

Figures

Nhan Nguyen

2020 M09 9

Figures

```
## Loading required package: here

## here() starts at D:/TGX/GitHub/lncRNA-EPI

## DOX_Tox_240_2 IDA_The_240_3
##      1312.99      4522.99

## Loading required package: S4Vectors

## Loading required package: stats4

## Loading required package: BiocGenerics

## Loading required package: parallel

##
## Attaching package: 'BiocGenerics'

## The following objects are masked from 'package:parallel':
##
##      clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,
##      clusterExport, clusterMap, parApply, parCapply, parLapply,
##      parLapplyLB, parRapply, parSapply, parSapplyLB

## 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, which.max, which.min
```

```

##
## Attaching package: 'S4Vectors'

## The following object is masked from 'package:base':
##
##     expand.grid

## Loading required package: IRanges

##
## Attaching package: 'IRanges'

## The following object is masked from 'package:grDevices':
##
##     windows

## Loading required package: GenomicRanges

## Loading required package: GenomeInfoDb

## Loading required package: SummarizedExperiment

## 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)".

## Loading required package: DelayedArray

## Loading required package: matrixStats

##
## Attaching package: 'matrixStats'

## The following objects are masked from 'package:Biobase':
##
##     anyMissing, rowMedians

##
## Attaching package: 'DelayedArray'

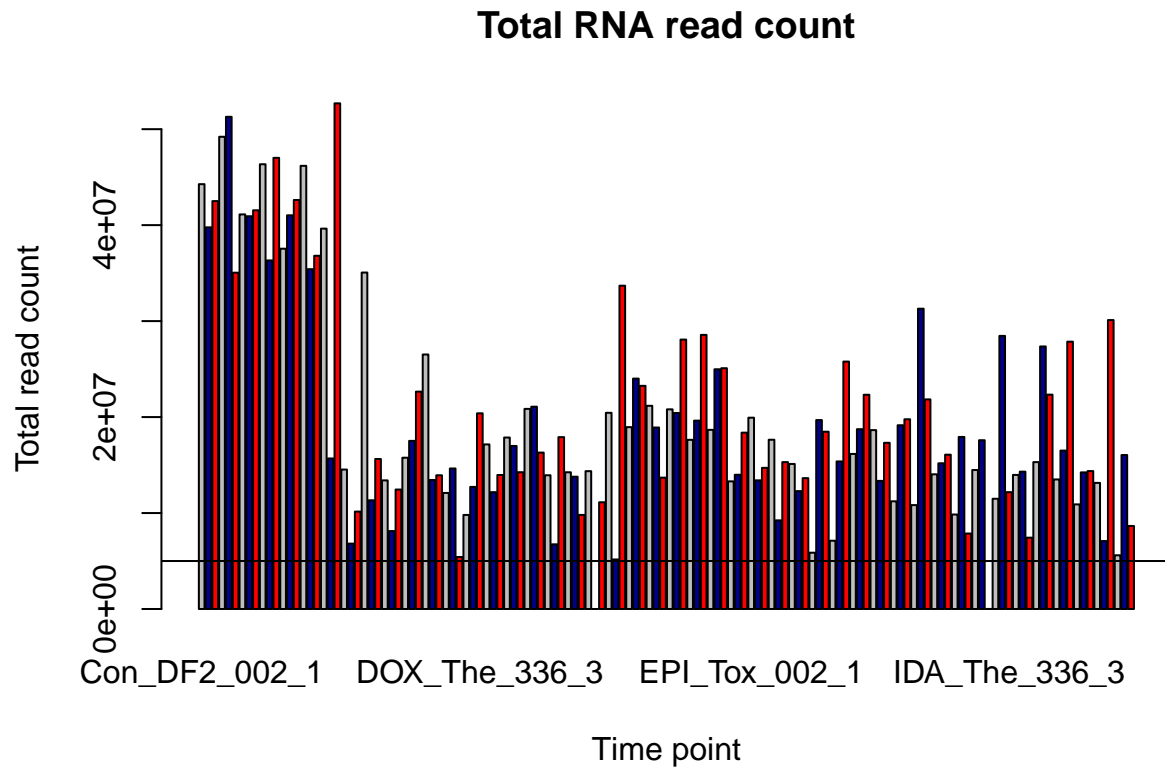
## The following objects are masked from 'package:matrixStats':
##
##     colMaxs, colMins, colRanges, rowMaxs, rowMins, rowRanges

## The following objects are masked from 'package:base':
##
##     aperm, apply, rowsum

```

```
## converting counts to integer mode
```

```
## Warning in DESeqDataSet(se, design = design, ignoreRank): some variables in  
## design formula are characters, converting to factors
```



