fq \
    --un 01_sRNA_MMHT2_bowtie_un-mRNAs.fq \
    -S 01_sRNA_MMHT2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
```

```
    -q \
    01_sRNA_MMHT2_bowtie_un-mRNAs.fq \
    --al 02_sRNA_MMHT2_bowtie_un-mRNAs_al-rRNA-biotypes.fq \
    --un 02_sRNA_MMHT2_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    -S 02_sRNA_MMHT2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.filtered-biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_sRNA_MMHT2_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    --al 03_sRNA_MMHT2_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --un 03_sRNA_MMHT2_bowtie_un-mRNAs_un-rRNA-biotypes_un-clust-filtered-ncRNAs.fq  \
    -S 03_sRNA_MMHT2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VFAB1.stdout.%j
#SBATCH --error=01_sRNA_VFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_VFAB1.fq \
    --al 01_sRNA_VFAB1_bowtie_al-mRNAs.fq \
    --un 01_sRNA_VFAB1_bowtie_un-mRNAs.fq \
    -S 01_sRNA_VFAB1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
```

```
    -a \
    -p 48 \
    -q \
    01_sRNA_VFAB1_bowtie_un-mRNAs.fq \
    --al 02_sRNA_VFAB1_bowtie_un-mRNAs_al-rRNA-biotypes.fq \
    --un 02_sRNA_VFAB1_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    -S 02_sRNA_VFAB1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.filtered-biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_sRNA_VFAB1_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    --al 03_sRNA_VFAB1_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --un 03_sRNA_VFAB1_bowtie_un-mRNAs_un-rRNA-biotypes_un-clust-filtered-ncRNAs.fq  \
    -S 03_sRNA_VFAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VFAB2.stdout.%j
#SBATCH --error=01_sRNA_VFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_VFAB2.fq \
    --al 01_sRNA_VFAB2_bowtie_al-mRNAs.fq \
    --un 01_sRNA_VFAB2_bowtie_un-mRNAs.fq \
    -S 01_sRNA_VFAB2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
```

```
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_VFAB2_bowtie_un-mRNAs.fq \
    --al 02_sRNA_VFAB2_bowtie_un-mRNAs_al-rRNA-biotypes.fq \
    --un 02_sRNA_VFAB2_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    -S 02_sRNA_VFAB2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.filtered-biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_sRNA_VFAB2_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    --al 03_sRNA_VFAB2_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --un 03_sRNA_VFAB2_bowtie_un-mRNAs_un-rRNA-biotypes_un-clust-filtered-ncRNAs.fq  \
    -S 03_sRNA_VFAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VFHT1.stdout.%j
#SBATCH --error=01_sRNA_VFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_VFHT1.fq \
    --al 01_sRNA_VFHT1_bowtie_al-mRNAs.fq \
    --un 01_sRNA_VFHT1_bowtie_un-mRNAs.fq \
    -S 01_sRNA_VFHT1.sam;

bowtie \
```

```
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_VFHT1_bowtie_un-mRNAs.fq \
    --al 02_sRNA_VFHT1_bowtie_un-mRNAs_al-rRNA-biotypes.fq \
    --un 02_sRNA_VFHT1_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    -S 02_sRNA_VFHT1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.filtered-biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_sRNA_VFHT1_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    --al 03_sRNA_VFHT1_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --un 03_sRNA_VFHT1_bowtie_un-mRNAs_un-rRNA-biotypes_un-clust-filtered-ncRNAs.fq  \
    -S 03_sRNA_VFHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VFHT2.stdout.%j
#SBATCH --error=01_sRNA_VFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_VFHT2.fq \
    --al 01_sRNA_VFHT2_bowtie_al-mRNAs.fq \
    --un 01_sRNA_VFHT2_bowtie_un-mRNAs.fq \
    -S 01_sRNA_VFHT2.sam;
```

```
bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_VFHT2_bowtie_un-mRNAs.fq \
    --al 02_sRNA_VFHT2_bowtie_un-mRNAs_al-rRNA-biotypes.fq \
    --un 02_sRNA_VFHT2_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    -S 02_sRNA_VFHT2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.filtered-biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_sRNA_VFHT2_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    --al 03_sRNA_VFHT2_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --un 03_sRNA_VFHT2_bowtie_un-mRNAs_un-rRNA-biotypes_un-clust-filtered-ncRNAs.fq  \
    -S 03_sRNA_VFHT2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VMAB1.stdout.%j
#SBATCH --error=01_sRNA_VMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_VMAB1.fq \
    --al 01_sRNA_VMAB1_bowtie_al-mRNAs.fq \
```

