

SPORTS1.0

Small non-coding RNA annotation Pipeline

Optimized for rRNA- and tRNA-Derived Small RNAs

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Requirements

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

Installation

1. Download SPORTS1.0 package.
wget https://github.com/junchaoshi/sports1.0/archive/master.zip
2. Download necessary software, packages and reference databases as listed below:
 - 2.1 Perl 5 (<https://www.perl.org>) (Tested version: v5.14.2, v5.22.1); Perl 5 could be already installed in the linux system.
 - 2.2 Bowtie [1] (<http://bowtie-bio.sourceforge.net/index.shtml>) (Tested version: 1.1.2, 1.2.1.1)
 - 2.3 SRA Toolkit (<https://ncbi.github.io/sra-tools/>) (Tested version: 2.8.2)
 - 2.4 cutadapt [2] (<http://cutadapt.readthedocs.io/en/stable/index.html>) (Tested version: 1.11)
 - 2.5 R (<https://www.r-project.org/>) (Tested version: 3.2.3, 3.2.5)
 - 2.6 Reference database (See lists and download link of all pre-compiled species' databases in [appendix](#))
3. Installation tutorial for software and packages.
 - 3.1 Install SPORTS1.0
 - 3.1.1 Unpack SPORTS1.0 package.
unzip sports1.0-master.zip
 - 3.1.2 Attach the SPORTS directory to your PATH:
echo 'export PATH=\$PATH:your_path_to_sports1.0-master/source' >> ~/.bashrc
 - 3.2 Install Bowtie
 - 3.2.1 Unpack bowtie-1.x.x-linux-x86_64.zip.
unzip sports1.0-master.zip
 - 3.2.2 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 bowtie:
sudo apt-get install bowtie

- 3.3 Install SRA Toolkit
 - 3.3.1 Unpack SRA toolkit files.
 - 3.3.2 Attach the SRA Toolkit executable path to your PATH:
echo 'export PATH=\$PATH:your_path_to_sra-toolkit/bin' >> ~/.bashrc
- 3.4 Install cutadapt
 - 3.4.1 Use pip on the command line to install latest version of cutadapt:
pip install --user --upgrade cutadapt
 - 3.4.2 Attach the cutadapt directory to your PATH:
echo 'export PATH=\$PATH:\$HOME/.Local/bin' >> ~/.bashrc
- 3.5 Install R and R package
 - 3.5.1 Unpack R-x.y.z.tar.gz with:
tar -xf R-x.y.z.tar.gz
 - 3.5.2 Enter into the R-x.y.z directory:

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

3.5.3 Type following command in terminal:

```
./configure
```

```
make
```

```
make check
```

```
make install
```

3.5.4 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 correctly install the software again.

Script description:

sports.pl

1. Input query format:

- a) .sra files.
- b) .fastq/.fq, .fasta/.fa files of deep sequencing reads.

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 multiple data, input each file/folder path per line).

-p <int> number of threads to launch (default = 1)

--Index:

- g <str> reference genome bowtie index
- m <str> miRNA database bowtie index (optional)
- r <str> rRNA database bowtie index (optional)
- t <str> tRNA database bowtie index (optional)
- w <str> piRNA database bowtie index (optional)
- e <str> ensembl noncoding RNA database bowtie index (optional)
- f <str> rfam database bowtie index (optional)

--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 wishes 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/genome
```

Example use 2:

The user wishes to map several already trimmed human sequencing files against 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/UCSC/hg38/Sequence/BowtieIndex/genome -m  
/Homo_sapiens/miRBase_21/miRBase_21-has -r /foo/bar/Homo_sapiens/rRNA_db/human_rRNA -t  
/foo/bar/Homo_sapiens/GtRNadb/hg19-tRNAs -w /foo/bar/Homo_sapiens/piRBase/piR_human -o  
/foo/bar/output/
```

Example use 3:

The user wishes to map several untrimmed mouse sequencing files downloaded from NCBI or somewhere else against mouse reference genome, miRNA database, tRNA database, rRNA database, piRNA database, ensembl noncoding 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.:

input folder structure:

| Level 1 directory | Level 2 directory | Level 3 directory | Level 4 directory |
|-------------------|-------------------|-------------------|-------------------|
| 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  
TGGGAATTCTCGGGTGCCAAGG -g /foo/bar/Mus_musculus/UCSC/mm10/Sequence/BowtieIndex/Genome -m  
/foo/bar/Mus_musculus/miRBase_21/miRbase_21-mmu -r  
/foo/bar/Mus_musculus/rRNA_db/mouse_rRNA -t /foo/bar/Mus_musculus/GtRNadb/mm10-tRNAs -w  
/foo/bar/Mus_musculus/piRBase/piR_mouse -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

| Level 1 directory | Level 2 directory | Level 3 directory | Annotation |
|-------------------|--------------------------------------|-------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------|
| 1_SeqFile | SeqFile_fa (if -k applied) | SeqFile.fa | unique seqs with reads number |
| | | SeqFile_disgarded_reads.fa | seqs that cannot pass adapter removing process |
| | | SeqFile_too_short_reads.fa | seqs that are lower than required minimal length threshold |
| | | SeqFile_too_long_reads.fa | seqs that are higher than required maximal length threshold |
| | | 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 can match to reference genome |
| | | SeqFile_unmatch_<X>_unmatch_genome.fa | seqs that match to neither <X> database nor reference genome |
| | SeqFile_processed (if -k applied) | SeqFile_output_match_genome | seqs that match to reference genome in SAM format |
| | | SeqFile_output_<X>_match_genome | seqs that match to <X> database but not reference genome in SAM format |
| | | SeqFile_output_<X>_unmatch_genome | seqs that match to both <X> database and reference genome in SAM format |
| | | SeqFile_output_tRNA_match_genome | seqs that match to both tRNA database and reference genome in SAM format |
| | | SeqFile_output_tRNA_unmatch_genome | seqs that match to tRNA database but not reference genome in SAM format |
| | | SeqFile_output_tRNA_5_tail_match_genome | seqs that match to both tRNA 5' end and reference genome in SAM format (included in SeqFile_output_tRNA_match_genome file) |
| | | SeqFile_output_tRNA_5_tail_unmatch_genome | seqs that match to tRNA 5' end but not reference genome in SAM format (included in SeqFile_output_tRNA_unmatch_genome file) |
| | | SeqFile_output_tRNA_3_tail_match_genome | seqs that match to both tRNA 3' end and reference genome in SAM format (included in SeqFile_output_tRNA_match_genome file) |
| | | SeqFile_output_tRNA_3_tail_unmatch_genome | seqs that match to tRNA 3' end but not reference genome in SAM format (included in SeqFile_output_tRNA_unmatch_genome file) |
| | | SeqFile_output_tRNA_CCA_tail_match_genome | seqs that match to both tRNA 3' CCA end and reference genome in SAM format |

| | | | |
|--|-----------------------------------|---------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------|
| | | | (excluded in SeqFile_output_tRNA_match_genome file) |
| | | SeqFile_output_tRNA_CCA_tail_unmatch_genome | seqs that match to tRNA 3' CCA end but not reference genome in SAM format (excluded in SeqFile_output_tRNA_unmatch_genome file) |
| | SeqFile_result | SeqFile_output.txt | 6 column table file including annotation information for every unique sequence |
| | | SeqFile_summary.txt | 3 column table file including reads number of each major- (e.g. rRNA) and sub- (e.g. 5S rRNA) classes |
| | | SeqFile_length_distribution.txt | 3 column table file including reads number of each length distribution of each major class |
| | | SeqFile_sncRNA_distribution.pdf | figure of length distribution of miRNA, rsRNA, tsRNA, piRNA and other RNAs, if sequence matches existed |
| | | SeqFile_rRNA_distribution.pdf | figure of length distribution of different types of rRNAs, if sequence matches existed |
| | | SeqFile_rRNA_mapping.pdf | figure of rsRNAs mapping against different types of rRNAs, if sequence matches existed |
| | 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;
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 <int> 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.

| | |
|------------|---------|
| >t00000001 | 1234567 |
|------------|---------|

| |
|----------------------------------|
| TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGC |
|----------------------------------|

't00000001' is the unique ID of the sequence, represents the abundance ranking among all the sequences. In this case, the abundance of this sequence is the highest.

