

SPORTS1.1

Small non-coding RNA annotation Pipeline Optimized for rRNA- and tRNA-Derived Small RNAs

If you use SPORTS1.1 in your work, please cite this paper:

SPORTS1.0: a tool for annotating and profiling non-coding RNAs optimized for rRNA-and tRNA-derived small RNAs

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Requirements

Linux system, enough disk space and Ram depending on the size of RNA deep sequencing data. (Tested system: ubuntu 12.04 LTS, ubuntu 16.04 LTS)

Installation

1. Download SPORTS1.1 pipeline package.

```
wget https://github.com/junchaoshi/SPORTS1.1/archive/master.zip
```

2. Download necessary software, packages and reference databases as listed below:

1. Perl 5 (<https://www.perl.org>) (Tested version: v5.14.2, v5.22.1); Perl 5 might be already installed in the linux system.

2. Bowtie [1] (<http://bowtie-bio.sourceforge.net/index.shtml>) (Tested version: 1.1.2, 1.2.1.1)
 3. SRA Toolkit (<https://ncbi.github.io/sra-tools/>) (Tested version: 2.8.2)
 4. cutadapt [2] (<http://cutadapt.readthedocs.io/en/stable/index.html>) (Tested version: 1.11)
 5. R (<https://www.r-project.org/>) (Tested version: 3.2.3, 3.2.5)
 6. Reference database (See lists and download link of all pre-compiled species' databases in Pre-compiled Databases Instruction)
3. Installation tutorial for software and packages.

1. Install SPORTS1.1

1. Unpack SPORTS1.1 package.

```
unzip SPORTS1.1-master.zip
```

2. Attach the SPORTS directory to your PATH:

```
echo 'export PATH=$PATH:your_path_to_SPORTS1.1-master/source'
>> ~/.bashrc
```

```
chmod 755 your_path_to_SPORTS1.1-master/source/sports.pl
```

2. Install Bowtie

1. Unpack bowtie-1.x.x-linux-x86_64.zip.

```
unzip bowtie-1.x.x-linux-x86_64.zip
```

2. Attach the bowtie directory to your PATH:

```
echo 'export PATH=$PATH:your_path_to_bowtie' >>
~/.bashrc
```

If you are administrator user, type the following command and password to easily install

```
sudo apt-get install bowtie
```

3. Install SRA Toolkit

1. Unpack SRA toolkit files.

2. Attach the SRA Toolkit executable path to your PATH:

```
echo 'export PATH=$PATH:your_path_to_sra-toolkit/bin'
>> ~/.bashrc
```

4. Install cutadapt

1. Use pip on the command line to install latest version of cutadapt:

```
pip install --user --upgrade cutadapt
```

2. Attach the cutadapt directory to your PATH:

```
echo 'export PATH=$PATH:$HOME/.local/bin' >> ~/.bashrc
```

5. Install R and R package

1. Unpack R-x.y.z.tar.gz with:

```
tar -xf R-x.y.z.tar.gz
```

2. Enter into the R-x.y.z directory:

```
cd R-x.y.z
```

3. Type following command in terminal:

```
./configure
```

```
make
```

```
make check
```

```
make install
```

4. Install R packages by typing following command in terminal:

```
R
```

```
install.packages('ggplot2', dependencies=TRUE, repos='http://cran.rstudio.com/')  
install.packages('data.table', dependencies=TRUE, repos='http://cran.rstudio.com/')  
install.packages('stringr', dependencies=TRUE, repos='http://cran.rstudio.com/')  
q()  
  
n
```

4. Start a new shell session to apply changes to environment variables:

```
source ~/.bashrc
```

5. Test if everything is installed properly:

```
perl -v
```

```
sports.pl -h
```

```
bowtie
```

```
fastq-dump
```

```
cutadapt -h
```

R --version

If you get any error messages you should install the software once again.

Script description

sports.pl

1. Input query format:

1. .sra files.
2. .fastq/.fq, .fasta/.fa files of deep sequencing reads.

Attention: compressed files need to be unpacked before input!

2. Options:

-Input:

-i <file> Input could be:

a .sra, .fastq/.fq or .fasta/.fa file;

a directory (will run all qualified files in the directory recursively);

a text document with absolute path information for each file/folder (when processing)

-Output:

-o <str> output address of annotation results (default: input address)

-k keep all the intermediate files generated during the running progress

-Alignment:

-l <int> the minimal length of the output sequences (default = 15)

-L <int> the maximal length of the output sequences (default = 45)

-M <int> the total number of mismatches in the entire alignment (default = 0)

-a Remove 5' / 3' adapters

-x <str> (if -a applied) 5' adapter sequence. Default = "GTTTCAGAGTTCTACAGTCCGACGATC"

-y <str> (if -a applied) 3' adapter sequence. Default = "TGGAATTCTCGGGTGCCAAGG"

-Others:

`-v` print version information

`-h` print this usage message

3. Example

- Example use 1:

The user wants to map a single fasta file against rat reference genome to get the mapping genome annotation only. (No output figures)

Type following command in terminal:

```
sports.pl -i reads.fa -g /foo/bar/Rattus_norvegicus/UCSC/rn6/Sequence/BowtieIndex/genom
```

- Example use 2:

The user wants to map several already trimmed human sequencing files to human reference genome, miRNA database, tRNA database, rRNA database and piRNA database by using 4 CPU threads, then to output the result to the address: `‘/foo/bar/output/’`.

Write all the fastq files’ addresses into a text document, e.g.:

`seq_address.txt`

```
-----  
/foo/bar/fold_1/seq_1.fastq  
/foo/bar/fold_2/seq_2.fq  
/foo/bar/fold_2/seq_3.fq  
/foo/bar/fold_3/seq_4.fasta  
/foo/bar/fold_4/seq_5.fa  
-----
```

Type following command in terminal:

```
sports.pl -i seq_address.txt -p 4 -g /foo/bar/Homo_sapiens/genome/hg38/genome  
-m /Homo_sapiens/miRBase/21/miRBase_21-has -r /foo/bar/Homo_sapiens/rRNadb/human_rRNA  
-t /foo/bar/Homo_sapiens/GtRNadb/hg19/hg19-tRNAs -w /foo/bar/Homo_sapiens/piRBase/piR_h  
-o /foo/bar/output/
```

- Example use 3:

The user wants to map several untrimmed mouse sequencing files downloaded from NCBI or somewhere else to mouse reference genome, miRNA database, tRNA database, rRNA database, piRNA database, ensembl non-coding RNA database and Rfam database by using 4 CPU threads, then to output the result to the address: `‘/foo/bar/output/’` and keep all the intermediate files generated during the running progress.

