A Pan Cancer Atlas

```
setwd("~/desktop/THCA")
ex <- read.delim("~/Desktop/THCA/ex LUAD.tsv")
cn <- ex #backup
rownames(cn) <- cn$gene_id
cn \leftarrow cn[,-1:-2]
# Duplicated Counts from patients
cn \leftarrow cn[,-c(178,223,226,246,339,428,485,474)]
#sample types
library(dplyr)
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
       filter, lag
## The following objects are masked from 'package:base':
##
##
       intersect, setdiff, setequal, union
sampleID <- read.delim("~/desktop/THCA/TCGA-LUAD/Data/gdc_sample_sheet.2022-06-11.tsv")</pre>
i1 <- sampleID$Data.Type == "Gene Expression Quantification"
sampleID <- sampleID[i1, , drop = F]</pre>
sampleID <- sampleID[,7:8]</pre>
sampleID <- distinct(sampleID, Sample.ID, .keep_all = T)</pre>
a <- colnames(cn)
for(i in 1:3){a <- sub('\\.', '-', a)}</pre>
b <- data.frame(IDs = a)</pre>
c <- merge(b, sampleID, by.x = "IDs", by.y = "Sample.ID", sort = F)</pre>
cc <- data.frame(sample = sub("Primary Tumor", "PRT", c$Sample.Type))</pre>
cc <- data.frame(sample = sub("Solid Tissue Normal", "STN", cc$sample))</pre>
for(i in 1:3){c$IDs <- sub('\\-', '.', c$IDs)}</pre>
colnames(cn) <- cc$sample</pre>
head(cn)
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# we reached to our tidy data set
library(DESeq2)
## Loading required package: S4Vectors
```

```
## Loading required package: S4Vectors
## Loading required package: stats4
## Loading required package: BiocGenerics
##
## Attaching package: 'BiocGenerics'
## The following objects are masked from 'package:dplyr':
```

```
##
##
       combine, intersect, setdiff, union
## The following objects are masked from 'package:stats':
##
##
       IQR, mad, sd, var, xtabs
## The following objects are masked from 'package:base':
##
##
       anyDuplicated, append, as.data.frame, basename, cbind, colnames,
##
       dirname, do.call, duplicated, eval, evalq, Filter, Find, get, grep,
##
       grepl, intersect, is.unsorted, lapply, Map, mapply, match, mget,
       order, paste, pmax, pmax.int, pmin, pmin.int, Position, rank,
##
       rbind, Reduce, rownames, sapply, setdiff, sort, table, tapply,
##
       union, unique, unsplit, which.max, which.min
##
##
## Attaching package: 'S4Vectors'
## The following objects are masked from 'package:dplyr':
##
       first, rename
##
## The following objects are masked from 'package:base':
##
##
       expand.grid, I, unname
## Loading required package: IRanges
##
## Attaching package: 'IRanges'
## The following objects are masked from 'package:dplyr':
##
##
       collapse, desc, slice
## Loading required package: GenomicRanges
## Loading required package: GenomeInfoDb
## Loading required package: SummarizedExperiment
## Loading required package: MatrixGenerics
## Loading required package: matrixStats
##
## Attaching package: 'matrixStats'
## The following object is masked from 'package:dplyr':
##
##
       count
##
## Attaching package: 'MatrixGenerics'
## The following objects are masked from 'package:matrixStats':
##
##
       colAlls, colAnyNAs, colAnys, colAvgsPerRowSet, colCollapse,
       colCounts, colCummaxs, colCummins, colCumprods, colCumsums,
##
##
       colDiffs, colIQRDiffs, colIQRs, colLogSumExps, colMadDiffs,
       colMads, colMaxs, colMeans2, colMedians, colMins, colOrderStats,
##
```

```
##
       colProds, colQuantiles, colRanges, colRanks, colSdDiffs, colSds,
##
       colSums2, colTabulates, colVarDiffs, colVars, colWeightedMads,
##
       colWeightedMeans, colWeightedMedians, colWeightedSds,
       colWeightedVars, rowAlls, rowAnyNAs, rowAnys, rowAvgsPerColSet,
##
##
       rowCollapse, rowCounts, rowCummaxs, rowCummins, rowCumprods,
       rowCumsums, rowDiffs, rowIQRDiffs, rowIQRs, rowLogSumExps,
##
       rowMadDiffs, rowMads, rowMaxs, rowMeans2, rowMedians, rowMins,
##
       rowOrderStats, rowProds, rowQuantiles, rowRanges, rowRanks,
##
##
       rowSdDiffs, rowSds, rowSums2, rowTabulates, rowVarDiffs, rowVars,
       rowWeightedMads, rowWeightedMeans, rowWeightedMedians,
##
##
       rowWeightedSds, rowWeightedVars
## Loading required package: Biobase
## Welcome to Bioconductor
##
##
       Vignettes contain introductory material; view with
##
       'browseVignettes()'. To cite Bioconductor, see
##
       'citation("Biobase")', and for packages 'citation("pkgname")'.
##
## Attaching package: 'Biobase'
## The following object is masked from 'package:MatrixGenerics':
##
##
       rowMedians
## The following objects are masked from 'package:matrixStats':
##
       anyMissing, rowMedians
##
con <- factor(paste0(c$Sample.Type, seq_along(c$Sample.Type)))</pre>
gr <- factor(cc$sample)</pre>
#colSums(cn)
colData <- data.frame(condition = con,group = gr , type = "paired-end")</pre>
cds <- DESeqDataSetFromMatrix(cn, colData, design = ~group)</pre>
cds <- DESeq(cds) #Constructing DESeq2 dataset</pre>
## estimating size factors
## estimating dispersions
## gene-wise dispersion estimates
## mean-dispersion relationship
## final dispersion estimates
## fitting model and testing
## -- replacing outliers and refitting for 8106 genes
## -- DESeq argument 'minReplicatesForReplace' = 7
## -- original counts are preserved in counts(dds)
## estimating dispersions
## fitting model and testing
cnt <- log2(1+(counts(cds, normalize = T))) #qetting normalized counts `count matrix`</pre>
```