



## **RNA Structure Framework (v1.0.0a)**

### **User Manual**

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*Date released: 27th February 2016*

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**NGI – Next Generation Intelligence**

## 1. Introduction

The recent advent of high-throughput methods for probing RNA secondary structures has enabled for the transcriptome-wide analysis of the *RNA structurome*. Despite the establishment of several methods for querying RNA secondary structures on a genome-wide scale (CIRS-seq, SHAPE-seq, Structure-seq, DMS-seq, PARS), no tool has been developed to date to enable the rapid analysis and interpretation of these data.

The **RNA Structure Framework** is a modular toolkit developed to deal with RNA structure probing high-throughput data, from reads mapping to structure inference.

Its main features are:

- Automatic reference transcriptome creation
- Automatic reads preprocessing (adapter clipping and trimming) and mapping
- Scoring and data normalization
- Accurate RNA folding prediction by incorporating structural probing data

## 2. Requirements

- Linux/Mac system
- Bowtie v1.0.0 (<http://bowtie-bio.sourceforge.net/index.shtml>)
- SAMTools v1.2 or greater (<http://www.htslib.org/>)
- BEDTools v2.0 or greater (<https://github.com/arq5x/bedtools2/>)
- FASTX Toolkit ([http://hannonlab.cshl.edu/fastx\\_toolkit/](http://hannonlab.cshl.edu/fastx_toolkit/))
- ViennaRNA Package v2.2.0 or greater (<http://www.tbi.univie.ac.at/RNA/>)
- RNAstructure v5.6 or greater (<http://rna.urmc.rochester.edu/RNAstructure.html>)
- Perl v5.12 (or greater), with ithreads support
- Perl non-CORE modules (<http://search.cpan.org/>):
  - DBI
  - LWP::UserAgent
  - RNA (part of the ViennaRNA package)
  - XML::Simple

### 3. List of toolkit components

CORE modules	
<b>rsf-index</b>	Automatically queries UCSC genome database and builds the transcriptome Bowtie reference index for the RT Count module
<b>rt-count</b>	Performs reads pre-processing and mapping (where needed), and calculates per-base RT-stops and coverage
<b>rsf-norm</b>	Performs whole-transcriptome normalization of structure probing data
<b>rsf-fold</b>	Produces secondary structures for the analyzed transcripts using structure probing data to guide folding

Utilities	
<b>rsf-combine</b>	Allows combining SPD files from multiple experiments into a single structure profile
<b>spd2shape</b>	Converts SPD files into SHAPE Constraint files (required by RSF Fold)

## 4. Usage

### 4.1. *rsf-index*

The RSF Index tool is designed to automatically generate a Bowtie reference index, that will be used by the RT Count module for reads mapping.

This tool requires an internet connection, since it relies on querying the UCSC Genome database to obtain transcripts annotation and reference genome's sequence.

To list the required parameters, simply type:

```
$ rsf-index -h (or --help)
```

Parameter	Description
<b>-o or --output-dir</b>	Bowtie index output directory (Default: <assembly>_<annotation>, e.g. "mm9_refFlat")
<b>-ow or --overwrite</b>	Overwrites the output directory if already exists
<b>-g or --genome-assembly</b>	Genome assembly for the species of interest (Default: mm9). For a complete list of UCSC available assemblies, please refer to Appendix A, or to the UCSC website ( <a href="https://genome.ucsc.edu/FAQ/FAQreleases.html">https://genome.ucsc.edu/FAQ/FAQreleases.html</a> )
<b>-a or --annotation</b>	Name of the UCSC table containing the genes annotation (Default: refFlat). For a complete list of tables available for the chosen assembly, please refer to the UCSC website ( <a href="https://genome.ucsc.edu/cgi-bin/hgTables">https://genome.ucsc.edu/cgi-bin/hgTables</a> )
<b>-n or --gene-name</b>	When possible, gene names will be used instead of gene IDs/accessions
<b>-t or --timeout</b>	Connection's timeout in seconds (Default: 180)
<b>-r or --reference</b>	Path to a FASTA file containing chromosome (or scaffold) sequences for the chosen genome assembly.  <b>Note:</b> if no file is specified, RSF Index will try to obtain sequences from the UCSC DAS server. This process may take up to hours, depending on your connection's speed.
<b>-b or --bowtie-build</b>	Path to bowtie-build executable (Default: assumes bowtie-build is in PATH)
<b>-e or --bedtools</b>	Path to BEDTools executable (Default: assumes BEDTools is in PATH)

**Note:** For RNA structure probing experiments conducted over synthetic RNAs (or custom pools of RNAs), a reference can be generated by invoking directly the *bowtie-build* command, however it is necessary to first sort lexicographically the FASTA file by sequence IDs:

```
$ awk 'BEGIN{RS=">"} NR>1 {gsub("\n", "\t"); print ">"$0}' reference_unsorted.fa | \
LC_ALL=C sort -T "" -t ' ' -k2,2 | awk '{sub("\t", "\n"); gsub("\t", ""); print $0}' > reference_sorted.fa
```

```
$ bowtie-build reference_sorted.fa reference_sorted
```

```
$ ls -l
```

```
-rwxrwxrwx 1 danny epigenetics 96041105 5 mar 10.50 reference_sorted.1.ebwt  
-rwxrwxrwx 1 danny epigenetics 37313744 5 mar 10.50 reference_sorted.2.ebwt  
-rwxrwxrwx 1 danny epigenetics 1844468 5 mar 10.28 reference_sorted.3.ebwt  
-rwxrwxrwx 1 danny epigenetics 74627475 5 mar 10.28 reference_sorted.4.ebwt  
-rwxrwxrwx 1 danny epigenetics 302198817 5 mar 10.28 reference_sorted.fa  
-rwxrwxrwx 1 danny epigenetics 96041105 5 mar 11.11 reference_sorted.rev.1.ebwt  
-rwxrwxrwx 1 danny epigenetics 37313744 5 mar 11.11 reference_sorted.rev.2.ebwt  
-rwxrwxrwx 1 danny epigenetics 302198817 5 mar 10.28 reference_unsorted.fa
```

## 4.2. *rt-count*

The RT Count module is the core component of the toolkit. It can process any number of both FastQ or SAM/BAM files, also mixed. In case FastQ files are passed, reads are pre-processed (trimming and clipping), and mapped to the reference transcriptome. Each SAM/BAM file is then processed to calculate per-base RT-stops and reads coverage on each transcript.

To list the required parameters, simply type:

```
$ rt-count -h (or --help)
```

Parameter	Description
<b>-p or --processors</b>	Number of processors (threads) to use (Default: 1)
<b>-t or --tmp-dir</b>	Path to a directory for temporary files creation (Default: /tmp) <b>Note:</b> If the provided directory does not exist, it will be created
<b>-o or --output-dir</b>	Output directory for writing counts in RTC (RT Count) format (Default: rt_count/)
<b>-ow or --overwrite</b>	Overwrites the output directory if already exists
<b>-k or --keep</b>	Keeps SAM/BAM files after reads mapping (in case FastQ files are passed) <b>Note:</b> If unsorted SAM/BAM files are passed, this option will cause RT Count to keep the sorted SAM/BAM file
<b>-n or --no-bam</b>	Disables conversion of SAM files to BAM format (requires -k)
<b>-b or --bowtie</b>	Path to Bowtie v1 executable (Default: assumes Bowtie is in PATH)
<b>-fx or --fastx</b>	Path to FASTX Clipper executable (Default: assumes FASTX Clipper is in PATH)
<b>-s or --samtools</b>	Path to SAMTools executable (Default: assumes SAMTools is in PATH)
<b>-r or --sorted</b>	In case SAM/BAM files are passed, assumes that they are already sorted lexicographically by transcript ID, and numerically by position
<b>-t5 or --trim-5prime</b>	In case SAM/BAM files are passed, allows to specify a comma separated list (no spaces) of values indicating the number of bases trimmed from the 5'-end of reads in the respective sample SAM/BAM files (Default: 0)  <b>Note #1:</b> Values must be provided in the same order as the input files (e.g. <i>rt-counter -t5 0,5 file1.bam file2.bam</i> , will consider 0 bases trimmed from <i>file1</i> reads, and 5 bases trimmed from <i>file2</i> reads). <b>Note #2:</b> If a single value is specified along with multiple SAM/BAM files, it will be used for all files.

