Package 'Meth27QC'

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Type Package

Title Meth27QC: sample quality analysis, and sample control analysis

Version 1.1

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Description Meth27QC is a tool for analyzing Illumina Infinium
HumanMethylation27 BeadChip Data and generating QC reports.
This package allows users quickly assess data quality of the
Assay. Users can evaluate the data quality in the way that
Illumina GenomeStudio/BeadStudio recommended based on the
control probes. The package reads files exported from
GenomeStudio/BeadStudio software, generating intensity and
standard deviation plots grouped by the types of the control
probes. Meth27 carries 40 control probes for staining,
hybridization, target removal, extension, bisulfite conversion,
specificity, negative and non-polymorphic controls. Details of
those control probes can be found in the Infinium Assay for
Methylation Protocol Guide from Illumina.We also used the other
non-control probes to plot intensity of detected genes, signal
average for green and red. Outliers can be identified.

Depends gplots,tcltk

License GPL-2

Repository CRAN

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NeedsCompilation no

R topics documented:

Meth27QC	*Generate a subdirectory,which is composed of QC Reports for Illuminas Infinium HumanMethylation27 BeadChip methylation assay*

Description

Meth27QC is a tool analyzing Illumina Infinium HumanMethylation27 BeadChip Data and generating QC reports. This package allows users quickly assess data quality of the Assay. Users can evaluate the data quality in the way that Illumina GenomeStudio/BeadStudio recommended based on the control probes. The package reads files exported from GenomeStudio/BeadStudio software, generating intensity and standard deviation plots grouped by the types of the control probes. Meth27 carries 40 control probes for staining, hybridization, target removal, extension, bisulfite conversion, specificity, negative and non-polymorphic controls. Details of those control probes can be found in the Infinium Assay for Methylation Protocol Guide from Illumina. We also used the other non-control probes to plot intensity of detected genes, signal average for green and red. Outliers can be identified.

Usage

```
Meth27QC(Dir,controlfile,sampfile)
```

Arguments

Dir	directory path where the control profile and sample file are included
controlfile	control probe file name,exported from BeadStudio/GenomeStudio
sampfile	sample table file name,exported from BeadStudio/GenomeStudio

Author(s)

ling teng,chao chen, chunyu liu

References

R core development. "Writing R Extentions". 2007.

QCRep	*Generate a subdirectory,which is composed of QC Reports for Illuminas Infinium HumanMethylation27 BeadChip methylation assay*

Description

QCRep is a subfunction in the main function Meth27QC

Usage

```
QCRep(Dir,controlfile,sampfile)
```

Arguments

`Dir`	directory path where the control profile and sample file are included
`controlfile`	control probe file name,exported from BeadStudio/GenomeStudio
`sampfile`	sample table file name,exported from BeadStudio/GenomeStudio

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