

Class13

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Section 1. Differential Expression Analysis

first step is to read and analyze the data:

```
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 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, colAvgPerRowSet, 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, rowAvgPerColSet,
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

```
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
```

```
# Import countdata
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

we will need to remove that odd first column in `countData` namely `countData$length`:

Q1. Complete the code below to remove the troublesome first column from `countData`

```
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

we are going to eliminate the zeros:

Q2. Complete the code below to filter `countData` to exclude genes (i.e. rows) where we have 0 read count across all samples (i.e. columns).

```
remove <- rowSums(countData) == 0
countData <- countData[!remove, ]

# Filter count data where you have 0 read count across all samples.
to_keep <- rowSums(countData)>0
countData <- countData[to_keep, ]
```

Running DESeq2

now lets setup the DESeqDataSet object required for the **DESeq()** :

```
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
```

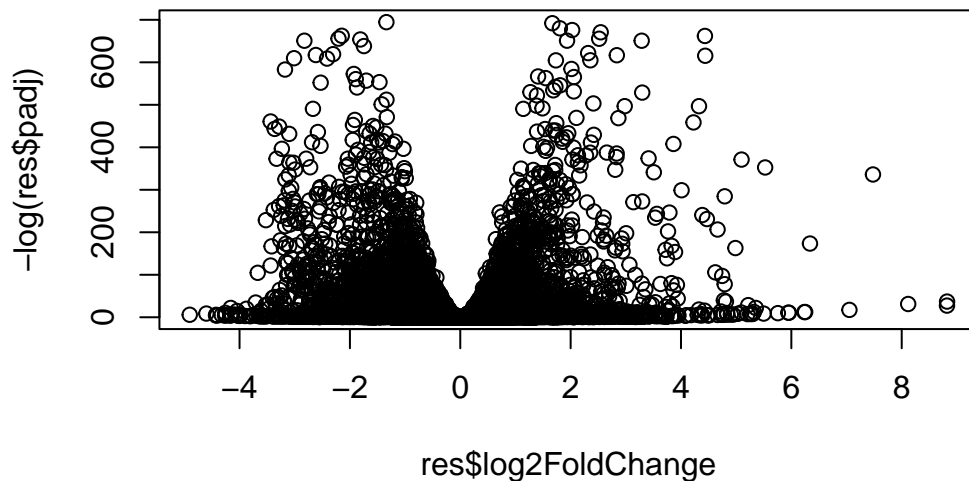
```
res = results(dds, contrast=c("condition", "hoxa1_kd", "control_sirna"))
```

Q3. Call the `summary()` function on your results to get a sense of how many genes are up or down-regulated at the default 0.1 p-value cutoff.

```
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) )
```



Q4. Improve this plot by completing the below code, which adds color and axis labels

```

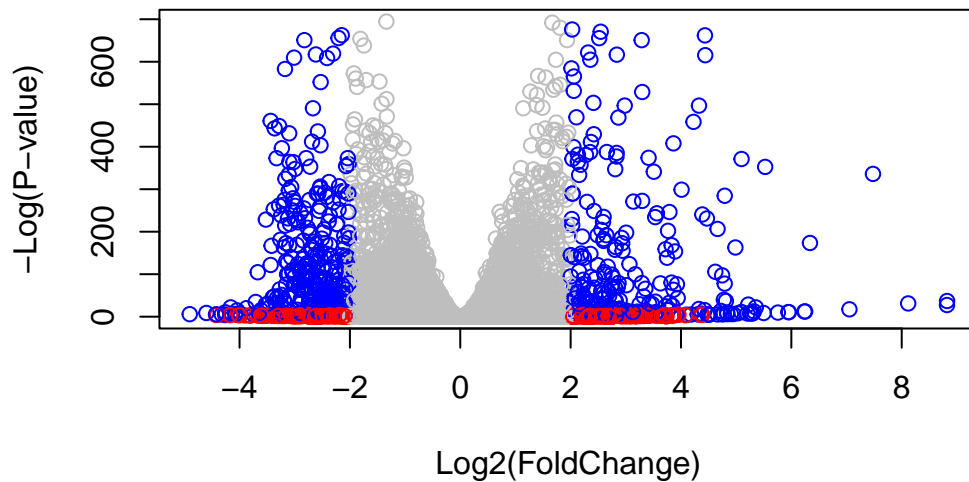
# Make a color vector for all genes
mycols <- rep("gray", nrow(res) )

