

HTqPCR - high-throughput qPCR analysis in R and Bioconductor

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1 Introduction

The package *HTqPCR* is designed for the analysis of cycle threshold (Ct) values from quantitative real-time PCR data. The main areas of functionality comprise data import, quality assessment, normalisation, data visualisation, and testing for statistical significance in Ct values between different features (genes, miRNAs).

Example data is included from TaqMan Low Density Arrays (TLDA), a proprietary format of Applied Biosystems, Inc. However, most functions can be applied to any kind of qPCR data, regardless of the nature of the experimental samples and whether genes or miRNAs were measured.

```
> library("HTqPCR")
```

The package employs functions from other packages of the Bioconductor project ([Gentleman et al., 2004](#)). Dependencies include *Biobase*, *RColorBrewer*, *limma*, *statmod*, *affy* and *gplots*.

Examples from the vignette

This vignette was developed in Sweave, so the embedded R code was compiled when the PDF was generated, and its output produced the results and plots that appear throughout the document. The following commands will extract all of the code from this file:

```
> all.R.commands <- system.file("doc", "HTqPCR.Rnw",  
+   package = "HTqPCR")  
> Stangle(all.R.commands)
```

This will create a file called HTqPCR.R in your current working directory, and this file can then either be sourced directly, or the commands run individually.

General workflow

The main functions and their use are outlined in [Figure 1](#). Note that the QC plotting functions can be used both before and after normalisation, in order to examine the quality of the data or look for particular trends.

For the full set of available functions type:

```
> ls("package:HTqPCR")
```

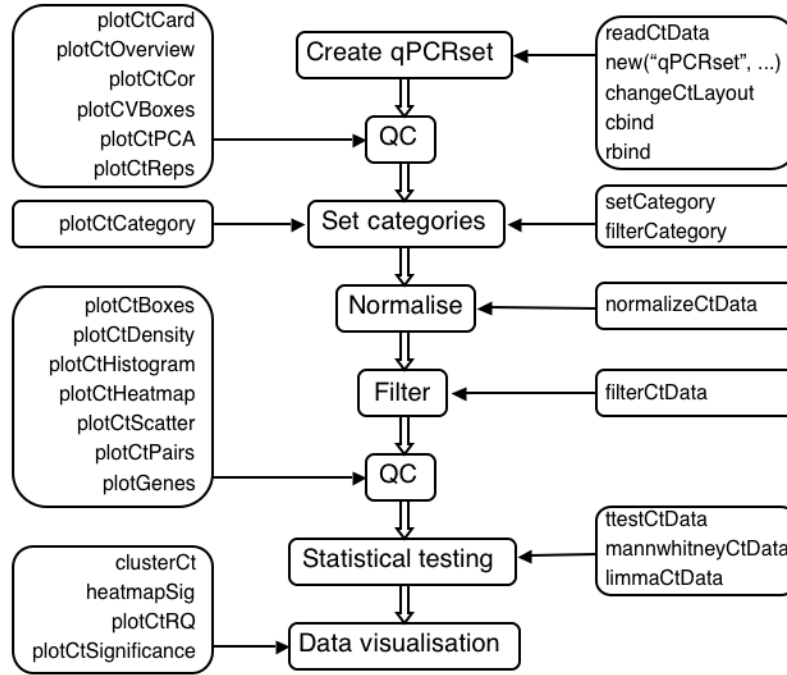


Figure 1: Workflow in *HTqPCR* analysis of qPCR data. Centre column: The main procedural steps in a typical qPCR analysis; Left: examples of visualisation functions; Right: data analysis functions.

[1] "cbind.qPCRset"	"changeCtLayout"
[3] "clusterCt"	"featureCategory"
[5] "featureCategory<-"	"featureClass"
[7] "featureClass<-"	"featurePos"
[9] "featurePos<-"	"featureType"
[11] "featureType<-"	"filterCategory"
[13] "filterCtData"	"flag"
[15] "flag<-"	"getCt"
[17] "getCtHistory"	"heatmapSig"
[19] "limmaCtData"	"mannwhitneyCtData"
[21] "n.samples"	"n.wells"
[23] "normalizeCtData"	"plotCtBoxes"
[25] "plotCtCard"	"plotCtCategory"
[27] "plotCtCor"	"plotCtDensity"
[29] "plotCtHeatmap"	"plotCtHistogram"
[31] "plotCtLines"	"plotCtOverview"
[33] "plotCtPairs"	"plotCtPCA"
[35] "plotCtReps"	"plotCtRQ"
[37] "plotCtScatter"	"plotCtSignificance"
[39] "plotCVBoxes"	"rbind.qPCRset"
[41] "readCtData"	"setCategory"
[43] "setCt<-"	"summary"
[45] "ttestCtData"	

Getting help

Please send questions about *HTqPCR* to the Bioconductor mailing list.

See <http://www.bioconductor.org/docs/mailList.html>

2 *qPCRset* objects

The data is stored in an object of class *qPCRset*, which is similar to the *ExpressionSet* from package *Biobase* used for handling microarray data. The format is the same for raw and normalized data, and depending on how much information is available about the input data, the object can contain the following slots:

featureNames Object of class *character* giving the names of the features (genes, miRNAs) used in the experiment.

sampleNames Object of class *character* containing the sample names of the individual experiments.

exprs Object of class *matrix* containing the Ct values.

flag Object of class *data.frame* containing the flag for each Ct value, as supplied by the input files. These are typically set during the calculation of Ct values, and indicate whether the results are flagged as e.g. “Passed” or “Flagged”.

featureType Object of class *factor* representing the different types of features on the card, such as endogenous controls and target genes.

featurePos Object of class *character* representing the location “well” of a gene in case TLDA cards are used, or some other method containing a defined spatial layout of features.

featureClass Object of class *factor* with some meta-data about the genes, for example if it is a transcription factor, kinase, marker for different types of cancers or similar. This is typically set by the user.

featureCategory Object of class *data.frame* representing the quality of the measurement for each Ct value, such as “OK”, “Undetermined” or “Unreliable”. These can be set using the function **setCategories** depending on a number of parameters, such as how the Ct values are flagged, upper and lower limits of Ct values and variations between technical and biological replicates of the same feature.

history Object of class *data.frame* indicating what operations have been performed on the *qPCRset* object, and what the parameters were. Automatically set when any of the functions on the upper right hand side of figure 1 are called (**readCtData**, **setCategory**, **filterCategory**, **normalizeCtData**, **filterCtData**, **changeCtLayout**, **rbind**, **cbind**).

Generally, information can be handled in the *qPCRset* using the same kind of functions as for *ExpressionSet*, such as **exprs**, **featureNames** and **featureCategory** for extracting the data, and **exprs<-**, **featureNames<-** and **featureCategory<-** for replacing or modifying values.

The use of **exprs** might not be intuitive to users who are not used to dealing with microarray data, and hence *ExpressionSet*. The functions **getCt** and **setCt<-** that perform the same

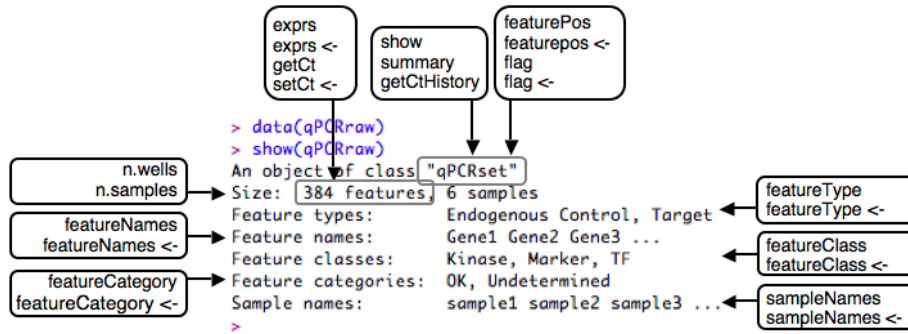


Figure 2: An example of a *qPCRset* object, and some of the functions that can be used to display and/or alter different aspects of the object, i.e. the accessor and replacement functions.

operations as `exprs` and `exprs<-` are therefore also included. For the sake of consistency, `exprs` will be used throughout this vignette for accessing the Ct values, but it can be replaced by `getCt` in all examples.

`qPCRset` objects can also be combined or reformatted in various ways (see 13).

Two `qPCRset` test objects are included in the package: one containing raw data, and the other containing processed values. An example is shown in figure 2, along with some of the functions that can typically be used for manipulating *qPCRset* objects.

```
> data(qPCRraw)
> data(qPCRpros)
> class(qPCRraw)
[1] "qPCRset"
attr(,"package")
[1] ".GlobalEnv"
```

3 Reading in the raw data

The standard input consists of tab-delimited text files containing the Ct values for a range of genes. Additional information, such as type of gene (e.g. target, endogenous control) or groupings of genes into separate classes (e.g. markers, kinases) can also be read in, or supplied later.

The package comes with example input files (from Applied Biosystem's TLDA cards), along with a text file listing sample file names and biological conditions.

```
> path <- system.file("exData", package = "HTqPCR")
> head(read.delim(file.path(path, "files.txt")))

  File Treatment
1 sample1.txt   Control
2 sample2.txt LongStarve
3 sample3.txt LongStarve
4 sample4.txt   Control
5 sample5.txt   Starve
6 sample6.txt   Starve
```

The data consist of 192 features represented twice on the array and labelled “Gene1”, “Gene2”, etc. There are three different conditions, “Control”, “Starve” and “LongStarve”, each having 2 replicates.

The input data consists of tab-delimited text files (one per sample); however, the format is likely to vary depending on the specific platform on which the data were obtained (e.g., TLDA cards, 96-well plates, or some other format). The only requirement is that columns containing the Ct values and feature names are present.

```
> files <- read.delim(file.path(path, "files.txt"))
> raw <- readCtData(files = files$File, path = path)
```

The *qPCRset* object looks like:

```
> show(raw)
An object of class "qPCRset"
Size: 384 features, 6 samples
Feature types:          Endogenous Control, Target
Feature names:          Gene1 Gene2 Gene3 ...
Feature classes:
Feature categories:      OK, Undetermined
Sample names:           sample1 sample2 sample3 ...
```

NB: This section only deals with data presented in general data format. For notes regarding other types of input data, see section 12.

4 Data visualisation

4.1 Overview of Ct values across all groups

To get a general overview of the data the (average) Ct values for a set of features across all samples or different condition groups can be displayed. In principle, all features in a sample might be chosen, but to make it less cluttered Figure 3 displays only the first 10 features. The top plot was made using just the Ct values, and shows the 95% confidence interval across replicates within and between samples. The bottom plot represents the same values but relative to a chosen calibrator sample, here the “Control”. Confidence intervals can also be added to the relative plot, in which case these will be calculated for all values compared to the average of the calibrator sample per gene.

```
> g <- featureNames(raw)[1:10]
> plotCtOverview(raw, genes = g, xlim = c(0, 50), groups = files$Treatment,
+   conf.int = TRUE, ylim = c(0, 55))

> plotCtOverview(raw, genes = g, xlim = c(0, 50), groups = files$Treatment,
+   calibrator = "Control")
```

4.2 Spatial layout

When the features are organised in a particular spatial pattern, such as the 96- or 384-well plates, it is possible to plot the Ct values or other characteristics of the features using this layout. Figure 4 shows an example of the Ct values, as well as the location of different classes of features (using random examples here), across all the wells of a TLDA microfluidic card.