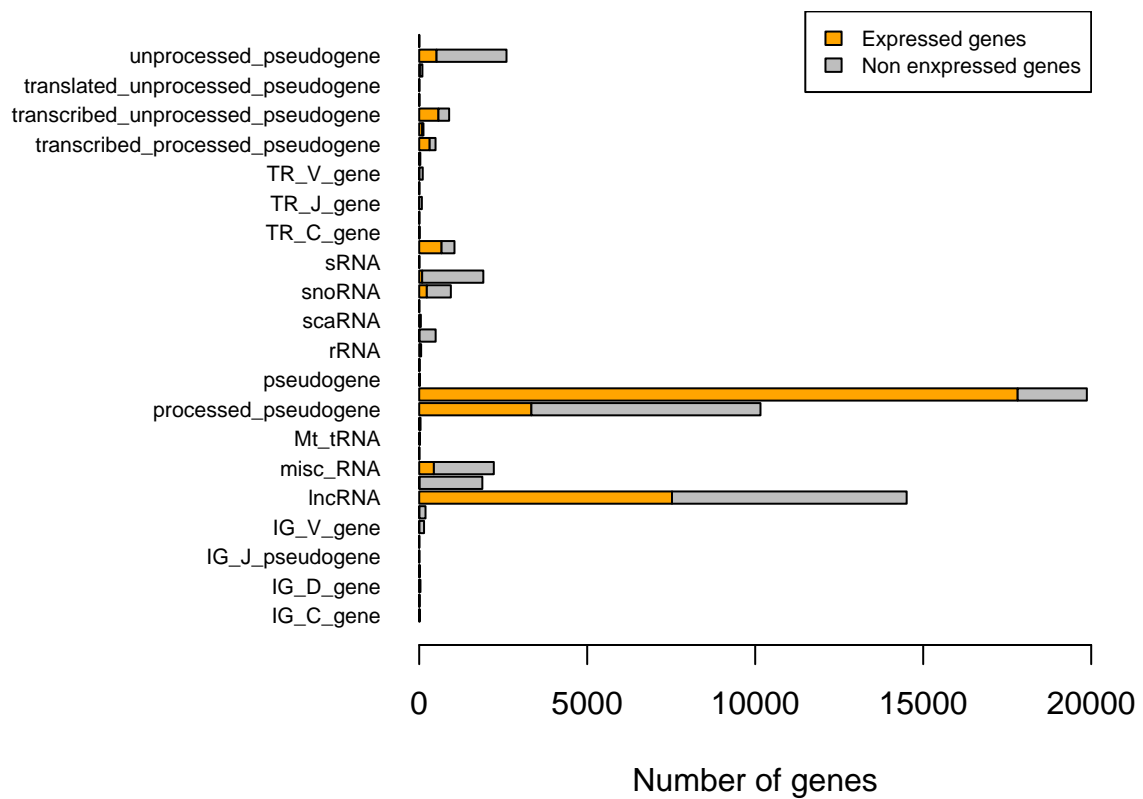


Figure 1: The proportion of gene expressed in each gene type in the RNA-seq data.

PCA samples:

```
## Loading required package: ggplot2
```

```
## Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa
```