<b>-f or --fasta</b>	<p>Path to a FASTA file containing the reference transcripts</p> <p><b>Note #1:</b> Transcripts in this file must match transcripts in SAM/BAM file headers.  <b>Note #2:</b> This can be omitted if a Bowtie index is specified by -bi (or --bowtie-index)</p>
----------------------	---

FASTX Clipper options	
<b>-fa or --fastx-adapter</b>	Sequence of 3' adapter for clipping (Default: TGGAATTCTCGGGTGCCAAGG, Illumina TruSeq Small RNA 3' Adapter)
<b>-fq or --fastx-qual</b>	FastQ files quality scale (33 [Default], or 64)
<b>-fl or --fastx-len</b>	Minimum length to keep reads after clipping ( $\geq 35$ , Default: 35)
<b>-c or --clipped</b>	Assumes that reads have been already clipped

Bowtie options	
<b>-bn or --bowtie-n</b>	Use Bowtie mapper in -n mode (0-3 mismatches, Default: 2)
<b>-bv or --bowtie-v</b>	Use Bowtie mapper in -v mode (0-3 mismatches, Default: disabled). If both --bowtie-v and --bowtie-n parameters are passed, the -n mode will be overridden by the -v mode.
<b>-ba or --bowtie-all</b>	Report all equally scoring positions for multi-mapping reads (Default: disabled, reports only uniquely mapped reads)
<b>-bc or --bowtie-chunkmbs</b>	Maximum MB of RAM for best-first search frames (Default: 128)
<b>-bp or --bowtie-threads</b>	<p>Number of threads to use for each instance of Bowtie (Default: 1)</p> <p><b>Note:</b> RT Count executes 1 instance of Bowtie for each processor specified by -p. At least -p &lt;processors&gt; * bowtie-threads processors are required.</p>
<b>-bi or --bowtie-index</b>	Path to transcriptome reference index (see paragraph 4.1)

#### 4.2.1. RTC format

RT Count produces a RTC (RT Count) file for each analyzed sample. RTC files are proprietary binary files, that store transcript's sequence, per-base RT-stop counts, and per-base reads coverage. These files can be indexed for fast random access.

Each entry in a RTC file is structured as follows:

Field	Description	Type
<b>len_transcript_id</b>	Length of the transcript ID (plus 1, including NULL)	uint32_t
<b>transcript_id</b>	Transcript ID (NULL terminated)	char[len_transcript_id]
<b>len_seq</b>	Length of sequence	uint32_t
<b>seq</b>	4-bit encoded sequence: 'ACGTN' -> [0,4] (High nybble first)	uint8_t[(len_seq+1)/2]
<b>stops</b>	RT-stops at each base of transcript	uint32_t[len_seq]
<b>cov</b>	Coverage at each base of transcript	uint32_t[len_seq]

The RTC file EOF marker (last 8 bytes of file) is "\x5b\x65\x6f\x66\x72\x74\x63\x5d".

If the marker is absent, it means that the file is truncated or corrupted.

RTI index files are binary files, structured as follows:

Field	Description	Type
<b>len_transcript_id</b>	Length of the transcript ID (plus 1, including NULL)	uint32_t
<b>transcript_id</b>	Transcript ID (NULL terminated)	char[len_transcript_id]
<b>offset</b>	Offset position of transcript in the RTC file	uint32_t



### 4.3. rsf-norm

The RSF Norm tool takes one (Rouskin method), or two (Ding method) RTC files generated by the RT Count module, and performs normalization to obtain a per-base reactivity score for each transcript. Reactivity scores can be computed using two methods:

#### [1] Ding *et al.*, 2014

In this scoring approach, the signal per-base is calculated as the natural log (ln) of the ratio between the raw count of RT-stops/Nuclease cuts at a given position of a transcript, and the average of the ln of RT-stops/Nuclease cuts along the whole transcript's length:

$$U_i = \frac{\ln(n_{1i}+p)}{\left(\sum_{j=0}^l \frac{\ln(n_{1j}+p)}{l}\right)} \quad \text{and} \quad T_i = \frac{\ln(n_{2i}+p)}{\left(\sum_{j=0}^l \frac{\ln(n_{2j}+p)}{l}\right)}$$

where  $n_{1i}$  and  $n_{2i}$  are respectively the raw read counts in the untreated (or RNase V1) and treated (DMS, CMCT, SHAPE, or Nuclease S1) experiments at position  $i$  of the transcript,  $l$  is transcript's length, and  $p$  is a pseudocount added to deal with non-covered regions.  $U_i$  and  $T_i$  are respectively the normalized number of RT-stops at position  $i$  in the untreated and treated samples.

Score at position  $i$  is then calculated as:

$$S_i = \max(0, (T_i - U_i))$$

#### [2] Rouskin *et al.*, 2014

In this scoring approach, the untreated sample is not considered. Signal per-base is calculated within fixed size windows, by dividing the number of RT-stops on each residue, by the number of RT-stops on the most reactive residue within the same window after removing the outliers.

Once computed, reactivity scores are normalized. Three normalization methods are actually provided:

Parameter	Description
<b>2-8% Normalization</b>	From the top 10% of values, the top 2% is ignored, then any reactivity value along the entire transcript is divided by the average of the remaining 8%
<b>90% Winsorising</b>	Each reactivity value above the 95th percentile is set to the 95th percentile, and the reactivity at each position of the transcript is divided by the 95th percentile
<b>Box-plot Normalization</b>	<p>Values greater than 1.5x the interquartile range (numerical distance between the 25th and 75th percentiles) above the 75th percentile are removed.</p> <p>After excluding these outliers, the next 10% of reactivities are averaged, and all reactivities (including outliers) are divided by this value.</p> <p>In our implementation, since box-plot normalization returns values ranging from 0 to ~1.5, values greater than 1.5 are scaled to 1.5, then each reactivity is divided by 1.5 to obtain values in the range 0-1</p>

To list the parameters required to the RSF Norm tool, simply type:

\$ rsf-norm -h (or --help)

