Class 14: RNASeq Analysis Mini Project

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Differential Expression Analysis

Load our data files

```
library(DESeq2)
```

```
Loading required package: S4Vectors

Loading required package: stats4

Loading required package: BiocGenerics


Attaching package: 'BiocGenerics'

The following objects are masked from 'package:stats':

    IQR, mad, sd, var, xtabs

The following objects are masked from 'package:base':

    anyDuplicated, aperm, 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 object is masked from 'package:utils':

    findMatches

The following objects are masked from 'package:base':

    expand.grid, I, unname

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: MatrixGenerics

Loading required package: matrixStats


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
```

Import metadata and countdata, and take a peak

```
  metaFile <- "GSE37704_metadata.csv"
  countFile <- "GSE37704_featurecounts.csv"


  colData = read.csv(metaFile, row.names=1)
  head(colData)
```

```
            condition
SRR493366 control_sirna
SRR493367 control_sirna
SRR493368 control_sirna
```

```
SRR493369      hoxa1_kd
SRR493370      hoxa1_kd
SRR493371      hoxa1_kd
```

```
countData = read.csv(countFile, row.names=1)
head(countData)
```

```
                length SRR493366 SRR493367 SRR493368 SRR493369 SRR493370
ENSG00000186092    918         0         0         0         0         0
ENSG00000279928    718         0         0         0         0         0
ENSG00000279457   1982        23        28        29        29        28
ENSG00000278566    939         0         0         0         0         0
ENSG00000273547    939         0         0         0         0         0
ENSG00000187634   3214       124       123       205       207       212
                SRR493371
ENSG00000186092         0
ENSG00000279928         0
ENSG00000279457        46
ENSG00000278566         0
ENSG00000273547         0
ENSG00000187634       258
```

Note we need to remove the odd first$length col

```
countData <- as.matrix(countData[,-1])
```

```
head(countData)
```

```
                SRR493366 SRR493367 SRR493368 SRR493369 SRR493370 SRR493371
ENSG00000186092         0         0         0         0         0         0
ENSG00000279928         0         0         0         0         0         0
ENSG00000279457        23        28        29        29        28        46
ENSG00000278566         0         0         0         0         0         0
ENSG00000273547         0         0         0         0         0         0
ENSG00000187634       124       123       205       207       212       258
```

Filter the count data where you have 0 read count across all samples.

```
countData = countData[rowSums(countData) >0, ]
head(countData)
```

```
               SRR493366 SRR493367 SRR493368 SRR493369 SRR493370 SRR493371
ENSG00000279457        23        28        29        29        28        46
ENSG00000187634       124       123       205       207       212       258
ENSG00000188976      1637      1831      2383      1226      1326      1504
ENSG00000187961       120       153       180       236       255       357
ENSG00000187583        24        48        65        44        48        64
ENSG00000187642         4         9        16        14        16        16
```

Nice now lets setup the DESeqDataSet object required for the DESeq() function and then run the DESeq pipeline.

```
dds = DESeqDataSetFromMatrix(countData=countData,
                             colData=colData,
                             design=~condition)
```

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

```
dds = DESeq(dds)
```

estimating size factors

estimating dispersions

gene-wise dispersion estimates

mean-dispersion relationship

final dispersion estimates

fitting model and testing

```
dds
```

```
class: DESeqDataSet
dim: 15975 6
metadata(1): version
assays(4): counts mu H cooks
rownames(15975): ENSG00000279457 ENSG00000187634 ... ENSG00000276345
  ENSG00000271254
rowData names(22): baseMean baseVar ... deviance maxCooks
colnames(6): SRR493366 SRR493367 ... SRR493370 SRR493371
colData names(2): condition sizeFactor
```

