

# Package ‘EpiTxDb’

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**Type** Package

**Title** Storing and accessing epitranscriptomic information using the AnnotationDbi interface

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**Description** EpiTxDb facilitates the storage of epitranscriptomic information. More specifically, it can keep track of modification identity, position, the enzyme for introducing it on the RNA, a specifier which determines the position on the RNA to be modified and the literature references each modification is associated with.

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**biocViews** Software, Epitranscriptomics

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**Imports** methods, utils, httr, xml2, curl, rex, GenomicFeatures, txdbmaker, GenomicRanges, GenomeInfoDb, BiocGenerics, BiocFileCache, S4Vectors, IRanges, RSQLite, DBI, Biostrings, tRNAdbImport

**Suggests** BiocStyle, knitr, rmarkdown, testthat, httpptest, AnnotationHub, ensemblDb, ggplot2, EpiTxDb.Hs.hg38, BSgenome.Hsapiens.UCSC.hg38, BSgenome.Scerevisiae.UCSC.sacCer3, TxDb.Hsapiens.UCSC.hg38.knownGene

**Collate** 'AllGenerics.R' 'EpiTxDb-SELECT-helpers.R' 'EpiTxDb-schema.R' 'EpiTxDb.R' 'EpiTxDb-class.R' 'makeEpiTxDb.R' 'makeEpiTxDbFromGRanges.R' 'shiftGenomicToTranscript.R' 'makeEpiTxDbFromRMBase.R' 'makeEpiTxDbFromRNAdb.R' 'modifications.R' 'modificationsBy.R' 'ranges-helpers.R' 'select-methods.R'

**RoxygenNote** 7.3.1

**BugReports** <https://github.com/FelixErnst/EpiTxDb/issues>

**URL** <https://github.com/FelixErnst/EpiTxDb>

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EpiTxDb-package	<i>EpiTxDb: Storing and accessing epitranscriptomic information using the AnnotationDbi interface</i>
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## Description

EpiTxDb facilitates the storage of epitranscriptomic information. More specifically, it can keep track of modification identity, position, the enzyme for introducing it on the RNA, a specifier which determines the position on the RNA to be modified and the literature references each modification is associated with.

## Author(s)

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## See Also

Useful links:

- <https://github.com/FelixErnst/EpiTxDb>
- Report bugs at <https://github.com/FelixErnst/EpiTxDb/issues>

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EpiTxDb-class

*EpiTxDb objects*

---

## Description

The EpiTxDb class is a [AnnotationDb](#) type container for storing Epitranscriptomic information.

The information are typically stored on a per transcript and not as genomic coordinates, but the EpiTxDb class is agnostic to this. In case of genomic coordinates `transcriptsBy` will return modifications per chromosome.

## Usage

```
## S4 method for signature 'EpiTxDb'  
organism(object)
```

```
## S4 method for signature 'EpiTxDb'  
seqinfo(x)
```

```
## S4 method for signature 'EpiTxDb'  
seqlevels(x)
```

```
## S4 method for signature 'EpiTxDb'  
as.list(x)
```

## Arguments

`x, object`      a EpiTxDb object

## Value

For

- `organism()` and `seqlevels()` a character vector
- `seqinfo()` a [Seqinfo](#) object
- `as.list()` a list

## See Also

- [makeEpiTxDbFromGRanges](#) for creating a EpiTxDb object from a [GRanges](#) object and it's metadata columns
- [makeEpiTxDbFromRMBase](#) for creating a EpiTxDb object from RMBase online resources
- [makeEpiTxDbFromtRNAdb](#) for creating a EpiTxDb object from tRNAdb online resources
- [makeEpiTxDb](#) for creating a EpiTxDb object from `data.frames`
- [modifications](#), [modificationsBy](#) for getting epitranscriptomic modification locations
- [select](#) for using the default interface of [AnnotationDb](#) objects.
- [shiftGenomicToTranscript](#) and [shiftTranscriptToGenomic](#) for transferring genomic to transcript coordinates and back again.