'1234567' represents the reads number of sequence 'TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGC'

4. Options:

-

5. Example usage:

combine_reads.pl reads.fa > combined_reads.fa

tRNA_tail_annotation.pl

1. Description:

This script annotates (perfect match) RNA sequences to tRNA 5' end, tRNA 3' end (without -CCA) and tRNA 3' end (with -CCA).

2. Input:

The reference tRNA database file in .fa format

A fasta file

3. output:

3.1 A 4-column table file describes sequences mapping to tRNA 5' end, including ID, sequence, length and annotation information. e.g.:

| | | | |
|-----------|----------------------------------|----|--------------------|
| t00000001 | TCCCTGGTGGTCTAGTGGTTAGGATTCGGCGC | 32 | tRNA_Glu_CTC_5_end |
|-----------|----------------------------------|----|--------------------|

3.2 A 4-column table file describes sequences mapping to tRNA 3' end (without -CCA), same format as in output 3.1

3.3 A 4-column table file describes sequences mapping to tRNA 3' end (with -CCA), same format as in output 3.1

3.4 A fasta file including sequences that not mapping to tRNA end

4. Options:

-

5. Example usage:

tRNA_tail_annotation.pl refer_file in_file

annotation.pl

1. Description:

Combine the annotation information generated from sports.pl

2. Input:

sports.pl output folder address <SPORTS_output_fold_address>

3. Output:

3.1 <seq_fold>_output.txt: A 6 column table file including annotation information for every unique sequence.

| ID | Sequence | Length | Reads | Match_Genome | Annotation |
|-----------|--------------------------------------|--------|---------|--------------|--------------------|
| t00000001 | TCCCTGGTGGTCTAGTGGTT AGGATTCGGCGC | 32 | 1234567 | Yes | tRNA-Glu-CTC_5_end |

-ID: t00000001 --Represents the unique ID of the sequence, represents the abundance ranking among all the sequences. In this case, the abundance of this sequence is the highest.

-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 or not.

-Annotation: tRNA-Glu-CTC_5_end --The annotation of the sequence. This sequence mapped against the 5' end of tRNA-Glu-CTC sequence.

3.2 <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.

3.3 <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>

overall_RNA_length_distribution.R

1. Description:

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

2. Input:

Files generated by annotation.pl

3. Output:

<seq_fold>_sncRNA_distribution.pdfGenerate figure of length distribution of different types of rRNAs, if sequence matches existed.

4. Options:

-

5. Example usage:

***Rscript --vanilla overall_RNA_length_distribution.R <SPAR_output_fold_address>
<dataset_name>***

rRNA_length_distribution.R

1. Description:

Generate figure of length distribution of 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_distribution.pdf

4. Options:

-

5. Example usage:

```
Rscript --vanilla r_RNA_length_distribution.R <SPAR_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 <SPAR_output_fold_address> <dataset_name>
```

Appendix

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_name

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

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

Main database source:

- mirbase 21 database [4] (Original source: <http://www.mirbase.org/index.shtml>)
- rRNA database (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)
- GtRNadb 2.0 database [5] (Original source: <http://gtrnadb.ucsc.edu/>)
- piRBase database [6] (Original source: <http://www.regulatoryrna.org/database/piRNA/>)
- piRNABank [7] (Original source: <http://pirnabank.ibab.ac.in/index.shtml>)
- ensembl ncRNA database [8] (Original source: <http://www.ensembl.org/index.html>)
- rfam 12.3 database [9] (Original source: <http://rfam.xfam.org/>)

1. Homo sapiens (Human)

- 1.1 annotation databases: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0773ed3d5f6b74f35bbd643e1af221c31&authkey=AcRx8walnGUIEhgl--8CDc)
 - genome with bowtie-index (UCSC hg38) (Original source: ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Homo_sapiens/UCSC/hg38/Homo_sapiens_UCSC_hg38.tar.gz)
 - mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
 - rRNA database with bowtie-index (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)
 - tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/genomes/eukaryota/Hsapi19/hg19-tRNAs.fa>)
 - piRNA database with bowtie-index (Original source: <http://www.regulatoryrna.org/database/piRNA/> && <http://pirnabank.ibab.ac.in/request.html>)
 - ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensembl.org/pub/release-89/fasta/mus_musculus/ncrna/)
 - rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
- 1.2 SPORTS1.0 related parameters if you download recommend reference database:
 - g /<your_defined_address>/Homo_sapiens/UCSC/hg38/Sequence/BowtieIndex/genome
 - m /<your_defined_address>/Homo_sapiens/miRBase_21/miRBase_21-has
 - r /<your_defined_address>/Homo_sapiens/rRNA_db/human_rRNA
 - t /<your_defined_address>/Homo_sapiens/GtRNadb/hg19-tRNAs
 - w /<your_defined_address>/Homo_sapiens/piRBase/piR_human
 - e /<your_defined_address>/Homo_sapiens/Ensembl/Homo_sapiens.GRCh38.ncrna
 - f /<your_defined_address>/Homo_sapiens/Rfam_12.3/Rfam-12.3-human

2. Gorilla gorilla gorilla (Gorilla)

- 2.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=03a9a8d26cca14b458007e9c6ee4541f7&authkey=Aag330X-ljvagrWePhYNF3k)
 - genome with bowtie-index (UCSC gorGor5) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/gorGor5/bigZips/gorGor5.fa.gz>)
 - mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
 - tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Acaro2/anoCar2-tRNAs.fa>)

-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

2.2 SPORTS1.0 related parameters if you download recommend 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)

3.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=03a74e9f6c2594f1e86a31acd8e554621&authkey=AYrgOm8rrAY7hrFYQ03gmTA)

-genome with bowtie-index (UCSC panPan1) (Original source:
<http://hgdownload.soe.ucsc.edu/goldenPath/panPan1/bigZips/panPan1.fa.gz>)
-mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

3.2 SPORTS1.0 related parameters if you download recommend 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)

4.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=09c13507ee7414365843de3450aa9ad3e&authkey=AdsLOHA5q2--SbiP2C6Qjpc)

-genome with bowtie-index (Ensembl CHIMP2.1.4) (Original source: ftp://igenome.G3nom3s4u@ussd-ftp.illumina.com/Pan_troglodytes/Ensembl/CHIMP2.1.4/Pan_troglodytes_Ensembl_CHIMP2.1.4.tar.gz)
-mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
-tRNA database with bowtie-index (Original source:
<http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Ptrog4/panTro4-tRNAs.fa>)
-ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensembl.org/pub/release-89/fasta/pan_troglodytes/ncrna/)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

4.2 SPORTS1.0 related parameters if you download recommend reference database:

-g /<your_defined_address>/Pan_troglodytes/Ensembl/CHIMP2.1.4/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)

- 5.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=037168296877942ecb9735f26afcb450a&authkey=AZkU5ib3A0KOiT4KxrhgTGQ)
- genome with bowtie-index (UCSC ponAbe2) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/ponAbe2/bigZips/chromFa.tar.gz>)
 - mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
 - tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Ppygm2/ponAbe2-tRNAs.fa>)
 - ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensembl.org/pub/release-89/fasta/pongo_abelii/ncrna/)
 - rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
- 5.2 SPORTS1.0 related parameters if you download recommend reference database:
- g /<your_defined_address>/Pongo_pygmaeus/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.aspx?docid=068ef6629d31b4fb28100f667050be1d1&authkey=AWEPi3HUmOVD PPPnkMhdvs)
- genome with bowtie-index (UCSC nomLeu3) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/nomLeu3/bigZips/nomLeu3.fa.gz>)
 - tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Nleuc3/nomLeu3-tRNAs.fa>)
 - rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
- 6.2 SPORTS1.0 related parameters if you download recommend reference database:
- g /<your_defined_address>/Nomascus_leucogenys/UCSC/nomLeu3/Sequence/BowtieIndex/genome
 - t /<your_defined_address>/Nomascus_leucogenys/GtRNAdb/nomLeu3-tRNAs
 - f /<your_defined_address>/Nomascus_leucogenys/Rfam_12.3/Rfam-12.3-gibbon

7. Macaca mulatta (Rhesus)

- 7.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=037168296877942ecb9735f26afcb450a&authkey=AZkU5ib3A0KOiT4KxrhgTGQ)

my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=07fededf7468444ba9b863b74316b8504&authkey=Aa6X06J4ExLvKtH8mJ-CESs)

