

# Package ‘ribosomeProfilingQC’

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**Type** Package

**Title** Ribosome Profiling Quality Control

**Version** 1.17.0

**Description** Ribo-Seq (also named ribosome profiling or footprinting) measures translato~~me~~me (unlike RNA-Seq, which sequences the transcriptome) by direct quantification of the ribosome-protected fragments (RPFs). This package provides the tools for quality assessment of ribosome profiling. In addition, it can preprocess Ribo-Seq data for subsequent differential analysis.

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assignReadingFrame	<i>Assign reading frame</i>
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---

### Description

Set reading frame for each reads in CDS region to frame0, frame1 and frame2.

### Usage

```
assignReadingFrame(reads, CDS, txdb, ignore.seqlevelsStyle = FALSE)
```

### Arguments

reads	Output of <a href="#">getPsiteCoordinates</a>
CDS	Output of <a href="#">prepareCDS</a>
txdb	A TxDb object. If it is set, assign reading frame for all reads. Default missing, only assign rading frame for reads in CDS.
ignore.seqlevelsStyle	Ignore the sequence name style detection or not.

### Value

An GRanges object of reads with reading frame information.

### Examples

```
library(Rsamtools)
bamfilename <- system.file("extdata", "RPF.WT.1.bam",
                           package="ribosomeProfilingQC")

yieldSize <- 10000000
bamfile <- BamFile(bamfilename, yieldSize = yieldSize)
pc <- getPsiteCoordinates(bamfile, bestpsite=13)
pc.sub <- pc[pc$qwidth %in% c(29, 30)]
#library(GenomicFeatures)
library(BSgenome.Drerio.UCSC.danRer10)
#txdb <- makeTxDbFromGFF(system.file("extdata",
#                                   "Danio_rerio.GRCz10.91.chr1.gtf.gz",
#                                   package="ribosomeProfilingQC"),
#                       organism = "Danio rerio",
#                       chrominfo = seqinfo(Drerio)["chr1"],
#                       taxonomyId = 7955)
#CDS <- prepareCDS(txdb)
CDS <- readRDS(system.file("extdata", "CDS.rds",
                           package="ribosomeProfilingQC"))
pc.sub <- assignReadingFrame(pc.sub, CDS)
```

---

codonBias

*Codon usage bias*


---

### Description

Calculate the codon usage for the reads in the identified CDSs. And then compared to the reference codon usage.

### Usage

```
codonBias(
  RPFs,
  gtf,
  genome,
  bestpsite = 13,
  readsLen = c(28, 29),
  anchor = "5end",
  ignore.seqlevelsStyle = FALSE,
  summary = TRUE,
  removeDuplicates = TRUE,
  ...
)
```

### Arguments

RPFs	Bam file names of RPFs.
gtf	GTF file name for annotation or a TxDb object.
genome	A BSgenome object.
bestpsite	P site postion.
readsLen	Reads length to keep.
anchor	5end or 3end. Default is 5end.
ignore.seqlevelsStyle	Ignore the sequence name style detection or not.
summary	Return the summary of codon usage bias or full list.
removeDuplicates	Remove the PCR duplicates or not. Default TRUE.
...	Parameters pass to <a href="#">makeTxDbFromGFF</a>

### Value

A list of data frame of codon count table if summary is TRUE. list 'reads' means the counts by raw reads. list 'reference' means the counts by sequence extracted from reference by the coordinates of mapped reads. Otherwise, return the counts (reads/reference) table for each reads.

## Examples

```
path <- system.file("extdata", package="ribosomeProfilingQC")
RPFs <- dir(path, "RPF.*?\\. [12].bam$", full.names=TRUE)
gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
library(BSgenome.Drerio.UCSC.danRer10)
cb <- codonBias(RPFs[c(1,2)], gtf=gtf, genome=Drerio)
```

---

codonUsage	<i>Start or Stop codon usage</i>
------------	----------------------------------

---

## Description

Calculate the start or stop codon usage for the identified CDSs.

## Usage

```
codonUsage(reads, start = TRUE, genome)
```

## Arguments

reads	Output of <a href="#">assignReadingFrame</a> .
start	Calculate for start codon or stop codon.
genome	A BSgenome object.

## Value

Table of codon usage.

## Examples

```
pcs <- readRDS(system.file("extdata", "samplePc.rds",
                          package="ribosomeProfilingQC"))
library(BSgenome.Drerio.UCSC.danRer10)
codonUsage(pcs, genome=Drerio)
codonUsage(pcs, start=FALSE, genome=Drerio)
```

---

countReads	<i>Extract counts for RPFs and RNAs</i>
------------	---

---

### Description

Calculate the reads counts for gene level or transcript level.

### Usage

```
countReads(
  RPFs,
  RNAs,
  gtf,
  level = c("tx", "gene"),
  bestpsite = 13,
  readsLen = c(28, 29),
  anchor = "5end",
  ignore.seqlevelsStyle = FALSE,
  ...
)
```

### Arguments

RPFs	Bam file names of RPFs.
RNAs	Bam file names of RNAseq.
gtf	GTF file name for annotation.
level	Transcript or gene level.
bestpsite	numeric(1). P site postion.
readsLen	numeric(1). reads length to keep.
anchor	5end or 3end. Default is 5end.
ignore.seqlevelsStyle	Ignore the sequence name style detection or not.
...	Parameters pass to <a href="#">featureCounts</a> except isGTFAnnotationFile, GTF.attrType, and annot.ext.

### Value

A list with reads counts.

### Examples

```
path <- system.file("extdata", package="ribosomeProfilingQC")
RPFs <- dir(path, "RPF.*?.[12].bam$", full.names=TRUE)
gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
RNAs <- dir(path, "mRNA.*?.[12].bam$", full.names = TRUE)
cnts <- countReads(RPFs[1], gtf=gtf, level="gene", readsLen=29)
#cnts <- countReads(RPFs[1], RNAs[1], gtf=gtf, level="gene", readsLen=29)
```

---

coverageDepth	<i>Extract coverage depth for gene level or transcript level</i>
---------------	--

---

### Description

Calculate the coverage depth for gene level or transcript level. Coverage for RPFs will be the best P site coverage. Coverage for RNAs will be the coverage for 5' end of reads.