**Examples**

```

etdb_file <- system.file("extdata", "EpiTxDb.Hs.hg38.snoRNadb.sqlite",
                        package="EpiTxDb")
etdb <- loadDb(etdb_file)
etdb

# general methods
seqinfo(etdb) #
seqlevels(etdb) # easy access to all transcript names

```

---

EpiTxDb-data	<i>EpiTxDb internal data</i>
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---

**Description**

EpiTxDb internal data

**Usage**

```
data(rmbase_data)
```

**Format**

data.frame

---

EpiTxDb-package#'	<i>EpiTxDb - Storing and accessing epitranscriptomic information using the AnnotationDbi interface</i>
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**Description**

title

**Author(s)**

Felix G M Ernst [aut]

**References**

Jia-Jia Xuan, Wen-Ju Sun, Ke-Ren Zhou, Shun Liu, Peng-Hui Lin, Ling-Ling Zheng, Liang-Hu Qu, Jian-Hua Yang (2017): "RMBase v2.0: Deciphering the Map of RNA Modifications from Epitranscriptome Sequencing Data." *Nucleic Acids Research*, Volume 46, Issue D1, 4 January 2018, Pages D327–D334. doi: 10.1093/nar/gkx934

Jühling, Frank; Mörl, Mario; Hartmann, Roland K.; Sprinzl, Mathias; Stadler, Peter F.; Pütz, Jörn (2009): "TRNAdb 2009: Compilation of tRNA Sequences and tRNA Genes." *Nucleic Acids Research* 37 (suppl\_1): D159–D162. doi: 10.1093/nar/gkn772

Sprinzl, Mathias; Vassilenko, Konstantin S. (2005): "Compilation of tRNA Sequences and Sequences of tRNA Genes." *Nucleic Acids Research* 33 (suppl\_1): D139–D140. doi: 10.1093/nar/gki012

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makeEpiTxDb

*Creating a EpiTxDb from user supplied annotations as data.frames*


---

## Description

makeEpiTxDb is a low-level constructor for creating a [EpiTxDb](#) object from user supplied annotations.

This functions typically will not be used by regular users.

## Usage

```
makeEpiTxDb(
  modifications,
  reactions = NULL,
  specifiers = NULL,
  references = NULL,
  metadata = NULL,
  reassign.ids = FALSE
)
```

## Arguments

**modifications** A data.frame containing the following columns:

- **mod\_id**: a unique integer value per modification.
- **mod\_type**: the modification type as a character or factor value. Must be a value from `shortName(ModRNAString())`.
- **mod\_name**: a character or factor name for the specific modification
- **mod\_start**: the start position for the modification as integer value. Usually `mod_start = mod_end`
- **mod\_end**: the end position for the modification as integer value. Usually `mod_start = mod_end`
- **mod\_strand**: the strand information for the modification as a character or factor.
- **sn\_id**: a integer value per unique sequence
- **sn\_name**: a character or factor as sequence name, e.g a chromosome or a transcript identifier like `chr1`.

The first six are mandatory, whereas one of the last two has to be set. `sn_id` will be generated from `sn_name`, if `sn_id` is not set.

**reactions** An optional data.frame containing the following columns:

- **mod\_id**: a integer value per modification and the link to the modification data.frame.
- **rx\_genename**: a character or factor referencing a gene name for the enzyme incorporating the modification.
- **rx\_rank**: a integer for sorting enzyme reactions, if multiple enzymes are involved in the modification's incorporation/maintenance.
- **rx\_ensembl**: a character or factor with an ensembl identifier for the gene name of the enzyme.

	<ul style="list-style-type: none"> <li>• rx_ensembltrans: a character or factor with an ensembl identifier for the transcript being translated into the enzyme.</li> <li>• rx_entrezid: a character or factor with an entrezid for the gene name of the enzyme.</li> </ul>
	(default: reactions = NULL)
specifiers	<p>An optional data.frame containing the following columns:</p> <ul style="list-style-type: none"> <li>• mod_id: an integer value per modification and the link to the modification data.frame.</li> <li>• spec_type: a character or factor referencing a type of specifier, e.g. snoRNA. Not checked for validity.</li> <li>• spec_gene_name: a character or factor referencing a gene name for the specifier directing an enzyme to the specific location for the modification to be incorporated.</li> <li>• spec_ensembl: a character or factor with an ensembl identifier for the gene name of the specifier.</li> <li>• spec_ensembltrans: a character or factor with an ensembl identifier for the transcript being translated into the specifier.</li> <li>• spec_entrezid: a character or factor with an entrezid for the gene name of the specifier.</li> </ul>
	(default: specifiers = NULL)
references	<p>An optional data.frame containing the following columns:</p> <ul style="list-style-type: none"> <li>• mod_id: an integer value per modification and the link to the modification data.frame.</li> <li>• ref_type: a character or factor with a reference type, e.g. PMID. Is not checked for validity.</li> <li>• ref: a character or factor with a reference value, e.g. a specific pubmed id or a journal article. Is not checked for validity.</li> </ul>
	(default: references = NULL)
metadata	<p>An optional data.frame containing the following columns:</p> <ul style="list-style-type: none"> <li>• name: a character value used as name</li> <li>• value: a character value</li> </ul>
	This dataframe will be returned by metadata() (default: metadata = NULL)
reassign.ids	TRUE or FALSE Controls how internal mod_ids should be assigned. If reassign.ids is FALSE (the default) and if the ids are supplied, then they are used as the internal ids, otherwise the internal ids are assigned in a way that is compatible with the order defined by ordering the modifications first by chromosome, then by strand, then by start, and finally by end.