Next, get results for the HoxA1 knockdown versus control siRNA (remember that these were labeled as "hoxa1_kd" and "control_sirna" in our original colData metaFile input to DESeq, you can check this above and by running resultsNames(dds) command).

```
res = results(dds, contrast=c("condition", "hoxa1_kd", "control_sirna"))
```

```
summary(res)
```

```
out of 15975 with nonzero total read count
adjusted p-value < 0.1
LFC > 0 (up)       : 4349, 27%
LFC < 0 (down)     : 4396, 28%
outliers [1]       : 0, 0%
low counts [2]     : 1237, 7.7%
(mean count < 0)
[1] see 'cooksCutoff' argument of ?results
[2] see 'independentFiltering' argument of ?results
```
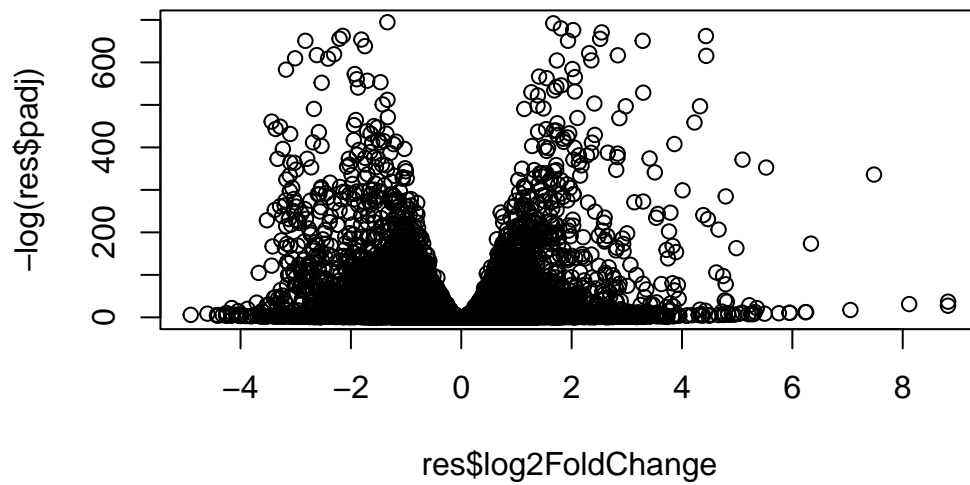
Make a plot

```
plot(res$log2FoldChange, -log(res$padj))
```

```r
# Make a color vector for all genes
mycols <- rep("gray", nrow(res) )

# Color red the genes with absolute fold change above 2
mycols[ abs(res$log2FoldChange) > 2 ] <- "red"

# Color blue those with adjusted p-value less than 0.01
#  and absolute fold change more than 2
inds <- (res$padj<0.01) & (abs(res$log2FoldChange) > 2 )
mycols[ inds ] <- "blue"

plot( res$log2FoldChange, -log(res$padj), col=mycols, xlab="Log2(FoldChange)", ylab="-Log(
```

Adding gene annotation

```
library("AnnotationDbi")
library("org.Hs.eg.db")
```

```
columns(org.Hs.eg.db)
```

```
 [1] "ACCNUM"      "ALIAS"       "ENSEMBL"      "ENSEMBLPROT"   "ENSEMBLTRANS"
 [6] "ENTREZID"    "ENZYME"      "EVIDENCE"     "EVIDENCEALL"   "GENENAME"
[11] "GENETYPE"    "GO"          "GOALL"        "IPI"           "MAP"
[16] "OMIM"        "ONTOLOGY"    "ONTOLOGYALL"  "PATH"          "PFAM"
[21] "PMID"        "PROSITE"     "REFSEQ"       "SYMBOL"        "UCSCKG"
[26] "UNIPROT"
```

```
res$symbol = mapIds(org.Hs.eg.db,
                    keys=row.names(res),
                    keytype="ENSEMBL",
                    column="SYMBOL",
```

```
                    multiVals="first")
```

'select()' returned 1:many mapping between keys and columns

```
res$entrez = mapIds(org.Hs.eg.db,
                    keys=row.names(res),
                    keytype="ENSEMBL",
                    column="ENTREZID",
                    multiVals="first")
```

'select()' returned 1:many mapping between keys and columns

```
res$name =   mapIds(org.Hs.eg.db,
                    keys=row.names(res),
                    keytype="ENSEMBL",
                    column="GENENAME",
                    multiVals="first")
```