### Usage

```
coverageDepth(
  RPFs,
  RNAs,
  gtf,
  level = c("tx", "gene"),
  bestpsite = 13,
  readsLen = c(28, 29),
  anchor = "5end",
  region = "cds",
  ext = 5000,
  ignore.seqlevelsStyle = FALSE,
  ...
)
```

### Arguments

RPFs	Bam file names of RPFs.
RNAs	Bam file names of RNAseq.
gtf	GTF file name for annotation or a TxDb object.
level	Transcript or gene level.
bestpsite	P site position.
readsLen	Reads length to keep.
anchor	5end or 3end. Default is 5end.
region	Annotation region. It could be "cds", "utr5", "utr3", "exon", "transcripts", "feature with extension".
ext	Extension region for "feature with extension".
ignore.seqlevelsStyle	Ignore the sequence name style detection or not.
...	Parameters pass to <a href="#">makeTxDbFromGFF</a>

### Value

A cvgd object with coverage depth.

## Examples

```
path <- system.file("extdata", package="ribosomeProfilingQC")
RPFs <- dir(path, "RPF.*?\\. [12].bam$", full.names=TRUE)
gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
cvgs <- coverageDepth(RPFs[1], gtf=gtf, level="gene")
```

---

coverageRates	<i>Calculate coverage rate</i>
---------------	--------------------------------

---

## Description

Coverage is a measure as percentage of position with reads along the CDS. Coverage rate calculate coverage rate for RPFs and mRNAs in gene level. Coverage will be calculated based on best P sites for RPFs and 5'end for RNA-seq.

## Usage

```
coverageRates(cvgs, RPFsampleOrder, mRNAsampleOrder)
```

## Arguments

cvgs                    Output of [coverageDepth](#)

RPFsampleOrder, mRNAsampleOrder  
Sample order of RPFs and mRNAs. The parameters are used to make sure that the order of RPFs and mRNAs in cvgs is corresponding samples.

## Value

A list with coverage rate.

## Examples

```
path <- system.file("extdata", package="ribosomeProfilingQC")
RPFs <- dir(path, "RPF.*?\\. [12].bam$", full.names=TRUE)
gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
cvgs <- coverageDepth(RPFs[1], gtf=gtf, level="gene")
cr <- coverageRates(cvgs)
```



---

cvgd-class	Class "cvgd"
------------	--------------

---

## Description

An object of class "cvgd" represents output of coverageDepth.

## Usage

```
cvgd(...)

## S4 method for signature 'cvgd'
x$name

## S4 replacement method for signature 'cvgd'
x$name <- value

## S4 method for signature 'cvgd,ANY,ANY'
x[[i, j, ..., exact = TRUE]]

## S4 replacement method for signature 'cvgd,ANY,ANY,ANY'
x[[i, j, ...]] <- value

## S4 method for signature 'cvgd'
show(object)
```

## Arguments

...	Each argument in ... becomes an slot in the new "cvgd"-class.
x	cvgd object.
name	A literal character string or a name (possibly backtick quoted).
value	value to replace.
i, j	indexes specifying elements to extract or replace.
exact	see <a href="#">Extract</a>
object	cvgd object.

## Value

A cvgd object.

## Slots

coverage "list", list of [CompressedRleList](#), specify the coverage of features of each sample.  
 granges [CompressedGRangesList](#), specify the features.

## Examples

```
cvgd()
```

---

estimatePsite	<i>Estimate P site position</i>
---------------	---------------------------------

---

## Description

Estimate P site position from a subset reads.

## Usage

```
estimatePsite(  
  bamfile,  
  CDS,  
  genome,  
  anchor = "5end",  
  readLen = c(25:30),  
  ignore.seqlevelsStyle = FALSE  
)
```

## Arguments

bamfile	A BamFile object.
CDS	Output of <a href="#">prepareCDS</a>
genome	A BSgenome object.
anchor	5end or 3end. Default is 5end.
readLen	The reads length used to estimate.
ignore.seqlevelsStyle	Ignore the sequence name style detection or not.

## Value

A best P site position.

## References

1: Bazzini AA, Johnstone TG, Christiano R, Mackowiak SD, Obermayer B, Fleming ES, Vejnar CE, Lee MT, Rajewsky N, Walther TC, Giraldez AJ. Identification of small ORFs in vertebrates using ribosome footprinting and evolutionary conservation. *EMBO J.* 2014 May 2;33(9):981-93. doi: 10.1002/embj.201488411. Epub 2014 Apr 4. PubMed PMID: 24705786; PubMed Central PMCID: PMC4193932.

**Examples**

```

library(Rsamtools)
bamfilename <- system.file("extdata", "RPF.WT.1.bam",
                           package="ribosomeProfilingQC")

yieldSize <- 10000000
bamfile <- BamFile(bamfilename, yieldSize = yieldSize)
#library(GenomicFeatures)
library(BSgenome.Drerio.UCSC.danRer10)
#txdb <- makeTxDbFromGFF(system.file("extdata",
#   "Danio_rerio.GRCz10.91.chr1.gtf.gz",
#   package="ribosomeProfilingQC"),
#   organism = "Danio rerio",
#   chrominfo = seqinfo(Drerio)["chr1"],
#   taxonomyId = 7955)
#CDS <- prepareCDS(txdb)
CDS <- readRDS(system.file("extdata", "CDS.rds",
                           package="ribosomeProfilingQC"))
estimatePsite(bamfile, CDS, Drerio)

```

---

filterCDS

*Filter CDS by size*


---

**Description**

Filter CDS by CDS size.

