

# Package: basecallQC (via r-universe)

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**Type** Package

**Title** Working with Illumina Basecalling and Demultiplexing input and output files

**Version** 1.29.0

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**Description** The basecallQC package provides tools to work with Illumina bcl2Fastq (versions  $\geq 2.1.7$ ) software. Prior to basecalling and demultiplexing using the bcl2Fastq software, basecallQC functions allow the user to update Illumina sample sheets from versions  $\leq 1.8.9$  to  $\geq 2.1.7$  standards, clean sample sheets of common problems such as invalid sample names and IDs, create read and index basemasks and the bcl2Fastq command. Following the generation of basecalled and demultiplexed data, the basecallQC packages allows the user to generate HTML tables, plots and a self contained report of summary metrics from Illumina XML output files.

**LazyData** TRUE

**biocViews** Sequencing, Infrastructure, DataImport, QualityControl

**License** GPL ( $\geq 3$ )

**Depends** R ( $\geq 3.4$ ), stats, utils, methods, rmarkdown, knitr, prettydoc, yaml

**Imports** ggplot2, stringr, XML, raster, dplyr, data.table, tidyr, magrittr, DT, lazyeval, ShortRead

**Suggests** testthat, BiocStyle

**VignetteBuilder** knitr

**SystemRequirements** bcl2Fastq (versions  $\geq 2.1.7$ )

**Collate** processIlluminaSamplesheets\_Functions.R  
processXMLs\_Functions.R allClasses.R allMethods.R  
processExternalFormats\_Functions.R plots.R reporting.R tables.R  
FastQCShortRead\_Functions.R processInterOps\_Functions.R

**RoxygenNote** 7.1.0

**Repository** <https://bioc.r-universe.dev>

**RemoteUrl** <https://github.com/bioc/basecallQC>

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baseCallMetrics	<i>Gather basecalling metrics from a Run (using Run's ConversionStats.xml file).</i>
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### Description

Gather basecalling metrics from a Run (using Run's ConversionStats.xml file).

### Usage

```
baseCallMetrics(bcl2fastqparams)
```

### Arguments

bcl2fastqparams

A BCL2FastQparams object as created by BCL2FastQparams() constructor.

**Value**

A list of length two containing the full basecalling metrics from a Run (using Run's Conversion-Stats.xml file). Contains an unsummarised data.frame and basecalling metrics summarised to Sample, Lane, Sample by lane, and Sample by Lane and Tile.

**Examples**

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)
convMetrics <- baseCallMetrics(bcl2fastqparams)
```

---

basecallQC-class      *The basecallQC object and constructor.*

---

**Description**

Object and method to handle Illumina basecalling/demultiplexing inputs and output files. Provides sample sheet cleanup, basecall command and summary QC statistics for basecalling/demultiplexing.

The basecallQC object and constructor.

**Usage**

```
basecallQC(bcl2fastqparams, RunMetaData = NULL, sampleSheet = NULL,
  doFQMetric = FALSE)
```

**Arguments**

bcl2fastqparams	A BCL2FastQparams object as created by BCL2FastQparams() constructor.
RunMetaData	Any run metadata to attach (data.frame)
sampleSheet	A sample sheet for Illumina basecalling using bcl2Fastq (See vignette for more details).
doFQMetric	TRUE or FALSE. Perform ShortRead FastQ quality assessment using Short-Read's qa and report function

**Details**

The basecallQC object contains slots BCL2FastQparams, cleanedSampleSheet, baseMasks, BCLCommand, baseCallMetrics, demultiplexMetrics and fqQCmetrics.

- "BCL2FastQparams" A BCL2FastQparams object
- "cleanedSampleSheet" A data.frame containing the cleaned sample sheet for Illumina basecalling using bcl2Fastq versions >= 2.1.7

- "baseMasks" A data.frame containing basecall masks per lane for use with bcl2Fastq versions >= 2.1.7. Basemasks in data.frame for reads and indexes as well as the total basemasks for each lane.
- "BCLCommand" A character string containing the command to be used for basecalling using bcl2Fastq (versions >= 2.1.7).
- "baseCallMetrics" A list containing the full basecalling metrics from ConversionStats.xml. Contains an unsummarised data.frame and basecalling metrics summarised to Sample, Lane, Sample by lane, and Sample by Lane and Tile
- "demultiplexMetrics" A list containing the full demultiplexing metrics from DemultiplexingStats.xml. Contains an unsummarised data.frame and demultiplexing metrics filtered to per Sample metrics
- "fqQCmetrics" A list containing a data.frame of read counts and links to ShortRead QA reports and a ShortRead QA object containing quality information for generated fastQs.

### Value

basecallQC a basecallQC object (See details for more information)

### Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)
bclQC <- basecallQC(bcl2fastqparams,RunMetaData=NULL,sampleSheet)
```