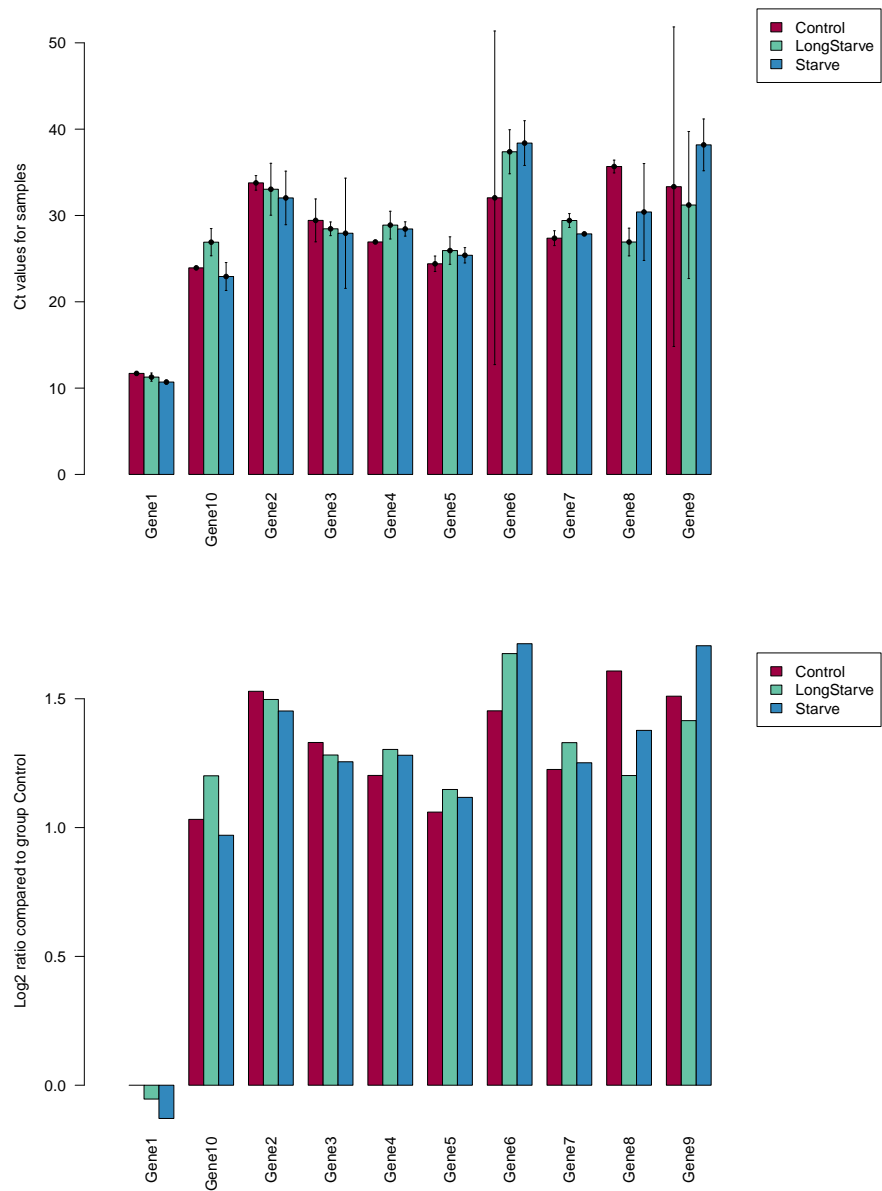


Figure 3: Overview of Ct values for the raw data.

```
> plotCtCard(raw, col.range = c(10, 35), well.size = 2.6)

> featureClass(raw) <- factor(c("Marker", "TF", "Kinase")[sample(c(1,
+ 1, 2, 2, 1, 3), 384, replace = TRUE)])
> plotCtCard(raw, plot = "class", well.size = 2.6)
```

5 Feature categories and filtering

Each Ct values in HTqPCR has an associated feature category. This is an important component to indicate the reliability of the qPCR data. Aside from the “OK” indicator, there are two other categories: “Undetermined” is used to flag Ct values above a user-selected threshold, and “Unreliable” indicates Ct values that are either so low as to be estimated by the user to be problematic, or that arise from deviation between individual Ct values across replicates. By default, only Ct values labelled as “undetermined” in the input data files are placed into the “Undetermined” category, and the rest are classified as “OK”. However, either before or after normalisation these categories can be altered depending on various criteria.

Range of Ct values Some Ct values might be too high or low to be considered a reliable measure of gene expression in the sample, and should therefore not be marked as “OK”.

Flags Depending on the qPCR input the values might have associated flags, such as “Passed” or “Failed”, which are used for assigning categories.

Biological and technical replicates If features are present multiple times within each sample, or if samples are repeated in the form of technical or biological replicates, then these values can be compared. Ct values lying outside a user-selected confidence interval (90% by default) will be marked as “Unreliable”.

```
> raw.cat <- setCategory(raw, groups = files$Treatment,
+ quantile = 0.8)
```

Categories after Ct.max and Ct.min filtering:

	sample1	sample2	sample3	sample4	sample5	sample6
OK	313	264	327	295	296	286
Undetermined	68	119	56	86	86	96
Unreliable	3	1	1	3	2	2

Categories after standard deviation filtering:

	sample1	sample2	sample3	sample4	sample5	sample6
OK	301	254	319	274	277	275
Undetermined	68	119	56	86	86	96
Unreliable	15	11	9	24	21	13

A summary plot for the sample categories is depicted in Figure 5. The result can be stratified by `featureType` or `featureClass`, for example to determine whether one class of features performed better or worse than others.

```
> plotCtCategory(raw.cat)
```

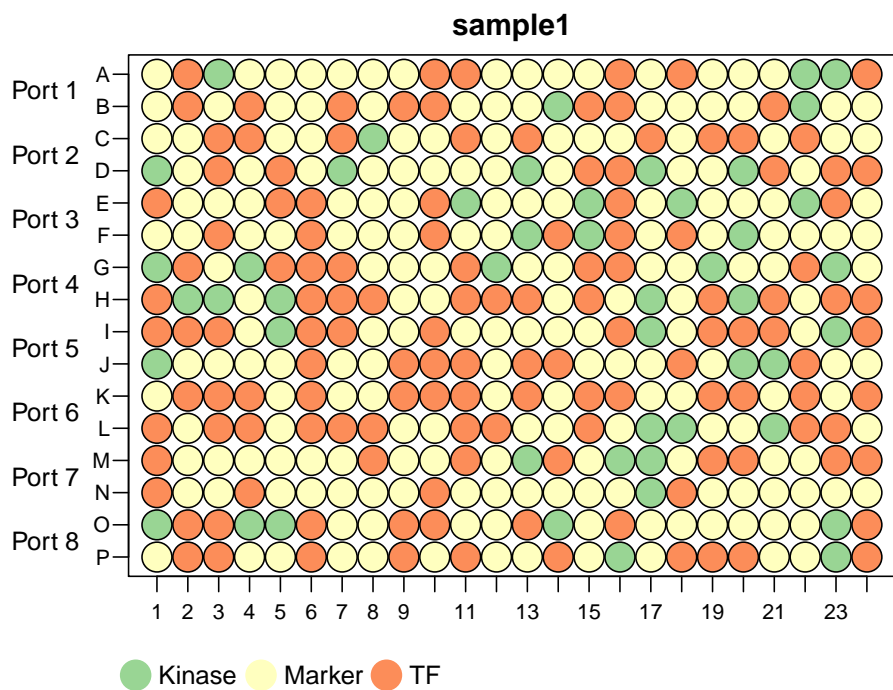
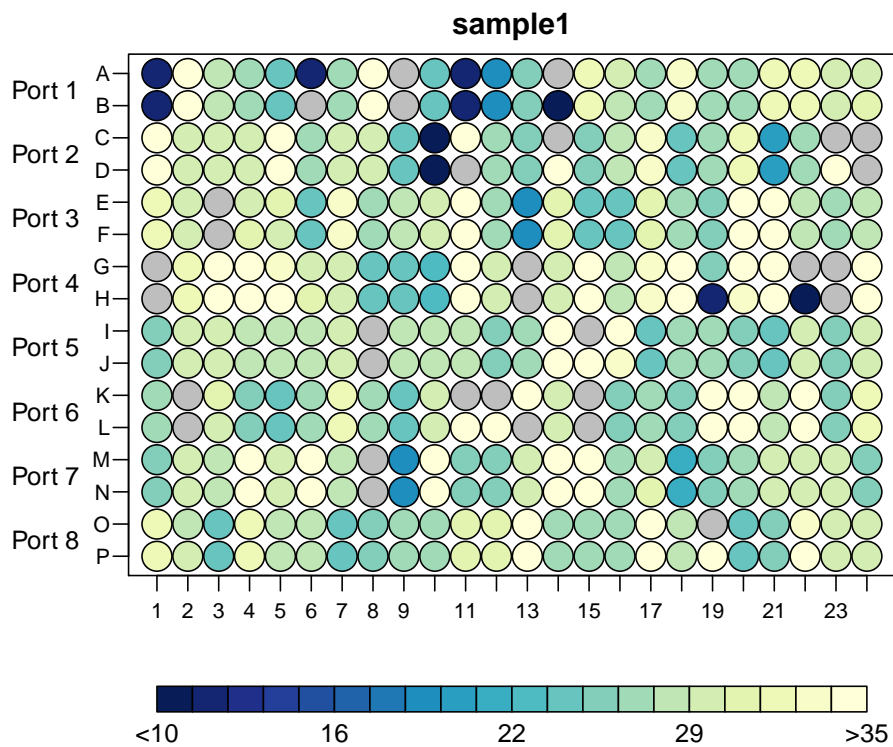


Figure 4: Ct values for the first sample (top)⁸, and the location of different feature classes (bottom). Ct values are visualised using colour intensity, and grey circles are features that were marked “undetermined” in the input file.

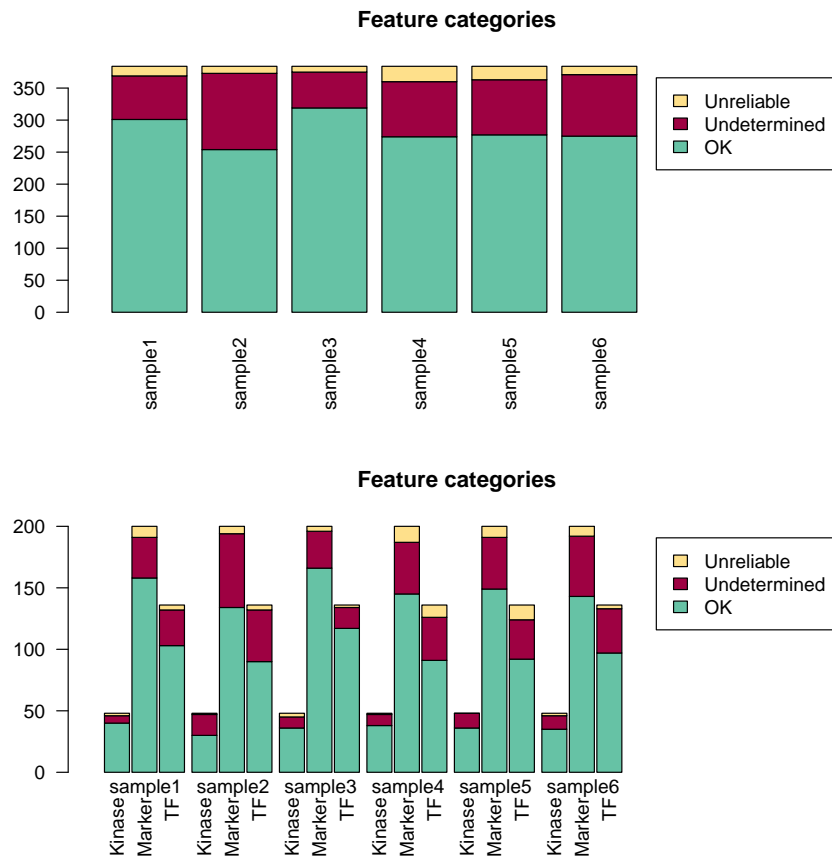


Figure 5: Summary of the categories, either for each sample individually or stratified by feature class.