**Usage**

```
filterCDS(CDS, sizeCutoff = 100L)
```

**Arguments**

CDS	Output of preparedCDS
sizeCutoff	numeric(1). Cutoff size for CDS. If the size of CDS is less than the cutoff, it will be filtered out.

**Value**

A GRanges object with filtered CDS.

**Examples**

```

#library(GenomicFeatures)
library(BSgenome.Drerio.UCSC.danRer10)
#txdb <- makeTxDbFromGFF(system.file("extdata",
#   "Danio_rerio.GRCz10.91.chr1.gtf.gz",
#   package="ribosomeProfilingQC"),
#   organism = "Danio rerio",

```

```

#       chrominfo = seqinfo(Drerio)["chr1"],
#       taxonomyId = 7955)
#CDS <- prepareCDS(txdb)
CDS <- readRDS(system.file("extdata", "CDS.rds",
                          package="ribosomeProfilingQC"))
filterCDS(CDS)

```

---

FLOSS

*Fragment Length Organization Similarity Score (FLOSS)*


---

### Description

The FLOSS will be calculated from a histogram of read lengths for footprints on a transcript or reading frame.

### Usage

```

FLOSS(
  reads,
  ref,
  CDS,
  readLengths = c(26:34),
  level = c("tx", "gene"),
  draw = FALSE,
  ignore.seqlevelsStyle = FALSE
)

```

### Arguments

reads	Output of <a href="#">getPsiteCoordinates</a>
ref	Reference id list. If level is set to tx, the id should be transcript names. If level is set to gene, the id should be gene id.
CDS	Output of <a href="#">prepareCDS</a>
readLengths	Read length used for calculation
level	Transcript or gene level
draw	Plot FLOSS vs total reads or not.
ignore.seqlevelsStyle	Ignore the sequence name style detection or not.

### Value

A data frame with colnames as id, FLOSS, totalReads, wilcox.test.pval, cook's distance.

## References

1: Ingolia NT, Brar GA, Stern-Ginossar N, Harris MS, Talhouarne GJ, Jackson SE, Wills MR, Weissman JS. Ribosome profiling reveals pervasive translation outside of annotated protein-coding genes. *Cell Rep.* 2014 Sep 11;8(5):1365-79. doi: 10.1016/j.celrep.2014.07.045. Epub 2014 Aug 21. PubMed PMID: 25159147; PubMed Central PMCID: PMC4216110.

## Examples

```
library(Rsamtools)
bamfilename <- system.file("extdata", "RPF.WT.1.bam",
                           package="ribosomeProfilingQC")
yieldSize <- 10000000
bamfile <- BamFile(bamfilename, yieldSize = yieldSize)
pc <- getPsiteCoordinates(bamfile, bestpsite=13)
#library(GenomicFeatures)
library(BSgenome.Drerio.UCSC.danRer10)
#txdb <- makeTxDbFromGFF(system.file("extdata",
#   "Danio_rerio.GRCz10.91.chr1.gtf.gz",
#   package="ribosomeProfilingQC"),
#   organism = "Danio rerio",
#   chrominfo = seqinfo(Drerio)["chr1"],
#   taxonomyId = 7955)
#CDS <- prepareCDS(txdb)
CDS <- readRDS(system.file("extdata", "CDS.rds",
                           package="ribosomeProfilingQC"))

set.seed(123)
ref <- sample(unique(CDS$gene_id), 100)
fl <- FLOSS(pc, ref, CDS, level="gene")
```

---

frameCounts

*Extract counts for gene level or transcript level*

---

## Description

Calculate the reads counts or coverage rate for gene level or transcript level. Coverage is determined by measuring the proportion of in-frame CDS positions with  $\geq 1$  reads.

## Usage

```
frameCounts(
  reads,
  level = c("tx", "gene"),
  frame0only = TRUE,
  coverageRate = FALSE
)
```

**Arguments**

reads	Output of <a href="#">assignReadingFrame</a> .
level	Transcript or gene level
frame0only	Only count for reading frame 0 or not
coverageRate	Calculate for coverage or not

**Value**

A numeric vector with reads counts.

**Examples**

```
pcs <- readRDS(system.file("extdata", "samplePc.rds",
                          package="ribosomeProfilingQC"))
cnts <- frameCounts(pcs)
cnts.gene <- frameCounts(pcs, level="gene")
cvg <- frameCounts(pcs, coverageRate=TRUE)
```

---

getFPKM

*Get FPKM values for counts*


---

**Description**

Calculate Fragments Per Kilobase of transcript per Million mapped reads (FPKM) for counts.

**Usage**

```
getFPKM(counts, gtf, level = c("gene", "tx"))
```

**Arguments**

counts	Output of <a href="#">countReads</a> or <a href="#">normByRUVs</a>
gtf	GTF file name for annotation.
level	Transcript or gene level.

**Value**

A list with FPKMs

**Examples**

```
path <- system.file("extdata", package="ribosomeProfilingQC")
#RPFs <- dir(path, "RPF.*?.[12].bam$", full.names=TRUE)
#RNAs <- dir(path, "mRNA.*?.[12].bam$", full.names=TRUE)
#gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
#cnts <- countReads(RPFs, RNAs, gtf, level="gene")
cnts <- readRDS(file.path(path, "cnts.rds"))
fpkm <- getFPKM(cnts)
```

---

getORFscore	<i>Calculate ORFscore</i>
-------------	---------------------------

---

### Description

To calculate the ORFscore, reads were counted at each position within the ORF.

$$ORFscore = \log_2\left(\left(\sum_{n=1}^3 \frac{(F_n - \bar{F})^2}{\bar{F}}\right) + 1\right)$$

where  $F_n$  is the number of reads in reading frame  $n$ ,  $\bar{F}$  is the total number of reads across all three frames divided by 3. If  $F_1$  is smaller than  $F_2$  or  $F_3$ ,  $ORFscore = -1XORFscore$ .