'select()' returned 1:many mapping between keys and columns

```
head(res, 10)
```

log2 fold change (MLE): condition hoxa1_kd vs control_sirna
Wald test p-value: condition hoxa1 kd vs control sirna
DataFrame with 10 rows and 9 columns
                  baseMean log2FoldChange   lfcSE   stat   pvalue
                 <numeric>   <numeric> <numeric>   <numeric>   <numeric>
ENSG00000279457   29.913579   0.1792571 0.3248216   0.551863 5.81042e-01
ENSG00000187634 183.229650   0.4264571 0.1402658   3.040350 2.36304e-03
ENSG00000188976 1651.188076   -0.6927205 0.0548465 -12.630158 1.43990e-36
ENSG00000187961 209.637938   0.7297556 0.1318599   5.534326 3.12428e-08
ENSG00000187583   47.255123   0.0405765 0.2718928   0.149237 8.81366e-01
ENSG00000187642   11.979750   0.5428105 0.5215598   1.040744 2.97994e-01
ENSG00000188290 108.922128   2.0570638 0.1969053   10.446970 1.51282e-25
ENSG00000187608 350.716868   0.2573837 0.1027266   2.505522 1.22271e-02
ENSG00000188157 9128.439422   0.3899088 0.0467163   8.346304 7.04321e-17
ENSG00000237330   0.158192   0.7859552 4.0804729   0.192614 8.47261e-01
```

```
                      padj      symbol      entrez                        name
                 <numeric> <character> <character>                 <character>
ENSG00000279457 6.86555e-01          NA          NA                          NA
ENSG00000187634 5.15718e-03      SAMD11      148398 sterile alpha motif ..
ENSG00000188976 1.76549e-35       NOC2L       26155 NOC2 like nucleolar ..
ENSG00000187961 1.13413e-07      KLHL17      339451 kelch like family me..
ENSG00000187583 9.19031e-01     PLEKHN1       84069 pleckstrin homology ..
ENSG00000187642 4.03379e-01       PERM1       84808 PPARGC1 and ESRR ind..
ENSG00000188290 1.30538e-24        HES4       57801 hes family bHLH tran..
ENSG00000187608 2.37452e-02       ISG15        9636 ISG15 ubiquitin like..
ENSG00000188157 4.21963e-16        AGRN      375790                       agrin
ENSG00000237330          NA      RNF223      401934 ring finger protein ..
```

Finally for this section let's reorder these results by adjusted p-value and save them to a CSV file in your current project directory.

```
res = res[order(res$pvalue),]
write.csv(res, file="deseq_results.csv")
```

Pathway Analysis

```
library(pathview)
```

```
##############################################################################
Pathview is an open source software package distributed under GNU General
Public License version 3 (GPLv3). Details of GPLv3 is available at
http://www.gnu.org/licenses/gpl-3.0.html. Particullary, users are required to
formally cite the original Pathview paper (not just mention it) in publications
or products. For details, do citation("pathview") within R.

The pathview downloads and uses KEGG data. Non-academic uses may require a KEGG
license agreement (details at http://www.kegg.jp/kegg/legal.html).
##############################################################################
```

```
library(gage)
```

```
library(gageData)

data(kegg.sets.hs)
data(sigmet.idx.hs)