---

BCL2FastQparams-class *The Parameters for BCL2FastQparams object.*

---

### Description

Parameter class and accessors for use with basecallQC

Parameter class and accessors

### Usage

```
BCL2FastQparams(runXML = NULL, config = NULL, runDir = NULL,
  outDir = NULL, verbose = TRUE)
```

### Arguments

runXML	file path to runParameters.xml ,if not specified looks in top level of run directory.
config	file path to config.ini ,if not specified looks in top level of run directory.
runDir	file path to run directory.
outDir	file path to out directory.
verbose	TRUE or FALSE. Messages on or off. Warnings/errors persist

**Details**

The BCL2FastQparams object contains slots RunDir, OutDir and RunParameters

- "RunDir" Character string specifying the top level Run directory
- "OutDir" Character string specifying the output directory
- "RunParameters" A data.frame containing the information from runParameters.xml (See vignette for more details).

**Value**

A BCL2FastQparams object (See details).

**Examples**

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
BCL2FastQparams(runXML,config,runDir=getwd(),verbose=FALSE)
```

---

createBasemasks	<i>Function to create basemasks for basecalling from Illumina samplesheet (for bcl2Fastq versions &gt;= 2.1.7).</i>
-----------------	---

---

**Description**

Parses the Illumina sample sheet for versions >= 2.1.7 and creates basemasks.

**Usage**

```
createBasemasks(cleanedSampleSheet, param)
```

**Arguments**

cleanedSampleSheet	Data.frame of cleaned samplesheet for Illumina basecalling using bcl2Fastq versions >= 2.1.7 (see vignette for more details)
param	A BCL2FastQparams object

**Value**

A data.frame containing basecall masks per lane for reads and indexes as well as per lane complete basemasks.

**Author(s)**

Thomas Carroll and Marian Dore

## Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),verbose=FALSE)

cleanedSampleSheet <- validateBCLSheet(sampleSheet,param=bcl2fastqparams)
basemasks <- createBasemasks(cleanedSampleSheet,param=bcl2fastqparams)
```

---

createBCLcommand	<i>Function to create command for Illumina basecalling/demultiplexing using bcl2fastq versions &gt;= 2.1.7.</i>
------------------	---

---

## Description

Creates the command to be used for basecalling/demultiplexing with bcl2fastq versions >= 2.1.7

## Usage

```
createBCLcommand(bcl2fastqparams, cleanedSampleSheet, baseMasks)
```

## Arguments

bcl2fastqparams	A BCL2FastQparams object.
cleanedSampleSheet	Data.frame of cleaned samplesheet for Illumina basecalling/demultiplexing using bcl2fastq versions >= 2.1.7 (see vignette for more details)
baseMasks	A data.frame of basemasks as created by createBasemasks() function

## Value

A character vector containing the command for Illumina basecalling using bcl2fastq versions >= 2.1.7

## Author(s)

Thomas Carroll and Marian Dore

## Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),verbose=FALSE)

cleanedSampleSheet <- validateBCLSheet(sampleSheet,param=bcl2fastqparams)
baseMasks <- createBasemasks(cleanedSampleSheet,param=bcl2fastqparams)
toSubmit <- createBCLcommand(bcl2fastqparams,cleanedSampleSheet,baseMasks)
```

---

demultiplexMetrics	<i>Gather demultiplexing metrics from a Run (using Run's DemultiplexingStats.xml file).</i>
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---

## Description

Gather demultiplexing metrics from a Run (using Run's DemultiplexingStats.xml file).

## Usage

```
demultiplexMetrics(bcl2fastqparams)
```

## Arguments

bcl2fastqparams

A BCL2FastQparams object as created by BCL2FastQparams() constructor.

## Value

A list of length two containing the full demultiplexing metrics from a Run (using Run's DemultiplexingStats.xml file). Contains an unsummarised data.frame and demultiplexing metrics filtered to per Sample metrics

## Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)
demuxMetrics <- demultiplexMetrics(bcl2fastqparams)
```

---

demuxBarplot

*Barplot of Illumina demultiplexing statistics.*

---

## Description

Produces a barplot of demultiplexing statistics of reads with perfect/mismatched barcode.