**Value**

a EpiTxDb object.

**See Also**

- [makeEpiTxDbFromGRanges](#) for creating a EpiTxDb object from a [GRanges](#) object and its metadata columns
- [makeEpiTxDbFromRMBase](#) for creating a EpiTxDb object from RMBase online resources
- [makeEpiTxDbFromtRNADB](#) for creating a EpiTxDb object from tRNADB online resources
- [shortName](#) and [ModRNAStrng](#) for information on ModRNAStrng objects.

**Examples**

```

mod <- data.frame("mod_id" = 1L,
                  "mod_type" = "m1A",
                  "mod_name" = "m1A_1",
                  "mod_start" = 1L,
                  "mod_end" = 1L,
                  "mod_strand" = "+",
                  "sn_id" = 1L,
                  "sn_name" = "test")
rx <- data.frame(mod_id = 1L,
                 rx_genename = "test",
                 rx_rank = 1L,
                 rx_ensembl = "test",
                 rx_ensembltrans = "test",
                 rx_entrezid = "test")
spec <- data.frame(mod_id = 1L,
                   spec_type = "test",
                   spec_genename = "test",
                   spec_ensembl = "test",
                   spec_ensembltrans = "test",
                   spec_entrezid = "test")
ref <- data.frame(mod_id = 1L,
                  ref_type = "test",
                  ref = "test")
etdb <- makeEpiTxDb(mod,rx,spec,ref)

```

---

makeEpiTxDbFromGRanges

*Create a EpiTxDb object from a GRanges object*

---

**Description**

makeEpiTxDbFromGRanges extracts informations from a [GRanges](#) object. The following metadata columns can be used:

- mod\_id, mod\_type, mod\_name and tx\_ensembl. The first three are mandatory, whereas tx\_ensembl is optional.
- rx\_genename, rx\_rank, rx\_ensembl, rx\_ensembltrans and rx\_entrezid
- spec\_type, spec\_genename, spec\_ensembl, spec\_ensembltrans and spec\_entrezid
- ref\_type and ref

... and passed on the [makeEpiTxDb](#).

**Usage**

```
makeEpiTxDbFromGRanges(gr, metadata = NULL, reassign.ids = FALSE)
```

**Arguments**

gr	A <a href="#">GRanges</a> object, which contains at least the mandatory columns.
metadata	A 2-column data.frame containing meta information to be included in the EpiTxDb object. This data.frame is just passed to <a href="#">makeEpiTxDb</a> . See <a href="#">makeEpiTxDb</a> for more information about the format of metadata. (default: metadata = NULL)
reassign.ids	= FALSE

**Value**

a EpiTxDb object.

**Examples**

```
library(GenomicRanges)
gr <- GRanges(seqnames = "test",
              ranges = IRanges::IRanges(1,1),
              strand = "+",
              DataFrame(mod_id = 1L,
                       mod_type = "Am",
                       mod_name = "Am_1"))
etdb <- makeEpiTxDbFromGRanges(gr)
```

---

makeEpiTxDbFromRMBase *Create a EpiTxDb object from RMBase v2.0 online resources*

---

**Description**

makeEpiTxDbFromRMBase will make use of the RMBase v2.0 online resources.