-genome with bowtie-index (Ensembl Gm01) (Original source: ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Glycine_max/Ensembl/Gm01/Glycine_max/Ensembl_Gm01.tar.gz)

-mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)

-tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNADB2/genomes/eukaryota/Mmula3/rheMac3-tRNAs.fa>)

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

-rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

7.2 SPORTS1.0 related parameters if you download recommend reference database:

-g /<your_defined_address>/Macaca_mulatta/UCSC/rheMac8/Sequence/BowtieIndex/genome

-m /<your_defined_address>/Macaca_mulatta/miRBase_21/miRBase_21-mm1

-r /<your_defined_address>/Macaca_mulatta/rRNA_db/rhesus_rRNA

-t /<your_defined_address>/Macaca_mulatta/GtRNADB/rheMac3-tRNAs

-e /<your_defined_address>/Macaca_mulatta/Ensembl/Pan_troglodytes.CHIMP2.1.4.ncrna

-f /<your_defined_address>/Macaca_mulatta/Rfam_12.3/Rfam-12.3-rhesus

8. Papio anubis (Baboon)

8.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=03a22a2092c7b46fb93a8fc49cf234720&authkey=Ad_hzH3MUIMh0-9BLoH_Vmw)

-genome with bowtie-index (UCSC papAnu2) (Original source:

<http://hgdownload.soe.ucsc.edu/goldenPath/papAnu2/bigZips/papAnu2.fa.gz>)

-tRNA database with bowtie-index (Original source:

<http://gtrnadb.ucsc.edu/GtRNADB2/genomes/eukaryota/Panub2/papAnu2-tRNAs.fa>)

-rfam 12.3 database with bowtie-index (Original source:

ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

8.2 SPORTS1.0 related parameters if you download recommend 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)

9.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=077698888fa8d40408df8c979e91146e4&authkey=AeoDYI5a3IKyF-CWgupu6IA)

-genome with bowtie-index (UCSC calJac3) (Original source:

<http://hgdownload.soe.ucsc.edu/goldenPath/calJac3/bigZips/calJac3.fa.gz>)

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

-tRNA database with bowtie-index (Original source:

<http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Cjacc3/calJac3-tRNAs.fa>)

-rfam 12.3 database with bowtie-index (Original source:

ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

9.2 SPORTS1.0 related parameters if you download recommend 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)

10.1 annotation database: (We provide a download link for all databases listed below: [https://ncrnainfo-](https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0c761313792b64396b87a66a6e04101be&authkey=AZBsJTAS-hXdASOlmxNL4I)

[my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0c761313792b64396b87a66a6e04101be&authkey=AZBsJTAS-hXdASOlmxNL4I](https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0c761313792b64396b87a66a6e04101be&authkey=AZBsJTAS-hXdASOlmxNL4I))

-genome with bowtie-index (UCSC tarSyr2) (Original source:

<http://hgdownload.soe.ucsc.edu/goldenPath/tarSyr2/bigZips/tarSyr2.fa.gz>)

-tRNA database with bowtie-index (Original source:

<http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Tsyr2/tarSyr2-tRNAs.fa>)

-rfam 12.3 database with bowtie-index (Original source:

ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

10.2 SPORTS1.0 related parameters if you download recommend 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)

11.1 annotation database: (We provide a download link for all databases listed below: [https://ncrnainfo-](https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0b2cacd8453104b2abb60298863fc4c16&authkey=AZAYeCOsLKuc_ml-QMqBJoQ)

[my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0b2cacd8453104b2abb60298863fc4c16&authkey=AZAYeCOsLKuc_ml-QMqBJoQ](https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0b2cacd8453104b2abb60298863fc4c16&authkey=AZAYeCOsLKuc_ml-QMqBJoQ))

-genome with bowtie-index (UCSC rn6) (Original source: [ftp://igenome:G3nom3s4u@ussd-](ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Rattus_norvegicus/UCSC/rn6/Rattus_norvegicus_UCSC_rn6.tar.gz)

[ftp.illumina.com/Rattus_norvegicus/UCSC/rn6/Rattus_norvegicus_UCSC_rn6.tar.gz](ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Rattus_norvegicus/UCSC/rn6/Rattus_norvegicus_UCSC_rn6.tar.gz))

-mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)

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

-tRNA database with bowtie-index (Original source:

<http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Rnorv5/rn5-tRNAs.fa>)

-piRNA database with bowtie-index (Original source: <http://www.regulatoryrna.org/database/piRNA/> &&

<http://pirnabank.ibab.ac.in/request.html>)

-ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensembl.org/pub/release-89/fasta/rattus_norvegicus/ncrna/)

-rfam 12.3 database with bowtie-index (Original source:

ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

11.2 SPORTS1.0 related parameters if you download recommend 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/rRNA_db/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)

12.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0833653a140eb47f098267d7a23d3b63c&authkey=Ab8aoYC8paqFI2yRabIo7Ok)

- genome with bowtie-index (UCSC mm10) (Original source: ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Mus_musculus/UCSC/mm10/Mus_musculus_UCSC_mm10.tar.gz)
- mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
- rRNA database with bowtie-index (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)
- tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/genomes/eukaryota/Mmusc10/mm10-tRNAs.fa>)
- piRNA database with bowtie-index (Original source: <http://www.regulatoryrna.org/database/piRNA/> && <http://pirnabank.ibab.ac.in/request.html>)
- ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensembl.org/pub/release-89/fasta/mus_musculus/ncrna/)
- rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

12.2 SPORTS1.0 related parameters if you download recommend reference database:

- g /<your_defined_address>/Mus_musculus/UCSC/mm10/Sequence/BowtieIndex/genome
- m /<your_defined_address>/Mus_musculus/miRBase_21/miRBase_21-mmu
- r /<your_defined_address>/Mus_musculus/rRNA_db/mouse_rRNA
- t /<your_defined_address>/Mus_musculus/GtRNAdb/mm10-tRNAs
- w /<your_defined_address>/Mus_musculus/piRBase/piR_mouse
- e /<your_defined_address>/Mus_musculus/Ensembl/Mus_musculus.GRCm38.ncrna
- f /<your_defined_address>/Mus_musculus/Rfam_12.3/Rfam-12.3-mouse

13. Cricetus griseus (Hamster)

13.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0b0ac3830026f4007958774cbdb421632&authkey=AZnURBxU1PYzUO1yyrcoZ_M)

- genome with bowtie-index (UCSC criGri1) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/criGri1/bigZips/criGri1.fa.gz>)
- mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
- rRNA database with bowtie-index (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)

-tRNA database with bowtie-index (Original source:
<http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Cgris1/criGri1-tRNAs.fa>)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

13.2 SPORTS1.0 related parameters if you download recommend 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)

14.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0d27261e6ae9c4402bbc9465addb544de&authkey=Ad1xIk56DNm0StozUWDqCYw)

-genome with bowtie-index (UCSC cavPor3) (Original source:
<http://hgdownload.soe.ucsc.edu/goldenPath/cavPor3/bigZips/cavPor3.fa.gz>)
-rRNA database with bowtie-index (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)
-tRNA database with bowtie-index (Original source:
<http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Cporc3/cavPor3-tRNAs.fa>)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

14.2 SPORTS1.0 related parameters if you download recommend 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)

15.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0ceff76c620884395899bcd385bfaa098&authkey=ATiBTnSjWKqY0zPKQOmM6kU)

-genome with bowtie-index (UCSC hetGla2) (Original source:
<http://hgdownload.soe.ucsc.edu/goldenPath/hetGla2/bigZips/hetGla2.fa.gz>)
-rRNA database with bowtie-index (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)
-tRNA database with bowtie-index (Original source:
<http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Hglab2/hetGla2-tRNAs.fa>)
-rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

15.2 SPORTS1.0 related parameters if you download recommend 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)

- 16.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0419ea57bd00548cc94574d8ce9717fcd&authkey=Aa1pkb9R7850Ss3GFmB6GzM)
- genome with bowtie-index (UCSC speTri2) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/speTri2/bigZips/speTri2.fa.gz>)
 - tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNADB2/genomes/eukaryota/Strid2/speTri2-tRNAs.fa>)
 - rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
- 16.2 SPORTS1.0 related parameters if you download recommend 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)