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

Q5. Use the `mapIDs()` function multiple times to add SYMBOL, ENTREZID and GENE-NAME annotation to our results by completing the code below.

```
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 ..	

Q6. 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$padj), ]
write.csv(res, file = "deseq_results.csv")
```

Section 2. Pathway Analysis

KEGG pathways

First we need to do our one time install of these required bioconductor packages:

```
# Run in your R console (i.e. not your Rmarkdown doc!)
# BiocManager::install( c("pathview", "gage", "gageData") )
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

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

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

```
Info: Working in directory /Users/mahsa/Desktop/BioInformatics/Class13
```

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



```
## 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/mahsa/Desktop/BioInformatics/Class13
```

```
Info: Writing image file hsa04640.pathview.png
```

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

```
Info: Working in directory /Users/mahsa/Desktop/BioInformatics/Class13
```

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

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

```
Info: Working in directory /Users/mahsa/Desktop/BioInformatics/Class13
```

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

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

```
Info: Working in directory /Users/mahsa/Desktop/BioInformatics/Class13
```

```
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/mahsa/Desktop/BioInformatics/Class13

Info: Writing image file hsa04330.pathview.png

Q7. Can you do the same procedure as above to plot the pathview figures for the top 5 down-regulated pathways?

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

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

```
[1] "hsa04110" "hsa03030" "hsa03013" "hsa03440" "hsa04114"
```

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

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

Info: Working in directory /Users/mahsa/Desktop/BioInformatics/Class13

Info: Writing image file hsa04110.pathview.png

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

Info: Working in directory /Users/mahsa/Desktop/BioInformatics/Class13

Info: Writing image file hsa03030.pathview.png

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

Info: Working in directory /Users/mahsa/Desktop/BioInformatics/Class13

Info: Writing image file hsa03013.pathview.png

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

Info: Working in directory /Users/mahsa/Desktop/BioInformatics/Class13

Info: Writing image file hsa03440.pathview.png

Info: Writing image file hsa04114.pathview.png



DNA polymerase III holoenzyme

			θ	Pol III core
			ε	
			α	
			γ δ τ	
Clamp	ψ	δ	y6 complex	
	β	χ		

Helicase
DnaB

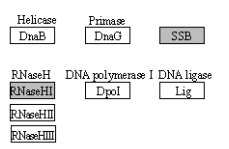
Primase
DnaG

SSB

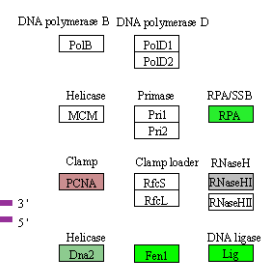
RNaseH
RNaseHII
RNaseHIII

DNA polymerase I
Dpol

DNA ligase
Lig



DNA polymerase B		DNA polymerase D	
PoIb	PoId1 PoId2		
Helicase	Primase	RPA/SSB	
MCM	Pri1 Pri2	RPA	
Clamp	Clamp loader	RNaseH	
PCNA	RfcS RfcL	RNaseH1 RNaseH2	
Helicase		DNA ligase	
Dna2	Fen1	Lig	



DNA polymerase α -primease complex

$\alpha 1$ $\alpha 2$ PriI Pri2

DNA polymerase δ complex

$\delta 1$ $\delta 2$ $\delta 3$ $\delta 4$

DNA polymerase ϵ complex

$\epsilon 1$ $\epsilon 2$ $\epsilon 3$ $\epsilon 4$

MCM complex (helicase)