Parameter	Description
<b>-u or --untreated</b>	Path to the RTC file for the non-treated (or RNase V1) sample
<b>-t or --treated</b>	Path to the RTC file for the treated (DMS, SHAPE, or Nuclease S1) sample
<b>-i or --index</b>	<p>A comma separated (no spaces) list of RTI index files for the provided RTC files</p> <p><b>Note #1:</b> RTI files must be provided in the order 1. Untreated, 2. Treated</p> <p><b>Note #2:</b> If a single RTI file is specified along with both untreated and treated samples, it will be used for both samples</p> <p><b>Note #3:</b> If no RTI index is provided, it will be generated at runtime, and stored in the same folder of the untreated/treated samples</p>
<b>-p or --processors</b>	Number of processors (threads) to use (Default: 1)
<b>-o or --output-dir</b>	Output directory for writing normalized data in SPD (Structure Probing Data file) format (Default: <treated>_vs_<untreated>_norm/ for Ding method, <treated>_norm/ for Rouskin method)
<b>-ow or --overwrite</b>	Overwrites the output directory if already exists
<b>-c or --config-file</b>	<p>Path to a configuration file with normalization parameters (see paragraph 4.2.1)</p> <p><b>Note #1:</b> If the provided file exists, the loaded configuration will override any command-line specified parameter</p> <p><b>Note #2:</b> If the provided file doesn't exist, it will be generated using the command-line specified (or the default) parameters</p>
<b>-sm or --scoring-method</b>	Score calculation method (1-2, Default: 1), where: 1. Ding <i>et al.</i> , 2014; 2. Rouskin <i>et al.</i> , 2014
<b>-nm or --norm-method</b>	Score normalization method (1-3, Default: 1), where: 1. 2-8% normalization; 2. 90% Winsorising; 3. Box-plot normalization
<b>-rb or --reactive-bases</b>	<p>Reactive bases to consider for signal normalization (Default: N [ACGT])</p> <p><b>Note:</b> This parameter accepts any IUPAC code, or combinations of them (e.g. <i>-rb M</i>, or <i>-rb AC</i>). Reactivity for any other base will be reported as NaN.</p>
<b>-ni or --norm-independent</b>	Each one of the reactive bases will be normalized independently (e.g. <i>-rb AC -ni</i> will normalize independently A and C residues)
<b>-mc or --mean-coverage</b>	Discards any transcript with mean coverage below this threshold ( $\geq 0$ , Default: 1)
<b>-ec or --median-coverage</b>	Discards any transcript with median coverage below this threshold ( $\geq 0$ , Default: 1)

<b>-d or --decimals</b>	Number of decimals for reporting reactivities (1-10, Default: 3)
<b>-n or --nan</b>	Non-covered transcript positions will be reported as NaN in the reactivity profile

<b>Scoring method #1 options (Ding <i>et al.</i>, 2014)</b>	
<b>-pc or --pseudocount</b>	Pseudocount added to reactivities to avoid division by 0 (>0, Default: 1)
<b>-s or --max-score</b>	Score threshold for capping raw reactivities (>1, Default: 10)

<b>Scoring method #2 options (Rouskin <i>et al.</i>, 2014)</b>	
<b>-nw or --norm-window</b>	Window size (in nt) for signal normalization ( $\geq 3$ , Default: 50)
<b>-wo or --window-offset</b>	Offset for sliding window during normalization (Default: 0, non-overlapping windows)

#### 4.3.1. Configuration files

RSF Norm configuration files are used to provide normalization parameters for the analysis, without the need to manually specify them from the command-line.

Configuration files are composed of a list of key/value pairs, separated by the equal sign (=), or by the colon punctuation mark (:). Keys and values are *case-insensitive*.

Accepted key/value pairs are:

Parameter	Accepted values	Default value
scoreMethod	"Ding" (or 1); "Rouskin" (or 2)	Ding
normMethod	"2-8%" (or 1); "90% Winsorising" (or 2); "Box-plot" (or 3)	2-8%
reactiveBases	[ACGTURYSWKMBDHSV] (or "all")	all
normIndependent	TRUE/FALSE; Yes/No; 1/0	FALSE
meanCoverage	Positive integer $\geq 0$	1
medianCoverage	Positive integer $\geq 0$	1

Scoring method #1 parameters (Ding <i>et al.</i> , 2014)		
maxScore	Positive integer $\geq 1$	10
pseudoCount	Positive integer $\geq 1$	1

Scoring method #2 parameters (Rouskin <i>et al.</i> , 2014)		
normWindow	Positive integer $\geq 3$	50
windowOffset	Positive integer $\geq 0$	0

e.g. A typical configuration file

```
scoreMethod=Ding
normMethod=2-8%
maxScore=50
pseudoCount=1
reactiveBases=ACGT
normIndependent=no
meanCoverage=1
mediancoverage=1
```

### 4.3.2. Structure Probing Data (SPD) files

RSF Norm produces a set of SPD files, one for each transcript being analyzed. These files are essentially XML files, and therefore can be parsed using any standard XML parsing library. SPD files tree structure is the following:

```
<?xml version="1.0" encoding="UTF-8"?>
<data [attributes]>
  <transcript id="Transcript ID" length="Transcript length">
    <sequence>
      Transcript sequence
    </sequence>
    <reactivity>
      Comma-separated list of reactivity values
    </reactivity>
    <error>
      Comma-separated list of standard deviations from multiple experiments
    </error>
  </transcript>
</data>
```

The “error” tag is optional. It is introduced by RSF Combine when multiple experiments are combined into a single SPD profile, and stores the per-base standard deviation of the normalized reactivity.

The “data” tag’s attributes allow keeping track of the analysis performed to obtain the SPD file:

Attribute	Description
<b>combined</b>	Whether multiple experiments have been combined into a single profile (TRUE or FALSE, see paragraph 5.1)
<b>scoring</b>	Scoring method (Ding or Rouskin)
<b>norm</b>	Normalization method (2-8%, Winsorising 90%, or Box-plot)
<b>reactive</b>	Reactive bases

Scoring method #1 attributes (Ding <i>et al.</i> , 2014)	
<b>max</b>	Score threshold for reactivity capping
<b>pseudo</b>	Pseudocount added during score calculation

Scoring method #2 attributes (Rouskin <i>et al.</i> , 2014)	
<b>win</b>	Normalization window’s size (in nt)
<b>offset</b>	Offset for normalization window sliding

### 4.3. rsf-fold

The RSF Fold tool is designed to allow the transcriptome-wide reconstruction of RNA structures, starting from SPD files generated using the RSF Norm tool.

This tool can process a single, or an entire directory of SPD files, and produces the inferred secondary structures (either in dot-bracket notation, or CT format) and their graphical representation (either in Postscript, or SVG format).

To allow higher analysis flexibility, the tool incorporates two different prediction methods:

[1] ViennaRNA

[2] RNAstructure

**Note #1:** Only the new v2.2.0 ViennaRNA soft-constraint approach is provided, since hard-constraint predictions are in most cases totally unreliable.

**Note #2:** The Iterative Cluster Refinement method (Incarnato *et al.*, 2016) has been temporary removed due to a change in the ViennaRNA APIs, and will be added back in a future release.

To list the parameters required to the RSF Fold tool, simply type:

```
$ rsf-fold -h (or --help)
```

Parameter	Description
<b>-o or --output-dir</b>	Output directory for writing structural data (Default: structurome/)
<b>-ow or --overwrite</b>	Overwrites output directory (if the specified path already exists)
<b>-ct or --connectivity-table</b>	Writes predicted structures in CT format (Default: Dot-bracket notation)
<b>-m or --folding-method</b>	Specifies the folding method (1-2, Default: 1): 1. ViennaRNA; 2. RNAstructure
<b>-p or --processors</b>	Number of processors to use for the analysis (Default: 1)
<b>-g or --img</b>	Enables generation of structure representations (Default: Postscript format)
<b>-s or --svg</b>	Structure representations are generated in SVG format (requires -g)
<b>-sl or --slope</b>	Sets slope used with structure probing data restraints (Default: 1.8 [kcal/mol])
<b>-in or --intercept</b>	Sets intercept used with structure probing data restraints (Default: -0.6 [kcal/mol])
<b>-m or --maximum-distance</b>	Sets the maximum pairing distance in nucleotides between transcript's residues (Default: 0, [no limit])