```
    --un 01_sRNA_VMAB1_bowtie_un-mRNAs.fq \
    -S 01_sRNA_VMAB1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_VMAB1_bowtie_un-mRNAs.fq \
    --al 02_sRNA_VMAB1_bowtie_un-mRNAs_al-rRNA-biotypes.fq \
    --un 02_sRNA_VMAB1_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    -S 02_sRNA_VMAB1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.filtered-biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_sRNA_VMAB1_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    --al 03_sRNA_VMAB1_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --un 03_sRNA_VMAB1_bowtie_un-mRNAs_un-rRNA-biotypes_un-clust-filtered-ncRNAs.fq  \
    -S 03_sRNA_VMAB1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VMAB2.stdout.%j
#SBATCH --error=01_sRNA_VMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
```

```
    sRNA_VMAB2.fq \
    --al 01_sRNA_VMAB2_bowtie_al-mRNAs.fq \
    --un 01_sRNA_VMAB2_bowtie_un-mRNAs.fq \
    -S 01_sRNA_VMAB2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_VMAB2_bowtie_un-mRNAs.fq \
    --al 02_sRNA_VMAB2_bowtie_un-mRNAs_al-rRNA-biotypes.fq \
    --un 02_sRNA_VMAB2_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    -S 02_sRNA_VMAB2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.filtered-biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_sRNA_VMAB2_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    --al 03_sRNA_VMAB2_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --un 03_sRNA_VMAB2_bowtie_un-mRNAs_un-rRNA-biotypes_un-clust-filtered-ncRNAs.fq  \
    -S 03_sRNA_VMAB2.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VMHT1.stdout.%j
#SBATCH --error=01_sRNA_VMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
```

```
    -p 48 \
    -q \
    sRNA_VMHT1.fq \
    --al 01_sRNA_VMHT1_bowtie_al-mRNAs.fq \
    --un 01_sRNA_VMHT1_bowtie_un-mRNAs.fq \
    -S 01_sRNA_VMHT1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_VMHT1_bowtie_un-mRNAs.fq \
    --al 02_sRNA_VMHT1_bowtie_un-mRNAs_al-rRNA-biotypes.fq \
    --un 02_sRNA_VMHT1_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    -S 02_sRNA_VMHT1.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.filtered-biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_sRNA_VMHT1_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    --al 03_sRNA_VMHT1_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --un 03_sRNA_VMHT1_bowtie_un-mRNAs_un-rRNA-biotypes_un-clust-filtered-ncRNAs.fq  \
    -S 03_sRNA_VMHT1.sam;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_VMHT2.stdout.%j
#SBATCH --error=01_sRNA_VMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
```

```
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_VMHT2.fq \
    --al 01_sRNA_VMHT2_bowtie_al-mRNAs.fq \
    --un 01_sRNA_VMHT2_bowtie_un-mRNAs.fq \
    -S 01_sRNA_VMHT2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_VMHT2_bowtie_un-mRNAs.fq \
    --al 02_sRNA_VMHT2_bowtie_un-mRNAs_al-rRNA-biotypes.fq \
    --un 02_sRNA_VMHT2_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    -S 02_sRNA_VMHT2.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.filtered-biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    02_sRNA_VMHT2_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    --al 03_sRNA_VMHT2_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --un 03_sRNA_VMHT2_bowtie_un-mRNAs_un-rRNA-biotypes_un-clust-filtered-ncRNAs.fq  \
    -S 03_sRNA_VMHT2.sam;
```

12.2 Experiment04_sRNAs_Salmon_Commands

```
module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    index \
    --transcripts Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.filtered-biotype-rRNA.fa \
    --threads 48 \
    --index salmon_index \
    --kmerLen 9;
```

```
mkdir 04_sRNA_MFAB1;
mkdir 04_sRNA_MFAB2;
mkdir 04_sRNA_MFHT1;
mkdir 04_sRNA_MFHT2;
mkdir 04_sRNA_MMAB1;
mkdir 04_sRNA_MMAB2;
mkdir 04_sRNA_MMHT1;
mkdir 04_sRNA_MMHT2;
mkdir 04_sRNA_VFAB1;
mkdir 04_sRNA_VFAB2;
mkdir 04_sRNA_VFHT1;
mkdir 04_sRNA_VFHT2;
mkdir 04_sRNA_VMAB1;
mkdir 04_sRNA_VMAB2;
mkdir 04_sRNA_VMHT1;
mkdir 04_sRNA_VMHT2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_MFAB1.stdout.%j
#SBATCH --error=04_sRNA_MFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
```

