Class_16

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```
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, 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:base':
##
##     expand.grid, I, unname

## Loading required package: IRanges

## 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
```

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

# Import metadata and take a peak
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
```

```r
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
```

#Remove the first $length col

```r
countData1 <- as.matrix(countData[,-1])
head(countData1)
```

```
##                 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
```

```r
countData1 = countData1[-which(rowSums(countData1) == 0), ]
head(countData1)
```

```
##                 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
```

#Run PCR To see that the data looks ok

```
pca <- prcomp(t(countData1))
plot(pca$x[,1:2])
```
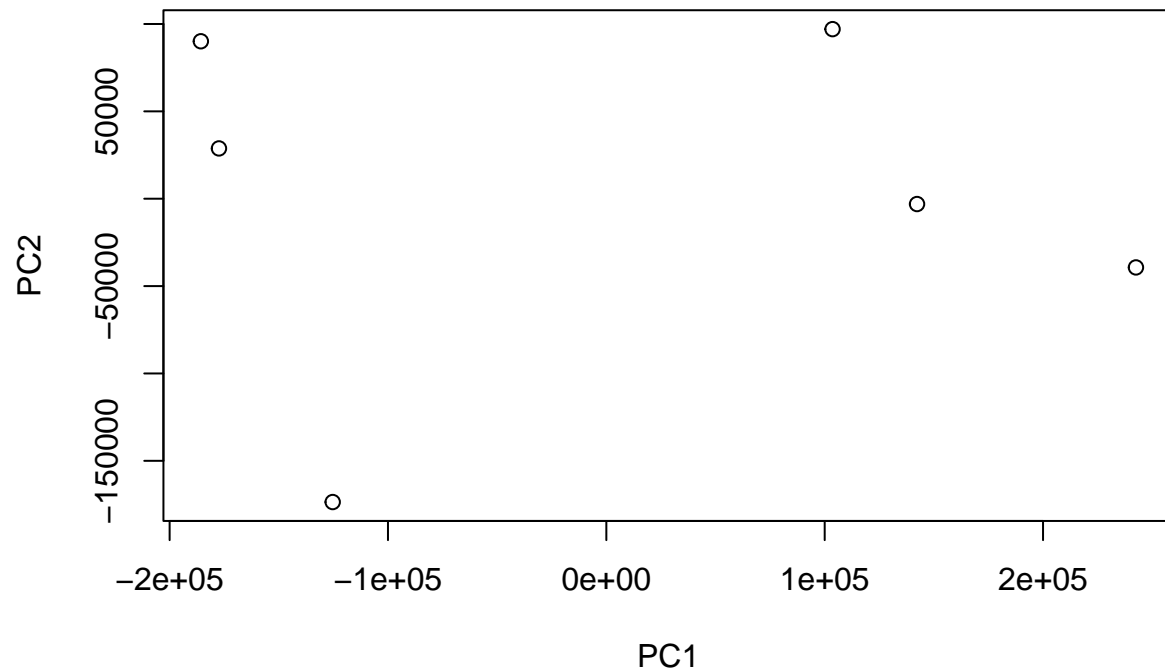

#setup the DESeqDataSet object required for the DESeq() function and then run the DESeq pipeline

```
dds = DESeqDataSetFromMatrix(countData=countData1,
                              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
```

#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)
```

```
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
```

```
plot( res$log2FoldChange, -log(res$padj) )
```
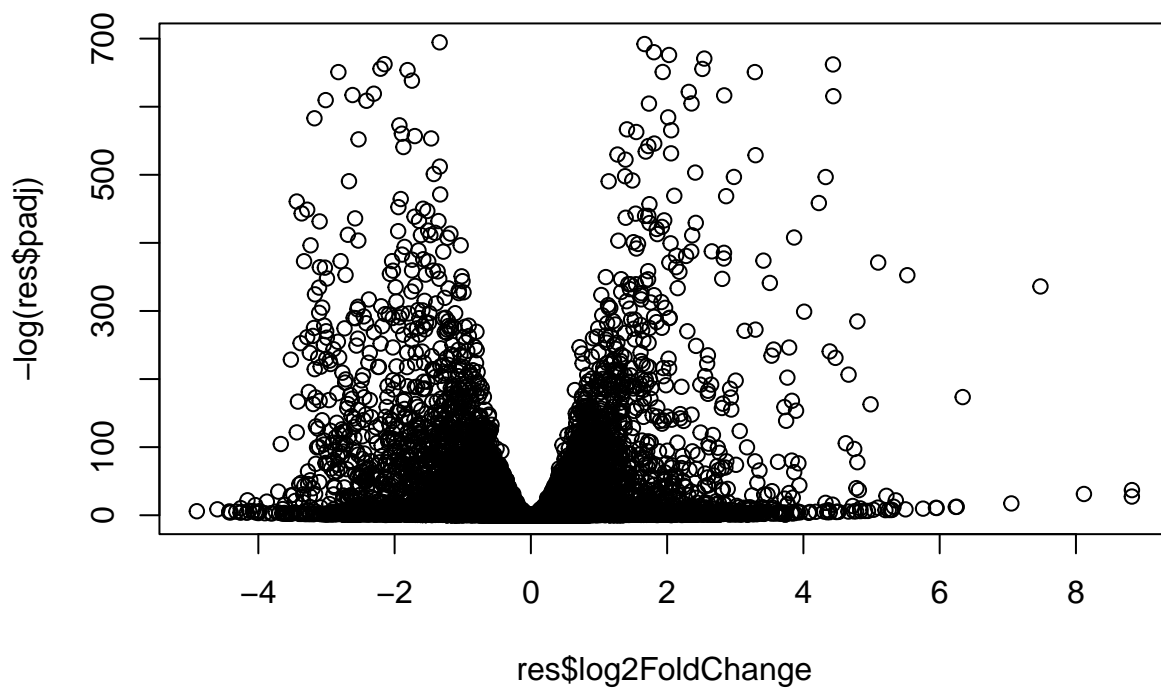
```r
# Make a color vector for all genes
mycols <- rep("gray", nrow(res) )