Folding method #1 options (ViennaRNA)	
<b>-v or --viennarna</b>	Path to ViennaRNA RNAfold executable (Default: assumes RNAfold is in PATH)
<b>-nlp or --no-lonely-pairs</b>	Disallows lonely (unstacked) base-pairs inside predicted structure
<b>-ngu or --no-closing-gu</b>	Disallows G:U wobbles at the end of helices
<b>-cm or --constraint-method</b>	Method for converting SPD reactivities into pseudo-energies (1-2, Default: 1): 1. Zarringhalam <i>et al.</i> , 2012; 2. Deigan <i>et al.</i> , 2009

Zarringhalam <i>et al.</i> , 2012 method options	
<b>-cc or --constraint-conversion</b>	Method for converting SPD reactivities to pairing probabilities (1-5, Default: 1): 1. Skip normalization step (SPD reactivities are treated as pairing probabilities) 2. Linear mapping according to Zarringhalam <i>et al.</i> , 2012 3. Use a cutoff to divide into paired and unpaired nucleotides 4. Linear model for converting SPD reactivities into probabilities of being unpaired 5. Linear model for converting the logarithm of SPD reactivities into probabilities of being unpaired
<b>-bf or --beta-factor</b>	Sets the magnitude of penalties for deviations from the observed pairing probabilities (Default: 0.5)
<b>-f or --cutoff</b>	Cutoff for constraining a position as unpaired (0-1, Default: 0.7) <b>Note:</b> This option requires constraint conversion method #3
<b>-ms or --model-slope</b>	Sets the slope used by the linear model (Default: 0.68 [Method #4], or 1.6 [Method #5]) <b>Note:</b> This option requires constraint conversion methods #4 or #5
<b>-mi or --model-intercept</b>	Sets the intercept used by the linear model (Default: 0.2 [Method #4], or -2.29 [Method #5]) <b>Note:</b> This option requires constraint conversion methods #4 or #5

Folding method #2 options (RNAstructure)	
<b>-r or --rnastructure</b>	Path to RNAstructure Fold executable (Default: assumes RNAstructure is in PATH)
<b>-dp or --data-path</b>	Path to RNAstructure data tables (Default: assumes DATAPATH environment variable is already set)

**Note:** ViennaRNA constraint method #2 (Deigan *et al.*, 2009) is essentially the same employed by RNAstructure, therefore the two approaches should yield approximately the same results.

For additional details relatively to ViennaRNA soft-constraint prediction methods, please refer to the ViennaRNA manual, or to Lorenz *et al.*, 2016.

## 5. Utilities

### 5.1. *rsf-combine*

RSF Combine allows combining multiple experiments into a single reactivity profile. This is useful for example when performing CIRS-seq experiments, to combine into a single profile both the reactivity of A/C residues probed with DMS, and of G/U residues probed with CMCT. Alternatively, RSF Combine is able to combine into a single profile multiple replicates of the same probing experiment. In these cases, the resulting SPD file may contain the optional “error” tag, in which the per-base standard deviation of the reactivity is reported.

When combining SPD files generated using the *-n* (or *--nan*) option of RSF Norm, only positions covered in all the experiments will be combined, while the others will be reported as NaN.

There’s no limit to the number of experiments that RSF Combine can handle. Moreover, it can be used both on individual SPD files, or on whole SPD folders by RSF Norm.

**Note:** RSF Combine does not allow combining SPD files generated using different scoring/normalization methods, since this will produce inconsistent data

To list the parameters required to the RSF Combine tool, simply type:

```
$ rsf-combine -h (or --help)
```

Parameter	Description
<b>-p or --processors</b>	Number of processors (threads) to use (Default: 1)
<b>-o or --output-dir</b>	Output directory for writing combined SPD (Structure Probing Data) files (Default: combined/)
<b>-ow or --overwrite</b>	Overwrites the output directory if already exists
<b>-s or --stdev</b>	When multiple replicates are combined, an optional “error” tag will be reported within the output SPD files, containing the per-base reactivity’s standard deviation
<b>-d or --decimals</b>	Number of decimals for reporting reactivities (1-10, Default: 3)



## 5.2. *spd2shape*

The SPD2SHAPE utility takes a SPD file in input, and generates a SHAPE constraint file that can be used by the RNAstructure and ViennaRNA programs to guide RNA folding. This utility is required by the *rsf-fold* module.

SPD2SHAPE doesn't require any parameters. The SPD file is passed in input, and the SHAPE constraint file is written to the standard output.

```
$ spd2shape ENS0000054321.spd > constraint.shape
```

```
$ cat constraint.shape
```

```
1 0.369
2 0.474
3 0.364
4 0.865
5 0
6 0
7 0.060
8 0.153
9 0.045
10 0.104
11 0.192
12 0.306
13 1.000
14 0.820
15 0.677
16 0.802
17 0.760
18 0.982
19 1.000
20 0.781
21 0.251
22 0.216
23 0.438
```

```
-- cut --
```

```
94 0
95 1.000
96 0.276
97 0
```

**Note:** bases that have not been covered in the probing experiment, will be excluded from the output file

## 6. Application case

### **Analysis of PARS data on GM12878 native deproteinized RNA structures**

**Reference:** Wan, Y. *et al.* (2014) Landscape and variation of RNA secondary structure across the human transcriptome. *Nature*, **505**, 706–709.

**GEO Dataset:** GSE50676

**Description:** In this work, Wan and colleagues used PARS to probe transcriptome-wide the structures of RNA from GM12878 cells in native deproteinized conformation, following phenol-chloroform extraction.

First of all, data in Sequence Read Archive (SRA) format should be downloaded from the Gene Expression Omnibus database:

```
$ wget 'ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-
instant/reads/ByExp/sra/SRX%2FSRX346%2FSRX346863/SRR972714/SRR972714.sra' -O S1.sra
$ wget 'ftp://ftp-trace.ncbi.nlm.nih.gov/sra/sra-
instant/reads/ByExp/sra/SRX%2FSRX346%2FSRX346864/SRR972715/SRR972715.sra' -O V1.sra
```

These commands will download the SRA files for the Nuclease S1 and RNase V1 treatments. Once downloaded, SRA files should be converted to FastQ format. To perform conversion, it is necessary first to download and install the NCBI SRA Toolkit (<http://www.ncbi.nlm.nih.gov/Traces/sra/sra.cgi?view=software>). Issue the following commands to convert the SRA files into FastQ files:

```
$ fastq-dump S1.sra
$ fastq-dump V1.sra
```