Put all the sequencing files into a folder, e.g.:

folder structure:

```

-----
download_seq

    fold_1

        seq_1.sra

        seq_2.sra

    fold_2

        fold_3

            seq_3.fastq

            seq_4.fq

            seq_5.fasta

        seq_6.fa
-----

```

Type following command in terminal:

```

sports.pl -i /foo/bar/download_seq/ -p 4 -a -x GTTCAGAGTTCTACAGTCCGACGATC
-y TGGAAATTCTCGGGTGCCAAGG -g /foo/bar/Mus_musculus/genome/mm10/genome
-m /foo/bar/Mus_musculus/miRBase/21/miRbase_21-mmu -r /foo/bar/Mus_musculus/rRNadb/mous
-t /foo/bar/Mus_musculus/GtRNadb/mm10/mm10-tRNAs -w /foo/bar/Mus_musculus/piRBase/piR_m
-e /foo/bar/Mus_musculus/Ensembl/Mus_musculus.GRCm38.ncrna
-f /foo/bar/Mus_musculus/Rfam/12.3/Rfam-12.3-mouse -o /foo/bar/output/
-k

```

4. Example output file structure for 1 query file input (e.g. SeqFile):

Output folder structure

1_SeqFile

SeqFile_fa (if -k applied)

SeqFile.fa ---unique seqs with reads number

SeqFile_disgarded_reads.fa ---seqs that cannot pass adapter removing

SeqFile_too_short_reads.fa ---seqs that are lower than required mini

SeqFile_too_long_reads.fa ---seqs that are higher than required max

SeqFile_match_genome.fa	---	seqs that can match to reference genome
SeqFile_unmatch_genome.fa	---	seqs that cannot match to reference genome
SeqFile_match_<X>_match_genome.fa	---	seqs that can match to both <X> database and reference genome
SeqFile_match_<X>_unmatch_genome.fa	---	seqs that can match to <X> database but not reference genome
SeqFile_unmatch_<X>_match_genome.fa	---	seqs that cannot match to <X> database but match reference genome
SeqFile_unmatch_<X>_unmatch_genome.fa	---	seqs that match to <X> rfam database but not reference genome
SeqFile_processed (if -k applied)		
SeqFile_output_match_genome	---	seqs that match to reference genome in output
SeqFile_output_<X>_match_genome	---	seqs that match to both miRNA database and reference genome in output
SeqFile_output_<X>_unmatch_genome	---	seqs that match to miRNA database but not reference genome in output
SeqFile_result		
SeqFile_output.txt	---	6 column table file including annotation
SeqFile_summary.txt	---	3 column table file including reads number
SeqFile_length_distribution.txt	---	3 column table file including reads number
SeqFile_mismatch_summary.txt	---	11 column table file including mismatch
SeqFile_sncRNA_distribution.pdf	---	figure of length distribution of sncRNA
SeqFile_rRNA_distribution.pdf	---	figure of length distribution of rRNA
SeqFile_rRNA_mapping.pdf	---	figure of rRNAs mapping against different databases
SeqFile_tRNA_mapping.pdf	---	figure of length distribution of different tRNAs
processing_report (if -k applied)		
1_SeqFile.txt	---	processing log file
sh_file (if -k applied)		
1__SeqFile.sh	---	processing script file

Some output folders only exist when '-k' parameter is applied in sports.pl;

SeqFile_mismatch_summary.txt only exist when '-M' parameter is larger than 0 in sports.pl

Some output files might not exist if the file size is zero.

fastq2fasta.pl

Extracted from miRDeep2 [3] (<https://github.com/rajewsky-lab/mirdeep2>)

1. Description:

Parses fastq format files into fasta format.

2. Input:

A fastq file.

3. Output:

A fasta file, one sequence per line (the sequences are expanded).

4. options:

-

5. Example usage:

```
fastq2fasta.pl reads.fq > reads.fa
```

fastaparse.pl

Extracted from miRDeep2 [3] (<https://github.com/rajewsky-lab/mirdeep2>)

1. Description:

Performs simple filtering of entries in a fasta file.

2. Input:

A fasta file

3. Output:

A filtered fasta file

4. Options:

-a only output entries where the sequence is minimum int nts long

-b remove all entries that have a sequence that contains letters other than
a,c,g,t,u,n,A,C,G,T,U,N.

-s output progress

5. Example usage:

```
fastaparse.pl reads.fa -a 15 -s > reads_no_short.fa 2>
reads_discarded.fa
```

combine_reads.pl

1. Description:

Combine reads in the fasta file to get unique sequence and its read number.

2. Input:

A fasta file

3. Output:

A filtered fasta file.

```
-----
>t000000001 1234567
TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGC
-----
```

't000000001' is the unique ID of the sequence, representing the abundance ranking among all sequences.
'1234567' represents the reads number of sequence 'TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGC'

4. Options:

-

5. Example usage:

```
combine_reads.pl reads.fa > combined_reads.fa
```

tRNA_db_processing.pl

1. Description:

This script adds CCA end to original genomic tRNA 3' end and add G to Histidine tRNA 5' end.

2. Input:

The reference tRNA database file in .fa format

A fasta file

3. Options: -

4. Example usage:

```
tRNA_db_processing.pl input_tRNA_file.fa
```

annotation.pl

1. Description:

Combine the annotation information generated from sports.pl

2. Input:

sports.pl output folder address:

3. Output:

1. __output.txt: A 6 column table file including annotation information for every unique sequence.

ID	Sequence	Length	Reads	Match_Genome
t00000001	TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGC	32	1234567	Yes

-ID: t00000001 --Represents the unique ID of the sequence.

-Sequence: TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGC --Represents the sequence.

-Length: 32 --Length of the sequence.

-Reads: 1234567 --Reads number of the sequence.

-Match_Genome: Yes --If the sequence can match the reference genome.

-Annotation: tRNA-Glu-CTC_5_end --The annotation of the sequence. The annotation is the same as the one in the sports.pl output.

2. <seq_fold>_summary.txt: A 3 column table file including reads number of each major- and sub- classes.

Class	Sub_Class	Reads
tRNAdb-tRNA_5_end_Match_Genome	-	123456
-	tRNA-Glu-CTC_5_end	78910

-Class: tRNAdb-tRNA_5_end_Match_Genome --The major class name.

-Sub_Class: tRNA-Glu-CTC_5_end --The sub class name.

-Reads: 123456 --The reads number of the class.

3. <seq_fold>_length_distribution.txt: A 3 column table file including reads number of each length distribution of each major class.

Class	Length	Reads
-------	--------	-------

tRNAdb-tRNA_5_end_Match_Genome	30	1234
tRNAdb-tRNA_5_end_Match_Genome	31	23456
tRNAdb-tRNA_5_end_Match_Genome	32	34567
tRNAdb-tRNA_5_end_Match_Genome	33	4567
.....		

```

-----
-Class: tRNAdb-tRNA_5_end_Match_Genome    --The major class name.
-Length: 30                                --Length of the sequence.
-Reads: 1234                               --The reads number of the class.

```

4. Options:

-

5. Example usage:

```
annotation.pl <SPORTS_output_fold_address>
```

tRNA_mapping.pl

1. Description:

Perl script calculates expression level of genomic loci by bowtie 1 output information.

2. Input:

bowtie 1 output file

3. Output:

expression summary file

4. Options:

-

5. Example usage:

```
tRNA_mapping.pl bowtie_output_file summary_file
```

mismatch_summary.pl

1. Description:

Perl script summarizes mismatch information generated by Bowtie 1 if parameter '-M' >0 applied in sports.pl

2. Input:

bowtie 1 output file and threshold of reads number.

3. Output:

mismatch summary file

4. Options:

-

5. Example usage:

```
mismatch_summary.pl bowtie_output_file 10 > mismatch_summary.txt
```

overall_RNA_length_distribution.R

1. Description:

Generate figure of length distribution of miRNA, rsRNA, tsRNA, piRNA and other RNAs, if sequence matches exists.

2. Input:

Files generated by annotation.pl

3. Output:

<seq_fold>_sncRNA_distribution.pdf Generate figure of length distribution of different types of rRNAs, if sequence matches exists.

4. Options:

-

5. Example usage:

```
Rscript --vanilla overall_RNA_length_distribution.R <SPORTS_output_fold_address>  
<dataset_name>
```

rRNA_length_distribution.R

1. Description:

Generate figure of length distribution of different types of rRNAs, if sequence matches exists. (e.g. 4.5S, 5S, 5.3S, 5.8S, 12S, 16S, 18S, 28S, 45S ...)