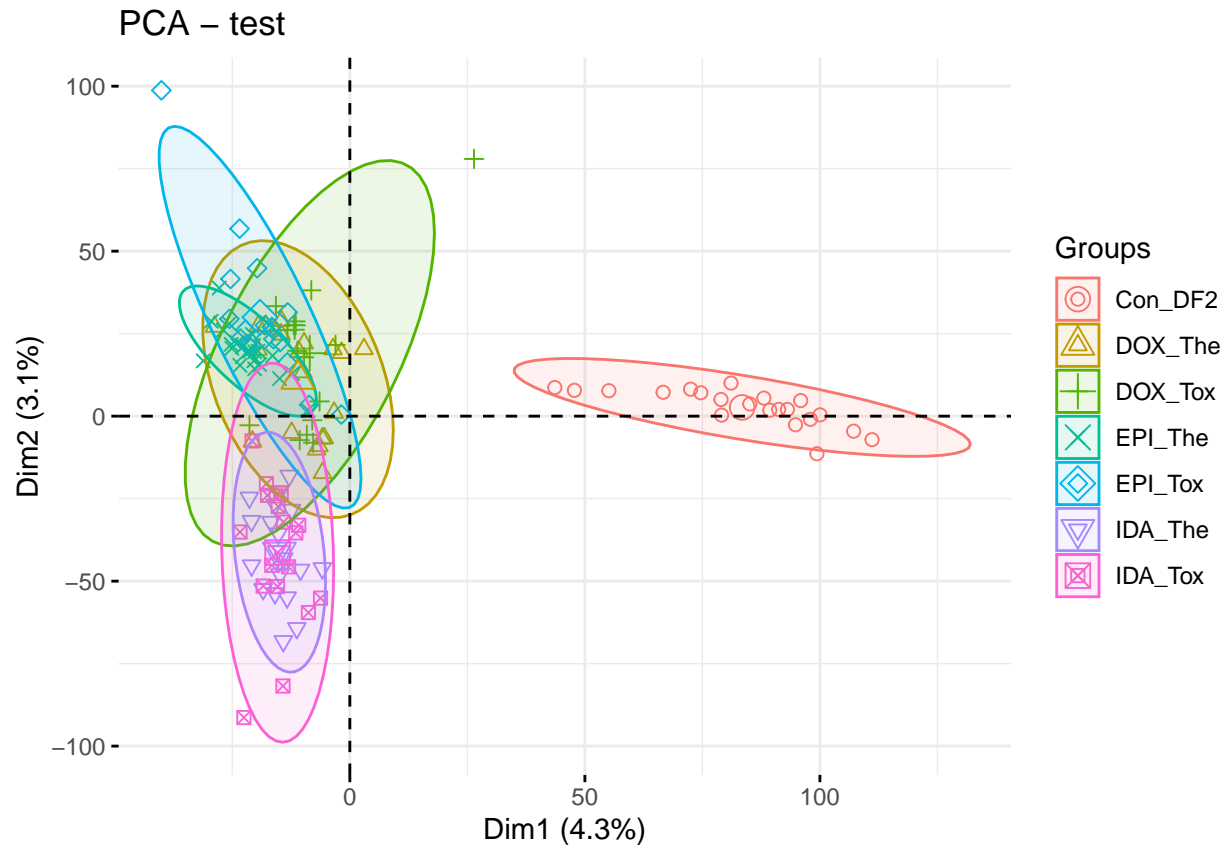


Figure 2: PCA of the samples

expression:

```
##
## Attaching package: 'plyr'

## The following object is masked from 'package:matrixStats':
##
##   count

## The following object is masked from 'package:IRanges':
##
##   desc

## The following object is masked from 'package:S4Vectors':
##
##   rename

## The following object is masked from 'package:here':
##
##   here

##
## Attaching package: 'gridExtra'
```

```

## The following object is masked from 'package:Biobase':
##
##      combine

## The following object is masked from 'package:BiocGenerics':
##
##      combine

##
## Attaching package: 'dplyr'

## The following object is masked from 'package:gridExtra':
##
##      combine

## The following objects are masked from 'package:plyr':
##
##      arrange, count, desc, failwith, id, mutate, rename, summarise,
##      summarize

## The following object is masked from 