Package 'DNAfusion'

April 10, 2023

Title Identification of gene fusions using paired-end sequencing

Version 1.0.0

biocViews TargetedResequencing, Genetics, GeneFusionDetection, Sequencing

Description Paired-end sequencing of cfDNA generated BAM files can be used as input to discover EML4-ALK variants. This package was developed using position deduplicated BAM files generated with the AVENIO Oncology Analysis Software. These files are made using the AVENIO ctDNA surveillance kit and Illumina Nextseq 500 sequencing. This is a targeted hybridization NGS approach and includes ALK-specific but not EML4-specific probes.

License GPL-3

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.1

Suggests knitr, rmarkdown, testthat, sessioninfo, BiocStyle,

VignetteBuilder knitr

Imports bamsignals, GenomicRanges, IRanges, Rsamtools, GenomicAlignments, BiocBaseUtils, S4Vectors

Depends R (>= 4.2.0)

BugReports https://github.com/CTrierMaansson/DNAfusion/issues

URL https://github.com/CTrierMaansson/DNAfusion

git_url https://git.bioconductor.org/packages/DNAfusion

git_branch RELEASE_3_16

git_last_commit 163dcf2

git_last_commit_date 2022-11-01

Date/Publication 2023-04-10

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`ALK_sequence` *Identification of ALK breakpoint bases*

Description

This function identifies the basepairs following the ALK breakpoint.

Usage

```
ALK_sequence(reads, basepairs = 20)
```

Arguments

`reads`	`GAlignments` returned by `EML4_ALK_detection()`.
`basepairs`	`integer`, number of basepairs identified from the EML4-ALK fusion. Default=20.

Value

If EML4-ALK is detected, returns a `table` of identified ALK basepairs with the number of corresponding reads for each sequence. If no EML4-ALK is detected "No EML4-ALK was detected" is returned.

Examples

```
H3122_bam <- system.file("extdata",
"H3122_EML4.bam",
package="DNAfusion")
HCC827_bam <-  system.file("extdata",
"HCC827_EML4.bam",
package="DNAfusion")

ALK_sequence(EML4_ALK_detection(file=H3122_bam,
                                genome="hg38",
                                mates=2),
```

```
                basepairs=20)
ALK_sequence(EML4_ALK_detection(file=HCC827_bam,
                                genome="hg38",
                                mates=2),
                basepairs=20)
```

`break_position` *EML4-ALK breakpoint*

Description

This function identifies the genomic position in EML4 where the breakpoint has happened.

Usage

```
break_position(reads)
```

Arguments

`reads`	`GAlignments` object returned by `EML4_ALK_detection()`.

Value

If EML4-ALK is detected, returns a `table` of genomic positions with the number of corresponding reads for each sequence. If no EML4-ALK is detected "No EML4-ALK was detected" is returned.

Examples

```
H3122_bam <- system.file("extdata",
"H3122_EML4.bam",
package="DNAfusion")
HCC827_bam <-  system.file("extdata",
"HCC827_EML4.bam",
package="DNAfusion")

break_position(EML4_ALK_detection(file=H3122_bam,
                                  genome="hg38",
                                  mates=2))
break_position(EML4_ALK_detection(file=HCC827_bam,
                                  genome="hg38",
                                  mates=2))
```

break_position_depth *Read depth at breakpoint*

Description

This function identifies the read depth at the basepair before the breakpoint in EML4.

Usage

```
break_position_depth(file, reads)
```

Arguments

file	The name of the file which the data are to be read from.
reads	GAlignments object returned by EML4_ALK_detection().

Value

If EML4-ALK is detected a single integer corresponding to the read depth at the breakpoint is returned. If no EML4-ALK is detected "No EML4-ALK was detected" is returned.