### Usage

```
getORFscore(reads)
```

### Arguments

reads                      Output of [getPsiteCoordinates](#)

### Value

A numeric vector with ORFscore.

### References

1: Bazzini AA, Johnstone TG, Christiano R, Mackowiak SD, Obermayer B, Fleming ES, Vejnar CE, Lee MT, Rajewsky N, Walther TC, Giraldez AJ. Identification of small ORFs in vertebrates using ribosome footprinting and evolutionary conservation. EMBO J. 2014 May 2;33(9):981-93. doi: 10.1002/emboj.201488411. Epub 2014 Apr 4. PubMed PMID: 24705786; PubMed Central PMCID: PMC4193932.

### Examples

```
pcs <- readRDS(system.file("extdata", "samplePc.rds",
                           package="ribosomeProfilingQC"))
ORFscore <- getORFscore(pcs)
```

---

getPsiteCoordinates    *Get P site coordinates*

---

## Description

Extract P site coordinates from a bam file to a GRanges object.

## Usage

```
getPsiteCoordinates(  
  bamfile,  
  bestpsite,  
  anchor = "5end",  
  param = ScanBamParam(what = c("qwidth"), tag = character(0), flag =  
    scanBamFlag(isSecondaryAlignment = FALSE, isUnmappedQuery = FALSE,  
    isNotPassingQualityControls = FALSE, isSupplementaryAlignment = FALSE))  
)
```

## Arguments

bamfile	A BamFile object.
bestpsite	P site position. See <a href="#">estimatePsite</a>
anchor	5end or 3end. Default is 5end.
param	A ScanBamParam object. Please note the 'qwidth' is required.

## Value

A GRanges object with qwidth metadata which indicates the width of reads.

## Examples

```
library(Rsamtools)  
bamfilename <- system.file("extdata", "RPF.WT.1.bam",  
                           package="ribosomeProfilingQC")  
yieldSize <- 10000000  
bamfile <- BamFile(bamfilename, yieldSize = yieldSize)  
pc <- getPsiteCoordinates(bamfile, bestpsite=13)
```



---

ggBar	<i>barplot by ggplot2</i>
-------	---------------------------

---

**Description**

barplot with number in top.

**Usage**

```
ggBar(height, fill = "gray80", draw = TRUE, xlab, ylab, postfix)
```

**Arguments**

height	data for plot
fill, xlab, ylab	parameters pass to ggplot.
draw	plot or not
postfix	Postfix of text labled in top of bar.

**Value**

ggplot object.

**Examples**

```
ribosomeProfilingQC::ggBar(sample.int(100, 3))
```

---

metaPlot	<i>Metagene analysis plot</i>
----------	-------------------------------

---

**Description**

Plot the average coverage of UTR5, CDS and UTR3.

**Usage**

```
metaPlot(  
  UTR5coverage,  
  CDScoverage,  
  UTR3coverage,  
  sample,  
  xaxis = c("RPFs", "mRNA"),  
  bins = c(UTR5 = 100, CDS = 500, UTR3 = 100),  
  ...  
)
```

**Arguments**

UTR5coverage, CDScoverage, UTR3coverage  
 Coverages of UTR5, CDS, and UTR3 region. Output of [coverageDepth](#)

sample            character(1). Sample name to plot.

xaxis            What to plot for x-axis.

bins             Bins for UTR5, CDS and UTR3.

...              Parameter pass to plot.

**Value**

A list contain the data for plot.

**Examples**

```
## Not run:
path <- system.file("extdata", package="ribosomeProfilingQC")
RPFs <- dir(path, "RPF.*?\\.[12].bam$", full.names=TRUE)
RNAs <- dir(path, "mRNA.*?\\.[12].bam$", full.names=TRUE)
gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
cvgs <- coverageDepth(RPFs[1], RNAs[1], gtf)
cvgs.utr3 <- coverageDepth(RPFs[1], RNAs[1], gtf, region="utr3")
cvgs.utr5 <- coverageDepth(RPFs[1], RNAs[1], gtf, region="utr5")
metaPlot(cvgs.utr5, cvgs, cvgs.utr3, sample=1)

## End(Not run)
```

---

normalizeTEbyLoess      *Normalize the TE by Loess*

---

**Description**

Fitting the translational efficiency values with the mRNA value by [loess](#).

**Usage**

```
normalizeTEbyLoess(
  TE,
  log2 = TRUE,
  pseudocount = 0.001,
  span = 2/3,
  family.loess = "symmetric"
)
```

**Arguments**

TE	output of <a href="#">translationalEfficiency</a> .
log2	logical(1L). Do log2 transform for TE or not. If TE value is not log2 transformed, please set it as TRUE.
pseudocount	The number will be add to sum of reads count to avoid X/0.
span, family.loess	Parameters will be passed to <a href="#">loess</a>

**Value**

A list with RPFs, mRNA levels and TE as a matrix with log2 transformed translational efficiency.

**Examples**

```
path <- system.file("extdata", package="ribosomeProfilingQC")
cnts <- readRDS(file.path(path, "cnts.rds"))
fpkm <- getFPKM(cnts)
te <- translationalEfficiency(fpkm)
te1 <- normalizeTEbyLoess(te)
plotTE(te)
plotTE(te1, log2=FALSE)
```

---

normBy	<i>Normalization by edgeR, DESeq2 or RUVSeq</i>
--------	---

---

**Description**

Normalization by multiple known methods

**Usage**

```
normBy(counts, method = c("edgeR", "DESeq2", "RUVs", "fpkm", "vsr"), ...)
```

**Arguments**

counts	Output of <a href="#">countReads</a>
method	Character(1L) to indicate the method for normalization.
...	parameters will be passed to <a href="#">normByRUVs</a> or <a href="#">getFPKM</a>

**Value**

Normalized counts list

**Examples**

```

path <- system.file("extdata", package="ribosomeProfilingQC")
cnts <- readRDS(file.path(path, "cnts.rds"))
norm <- normBy(cnts, method = 'edgeR')
norm2 <- normBy(cnts, method = 'DESeq2')
norm3 <- normBy(cnts, 'vsn')