# Focus on signaling and metabolic pathways only
kegg.sets.hs = kegg.sets.hs[sigmet.idx.hs]

# Examine the first 3 pathways
head(kegg.sets.hs, 3)
```

$`hsa00232 Caffeine metabolism`
[1] "10"   "1544" "1548" "1549" "1553" "7498" "9"

$`hsa00983 Drug metabolism - other enzymes`
 [1] "10"   "1066"   "10720" "10941" "151531" "1548"   "1549"   "1551"
 [9] "1553"   "1576"   "1577"   "1806"   "1807"   "1890"   "221223" "2990"
[17] "3251"   "3614"   "3615"   "3704"   "51733" "54490" "54575" "54576"
[25] "54577" "54578" "54579" "54600" "54657" "54658" "54659" "54963"
[33] "574537" "64816" "7083"   "7084"   "7172"   "7363"   "7364"   "7365"
[41] "7366"   "7367"   "7371"   "7372"   "7378"   "7498"   "79799" "83549"
[49] "8824"   "8833"   "9"   "978"

$`hsa00230 Purine metabolism`
  [1] "100"   "10201" "10606" "10621" "10622" "10623" "107"   "10714"
  [9] "108"   "10846" "109"   "111"   "11128" "11164" "112"   "113"
 [17] "114"   "115"   "122481" "122622" "124583" "132"   "158"   "159"
 [25] "1633"   "171568" "1716"   "196883" "203"   "204"   "205"   "221823"
 [33] "2272"   "22978" "23649" "246721" "25885" "2618"   "26289" "270"
 [41] "271"   "27115" "272"   "2766"   "2977"   "2982"   "2983"   "2984"
 [49] "2986"   "2987"   "29922" "3000"   "30833" "30834" "318"   "3251"
 [57] "353"   "3614"   "3615"   "3704"   "377841" "471"   "4830"   "4831"
 [65] "4832"   "4833"   "4860"   "4881"   "4882"   "4907"   "50484" "50940"
 [73] "51082" "51251" "51292" "5136"   "5137"   "5138"   "5139"   "5140"
 [81] "5141"   "5142"   "5143"   "5144"   "5145"   "5146"   "5147"   "5148"
 [89] "5149"   "5150"   "5151"   "5152"   "5153"   "5158"   "5167"   "5169"
 [97] "51728" "5198"   "5236"   "5313"   "5315"   "53343" "54107" "5422"
[105] "5424"   "5425"   "5426"   "5427"   "5430"   "5431"   "5432"   "5433"
[113] "5434"   "5435"   "5436"   "5437"   "5438"   "5439"   "5440"   "5441"
[121] "5471"   "548644" "55276" "5557"   "5558"   "55703" "55811" "55821"
[129] "5631"   "5634"   "56655" "56953" "56985" "57804" "58497" "6240"
[137] "6241"   "64425" "646625" "654364" "661"   "7498"   "8382"   "84172"
```

```
[145] "84265"  "84284"  "84618"  "8622"   "8654"   "87178"  "8833"   "9060"
[153] "9061"   "93034"  "953"    "9533"   "954"    "955"    "956"    "957"
[161] "9583"   "9615"
```

```
foldchanges = res$log2FoldChange
names(foldchanges) = res$entrez
head(foldchanges)
```

```
     1266     54855     1465     51232     2034     2317
-2.422719  3.201955 -2.313738 -2.059631 -1.888019 -1.649792
```

Get the results

```
keggres = gage(foldchanges, gsets=kegg.sets.hs)
```

```
attributes(keggres)
```

```
$names
[1] "greater" "less"    "stats"
```

Look at the first few down (less) pathways

```
head(keggres$less)
```

```
                                          p.geomean stat.mean       p.val
hsa04110 Cell cycle                    8.995727e-06 -4.378644 8.995727e-06
hsa03030 DNA replication               9.424076e-05 -3.951803 9.424076e-05
hsa03013 RNA transport                 1.375901e-03 -3.028500 1.375901e-03
hsa03440 Homologous recombination      3.066756e-03 -2.852899 3.066756e-03
hsa04114 Oocyte meiosis                3.784520e-03 -2.698128 3.784520e-03
hsa00010 Glycolysis / Gluconeogenesis  8.961413e-03 -2.405398 8.961413e-03
                                             q.val set.size         exp1
hsa04110 Cell cycle                    0.001448312      121 8.995727e-06
hsa03030 DNA replication               0.007586381       36 9.424076e-05
hsa03013 RNA transport                 0.073840037      144 1.375901e-03
hsa03440 Homologous recombination      0.121861535       28 3.066756e-03
hsa04114 Oocyte meiosis                0.121861535      102 3.784520e-03
hsa00010 Glycolysis / Gluconeogenesis  0.212222694       53 8.961413e-03
```

```r
pathview(gene.data=foldchanges, pathway.id="hsa04110")
```

'select()' returned 1:1 mapping between keys and columns

Info: Working in directory C:/Users/wolfi/Downloads/UCSD & UCLA Folder/UCSD/UCSD Classes/202

Info: Writing image file hsa04110.pathview.png

```r
pathview(gene.data=foldchanges, pathway.id="hsa04110", kegg.native=FALSE)
```

'select()' returned 1:1 mapping between keys and columns

Warning: reconcile groups sharing member nodes!

```
     [,1] [,2]
[1,] "9"  "300"
[2,] "9"  "306"
```