## Usage

```
## S4 method for signature 'baseCallQC'
demuxBarplot(object,groupBy)

## S4 method for signature 'basecallQC'
demuxBarplot(object = "basecallQC",
             groupBy = c("Lane"))

## S4 method for signature 'list'
demuxBarplot(object = "basecallQC", groupBy = c("Lane"))
```

## Arguments

object	A basecallQC object or list from call to demultiplexMetrics()
groupBy	Character vector of how data is grouped for plotting. Should be either "Project", "Sample" or "Lane".

## Value

A ggplot2 object.

## Author(s)

Thomas Carroll and Marian Dore

## Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)
bclQC <- basecallQC(bcl2fastqparams,RunMetaData=NULL,sampleSheet)
plot <- demuxBarplot(bclQC)
```



---

`demuxBoxplot`*Boxplot of Illumina demultiplexing statistics.*

---

## Description

Produces a boxplot of demultiplexing statistics of reads with perfect/mismatched barcode.

## Usage

```
## S4 method for signature 'baseCallQC'  
demuxBoxplot(object,groupBy)  
  
## S4 method for signature 'basecallQC'  
demuxBoxplot(object = "basecallQC",  
             groupBy = c("Lane"))  
  
## S4 method for signature 'list'  
demuxBoxplot(object = "basecallQC", groupBy = c("Lane"))
```

## Arguments

<code>object</code>	A basecallQC object or list from call to demultiplexMetrics()
<code>groupBy</code>	Character vector of how data is grouped for plotting. Should be either "Project", "Sample" or "Lane".

## Value

A ggplot2 object.

## Author(s)

Thomas Carroll and Marian Dore

## Examples

```
fileLocations <- system.file("extdata",package="basecallQC")  
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)  
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)  
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)  
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")  
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)  
bclQC <- basecallQC(bcl2fastqparams,RunMetaData=NULL,sampleSheet)  
plot <- demuxBoxplot(bclQC)
```

---

indexlengths	<i>Index lengths</i>
--------------	----------------------

---

**Description**

Index lengths as defined by runParameters.xml

**Usage**

```
## S4 method for signature 'BCL2FastQparams'
indexlengths(object)
```

```
## S4 method for signature 'BCL2FastQparams'
indexlengths(object = "BCL2FastQparams")
```

**Arguments**

object            A BCL2FastQparams object

**Value**

Index lengths as defined runParameters.xml.

**Author(s)**

Thomas Carroll

**Examples**

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),verbose=FALSE)
indexlength <- indexlengths(bcl2fastqparams)
```

---

interOpsReport	<i>Function to parse InterOps files and generate summary reports</i>
----------------	--

---

**Description**

Parses the InterOps binary files produced by Illumina's Real Time Analysis software and used by Illumina's SAV software. InterOp binary files contain information on phasing/prephasing, yield, read numbers and basecalling quality score distributions per cycle. This interOpsReport functions parses and summarises the InterOps files, TileMetrics.bin and QMetrics.bin, and the Stats directory XML files, ConversionStats.xml and DemultiplexingStats.xml.

**Usage**

```
interOpsReport(bc12fastqparams, verbose = TRUE)
```

**Arguments**

bc12fastqparams      A BCL2FastQparams object.

verbose              TRUE or FALSE . TRUE reports progress through file parsing.

**Details**

The interOpsReport function returns a list of machine and run information, basecalling quality information and demultiplexing information. The three named elements are described below.

- "machineReport" A data.frame containing information machine and software parameters
- "sequencingReport" A data.frame of mean cluster density, percentage clusters passing filter, phasing and prephasing percentages, number of reads total/passing filter and percent of reads with mean quality score > Q30 grouped by lane and read
- "demuxReport" A data.frame of demultiplexing results containing yield, number of reads, percentage of reads with quality scores greater than >Q30 and the percent of total reads per lane. Results are summarised per lane for samples, underdetermined indexes and all indexes (identified and unidentified).

**Value**

A named list of length 3 containing machine and run information, basecalling quality information and demultiplexing information.

**Author(s)**

Thomas Carroll.