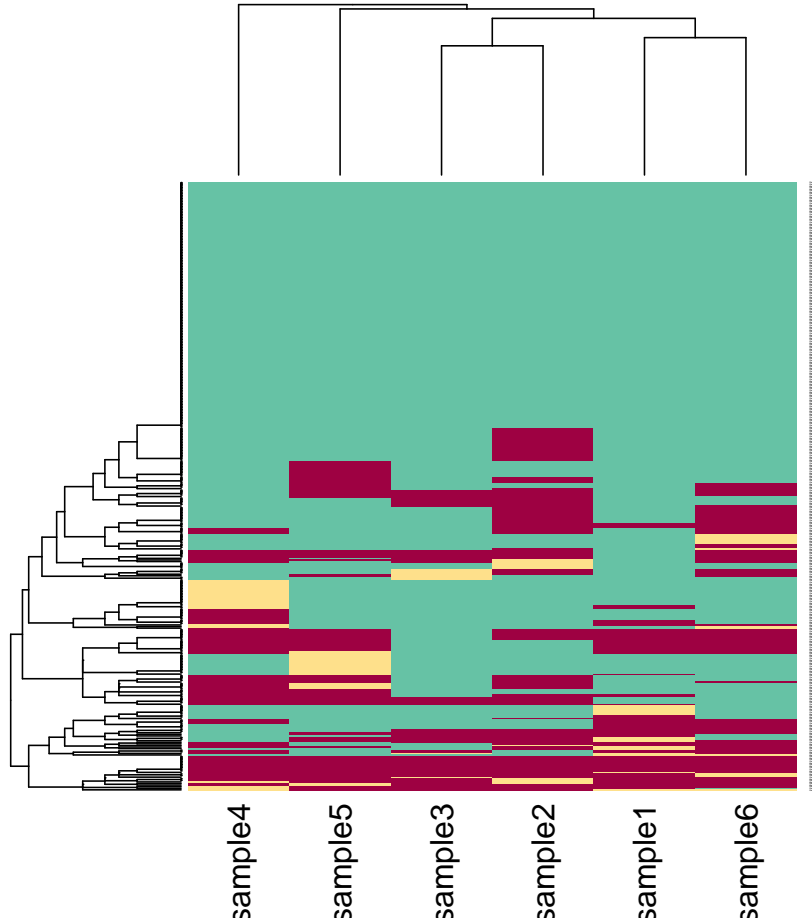


Figure 6: Summary of the categories, clustered across features.

```
> plotCtCategory(raw.cat, stratify = "class")
```

The results can also be shown per feature rather than averaged across samples (Figure 6).

```
> plotCtCategory(raw.cat, by.feature = TRUE, cexRow = 0.1)
```

If one doesn't want to include unreliable or undetermined data in part of the analysis, these Ct values can be set to NA using `filterCategory`. However, the presence of NAs could make the tests for differential expression less robust. When testing for differential expression the result will come with an associated category ("OK" or "Unreliable") that can instead be used to assess the quality of the results. For the final results both "Undetermined" and "Unreliable" are pooled together as being "Unreliable". However, the label for each feature can either be set according to whether half or more of the samples are unreliable, or whether only a single non-"OK" category is present, depending on the level of stringency the user wishes to enforce.

6 Normalisation

Four different normalisation methods are currently implemented in *HTqPCR*. Two of these (`scale.rankinvariant` and `deltaCt`) will scale each individual sample by a given value, whereas the remaining two will change the distribution of Ct values.

quantile Will make the distribution of Ct values more or less identical across samples.

norm.rankinvariant Computes all rank-invariant sets of features between pairwise comparisons of each sample against a reference, such as a pseudo-mean. The rank-invariant features are used as a reference for generating a smoothing curve, which is then applied to the entire sample.

scale.rankinvariant Also computes the pairwise rank-invariant features, but then takes only the features found in a certain number of samples, and used the average Ct value of those as a scaling factor for correcting all Ct values.

deltaCt Calculates the standard deltaCt values, i.e. subtracts the mean of the chosen controls from all other values in the feature set.

For the rank-invariant normalisation methods, Ct values above a given threshold can be excluded from the calculation of a scaling factor or normalisation curve. This is useful so that a high proportion of “Undetermined” Ct values (assigned a value of 40 by default) in a given sample doesn’t bias the normalisation of the remaining features.

In the example dataset, Gene1 and Gene60 correspond to 18S RNA and GADPH, and are used as endogenous controls. Normalisation methods can be run as follows:

```
> q.norm <- normalizeCtData(raw.cat, norm = "quantile")
> sr.norm <- normalizeCtData(raw.cat, norm = "scale.rank")
```

Scaling Ct values

Using rank invariant genes: Gene1 Gene29

Scaling factors: 1.00 1.06 1.00 1.03 1.00 1.00

```
> nr.norm <- normalizeCtData(raw.cat, norm = "norm.rank")
```

Normalizing Ct values

Using rank invariant genes:

sample1: 75 rank invariant genes

sample2: 33 rank invariant genes

sample3: 48 rank invariant genes

sample4: 69 rank invariant genes

sample5: 18 rank invariant genes

sample6: 67 rank invariant genes

```
> d.norm <- normalizeCtData(raw.cat, norm = "deltaCt",
+   deltaCt.genes = c("Gene1", "Gene60"))
```

Calculating deltaCt values

Using control gene(s): Gene1 Gene60

Card 1:	Mean=14.45	Stdev=4.25
---------	------------	------------

Card 2:	Mean=15.19	Stdev=5.27
---------	------------	------------

Card 3:	Mean=14.50	Stdev=5.8
---------	------------	-----------

Card 4:	Mean=14.79	Stdev=4.79
---------	------------	------------

Card 5:	Mean=14.07	Stdev=5.32
---------	------------	------------

Card 6:	Mean=13.82	Stdev=4.75
---------	------------	------------

Comparing the raw and normalised values gives an idea of how much correction has been performed (Figure 7), as shown below for the q.norm object. Note that the scale on the y-axis varies.

```
> plot(exprs(raw), exprs(q.norm), pch = 20, main = "Quantile normalisation",
+   col = rep(brewer.pal(6, "Spectral"), each = 384))
```

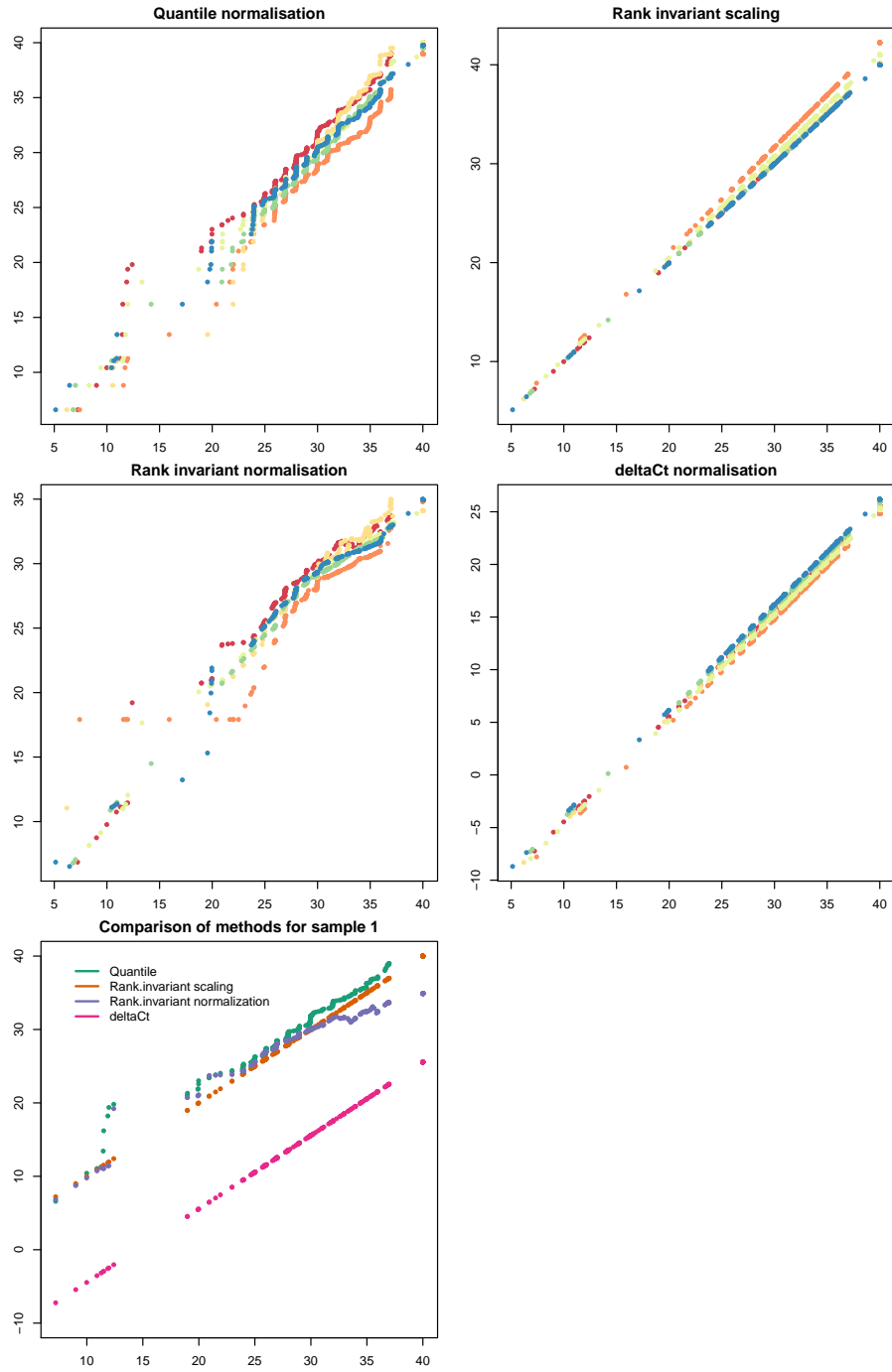


Figure 7: Normalized versus raw data, using a separate colour for each sample. The raw data is plotted along the x-axis and the normalised along y. The last plot is a comparison between normalization methods for the first sample, still with the raw Ct values along the x-axis.

7 Filtering and subsetting the data

At any point during the analysis it's possible to filter out both individual features or groups of features that are either deemed to be of low quality, or not of interest for a particular aspect of the analysis. This can be done using any of the feature characteristics that are included in the `featureNames`, `featureType`, `featureClass` and/or `featureCategory` slots of the data object. Likewise, the `qPCRset` object can be turned into smaller subsets, for example if only a particular class of features are to be used, or some samples should be excluded.

Simple subsetting can be done using the standard `[,]` notation of R, for example:

```
> nr.norm[1:10, ]
An object of class "qPCRset"
Size: 10 features, 6 samples
Feature types:          Endogenous Control, Target
Feature names:          Gene1 Gene2 Gene3 ...
Feature classes:        Kinase, Marker, TF
Feature categories:      OK, Unreliable, Undetermined
Sample names:           sample1 sample2 sample3 ...

> nr.norm[, c(1, 3, 5)]
An object of class "qPCRset"
Size: 384 features, 3 samples
Feature types:          Endogenous Control, Target
Feature names:          Gene1 Gene2 Gene3 ...
Feature classes:        Kinase, Marker, TF
Feature categories:      OK, Unreliable, Undetermined
Sample names:           sample1 sample3 sample5 ...
```

Filtering is done by specifying the components to remove, either by just using a single criteria, or by combining multiple filters:

```
> qFilt <- filterCtData(nr.norm, remove.type = "Endogenous Control")
Removed 4 'Endogenous Control' features based on featureType(q).

> qFilt <- filterCtData(nr.norm, remove.name = c("Gene1",
+       "Gene20", "Gene30"))
Removed 8 'Gene1/Gene20/Gene30' features based on featureNames(q).

> qFilt <- filterCtData(nr.norm, remove.class = "Kinase")
Removed 48 'Kinase' features based on featureClass(q).

> qFilt <- filterCtData(nr.norm, remove.type = c("Endogenous Control"),
+       remove.name = c("Gene1", "Gene20", "Gene30"))
Removed 4 'Endogenous Control' features based on featureType(q).
Removed 4 'Gene1/Gene20/Gene30' features based on featureNames(q).
```

The data can also be adjusted according to feature categories. With `filterCategory` mentioned previously it's possible to replace certain Ct values with NA, but one might want to completely exclude features where a certain number of the Ct values are for example unreliable.

```
> qFilt <- filterCtData(nr.norm, remove.category = "Undetermined")
Removed 64 features with >3 'Undetermined' based on featureCategory(q).
```

```
> qFilt <- filterCtData(nr.norm, remove.category = "Undetermined",
+   n.category = 5)
Removed 10 features with >5 'Undetermined' based on featureCategory(q).
```

Another typical filtering step would be to remove features showing little or no variation across samples, prior to testing for statistical significance of genes between samples. Features with relatively constant Ct levels are less likely to be differentially expressed, so including them in the downstream analysis would cause some loss of power when adjusting the p-values for multiple testing (the feature-by-feature hypothesis testing). Variation across samples can be assessed using for example the interquartile range (IQR) values for each feature (Figure 8).

```
> iqr.values <- apply(exprs(nr.norm), 1, IQR)
> hist(iqr.values, n = 20, main = "", xlab = "IQR across samples")
> abline(v = 1.5, col = 2)
```

All features with IQR below a certain threshold can then be filtered out.

```
> qFilt <- filterCtData(nr.norm, remove.IQR = 1.5)
Removed 207 features with IQR <1.5 based on exprs(q).
```

Note that filtering prior to normalisation can affect the outcome of the normalisation procedure. In some cases this might be desirable, for example if a particular feature class are heavily biasing the results so it's preferable to split the `qPCRset` object into smaller data sets. However, in other cases it might for example make it difficult to identify a sufficient number of rank invariant features for `thenorm.rankinvariant` and `scale.rankinvariant` methods. Whether to perform filtering, and if so then during what step of the analysis, depends on the genes and biological samples being analysed, as well as the quality of the data. It's therefore advisable to perform a detailed quality assessment and data comparison, as mentioned in the next section.