Mmm2 Mmm3
Mmm4 Mmm5
Mmm6 Mmm7

RPA

RPA1
RFA2/4
RPA3

Clamp loader

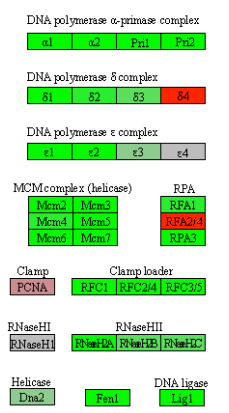
PCNA RFC1 RFC2/4 RFC3/6

RNaseH

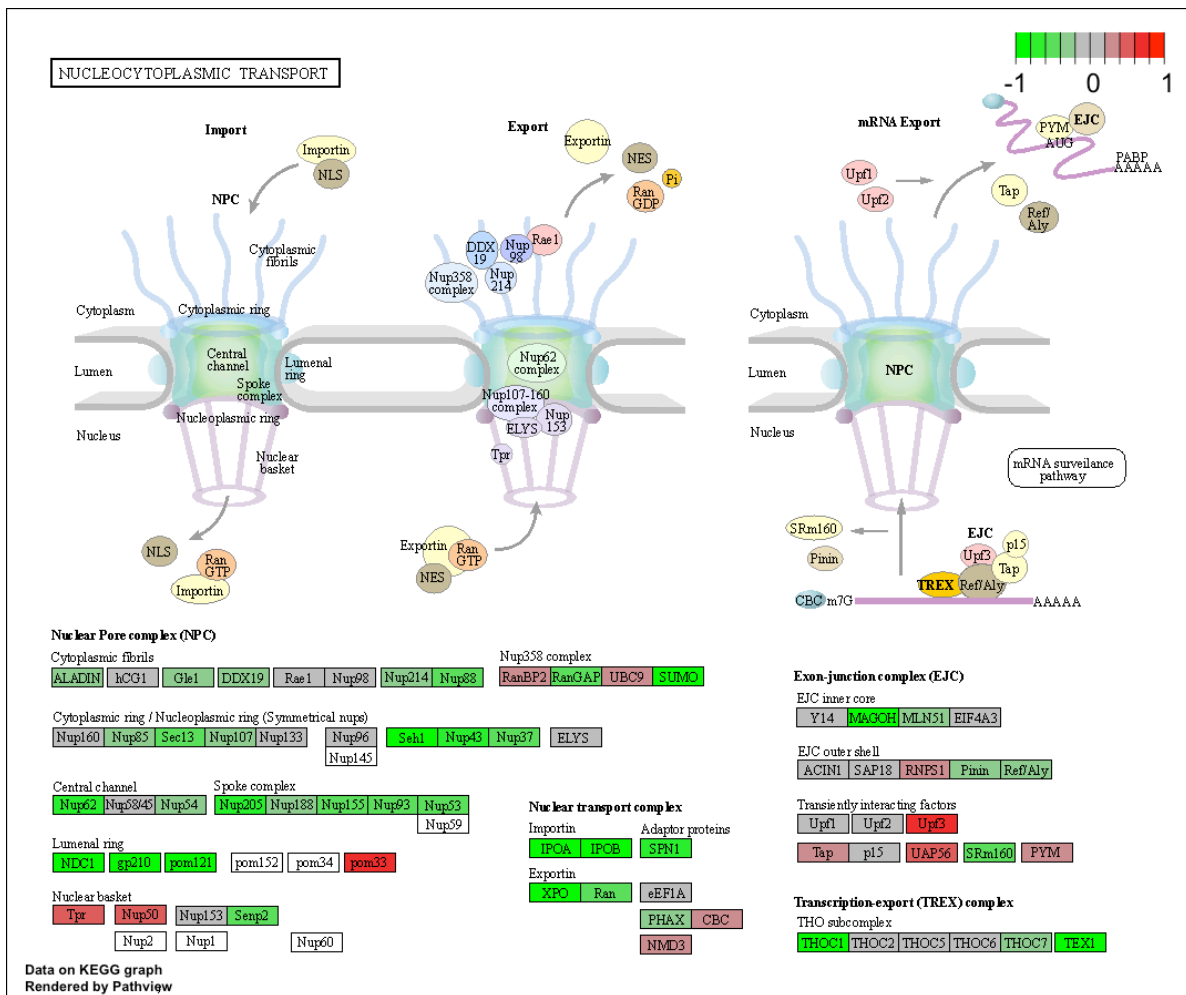
RNaseHI RNaseHII

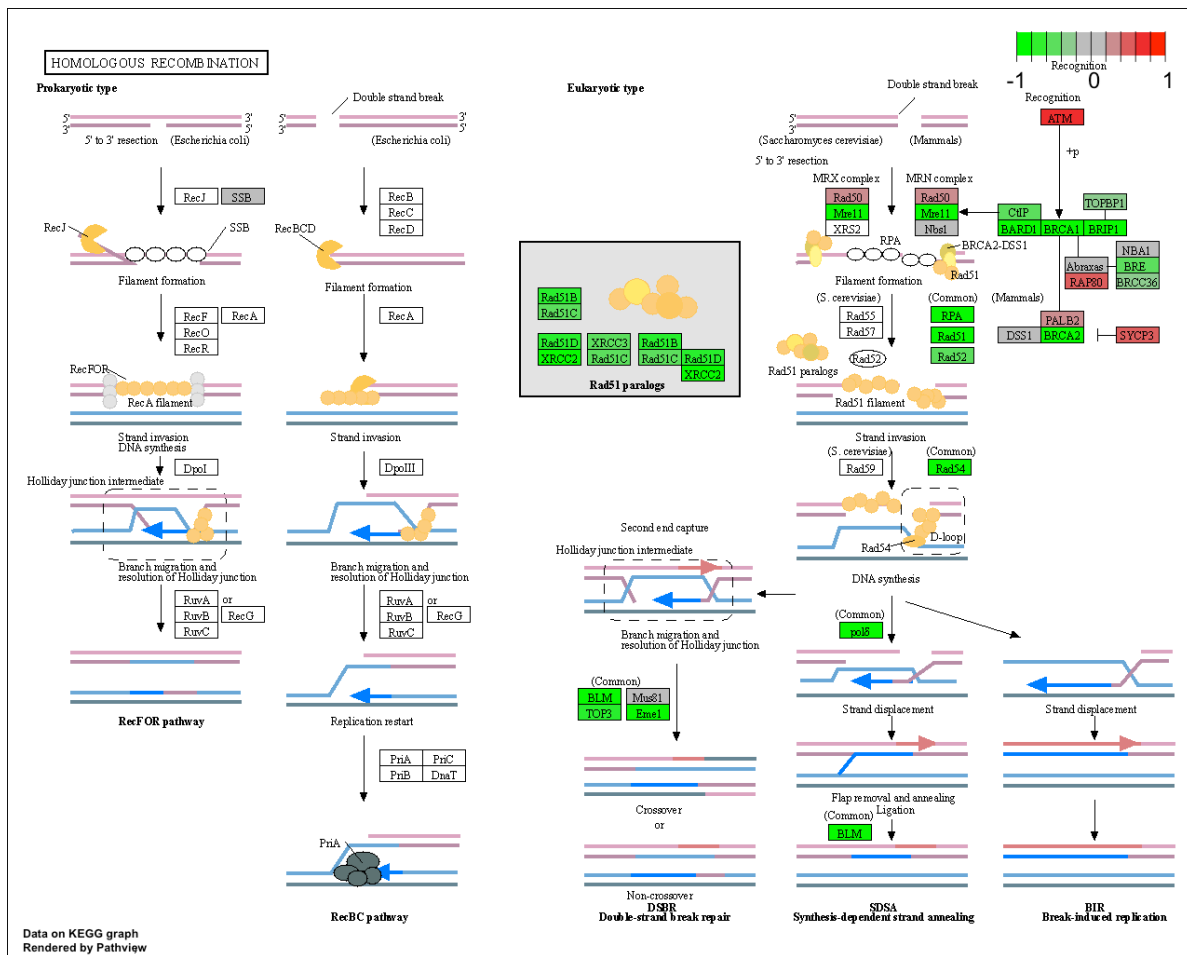
Helicase

Dna2 Fen1 Lig1



22





G0:0007156	homophilic cell adhesion	8.519724e-05	3.824205	8.519724e-05
G0:0002009	morphogenesis of an epithelium	1.396681e-04	3.653886	1.396681e-04
G0:0048729	tissue morphogenesis	1.432451e-04	3.643242	1.432451e-04
G0:0007610	behavior	2.195494e-04	3.530241	2.195494e-04
G0:0060562	epithelial tube morphogenesis	5.932837e-04	3.261376	5.932837e-04
G0:0035295	tube development	5.953254e-04	3.253665	5.953254e-04

		q.val	set.size	exp1
G0:0007156	homophilic cell adhesion	0.1951953	113	8.519724e-05
G0:0002009	morphogenesis of an epithelium	0.1951953	339	1.396681e-04
G0:0048729	tissue morphogenesis	0.1951953	424	1.432451e-04
G0:0007610	behavior	0.2243795	427	2.195494e-04
G0:0060562	epithelial tube morphogenesis	0.3711390	257	5.932837e-04
G0:0035295	tube development	0.3711390	391	5.953254e-04

\$less