- 17.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=068d8da8388b74c38943e50237a259a88&authkey=AemP73yDCDiObexIk-DcRVQ)
- genome with bowtie-index (UCSC ochPri3) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/ochPri3/bigZips/ochPri3.fa.gz>)
 - tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNADB2/genomes/eukaryota/Oprin3/ochPri3-tRNAs.fa>)
 - rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
- 17.2 SPORTS1.0 related parameters if you download recommend 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)

- 18.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=01b2d69333c97448196cc69b212e92fc9&authkey=ARbwyo0-WJX10nDdXwvNygC)

- genome with bowtie-index (UCSC oryCun2) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/oryCun2/bigZips/oryCun2.fa.gz>)
- mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
- rRNA database with bowtie-index (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)
- tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Ocuni2/oryCun2-tRNAs.fa>)
- rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

18.2 SPORTS1.0 related parameters if you download recommend 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)

19.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0e880ae29a16747bebf5b9afdb5956921&authkey=AYIP0UkTwtVuiul45XA7mYE)

- genome with bowtie-index (UCSC oviAri3) (Original source: <http://hgdownload.cse.ucsc.edu/goldenPath/oviAri3/bigZips/oviAri3.fa.gz>)
- mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
- tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Zmays5/zeaMay5-tRNAs.fa>)
- rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

19.2 SPORTS1.0 related parameters if you download recommend 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)

20.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0a58e56dc7cb743299631fec15b72e69d&authkey=AeosGslpVMdvtZa6qtKJBCE)

- genome with bowtie-index (UCSC bosTau8) (Original source: ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Bos_taurus/UCSC/bosTau8/Bos_taurus_UCSC_bosTau8.tar.gz)
- mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
- tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Btaur8/bosTau8-tRNAs.fa>)

- rRNA database with bowtie-index (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)
- ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensembl.org/pub/release-89/fasta/bos_taurus/ncrna/)
- rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

20.2 SPORTS1.0 related parameters if you download recommend 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)

21.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0e15d39ac05b24a9b899e7a9dfcf96773&authkey=AYaNWQ9KLlqq7f2qbWzchc)

- genome with bowtie-index (UCSC susScr3) (Original source: ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Sus_scrofa/UCSC/susScr3/Sus_scrofa_UCSC_susScr3.tar.gz)
- mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
- rRNA database with bowtie-index (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)
- tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Sscro3/susScr3-tRNAs.fa>)
- rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

21.2 SPORTS1.0 related parameters if you download recommend 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)

22.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=08396ad3619a247d695508aee771e3991&authkey=AVKuiimDuoOGVKfGvZcK_ik)

- genome with bowtie-index (UCSC turTru2) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/turTru2/bigZips/turTru2.fa.gz>)
- tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Ttrun2/turTru2-tRNAs.fa>)
- rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

22.2 SPORTS1.0 related parameters if you download recommend 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)

23.1 annotation database: (We provide a download link for all databases listed below: [https://ncrnainfo-](https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0d27ad173ffdb4dcc8a4954f9ba5426eb&authkey=AUdYvbA-q0IzVEEBIth8V8)

[my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0d27ad173ffdb4dcc8a4954f9ba5426eb&authkey=AUdYvbA-q0IzVEEBIth8V8](https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0d27ad173ffdb4dcc8a4954f9ba5426eb&authkey=AUdYvbA-q0IzVEEBIth8V8))

-genome with bowtie-index (UCSC balAcu1) (Original source:

<http://hgdownload.soe.ucsc.edu/goldenPath/balAcu1/bigZips/balAcu1.fa.gz>)

-tRNA database with bowtie-index (Original source:

<http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Bacut1/balAcu1-tRNAs.fa>)

-rfam 12.3 database with bowtie-index (Original source:

ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

23.2 SPORTS1.0 related parameters if you download recommend 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)

24.1 annotation database: (We provide a download link for all databases listed below: [https://ncrnainfo-](https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0633e2d7781ab4aefb59fc03f1347657b&authkey=AXrP4XnyiHQqkC5WOUhhS5w)

[my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0633e2d7781ab4aefb59fc03f1347657b&authkey=AXrP4XnyiHQqkC5WOUhhS5w](https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0633e2d7781ab4aefb59fc03f1347657b&authkey=AXrP4XnyiHQqkC5WOUhhS5w))

-genome with bowtie-index (UCSC eriEur2) (Original source:

<http://hgdownload.soe.ucsc.edu/goldenPath/eriEur2/bigZips/eriEur2.fa.gz>)

-tRNA database with bowtie-index (Original source:

<http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Eeuro2/eriEur2-tRNAs.fa>)

-rfam 12.3 database with bowtie-index (Original source:

ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

24.2 SPORTS1.0 related parameters if you download recommend 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)

25.1 annotation database: (We provide a download link for all databases listed below: <https://ncrnainfo->

my.sharepoint.com/personal/sports_ncrna_info/layouts/15/guestaccess.aspx?docid=0399046c56fb246c39630c84db61a23ad&authkey=AWE7pAlGt1TAAUyID4goE9A)

-genome with bowtie-index (UCSC sorAra2) (Original source:

<http://hgdownload.soe.ucsc.edu/goldenPath/sorAra2/bigZips/sorAra2.fa.gz>)

-tRNA database with bowtie-index (Original source:

<http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Saran2/sorAra2-tRNAs.fa>)

-rfam 12.3 database with bowtie-index (Original source:

ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

25.2 SPORTS1.0 related parameters if you download recommend 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 lupus familiaris (Dog)

26.1 annotation database: (We provide a download link for all databases listed below: [https://ncrnainfo-](https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/layouts/15/guestaccess.aspx?docid=06a45d60105a04796b5e96a9417d86f4c&authkey=AY37yxKX-C5u9DG71tztFEI)

[my.sharepoint.com/personal/sports_ncrna_info/layouts/15/guestaccess.aspx?docid=06a45d60105a04796b5e96a9417d86f4c&authkey=AY37yxKX-C5u9DG71tztFEI](https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/layouts/15/guestaccess.aspx?docid=06a45d60105a04796b5e96a9417d86f4c&authkey=AY37yxKX-C5u9DG71tztFEI))

-genome with bowtie-index (UCSC canFam3) (Original source: ftp://igenome:G3nom3s4u@usdd-ftp.illumina.com/Canis_familiaris/UCSC/canFam3/Canis_familiaris_UCSC_canFam3.tar.gz)

-mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)

-tRNA database with bowtie-index (Original source:

<http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Cfami3/canFam3-tRNAs.fa>)

-rfam 12.3 database with bowtie-index (Original source:

ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

26.2 SPORTS1.0 related parameters if you download recommend 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)

27.1 annotation database: (We provide a download link for all databases listed below: [https://ncrnainfo-](https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/layouts/15/guestaccess.aspx?docid=0ef4e067d42f241359e2e606b14e0d8f9&authkey=AUW2yr7SM356KpD5uhBNOeM)

[my.sharepoint.com/personal/sports_ncrna_info/layouts/15/guestaccess.aspx?docid=0ef4e067d42f241359e2e606b14e0d8f9&authkey=AUW2yr7SM356KpD5uhBNOeM](https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/layouts/15/guestaccess.aspx?docid=0ef4e067d42f241359e2e606b14e0d8f9&authkey=AUW2yr7SM356KpD5uhBNOeM))

-genome with bowtie-index (UCSC musFur1) (Original source:

<http://hgdownload.soe.ucsc.edu/goldenPath/musFur1/bigZips/musFur1.fa.gz>)

-tRNA database with bowtie-index (Original source:

<http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Mputo1/musFur1-tRNAs.fa>)

-rfam 12.3 database with bowtie-index (Original source:

ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

27.2 SPORTS1.0 related parameters if you download recommend 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/Rfam-12.3-ferret

28. Ailuropoda melanoleuca (Panda)

28.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0215799b172f94c909c5251061e317540&authkey=AdE82hkEi1MHI3OL1vY92b8)

- genome with bowtie-index (UCSC ailMel1) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/ailMel1/bigZips/ailMel1.fa.gz>)
- tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNADB2/genomes/eukaryota/Amela1/ailMel1-tRNAs.fa>)
- rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

28.2 SPORTS1.0 related parameters if you download recommend 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)

29.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0203fe1a0c8954879878ef8cabcf37cf&authkey=AZ32jdZl7FoFU_t8_NFb9o0)