8 Quality assessment

8.1 Correlation between samples

The overall correlation between different samples can be displayed visually, such as shown for the raw data in Figure 9.

```
> plotCtCor(raw, main = "Ct correlation")
```

8.2 Distribution of Ct values

It may be of interest to examine the general distribution of data both before and after normalisation. A simple summary of the data can be obtained using `summary` as shown below.

```
> summary(raw)
```

	sample1	sample2	sample3	sample4	sample5	sample6
Min.	" 7.218"	" 7.408"	" 6.19"	" 6.853"	" 6.787"	" 5.133"
1st Qu.	"26.738"	"28.855"	"27.90"	"26.964"	"27.913"	"27.514"
Median	"28.937"	"30.994"	"29.92"	"29.943"	"30.778"	"29.931"
Mean	"29.542"	"32.190"	"30.35"	"30.590"	"30.995"	"30.663"
3rd Qu.	"33.323"	"35.985"	"32.98"	"34.694"	"34.702"	"35.046"
Max.	"40.000"	"40.000"	"40.00"	"40.000"	"40.000"	"40.000"

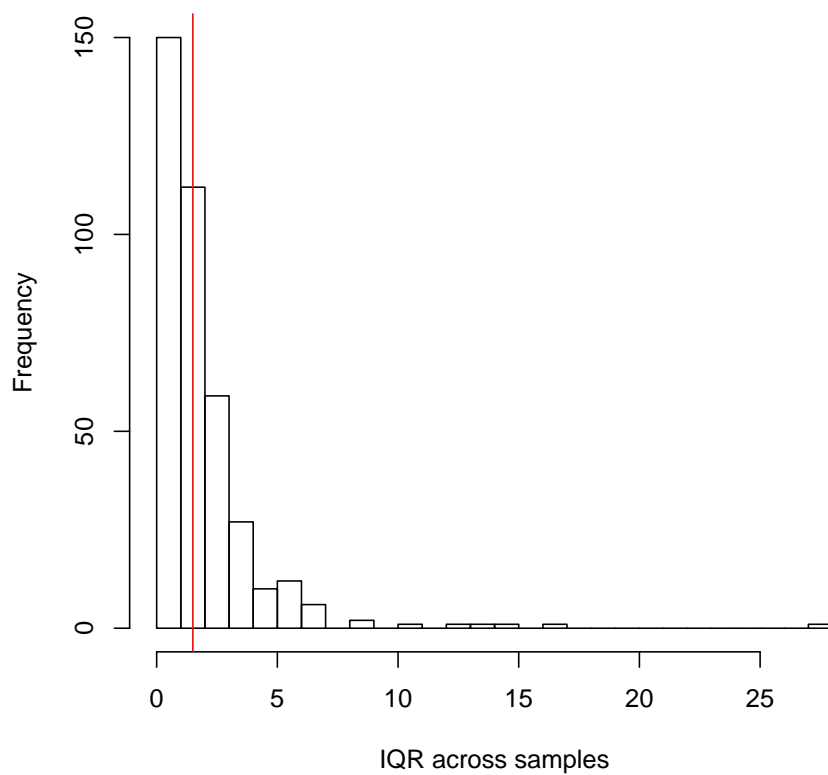


Figure 8: Histogram of the IQR values for all features across the samples, including the cut-off used in the filtering example.

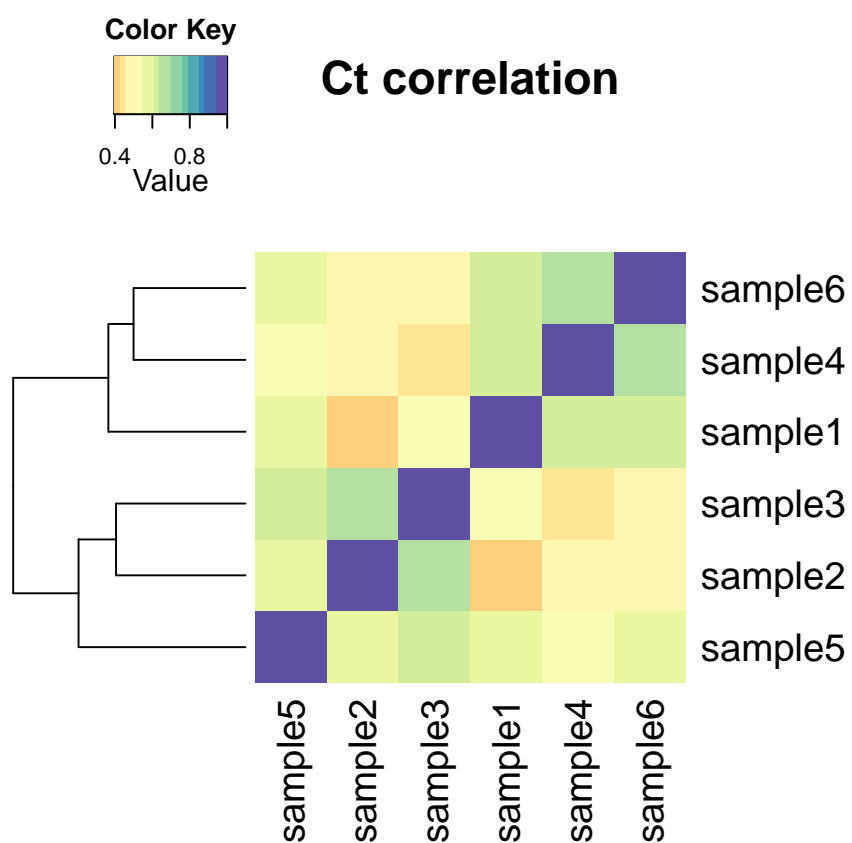


Figure 9: Correlation between raw Ct values.

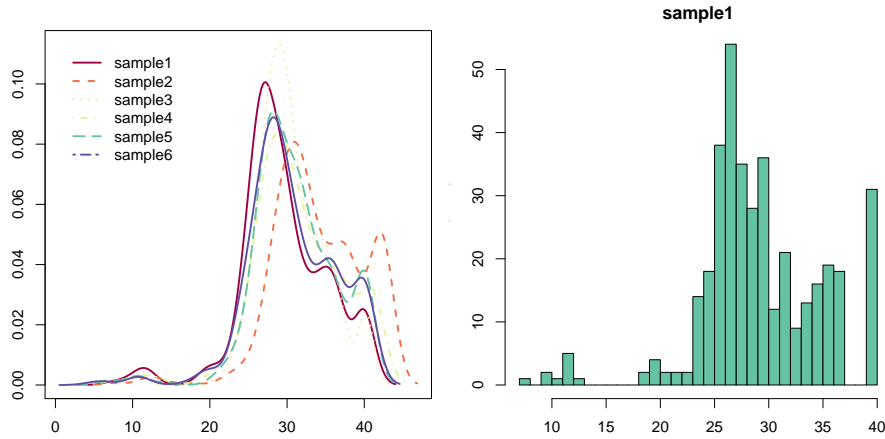


Figure 10: Distribution of Ct values for the individual samples, either using the density of all arrays (left) or a histogram of a single sample (right), after scale rank-invariant normalisation.

However, figures are often more informative. To that end, the range of Ct values can be illustrated using histograms or with the density distribution, as shown in Figure 10.

```
> plotCtDensity(sr.norm)

> plotCtHistogram(sr.norm)
```

Plotting the densities of the different normalisation methods lends insight into how they differ (Figure 11).

Ct values can also be displayed in boxplots, either with one box per sample or stratified by different attributes of the features, such as `featureClass` or `featureType` (Fig. 12).

```
> plotCtBoxes(sr.norm, stratify = "class")
```

8.3 Comparison of Ct values for two samples

It is often of interest to directly compare Ct values between two samples. In Figure 13, two examples are shown for the rank-invariant normalised data: one for different biological samples, and one for replicates.

```
> plotCtScatter(sr.norm, cards = c(1, 2), col = "type",
+   diag = TRUE)

> plotCtScatter(sr.norm, cards = c(1, 4), col = "class",
+   diag = TRUE)
```

8.4 Scatter across all samples

It is also possible to generate a scatterplot of Ct values between more than the two samples shown above. In Figure 14 all pairwise comparisons are shown, along with their correlation when all Ct values <35 are removed.

```
> plotCtPairs(sr.norm, col = "type", diag = TRUE)
```

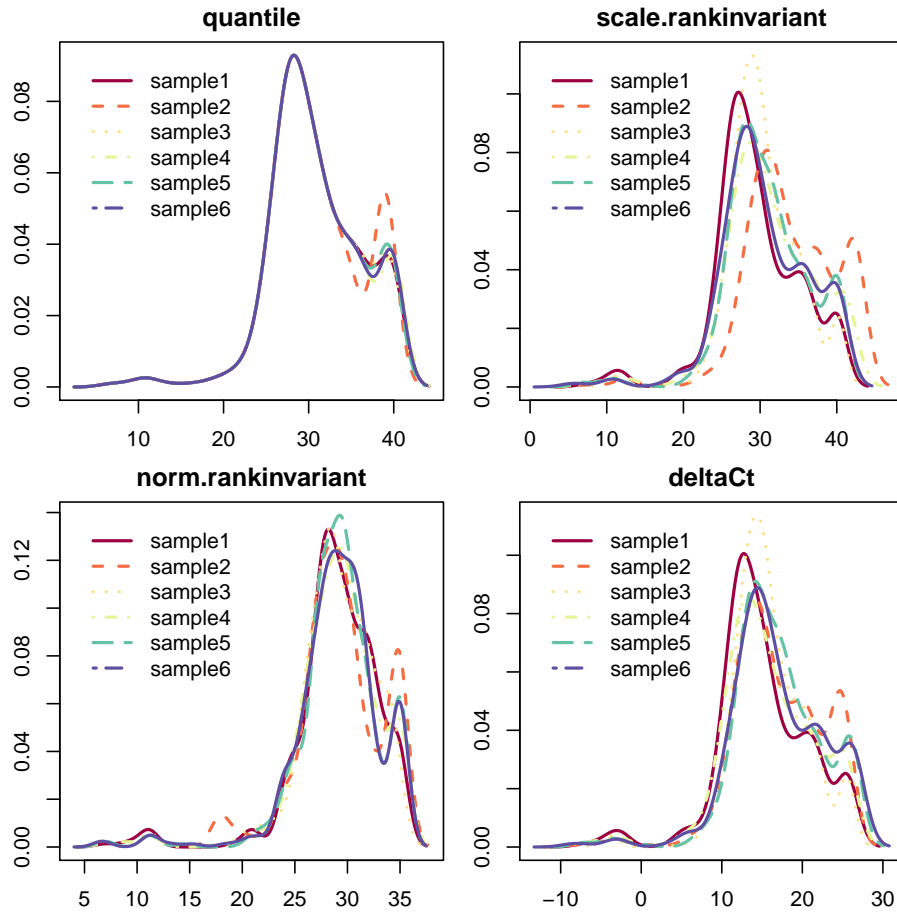


Figure 11: Densities of Ct values for all samples after each of the four normalisation methods. The peak at the high end originates from features with “Undetermined” Ct values, which are assigned the Ct value 40 by default.