		p.geomean	stat.mean	p.val
G0:0048285	organelle fission	1.536227e-15	-8.063910	1.536227e-15
G0:0000280	nuclear division	4.286961e-15	-7.939217	4.286961e-15
G0:0007067	mitosis	4.286961e-15	-7.939217	4.286961e-15
G0:0000087	M phase of mitotic cell cycle	1.169934e-14	-7.797496	1.169934e-14
G0:0007059	chromosome segregation	2.028624e-11	-6.878340	2.028624e-11
G0:0000236	mitotic prometaphase	1.729553e-10	-6.695966	1.729553e-10

		q.val	set.size	exp1
G0:0048285	organelle fission	5.841698e-12	376	1.536227e-15
G0:0000280	nuclear division	5.841698e-12	352	4.286961e-15
G0:0007067	mitosis	5.841698e-12	352	4.286961e-15
G0:0000087	M phase of mitotic cell cycle	1.195672e-11	362	1.169934e-14
G0:0007059	chromosome segregation	1.658603e-08	142	2.028624e-11
G0:0000236	mitotic prometaphase	1.178402e-07	84	1.729553e-10

\$stats

		stat.mean	exp1
G0:0007156	homophilic cell adhesion	3.824205	3.824205
G0:0002009	morphogenesis of an epithelium	3.653886	3.653886
G0:0048729	tissue morphogenesis	3.643242	3.643242
G0:0007610	behavior	3.530241	3.530241
G0:0060562	epithelial tube morphogenesis	3.261376	3.261376
G0:0035295	tube development	3.253665	3.253665

Section 4. Reactome Analysis

```
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
```

Q8: What pathway has the most significant “Entities p-value”? Do the most significant pathways listed match your previous KEGG results? What factors could cause differences between the two methods?

Cell cycle, mitotic has the most significant Entities p-value. The KEGG result is different from the Reactome result and factors like different database content could be a reason for different result. Another factor could be using different sets of genes and identifiers.

Section 5. GO online(optional)

performing Gene Set GO Enrichment online to determine over-represented or under-represented GO terms for a given set of genes:

Q9: What pathway has the most significant “Entities p-value”? Do the most significant pathways listed match your previous KEGG results? What factors could cause differences between the two methods?

the most significant is PRA1 Family protein 2 which is also different from KEGG result due to using different dataset.