- genome with bowtie-index (UCSC felCat8) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/felCat8/bigZips/felCat8.fa.gz>)
- rRNA database with bowtie-index (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)
- tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNADB2/genomes/eukaryota/Ocuni2/oryCun2-tRNAs.fa>)
- rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

29.2 SPORTS1.0 related parameters if you download recommend 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)

30.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0e7011a73d57545ea8be3c71335b3cf4c&authkey=AWHkBfbzVmwz_HjmQXo8IJU)

-genome with bowtie-index (UCSC equCab2) (Original source: ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Equus_caballus/UCSC/equCab2/Equus_caballus_UCSC_equCab2.tar.gz)

-mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)

-tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Ecaba2/equCab2-tRNAs.fa>)

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

-rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

30.2 SPORTS1.0 related parameters if you download recommend 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)

31.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0f836e7106664459bacda6f94dc15e22d&authkey=AVSh1b1dr84q53sLTqD9sRA)

-genome with bowtie-index (UCSC cerSim1) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/cerSim1/bigZips/cerSim1.fa.gz>)

-tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Csimu1/cerSim1-tRNAs.fa>)

-rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

31.2 SPORTS1.0 related parameters if you download recommend 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)

32.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=03dcc351bbc274cfc8692e5f2b1f5d0f3&authkey=AbjlxSozqu1c-2sRUrTGn7k)

-genome with bowtie-index (UCSC myoLuc2) (Original source:

<http://hgdownload.soe.ucsc.edu/goldenPath/myoLuc2/bigZips/myoLuc2.fa.gz>)

-tRNA database with bowtie-index (Original source:

<http://gtrnadb.ucsc.edu/GtRNADB2/genomes/eukaryota/Mluci2/myoLuc2-tRNAs.fa>)

-rfam 12.3 database with bowtie-index (Original source:

ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

32.2 SPORTS1.0 related parameters if you download recommend 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)

33.1 annotation database: (We provide a download link for all databases listed below: [https://ncrnainfo-](https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=06448172c574b4b9cbe0d906cf75bc68b&authkey=AX_fEuPmr18NZPEFbcg9nEQ)

[my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=06448172c574b4b9cbe0d906cf75bc68b&authkey=AX_fEuPmr18NZPEFbcg9nEQ](https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=06448172c574b4b9cbe0d906cf75bc68b&authkey=AX_fEuPmr18NZPEFbcg9nEQ))

-genome with bowtie-index (UCSC triMan1) (Original source:

<http://hgdownload.soe.ucsc.edu/goldenPath/triMan1/bigZips/triMan1.fa.gz>)

-tRNA database with bowtie-index (Original source:

<http://gtrnadb.ucsc.edu/GtRNADB2/genomes/eukaryota/Tmana1/triMan1-tRNAs.fa>)

-rfam 12.3 database with bowtie-index (Original source:

ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

33.2 SPORTS1.0 related parameters if you download recommend 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)

34.1 annotation database: (We provide a download link for all databases listed below: [https://ncrnainfo-](https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0e0146e32fe4745bba50bbede409efddc&authkey=AT8bNP2DhjKysDaGD4Qy-7s)

[my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0e0146e32fe4745bba50bbede409efddc&authkey=AT8bNP2DhjKysDaGD4Qy-7s](https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0e0146e32fe4745bba50bbede409efddc&authkey=AT8bNP2DhjKysDaGD4Qy-7s))

-genome with bowtie-index (UCSC loxAfr3) (Original source:

<http://hgdownload.soe.ucsc.edu/goldenPath/loxAfr3/bigZips/loxAfr3.fa.gz>)

-tRNA database with bowtie-index (Original source:

<http://gtrnadb.ucsc.edu/GtRNADB2/genomes/eukaryota/Lafri3/loxAfr3-tRNAs.fa>)

-rfam 12.3 database with bowtie-index (Original source:

ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

34.2 SPORTS1.0 related parameters if you download recommend 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)

- 35.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0c68adc6b2afc447a9dfe45a1a5eedd49&authkey=AUPTS51dr88E3AMvcZtljrk)
- genome with bowtie-index (UCSC dasNov3) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/dasNov3/bigZips/dasNov3.fa.gz>)
 - tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Dnove3/dasNov3-tRNAs.fa>)
 - rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
- 35.2 SPORTS1.0 related parameters if you download recommend reference database:
- g /<your_defined_address>/Dasypus_novemcinctus/UCSC/dasNov3/Sequence/BowtieIndex/genome
 - 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)

- 36.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=076db8740d2e34caabb25669fd6297e36&authkey=AWv-dFi1Mm7C0QH9K00WHH4)
- genome with bowtie-index (UCSC macEug2) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/macEug2/bigZips/macEug2.fa.gz>)
 - mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
 - tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Meuge2/macEug2-tRNAs.fa>)
 - rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
- 36.2 SPORTS1.0 related parameters if you download recommend reference database:
- g /<your_defined_address>/Notamacropus_eugenii/UCSC/macEug2/Sequence/BowtieIndex/genome
 - 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)

- 37.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0469dc3788cbb40bab7472ee70a230dc0&authkey=AXA1nDb4QpYeuIJFC-D6mL0)
- genome with bowtie-index (UCSC sarHar1) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/sarHar1/bigZips/sarHar1.fa.gz>)
 - mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)

-tRNA database with bowtie-index (Original source:
<http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Sharr1/sarHar1-tRNAs.fa>)
 -rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

37.2 SPORTS1.0 related parameters if you download recommend reference database:

-g /<your_defined_address>/Sarcophilus_harrisii/UCSC/sarHar1/Sequence/BowtieIndex/genome
 -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)

38.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=05e9cd2f3891a4761ade95d98aa3ebc78&authkey=Ae_jBKIdBC7HypVTN7S98Rw)

-genome with bowtie-index (UCSC monDom5) (Original source:
<http://hgdownload.soe.ucsc.edu/goldenPath/monDom5/bigZips/chromFa.tar.gz>)
 -mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
 -tRNA database with bowtie-index (Original source:
<http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Mdome5/monDom5-tRNAs.fa>)
 -ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensembl.org/pub/release-89/fasta/monodelphis_domestica/ncrna/)
 -rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

38.2 SPORTS1.0 related parameters if you download recommend reference database:

-g /<your_defined_address>/Monodelphis_domestica/UCSC/monDom5/Sequence/BowtieIndex/genome
 -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.BROADO5.ncrna
 -f /<your_defined_address>/Monodelphis_domestica/Rfam_12.3/Rfam-12.3-opossum

39. Ornithorhynchus anatinus (Platypus)

39.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=07f0f4ed088844a86afa5db763407699c&authkey=AUFx9yWXHtg1CQc-wfpJ81M)

-genome with bowtie-index (UCSC ornAna2) (Original source:
<http://hgdownload.soe.ucsc.edu/goldenPath/ornAna2/bigZips/ornAna2.fa.gz>)
 -mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
 -tRNA database with bowtie-index (Original source:
<http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Oanat1/ornAna1-tRNAs.fa>)
 -piRNA database with bowtie-index (Original source: <http://pirnabank.ibab.ac.in/request.html>)
 -ensembl ncRNA database with bowtie-index (Original source: <ftp://ftp.ensembl.org/pub/release->

[89/fasta/ornithorhynchus_anatinus/ncrna/](#)

-rfam 12.3 database with bowtie-index (Original source:

[ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/](#))

39.2 SPORTS1.0 related parameters if you download recommend reference database:

-g /<your_defined_address>/Ornithorhynchus_anatinus/UCSC/ornAna2/Sequence/BowtieIndex/genome

-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_anatinus.OANA5.ncrna

-f /<your_defined_address>/Ornithorhynchus_anatinus/Rfam_12.3/Rfam-12.3-platypus

40. Taeniopygia guttata (Zebra finch)

40.1 annotation database: (We provide a download link for all databases listed below: [https://ncrnainfo-](https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0defbf712045f4e7f85b373b0eba4cd1b&authkey=AbieXkq6akbsD8tY1oGctDI)

[my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0defbf712045f4e7f85b373b0eba4cd1b&authkey=AbieXkq6akbsD8tY1oGctDI](https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0defbf712045f4e7f85b373b0eba4cd1b&authkey=AbieXkq6akbsD8tY1oGctDI))

-genome with bowtie-index (UCSC taeGut2) (Original source:

<http://hgdownload.soe.ucsc.edu/goldenPath/taeGut2/bigZips/taeGut2.fa.gz>)

-mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)

-tRNA database with bowtie-index (Original source:

<http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Tgutt2/taeGut2-tRNAs.fa>)

-rfam 12.3 database with bowtie-index (Original source:

[ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/](#))

40.2 SPORTS1.0 related parameters if you download recommend reference database:

-g /<your_defined_address>/Taeniopygia_guttata/UCSC/taeGut2/Sequence/BowtieIndex/genome

-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)

41.1 annotation database: (We provide a download link for all databases listed below: [https://ncrnainfo-](https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0e0046ab3b1a9458a9a183b45507ea0c3&authkey=AWiCroVnVDQcPENZDX_76VM)

[my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0e0046ab3b1a9458a9a183b45507ea0c3&authkey=AWiCroVnVDQcPENZDX_76VM](https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0e0046ab3b1a9458a9a183b45507ea0c3&authkey=AWiCroVnVDQcPENZDX_76VM))

-genome with bowtie-index (UCSC melUnd1) (Original source:

<http://hgdownload.soe.ucsc.edu/goldenPath/melUnd1/bigZips/melUnd1.fa.gz>)

-tRNA database with bowtie-index (Original source:

<http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Mundu1/melUnd1-tRNAs.fa>)

-rfam 12.3 database with bowtie-index (Original source:

[ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/](#))

41.2 SPORTS1.0 related parameters if you download recommend reference database:

-g /<your_defined_address>/Melopsittacus_undulatus/UCSC/melUnd1/Sequence/BowtieIndex/genome

-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)

- 42.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0abafb326c4074fe9971d60a26497126c&authkey=AcRw_9ltjRXbdNAfmLRI_gg)
- genome with bowtie-index (UCSC galGal5) (Original source: ftp://igenome2:u7NMwVkm@ftp.illumina.com/Gallus_gallus/UCSC/galGal5/Gallus_gallus_UCSC_galGal5.tar.gz)
 - mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
 - tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Ggall4/galGal4-tRNAs.fa>)
 - rRNA database with bowtie-index (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)
 - piRNA database with bowtie-index (Original source: <http://www.regulatoryrna.org/database/piRNA/>)
 - ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensembl.org/pub/release-89/fasta/gallus_gallus/ncrna/)
 - rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
- 42.2 SPORTS1.0 related parameters if you download recommend 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.ncrna
 - f /<your_defined_address>/Gallus_gallus/Rfam_12.3/Rfam-12.3-chicken

43. Meleagris gallopavo (Turkey)

- 43.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0c88e1661f08e4b6d945d87e8120bdf07&authkey=AWICjj414nXNuNbrNM7mbE4)
- genome with bowtie-index (UCSC melGal1) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/melGal1/bigZips/melGal1.fa.gz>)
 - tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Mgall1/melGal1-tRNAs.fa>)
 - rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
- 43.2 SPORTS1.0 related parameters if you download recommend 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)

- 44.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0fbd62d91eb4442a88525f89684a74242&authkey=AY3fgBdvPRzWpqqD4yd_Sqw)
- genome with bowtie-index (UCSC chrPic1) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/chrPic1/bigZips/chrPic1.fa.gz>)
 - tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Ocuni2/oryCun2-tRNAs.fa>)
 - rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
- 44.2 SPORTS1.0 related parameters if you download recommend 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)

- 45.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=06986df31c45c4a00a6a2b47ce4ee7af2&authkey=AaE-i58-1fJeqcDHZUpLLo)
- genome with bowtie-index (UCSC anoCar2) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/anoCar2/bigZips/anoCar2.fa.gz>)
 - mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
 - tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Acaro2/anoCar2-tRNAs.fa>)
 - ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensembl.org/pub/release-89/fasta/anolis_carolinensis/ncrna/)
 - rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
- 45.2 SPORTS1.0 related parameters if you download recommend 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.AnoCar2.0.ncrna
 - f /<your_defined_address>/Anolis_carolinensis/Rfam_12.3/Rfam-12.3-lizard

46. *Xenopus laevis* (Frog)

- 46.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0d9b3d45b3bf3483c826c36d2b340f0fd&authkey=AdGZ969RHd1lpwBpm7lsGEQ)

- genome with bowtie-index (UCSC xenTro7) (Original source: <ftp://hgdownload.soe.ucsc.edu/goldenPath/xenTro7/bigZips/xenTro7.fa.gz>)
- mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
- tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Xtrop3/xenTro3-tRNAs.fa>)
- rRNA database with bowtie-index (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)
- piRNA database with bowtie-index (Original source: <http://www.regulatoryrna.org/database/piRNA/>)
- ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensembl.org/pub/release-89/fasta/xenopus_tropicalis/ncrna/)
- rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

46.2 SPORTS1.0 related parameters if you download recommend 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)

47.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0be8104aeb59d4ff89909d0c62d0a2f4e&authkey=AasK4DZcbB12a8wB8CNz6Ak)

- genome with bowtie-index (UCSC latCha1) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/latCha1/bigZips/latCha1.fa.gz>)
- rRNA database with bowtie-index (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)
- tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Lchal1/latCha1-tRNAs.fa>)
- rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

47.2 SPORTS1.0 related parameters if you download recommend 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)

48.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=06252eaadd5894a3795afe052716fd17&authkey=AWZ9FVt-iphIQFRDzuKoJtA)

- genome with bowtie-index (UCSC tetNig2) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/tetNig2/bigZips/chromFa.tar.gz>)
- mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
- tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Tnigr2/tetNig2-tRNAs.fa>)
- rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

48.2 SPORTS1.0 related parameters if you download recommend 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)

49.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=026501a5c4aa54930a00289acf9691f5f&authkey=AWUaDYW0_VZx-1dy5wnCfdQ)

- genome with bowtie-index (UCSC fr3) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/fr3/bigZips/fr3.fa.gz>)
- tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Trubr3/fr3-tRNAs.fa>)
- rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

49.2 SPORTS1.0 related parameters if you download recommend 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)

50.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0268db779d3654712b39d5450bac55894&authkey=AQwh0wJeAcvF78JRu4RHddM)

- genome with bowtie-index (UCSC gasAcu1) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/gasAcu1/bigZips/chromFa.tar.gz>)
- tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Gacul1/gasAcu1-tRNAs.fa>)
- ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensembl.org/pub/release-89/fasta/gasterosteus_aculeatus/ncrna/)
- rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

50.2 SPORTS1.0 related parameters if you download recommend 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.BROADS1.ncrna
- f /<your_defined_address>/Gasterosteus_aculeatus/Rfam_12.3/Rfam-12.3-stickleback

51. *Oryzias latipes* (Medaka)

51.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0f5089e2cc47245f28dca1a3f8f75343c&authkey=AV8N2wRviWth_LjhJqpB0zk)

- genome with bowtie-index (UCSC oryLat2)
(<http://hgdownload.soe.ucsc.edu/goldenPath/oryLat2/bigZips/oryLat2.fa.gz>)
- mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
- tRNA database with bowtie-index (Original source:
<http://gtrnadb.ucsc.edu/GtRNADB2/genomes/eukaryota/Olati2/oryLat2-tRNAs.fa>)
- rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

51.2 SPORTS1.0 related parameters if you download recommend 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)

52.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0cf791d1d99de4f4c8ed7f8de6d5694f8&authkey=AZZgbe3d1aKb7GDuCDlv81w)

- genome with bowtie-index (UCSC oreNil2) (Original source:
<http://hgdownload.soe.ucsc.edu/goldenPath/oreNil2/bigZips/oreNil2.fa.gz>)
- tRNA database with bowtie-index (Original source:
<http://gtrnadb.ucsc.edu/GtRNADB2/genomes/eukaryota/Onilo2/oreNil2-tRNAs.fa>)
- rfam 12.3 database with bowtie-index (Original source:
ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

52.2 SPORTS1.0 related parameters if you download recommend reference database:

- g /<your_defined_address>/Oreochromis_niloticus/UCSC/oreNil2/Sequence/BowtieIndex/genome
- 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)

53.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=08f5a65a279f34d518cc4017cb04fe469&authkey=ASMQLlwmWReD_bVW922N0lo)

-genome with bowtie-index (UCSC gadMor1) (Original source:

<http://hgdownload.soe.ucsc.edu/goldenPath/gadMor1/bigZips/gadMor1.fa.gz>)

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

-tRNA database with bowtie-index (Original source:

<http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Gmorh1/gadMor1-tRNAs.fa>)

-rfam 12.3 database with bowtie-index (Original source:

ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

53.2 SPORTS1.0 related parameters if you download recommend 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)

54.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=07d3448d6cd29485498e70f8f067a619d&authkey=Aa1-VjshX-GKLZI7limHFlo)

-genome with bowtie-index (UCSC danRer10) (Original source: ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Danio_rerio/UCSC/danRer10/Danio_rerio_UCSC_danRer10.tar.gz)

-mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)

-tRNA database with bowtie-index (Original source:

http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Dreri_v8/danRer6-tRNAs.fa)

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

-piRNA database with bowtie-index (Original source: <http://www.regulatoryrna.org/database/piRNA/>)

-ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensembl.org/pub/release-89/fasta/danio_rerio/ncrna/)

-rfam 12.3 database with bowtie-index (Original source:

ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

54.2 SPORTS1.0 related parameters if you download recommend 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)

- 55.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=053976e5c17b9435982d2223b9389eba&authkey=ASL1VUPU4OI2PskRXpj94t4)
- genome with bowtie-index (UCSC calMil1) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/calMil1/bigZips/calMil1.fa.gz>)
 - tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNADB2/genomes/eukaryota/Cmili1/calMil1-tRNAs.fa>)
 - rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
- 55.2 SPORTS1.0 related parameters if you download recommend reference database:
- g /<your_defined_address>/Callorhinchus_milii/UCSC/calMil1/Sequence/BowtieIndex/genome
 - 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)

- 56.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=013a1f7a5585b462b801f1cfe3faf2cdd&authkey=AVN94xcHd1_Aa2ofYovsw8Q)
- genome with bowtie-index (UCSC petMar2) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/petMar2/bigZips/petMar2.fa.gz>)
 - rRNA database with bowtie-index (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)
 - tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNADB2/genomes/eukaryota/Pmari2/petMar2-tRNAs.fa>)
 - rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
- 56.2 SPORTS1.0 related parameters if you download recommend reference database:
- g /<your_defined_address>/Petromyzon_marinus/UCSC/petMar2/Sequence/BowtieIndex/genome
 - 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)

- 57.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0840567689dbe4ff49852c8744056f172&authkey=AWhmaQmPgN5fuB1RXIKc69U)
- genome with bowtie-index (UCSC strPur2) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/strPur2/bigZips/strPur2.fa.gz>)
 - mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)

- rRNA database with bowtie-index (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)
- tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNADB2/genomes/eukaryota/Spurp/Spurp-tRNAs.fa>)
- ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensemblgenomes.org/pub/metazoa/release-36/fasta/strongylocentrotus_purpuratus/ncrna/)
- rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

57.2 SPORTS1.0 related parameters if you download recommend reference database:

- g /<your_defined_address>/Strongylocentrotus_purpuratus/UCSC/strPur2/Sequence/BowtieIndex/genome
- 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_purpuratus.GCA_000002235.2.ncrna
- f /<your_defined_address>/Strongylocentrotus_purpuratus/Rfam_12.3/Rfam-12.3-urchin

58. Drosophila melanogaster (Drosophila)

58.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=06d15ec2032e141648ce4eedd413b0e0c&authkey=ARejQLC8ofAhQq9lwwB0Pw)

- genome with bowtie-index (UCSC dm6) (Original source: ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Drosophila_melanogaster/UCSC/dm6/Drosophila_melanogaster_UCSC_dm6.tar.gz)
- mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
- tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/genomes/eukaryota/Dmela6/dm6-tRNAs.fa>)
- rRNA database with bowtie-index (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)
- piRNA database with bowtie-index (Original source: <http://www.regulatoryrna.org/database/piRNA/>)
- ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensemblgenomes.org/pub/metazoa/release-36/fasta/drosophila_melanogaster/ncrna/)
- rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

58.2 SPORTS1.0 related parameters if you download recommend reference database:

- g /<your_defined_address>/Drosophila_melanogaster/UCSC/dm6/Sequence/BowtieIndex/genome
- 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.BDGP6.ncrna
- f /<your_defined_address>/Drosophila_melanogaster/Rfam_12.3/Rfam-12.3-drosophila

59. Anopheles gambiae (Mosquito)

59.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=003bfc542d06b42edb24a94969bb12b36&authkey=AdgdWQ5emWRWTYvXcgPT0Fo)

- genome with bowtie-index (UCSC anoGam1) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/anoGam1/bigZips/chromFa.zip>)
- mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
- tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Agamb/Agamb-tRNAs.fa>)
- ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensemblgenomes.org/pub/metazoa/release-36/fasta/anopheles_gambiae/ncrna/)
- rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

59.2 SPORTS1.0 related parameters if you download recommend reference database:

- g /<your_defined_address>/Anopheles_gambiae/UCSC/anoGam1/Sequence/BowtieIndex/genome
- 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)

60.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0877c09c8493b47e9b9fb6c2c0bdc6015&authkey=AQJrbZlyZz9MDnPB9uYxMYE)

- genome with bowtie-index (UCSC priPac1) (Original source: <http://hgdownload.soe.ucsc.edu/goldenPath/priPac1/bigZips/chromFa.tar.gz>)
- mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
- tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Ppaci1/priPac1-tRNAs.fa>)
- rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

60.2 SPORTS1.0 related parameters if you download recommend reference database:

- g /<your_defined_address>/Pristionchus_pacificus/UCSC/priPac1/Sequence/BowtieIndex/genome
- 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):

61.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0cffdc7d5a3844567bc5303adca47fb81&authkey=AdA1jCVLRJkz2k8oSVU-pCI)

- genome with bowtie-index (UCSC ce10) (Original source: ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Caenorhabditis_elegans/UCSC/ce10/Caenorhabditis_elegans_UCSC_ce10.tar.gz)
- mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
- tRNA database with bowtie-index (Original source: http://gtrnadb.ucsc.edu/genomes/eukaryota/Celeg_WS220/ce10-tRNAs.fa)
- rRNA database with bowtie-index (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)
- piRNA database with bowtie-index (Original source: <http://www.regulatoryrna.org/database/piRNA/>)
- ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensemblgenomes.org/pub/metazoa/release-36/fasta/caenorhabditis_elegans/ncrna/)
- rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

61.2 *Caenorhabditis elegans* (Nematode):

- g /<your_defined_address>/Caenorhabditis_elegans/UCSC/ce10/Sequence/BowtieIndex/genome
- 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.WBcel235.ncrna
- f /<your_defined_address>/Caenorhabditis_elegans/Rfam_12.3/Rfam-12.3-nematode

62. *Saccharomyces cerevisiae* (Yeast)

62.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0a974d08ffcb842dea8d18462dcfaf2f4&authkey=AQ6wsr9hNwVfCfqvuScKStE)

- genome with bowtie-index UCSC sacCer3) (Original source: ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Saccharomyces_cerevisiae/UCSC/sacCer3/Saccharomyces_cerevisiae_UCSC_sacCer3.tar.gz)
- tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Scere3/sacCer3-tRNAs.fa>)
- rRNA database with bowtie-index (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)
- ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensemblgenomes.org/pub/fungi/release-36/fasta/saccharomyces_cerevisiae/ncrna/)
- rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

62.2 SPORTS1.0 related parameters if you download recommend reference database:

- g /<your_defined_address>/Saccharomyces_cerevisiae/UCSC/sacCer3/Sequence/BowtieIndex/genome
- 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.R64-1-1.ncrna

-f /<your_defined_address>/Saccharomyces_cerevisiae/Rfam_12.3/Rfam-12.3-yeast

63. Zea mays (Corn)

- 63.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0abdce07adf9449e89bdc&b89d4d4609a4&authkey=AViNEp3y6Y4hNBYSuW_sYg)
- genome with bowtie-index (Ensembl AGPv4) (Original source: ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Zea_mays/Ensembl/AGPv4/Zea_mays_Ensembl_AGPv4.tar.gz)
 - mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
 - rRNA database with bowtie-index (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)
 - tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Zmays5/zeaMay5-tRNAs.fa>)
 - ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensemblgenomes.org/pub/plants/release-36/fasta/zea_mays/ncrna/)
 - rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
- 63.2 SPORTS1.0 related parameters if you download recommend 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)