Info: Working in directory C:/Users/wolfi/Downloads/UCSD & UCLA Folder/UCSD/UCSD Classes/202

Info: Writing image file hsa04110.pathview.pdf

Extract the 8 character long IDs part of each string

```r
keggrespathways <- rownames(keggres$greater)[1:5]

keggresids = substr(keggrespathways, start=1, stop=8)
keggresids
```

```
[1] "hsa04640" "hsa04630" "hsa00140" "hsa04142" "hsa04330"
```

```r
pathview(gene.data=foldchanges, pathway.id=keggresids, species="hsa")
```

'select()' returned 1:1 mapping between keys and columns

```
Info: Working in directory C:/Users/wolfi/Downloads/UCSD & UCLA Folder/UCSD/UCSD Classes/2023

Info: Writing image file hsa04640.pathview.png

'select()' returned 1:1 mapping between keys and columns

Info: Working in directory C:/Users/wolfi/Downloads/UCSD & UCLA Folder/UCSD/UCSD Classes/2023

Info: Writing image file hsa04630.pathview.png

'select()' returned 1:1 mapping between keys and columns

Info: Working in directory C:/Users/wolfi/Downloads/UCSD & UCLA Folder/UCSD/UCSD Classes/2023

Info: Writing image file hsa00140.pathview.png

'select()' returned 1:1 mapping between keys and columns

Info: Working in directory C:/Users/wolfi/Downloads/UCSD & UCLA Folder/UCSD/UCSD Classes/2023

Info: Writing image file hsa04142.pathview.png

'select()' returned 1:1 mapping between keys and columns

Info: Working in directory C:/Users/wolfi/Downloads/UCSD & UCLA Folder/UCSD/UCSD Classes/2023

Info: Writing image file hsa04330.pathview.png
```

Gene Ontology (GO)

```r
data(go.sets.hs)
data(go.subs.hs)

gobpsets = go.sets.hs[go.subs.hs$BP]

gobpres = gage(foldchanges, gsets=gobpsets, same.dir=TRUE)
```

```
lapply(gobpres, head)
```

$greater
```
                                         p.geomean stat.mean          p.val
GO:0007156 homophilic cell adhesion      8.519724e-05  3.824205 8.519724e-05
GO:0002009 morphogenesis of an epithelium 1.396681e-04  3.653886 1.396681e-04
GO:0048729 tissue morphogenesis         1.432451e-04  3.643242 1.432451e-04
GO:0007610 behavior                     1.925222e-04  3.565432 1.925222e-04
GO:0060562 epithelial tube morphogenesis 5.932837e-04  3.261376 5.932837e-04
GO:0035295 tube development             5.953254e-04  3.253665 5.953254e-04
                                             q.val set.size         exp1
GO:0007156 homophilic cell adhesion      0.1952430      113 8.519724e-05
GO:0002009 morphogenesis of an epithelium 0.1952430      339 1.396681e-04
GO:0048729 tissue morphogenesis         0.1952430      424 1.432451e-04
GO:0007610 behavior                     0.1968058      426 1.925222e-04
GO:0060562 epithelial tube morphogenesis 0.3566193      257 5.932837e-04
GO:0035295 tube development             0.3566193      391 5.953254e-04


$less
                                          p.geomean stat.mean          p.val
GO:0048285 organelle fission            1.536227e-15 -8.063910 1.536227e-15
GO:0000280 nuclear division             4.286961e-15 -7.939217 4.286961e-15
GO:0007067 mitosis                      4.286961e-15 -7.939217 4.286961e-15
GO:0000087 M phase of mitotic cell cycle 1.169934e-14 -7.797496 1.169934e-14
GO:0007059 chromosome segregation       2.028624e-11 -6.878340 2.028624e-11
GO:0000236 mitotic prometaphase         1.729553e-10 -6.695966 1.729553e-10
                                             q.val set.size         exp1
GO:0048285 organelle fission            5.843127e-12      376 1.536227e-15
GO:0000280 nuclear division             5.843127e-12      352 4.286961e-15
GO:0007067 mitosis                      5.843127e-12      352 4.286961e-15
GO:0000087 M phase of mitotic cell cycle 1.195965e-11      362 1.169934e-14
GO:0007059 chromosome segregation       1.659009e-08      142 2.028624e-11
GO:0000236 mitotic prometaphase         1.178690e-07       84 1.729553e-10


$stats
                                         stat.mean     exp1
GO:0007156 homophilic cell adhesion      3.824205 3.824205
GO:0002009 morphogenesis of an epithelium 3.653886 3.653886
GO:0048729 tissue morphogenesis         3.643242 3.643242
GO:0007610 behavior                     3.565432 3.565432
GO:0060562 epithelial tube morphogenesis 3.261376 3.261376
GO:0035295 tube development             3.253665 3.253665
```

