Package 'scMitoTracing'

January 8, 2022

Title What the Package Does (One Line, Title Case)

Version 0.0.0.9000

Description What the package does (one paragraph).

License `use_mit_license()`, `use_gpl3_license()` or friends to pick a license

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2

Suggests knitr, rmarkdown

VignetteBuilder knitr

Depends R (>= 2.10)

LazyData true

R topics documented:

`CW_mgatk.read` *Function to read in mitoV outputs*

Description

This function allows you to read raw data from XX/final folder, the output from mitoV

Usage

```
CW_mgatk.read(path, Processed = F)
```

Arguments

path	The XX/final folder, the output from mitoV
Processed	Boolean variable (Default F), if true directly readRDS("VariantsGTSummary.RDS") or, generate and saveout "VariantsGTSummary.RDS"

Value

this returns depth which is a list of 4 df (Total/VerySensitive/Sensitive/Specific), each is a genotype summary

Examples

```
WD<-"/lab/solexa_weissman/cweng/Projects/MitoTracing_Velocity/SecondaryAnalysis/Donor01_C
DN1CD34_1.VariantsGTSummary<-CW_mgatk.read(WD,Processed =T)
```

DepthSummary *Function to summarize the depth (Total that passed Q30)*

Description

This function allows you to summarize the depth

Usage

```
DepthSummary(path, Processed = T)
```

Arguments

path	The XX/final folder, the output from mitoV
Processed	Boolean variable(Default T), if true directly readRDS("depth.RDS") or, generate and saveout "depth.RDS"

Value

this returns depth which is a list of 4 list(Total/VerySensitive/Sensitive/Specific), each contains 2 df, summarize mito coverage by Pos/Cell

Examples

```
WD<-"/lab/solexa_weissman/cweng/Projects/MitoTracing_Velocity/SecondaryAnalysis/Donor01_C
DN1CD34_1.depth<-DepthSummary(WD,Processed = T)
```

GTSummary *Function to generate GTS summary*

Description

This function allows you to summarize the meta data for each genotyped variant

Usage

```
GTSummary(RawGenotypes, filterN = T)
```

Arguments

RawGenotypes	Well-named "RawGenotypes.Sensitive.StrandBalance" file in function CW_mgatk.read
filterN	Boolean variable, if true filter out the variant with "N"

Value

Genotypes.summary a dataframe that summarize several metrics for each genotype

Examples

```
Usually used inside of function CW_mgatk.read
```

MutationProfile.bulk *Function to plot bulk level mutation signatures*

Description

This function allows you to plot the mito mutation signatures

Usage

```
MutationProfile.bulk(cell_variants)
```

Arguments

cell_variants	a vector of variants formated as c('93_A_G"103_G_A"146_T_C'

Value

p from ggplot2

Examples

```
MutationProfile.bulk(DN1CD34_1.Variants.feature.lst[[name]]$Variants
```

plot_depth *Function to plot the mito depth summary*

Description

This function allows you to plot both position-wise and cell-wise mito depth summary

Usage

```
plot_depth(depth = DN1CD34_1.depth, name = "", w = 10, h = 3)
```

Arguments

depth	The .depth file by function DepthSummary
name	The plot name shown on top
w	the Width of the plot, default=10
h	the height of the plot default=3

Value

directly out put the plot

Examples

```
plot_depth(DN1CD34_1.depth$Total,"Total")
```

Vfilter_v3 *Function to filter variants*

Description

This function allows you to filter variants

Usage

```
Vfilter_v3(
  InputSummary,
  depth,
  Rmvhomo = F,
  Min_Cells = 2,
  Max_Count_perCell = 2,
  QualifyCellCut = 10
)
```

Arguments

InputSummary	The GTSummary file read in by function CW_mgatk.read
depth	The .depth file by function DepthSummary
Rmvhomo	Boolean (Default F) If true, remove the homozygous variants
Min_Cells	Default 2, A qualified variant needs the minimum number of cells that have this variant
Max_Count_perCell	Default 2, A qualified variant needs to show at least 2 counts in one cell
QualifyCellCut	Default 10, Minimum depth for a qualified cell

Value

this returns feature.list

Examples

```
plot_variant(DN1CD34_1.VariantsGTSummary,DN1CD34_1.Variants.feature.lst,depth=DN1CD34_1.d
c("Total","VerySensitive","Sensitive","Specific"),p4xlim = 30)
```

Index