2. Input:

Files generated by annotation.pl

3. Output:

<seq_fold>_rRNA_distribution.pdf

4. Options:

-

5. Example usage:

```
Rscript --vanilla r_RNA_length_distribution.R <SPORTS_output_fold_address>  
<dataset_name>
```

rRNA_mapping.R

1. Description:

Generate figure of rRNAs mapping against different types of rRNAs if sequence matches existed. (e.g. 4.5S, 5S, 5.3S, 5.8S, 12S, 16S, 18S, 28S, 45S ...)

2. Input:

Files generated by annotation.pl

3. Output:

<seq_fold>_rRNA_mapping.pdf

4. Options:

-

5. Example usage:

```
Rscript --vanilla rRNA_mapping.R <SPORTS_output_fold_address>  
<dataset_name>
```

tRNA_mapping.R

1. Description:

Generate figure of rRNAs mapping against different types of tRNAs if sequence matches existed.

2. Input:

Files generated by tRNA_mapping.pl

3. Output:

<seq_fold>_tRNA_mapping.pdf

4. Options:

-

5. Example usage:

```
Rscript --vanilla tRNA_mapping.R <SPORTS_output_fold_address>_tRNA_mapping.txt  
<dataset_name>_tRNA_mapping.pdf
```

mismatch_stat.R

1. Description:

Generate statistics result for mismatch information generated from mismatch_summary.pl

2. Input:

File generated by mismatch_summary.pl and base-calling error

3. Output:

<seq_fold>_mismatch_summary.txt

4. Options:

-

5. Example usage:

```
Rscript --vanilla mismatch_stat.R <SPORTS_output_fold_address>_mismatch_summary.txt  
0.01
```

Pre-compiled annotation databases instruction

Available species lists of bowtie-index based reference database

To build bowtie-index of your own:

```
cd /foo/bar/your_reference_database/
```

```
bowtie-build <your_reference_database_name>.fa <your_reference_database_name>
```

The built bowtie index will be: /foo/bar/your_reference_database/your_reference_database

Unpack reference genome (e.g. human genome):

```
tar zxvf Homo_sapiens_UCSC_hg38.tar.gz
```

Main database source:

-mirbase database [4] (Original source: <http://www.mirbase.org/index.shtml>)

-rRNA database (Original source: <https://www.ncbi.nlm.nih.gov/nuccore/>)

-GtRNAdb database [5] (Original source: <http://gtrnadb.ucsc.edu/>)

-mitotRNAdb database [6] (Original source: <http://mttrna.bioinf.uni-leipzig.de/mtDataOutput/>)

-piRBase database [7] (Original source: <http://www.regulatoryrna.org/database/piRNA/>)

-piRNABank [8] (Original source: <http://pirnabank.ibab.ac.in/index.shtml>)

-ensembl ncRNA database [9] (Original source: <http://www.ensembl.org/index.html>)

-rfam database [10] (Original source: <http://rfam.xfam.org/>)

To download annotation databases of multiple species please use this link:

https://ncrnainfo-my.sharepoint.com/:f/g/personal/sports_ncrna_info/EvZP50IfGFRJlNJwZRujI00BM-CP_w7gITsv8iU45m1rxQ?e=Pk89b9

1. Homo sapiens (Human)

1. annotation databases: (We provide a download link for all databases

listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest8CDc)

2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Homo_sapiens/genome/hg38/genome
-m /<your_defined_address>/Homo_sapiens/miRBase/21/miRBase_21-hsa
-r /<your_defined_address>/Homo_sapiens/rRNadb/human_rRNA
-t /<your_defined_address>/Homo_sapiens/GtRNadb/hg19/hg19-tRNAs
-w /<your_defined_address>/Homo_sapiens/piRBase/piR_human
-e /<your_defined_address>/Homo_sapiens/Ensembl/release-89/Homo_sapiens.GRCh38.ncrna
-f /<your_defined_address>/Homo_sapiens/Rfam/12.3/Rfam-12.3-human
```

2. Gorilla gorilla gorilla (Gorilla)

1. annotation database: (We provide a download link for all databases

listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestIjvagrWePhYNF3k)

2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Gorilla_gorilla/UCSC/gorGor5/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Gorilla_gorilla/miRBase_21/miRBase_21-ggo
-t /<your_defined_address>/Gorilla_gorilla/GtRNadb/gorGor3-tRNAs
-f /<your_defined_address>/Gorilla_gorilla/Rfam_12.3/Rfam-12.3-gorilla
```

3. Pan paniscus (Bonobo)

1. annotation database: (We provide a download link for all databases

listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest

2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Pan_paniscus/UCSC/panPan1/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Pan_paniscus/miRBase_21/miRBase_21-ppa
-f /<your_defined_address>/Pan_paniscus/Rfam_12.3/Rfam-12.3-Bonobo
```

4. Pan troglodytes (Chimp)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestview.aspx?web=1&id=84682828-4040-4040-8040-804080408040&e=1 SbiP2C6Qjpc)

2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Pan_troglodytes/UCSC/panTro4/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Pan_troglodytes/miRBase_21/miRBase_21-ptr
-t /<your_defined_address>/Pan_troglodytes/GtRNAdb/panTro4-tRNAs
-e /<your_defined_address>/Pan_troglodytes/Ensembl/Pan_troglodytes.CHIMP2.1.4.ncrna
-f /<your_defined_address>/Pan_troglodytes/Rfam_12.3/Rfam-12.3-chimp
```

5. *Pongo abelii* (Orangutan)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest

2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Pongo_abelii/UCSC/ponAbe2/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Pongo_abelii/miRBase_21/miRBase_21-ppy
-t /<your_defined_address>/Pongo_abelii/GtRNAdb/ponAbe2-tRNAs
-e /<your_defined_address>/Pongo_abelii/Ensembl/Pongo_abelii.PPYG2.ncrna
-f /<your_defined_address>/Pongo_abelii/Rfam_12.3/Rfam-12.3-orangutan
```

6. *Nomascus leucogenys* (Gibbon)

- 6.1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess)

- 6.2 SPORTS1.1 related parameters if you download recommended reference database:

...

```
-g /<your_defined_address>/Nomascus_leucogenys/UCSC/nomLeu3/Sequence/BowtieIndex/genome
-t /<your_defined_address>/Nomascus_leucogenys/GtRNAb/nomLeu3-tRNAs
-f /<your_defined_address>/Nomascus_leucogenys/Rfam_12.3/Rfam-12.3-gibbon
```

7. *Macaca mulatta* (Rhesus)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest CESs)

2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Macaca_mulatta/UCSC/rheMac8/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Macaca_mulatta/miRBase_21/miRBase_21-mml
-r /<your_defined_address>/Macaca_mulatta/rRNadb/rhesus_rRNA
-t /<your_defined_address>/Macaca_mulatta/GtRNadb/rheMac3-tRNAs
-f /<your_defined_address>/Macaca_mulatta/Rfam_12.3/Rfam-12.3-rhesus
```