```

normByRUVs

*Normalization by RUVSeq***Description**

Normalization by RUVSeq:RUVs methods

**Usage**

```
normByRUVs(counts, RPFgroup, mRNAgroup = RPFgroup, k = 1)
```

**Arguments**

counts            Output of [countReads](#)

RPFgroup, mRNAgroup  
                  Groups for RPF and mRNA files

k                 The number of factor of unwanted variation to be estimated from the data. See [RUVs](#)

**Value**

Normalized counts list

**Examples**

```

## Not run: ##waiting for EDASeq fix the issue.
path <- system.file("extdata", package="ribosomeProfilingQC")
#RPFs <- dir(path, "RPF.*?.[12].bam$", full.names=TRUE)
#RNAs <- dir(path, "mRNA.*?.[12].bam$", full.names=TRUE)
#gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
#cnts <- countReads(RPFs, RNAs, gtf, level="gene")
cnts <- readRDS(file.path(path, "cnts.rds"))
gp <- c("KD1", "KD1", "WT", "WT")
norm <- normByRUVs(cnts, gp, gp)

## End(Not run)

```

---

PAmotif	<i>Metaplot of P site distribution</i>
---------	--

---

**Description**

Metaplot of P site distribution in all the CDS aligned by the start codon or stop codon.

**Usage**

```
PAmotif(reads, genome, plot = TRUE, ignore.seqlevelsStyle = FALSE)
```

**Arguments**

reads	Output of <a href="#">assignReadingFrame</a> or <a href="#">shiftReadsByFrame</a> .
genome	A BSgenome object.
plot	Plot the motif or not.
ignore.seqlevelsStyle	Ignore the sequence name style detection or not.

**Value**

A [pcm](#) object

**Examples**

```
pcs <- readRDS(system.file("extdata", "samplePc.rds",
                          package="ribosomeProfilingQC"))
library(BSgenome.Drerio.UCSC.danRer10)
#PAmotif(pcs, Drerio)
```

---

plotDistance2Codon	<i>Metaplot of P site distribution</i>
--------------------	--

---

**Description**

Metaplot of P site distribution in all the CDS aligned by the start codon or stop codon.

**Usage**

```
plotDistance2Codon(
  reads,
  start = TRUE,
  anchor = 50,
  col = c(Frame_0 = "#009E73", Frame_1 = "#D55E00", Frame_2 = "#0072B2")
)
```

**Arguments**

reads	Output of <a href="#">assignReadingFrame</a> .
start	Plot for start codon or stop codon.
anchor	The maximal xlim or (min, max) position for plot.
col	Colors for different reading frame.

**Value**

Invisible height of the barplot.

**Examples**

```
pcs <- readRDS(system.file("extdata", "samplePc.rds",
                           package="ribosomeProfilingQC"))
plotDistance2Codon(pcs)
#plotDistance2Codon(pcs, start=FALSE)
#plotDistance2Codon(pcs, anchor=c(-10, 20))
```

---

plotFrameDensity      *Plot density for each reading frame*

---

**Description**

Plot density for each reading frame.

**Usage**

```
plotFrameDensity(
  reads,
  density = TRUE,
  col = c(Frame_0 = "#009E73", Frame_1 = "#D55E00", Frame_2 = "#0072B2")
)
```

**Arguments**

reads	Output of <a href="#">assignReadingFrame</a>
density	Plot density or counts
col	Colors for reading frames

**Value**

A ggplot object.

**Examples**

```
pcs <- readRDS(system.file("extdata", "samplePc.rds",
                           package="ribosomeProfilingQC"))
plotFrameDensity(pcs)
```

---

plotSpliceEvent	<i>Plot splice event</i>
-----------------	--------------------------

---

### Description

Plot the splice event

### Usage

```
plotSpliceEvent(
  se,
  tx_name,
  coverage,
  group1,
  group2,
  cutoffFDR = 0.05,
  resetIntronWidth = TRUE
)
```

### Arguments

se	Output of <a href="#">spliceEvent</a>
tx_name	Transcript name.
coverage	Coverages of feature region with extensions. Output of <a href="#">coverageDepth</a>
group1, group2	The sample names of group 1 and group 2
cutoffFDR	Cutoff of FDR
resetIntronWidth	logical(1). If set to true, reset the region with no read to minimal width.

### Value

A ggplot object.

### Examples

```
## Not run:
path <- system.file("extdata", package="ribosomeProfilingQC")
RPFs <- dir(path, "RPF.*?\\. [12].bam$", full.names=TRUE)
gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
coverage <- coverageDepth(RPFs, gtf=gtf, level="gene",
  region="feature with extension")
group1 <- c("RPF.KD1.1", "RPF.KD1.2")
group2 <- c("RPF.WT.1", "RPF.WT.2")
se <- spliceEvent(coverage, group1, group2)
plotSpliceEvent(se, se$feature[1], coverage, group1, group2)

## End(Not run)
```

---

plotTE *Plot translational efficiency*

---

### Description

Scatterplot of RNA/RPFs level compared to the translational efficiency.

### Usage

```
plotTE(
  TE,
  sample,
  xaxis = c("mRNA", "RPFs"),
  removeZero = TRUE,
  log2 = TRUE,
  theme = theme_classic(),
  type = "histogram",
  margins = "y",
  ...
)
```

### Arguments

TE	Output of <a href="#">translationalEfficiency</a>
sample	Sample names to plot.
xaxis	What to plot for x-axis.
removeZero	Remove the 0 values from plots.
log2	Do log2 transform for TE or not.
theme	Theme for ggplot2.
type, margins, ...	Parameters pass to ggMarginal

### Value

A ggExtraPlot object.