**Usage**

EPITXDB\_RMBASE\_URL

downloadRMBaseFiles(organism, genome, modtype)

```
makeEpiTxDbFromRMBase(
  organism,
  genome,
  modtype,
  tx = NULL,
  sequences = NULL,
  metadata = NULL,
  reassign.ids = FALSE,
  verbose = FALSE
)
```

getRMBaseDataAsGRanges(files, verbose = FALSE)

```
makeEpiTxDbFromRMBaseFiles(
  files,
  tx = NULL,
  sequences = NULL,
  metadata = NULL,
  reassign.ids = FALSE,
  verbose = FALSE
)
```

listAvailableOrganismsFromRMBase()



```
listAvailableGenomesFromRMBase(organism)
```

```
listAvailableModFromRMBase(organism, genome)
```

### Arguments

organism	A character value, which must match an organism descriptor on the RMBase download website.
genome	A character value, which must match a genome descriptor on the RMBase download website.
modtype	A character value, which must match one or more modification descriptors on the RMBase download website.
tx	A <a href="#">GRangesList</a> object which will be used to shift the genomic coordinates to transcript coordinates. This is optional, but highly recommended. (default: tx = NULL).
sequences	A named <a href="#">DNAStringSet</a> or <a href="#">RNAStringSet</a> , which will be used to check whether the defined modifications are compatible with the original base. This uses <a href="#">removeIncompatibleModi</a> function from the <a href="#">Modstrings</a> package.
metadata, reassign.ids	See <a href="#">makeEpiTxDb</a>
verbose	TRUE or FALSE: Should verbose message be printed?
files	From organism, genome and modtype the available files will be downloaded using the <a href="#">BiocFileCache</a> interface and passed on to <a href="#">makeEpiTxDbFromRMBaseFiles</a> . However, individual files can be provided as well.

### Format

An object of class character of length 1.

### Value

a EpiTxDb object.

---

`makeEpiTxDbFromtRNAdb` *Create a EpiTxDb object from tRNAdb resources*

---

### Description

`makeEpiTxDbFromtRNAdb` will make use of the tRNAdb online resources and extract the modification information from the RNA database.

If a named [DNAStringSet](#) is provided as sequences, the result from the tRNAdb will be matched against the sequences. Valid matches will be used as transcript identifiers and returned after a check of modification compatibility with the provided sequence. By this process multiple copies of transcripts can be associated with a single modification.

`makeEpiTxDbFromtRNAdb` uses the functions provided by the [tRNAdbImport](#) package. `import.tRNAdb` will be used with `database = "RNA"` and the three different values for `origin`.

**Usage**

```

gettRNAdbDataAsGRanges(
  organism,
  sequences = NULL,
  dbURL = tRNAdbImport::TRNA_DB_URL
)

makeEpiTxDbFromtRNAdb(
  organism,
  sequences = NULL,
  metadata = NULL,
  dbURL = tRNAdbImport::TRNA_DB_URL
)

listAvailableOrganismsFromtRNAdb()

```

**Arguments**

organism	A character value for an organism available on the tRNAdb website.
sequences	A named DNASTringSet or RNASTringSet, which will be used to associate a tRNAdb result with a specific transcript.
dbURL	The URL to the tRNA db website.
metadata	See <a href="#">makeEpiTxDb</a>

**Value**

a EpiTxDb object.

**References**

Juehling F, Moerl M, Hartmann RK, Sprinzl M, Stadler PF, Puetz J. 2009. "tRNAdb 2009: compilation of tRNA sequences and tRNA genes." *Nucleic Acids Research*, Volume 37 (suppl\_1): D159–162. doi:10.1093/nar/gkn772.

**Examples**

```

## Not run:
# getting just the annotation data
etdb <- makeEpiTxDbFromtRNAdb("Saccharomyces cerevisiae")

# For associating the result with transcripts, provide and additional
# named DNASTringSet object. Matching will be done against each sequence
# allowing 5 mismatches and indels. The final result will be checked for
# validity regarding the identity of the modifications
etdb <- makeEpiTxDbFromtRNAdb("Saccharomyces cerevisiae",
                             some_transcript_sequences)

## End(Not run)

```

---

modifications

*Getting modification data from a EpiTxDb-object*

---

## Description

modifications and modificationsBy are functions to extract modification annotation from a [EpiTxDb](#) object.

modifiedSeqsByTranscript returns a [ModRNAStringSet](#) from a EpiTxDb object and compatible RNAStringSet object. This used the [combineIntoModstrings\(\)](#) function from the Modstrings package.