To build the reference index for the *Homo sapiens* genome (hg19 assembly), using the Ensembl gene annotation, run the *RSF Reference Builder* module with the following parameters:

```
$ rsf-index -g hg19 -a ensGene
```

```
[+] Making output directory...
[+] Connecting to UCSC genome database (genome-mysql.cse.ucsc.edu:3306)...
[+] Connected. Searching annotation...
[+] Annotation found. Validating columns...
[+] Downloading annotation data. Please wait...

[!] Warning: No reference multi-FASTA file has been provided.
            RSF Index will now try to download reference genome sequence
            from UCSC DAS server.
            This may take up to hours, depending on your connection's speed.

[+] Downloading sequence data for 52 chromosomes. Please wait...

[*] Chromosome chr1 [100.00%]
[*] Chromosome chr10 [100.00%]
[*] Chromosome chr11 [100.00%]
[*] Chromosome chr12 [100.00%]
[*] Chromosome chr13 [100.00%]
[*] Chromosome chr14 [100.00%]
[*] Chromosome chr15 [100.00%]
[*] Chromosome chr16 [100.00%]
[*] Chromosome chr17 [100.00%]
[*] Chromosome chr17_ctg5_hap1 [100.00%]
[*] Chromosome chr17_g1000205_random [100.00%]
[*] Chromosome chr18 [100.00%]
[*] Chromosome chr19 [100.00%]
[*] Chromosome chr19_g1000209_random [100.00%]
[*] Chromosome chr1_g1000191_random [100.00%]
[*] Chromosome chr1_g1000192_random [100.00%]
[*] Chromosome chr2 [100.00%]
[*] Chromosome chr20 [100.00%]
[*] Chromosome chr21 [100.00%]
[*] Chromosome chr22 [100.00%]
[*] Chromosome chr3 [100.00%]
[*] Chromosome chr4 [100.00%]
[*] Chromosome chr4_ctg9_hap1 [100.00%]
[*] Chromosome chr4_g1000193_random [100.00%]
[*] Chromosome chr4_g1000194_random [100.00%]
[*] Chromosome chr5 [100.00%]
```

```

[*] Chromosome chr6 [100.00%]
[*] Chromosome chr6_apd_hap1 [100.00%]
[*] Chromosome chr6_cox_hap2 [100.00%]
[*] Chromosome chr6_dbb_hap3 [100.00%]
[*] Chromosome chr6_mann_hap4 [100.00%]
[*] Chromosome chr6_mcf_hap5 [100.00%]
[*] Chromosome chr6_qbl_hap6 [100.00%]
[*] Chromosome chr6_ssto_hap7 [100.00%]
[*] Chromosome chr7 [100.00%]
[*] Chromosome chr7_gl000195_random [100.00%]
[*] Chromosome chr8 [100.00%]
[*] Chromosome chr9 [100.00%]
[*] Chromosome chrUn_gl000211 [100.00%]
[*] Chromosome chrUn_gl000212 [100.00%]
[*] Chromosome chrUn_gl000213 [100.00%]
[*] Chromosome chrUn_gl000215 [100.00%]
[*] Chromosome chrUn_gl000218 [100.00%]
[*] Chromosome chrUn_gl000219 [100.00%]
[*] Chromosome chrUn_gl000220 [100.00%]
[*] Chromosome chrUn_gl000222 [100.00%]
[*] Chromosome chrUn_gl000223 [100.00%]
[*] Chromosome chrUn_gl000227 [100.00%]
[*] Chromosome chrUn_gl000228 [100.00%]
[*] Chromosome chrUn_gl000241 [100.00%]
[*] Chromosome chrX [100.00%]
[*] Chromosome chrY [100.00%]

```

```

[+] Extracting transcript sequences...
[+] Building Bowtie transcriptome index from sequences. Please wait...
[+] All done.

```

Once the reference index has been prepared, the “*hg19\_ensGene*” folder should appear in the current path, containing all the relevant index files. The FastQ files can now be passed to the RT Count module that will perform reads mapping, and compute normalized reactivity scores for all covered transcripts. The module will also perform all the necessary pre-processing steps on the FastQ files (trimming and adapter clipping). These steps are not mandatory, and can be skipped by simply setting “-t5 0” or “-t3 0” to either disable trimming from the 5’- or 3’-end of the reads, and “--clipped” to disable adapter clipping. According to the GEO datasets page, the last 51 nt of each read should be trimmed (moreover, following analysis of FastQ files with FASTX Toolkit, we also decided to trim the first 3 nt of each read). To perform reads mapping, and data normalization, run the RT Counter module with the following parameters:

```
$ rt-counter -t tmp/ -k -b5 3 -b3 51 -c -bm 20 -bc 3200000 -bi hg19_ensGene/hg19_ensGene S1.fq V1.fq
```

```

[+] Reference FASTA file is present. Skipping FASTA regeneration...
[+] Making output directory...
[+] Guessing file types:

```

<u>Sample</u>	<u>Type</u>	<u>5'-end trimming</u>
S1	FastQ	3 nt
V1	FastQ	3 nt

```

[+] Processing FastQ files...
[+] Input FastQ files are already clipped. Skipping adapter clipping...
[+] Mapping reads to transcriptome...

```

```

[-] Mapping sample "S1" (PID: 19759)
[-] Mapping sample "V1" (PID: 19760)

```

```
[+] Mapping statistics:
```

```

[*] Sample "S1" [Mapped: 68.82%; Failed: 29.08%; Suppressed: 2.11%]
[*] Sample "V1" [Mapped: 65.15%; Failed: 29.81%; Suppressed: 5.04%]

```

```
[+] Sorting BAM files...
```

```

[-] Sorting sample "S1.bam" (PID: 19879)
[-] Sorting sample "V1.bam" (PID: 19880)

```

```

[+] Getting transcripts from reference, and building count table base structure...
[+] Validating SAM/BAM file headers...
[+] Calculating per-base RT-stops and coverage. This may take a while...

```

```

[-] Processing sample "S1" (Thread #2)...
[-] Processing sample "V1" (Thread #1)...

```

```
[+] Statistics:

[*] Sample "S1": 58725 transcripts covered
[*] Sample "V1": 98452 transcripts covered

[+] Cleaning up temporary files...
[+] All done.
```

The program reports mapping statistics, and the number of covered transcripts. RT Count has generated a folder named *“rt\_counter”*, which contains two folders:

1. a *“BAM”* folder containing mapped reads for both samples
2. a *“counts”* folder containing per-base transcript RT-stops in RTC (RT Count) format (see paragraph 4.2.1), and a RTI index file for fast RTC files random access:

**\$ ls -l**

```
rt_counter/BAM:
-rw-r--r-- 1 danny epigenetics 136030227  8 feb 12.04 S1.bam
-rw-r--r-- 1 danny epigenetics 130537439  8 feb 12.07 V1.bam

rt_counter/counts:
-rw-r--r-- 1 danny epigenetics   102  8 feb 12.02 index.rti
-rw-r--r-- 1 danny epigenetics 63658  8 feb 12.17 S1.rtc
-rw-r--r-- 1 danny epigenetics 63658  8 feb 12.22 V1.rtc
```

The RTC files can now be used as input for the RSF Norm module, that will normalize per-base signals. In this case, the V1 sample will be used as the untreated sample, while the S1 sample as the treated sample:

**\$ rsf-norm -u rt\_counter/counts/V1.rtc -t rt\_counter/counts/S1.rtc -c parameters.conf**

```
[+] Parsing configuration...

[!] Warning: Provided configuration file doesn't exist. Will be created...

[+] Configuration summary:

  Parameter                                Value

Scoring method                               Ding
Normalization method                         2-8%
Pseudocount                                  1
Maximum score                                10
Reactive bases                               ACGT
Normalize each base independently             No
Minimum mean coverage                        1
Minimum median coverage                      1

[+] Making output directory...
[+] Regenerating RTI index files...
[+] Loading transcript IDs... 204940 transcripts loaded.
[+] Normalizing reactivities [Last: ENST00000610125]
[+] Normalization statistics:

  [*] Covered transcripts:  3359
  [*] Discarded transcripts: 201581 total
                             201581 insufficient coverage
                             0 mismatch between treated and untreated sample sequence
                             0 absent in untreated sample reference

[+] All done.
```

RSF Norm has generated a folder containing one SPD (Structure Probing Data) file (see paragraph 4.3.2) for each transcript being analyzed, named *“S1\_vs\_V1\_norm”*, and a configuration file with the parameters used for the analysis named *“parameters.conf”*:

**\$ ls -l**

```
-rw-r--r-- 1 danny epigenetics      129 12 feb 17.51 parameters.conf
drwxr-xr-x 3 danny epigenetics     4096 13 feb 10.36 rt_counter
drwxr-xr-x 2 danny epigenetics    135168 13 feb 12.52 S1_vs_V1_norm
```