8. Papio anubis (Baboon)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest9BLoH_Vmw)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Papio_anubis/UCSC/papAnu2/Sequence/BowtieIndex/genome
-t /<your_defined_address>/Papio_anubis/GtRNadb/papAnu2-tRNAs
-f /<your_defined_address>/Papio_anubis/Rfam_12.3/Rfam-12.3-baboon
```

9. Callithrix jacchus (Marmoset)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestCWgupu6IA)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Callithrix_jacchus/UCSC/calJac3/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Callithrix_jacchus/rRNadb/marmoset_rRNA
-t /<your_defined_address>/Callithrix_jacchus/GtRNadb/calJac3-tRNAs
-f /<your_defined_address>/Callithrix_jacchus/Rfam_12.3/Rfam-12.3-marmoset
```

10. Carlito syrichta (Tarsier)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guesthXdASOIimxNL4I)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Carlito_syrichta/UCSC/tarSyr2/Sequence/BowtieIndex/genome
-t /<your_defined_address>/Carlito_syrichta/GtRNadb/tarSyr2-tRNAs
-f /<your_defined_address>/Carlito_syrichta/Rfam_12.3/Rfam-12.3-tarsier
```

11. Rattus norvegicus (rat)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestQMqBJoQ)

2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Rattus_norvegicus/UCSC/rn6/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Rattus_norvegicus/miRBase_21/miRBase_21-rno
-r /<your_defined_address>/Rattus_norvegicus/rRNAdb/mouse_rRNA
-t /<your_defined_address>/Rattus_norvegicus/GtRNAdb/rn5-tRNAs
-w /<your_defined_address>/Rattus_norvegicus/piRBase/piR_rat
-e /<your_defined_address>/Rattus_norvegicus/Ensembl/Rattus_norvegicus.Rnor_6.0.ncrna
-f /<your_defined_address>/Rattus_norvegicus/Rfam_12.3/Rfam-12.3-rat
```

12. Mus musculus (mouse)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestQMqBJoQ)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Mus_musculus/genome/mm10/genome
-m /<your_defined_address>/Mus_musculus/miRBase/21/miRBase_21-mmu
-r /<your_defined_address>/Mus_musculus/rRNAdb/mouse_rRNA
-t /<your_defined_address>/Mus_musculus/GtRNAdb/mm10/mm10-tRNAs
-w /<your_defined_address>/Mus_musculus/piRBase/piR_mouse
-e /<your_defined_address>/Mus_musculus/Ensembl/release-89/Mus_musculus.GRCm38.ncrna
-f /<your_defined_address>/Mus_musculus/Rfam/12.3/Rfam-12.3-mouse
```

13. Cricetulus griseus (Hamster)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestQMqBJoQ)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Cricetulus_griseus/UCSC/criGri1/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Cricetulus_griseus/miRBase_21/miRBase_21-cgr
-r /<your_defined_address>/Cricetulus_griseus/rRNA_db/hamster_rRNA
-t /<your_defined_address>/Cricetulus_griseus/GtRNAdb/criGri1-tRNAs
-f /<your_defined_address>/Cricetulus_griseus/Rfam_12.3/Rfam-12.3-hamster
```

14. Cavia porcellus (Guinea pig)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestQMqBJoQ)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Cavia_porcellus/UCSC/cavPor3/Sequence/BowtieIndex/genome
-r /<your_defined_address>/Cavia_porcellus/rRNA_db/guinea_rRNA
-t /<your_defined_address>/Cavia_porcellus/GtRNadb/cavPor3-tRNAs
-f /<your_defined_address>/Cavia_porcellus/Rfam_12.3/Rfam-12.3-guinea
```

15. *Heterocephalus glaber* (Naked mole-rat)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Heterocephalus_glaber/UCSC/hetGla2/Sequence/BowtieIndex/genome
-r /<your_defined_address>/Heterocephalus_glaber/rRNA_db/mole_rRNA
-t /<your_defined_address>/Heterocephalus_glaber/GtRNadb/hetGla2-tRNAs
-f /<your_defined_address>/Heterocephalus_glaber/Rfam_12.3/Rfam-12.3-mole
```

16. *Ictidomys tridecemlineatus* (Squirrel)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Ictidomys_tridecemlineatus/UCSC/speTri2/Sequence/BowtieIndex/genome
-t /<your_defined_address>/Ictidomys_tridecemlineatus/GtRNadb/speTri2-tRNAs
-f /<your_defined_address>/Ictidomys_tridecemlineatus/Rfam_12.3/Rfam-12.3-squirrel
```

17. *Ochotona princeps* (Pika)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest DcRVQ)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Ochotona_princeps/UCSC/ochPri3/Sequence/BowtieIndex/genome
-t /<your_defined_address>/Ochotona_princeps/GtRNadb/ochPri3-tRNAs
-f /<your_defined_address>/Ochotona_princeps/Rfam_12.3/Rfam-12.3-pika
```

18. *Oryctolagus cuniculus* (Rabbit)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest WJX10nDdXwvNygc)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Oryctolagus_cuniculus/UCSC/oryCun2/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Oryctolagus_cuniculus/miRBase_21/miRBase_21-ocu
```

```
-r /<your_defined_address>/Oryctolagus_cuniculus/rRNA_db/rabbit_rRNA
-t /<your_defined_address>/Oryctolagus_cuniculus/GtRNAdb/oryCun2-tRNAs
-f /<your_defined_address>/Oryctolagus_cuniculus/Rfam_12.3/Rfam-12.3-rabbit
```

19. *Ovis aries* (Sheep)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Ovis_aries/UCSC/oviAri3/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Ovis_aries/miRBase_21/miRBase_21-oar
-t /<your_defined_address>/Ovis_aries/GtRNAdb/oviAri1-tRNAs
-f /<your_defined_address>/Ovis_aries/Rfam_12.3/Rfam-12.3-sheep
```

20. *Bos taurus* (Cow)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Bos_taurus/UCSC/bosTau8/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Bos_taurus/miRBase_21/miRBase_21-bta
-r /<your_defined_address>/Bos_taurus/rRNA_db/cow_rRNA
-t /<your_defined_address>/Bos_taurus/GtRNAdb/bosTau8-tRNAs
-e /<your_defined_address>/Bos_taurus/Ensembl/Bos_taurus.UMD3.1.ncrna
-f /<your_defined_address>/Bos_taurus/Rfam_12.3/Rfam-12.3-cow
```

21. *Sus scrofa* (Pig)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Sus_scrofa/UCSC/susScr3/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Sus_scrofa/miRBase_21/miRBase_21-ssc
-r /<your_defined_address>/Sus_scrofa/rRNA_db/pig_rRNA
-t /<your_defined_address>/Sus_scrofa/GtRNAdb/susScr3-tRNAs
-f /<your_defined_address>/Sus_scrofa/Rfam_12.3/Rfam-12.3-pig
```

22. *Tursiops truncatus* (Dolphin)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Tursiops_truncatus/UCSC/turTru2/Sequence/BowtieIndex/genome
-t /<your_defined_address>/Tursiops_truncatus/GtRNADB/turTru2-tRNAs
-f /<your_defined_address>/Tursiops_truncatus/Rfam_12.3/Rfam-12.3-dolphin
```

23. *Balaenoptera acutorostrata* (Minke whale)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest-q0lzVEEBIth8V8)

2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Balaenoptera_acutorostrata/UCSC/balAcu1/Sequence/BowtieIndex/genome
-t /<your_defined_address>/Balaenoptera_acutorostrata/GtRNADB/balAcu1-tRNAs
-f /<your_defined_address>/Balaenoptera_acutorostrata/Rfam_12.3/Rfam-12.3-whale
```

24. *Erinaceus europaeus* (Hedgehog)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest-q0lzVEEBIth8V8)