Reactome Analysis

First, Using R, output the list of significant genes at the 0.05 level as a plain text file:

```
sig_genes <- res[res$padj <= 0.05 & !is.na(res$padj), "symbol"]
print(paste("Total number of significant genes:", length(sig_genes)))
```

```
[1] "Total number of significant genes: 8147"
```

```
write.table(sig_genes, file="significant_genes.txt", row.names=FALSE, col.names=FALSE, quo
```

```
sessionInfo()
```

```
R version 4.3.3 (2024-02-29 ucrt)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows 11 x64 (build 22631)

Matrix products: default


locale:
[1] LC_COLLATE=English_United States.utf8
[2] LC_CTYPE=English_United States.utf8
[3] LC_MONETARY=English_United States.utf8
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.utf8

time zone: America/Los_Angeles
tzcode source: internal

attached base packages:
[1] stats4    stats     graphics  grDevices utils     datasets  methods
[8] base

other attached packages:
 [1] gageData_2.40.0             gage_2.52.0
 [3] pathview_1.42.0             org.Hs.eg.db_3.18.0
 [5] AnnotationDbi_1.64.1        DESeq2_1.42.1
 [7] SummarizedExperiment_1.32.0 Biobase_2.62.0
 [9] MatrixGenerics_1.14.0       matrixStats_1.3.0
```

```
[11] GenomicRanges_1.54.1       GenomeInfoDb_1.38.8
[13] IRanges_2.36.0            S4Vectors_0.40.2
[15] BiocGenerics_0.48.1

loaded via a namespace (and not attached):
 [1] KEGGREST_1.42.0         gtable_0.3.4         xfun_0.43
 [4] ggplot2_3.5.0           lattice_0.22-5       vctrs_0.6.5
 [7] tools_4.3.3             bitops_1.0-7         generics_0.1.3
[10] parallel_4.3.3          tibble_3.2.1         fansi_1.0.6
[13] RSQLite_2.3.6           blob_1.2.4           pkgconfig_2.0.3
[16] Matrix_1.6-5            graph_1.80.0         lifecycle_1.0.4
[19] GenomeInfoDbData_1.2.11 compiler_4.3.3       Biostrings_2.70.3
[22] munsell_0.5.1           codetools_0.2-19     htmltools_0.5.8.1
[25] RCurl_1.98-1.14         yaml_2.3.8           GO.db_3.18.0
[28] pillar_1.9.0            crayon_1.5.2         BiocParallel_1.36.0
[31] DelayedArray_0.28.0     cachem_1.0.8         abind_1.4-5
[34] tidyselect_1.2.1        locfit_1.5-9.9       digest_0.6.35
[37] dplyr_1.1.4             fastmap_1.1.1        grid_4.3.3
[40] colorspace_2.1-0        cli_3.6.2            SparseArray_1.2.4
[43] magrittr_2.0.3          S4Arrays_1.2.1       XML_3.99-0.16.1
[46] utf8_1.2.4              scales_1.3.0         bit64_4.0.5
[49] httr_1.4.7              rmarkdown_2.26       XVector_0.42.0
[52] bit_4.0.5               png_0.1-8            memoise_2.0.1
[55] evaluate_0.23           knitr_1.46          rlang_1.1.3
[58] Rcpp_1.0.12             glue_1.7.0           DBI_1.2.2
[61] Rgraphviz_2.46.0        KEGGgraph_1.62.0     rstudioapi_0.16.0
[64] jsonlite_1.8.8          R6_2.5.1             zlibbioc_1.48.2
```