### Examples

```
path <- system.file("extdata", package="ribosomeProfilingQC")
#RPFs <- dir(path, "RPF.*?\\. [12].bam$", full.names=TRUE)
#RNAs <- dir(path, "mRNA.*?\\. [12].bam$", full.names=TRUE)
#gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
#cnts <- countReads(RPFs, RNAs, gtf, level="gene")
cnts <- readRDS(file.path(path, "cnts.rds"))
fpkm <- getFPKM(cnts)
te <- translationalEfficiency(fpkm)
plotTE(te, 1)
```



---

plotTranscript	<i>Plot reads P site abundance for a specific transcript</i>
----------------	--

---

**Description**

Plot the bundances of P site on a transcript.

**Usage**

```
plotTranscript(  
  reads,  
  tx_name,  
  col = c(Frame_0 = "#009E73", Frame_1 = "#D55E00", Frame_2 = "#0072B2")  
)
```

**Arguments**

reads	Output of <a href="#">assignReadingFrame</a>
tx_name	Transcript names.
col	Colors for reading frames

**Value**

Invisible heights of the barplot.

**Examples**

```
pcs <- readRDS(system.file("extdata", "samplePc.rds",  
  package="ribosomeProfilingQC"))  
  
plotTranscript(pcs, c("ENS DART00000152562", "ENS DART00000054987"))
```

---

prepareCDS	<i>Prepare CDS</i>
------------	--------------------

---

**Description**

Prepare CDS library from a TxDb object.

**Usage**

```
prepareCDS(txdb, withUTR = FALSE)
```

**Arguments**

txdb	A TxDb object.
withUTR	Including UTR information or not.

**Value**

A GRanges object with metadata which include: tx\_id: transcript id; tx\_name: transcript name; gene\_id: gene id; isFirstExonInCDS: is first exon in CDS or not; idFirstExonInCDS: the id for the first exon; isLastExonInCDS: is last exon in CDS or not; wid.cumsu: cumulative sums of number of bases in CDS; internalPos: offset position from 1 base;

**Examples**

```
library(GenomicFeatures)
txdb_file <- system.file("extdata", "Biomart_Ensembl_sample.sqlite",
                          package="GenomicFeatures")
txdb <- loadDb(txdb_file)
CDS <- prepareCDS(txdb)
```

---

readsDistribution      *Plot reads distribution in genomic elements*

---

**Description**

Plot the percentage of reads in CDS, 5'UTR, 3'UTR, introns, and other elements.

**Usage**

```
readsDistribution(
  reads,
  txdb,
  upstreamRegion = 3000,
  downstreamRegion = 3000,
  plot = TRUE,
  precedence = NULL,
  ignore.seqlevelsStyle = FALSE,
  ...
)
```

**Arguments**

reads	Output of <a href="#">getPsiteCoordinates</a>
txdb	A TxDb object
upstreamRegion, downstreamRegion	The range for promoter region and downstream region.
plot	Plot the distribution or not
precedence	If no precedence specified, double count will be enabled, which means that if the reads overlap with both CDS and 5'UTR, both CDS and 5'UTR will be incremented. If a precedence order is specified, for example, if promoter is specified before 5'UTR, then only promoter will be incremented for the same example. The values could be any combinations of "CDS", "UTR5", "UTR3", "OtherExon", "Intron", "upstream", "downstream" and "InterGenic", Default=NULL

```

ignore.seqlevelsStyle      Ignore the sequence name style detection or not.
...                          Not use.

```

**Value**

The reads with distribution assignment

**Examples**

```

library(Rsamtools)
bamfilename <- system.file("extdata", "RPF.WT.1.bam",
                           package="ribosomeProfilingQC")

yieldSize <- 10000000
bamfile <- BamFile(bamfilename, yieldSize = yieldSize)
pc <- getPsiteCoordinates(bamfile, bestpsite=11)
pc.sub <- pc[pc$qwidth %in% c(29, 30)]
library(GenomicFeatures)
library(BSgenome.Drerio.UCSC.danRer10)
txdb <- makeTxDbFromGFF(system.file("extdata",
                                   "Danio_rerio.GRCz10.91.chr1.gtf.gz",
                                   package="ribosomeProfilingQC"),
                       organism = "Danio rerio",
                       chrominfo = seqinfo(Drerio)["chr1"],
                       taxonomyId = 7955)
pc.sub <- readsDistribution(pc.sub, txdb, las=2)
pc.sub <- readsDistribution(pc.sub, txdb, las=2,
                           precedence=c(
                             "CDS", "UTR5", "UTR3", "OtherExon",
                             "Intron", "upstream", "downstream",
                             "InterGenic"
                           ))

```

---

readsEndPlot

*Plot start/stop windows*

---

**Description**

Plot the reads shifted from start/stop position of CDS.

**Usage**

```

readsEndPlot(
  bamfile,
  CDS,
  toStartCodon = TRUE,
  fiveEnd = TRUE,
  shift = 0,
  window = c(-29, 30),

```

```

    readLen = 25:30,
    ignore.seqlevelsStyle = FALSE
  )

```

### Arguments

bamfile	A BamFile object.
CDS	Output of <a href="#">prepareCDS</a>
toStartCodon	What to search: start or end codon
fiveEnd	Search from five or three ends of the reads.
shift	number(1). Search from 5' end or 3' end of given number. if fiveEnd set to false, please set the shift as a negative number.
window	The window of CDS region to plot
readLen	The reads length used to plot
ignore.seqlevelsStyle	Ignore the sequence name style detection or not.

### Value

The invisible list with counts numbers and reads in GRanges.