2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Erinaceus_europaeus/UCSC/eriEur2/Sequence/BowtieIndex/genome
-t /<your_defined_address>/Erinaceus_europaeus/GtRNADB/eriEur2-tRNAs
-f /<your_defined_address>/Erinaceus_europaeus/Rfam_12.3/Rfam-12.3-hedgehog
```

25. *Sorex araneus* (Shrew)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest-q0lzVEEBIth8V8)

2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Sorex_araneus/UCSC/sorAra2/Sequence/BowtieIndex/genome
-t /<your_defined_address>/Sorex_araneus/GtRNADB/sorAra2-tRNAs
-f /<your_defined_address>/Sorex_araneus/Rfam_12.3/Rfam-12.3-shrew
```

26. *Canis familiaris* (Dog)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest-q0lzVEEBIth8V8)

2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Canis_familiaris/UCSC/canFam3/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Canis_familiaris/miRBase_21/miRBase_21-cfa
-t /<your_defined_address>/Canis_familiaris/GtRNADB/canFam3-tRNAs
-f /<your_defined_address>/Canis_familiaris/Rfam_12.3/Rfam-12.3-dog
```

27. *Mustela putorius furo* (Ferret)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Mustela_furo/UCSC/musFur1/Sequence/BowtieIndex/genome  
-t /<your_defined_address>/Mustela_furo/GtRNAdb/musFur1-tRNAs  
-f /<your_defined_address>/Mustela_furo/Rfam_12.3-ferret
```

28. *Ailuropoda melanoleuca* (Panda)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Ailuropoda_melanoleuca/UCSC/ailMel1/Sequence/BowtieIndex/genome  
-t /<your_defined_address>/Ailuropoda_melanoleuca/GtRNAdb/ailMel1-tRNAs  
-f /<your_defined_address>/Ailuropoda_melanoleuca/Rfam-12.3-panda
```

29. *Felis catus* (Cat)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Felis_catus/UCSC/felCat8/Sequence/BowtieIndex/genome  
-r /<your_defined_address>/Felis_catus/rRNA_db/cat_rRNA  
-t /<your_defined_address>/Felis_catus/GtRNAdb/felCat5-tRNAs  
-f /<your_defined_address>/Felis_catus/Rfam_12.3/Rfam-12.3-cat
```

30. *Equus caballus* (Horse)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Equus_caballus/UCSC/equCab2/Sequence/BowtieIndex/genome  
-m /<your_defined_address>/Equus_caballus/miRBase_21/miRBase_21-eca  
-r /<your_defined_address>/Equus_caballus/rRNA_db/horse_rRNA  
-t /<your_defined_address>/Equus_caballus/GtRNAdb/equCab2-tRNAs  
-f /<your_defined_address>/Equus_caballus/Rfam_12.3/Rfam-12.3-horse
```

31. *Ceratotherium simum* (White rhinoceros)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
 2. SPORTS1.1 related parameters if you download recommended reference database:


```
-g /<your_defined_address>/Ceratotherium_simum/UCSC/cerSim1/Sequence/BowtieIndex/genome
-t /<your_defined_address>/Ceratotherium_simum/GtRNADB/cerSim1-tRNAs
-f /<your_defined_address>/Ceratotherium_simum/Rfam_12.3/Rfam-12.3-rhinoceros
```
32. *Myotis lucifugus* (Microbat)
1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest 2sRUrTGn7k)
 2. SPORTS1.1 related parameters if you download recommended reference database:


```
-g /<your_defined_address>/Myotis_lucifugus/UCSC/myoLuc2/Sequence/BowtieIndex/genome
-t /<your_defined_address>/Myotis_lucifugus/GtRNADB/myoLuc2-tRNAs
-f /<your_defined_address>/Myotis_lucifugus/Rfam_12.3/Rfam-12.3-bat
```
33. *Trichechus manatus* (Manatee)
1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
 2. SPORTS1.1 related parameters if you download recommended reference database:


```
-g /<your_defined_address>/Trichechus_manatus/UCSC/triMan1/Sequence/BowtieIndex/genome
-t /<your_defined_address>/Trichechus_manatus/GtRNADB/triMan1-tRNAs
-f /<your_defined_address>/Trichechus_manatus/Rfam_12.3/Rfam-12.3-manatee
```
34. *Loxodonta africana* (Elephant)
1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest 7s)
 2. SPORTS1.1 related parameters if you download recommended reference database:


```
-g /<your_defined_address>/Loxodonta_africana/UCSC/loxAfr3/Sequence/BowtieIndex/genome
-t /<your_defined_address>/Loxodonta_africana/GtRNADB/loxAfr3-tRNAs
-f /<your_defined_address>/Loxodonta_africana/Rfam_12.3/Rfam-12.3-elephant
```
35. *Dasypus novemcinctus* (Armadillo)
1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)

2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Dasypus_novemcinctus/UCSC/dasNov3/Sequence/BowtieIndex/g
-t /<your_defined_address>/Dasypus_novemcinctus/GtRNAdb/dasNov3-tRNAs
-f /<your_defined_address>/Dasypus_novemcinctus/Rfam_12.3/Rfam-12.3-armadillo
```

36. *Notamacropus eugenii* (Wallaby)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestdFi1Mm7C0QH9K00WHH4)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Notamacropus_eugenii/UCSC/macEug2/Sequence/BowtieIndex/g
-m /<your_defined_address>/Notamacropus_eugenii/miRBase_21/miRBase_21-meu
-t /<your_defined_address>/Notamacropus_eugenii/GtRNAdb/macEug2-tRNAs
-f /<your_defined_address>/Notamacropus_eugenii/Rfam_12.3/Rfam-12.3-wallaby
```

37. *Sarcophilus harrisii* (Tasmanian devil)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestD6mL0)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Sarcophilus_harrisii/UCSC/sarHar1/Sequence/BowtieIndex/g
-m /<your_defined_address>/Sarcophilus_harrisii/miRBase_21/miRBase_21-sha
-t /<your_defined_address>/Sarcophilus_harrisii/GtRNAdb/sarHar1-tRNAs
-f /<your_defined_address>/Sarcophilus_harrisii/Rfam_12.3/Rfam-12.3-tasmanian
```

38. *Monodelphis domestica* (Opossum)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Monodelphis_domestica/UCSC/monDom5/Sequence/BowtieIndex/
-m /<your_defined_address>/Monodelphis_domestica/miRBase_21/miRBase_21-mdo
-t /<your_defined_address>/Monodelphis_domestica/GtRNAdb/monDom5-tRNAs
-e /<your_defined_address>/Monodelphis_domestica/Ensembl/Monodelphis_domestica.BROA
-f /<your_defined_address>/Monodelphis_domestica/Rfam_12.3/Rfam-12.3-opossum
```

39. *Ornithorhynchus anatinus* (Platypus)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestwfpJ81M)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Ornithorhynchus_anatinus/UCSC/ornAna2/Sequence/BowtieIndex/
-m /<your_defined_address>/Ornithorhynchus_anatinus/miRBase_21/miRBase_21-oan
-t /<your_defined_address>/Ornithorhynchus_anatinus/GtRNAdb/ornAna1-tRNAs
-w /<your_defined_address>/Ornithorhynchus_anatinus/piRBase/piR_platypus
-e /<your_defined_address>/Ornithorhynchus_anatinus/Ensembl/Ornithorhynchus_anatinu
-f /<your_defined_address>/Ornithorhynchus_anatinus/Rfam_12.3/Rfam-12.3-platypus
```