**Examples**

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
bc12fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),verbose=FALSE)

# myRes_BCAGJ8ANXX <- interOpsReport(bc12fastqparams,verbose=TRUE)
```

---

makeFQTable	<i>Generate an HTML table linking to per sample summary fastq QC statistics from ShortRead</i>
-------------	--

---

## Description

Creates an HTML table linking to per sample summary fastq QC statistics from ShortRead

## Usage

```
makeFQTable(object, output = "static")
```

## Arguments

object	A basecall QC object as returned from basecallQC function
output	Whether the report contains frozen or sortable tables. Options are "static" and "html"

## Value

A HTML table for reporting fastq QC results from ShortRead. Table contains read counts and links to ShortRead QA reports per sample.

## Author(s)

Thomas Carroll

## Examples

```
fileLocations <- system.file("extdata", package="basecallQC")
runXML <- dir(fileLocations, pattern="runParameters.xml", full.names=TRUE)
config <- dir(fileLocations, pattern="config.ini", full.names=TRUE)
sampleSheet <- dir(fileLocations, pattern="*\\.csv", full.names=TRUE)
outDir <- file.path(fileLocations, "Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML, config, runDir=getwd(), outDir, verbose=FALSE)
bclQC <- basecallQC(bcl2fastqparams, RunMetaData=NULL, sampleSheet)
#makeFQTable(bclQC, output="static")
```

---

passFilterBar	<i>Barplot of Illumina basecalling statistics for reads passing filter.</i>
---------------	---

---

### Description

Produces a barplot of Illumina basecalling statistics for reads passing filter.

### Usage

```
## S4 method for signature 'baseCallQC'  
passFilterBar(object,groupBy,metricToPlot)  
  
## S4 method for signature 'basecallQC'  
passFilterBar(object = "basecallQC",  
  groupBy = c("Lane"), metricToPlot = "Yield")  
  
## S4 method for signature 'list'  
passFilterBar(object = "basecallQC", groupBy = c("Lane"),  
  metricToPlot = "Yield")
```

### Arguments

object	A basecallQC object or list from call to baseCallMetrics()
groupBy	Character vector of how data is grouped for plotting. Should be either "Project","Sample","Lane","Tile","P
metricToPlot	Character vector defining which metric will be displayed in plot. Should be either "Yield","Yield30","QualityScoreSum" or "ClusterCount".

### Value

A ggplot2 object.

### Author(s)

Thomas Carroll and Marian Dore

### Examples

```
fileLocations <- system.file("extdata",package="basecallQC")  
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)  
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)  
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)  
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")  
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)  
bclQC <- basecallQC(bcl2fastqparams,RunMetaData=NULL,sampleSheet)  
plot <- passFilterBar(bclQC)
```

---

passFilterBoxplot      *Boxplot of Illumina basecalling statistics for reads passing filter.*

---

### Description

Produces a boxplot of basecalling statistics for reads passing filter.

### Usage

```
## S4 method for signature 'baseCallQC'
passFilterBoxplot(object,groupBy,metricToPlot)

## S4 method for signature 'basecallQC'
passFilterBoxplot(object = "basecallQC",
  groupBy = c("Lane"), metricToPlot = "Yield")

## S4 method for signature 'list'
passFilterBoxplot(object = "basecallQC",
  groupBy = c("Lane"), metricToPlot = "Yield")
```

### Arguments

object	A basecallQC object or list from call to baseCallMetrics()
groupBy	Character vector of how data is grouped for plotting. Should be either "Project","Sample","Lane","Tile","TileID"
metricToPlot	Character vector defining which metric will be displayed in plot. Should be either "Yield","Yield30","QualityScoreSum" or "ClusterCount".

### Value

A ggplot2 object.

### Author(s)

Thomas Carroll and Marian Dore

### Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)
bclQC <- basecallQC(bcl2fastqparams,RunMetaData=NULL,sampleSheet)
plot <- passFilterBoxplot(bclQC,groupBy = "Sample")
```

---

passFilterTilePlot      *Tile plot of Illumina basecalling statistics for reads passing filter.*

---

### Description

Produces a plot of metric per Tile for basecalling statistics of reads passing/failing filter.

### Usage

```
## S4 method for signature 'baseCallQC'
passFilterTilePlot(object,metricToPlot)

## S4 method for signature 'basecallQC'
passFilterTilePlot(object = "basecallQC",
  metricToPlot = "Yield")

## S4 method for signature 'list'
passFilterTilePlot(object = "basecallQC",
  metricToPlot = "Yield")
```

### Arguments

**object**            A basecallQC object or list from call to baseCallMetrics()

**metricToPlot**    Character vector defining which metric will be displayed in plot. Should be either "Yield","Yield30","QualityScoreSum" or "ClusterCount".

### Value

A ggplot2 object.