### Examples

```

library(Rsamtools)
bamfilename <- system.file("extdata", "RPF.WT.1.bam",
                           package="ribosomeProfilingQC")

yieldSize <- 10000000
bamfile <- BamFile(bamfilename, yieldSize = yieldSize)
#library(GenomicFeatures)
library(BSgenome.Drerio.UCSC.danRer10)
#txdb <- makeTxDbFromGFF(system.file("extdata",
#   "Danio_rerio.GRCz10.91.chr1.gtf.gz",
#   package="ribosomeProfilingQC"),
#   organism = "Danio rerio",
#   chrominfo = seqinfo(Drerio)["chr1"],
#   taxonomyId = 7955)
#CDS <- prepareCDS(txdb)
CDS <- readRDS(system.file("extdata", "CDS.rds",
                           package="ribosomeProfilingQC"))

re <- readsEndPlot(bamfile, CDS, toStartCodon=TRUE)
readsEndPlot(re$reads, CDS, toStartCodon=TRUE, fiveEnd=FALSE)
#re <- readsEndPlot(bamfile, CDS, toStartCodon=FALSE)
#readsEndPlot(re$reads, CDS, toStartCodon=FALSE, fiveEnd=FALSE)
readsEndPlot(bamfile, CDS, shift=13)
#readsEndPlot(bamfile, CDS, fiveEnd=FALSE, shift=-16)

```

---

readsLenToKeep      *Get reads length to keep by cutoff percentage*

---

**Description**

Set the percentage to filter the reads.

**Usage**

```
readsLenToKeep(readsLengthDensity, cutoff = 0.8)
```

**Arguments**

readsLengthDensity      Output of [summaryReadsLength](#)  
 cutoff      Cutoff value.

**Value**

Reads length to be kept.

**Examples**

```
reads <- GRanges("chr1", ranges=IRanges(seq.int(100), width=1),
                 qwidth=sample(25:31, size = 100, replace = TRUE,
                               prob = c(.01, .01, .05, .1, .77, .05, .01)))
readsLenToKeep(summaryReadsLength(reads, plot=FALSE))
```

---

ribosomeReleaseScore      *Ribosome Release Score (RRS)*

---

**Description**

RRS is calculated as the ratio of translational efficiency in the CDS with RPFs in the 3'UTR.

**Usage**

```
ribosomeReleaseScore(
  cdsTE,
  utr3TE,
  CDSsampleOrder,
  UTR3sampleOrder,
  pseudocount = 0,
  log2 = FALSE
)
```

**Arguments**

cdsTE, utr3TE	Translational efficiency of CDS and UTR3 region. Output of <a href="#">translationalEfficiency</a>
CDSsampleOrder, UTR3sampleOrder	Sample order of cdsTE and utr3TE. The parameters are used to make sure that the order of CDS and UTR3 in TE is corresponding samples.
pseudocount	The number will be add to sum of reads count to avoid X/0.
log2	Do log2 transform or not.

**Value**

A vector of RRS.

**Examples**

```
## Not run:
path <- system.file("extdata", package="ribosomeProfilingQC")
RPFs <- dir(path, "RPF.*?\\.[12].bam$", full.names=TRUE)
RNAs <- dir(path, "mRNA.*?\\.[12].bam$", full.names=TRUE)
gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
cvgs <- coverageDepth(RPFs, RNAs, gtf)
cvgs.utr3 <- coverageDepth(RPFs, RNAs, gtf, region="utr3")
TE90 <- translationalEfficiency(cvgs, window = 90)
TE90.utr3 <- translationalEfficiency(cvgs.utr3, window = 90)
rrs <- ribosomeReleaseScore(TE90, TE90.utr3)

## End(Not run)
```

---

shiftReadsByFrame      *Shift reads by reading frame*

---

**Description**

Shift reads P site position by reading frame. After shifting, all reading frame will be set as 0

**Usage**

```
shiftReadsByFrame(reads, txdb, ignore.seqlevelsStyle = FALSE)
```

**Arguments**

reads	Output of <a href="#">getPsiteCoordinates</a>
txdb	A TxDb object.
ignore.seqlevelsStyle	Ignore the sequence name style detection or not.

**Value**

Reads with reading frame information

**Examples**

```
library(Rsamtools)
bamfilename <- system.file("extdata", "RPF.WT.1.bam",
                           package="ribosomeProfilingQC")

yieldSize <- 10000000
bamfile <- BamFile(bamfilename, yieldSize = yieldSize)
pc <- getPsiteCoordinates(bamfile, bestpsite=11)
pc.sub <- pc[pc$qwidth %in% c(29, 30)]
library(GenomicFeatures)
library(BSgenome.Drerio.UCSC.danRer10)
txdb <- makeTxDbFromGFF(system.file("extdata",
                                   "Danio_rerio.GRCz10.91.chr1.gtf.gz",
                                   package="ribosomeProfilingQC"),
                       organism = "Danio rerio",
                       chrominfo = seqinfo(Drerio)["chr1"],
                       taxonomyId = 7955)
pc.sub <- shiftReadsByFrame(pc.sub, txdb)
```

---

simulateRPF

*Simulation function*

---

**Description**

Simulate the RPFs reads in CDS, 5'UTR and 3'UTR

**Usage**

```
simulateRPF(
  txdb,
  outPath,
  genome,
  samples = 6,
  group1 = c(1, 2, 3),
  group2 = c(4, 5, 6),
  readsPerSample = 1e+06,
  readsLen = 28,
  psite = 13,
  frame0 = 0.9,
  frame1 = 0.05,
  frame2 = 0.05,
  DRegions = GRanges(),
  size = 1,
  sd = 0.02,
```

```

    minDElevel = log2(2),
    includeReadsSeq = FALSE
  )

```

### Arguments

txdb	A TxDb object
outPath	Output folder for the bam files
genome	A BSgenome object
samples	Total samples to simulate.
group1, group2	Numeric to index the sample groups.
readsPerSample	Total reads number per sample.
readsLen	Reads length, default 100bp.
psite	P-site position. default 13.
frame0, frame1, frame2	Percentage of reads distribution in frame0, frame1 and frame2
DEregions	The regions with differential reads in exon, utr5 and utr3.
size	Dispersion parameter. Must be strictly positive.
sd	Standard deviations.
minDElevel	Minimal differential level. default: log2(2).
includeReadsSeq	logical(1). Include reads sequence or not.