'package:matrixStats':
##
##      count

## The following object is masked from 'package:Biobase':
##
##      combine

## The following objects are masked from 'package:GenomicRanges':
##
##      intersect, setdiff, union

## The following object is masked from 'package:GenomeInfoDb':
##
##      intersect

## The following objects are masked from 'package:IRanges':
##
##      collapse, desc, intersect, setdiff, slice, union

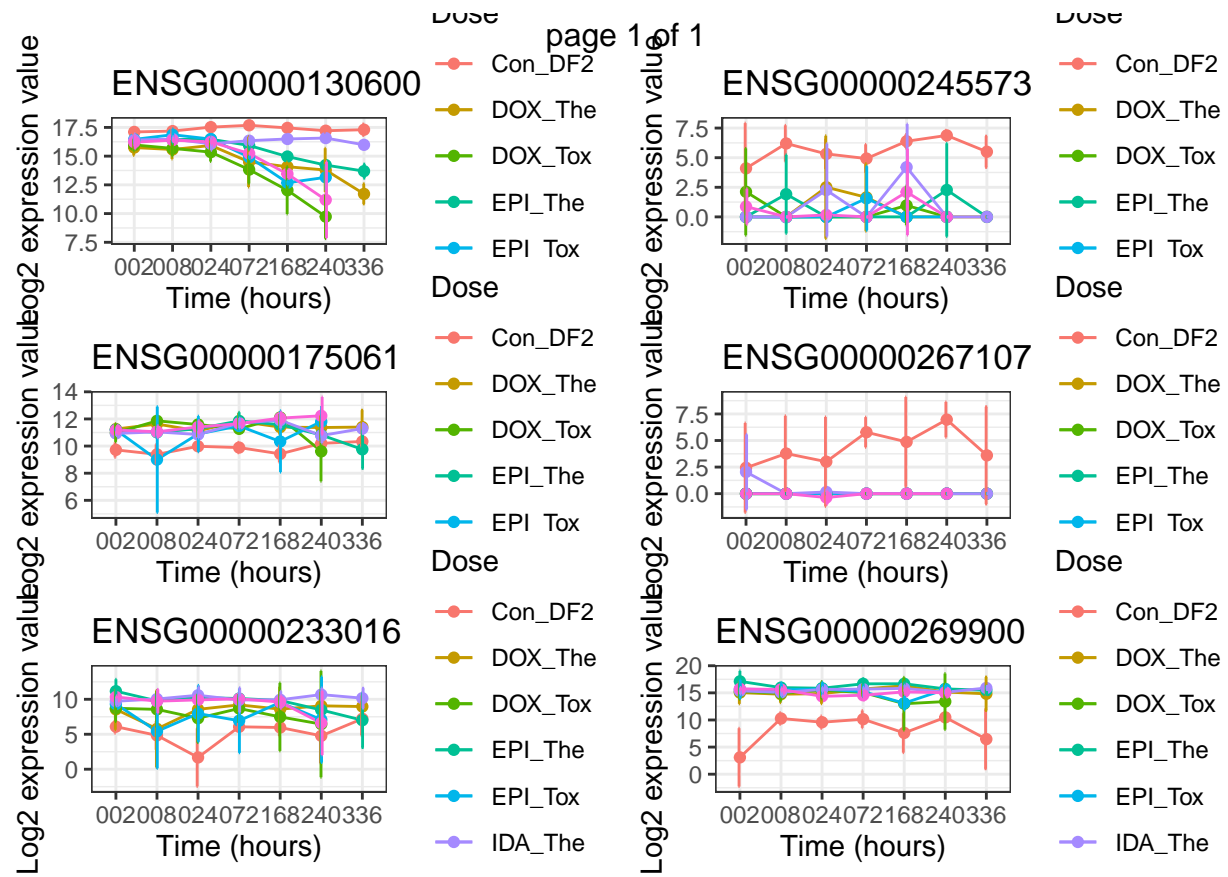
## The following objects are masked from 'package:S4Vectors':
##
##      first, intersect, rename, setdiff, setequal, union

## The following objects are masked from 'package:BiocGenerics':
##
##      combine, intersect, setdiff, union

## The following objects are masked from 'package:stats':
##
##      filter, lag

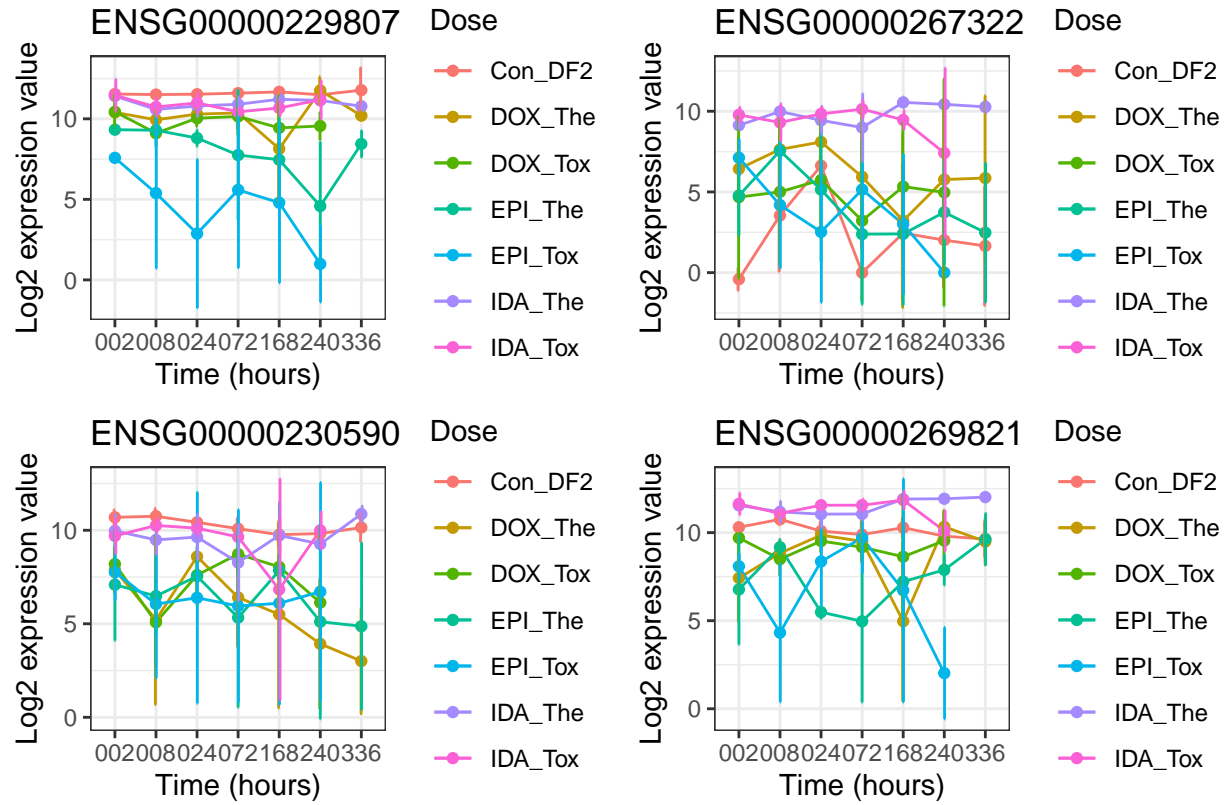
```

```
## The following objects are masked from 'package:base':
##
## intersect, setdiff, setequal, union
```