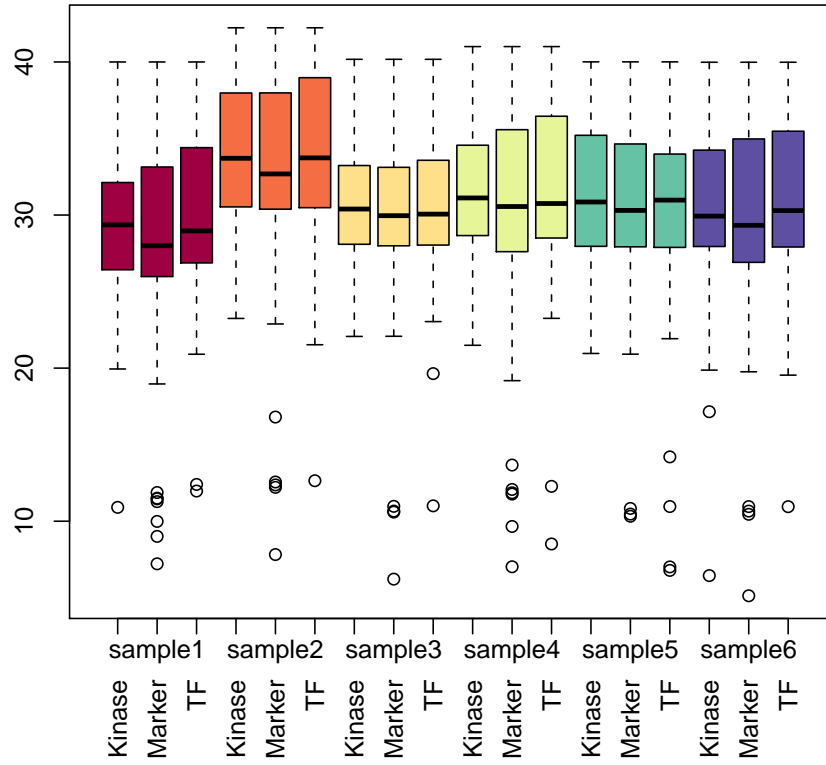


Figure 12: Boxplot of Ct values across all samples, stratified by feature classes.

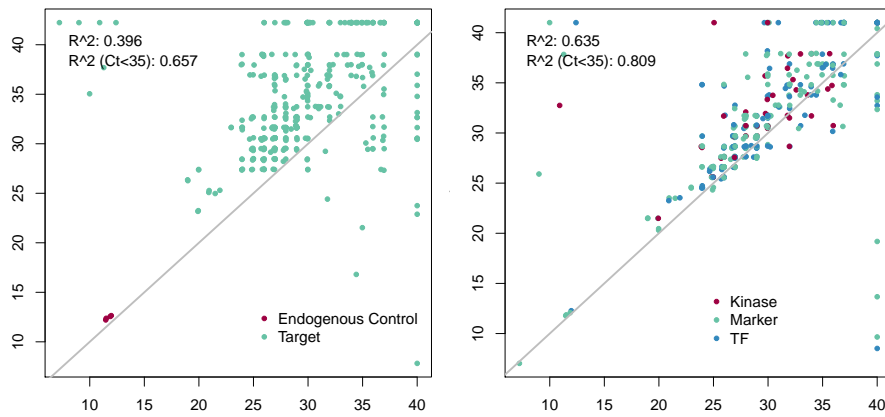


Figure 13: Scatter plot of Ct values in different samples, with points marked either by featureType (left) or featureClass (right) and the diagonal through $x = y$ marked with a grey line.

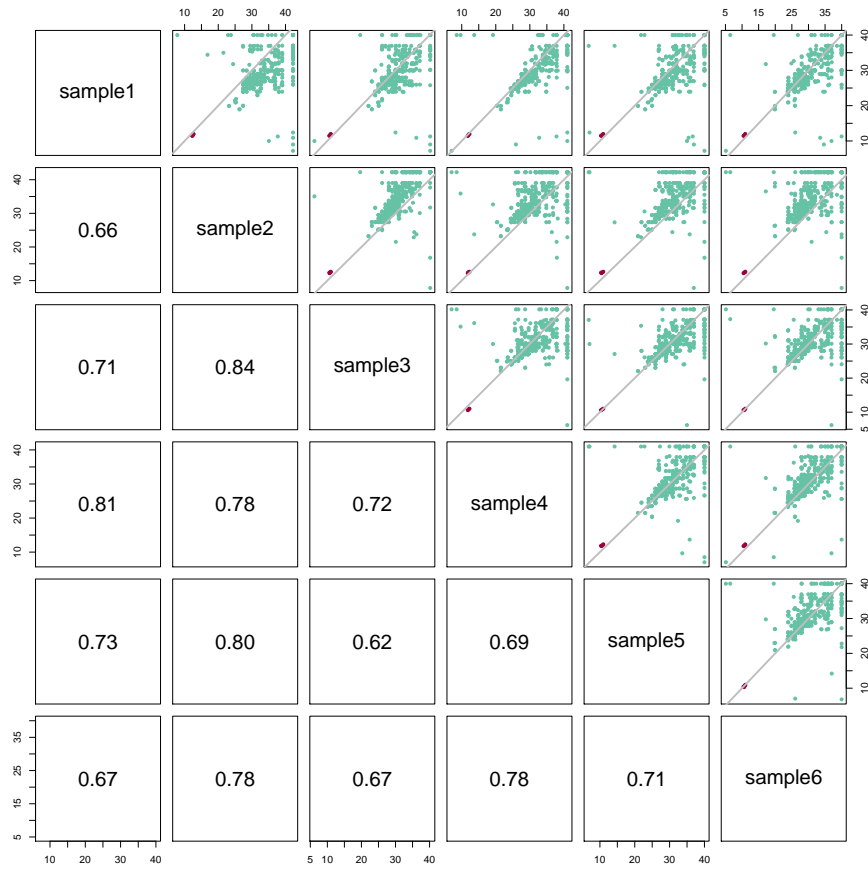


Figure 14: Scatterplot for all pairwise comparisons between samples, with spots marked depending on `featureType`, i.e. whether they represent endogenous controls or targets.

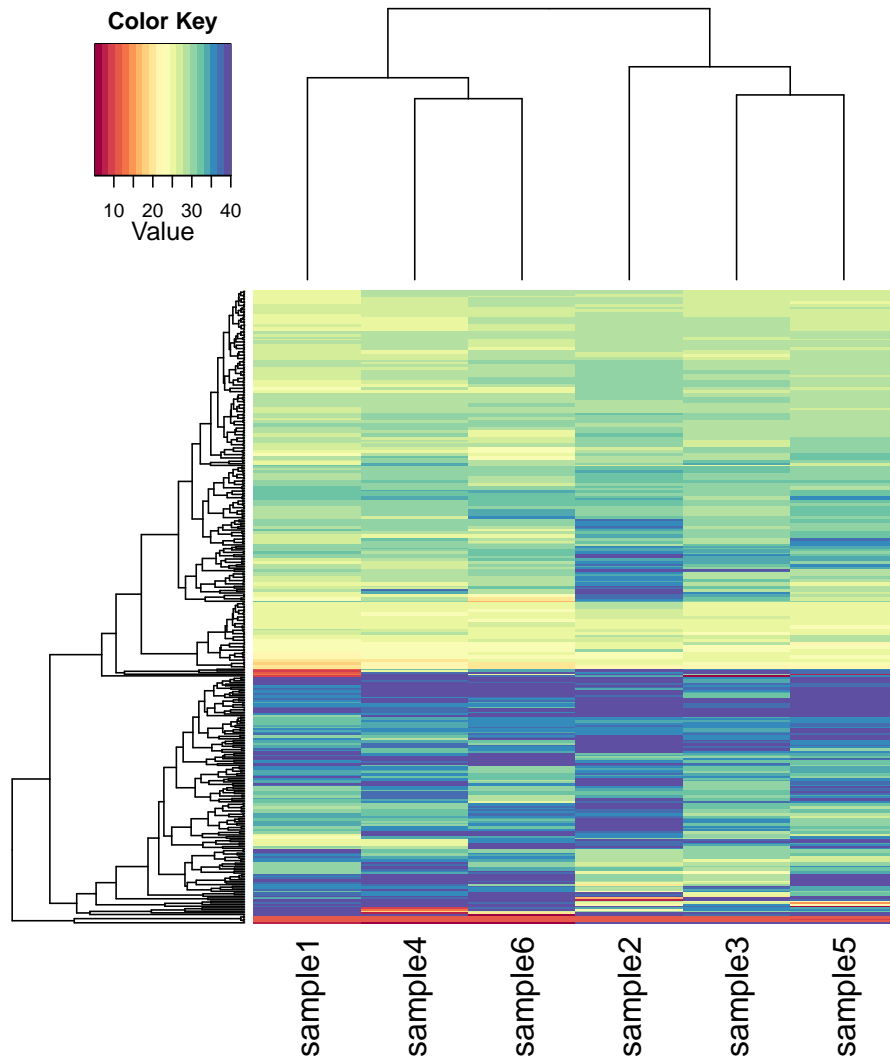


Figure 15: Heatmap for all samples and genes, based on the Euclidean distance between Ct values.

8.5 Ct heatmaps

Heatmaps provide a convenient way to visualise clustering of features and samples at the same time, and show the levels of Ct values (Figure 15). The heatmaps can be based on either Pearson correlation coefficients or Euclidean distance clustering. Euclidean-based heatmaps will focus on the magnitude of Ct values, whereas Pearson clusters the samples based on similarities between the Ct profiles.

```
> plotCtHeatmap(raw, gene.names = "", dist = "euclidean")
```

8.6 Comparison of replicated features within samples

When a sample contains duplicate measurements for some or all features, the Ct values of these duplicates can be plotted against each other to measure accordance between duplicates. In Figure 16 the duplicates in sample2 are plotted against each other, and those where the Ct values differ more than 20% from the average of a given feature are marked.

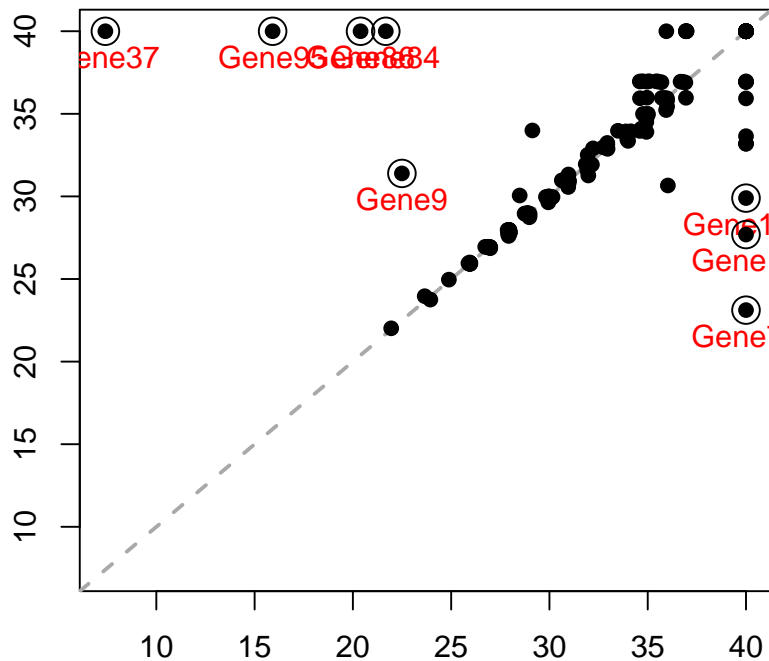


Figure 16: Concordance between duplicated Ct values in sample 2, marking features differing >20% from their mean.

```
> plotCtReps(qPCRraw, card = 2, percent = 20)
Replicates differing > 20% on card 2:
      rep1      rep2
Gene135 40.000000 29.90044
Gene14  40.000000 27.69185
Gene37   7.408248 40.00000
Gene73  40.000000 23.11949
Gene84  21.673946 40.00000
Gene86  20.389658 40.00000
Gene9   22.494440 31.39404
Gene95  15.916160 40.00000
```

Differences will often arise due to one of the duplicates marked as “Undetermined”, thus contributing to an artificially high Ct value, but other known cases exist as well.