Examples

```
H3122_bam <- system.file("extdata",
"H3122_EML4.bam",
package="DNAfusion")
HCC827_bam <-  system.file("extdata",
"HCC827_EML4.bam",
package="DNAfusion")

break_position_depth(file=H3122_bam,
                        EML4_ALK_detection(file=H3122_bam,
                                           genome="hg38",
                                           mates=2))
break_position_depth(file=HCC827_bam,
                        EML4_ALK_detection(file=HCC827_bam,
                                           genome="hg38",
                                           mates=2))
```

EML4_ALK_analysis *Complete EML4-ALK analysis*

Description

This functions collects the results from the other functions of the package.

Usage

```
EML4_ALK_analysis(file, genome = "hg38", mates = 2, basepairs = 20)
```

Arguments

file	The name of the file which the data are to be read from.
genome	character representing the reference genome. Can be either "hg38" or "hg19". Default="hg38".
mates	interger, the minimum number EML4-ALK mate pairs needed to be detected in order to call a variant. Default=2.
basepairs	integer, number of basepairs identified from the EML4-ALK fusion. Default=20.

Value

A list object with clipped_reads corresponding to EML4_ALK_detection(), last_EML4 corresponding to EML4_sequence(), first_ALK corresponding to ALK_sequence(), breakpoint corresponding to break_position(), and read_depth corresponding to break_position_depth(). If no EML4-ALK is detected an empty GAlignments is returned.

Examples

```
H3122_bam <- system.file("extdata",
"H3122_EML4.bam",
package="DNAfusion")
HCC827_bam <-  system.file("extdata",
"HCC827_EML4.bam",
package="DNAfusion")

EML4_ALK_analysis(file=H3122_bam,
                    genome="hg38",
                    mates=2,
                    basepairs=20)
EML4_ALK_analysis(file=HCC827_bam,
                    genome="hg38",
                    mates=2,
                    basepairs=20)
```

EML4_ALK_detection *Detection of EML4-ALK variants*

Description

This function looks for EML4-ALK mate pair reads in the BAM file.

Usage

```
EML4_ALK_detection(file, genome = "hg38", mates = 2)
```

Arguments

file	The name of the file which the data are to be read from.
genome	Character string representing the reference genome. Can be either "hg38" or "hg19". Default="hg38".
mates	Interger, the minimum number EML4-ALK mate pairs needed to be detected in order to call a variant. Default=2.

Value

A GAlignments object with soft-clipped reads representing EML4-ALK is returned. If no EML4-ALK is detected the GAlignments is empty.

Examples

```
H3122_bam <- system.file("extdata",
"H3122_EML4.bam",
package="DNAfusion")
HCC827_bam <-  system.file("extdata",
"HCC827_EML4.bam",
package="DNAfusion")

EML4_ALK_detection(file=H3122_bam,
                   genome="hg38",
                   mates=2)
EML4_ALK_detection(file=HCC827_bam,
                   genome="hg38",
                   mates=2)
```

EML4_sequence *Identification of EML4 breakpoint bases*

Description

This function identifies the basepairs leading up to the EML4 breakpoint.

Usage

```
EML4_sequence(reads, basepairs = 20)
```

Arguments

reads	GAlignments object returned by EML4_ALK_detection().
basepairs	Integer, number of basepairs identified from the EML4-ALK fusion. Default=20.

Value

If EML4-ALK is detected, returns a table of identified EML4 basepairs with the number of corresponding reads for each sequence. If no EML4-ALK is detected "No EML4-ALK was detected" is returned.

Examples

```
H3122_bam <- system.file("extdata",
"H3122_EML4.bam",
package="DNAfusion")
HCC827_bam <-  system.file("extdata",
"HCC827_EML4.bam",
package="DNAfusion")

EML4_sequence(EML4_ALK_detection(file=H3122_bam,
                                 genome="hg38",
                                 mates=2),
              basepairs=20)
EML4_sequence(EML4_ALK_detection(file=HCC827_bam,
                                 genome="hg38",
                                 mates=2),
              basepairs=20)
```

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