SPD files can now be used as input for the RSF Fold module to perform data-guided folding prediction. In the following example, we will pass the RSF-normalized reactivity profile for the U1 snRNA (Ensembl ID: ENST00000383861) to the *RSF Structure Deconvolver* module to perform prediction using the ViennaRNA package:

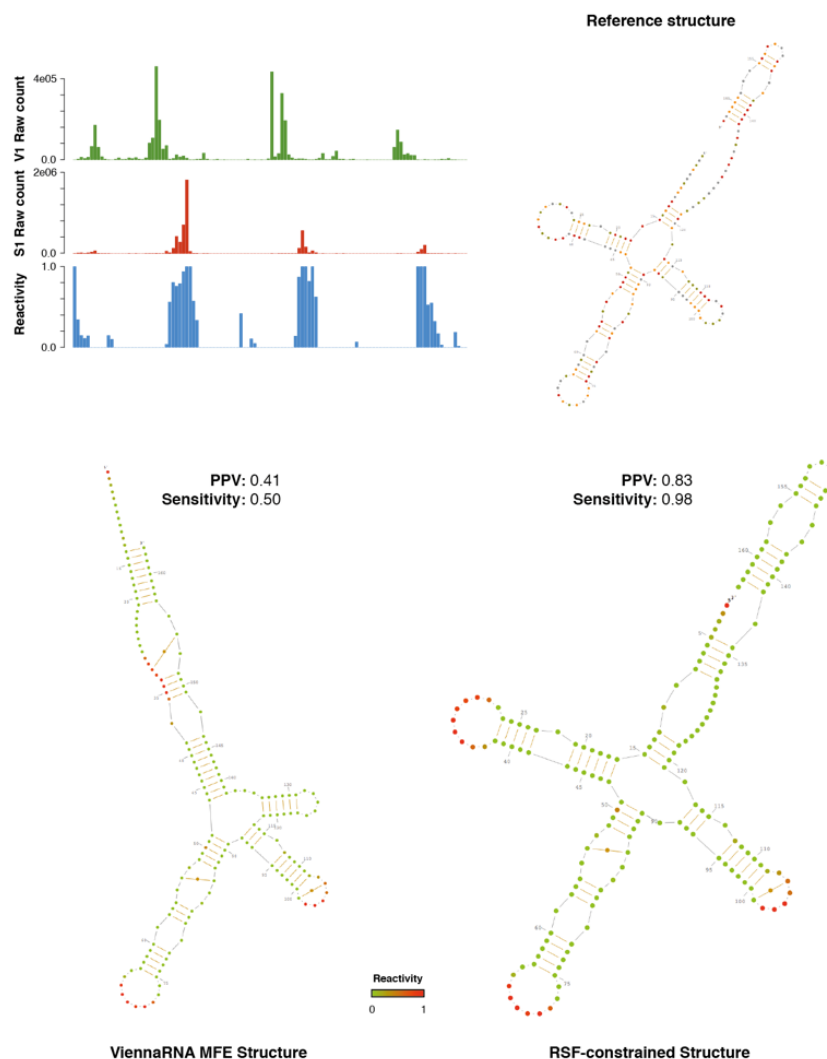
```
$ rsf-fold -m 1 -cm 1 -cc 3 -f 0.7 -g S1_vs_V1_norm/ENST00000383861.spd
```

```
[+] Checking method's requirements...
[+] Making output directory tree...
[+] Importing SPD file(s) [1 imported]
[+] Building RNA structurome [Last: ENST00000383861]
[+] Folding statistics:

[*] Folded transcripts: 1
[*] Discarded transcripts: 0 total
                        0 SPD parsing failed
                        0 constraint file generation failed
                        0 folding failed
                        0 I/O error

[+] All done.
```

As shown in the following figure, the RSF-constrained structure for the U1 snRNA (bottom right) better recapitulates the known reference structure (upper right) in terms of both Sensitivity and Positive Predictive Value (PPV) than the unconstrained MFE structure does (bottom left).



(Structure plots in this figure have been generated using the Assemble2 software, <http://bioinformatics.org/s2s/>)

**Appendix A. List of UCSC genome assembly releases** (<https://genome.ucsc.edu/FAQ/FAQreleases.html>)

Species	UCSC Version	Release date	Release name	Status
<b>Mammals</b>				
<b>Human</b>	hg38	Dec. 2013	Genome Reference Consortium GRCh38	<b>Available</b>
	hg19	Feb. 2009	Genome Reference Consortium GRCh37	<b>Available</b>
	hg18	Mar. 2006	NCBI Build 36.1	<b>Available</b>
	hg17	May 2004	NCBI Build 35	<b>Available</b>
	hg16	Jul. 2003	NCBI Build 34	<b>Available</b>
	hg15	Apr. 2003	NCBI Build 33	<b>Archived</b>
	hg13	Nov. 2002	NCBI Build 31	<b>Archived</b>
	hg12	Jun. 2002	NCBI Build 30	<b>Archived</b>
	hg11	Apr. 2002	NCBI Build 29	<b>Archived (data only)</b>
	hg10	Dec. 2001	NCBI Build 28	<b>Archived (data only)</b>
	hg8	Aug. 2001	UCSC-assembled	<b>Archived (data only)</b>
	hg7	Apr. 2001	UCSC-assembled	<b>Archived (data only)</b>
	hg6	Dec. 2000	UCSC-assembled	<b>Archived (data only)</b>
	hg5	Oct. 2000	UCSC-assembled	<b>Archived (data only)</b>
	hg4	Sep. 2000	UCSC-assembled	<b>Archived (data only)</b>
	hg3	Jul. 2000	UCSC-assembled	<b>Archived (data only)</b>
	hg2	Jun. 2000	UCSC-assembled	<b>Archived (data only)</b>
	hg1	May 2000	UCSC-assembled	<b>Archived (data only)</b>
<b>Alpaca</b>	vicPac2	Mar. 2013	Broad Institute Vicugna_pacos-2.0.1	<b>Available</b>
	vicPac1	Jul. 2008	Broad Institute VicPac1.0	<b>Available</b>
<b>Armadillo</b>	dasNov3	Dec. 2011	Broad Institute DasNov3	<b>Available</b>
<b>Bushbaby</b>	otoGar3	Mar. 2011	Broad Institute OtoGar3	<b>Available</b>
<b>Baboon</b>	papHam1	Nov. 2008	Baylor College of Medicine HGSC Pham_1.0	<b>Available</b>
	papAnu2	Mar. 2012	Baylor College of Medicine Panu_2.0	<b>Available</b>
<b>Cat</b>	felCat5	Sep. 2011	ICGSC Felis_catus-6.2	<b>Available</b>
	felCat4	Dec. 2008	NHGRI catChrV17e	<b>Available</b>
	felCat3	Mar. 2006	Broad Institute Release 3	<b>Available</b>
<b>Chimp</b>	panTro4	Feb. 2011	CGSC Build 2.1.4	<b>Available</b>
	panTro3	Oct. 2010	CGSC Build 2.1.3	<b>Available</b>
	panTro2	Mar. 2006	CGSC Build 2.1	<b>Available</b>
	panTro1	Nov. 2003	CGSC Build 1.1	<b>Available</b>
<b>Chinese hamster</b>	criGri1	Jul. 2013	Beijing Genomics Institution-Shenzhen C_griseus_v1.0	<b>Available</b>
<b>Cow</b>	bosTau7	Oct. 2011	Baylor College of Medicine HGSC Btau_4.6.1	<b>Available</b>
	bosTau6	Nov. 2009	University of Maryland v3.1	<b>Available</b>
	bosTau4	Oct. 2007	Baylor College of Medicine HGSC Btau_4.0	<b>Available</b>
	bosTau3	Aug. 2006	Baylor College of Medicine HGSC Btau_3.1	<b>Available</b>
	bosTau2	Mar. 2005	Baylor College of Medicine HGSC Btau_2.0	<b>Available</b>
	bosTau1	Sep. 2004	Baylor College of Medicine HGSC Btau_1.0	<b>Archived</b>
<b>Dog</b>	canFam3	Sep. 2011	Broad Institute v3.1	<b>Available</b>
	canFam2	May 2005	Broad Institute v2.0	<b>Available</b>
	canFam1	Jul. 2004	Broad Institute v1.0	<b>Available</b>
<b>Dolphin</b>	turTru2	Oct. 2011	Baylor College of Medicine Ttru_1.4	<b>Available</b>
<b>Elephant</b>	loxAfr3	Jul. 2009	Broad Institute LoxAfr3	<b>Available</b>
<b>Ferret</b>	musFur1	Apr. 2011	Ferret Genome Sequencing Consortium MusPutFur1.0	<b>Available</b>
<b>Gibbon</b>	nomLeu3	Oct. 2012	Gibbon Genome Sequencing Consortium Nleu3.0	<b>Available</b>