## Usage

```
modifications(  
  x,  
  columns = c("mod_id", "mod_type", "mod_name"),  
  filter = NULL,  
  use.names = FALSE,  
  ...  
)  
  
modificationsBy(  
  x,  
  by = c("seqnames", "mod_type", "reaction", "specifier", "specifier_type"),  
  ...  
)  
  
modifiedSeqsByTranscript(x, sequences, ...)  
  
## S4 method for signature 'EpiTxDb'  
modifications(  
  x,  
  columns = c("mod_id", "mod_type", "mod_name"),  
  filter = NULL,  
  use.names = FALSE  
)  
  
## S4 method for signature 'EpiTxDb'  
modificationsBy(  
  x,  
  by = c("seqnames", "modtype", "reaction", "specifier", "specifiertype")  
)  
  
## S4 method for signature 'EpiTxDb,DNAStringSet'  
modifiedSeqsByTranscript(x, sequences)
```

## Arguments

x a [EpiTxDb](#)

columns	Columns to include in the result. If the vector is named, those names are used for the corresponding column in the element metadata of the returned object. (default: columns = c("mod_id", "mod_type", "mod_name"))
filter	Either NULL or a named list of vectors to be used to restrict the output. Valid names for this list are: "mod_id", "mod_type", "mod_name", "sn_id", "sn_name", "rx_genename", "rx_ensembl", "rx_ensembltrans", "rx_entrezid", "spec_genename", "spec_type", "spec_ensembl", "spec_ensembltrans", "spec_entrezid", "ref_type" and "ref". (default: filter = NULL)
use.names	TRUE or FALSE. If TRUE, the modification names are set as the names of the returned object. (default: use.names = FALSE)
...	Not used.
by	By which information type should the result be split into? A character value from one of the following values: <ul style="list-style-type: none"> <li>• seqnames</li> <li>• mod_type</li> <li>• reaction</li> <li>• specifier</li> <li>• specifier_type</li> </ul>
sequences	A RNAStringSet, which can be used as input for <code>combineIntoModstrings()</code> . See <code>?combineIntoModstrings</code> for additional details.

**Value**

a `GRanges` object for modifications and a `GRangesList` for modificationsBy.

**Examples**

```
etdb_file <- system.file("extdata", "EpiTxDb.Hs.hg38.snoRNADB.sqlite",
                        package="EpiTxDb")
etdb <- loadDb(etdb_file)
etdb
```

---

positionSequence      *Generate integer sequences from position information of Ranges*

---

**Description**

positionSequence generates sequences of integer values along the range information of x. This can be used for navigating specific positions on a range information.

**Usage**

```
positionSequence(x, order = FALSE, decreasing = FALSE)

## S4 method for signature 'Ranges'
positionSequence(x, order = FALSE, decreasing = FALSE)

## S4 method for signature 'RangesList'
positionSequence(x, order = FALSE, decreasing = FALSE)

## S4 method for signature 'Ranges'
as.integer(x)
```

**Arguments**

x	a Ranges object, like a <a href="#">GRanges</a> or <a href="#">IRanges</a> , or a RangesList object, like a <a href="#">GRangesList</a> or <a href="#">IRangesList</a>
order	TRUE or FALSE: Should the position be ordered? (default: order = FALSE)
decreasing	TRUE or FALSE: If order = TRUE Should the position be ordered in a decreasing order? (default: order = FALSE)

**Value**

a integer vector if x is a [GRanges](#) object and a IntegerList if x is a [GRangesList](#)

**Examples**

```
library(GenomicRanges)
# Returns an integer vector
gr <- GRanges("chr1:1-5:+")
positionSequence(gr)
gr2 <- GRanges("chr1:1-5:-")
positionSequence(gr)
# returns an IntegerList
grl <- GRangesList("1" = gr,"2" = gr,"3" = gr2) # must be named
positionSequence(grl)
```

rescale

*Rescaling Ranges object***Description**

rescale() rescales IRanges, GRanges, IRangesList and GRangesList by using minima and maxima derived from to and from.

**Usage**

```
rescale(x, to = 1L, from = 1L)

## S4 method for signature 'IRanges'
rescale(x, to = 1L, from = 1L)

## S4 method for signature 'IRangesList'
rescale(x, to = 1L, from = 1L)

## S4 method for signature 'GRanges'
rescale(x, to = 1L, from = 1L)

## S4 method for signature 'GRangesList'
rescale(x, to = 1L, from = 1L)
```

**Arguments**

x	a IRanges, GRanges, IRangesList and GRangesList object
to, from	an IRanges object, a character vector coercible to IRanges or a integer vector parallel to x or with length = 1L.