- 64.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0335fb9b05a024e61819c04db7ffd2a51&authkey=AdMT31NWtny7F1NzJNn3zZI)
- genome with bowtie-index (Ensembl Sbi1) (Original source: ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Sorghum_bicolor/Ensembl/Sbi1/Sorghum_bicolor_Ensembl_Sbi1.tar.gz)
 - mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
 - tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNAdb2/genomes/eukaryota/Sbico/Sbico-tRNAs.fa>)
 - rRNA database with bowtie-index (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)
 - ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensemblgenomes.org/pub/plants/release-36/fasta/sorghum_bicolor/ncrna/)
 - rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)
- 64.2 SPORTS1.0 related parameters if you download recommend 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_v2.ncrna
- f /<your_defined_address>/Sorghum_bicolor/Rfam_12.3/Rfam-12.3-sorghum

65. Oryza sativa (Rice)

65.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0510818bde4a342868928f982420dd07c&authkey=ASfslUL0BX2HYew7xrw2x1A)

- genome with bowtie-index (Ensembl IRGSP-1.0) (Original source: ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Oryza_sativa_japonica/Ensembl/IRGSP-1.0/Oryza_sativa_japonica_Ensembl_IRGSP-1.0.tar.gz)
- mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
- tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Osati/Osati-tRNAs.fa>)
- rRNA database with bowtie-index (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)
- ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensemblgenomes.org/pub/plants/release-36/fasta/oryza_sativa/ncrna/)
- rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

65.2 SPORTS1.0 related parameters if you download recommend 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/GtRNadb/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)

66.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=08ec312d8fc7d4211952170468dfbb202&authkey=AeVag9p4ifZJG58C5UbXstE)

- genome with bowtie-index (Ensembl TAIR10) (Original source: ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Arabidopsis_thaliana/Ensembl/TAIR10/Arabidopsis_thaliana_Ensembl_TAIR10.tar.gz)
- mirbase 21 with bowtie-index (Original source: <http://www.mirbase.org/ftp.shtml>)
- tRNA database with bowtie-index (Original source: <http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Athal10/araTha1-tRNAs.fa>)
- rRNA database with bowtie-index (Original source: <https://www.ncbi.nlm.nih.gov/nuccore>)
- ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensemblgenomes.org/pub/plants/release-36/fasta/arabidopsis_thaliana/ncrna/)
- rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta_files/)

66.2 SPORTS1.0 related parameters if you download recommend reference database:

```
-g /<your_defined_address>/Arabidopsis_thaliana/Ensembl/TAIR10/Sequence/BowtieIndex/genome  
-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/GtRNadb/araTha1-tRNAs  
-e /<your_defined_address>/Arabidopsis_thaliana/Ensembl/Arabidopsis_thaliana.TAIR10.ncrna  
-f /<your_defined_address>/Arabidopsis_thaliana/Rfam_12.3/Rfam-12.3-arabidopsis
```

67. Glycine max (Soybean)

67.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=079974655bb2e4f62b669c3d1701fffeb&authkey=AWVriz_LNaTMDsBjbMXDS60)

```
-genome with bowtie-index (Ensembl Gm01) (Original source: ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Glycine\_max/Ensembl/Gm01/Glycine\_max\_Ensembl\_Gm01.tar.gz)  
-mirbase 21 with bowtie-index (Original source: http://www.mirbase.org/ftp.shtml)  
-tRNA database with bowtie-index (Original source: http://gtrnadb.ucsc.edu/GtRNadb2/genomes/eukaryota/Gmax2/glyMax2-tRNAs.fa)  
-rRNA database with bowtie-index (Original source: https://www.ncbi.nlm.nih.gov/nuccore)  
-rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta\_files/)
```

67.2 SPORTS1.0 related parameters if you download recommend 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/GtRNadb/glyMax2-tRNAs  
-f /<your_defined_address>/Glycine_max/Rfam_12.3/Rfam-12.3-soybean
```

68. Escherichia coli (E.coli)

68.1 annotation database: (We provide a download link for all databases listed below: https://ncrnainfo-my.sharepoint.com/personal/sports_ncrna_info/_layouts/15/guestaccess.aspx?docid=0645cc2a0024d41fdb5be31a17bd5374&authkey=AaR4ui2QEXqh2-SpOlxaUik)

```
-genome with bowtie-index (Ensembl EB1) (Original source: ftp://igenome:G3nom3s4u@ussd-ftp.illumina.com/Escherichia\_coli\_K\_12\_DH10B/Ensembl/EB1/Escherichia\_coli\_K\_12\_DH10B\_Ensembl\_EB1.tar.gz)  
-tRNA database with bowtie-index (Original source: http://gtrnadb.ucsc.edu/GtRNadb2/genomes/bacteria/Esch\_coli/eschColi-tRNAs.fa)  
-rRNA database with bowtie-index (Original source: https://www.ncbi.nlm.nih.gov/nuccore)  
-ensembl ncRNA database with bowtie-index (Original source: ftp://ftp.ensemblgenomes.org/pub/bacteria/release-36/fasta/bacteria\_91\_collection/escherichia\_coli/ncrna/)  
-rfam 12.3 database with bowtie-index (Original source: ftp://ftp.ebi.ac.uk/pub/databases/Rfam/12.3/fasta\_files/)
```

68.2 SPORTS1.0 related parameters if you download recommend 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/GtRNAdb/eschColi-tRNAs  
-e /<your_defined_address>/Escherichia_coli/Ensembl/Escherichia_coli.HUSEC2011CHR1.ncrna  
-f /<your_defined_address>/Escherichia_coli/Rfam_12.3/Rfam-12.3-e_coli
```

References

1. Langmead B, Trapnell C, Pop M, Salzberg SL. Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. *Genome Biol.* 2009;10(3):R25. doi: 10.1186/gb-2009-10-3-r25. PubMed PMID: 19261174; PubMed Central PMCID: PMC2690996.
2. Martin M. Cutadapt removes adapter sequences from high-throughput sequencing reads. *EMBnetjournal.* 2011;17(1):3. doi: <http://dx.doi.org/10.14806/ej.17.1.200>.
3. Friedlander MR, Chen W, Adamidi C, Maaskola J, Einspanier R, Knespel S, et al. Discovering microRNAs from deep sequencing data using miRDeep. *Nat Biotechnol.* 2008;26(4):407-15. doi: 10.1038/nbt1394. PubMed PMID: 18392026.
4. Kozomara A, Griffiths-Jones S. miRBase: annotating high confidence microRNAs using deep sequencing data. *Nucleic acids research.* 2014;42(Database issue):D68-73. doi: 10.1093/nar/gkt1181. PubMed PMID: 24275495; PubMed Central PMCID: PMC3965103.
5. Chan PP, Lowe TM. GtRNAdb 2.0: an expanded database of transfer RNA genes identified in complete and draft genomes. *Nucleic acids research.* 2016;44(D1):D184-9. doi: 10.1093/nar/gkv1309. PubMed PMID: 26673694; PubMed Central PMCID: PMC4702915.
6. Zhang P, Si X, Skogerbo G, Wang J, Cui D, Li Y, et al. piRBase: a web resource assisting piRNA functional study. *Database (Oxford).* 2014;2014:bau110. doi: 10.1093/database/bau110. PubMed PMID: 25425034; PubMed Central PMCID: PMC4243270.
7. Sai Lakshmi S, Agrawal S. piRNABank: a web resource on classified and clustered Piwi-interacting RNAs. *Nucleic acids research.* 2008;36(Database issue):D173-7. doi: 10.1093/nar/gkm696. PubMed PMID: 17881367; PubMed Central PMCID: PMC2238943.
8. Yates A, Akanni W, Amodio MR, Barrell D, Billis K, Carvalho-Silva D, et al. Ensembl 2016. *Nucleic acids research.* 2016;44(D1):D710-6. doi: 10.1093/nar/gkv1157. PubMed PMID: 26687719; PubMed Central PMCID: PMC4702834.
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. PubMed PMID: 25392425; PubMed Central PMCID: PMC4383904.

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Contact information

Contact author: Junchao Shi

E-mail: sports.rna@gmail.com; junchao.shi@yahoo.com