```
    -r 03_sRNA_MFAB1_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_sRNA_MFAB1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_MFAB2.stdout.%j
#SBATCH --error=04_sRNA_MFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_sRNA_MFAB2_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_sRNA_MFAB2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_MFHT1.stdout.%j
#SBATCH --error=04_sRNA_MFHT1.stderr.%j

module purge
module load GCC/9.3.0
```

```
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_sRNA_MFHT1_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_sRNA_MFHT1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_MFHT2.stdout.%j
#SBATCH --error=04_sRNA_MFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_sRNA_MFHT2_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_sRNA_MFHT2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
```

```
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_MMAB1.stdout.%j
#SBATCH --error=04_sRNA_MMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_sRNA_MMAB1_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_sRNA_MMAB1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_MMAB2.stdout.%j
#SBATCH --error=04_sRNA_MMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_sRNA_MMAB2_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_sRNA_MMAB2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_MMHT1.stdout.%j
#SBATCH --error=04_sRNA_MMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_sRNA_MMHT1_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_sRNA_MMHT1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_MMHT2.stdout.%j
#SBATCH --error=04_sRNA_MMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_sRNA_MMHT2_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --validateMappings \
```

```
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_sRNA_MMHT2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_VFAB1.stdout.%j
#SBATCH --error=04_sRNA_VFAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_sRNA_VFAB1_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_sRNA_VFAB1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_VFAB2.stdout.%j
#SBATCH --error=04_sRNA_VFAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0
```

```
salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_sRNA_VFAB2_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_sRNA_VFAB2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_VFHT1.stdout.%j
#SBATCH --error=04_sRNA_VFHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_sRNA_VFHT1_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_sRNA_VFHT1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
```

```
#SBATCH --output=04_sRNA_VFHT2.stdout.%j
#SBATCH --error=04_sRNA_VFHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_sRNA_VFHT2_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_sRNA_VFHT2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_VMAB1.stdout.%j
#SBATCH --error=04_sRNA_VMAB1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_sRNA_VMAB1_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_sRNA_VMAB1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_VMAB2.stdout.%j
#SBATCH --error=04_sRNA_VMAB2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_sRNA_VMAB2_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_sRNA_VMAB2;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_VMHT1.stdout.%j
#SBATCH --error=04_sRNA_VMHT1.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_sRNA_VMHT1_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
```

```
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_sRNA_VMHT1;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_VMHT2.stdout.%j
#SBATCH --error=04_sRNA_VMHT2.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_sRNA_VMHT2_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_sRNA_VMHT2;
```

---

13 Experiment04_sRNAs_all

13.1 Experiment04_sRNAs_All_Bowtie_Commands

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=01_sRNA_MVABHT.stdout.%j
#SBATCH --error=01_sRNA_MVABHT.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Bowtie/1.3.0

bowtie \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    sRNA_MVABHT.fq \
    --al 01_sRNA_MVABHT_bowtie_al-mRNAs.fq \
    --un 01_sRNA_MVABHT_bowtie_un-mRNAs.fq \
    -S 01_sRNA_MVABHT.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
    01_sRNA_MVABHT_bowtie_un-mRNAs.fq \
    --al 02_sRNA_MVABHT_bowtie_un-mRNAs_al-rRNA-biotypes.fq \
    --un 02_sRNA_MVABHT_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
    -S 02_sRNA_MVABHT.sam;

bowtie \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.filtered-biotype-rRNA.fa \
    --best \
    --strata \
    -t \
    -a \
    -p 48 \
    -q \
```

```
02_sRNA_MVABHT_bowtie_un-mRNAs_un-rRNA-biotypes.fq \
--al 03_sRNA_MVABHT_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
--un 03_sRNA_MVABHT_bowtie_un-mRNAs_un-rRNA-biotypes_un-clust-filtered-ncRNAs.fq  \
-S 03_sRNA_MVABHT.sam;
```

13.2 Experiment04_sRNAs_All_Salmon_Commands

```
module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    index \
    --transcripts Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.filtered-biotype-rRNA.fa \
    --threads 48 \
    --index salmon_index \
    --kmerLen 9;
```

```
mkdir 04_sRNA_MVABHT;
```

```
#! /bin/bash
#SBATCH --export=NONE
#SBATCH --job-name=Filter
#SBATCH --time=1-00:00:00
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=04_sRNA_MVABHT.stdout.%j
#SBATCH --error=04_sRNA_MVABHT.stderr.%j

module purge
module load GCC/9.3.0
module load OpenMPI/4.0.3
module load Salmon/1.3.0

salmon \
    quant \
    -i salmon_index \
    --libType U \
    -r 03_sRNA_MVABHT_bowtie_un-mRNAs_un-rRNA-biotypes_al-clust-filtered-ncRNAs.fq \
    --validateMappings \
    --seqBias \
    --gcBias \
    --threads 48 \
    --geneMap Drosophila_melanogaster.BDGP6.28.47.gtf \
    --numBootstraps 100 \
    --output 04_sRNA_MVABHT;
```