

```
HTqPSR_script.R x files x
Source on Save Run Source
3 library(HTqPCR)
4
5 path="C:/Users/Hoffmann/Desktop/Master_Biomedizin/3_Semester/Praktikum_AG_Hansmann/Raw_data_t
6
7 files <- read.delim(file.path(path, "Files.txt"))
8 raw <- readCtData(files = files$File, path = path)
9
10
11 head(read.delim(file.path(path, "Files.txt")))
12
13 #####
14 g <- featureNames(raw)[1:10]
15 plotCtOverview(raw, genes=g, xlim=c(0,50), groups=files$Treatment, conf.int=TRUE,
16               ylim=c(0,55))
17
18
19 #####
20 ### code chunk number 11: Ct overview ex 2
21 #####
22 plotCtOverview(raw, genes=g, xlim=c(0,50), groups=files$Treatment,
23               calibrator="NxB")
19:1 (Untitled) R Script

Console ~/
2 NxRV61_CARDA.txt      NxA
> #####
> g <- featureNames(raw)[1:10]
Error in (function (classes, fdef, mtable) :
  unable to find an inherited method for function 'featureNames' for signature "'function'"
> plotCtOverview(raw, genes=g, xlim=c(0,50), groups=files$Treatment, conf.int=TRUE,
+               ylim=c(0,55))
Error in (function (classes, fdef, mtable) :
  unable to find an inherited method for function 'exprs' for signature "'function'"
> rm(list=ls(all=TRUE))
> #####
> ### code chunk number 11: Ct overview ex 2
> #####
> plotCtOverview(raw, genes=g, xlim=c(0,50), groups=files$Treatment,
+               calibrator="NxB")
Error in (function (classes, fdef, mtable) :
  unable to find an inherited method for function 'exprs' for signature "'function'"
> |
```