8.7 Coefficients of variation

The coefficients of variation (CV) can be calculated for each feature across all samples. Stratifying the CV values by `featureType` or `featureClass` can help to determine whether one class of features is more variable than another (Figure 17). For the example data feature

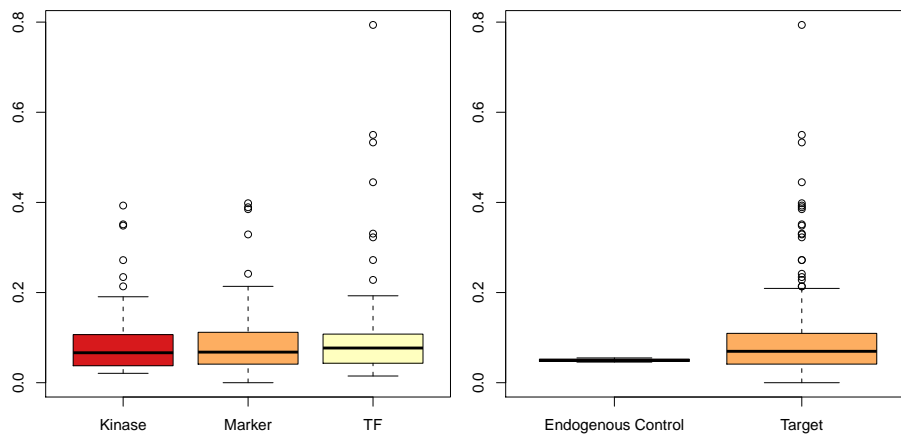


Figure 17: Coefficients of variation for each feature across all samples.

classes have been assigned randomly, and the CVs are therefore similar, whereas for the feature types there's a clear difference between controls and targets.

```
> plotCVBoxes(qPCRraw, stratify = "class")
> plotCVBoxes(qPCRraw, stratify = "type")
```

9 Clustering

At the moment there are two default methods present in *HTqPCR* for clustering; hierarchical clustering and principal components analysis (PCA).

9.1 Hierarchical clustering

Both features and samples can be subjected to hierarchical clustering using either Euclidean or Pearson correlation distances, to display similarities and differences within groups of data. Individual subclusters can be selected, either using pre-defined criteria such as number of clusters, or interactively by the user. The content of each cluster is then saved to a list, to allow these features to be extracted from the full data set if desired.

An example of a clustering of samples is shown in Figure 18. In Figure 19 these data are clustered by features, and the main subclusters are marked.

```
> clusterCt(sr.norm, type = "samples")

> cluster.list <- clusterCt(sr.norm, type = "genes",
+   n.cluster = 6, cex = 0.5)

> c6 <- cluster.list[[6]]
> print(c6)
  Gene9  Gene13  Gene46  Gene50  Gene75  Gene93  Gene75  Gene103
    9    14    71    99    148    166    172    200
Gene132 Gene151 Gene151
  277    296    320
```

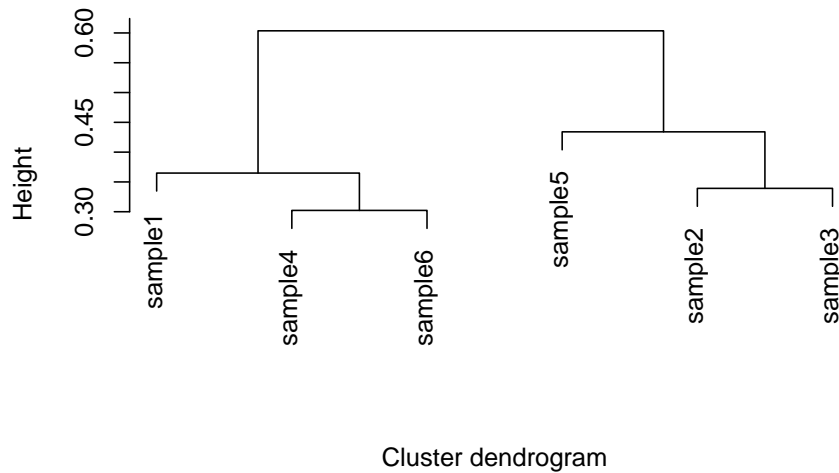


Figure 18: Hierarchical clustering of samples.

```
> show(sr.norm[c6, ])
An object of class "qPCRset"
Size: 11 features, 6 samples
Feature types:      Endogenous Control, Target
Feature names:      Gene9 Gene13 Gene46 ...
Feature classes:    Kinase, Marker, TF
Feature categories: Undetermined, Unreliable, OK
Sample names:      sample1 sample2 sample3 ...
```

9.2 Principal components analysis

PCA is performed across the selected features and samples (observations and variables), and can be visualized either in a biplot, or showing just the clustering of the samples (Figure 20).

```
> plotCtPCA(qPCRRaw)
> plotCtPCA(qPCRRaw, features = FALSE)
```

10 Differential expression

At this stage multiple filterings might have been performed on the data set(s). To remind yourself about those, you can use the `getCtHistory` function on the *qPCRset* object.

```
> getCtHistory(sr.norm)
history
1      readCtData(files = files$File, path = path)
2 setCategory(q = raw, quantile = 0.8, groups = files$Treatment)
3      normalizeCtData(q = raw.cat, norm = "scale.rank")
> getCtHistory(qFilt)
```

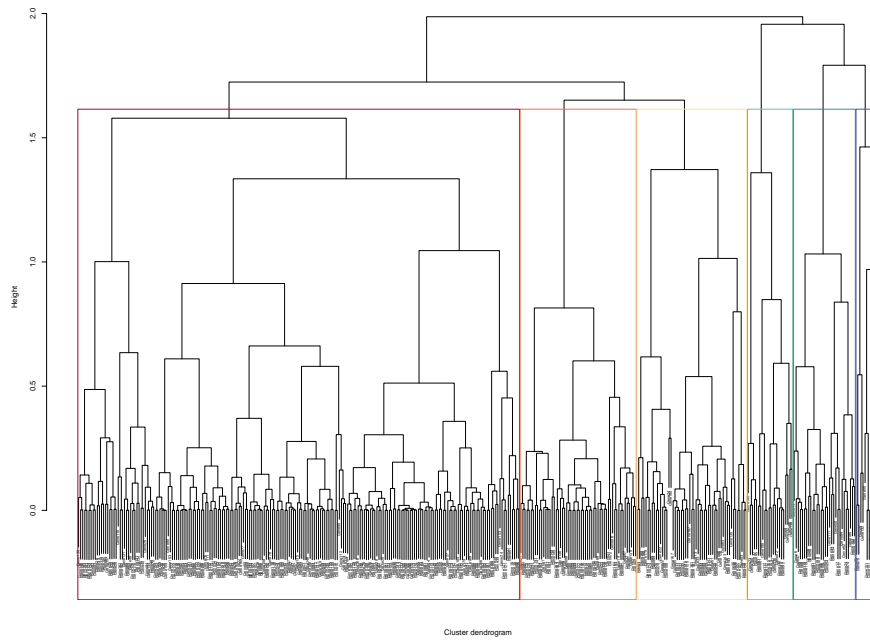



Figure 19: Hierarchical clustering of features, with subclusters marked.

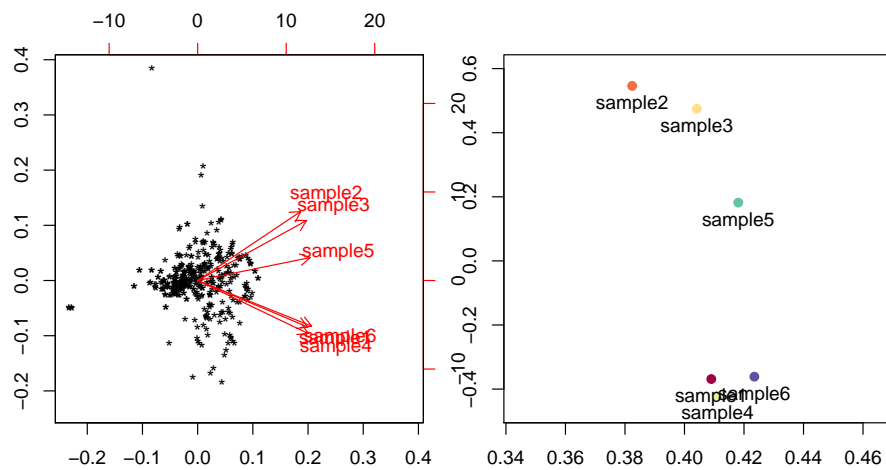


Figure 20: Left: a biplot including all features, with samples represented by vectors. Right: the same plot, including only the samples.

```

                                history
1      readCtData(files = files$File, path = path)
2 setCategory(q = raw, quantile = 0.8, groups = files$Treatment)
3      normalizeCtData(q = raw.cat, norm = "norm.rank")
4      filterCtData(q = nr.norm, remove.IQR = 1.5)

```

In general there are three approaches in *HTqPCR* for testing the significance of differences in Ct values between samples.

t-test Performing a standard t-test between two sample groups. This function will incorporate information about replicates to calculate t and p-values. This is a fairly simple approach, typically used when comparing a single treatment and control sample, and multiple pair-wise tests can be carried out one-by-one by the user.

Mann-Whitney This is a non-parametric test, also known as a two sample Wilcoxon test. Similar to the t-test, multiple pair-wise tests will have to be carried out one by one if more than two types of samples are present. This is a rank-based test that doesn't make any assumptions about the population distribution of Ct values.

limma Using a wrapper for functions from the package *limma* (Smyth, 2005) to calculate more sophisticated t and p-values for any number of groups present across the experiment. This is more flexible in terms of what types of comparisons can be made, but the users need to familiarise themselves with the *limma* conventions for specifying what contrasts are of interest.

Examples of how to use each of these are given in the next sections. In all cases the output is similar; a data frame containing the test statistics for each feature, along with fold change and information about whether the Ct values are "OK" or "Unreliable". This result can be written to a file using standard functions such as `write.table`.

10.1 Two sample types - t-test

This section shows how to compare two samples, e.g. the control and long starvation samples from the example data. A subset of the `qPCRset` data is created to encompass only these samples, and a t-test is then performed.

```

> qDE.ttest <- ttestCtData(sr.norm[, 1:4], groups = files$Treatment[1:4],
+   calibrator = "Control")
> qDE.ttest[1:10, ]

```

	genes	feature.pos	t.test	p.value	adj.p.value
2	Gene10	A10;B10	-13.705640	9.812948e-06	0.001874273
22	Gene118	I23;J23	-10.407281	8.661980e-05	0.008272191
36	Gene130	K11;L11	7.644065	3.156334e-04	0.019863762
164	Gene74	G3;H3	7.201124	4.768225e-04	0.019863762
30	Gene125	K6;L6	-7.203614	5.199938e-04	0.019863762
33	Gene128	K9;L9	-10.357650	6.826374e-04	0.020708859
76	Gene167	M24;N24	-12.360918	7.589634e-04	0.020708859
51	Gene144	M1;N1	-7.847655	1.087976e-03	0.025975434
167	Gene77	G6;H6	-8.643118	1.397709e-03	0.027536277
118	Gene32	C9;D9	-6.332114	1.441690e-03	0.027536277

```

      ddCt      FC meanCalibrator meanTarget
2  3.460492 9.084231e-02      24.23106    27.69156

```

22	8.982157	1.977430e-03	26.70531	35.68746
36	-9.433460	6.914400e+02	39.74414	30.31068
164	-5.178293	3.620942e+01	35.40699	30.22869
30	7.052337	7.534164e-03	28.28445	35.33679
33	5.210558	2.700635e-02	25.61542	30.82598
76	13.401172	9.243685e-05	26.25075	39.65192
51	3.582610	8.346932e-02	26.17539	29.75800
167	11.067840	4.658522e-04	29.36973	40.43757
118	5.645620	1.997556e-02	25.73270	31.37832

	categoryCalibrator	categoryTarget
2	Undetermined	OK
22	OK	Undetermined
36	Undetermined	OK
164	Undetermined	OK
30	OK	OK
33	OK	OK
76	Undetermined	Undetermined
51	OK	Undetermined
167	OK	Undetermined
118	OK	OK