# 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$pvalue < 0.01) & (abs(res$log2FoldChange) > 2 )
mycols[ inds ] <- "blue"

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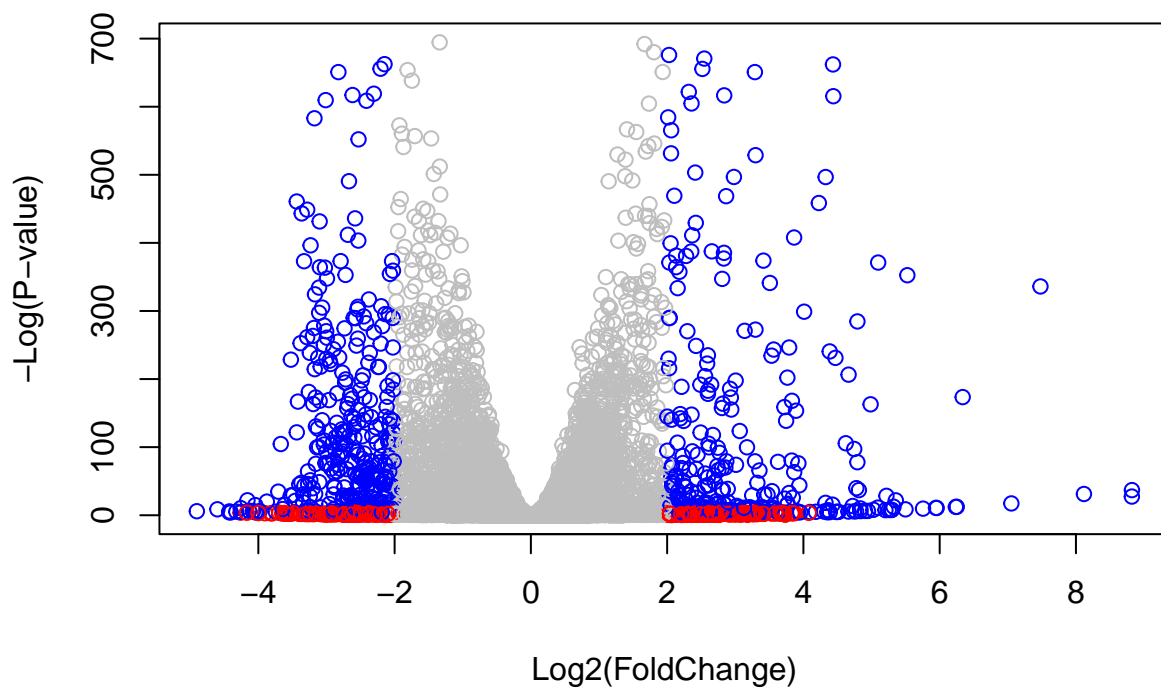
```r
library("AnnotationDbi")
```

```
## Warning: package 'AnnotationDbi' was built under R version 4.1.2
```

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

```
##
```

```r
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"
```

```r
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      WASH9P   102723897 WAS protein family h..
## 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 ..
```

#Reorder the 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")
```

```
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"
```

```r
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
```

#Now, let's run the gage pathway analysis.

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

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

```r
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 /Users/elizabethwest/Documents/Classes/Bioinformatics/R Files/bggn213/Cla
```

```
## Info: Writing image file hsa04110.pathview.png
```

10

```
## Focus on top 5 upregulated pathways here for demo purposes only
keggrespathways <- rownames(keggres$greater)[1:5]

# Extract the 8 character long IDs part of each string
keggresids = substr(keggrespathways, start=1, stop=8)
keggresids
```

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

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

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

Info: Working in directory /Users/elizabethwest/Documents/Classes/Bioinformatics/R Files/bggn213/Clas

Info: Writing image file hsa04640.pathview.png

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

Info: Working in directory /Users/elizabethwest/Documents/Classes/Bioinformatics/R Files/bggn213/Clas