40. Taeniopygia guttata (Zebra finch)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestwfpJ81M)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Taeniopygia_guttata/UCSC/taeGut2/Sequence/BowtieIndex/g
-m /<your_defined_address>/Taeniopygia_guttata/miRBase_21/miRBase_21-tgu
-t /<your_defined_address>/Taeniopygia_guttata/GtRNAdb/taeGut2-tRNAs
-f /<your_defined_address>/Taeniopygia_guttata/Rfam_12.3/Rfam-12.3-finch
```

41. Melopsittacus undulatus (Budgerigar)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestwfpJ81M)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Melopsittacus_undulatus/UCSC/melUnd1/Sequence/BowtieIndex/
-t /<your_defined_address>/Melopsittacus_undulatus/GtRNAdb/melUnd1-tRNAs
-f /<your_defined_address>/Melopsittacus_undulatus/Rfam_12.3/Rfam-12.3-budgerigar
```

42. Gallus gallus (Chicken)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestwfpJ81M)
2. PORTS1.0 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Gallus_gallus/UCSC/galGal5/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Gallus_gallus/miRBase_21/miRBase_21-gga
-r /<your_defined_address>/Gallus_gallus/rRNA_db/chicken_rRNA
-t /<your_defined_address>/Gallus_gallus/GtRNAdb/galGal4-tRNAs
-w /<your_defined_address>/Gallus_gallus/piRBase/piR_gga_v1.0
-e /<your_defined_address>/Gallus_gallus/Ensembl/Gallus_gallus.Gallus_gallus-5.0.no
```

- f /<your_defined_address>/Gallus_gallus/Rfam_12.3/Rfam-12.3-chicken
43. *Meleagris gallopavo* (Turkey)
1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
 2. SPORTS1.1 related parameters if you download recommended reference database:


```
-g /<your_defined_address>/Meleagris_gallopavo/UCSC/melGal1/Sequence/BowtieIndex/genome
-t /<your_defined_address>/Meleagris_gallopavo/GtRNadb/melGal1-tRNAs
-f /<your_defined_address>/Meleagris_gallopavo/Rfam_12.3/Rfam-12.3-turkey
```
44. *Chrysemys picta* (Painted Turtle)
1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
 2. SPORTS1.1 related parameters if you download recommended reference database:


```
-g /<your_defined_address>/Chrysemys_picta/UCSC/chrPic1/Sequence/BowtieIndex/genome
-t /<your_defined_address>/Chrysemys_picta/GtRNadb/chrPic1-tRNAs
-f /<your_defined_address>/Chrysemys_picta/Rfam_12.3/Rfam-12.3-turtle
```
45. *Anolis carolinensis* (Lizard)
1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest i58-1fjJeqcDHZUpLLo)
 2. SPORTS1.1 related parameters if you download recommended reference database:


```
-g /<your_defined_address>/Anolis_carolinensis/UCSC/anoCar2/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Anolis_carolinensis/miRBase_21/miRBase_21-aca
-t /<your_defined_address>/Anolis_carolinensis/GtRNadb/anoCar2-tRNAs
-e /<your_defined_address>/Anolis_carolinensis/Ensembl/Anolis_carolinensis.AnoCar2
-f /<your_defined_address>/Anolis_carolinensis/Rfam_12.3/Rfam-12.3-lizard
```
46. *Xenopus laevis* (Frog)
1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
 2. SPORTS1.1 related parameters if you download recommended reference database:


```
-g /<your_defined_address>/Xenopus_laevis/UCSC/xenTro7/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Xenopus_laevis/miRBase_21/miRBase_21-xtr
-r /<your_defined_address>/Xenopus_laevis/rRNA_db/frog_rRNA
-t /<your_defined_address>/Xenopus_laevis/GtRNadb/xenTro3-tRNAs
-w /<your_defined_address>/Xenopus_laevis/piRBase/piR_xtr_v1.0
```

```
-e /<your_defined_address>/Xenopus_laevis/Ensembl/Xenopus_tropicalis.JGI_4.2.ncrna
-f /<your_defined_address>/Xenopus_laevis/Rfam_12.3/Rfam-12.3-frog
```

47. *Latimeria chalumnae* (Coelacanth)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestiphiQFRDzuKoJtA)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Latimeria_chalumnae/UCSC/latCha1/Sequence/BowtieIndex/genome
-r /<your_defined_address>/Latimeria_chalumnae/rRNA_db/coelacanth_rRNA
-t /<your_defined_address>/Latimeria_chalumnae/GtRNadb/latCha1-tRNAs
-f /<your_defined_address>/Latimeria_chalumnae/Rfam_12.3/Rfam-12.3-coelacanth
```

48. *Tetraodon nigroviridis* (Tetraodon)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestiphiQFRDzuKoJtA)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Tetraodon_nigroviridis/UCSC/tetNig2/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Tetraodon_nigroviridis/miRBase_21/miRBase_21-tni
-t /<your_defined_address>/Tetraodon_nigroviridis/GtRNadb/tetNig2-tRNAs
-f /<your_defined_address>/Tetraodon_nigroviridis/Rfam_12.3/Rfam-12.3-tetraodon
```

49. *Takifugu rubripes* (Fugu)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest1dy5wnCfdQ)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Takifugu_rubripes/UCSC/fr3/Sequence/BowtieIndex/genome
-t /<your_defined_address>/Takifugu_rubripes/GtRNadb/fr3-tRNAs
-f /<your_defined_address>/Takifugu_rubripes/Rfam_12.3/Rfam-12.3-fugu
```

50. *Gasterosteus aculeatus* (Stickleback)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest1dy5wnCfdQ)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Gasterosteus_aculeatus/UCSC/gasAcu1/Sequence/BowtieIndex/genome
-t /<your_defined_address>/Gasterosteus_aculeatus/GtRNadb/gasAcu1-tRNAs
-e /<your_defined_address>/Gasterosteus_aculeatus/Ensembl/Gasterosteus_aculeatus.BF
```

- f /<your_defined_address>/Gasterosteus_aculeatus/Rfam_12.3/Rfam-12.3-stickleback
51. *Oryzias latipes* (Medaka)
1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
 2. SPORTS1.1 related parameters if you download recommended reference database:


```
-g /<your_defined_address>/Oryzias_latipes/UCSC/oryLat2/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Oryzias_latipes/miRBase_21/miRBase_21-ola
-t /<your_defined_address>/Oryzias_latipes/GtRNAdb/oryLat2-tRNAs
-f /<your_defined_address>/Oryzias_latipes/Rfam_12.3/Rfam-12.3-medaka
```
52. *Oreochromis niloticus* (Nile tilapia)
1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
 2. SPORTS1.1 related parameters if you download recommended reference database:


```
-g /<your_defined_address>/Oreochromis_niloticus/UCSC/oreNil2/Sequence/BowtieIndex/
-t /<your_defined_address>/Oreochromis_niloticus/GtRNAdb/oreNil2-tRNAs
-f /<your_defined_address>/Oreochromis_niloticus/Rfam_12.3/Rfam-12.3-tilapia
```
53. *Gadus morhua* (Atlantic cod)
1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
 2. SPORTS1.1 related parameters if you download recommended reference database:


```
-g /<your_defined_address>/Gadus_morhua/UCSC/gadMor1/Sequence/BowtieIndex/genome
-r /<your_defined_address>/Gadus_morhua/rRNA_db/cod_rRNA
-t /<your_defined_address>/Gadus_morhua/GtRNAdb/gadMor1-tRNAs
-f /<your_defined_address>/Gadus_morhua/Rfam_12.3/Rfam-12.3-cod
```
54. *Danio rerio* (Zebrafish)
1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest VjshX-GKLZI7limHFlo)
 2. SPORTS1.1 related parameters if you download recommended reference database:


```
-g /<your_defined_address>/Danio_rerio/UCSC/danRer10/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Danio_rerio/miRBase_21/miRBase_21-dre
-r /<your_defined_address>/Danio_rerio/rRNA_db/zebrafish_rRNA
-t /<your_defined_address>/Danio_rerio/GtRNAdb/danRer6-tRNAs
-w /<your_defined_address>/Danio_rerio/piRBase/piR_dre_v1.0
```

```
-e /<your_defined_address>/Danio_rerio/Ensembl/Danio_rerio.GRCz10.ncrna
-f /<your_defined_address>/Danio_rerio/Rfam_12.3/Rfam-12.3-zebrafish
```

55. *Callorhinchus milii* (Elephant shark)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Callorhinchus_milii/UCSC/calMil1/Sequence/BowtieIndex/g
-t /<your_defined_address>/Callorhinchus_milii/GtRNAdb/calMil1-tRNAs
-f /<your_defined_address>/Callorhinchus_milii/Rfam_12.3/Rfam-12.3-shark
```

56. *Petromyzon marinus* (Lamprey)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Petromyzon_marinus/UCSC/petMar2/Sequence/BowtieIndex/gen
-r /<your_defined_address>/Petromyzon_marinus/rRNA_db/lamprey_rRNA
-t /<your_defined_address>/Petromyzon_marinus/GtRNAdb/petMar2-tRNAs
-f /<your_defined_address>/Petromyzon_marinus/Rfam_12.3/Rfam-12.3-lamprey
```

57. *Strongylocentrotus purpuratus* (Sea urchin)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Strongylocentrotus_purpuratus/UCSC/strPur2/Sequence/Bowt
-m /<your_defined_address>/Strongylocentrotus_purpuratus/miRBase_21/miRBase_21-spu
-r /<your_defined_address>/Strongylocentrotus_purpuratus/rRNA_db/urchin_rRNA
-t /<your_defined_address>/Strongylocentrotus_purpuratus/GtRNAdb/Spurp-tRNAs
-e /<your_defined_address>/Strongylocentrotus_purpuratus/Ensembl/Strongylocentrotus
-f /<your_defined_address>/Strongylocentrotus_purpuratus/Rfam_12.3/Rfam-12.3-urchin
```

58. *Drosophila melanogaster* (Drosophila)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Drosophila_melanogaster/UCSC/dm6/Sequence/BowtieIndex/g
-m /<your_defined_address>/Drosophila_melanogaster/miRBase_21/miRBase_21-dme
-r /<your_defined_address>/Drosophila_melanogaster/rRNA_db/drosophila_rRNA
```

```
-t /<your_defined_address>/Drosophila_melanogaster/GtRNadb/dm6-tRNAs
-w /<your_defined_address>/Drosophila_melanogaster/piRBase/piR_dme
-e /<your_defined_address>/Drosophila_melanogaster/Ensembl/Drosophila_melanogaster
-f /<your_defined_address>/Drosophila_melanogaster/Rfam_12.3/Rfam-12.3-drosophila
```

59. *Anopheles gambiae* (Mosquito)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Anopheles_gambiae/UCSC/anoGam1/Sequence/BowtieIndex/gen
-m /<your_defined_address>/Anopheles_gambiae/miRBase_21/miRBase_21-aga
-t /<your_defined_address>/Anopheles_gambiae/GtRNadb/Agamb-tRNAs
-e /<your_defined_address>/Anopheles_gambiae/Ensembl/Anopheles_gambiae.AgamP4.ncrna
-f /<your_defined_address>/Anopheles_gambiae/Rfam_12.3/Rfam-12.3-mosquito
```

60. *Pristionchus pacificus* (Roundworm)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Pristionchus_pacificus/UCSC/priPac1/Sequence/BowtieIndex
-m /<your_defined_address>/Pristionchus_pacificus/miRBase_21/miRBase_21-ppc
-r /<your_defined_address>/Pristionchus_pacificus/rRNA_db/roundworm_rRNA
-t /<your_defined_address>/Pristionchus_pacificus/GtRNadb/priPac1-tRNAs
-f /<your_defined_address>/Pristionchus_pacificus/Rfam_12.3/Rfam-12.3-roundworm
```

61. *Caenorhabditis elegans* (Nematode):

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest pCI)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Caenorhabditis_elegans/UCSC/ce10/Sequence/BowtieIndex/g
-m /<your_defined_address>/Caenorhabditis_elegans/miRBase_21/miRBase_21-cel
-r /<your_defined_address>/Caenorhabditis_elegans/rRNA_db/cel_rRNA
-t /<your_defined_address>/Caenorhabditis_elegans/GtRNadb/ce10-tRNAs
-w /<your_defined_address>/Caenorhabditis_elegans/piRBase/piR_cel_v1.0
-e /<your_defined_address>/Caenorhabditis_elegans/Ensembl/Caenorhabditis_elegans.W
-f /<your_defined_address>/Caenorhabditis_elegans/Rfam_12.3/Rfam-12.3-nematode
```

62. *Saccharomyces cerevisiae* (Yeast)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:


```
-g /<your_defined_address>/Saccharomyces_cerevisiae/UCSC/sacCer3/Sequence/BowtieIndex
-r /<your_defined_address>/Saccharomyces_cerevisiae/rRNA_db/yeast_rRNA
-t /<your_defined_address>/Saccharomyces_cerevisiae/GtRNADB/sacCer3-tRNAs
-e /<your_defined_address>/Saccharomyces_cerevisiae/Ensembl/Saccharomyces_cerevisiae
-f /<your_defined_address>/Saccharomyces_cerevisiae/Rfam_12.3/Rfam-12.3-yeast
```

63. Zea mays (Corn)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:


```
-g /<your_defined_address>/Zea_mays/Ensembl/AGPv4/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Zea_mays/miRBase_21/miRBase_21-zma
-r /<your_defined_address>/Zea_mays/rRNA_db/corn_rRNA
-t /<your_defined_address>/Zea_mays/GtRNADB/zeaMay5-tRNAs
-e /<your_defined_address>/Zea_mays/Ensembl/Zea_mays.AGPv4.ncrna
-f /<your_defined_address>/Zea_mays/Rfam_12.3/Rfam-12.3-corn
```

64. Sorghum bicolor (Sorghum)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:


```
-g /<your_defined_address>/Sorghum_bicolor/Ensembl/Sbi1/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Sorghum_bicolor/miRBase_21/miRBase_21-sbi
-r /<your_defined_address>/Sorghum_bicolor/rRNA_db/sorghum_rRNA
-t /<your_defined_address>/Sorghum_bicolor/GtRNADB/Sbico-tRNAs
-e /<your_defined_address>/Sorghum_bicolor/Ensembl/Sorghum_bicolor.Sorghum_bicolor
-f /<your_defined_address>/Sorghum_bicolor/Rfam_12.3/Rfam-12.3-sorghum
```

65. Oryza sativa (Rice)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:


```
-g /<your_defined_address>/Oryza_sativa/Ensembl/IRGSP-1.0/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Oryza_sativa/miRBase_21/miRBase_21-osa
-r /<your_defined_address>/Oryza_sativa/rRNA_db/rice_rRNA
```

```
-t /<your_defined_address>/Oryza_sativa/GtRNAb/Osati-tRNAs
-e /<your_defined_address>/Oryza_sativa/Ensembl/Oryza_sativa.IRGSP-1.0.ncrna
-f /<your_defined_address>/Oryza_sativa/Rfam_12.3/Rfam-12.3-rice
```