10.2 Two sample types - Mann-Whitney

When only two samples are of interest, these can also be compared using a Mann-Whitney test. As in the section above, the function is demonstrated using the control and long starvation samples from the example data. A subset of the `qPCRset` data is created to encompass only these samples, and a Mann-Whitney test is performed.

```
> qDE.mwtest <- mannwhitneyCtData(sr.norm[, 1:4], groups = files$Treatment[1:4],
+   calibrator = "Control")
> qDE.mwtest[1:10, ]
```

	genes	feature.pos	MW.value	p.value	adj.p.value
26	Gene121	K2;L2	W = 0	0.02746864	0.07842053
134	Gene47	C24;D24	W = 16	0.02842954	0.07842053
157	Gene68	E21;F21	W = 0	0.02842954	0.07842053
185	Gene93	G22;H22	W = 0	0.02842954	0.07842053
36	Gene130	K11;L11	W = 16	0.02940105	0.07842053
54	Gene147	M4;N4	W = 0	0.02940105	0.07842053
58	Gene150	M7;N7	W = 0	0.02940105	0.07842053
59	Gene151	M8;N8	W = 16	0.02940105	0.07842053
69	Gene160	M17;N17	W = 0	0.02940105	0.07842053
95	Gene184	O17;P17	W = 0	0.02940105	0.07842053

	ddCt	FC	meanCalibrator	meanTarget
26	2.316925	2.006947e-01	38.88749	41.20441
134	-12.205480	4.722973e+03	40.50267	28.29719
157	6.547033	1.069416e-02	34.65738	41.20441
185	25.515391	2.084980e-08	15.68902	41.20441
36	-9.433460	6.914400e+02	39.74414	30.31068
54	3.765620	7.352505e-02	35.92123	39.68685
58	7.384220	5.985884e-03	29.81061	37.19483

59	-5.986312	6.339564e+01	36.26967	30.28336
69	7.130602	7.136332e-03	31.86682	38.99743
95	6.021983	1.538872e-02	34.36985	40.39183

	categoryCalibrator	categoryTarget
26	Undetermined	Undetermined
134	Undetermined	OK
157	Undetermined	Undetermined
185	Undetermined	Undetermined
36	Undetermined	OK
54	Undetermined	Undetermined
58	OK	Undetermined
59	Undetermined	OK
69	OK	Undetermined
95	OK	Undetermined

10.3 Multiple sample types - limma

In this example all three types of treatment are compared, as well as the control against both starvation samples combined. The data is sorted by feature names, to make easier use of replicated features.

```
> design <- model.matrix(~0 + files$Treatment)
> colnames(design) <- c("Control", "LongStarve", "Starve")
> print(design)
  Control LongStarve Starve
1       1         0      0
2       0         1      0
3       0         1      0
4       1         0      0
5       0         0      1
6       0         0      1
attr(,"assign")
[1] 1 1 1
attr(,"contrasts")
attr(,"contrasts")$`files$Treatment`
[1] "contr.treatment"

> contrasts <- makeContrasts(LongStarve - Control,
+   LongStarve - Starve, Starve - Control, (Starve +
+   LongStarve)/2 - Control, levels = design)
> colnames(contrasts) <- c("LS-C", "LS-S", "S-C", "bothS-C")
> print(contrasts)
      Contrasts
Levels      LS-C LS-S S-C bothS-C
Control     -1   0  -1   -1.0
LongStarve   1   1   0    0.5
Starve       0  -1   1    0.5

> sr.norm2 <- sr.norm[order(featureNames(sr.norm)),
+   ]
> qDE.limma <- limmaCtData(sr.norm2, design = design,
+   contrasts = contrasts, ndups = 2, spacing = 1)
```

The result is a list with one component per comparison. Each component is similar to the result from using `ttestCtData`.

```
> class(qDE.limma)
[1] "list"
> names(qDE.limma)
[1] "LS-C"    "LS-S"    "S-C"     "bothS-C" "Summary"
> qDE.limma[["LS-C"]][1:10, ]
      genes feature.pos  t.test      p.value adj.p.value
14  Gene11      A12;B12 7.603024 1.999665e-05 0.003839357
50  Gene142     K23;L23 6.271023 9.883760e-05 0.009488409
3   Gene10      A10;B10 5.076932 5.031756e-04 0.024152428
119 Gene32       C9;D9 5.217172 4.113509e-04 0.024152428
23  Gene118     I23;J23 4.812232 7.417071e-04 0.028481551
133 Gene45      C22;D22 4.195002 1.905657e-03 0.060981013
11  Gene107     I12;J12 3.943239 2.842798e-03 0.068227164
100 Gene188     O21;P21 3.973794 2.706901e-03 0.068227164
31  Gene125      K6;L6 3.689090 4.291790e-03 0.082561735
156 Gene66      E19;F19 3.687908 4.300090e-03 0.082561735
      ddCt      FC meanTarget meanCalibrator
14  6.051791 0.0150740287 26.23181 20.18002
50 10.752992 0.0005794645 36.48566 25.73267
3   3.460492 0.0908423086 27.69156 24.23106
119 5.645620 0.0199755612 31.37832 25.73270
23  8.982157 0.0019774303 35.68746 26.70531
133 6.108469 0.0144933090 34.42031 28.31184
11  4.515573 0.0437196812 31.32807 26.81250
100 3.004184 0.1246380522 29.29643 26.29224
31  7.052337 0.0075341638 35.33679 28.28445
156 3.055333 0.1202964947 29.26378 26.20845
      categoryTarget categoryCalibrator
14      OK      Undetermined
50  Undetermined      OK
3      OK      Undetermined
119      OK      OK
23  Undetermined      OK
133      OK      OK
11      OK      OK
100      OK      OK
31      OK      OK
156      OK      OK
```

Furthermore, there is a “Summary” component at the end where each feature is denoted with -1, 0 or 1 to respectively indicate down-regulation, no change, or up-regulation in each of the comparisons.

```
> qDE.limma[["Summary"]][21:30, ]
      Contrasts
      LS-C LS-S S-C bothS-C
Gene116      0      0      0      0
```

Gene117	0	0	0	0
Gene118	1	0	0	0
Gene119	0	0	0	0
Gene12	0	0	0	0
Gene120	0	0	0	0
Gene121	0	0	0	0
Gene122	0	0	0	0
Gene123	0	0	0	0
Gene124	0	0	0	0

11 Displaying the results

The results can be visualised using the generic `plotCtOverview` shown in Figure 3. However, *HTqPCR* also contains more specialised functions, for example to include information about whether differences are significant or not.

11.1 Fold changes: Relative quantification

The relative Ct levels between two groups can be plotted with the function `plotCtRQ`. Below are two examples: one the result of `ttestCtData` where the top 15 genes are selected (figure 21), and another from the first comparison in `limmaCtData` where all genes below a certain p-value are depicted (Figure 22).

```
> plotCtRQ(qDE.ttest, genes = 1:15)

> plotCtRQ(qDE.limma, p.val = 0.085, transform = "log10",
+         col = "#9E0142")
```

The hatching on the bars indicates whether the target and calibrator Ct samples were unreliable, but this also depend on whether the parameter `stringent=TRUE` or `stringent=FALSE` when testing for differential expression. See the help functions for details (`?ttestCtData` and `?limmaCtData`).

11.2 Fold changes: Detailed visualisation

In some cases it will be beneficial to more closely examine individual Ct data points from the fold changes, partly to look at the data dispersion, and partly to determine which of these values are in the “OK” versus “Unreliable”/“Undetermined” category. The function `plotCtSignificance` will take the result of `ttestCtData` or `limmaCtData`, along with the input data to these functions, and display a combined barplot showing the individual data points and marking those comparisons with a significant p-value.

```
> plotCtSignificance(qDE.limma, q = sr.norm, groups = files$Treatment,
+   target = "LongStarve", calibrator = "Control",
+   genes = featureNames(sr.norm)[11:20], un.col = "#3288BD",
+   jitter = 0.2)
```

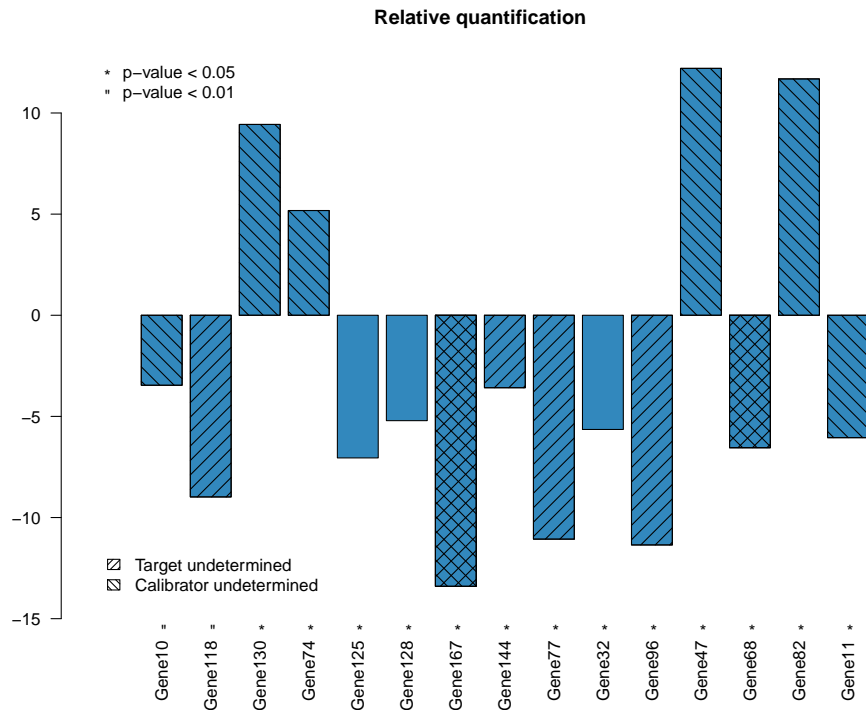


Figure 21: Relative quantification, using the top 15 features from ttestCtData.

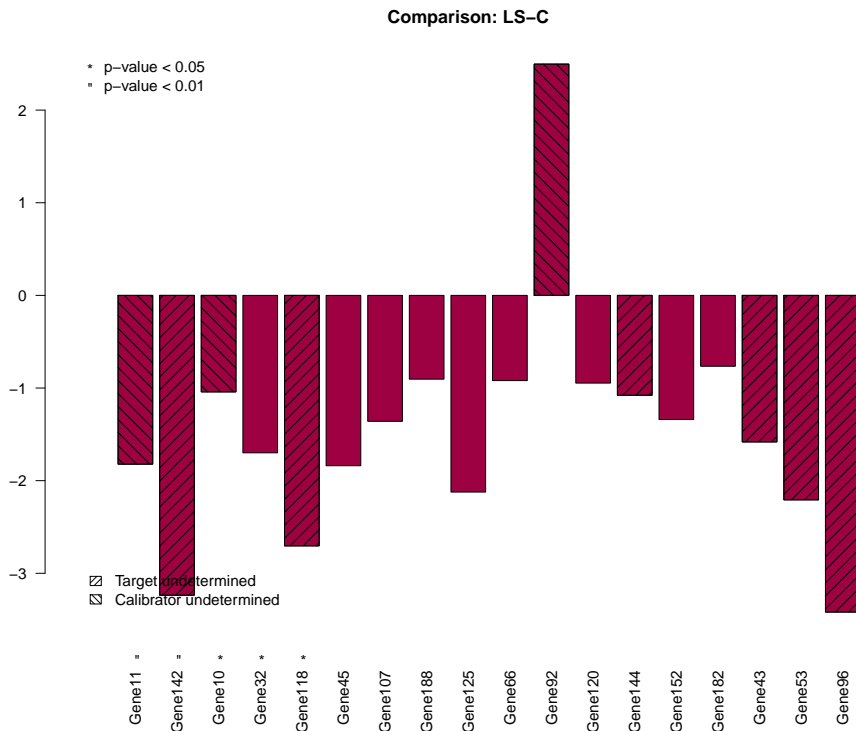


Figure 22: Relative quantification, using all features with p-value<0.085 from limmaCt-Data.