```
## Info: Writing image file hsa04630.pathview.png

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

## Info: Working in directory /Users/elizabethwest/Documents/Classes/Bioinformatics/R Files/bggn213/Clas

## Info: Writing image file hsa00140.pathview.png

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

## Info: Working in directory /Users/elizabethwest/Documents/Classes/Bioinformatics/R Files/bggn213/Clas

## Info: Writing image file hsa04142.pathview.png

## Info: some node width is different from others, and hence adjusted!

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

## Info: Working in directory /Users/elizabethwest/Documents/Classes/Bioinformatics/R Files/bggn213/Clas

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

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

# Focus on Biological Process subset of GO
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                     2.195494e-04  3.530241 2.195494e-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     0.1951953      113 8.519724e-05
## GO:0002009 morphogenesis of an epithelium 0.1951953      339 1.396681e-04
## GO:0048729 tissue morphogenesis         0.1951953      424 1.432451e-04
## GO:0007610 behavior                     0.2243795      427 2.195494e-04
## GO:0060562 epithelial tube morphogenesis 0.3711390      257 5.932837e-04
## GO:0035295 tube development             0.3711390      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                  5.841698e-12      376 1.536227e-15
## GO:0000280 nuclear division                   5.841698e-12      352 4.286961e-15
## GO:0007067 mitosis                            5.841698e-12      352 4.286961e-15
## GO:0000087 M phase of mitotic cell cycle      1.195672e-11      362 1.169934e-14
## GO:0007059 chromosome segregation             1.658603e-08      142 2.028624e-11
## GO:0000236 mitotic prometaphase               1.178402e-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                           3.530241 3.530241
## GO:0060562 epithelial tube morphogenesis      3.261376 3.261376
## GO:0035295 tube development                   3.253665 3.253665
```

```r
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"
```

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

STEROID HORMONE BIOSYNTHESIS

Steroid biosynthesis

Data on KEGG graph
Rendered by Pathview

NOTCH SIGNALING PATHWAY

Fringe Dvl Numb

Deltex

Delta Notch

Serrate

S3

S2

TACE

PSE2 PSEN
NCSTN APH-1

γ-Secretase complex

Ras/MAPK MAPK signaling pathway Gene expression

Co-activator

MAML
HATs SKIP

NICD
(Notch intracellular domain)

CSL DNA

Hairless SMRT

CtBP Gro/TLE CIR

Co-repressor HDAC ATXN1L

Hes1/5

Hey

PreTα

-1 0 1

Data on KEGG graph
Rendered by Pathview

LYSOSOME

bacterium

lysosomal acid hydrolase

Golgi body

transport vesicle

Phagocytosis

phagosome

cytosol
pH- 7.2

ATP ADP

ATPaV

H⁺
pH- 5.0

clathrin coat

Endocytosis

Endocytosis

early endosome

late endosome
multivesicular body (MVB)

MCLN1

acid hydrolase

lysosomal membrane protein

lysosome

Glycosaminoglycan degradation

Other glycan degradation

plasma membrane

mitochondria

Autophagy

autophagosome

Regulation of autophagy

Activation of lysosomal sulfatase precursor

FGE

lysosomal hydrase precursor

from ER mannose

M6P receptor

MPR

Receptor-dependent transport

M6P

M6P ATPaV

AP-3

lysosome

+pO

GNPT
NAGPA

M6P

clathrin AP-1 AP-3
GGAs AP-4

transport vesicle

mannose

mature lysosomal hydrase

Snare interactions in vesicular transport

cis Golgi network

trans Golgi network

Golgi body

Receptor recycling

AP-1

late endosome

Transport of synthesized lysosomal enzymes

Transport of synthesized lysosomal enzymes
(See below)

-1 0 1

Lysosomal acid hydrolases
proteases
cathepsins napsin LGMN TPP1

glycosidases
GLA GLB GAA GBA IDUA
NAGA NAGLU GALC GUSB FUCA1
HEXA/B MANB LAMAN NEU1 HYAL1

sulfatases
ARS GALNS GNS IDS SGSH

lipases nuclease phosphatase
LIPA LYPLA3 DNaseII ACP2 ACP5

sphingomyelinase ceramidase aspartylglucosaminidase
SMPD1 ASAH1 AGA

Other lysosomal enzymes and activators
saposin GM2A CLN1

Lysosomal membrane proteins
major lysosomal membrane proteins
LAMP LIMP

minor lysosomal membrane proteins
NPC reticulon sialin NRAMP LAPTM
ABCA2 ABCB9 ACP2 endolyn LALP70
sortilin CLN3 CLN5 CLN7 HGSNAT
MCLN1 LITAF

Data on KEGG graph
Rendered by Pathview

JAK-STAT SIGNALING PATHWAY

Data on KEGG graph
Rendered by Pathview

HEMATOPOIETIC CELL LINEAGE

Data on KEGG graph
Rendered by Pathview