### Author(s)

Thomas Carroll and Marian Dore

### Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)
bclQC <- basecallQC(bcl2fastqparams,RunMetaData=NULL,sampleSheet)
plot <- passFilterTilePlot(bclQC,metricToPlot="Yield")
```

---

readlengths	<i>Read lengths</i>
-------------	---------------------

---

**Description**

Read lengths as defined by runParameters.xml

**Usage**

```
## S4 method for signature 'BCL2FastQparams'
readlengths(object)

## S4 method for signature 'BCL2FastQparams'
readlengths(object = "BCL2FastQparams")
```

**Arguments**

object            A BCL2FastQparams object

**Value**

Read lengths as defined runParameters.xml

**Author(s)**

Thomas Carroll

**Examples**

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),verbose=FALSE)
readlength <- readlengths(bcl2fastqparams)
```

---

reportBCL	<i>Generate basecallQC report</i>
-----------	-----------------------------------

---

**Description**

Creates a summary report from basecalling and demultiplexing metrics.



**Usage**

```
## S4 method for signature 'basecallQC'
reportBCL(object,reportOut,reportOutDir,output,reportRMDfile,FQQC)

## S4 method for signature 'basecallQC'
reportBCL(object = "basecallQC",
  reportOut = "report.html", reportOutDir = getwd(), output = "static",
  reportRMDfile = NULL, FQQC = FALSE)
```

**Arguments**

object	A basecall QC object as returned from basecallQC() function
reportOut	Name of report file
reportOutDir	Directory for the report file
output	Whether the report contains frozen or sortable tables. Options are "static" and "html"
reportRMDfile	RMD to be used for reporting. (Default uses standard report template)
FQQC	TRUE or FALSE, whether to run ShortRead fastq QC on any fastQ in output directory.

**Value**

An HTML report is written to file.

**Author(s)**

Thomas Carroll

**Examples**

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)
bclQC <- basecallQC(bcl2fastqparams,RunMetaData=NULL,sampleSheet)
reportBCL(bclQC,"TestReport.html",output="html")
```

---

summaryConvStatsTable *Creates an HTML table of per sample summary statistics from basecalling results*

---

**Description**

Creates an HTML table of per sample summary statistics from basecalling results

**Usage**

```
## S4 method for signature 'baseCallQC'
summaryConvStatsTable(object)

## S4 method for signature 'basecallQC'
summaryConvStatsTable(object = "basecallQC",
  output = "static")

## S4 method for signature 'list'
summaryConvStatsTable(object = "basecallQC",
  output = "static")
```

**Arguments**

object	A basecallQC object or list from call to baseCallMetrics()
output	Whether the report contains frozen or sortable tables. Options are "static" and "html"

**Value**

An HTML table for reporting basecalling results.

**Author(s)**

Thomas Carroll

**Examples**

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)
bclQC <- basecallQC(bcl2fastqparams,RunMetaData=NULL,sampleSheet)
summaryDemuxTable(bclQC,output="static")
```

---

summaryDemuxTable	<i>Generate an HTML table of per sample summary demultiplexing statistics</i>
-------------------	---

---

**Description**

Generate an HTML table of per sample summary demultiplexing statistics

**Usage**

```
## S4 method for signature 'baseCallQC'
summaryDemuxTable(object)

## S4 method for signature 'basecallQC'
summaryDemuxTable(object = "basecallQC",
  output = "static")

## S4 method for signature 'list'
summaryDemuxTable(object = "basecallQC", output = "static")
```

**Arguments**

object	A basecallQC object or list from call to demultiplexMetrics()
output	Whether the report contains frozen or sortable tables. Options are "static" and "html"

**Value**

An HTML table for reporting demultiplexing results.

**Author(s)**

Thomas Carroll

**Examples**

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)
bclQC <- basecallQC(bcl2fastqparams,RunMetaData=NULL,sampleSheet)
summaryDemuxTable(bclQC,output="static")
```

---

validateBCLSheet	<i>Illumina sample sheet cleaning and updating for bcl2Fastq versions &gt;= 2.1.7</i>
------------------	---

---

**Description**

Parses an Illumina bcl2Fastq sample sheet to create a standardised/updated sample sheet for bcl2Fastq  
 >= Version 2.1.7

**Usage**

```
validateBCLSheet(sampleSheet, param = bcl2fastqparams)
```

**Arguments**

sampleSheet      File location of a sample sheet for Illumina basecalling using bcl2Fastq (See vignette for more details).  
param              A BCL2FastQparams object

**Value**

cleanedSampleSheet A data.frame containing the cleaned sample sheet for Illumina basecalling using bcl2Fastq versions  $\geq 2.1.7$ .

**Author(s)**

Thomas Carroll and Marian Dore

**Examples**

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),verbose=FALSE)
cleanedSampleSheet <- validateBCLSheet(sampleSheet,param=bcl2fastqparams)
```

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