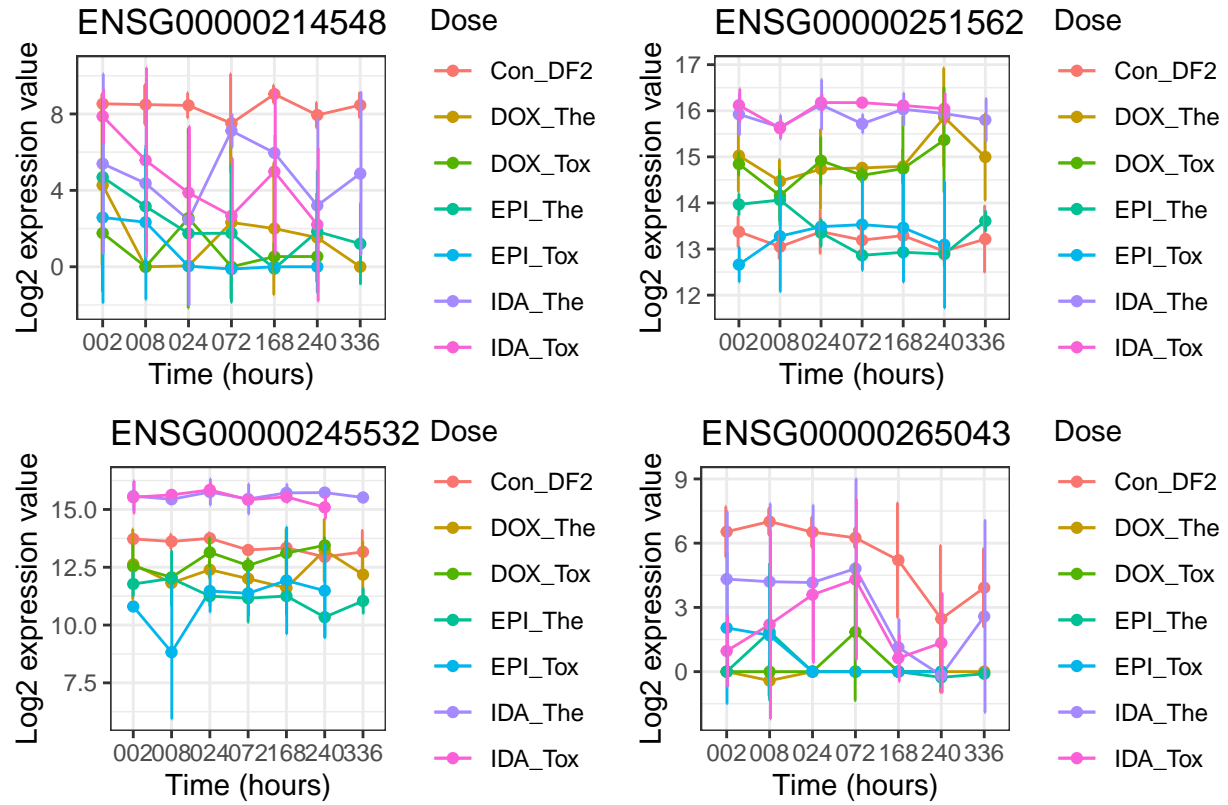
```
## [[1]]
## NULL
```

Figure 3.A: Overlapping DE lncRNAs in all ANT-treated samples



```
## [[1]]
## NULL
```

Figure 3.B: DE lncRNAs in DOX, EPI, iDA



```
## [[1]]
## NULL
```

Figure 3.C: DE lncRNAs in 2 of 3 ANT drugs