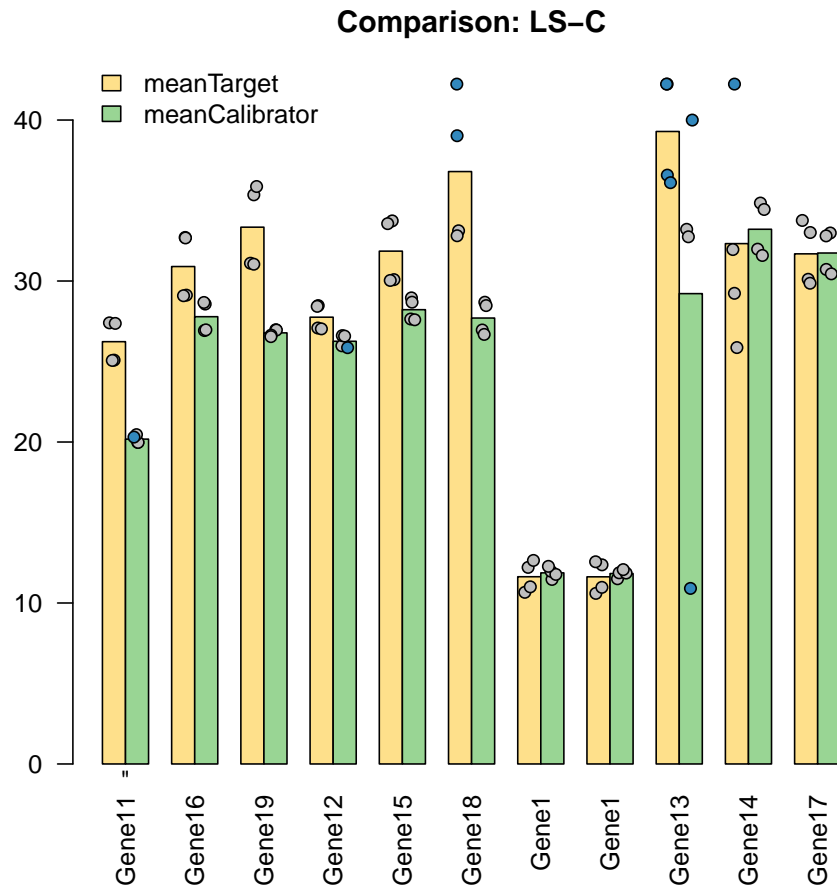


Figure 23: Ten genes from the data set, with the average Ct in two groups plotted along with the individual values. Points marked in blue are “Unreliable” or “Undetermined” whereas grey spots are “OK”.

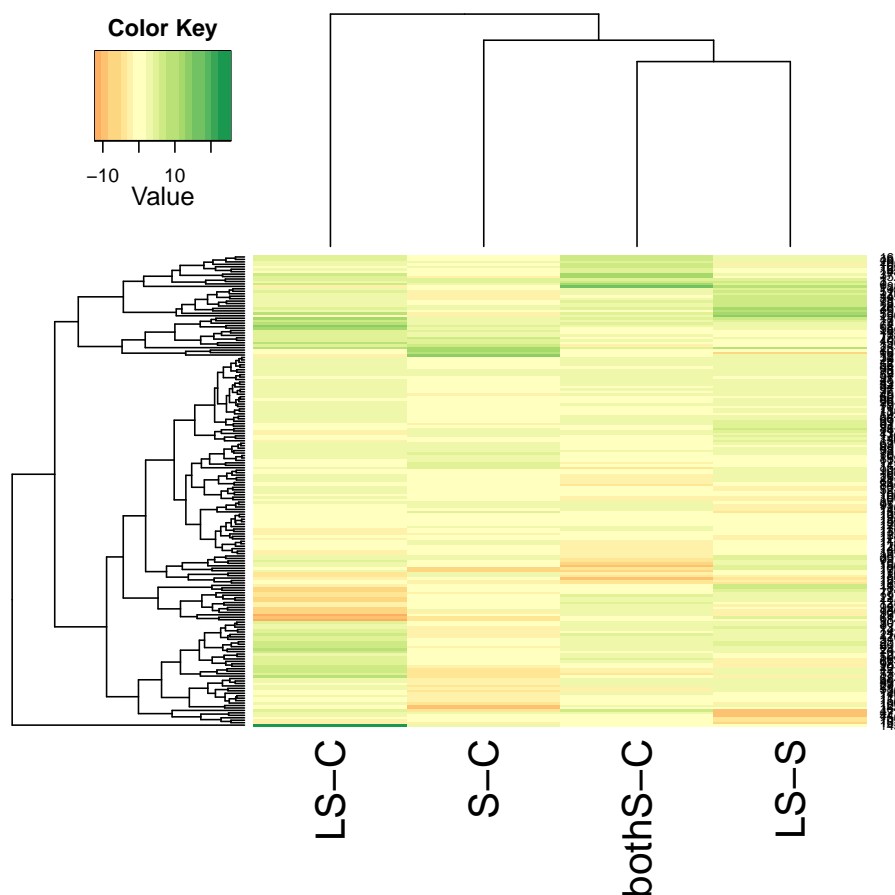


Figure 24: Fold changes across all comparisons, clustered based on Euclidean distance.

11.3 Heatmap across comparisons

When multiple conditions are compared with `limmaCtData`, the fold changes from all comparisons can be compared to see if features cluster together in groups (Figure 24).

```
> heatmapSig(qDE.limma, dist = "euclidean")
```

12 How to handle different input data

General information about how to read qPCR data into a *qPCRset* object is presented in section 3. Below, some more specific cases are illustrated.

12.1 Sequence Detection Systems format

The qPCR data might come from Sequence Detection Systems (SDS) software, in which case each file has a header containing some generic information about the initial Ct detection. This header varies in length depending on how many files were analysed simultaneously, and an example is shown below.

```
> path <- system.file("exData", package = "HTqPCR")
> cat(paste(readLines(file.path(path, "SDS_sample.txt"),
+   n = 19), "\n"))
```

```

SDS 2.3 RQ Results      1.2
Filename      Testscreen analys all.sdm
Assay Type    RQ Study
EmbeddedFile  FileA
Run DateTime  Fri May 15 17:10:28 BST 2009
Operator
ThermalCycleParams
EmbeddedFile  FileB
Run DateTime  Sat May 16 10:36:09 BST 2009
Operator
ThermalCycleParams
EmbeddedFile  FileC
Run DateTime  Sun May 17 13:21:05 BST 2009
Operator
ThermalCycleParams

```

#	Plate	Pos	Flag	Sample	Detector	Task
1	Control	A1	Passed	Sample01	Gene1	Endogenous
2	Control	A2	Passed	Sample01	Gene2	Target

Only the first 7 columns are shown, since the file shown here contains >30 columns (of which many are empty). All columns for the first 20 lines can be seen in an R terminal with the command:

```
> readLines(file.path(path, "SDS_sample.txt"), n = 20)
```

For these files the parameter `SDS=TRUE` can be set in `readCtData`. The first 100 lines of each file will be scanned, and all lines preceding the actual data will be skipped (in this case 17), even when the length of the header varies between files.

13 Manipulating qPCRset objects

Depending on the design of the qPCR card and how the data is to be analysed, it will sometimes be necessary to manipulate the `qPCRset` objects in different ways, such as by combining several objects or altering the layout of features x samples.

13.1 Multiple samples present on each plate

The result from each qPCR run of a given card typically gets presented together, such as in a file with 384 lines, one per feature, for 384 well plates. However, some cards may contain multiple samples, such as commercial cards that are designed to be loaded with two separate samples and then include 192 individual features.

Per default, `readCtData` reads each card into a `qPCRset` object as consisting of a single sample, and hence one column in the Ct data matrix. When this is not the case, the data can subsequently be split into the correct features x samples (rows x columns) dimensions using the function `changeCtLayout`. The parameter `sample.order` is a vector, that for each feature in the `qPCRset` indicates what sample it actually belongs to, and reformats all the information in the `qPCRset` (`exprs`, `featureCategory`, `flag` etc.) accordingly. The actual biological samples are likely to differ on each card, so `sample.order` merely indicates the *location* of different samples among the features present in the input data.

```

> sample2.order <- rep(c("subSampleA", "subSampleB"),
+   each = 192)
> sample4.order <- rep(c("subA", "subB", "subC", "subD"),
+   each = 96)
> qPCRnew2 <- changeCtLayout(sr.norm, sample.order = sample2.order)
> show(qPCRnew2)

An object of class "qPCRset"
Size: 192 features, 12 samples
Feature types:           Endogenous Control, Target
Feature names:           Gene1 Gene2 Gene3 ...
Feature classes:         Kinase, Marker, TF
Feature categories:      OK, Unreliable, Undetermined
Sample names:            subSampleA:sample1 subSampleA:sample2 subSampleA:sample3 .
> qPCRnew4 <- changeCtLayout(sr.norm, sample.order = sample4.order)
> show(qPCRnew4)

An object of class "qPCRset"
Size: 96 features, 24 samples
Feature types:           Endogenous Control, Target
Feature names:           Gene1 Gene2 Gene3 ...
Feature classes:         Kinase, Marker, TF
Feature categories:      OK, Unreliable, Undetermined
Sample names:            subA:sample1 subA:sample2 subA:sample3 ...

```

As with the other functions that manipulate the Ct data, the operation is stored in the history slot of the *qPCRset* for future reference.

```

> getCtHistory(qPCRnew4)

                                history
1          readCtData(files = files$File, path = path)
2 setCategory(q = raw, quantile = 0.8, groups = files$Treatment)
3      normalizeCtData(q = raw.cat, norm = "scale.rank")
4      changeCtLayout(q = sr.norm, sample.order = sample4.order)

```

13.2 Combining multiple qPCRset objects

In some cases it might be desirable to merge multiple *qPCRset* objects, that have been read into R or processed individually. The *HTqPCR* package contains two functions for combining multiple *qPCRset* objects into one, by either adding columns (samples) or rows (features). This can be done for either identical samples across multiple different cards (such as a 384 well plate), or if more samples have been run on cards with the same layout.

cbind combines data assuming that all experiments have been carried out on identical cards, i.e. that **featureNames**, **featureType**, **featurePos** and **featureClass** is identical across all the *qPCRset* objects. The number of features in each object must be identical, but number of samples can vary.

rbind combines data assuming that the same samples have been analysed using different *qPCR* cards. The number of samples in each object must be identical, but the number of features can vary.

Both these functions should be used with some care; consider e.g. whether to normalize before or after joining the samples, and what method to use.

In the examples here objects with different normalisation are combined, although in a real study the `qPCRset` objects would typically contain different data.

```
> q.comb <- cbind(q.norm[, 1:3], sr.norm[, 4], nr.norm[,
+               c(1, 5, 6)])
> q.comb
An object of class "qPCRset"
Size: 384 features, 7 samples
Feature types:      Endogenous Control, Target
Feature names:      Gene1 Gene2 Gene3 ...
Feature classes:    Kinase, Marker, TF
Feature categories: OK, Unreliable, Undetermined
Sample names:      sample1 sample2 sample3 ...
> q.comb2 <- rbind(q.norm, sr.norm[1:4, ], nr.norm)
> q.comb2
An object of class "qPCRset"
Size: 772 features, 6 samples
Feature types:      Endogenous Control, Target
Feature names:      Gene1 Gene2 Gene3 ...
Feature classes:    Kinase, Marker, TF
Feature categories: OK, Unreliable, Undetermined
Sample names:      sample1 sample2 sample3 ...
```

As with other functions where the `qPCRset` object is being manipulated, the information is stored in the history slot.

```
> getCtHistory(q.comb)
history
1          qPCRset1: readCtData(files = files$File, path = path)
2 qPCRset1: setCategory(q = raw, quantile = 0.8, groups = files$Treatment)
3          qPCRset1: normalizeCtData(q = raw.cat, norm = "quantile")
4          qPCRset2: readCtData(files = files$File, path = path)
5 qPCRset2: setCategory(q = raw, quantile = 0.8, groups = files$Treatment)
6          qPCRset2: normalizeCtData(q = raw.cat, norm = "scale.rank")
7          qPCRset3: readCtData(files = files$File, path = path)
8 qPCRset3: setCategory(q = raw, quantile = 0.8, groups = files$Treatment)
9          qPCRset3: normalizeCtData(q = raw.cat, norm = "norm.rank")
10                                     cbind(deparse.level, ..1, ..2, ..3)
```

14 Concluding remarks

This vignette was generated using:

- R version 2.11.0 (2010-04-22), x86_64-pc-mingw32
- Locale: LC_COLLATE=English_United States.1252,
LC_CTYPE=English_United States.1252,
LC_MONETARY=English_United States.1252, LC_NUMERIC=C,
LC_TIME=English_United States.1252
- Base packages: base, datasets, graphics, grDevices, methods, stats, tools, utils
- Other packages: Biobase 2.8.0, HTqPCR 1.2.0, limma 3.4.0, RColorBrewer 1.0-2,
statmod 1.4.6
- Loaded via a namespace (and not attached): affy 1.26.0, affyio 1.16.0, gdata 2.7.1,
gplots 2.7.4, gtools 2.6.1, preprocessCore 1.10.0

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