	nomLeu2	Jun. 2011	Gibbon Genome Sequencing Consortium Nleu1.1	Available
	nomLeu1	Jan. 2010	Gibbon Genome Sequencing Consortium Nleu1.0	Available
<b>Gorilla</b>	gorGor3	May 2011	Wellcome Trust Sanger Institute gorGor3.1	Available
<b>Guinea pig</b>	cavPor3	Feb. 2008	Broad Institute cavPor3	Available
<b>Hedgehog</b>	eriEur2	May 2012	Broad Institute EriEur2.0	Available
	eriEur1	Jun. 2006	Broad Institute Draft_v1	Available
<b>Horse</b>	equCab2	Sep. 2007	Broad Institute EquCab2	Available
	equCab1	Jan. 2007	Broad Institute EquCab1	Available
<b>Kangaroo rat</b>	dipOrd1	Jul. 2008	Baylor/Broad Institute DipOrd1.0	Available
<b>Manatee</b>	triMan1	Oct. 2011	Broad Institute TriManLat1.0	Available
<b>Marmoset</b>	calJac3	Mar. 2009	WUSTL Callithrix_jacchus-v3.2	Available
	calJac1	Jun. 2007	WUSTL Callithrix_jacchus-v2.0.2	Available
<b>Megabat</b>	pteVam1	Jul. 2008	Broad Institute Ptevap1.0	Available
<b>Microbat</b>	myoLuc2	Jul. 2010	Broad Institute MyoLuc2.0	Available
<b>Minke whale</b>	balAcu1	Oct. 2013	KORDI BalAcu1.0	Available
<b>Mouse</b>	mm10	Dec. 2011	Genome Reference Consortium GRCh38	Available
	mm9	Jul. 2007	NCBI Build 37	Available
	mm8	Feb. 2006	NCBI Build 36	Available
	mm7	Aug. 2005	NCBI Build 35	Available
	mm6	Mar. 2005	NCBI Build 34	Archived
	mm5	May 2004	NCBI Build 33	Archived
	mm4	Oct. 2003	NCBI Build 32	Archived
	mm3	Feb. 2003	NCBI Build 30	Archived
	mm2	Feb. 2002	MGSCv3	Archived
	mm1	Nov. 2001	MGSCv2	Archived (data only)
<b>Mouse lemur</b>	micMur1	Jul. 2007	Broad Institute MicMur1.0	Available
<b>Naked mole-rat</b>	hetGla2	Jan. 2012	Broad Institute HetGla_female_1.0	Available
	hetGla1	Jul. 2011	Beijing Genomics Institute HetGla_1.0	Available
<b>Opossum</b>	monDom5	Oct. 2006	Broad Institute release MonDom5	Available
	monDom4	Jan. 2006	Broad Institute release MonDom4	Available
	monDom1	Oct. 2004	Broad Institute release MonDom1	Available
<b>Orangutan</b>	ponAbe2	Jul. 2007	WUSTL Pongo_albelii-2.0.2	Available
<b>Panda</b>	ailMel1	Dec. 2009	BGI-Shenzhen AilMel 1.0	Available
<b>Pig</b>	susScr3	Aug. 2011	Swine Genome Sequencing Consortium Sscrofa10.2	Available
	susScr2	Nov. 2009	Swine Genome Sequencing Consortium Sscrofa9.2	Available
<b>Pika</b>	ochPri2	Jul. 2008	Broad Institute release OchPri2	Available
<b>Platypus</b>	ornAna1	Mar. 2007	WUSTL v5.0.1	Available
<b>Rabbit</b>	oryCun2	Apr. 2009	Broad Institute release OryCun2	Available
<b>Rat</b>	rn5	Oct. 2011	RGSC Rnor_5.0	Available
	rn4	Nov. 2004	Baylor College of Medicine HGSC v3.4	Available
	rn3	Jun. 2003	Baylor College of Medicine HGSC v3.1	Available
	rn2	Jan. 2003	Baylor College of Medicine HGSC v2.1	Archived
	rn1	Nov. 2002	Baylor College of Medicine HGSC v1.0	Archived
<b>Rhesus</b>	rheMac3	Oct. 2010	Beijing Genomics Institute CR_1.0	Available
	rheMac2	Jan. 2006	Baylor College of Medicine HGSC v1.0 Mmul_051212	Available
	rheMac1	Jan. 2005	Baylor College of Medicine HGSC Mmul_0.1	Archived
<b>Rock hyrax</b>	proCap1	Jul. 2008	Baylor College of Medicine HGSC Procap1.0	Available
<b>Sheep</b>	oviAri3	Aug. 2012	ISGC Oar_v3.1	Available
	oviAri1	Feb. 2010	ISGC Ovis aries 1.0	Available
<b>Shrew</b>	sorAra1	Jun. 2006	Broad Institute SorAra1.0	Available
<b>Sloth</b>	choHof1	Jul. 2008	Broad Institute ChoHof1.0	Available

