QC of the TCL38 PSet

Julia Nguyen

```
setwd("~/TCL38")
suppressMessages(library(data.table))
```

```
## Warning: package 'data.table' was built under R version 4.2.2
```

```
suppressMessages(library(S4Vectors))
suppressMessages(library(CoreGx))
```

```
## Warning: package 'matrixStats' was built under R version 4.2.2
```

```
suppressMessages(library(PharmacoGx))
load("PSet_TCL38_23.rds")
```

CHECK: colData for each molecularProfile matches sample dataframe

```
# get colData for each molecularProfile
variant_colData <- tcl38@molecularProfiles$variant@colData
rnaseq_colData <- tcl38@molecularProfiles$rnaseq@colData
acgh_colData <- tcl38@molecularProfiles$acgh@colData

# confirm all samples in colData can be mapped back to the PSet sample dataframe
table(rownames(variant_colData) %in% rownames(tcl38@sample))
```

```
##
## TRUE
##  145
```

```
table(rownames(rnaseq_colData) %in% rownames(tcl38@sample))
```

```
##
## TRUE
##  145
```

```
table(rownames(acgh_colData) %in% tcl38@sample$sampleid)
```

```
##
## TRUE
##   38
```

CHECK: colData matches assays for each molecularProfile

```
# get assays for each molecularProfile
variant_assay <- tcl38@molecularProfiles$variant@assays@data$assay
rnaseq_assay <- tcl38@molecularProfiles$rnaseq@assays@data$exprs
acgh_assay <- tcl38@molecularProfiles$acgh@assays@data$assay

# confirm all sample names map directly (same order) between assay and colData
table(colnames(variant_assay) == rownames(variant_colData))
```

```
##
## TRUE
##  145
```

```
table(colnames(rnaseq_assay) == rownames(rnaseq_colData))
```

```
##
## TRUE
##  145
```

```
table(colnames(acgh_assay) == rownames(acgh_colData))
```

```
##
## TRUE
##   38
```

CHECK: elementMetadata matches assays for each molecularProfile

```
# get elementMetadata for each molecularProfile
variant_emData <- tcl38@molecularProfiles$variant@elementMetadata
rnaseq_emData <- tcl38@molecularProfiles$rnaseq@elementMetadata
acgh_emData <- tcl38@molecularProfiles$acgh@elementMetadata

# confirm all genomic features map directly (same order) between assay and
# elementMetadata
table(rownames(variant_assay) == variant_emData$Coord)
```

```
##
##  TRUE
## 23720
```

```
table(rownames(rnaseq_assay) == rnaseq_emData$gene_id)
```

```
##
##  TRUE
## 60662
```

```
table(rownames(acgh_assay) ==
        paste0(acgh_emData$cellid,"_",acgh_emData$abberation_num))
```

```
##
## TRUE
## 3034
```