**Value**

an object of the same type and dimensions as `x`

**Author(s)**

H. Pagès, F. Ernst

**See Also**

[IRanges](#) for details on character vectors coercible to `IRanges`.

**Examples**

```
x <- IRanges("5-10")
# widen the ranges
rescale(x, 100, 10)
# widen and shift
rescale(x, "31-60", "5-14")
```

---

select

*Using the "select" interface on EpiTxDb objects*

---

**Description**

As expected for a `AnnotationDb` object, the general accessors `select`, `keys`, `columns` and `keytypes` can be used to get information from a [EpiTxDb](#) object.

**Usage**

```
## S4 method for signature 'EpiTxDb'
select(x, keys, columns, keytype, ...)

## S4 method for signature 'EpiTxDb'
columns(x)

## S4 method for signature 'EpiTxDb'
keys(x, keytype, ...)

## S4 method for signature 'EpiTxDb'
keytypes(x)
```

**Arguments**

`x` a [EpiTxDb](#) object  
`keys, columns, keytype, ...`  
 See [AnnotationDb](#) for more comprehensive description of the methods `select`, `keys`, `columns` and `keytypes` and their arguments.

**Value**

a `data.frame` object for `select()` and a character vector for `keytypes()`, `keys()` and `columns()`.

**Examples**

```
etdb_file <- system.file("extdata", "EpiTxDb.Hs.hg38.snoRNADB.sqlite",
                        package="EpiTxDb")
etdb <- loadDb(etdb_file)
etdb
```

---

```
shiftTranscriptToGenomic
```

*Shift GRanges coordinates based on another GRanges object*

---

**Description**

shiftGenomicToTranscript shifts positions of a [GRanges](#) object based on coordinates of another [GRanges](#) object. The most common application is to shift genomic coordinates to transcript coordinates, which is reflected in the name. shiftTranscriptToGenomic implements the reverse operation.

Matches are determined by [findOverlaps](#) for shiftGenomicToTranscript and by [findMatches](#) for shiftTranscriptToGenomic using the seqnames of the subject and the names of tx.

**Usage**

```
shiftTranscriptToGenomic(subject, tx)

shiftGenomicToTranscript(subject, tx)

## S4 method for signature 'GRanges,GRangesList'
shiftTranscriptToGenomic(subject, tx)

## S4 method for signature 'GRangesList,GRangesList'
shiftTranscriptToGenomic(subject, tx)

## S4 method for signature 'GRanges,GRangesList'
shiftGenomicToTranscript(subject, tx)

## S4 method for signature 'GRangesList,GRangesList'
shiftGenomicToTranscript(subject, tx)
```

**Arguments**

subject            a [GRanges](#) or [GRangesList](#) object  
tx                    a named [GRangesList](#) object.

**Value**

a [GRanges](#) or [GRangesList](#) object depending on the type of subject

**Examples**

```
library(GenomicRanges)
# Construct some example data
subject1 <- GRanges("chr1", IRanges(3, 6),
                    strand = "+")
subject2 <- GRanges("chr1", IRanges(c(17,23), width=3),
                    strand = c("+","-"))
subject3 <- GRanges("chr2", IRanges(c(51, 54), c(53, 59)),
                    strand = "-")
subject <- GRangesList(a=subject1, b=subject2, c=subject3)
tx1 <- GRanges("chr1", IRanges(1, 40),
               strand="+")
tx2 <- GRanges("chr1", IRanges(10, 30),
               strand="+")
tx3 <- GRanges("chr2", IRanges(50, 60),
               strand="-")
tx <- GRangesList(a=tx1, b=tx2, c=tx3)

# shift to transcript coordinates. Since the third subject does not have
# a match in tx it is dropped with a warning
shifted_gr1 <- shiftGenomicToTranscript(subject,tx)

# ... and back
shifted_gr12 <- shiftTranscriptToGenomic(shifted_gr1,tx)

# comparison of ranges work. However the seqlevels differ
ranges(shifted_gr12) == ranges(subject[[list(1,c(1,1),c(1,2))]])
```



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