<b>Squirrel</b>	speTri2	Nov. 2011	Broad Institute SpeTri2.0	<b>Available</b>
<b>Squirrel monkey</b>	saiBol1	Oct. 2011	Broad Institute SaiBol1.0	<b>Available</b>
<b>Tarsier</b>	tarSyr1	Aug. 2008	WUSTL/Broad Institute Tarsyr1.0	<b>Available</b>
<b>Tasmanian devil</b>	sarHar1	Feb. 2011	Wellcome Trust Sanger Institute Devil_refv7.0	<b>Available</b>
<b>Tenrec</b>	echTel2	Nov. 2012	Broad Institute EchTel2.0	<b>Available</b>
	echTel1	Jul. 2005	Broad Institute echTel1	<b>Available</b>
<b>Tree shrew</b>	tupBel1	Dec. 2006	Broad Institute Tupbel1.0	<b>Available</b>
<b>Wallaby</b>	macEug2	Sep. 2009	Tammar Wallaby Genome Sequencing Consortium Meug_1.1	<b>Available</b>
<b>White rhinoceros</b>	cerSim1	May 2012	Broad Institute CerSimSim1.0	<b>Available</b>
<b>American alligator</b>	allMis1	Aug. 2012	Int. Crocodilian Genomes Working Group allMis0.2	<b>Available</b>
<b>Atlantic cod</b>	gadMor1	May 2010	Genofisk GadMor_May2010	<b>Available</b>
<b>Budgerigar</b>	melUnd1	Sep. 2011	WUSTL v6.3	<b>Available</b>
<b>Chicken</b>	galGal4	Nov. 2011	ICGC Gallus-gallus-4.0	<b>Available</b>
	galGal3	May 2006	WUSTL Gallus-gallus-2.1	<b>Available</b>
	galGal2	Feb. 2004	WUSTL Gallus-gallus-1.0	<b>Available</b>
<b>Coelacanth</b>	latCha1	Aug. 2011	Broad Institute LatCha1	<b>Available</b>
<b>Elephant shark</b>	calMil1	Dec. 2013	IMCB Callorhinchus_milli_6.1.3	<b>Available</b>
<b>Fugu</b>	fr3	Oct. 2011	JGI v5.0	<b>Available</b>
	fr2	Oct. 2004	JGI v4.0	<b>Available</b>
	fr1	Aug. 2002	JGI v3.0	<b>Available</b>
<b>Lamprey</b>	petMar2	Sep. 2010	WUGSC 7.0	<b>Available</b>
	petMar1	Mar. 2007	WUSTL v3.0	<b>Available</b>
<b>Lizard</b>	anoCar2	May 2010	Broad Institute AnoCar2	<b>Available</b>
	anoCar1	Feb. 2007	Broad Institute AnoCar1	<b>Available</b>
<b>Medaka</b>	oryLat2	Oct. 2005	NIG v1.0	<b>Available</b>
<b>Medium ground finch</b>	geoFor1	Apr. 2012	BGI GeoFor_1.0 / NCBI 13302	<b>Available</b>
<b>Nile tilapia</b>	oreNil2	Jan. 2011	Broad Institute Release OreNil1.1	<b>Available</b>
<b>Painted turtle</b>	chrPic1	Dec. 2011	IPTGSC Chrysemys_picta_bellii-3.0.1	<b>Available</b>
<b>Stickleback</b>	gasAcu1	Feb. 2006	Broad Institute Release 1.0	<b>Available</b>
<b>Tetraodon</b>	tetNig2	Mar. 2007	Genoscope v7	<b>Available</b>
	tetNig1	Feb. 2004	Genoscope v7	<b>Available</b>
<b>Turkey</b>	melGal1	Dec. 2009	Turkey Genome Consortium v2.01	<b>Available</b>
<b><i>X. tropicalis</i></b>	xenTro3	Nov. 2009	JGI v.4.2	<b>Available</b>
	xenTro2	Aug. 2005	JGI v.4.1	<b>Available</b>
	xenTro1	Oct. 2004	JGI v.3.0	<b>Available</b>
<b>Zebra finch</b>	taeGut2	Feb. 2013	WUSTL v3.2.4	<b>Available</b>
	taeGut1	Jul. 2008	WUSTL v3.2.4	<b>Available</b>
<b>Zebrafish</b>	danRer7	Jul. 2010	Sanger Institute Zv9	<b>Available</b>
	danRer6	Dec. 2008	Sanger Institute Zv8	<b>Available</b>
	danRer5	Jul. 2007	Sanger Institute Zv7	<b>Available</b>
	danRer4	Mar. 2006	Sanger Institute Zv6	<b>Available</b>
	danRer3	May 2005	Sanger Institute Zv5	<b>Available</b>
	danRer2	Jun. 2004	Sanger Institute Zv4	<b>Archived</b>
	danRer1	Nov. 2003	Sanger Institute Zv3	<b>Archived</b>
<b>Deuterostomes</b>				
<b><i>C. intestinalis</i></b>	ci2	Mar. 2005	JGI v2.0	<b>Available</b>
	ci1	Dec. 2002	JGI v1.0	<b>Available</b>
<b>Lancelet</b>	braFlo1	Mar. 2006	JGI v1.0	<b>Available</b>
<b><i>S. purpuratus</i></b>	strPur2	Sep. 2006	Baylor College of Medicine HGSC v. Spur 2.1	<b>Available</b>
	strPur1	Apr. 2005	Baylor College of Medicine HGSC v. Spur_0.5	<b>Available</b>
<b>Insects</b>				
<b><i>A. mellifera</i></b>	apiMel2	Jan. 2005	Baylor College of Medicine HGSC v.Amel_2.0	<b>Available</b>



	apiMel1	Jul. 2004	Baylor College of Medicine HGSC v.Amel_1.2	Available
<b><i>A. gambiae</i></b>	anoGam1	Feb. 2003	IAGP v.MOZ2	Available
<b><i>D. ananassae</i></b>	droAna2	Aug. 2005	Agencourt Arachne release	Available
	droAna1	Jul. 2004	TIGR Celera release	Available
<b><i>D. erecta</i></b>	droEre1	Aug. 2005	Agencourt Arachne release	Available
<b><i>D. grimshawi</i></b>	droGri1	Aug. 2005	Agencourt Arachne release	Available
<b><i>D. melanogaster</i></b>	dm3	Apr. 2006	BDGP Release 5	Available
<b><i>D. melanogaster</i></b>	dm2	Apr. 2004	BDGP Release 4	Available
	dm1	Jan. 2003	BDGP Release 3	Available
<b><i>D. mojavensis</i></b>	droMoj2	Aug. 2005	Agencourt Arachne release	Available
	droMoj1	Aug. 2004	Agencourt Arachne release	Available
<b><i>D. persimilis</i></b>	droPer1	Oct. 2005	Broad Institute release	Available
<b><i>D. pseudoobscura</i></b>	dp3	Nov. 2004	Flybase Release 1.0	Available
	dp2	Aug. 2003	Baylor College of Medicine HGSC Freeze 1	Available
<b><i>D. sechellia</i></b>	droSec1	Oct. 2005	Broad Institute Release 1.0	Available
<b><i>D. simulans</i></b>	droSim1	Apr. 2005	WUSTL Release 1.0	Available
<b><i>D. virilis</i></b>	droVir2	Aug. 2005	Agencourt Arachne release	Available
	droVir1	Jul. 2004	Agencourt Arachne release	Available
<b><i>D. yakuba</i></b>	droYak2	Nov. 2005	WUSTL Release 2.0	Available
	droYak1	Apr. 2004	WUSTL Release 1.0	Available
<b>Nematodes</b>				
<b><i>C. brenneri</i></b>	caePb2	Feb. 2008	WUSTL 6.0.1	Available
	caePb1	Jan. 2007	WUSTL 4.0	Available
<b><i>C. briggsae</i></b>	cb3	Jan. 2007	WUSTL Cb3	Available
	cb1	Jul. 2002	WormBase v. cb25.agp8	Available
<b><i>C. elegans</i></b>	ce10	Oct. 2010	WormBase v. WS220	Available
	ce6	May 2008	WormBase v. WS190	Available
	ce4	Jan. 2007	WormBase v. WS170	Available
	ce2	Mar. 2004	WormBase v. WS120	Available
	ce1	May 2003	WormBase v. WS100	Archived
<b><i>C. japonica</i></b>	caeJap1	Mar. 2008	WUSTL 3.0.2	Available
<b><i>C. remanei</i></b>	caeRem3	May 2007	WUSTL 15.0.1	Available
	caeRem2	Mar. 2006	WUSTL 1.0	Available
<b><i>P. pacificus</i></b>	priPac1	Feb. 2007	WUSTL 5.0	Available
<b>Other</b>				
<b>Sea Hare</b>	aplCal1	Sep. 2008	Broad Release Aplcal2.0	Available
<b>Yeast</b>	sacCer3	apr-11	SGD April 2011 sequence	Available
	sacCer2	June 2008	SGD June 2008 sequence	Available