### Value

An invisible list of GAlignments.

### Examples

```

library(GenomicFeatures)
txdb_file <- system.file("extdata", "Biomart_Ensembl_sample.sqlite",
                        package="GenomicFeatures")
txdb <- loadDb(txdb_file)
simulateRPF(txdb, samples=1, readsPerSample = 1e3)
## Not run:
cds <- prepareCDS(txdb, withUTR = TRUE)
cds <- cds[width(cds)>200]
DEregions <- cds[sample(seq_along(cds), 10)]
simulateRPF(txdb, samples=6, readsPerSample = 1e5, DEregions=DEregions)

## End(Not run)

```



---

spliceEvent	<i>Get splicing events</i>
-------------	----------------------------

---

**Description**

Get differential usage of alternative Translation Initiation Sites, alternative Polyadenylation Sites or alternative splicing sites

**Usage**

```
spliceEvent(coverage, group1, group2)
```

**Arguments**

coverage            Coverages of feature region with extensions. Output of [coverageDepth](#)

group1, group2    The sample names of group 1 and group 2

**Value**

A GRanges object of splice events.

**Examples**

```
## Not run:
path <- system.file("extdata", package="ribosomeProfilingQC")
RPFs <- dir(path, "RPF.*?\\. [12].bam$", full.names=TRUE)
gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
coverage <- coverageDepth(RPFs, gtf=gtf,
                           level="gene", region="feature with extension")
group1 <- c("RPF.KD1.1", "RPF.KD1.2")
group2 <- c("RPF.WT.1", "RPF.WT.2")
se <- spliceEvent(coverage, group1, group2)

## End(Not run)
```

---

strandPlot	<i>Plot the distribution of reads in sense and antisense strand</i>
------------	---

---

**Description**

Plot the distribution of reads in sense and antisense strand to check the mapping is correct.

**Usage**

```
strandPlot(  
  reads,  
  CDS,  
  col = c("#009E73", "#D55E00"),  
  ignore.seqlevelsStyle = FALSE,  
  ...  
)
```

**Arguments**

reads	Output of <a href="#">getPsiteCoordinates</a>
CDS	Output of <a href="#">prepareCDS</a>
col	Color for sense and antisense strand.
ignore.seqlevelsStyle	Ignore the sequence name style detection or not.
...	Parameter passed to barplot

**Value**

A ggplot object.

**Examples**

```
library(Rsamtools)  
bamfilename <- system.file("extdata", "RPF.WT.1.bam",  
                           package="ribosomeProfilingQC")  
  
yieldSize <- 10000000  
bamfile <- BamFile(bamfilename, yieldSize = yieldSize)  
pc <- getPsiteCoordinates(bamfile, bestpsite=11)  
pc.sub <- pc[pc$qwidth %in% c(29, 30)]  
library(GenomicFeatures)  
library(BSgenome.Drerio.UCSC.danRer10)  
txdb <- makeTxDbFromGFF(system.file("extdata",  
                                   "Danio_rerio.GRCz10.91.chr1.gtf.gz",  
                                   package="ribosomeProfilingQC"),  
                       organism = "Danio rerio",  
                       chrominfo = seqinfo(Drerio)["chr1"],  
                       taxonomyId = 7955)  
CDS <- prepareCDS(txdb)  
strandPlot(pc.sub, CDS)
```

---

summaryReadsLength      *Summary the reads lengths*

---

**Description**

Plot the reads length distribution

**Usage**

```
summaryReadsLength(reads, widthRange = c(20:35), plot = TRUE, ...)
```

**Arguments**

reads	Output of getPsiteCoordinates
widthRange	The reads range to be plot
plot	Do plot or not
...	Not use.

**Value**

The reads length distribution

**Examples**

```
reads <- GRanges("chr1", ranges=IRanges(seq.int(100), width=1),
                qwidth=sample(25:31, size = 100, replace = TRUE,
                             prob = c(.01, .01, .05, .1, .77, .05, .01)))
summaryReadsLength(reads)
```

---

translationalEfficiency  
*Translational Efficiency*

---

**Description**

Calculate Translational Efficiency (TE). TE is defined as the ratios of the absolute level of ribosome occupancy divided by RNA levels for transcripts.

**Usage**

```
translationalEfficiency(
  x,
  window,
  RPFsampleOrder,
  mRNAsampleOrder,
  pseudocount = 1,
  log2 = FALSE,
  normByLibSize = FALSE,
  shrink = FALSE,
  ...
)
```

**Arguments**

x	Output of <a href="#">getFPKM</a> or <a href="#">normByRUVs</a> . if window is set, it must be output of <a href="#">coverageDepth</a> .
window	numeric(1). window size for maximal counts.
RPFsampleOrder, mRNAsampleOrder	Sample order of RPFs and mRNAs. The parameters are used to make sure that the order of RPFs and mRNAs in <code>cvgs</code> is corresponding samples.
pseudocount	The number will be add to sum of reads count to avoid X/0.
log2	Do log2 transform or not.
normByLibSize	Normalization by library size or not. If window size is provided and <code>normByLibSize</code> is set to TRUE, the coverage will be normalized by library size.
shrink	Shrink the TE or not.
...	Parameters will be passed to <code>ash</code> function from <code>ashr</code> .

**Value**

A list with RPFs, mRNA levels and TE as a matrix with translational efficiency

**Examples**

```
## Not run:
path <- system.file("extdata", package="ribosomeProfilingQC")
RPFs <- dir(path, "RPF.*?\\.[12].bam$", full.names=TRUE)
RNAs <- dir(path, "mRNA.*?\\.[12].bam$", full.names=TRUE)
gtf <- file.path(path, "Danio_rerio.GRCz10.91.chr1.gtf.gz")
cnts <- countReads(RPFs, RNAs, gtf, level="gene")
fpkm <- getFPKM(cnts)
te <- translationalEfficiency(fpkm)

## End(Not run)
```

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