66. Arabidopsis thaliana (Arabidopsis)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Arabidopsis_thaliana/Ensembl/TAIR10/Sequence/BowtieIndex
-m /<your_defined_address>/Arabidopsis_thaliana/miRBase_21/miRBase_21-ath
-r /<your_defined_address>/Arabidopsis_thaliana/rRNA_db/Arabidopsis_rRNA
-t /<your_defined_address>/Arabidopsis_thaliana/GtRNAb/araTha1-tRNAs
-e /<your_defined_address>/Arabidopsis_thaliana/Ensembl/Arabidopsis_thaliana.TAIR10
-f /<your_defined_address>/Arabidopsis_thaliana/Rfam_12.3/Rfam-12.3-arabidopsis
```

67. Glycine max (Soybean)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Glycine_max/Ensembl/Gm01/Sequence/BowtieIndex/genome
-m /<your_defined_address>/Glycine_max/miRBase_21/miRBase_21-gma
-r /<your_defined_address>/Glycine_max/rRNA_db/soybean_rRNA
-t /<your_defined_address>/Glycine_max/GtRNAb/glyMax2-tRNAs
-f /<your_defined_address>/Glycine_max/Rfam_12.3/Rfam-12.3-soybean
```

68. Escherichia coli (E.coli)

1. annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guest SpOIXaUik)
2. SPORTS1.1 related parameters if you download recommended reference database:

```
-g /<your_defined_address>/Escherichia_coli/Ensembl/EB1/Sequence/BowtieIndex/genome
-r /<your_defined_address>/Escherichia_coli/rRNA_db/e_coli_rRNA
-t /<your_defined_address>/Escherichia_coli/GtRNAb/eschColi-tRNAs
-e /<your_defined_address>/Escherichia_coli/Ensembl/Escherichia_coli.HUSEC2011CHR1
-f /<your_defined_address>/Escherichia_coli/Rfam_12.3/Rfam-12.3-e_coli
```

Instruction for compiling annotation database by user

1. Prepare the reference databases for your species X

1. Download the reference genome in .fa format into the defined folder address: <your_defined_address>; (necessary)
2. Download and extract the miRNA sequences belong to the species in .fa format from miRBase (<http://www.mirbase.org/>), convert RNA sequences to cDNA sequences (U -> T), then put the file X_mirbase.fa into the defined folder address: <your_defined_address>; (optional)
3. Download the rRNA sequences in .fa format from NCBI or anywhere else, convert RNA sequences to cDNA sequences (U -> T), name and list each rRNA sequences separately, as exemplified below, and put the files such X_rRNA_5S.fa, X_rRNA_5.8S.fa into the defined folder address: <your_defined_address>; (optional)

human_rRNA_5S.fa

>Human 5S ribosomal RNA

```
GTCTACGGCCATACCACCCTGAACGCGCCCGATCTCGTCTGATCTCGGAAGCTAAGCAGGGTCGGGCCTG
GTTAGTACTTGGATGGGAGACCGCCTGGGAATACCGGGTGCTGTAGGCTTT
```

human_rRNA_5.8S.fa

>Human 5.8S ribosomal RNA

```
CGACTCTTAGCGGTGGATCACTCGGCTCGTGCGTCGATGAAGAACGCAGCGCTAGCTGCGAGAATTAATG
TGAATTGCAGGACACATTGATCATCGACACTTCGAACGCACTTGCGGCCCCGGGTTCCTCCCGGGGCTAC
GCCTGTCTGAGCGTCGCTT
```

4. Download the high confidence tRNA sequences (X-tRNAs.fa) and high confidence mature tRNA sequences (X-mature-tRNAs.fa) in .fa format from GtRNAdb (<http://gtrnadb.ucsc.edu/>) and put the files X-mature-tRNAs.fa and X-tRNAs.fa into the defined folder address: <your_defined_address>; (optional)
5. Download the noncoding RNA sequences in .fa format from Ensembl database (<http://ensemblgenomes.org/>) and put the file X_ensembl_ncrna.fa into the defined folder address: <your_defined_address>; (optional)
6. Download and extract the noncoding RNA sequences in .fa format from Rfam database (<http://ensemblgenomes.org/>) and put the file X_rfam_ncrna.fa into the defined folder address: <your_defined_address>; (optional)
7. Download and extract the noncoding RNA sequences belong to the species in .fa format from Rfam database (<https://rfam.xfam.org/>) and put the file X_rfam.fa into the defined folder address: <your_defined_address>; (optional)
8. Download piRNA sequences in .fa format from piRNA databases and put the file X_piRNA.fa into the defined folder address:

<your_defined_address>. (optional)

2. Type following command in terminal:

```
sports.pl -i /foo/bar/download_seq/ -p 4 -g <your_defined_address>/X
-m <your_defined_address>/X_mirbase -r <your_defined_address>/X_rRNA
-t <your_defined_address>/X-tRNAs -e <your_defined_address>/X__ensembl_ncrna
-f <your_defined_address>/X_rfam_ncrna -w <your_defined_address>/X_piRNA
-o /foo/bar/output/
```

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9. Nawrocki EP, Burge SW, Bateman A, Daub J, Eberhardt RY, Eddy SR, et al. Rfam 12.0: updates to the RNA families database. *Nucleic acids research.* 2015;43(Database issue):D130-7. doi: 10.1093/nar/gku1063.

Update history

1.1.0 - 02/20/2020 1. The tsRNA annotation information has been refined to pre-tsRNA and mature-tsRNA based on updated tRNA database; 2. Annotation for Mitochondrial tRNAs (obtained from mitotRNAdb <http://mttrna.bioinf.uni-leipzig.de/mtDataOutput/>) and yRNAs (obtained from <https://www.ncbi.nlm.nih.gov/>) are now available. Pre-compiled databases for mouse and human have been updated (databases for other species will be updated soon if applicable), please re-download the databases for better results; 3. The miRNA annotation process has been optimized to get more accurate results. 4. Bowtie index building process has been imbedded in sports.pl to reduce the size of pre-compiled database; 5. New parameter '-z' is added to make mismatch information statistics optional ('-M' > 0 is needed for the statistics). 6. Instruction for compiling annotation database by user is added.

1.0.5 - 09/25/2018 1. Changed annotation strategy to fit more species tRNA annotation in GtRNAdb. 2. Fixed some bugs in the previous version. Thanks Catrin Lloyd to figure one out!

1.0.4 - 03/25/2018 1. New function added: if '-M' > 0 applied in sports.pl, statistics of mismatch information will be generated to predict potential nucleic acid modification loci; 2. The figure of tRNA mapping information will be generated if tRNA database is defined; 3. A sample output with the parameter '-M 1' of dataset GSM2304822 (mouse sperm) is uploaded here.

1.0.3 - 01/27/2018 1. Changed the mapping order to make the mapping results more accurate according to the paper "Juan Pablo Tosar, Carlos Rovira, Alfonso Cayota. Non-coding RNA fragments account for the majority of annotated piRNAs expressed in somatic non-gonadal tissues. Communications Biology. 2018;1, Article number: 2. doi: 10.1038/s42003-017-0001-7".

1.0.2 - 01/22/2018 1. Fixed bugs to generate more accurate mature tRNA database.

1.0.1 - 01/13/2018 1. Fixed bugs that caused unexpected exit. 2. Optimized script to speed up tRNA annotation process.

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