

# DE analysis - Day1

Sergey Naumenko

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## Overview

- Principal Investigator: Beth Overmoyer
- Experiment: RNAseq\_analysis\_of\_inflammatory\_breast\_cancer\_hbc04141
- study 6 was excluded because of low read depth in 3373-3
- <https://www.bioconductor.org/packages/release/bioc/vignettes/DEGreport/inst/doc/DEGreport.html>
- AnnotationHub. We use ensembl version matching bcbio pipeline - v94.
- HBC materials
- HBC materials - functional analysis
- <http://bioconductor.org/packages/release/bioc/vignettes/DESeq2/inst/doc/DESeq2.html>
- this is DE for Day1 samples

```
## Setup
### Bioconductor and CRAN libraries used

library(DESeq2)

## 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.max, which.min
##
## Attaching package: 'S4Vectors'
## The following object is masked from 'package:base':
##
##   expand.grid
## 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
library(tidyverse)

## -- Attaching packages ----- tidyverse 1.3.0 --
## v ggplot2 3.3.3    v purrr   0.3.4
## v tibble  3.1.0    v dplyr  1.0.5
## v tidyr   1.1.3    v stringr 1.4.0
## v readr   1.4.0    v forcats 0.5.1
##
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::collapse() masks IRanges::collapse()
## x dplyr::combine()  masks Biobase::combine(), BiocGenerics::combine()
## x dplyr::count()    masks matrixStats::count()

```

```
## x dplyr::desc()      masks IRanges::desc()
## x tidyr::expand()    masks S4Vectors::expand()
## x dplyr::filter()    masks stats::filter()
## x dplyr::first()     masks S4Vectors::first()
## x dplyr::lag()       masks stats::lag()
## x ggplot2::Position() masks BiocGenerics::Position(), base::Position()
## x purrr::reduce()    masks GenomicRanges::reduce(), IRanges::reduce()
## x dplyr::rename()    masks S4Vectors::rename()
## x dplyr::slice()     masks IRanges::slice()
```

```
library(RColorBrewer)
library(pheatmap)
library(DEGreport)
library(tximport)
library(ggplot2)
library(ggrepel)
library(knitr)
library(AnnotationHub)
```

```
## Loading required package: BiocFileCache
## Loading required package: dbplyr
##
## Attaching package: 'dbplyr'
## The following objects are masked from 'package:dplyr':
##
##     ident, sql
##
## Attaching package: 'AnnotationHub'
## The following object is masked from 'package:Biobase':
##
##     cache
```

```
library(ensembladb)
```

```
## Loading required package: GenomicFeatures
## Loading required package: AnnotationDbi
##
## Attaching package: 'AnnotationDbi'
## The following object is masked from 'package:dplyr':
##
##     select
## Loading required package: AnnotationFilter
##
## Attaching package: 'ensembladb'
## The following object is masked from 'package:dplyr':
##
##     filter
## The following object is masked from 'package:stats':
##
```

```
##      filter
ggplot2::theme_set(theme_light(base_size = 14))

opts_chunk[["set"]](
  cache = FALSE,
  dev = c("png", "pdf"),
  error = TRUE,
  highlight = TRUE,
  message = FALSE,
  prompt = FALSE,
  tidy = FALSE,
  warning = FALSE)

# Have a folder called 'data', and copy your Salmon folders here from the cluster.
## List all directories containing data
### change the pattern to something specific to your Salmon folders
samples <- list.files(path = "./data/final",
                      full.names = T,
                      pattern = "^S")

## Obtain a vector of all filenames including the path
files <- file.path(samples, "salmon", "quant.sf")
files

## [1] "./data/final/S3154-2/salmon/quant.sf"
## [2] "./data/final/S3169-2/salmon/quant.sf"
## [3] "./data/final/S3188-2/salmon/quant.sf"
## [4] "./data/final/S3190-4/salmon/quant.sf"
## [5] "./data/final/S3193-1/salmon/quant.sf"
## [6] "./data/final/S3194-3/salmon/quant.sf"
## [7] "./data/final/S3220-1/salmon/quant.sf"
## [8] "./data/final/S3234-1/salmon/quant.sf"
## [9] "./data/final/S3291-3/salmon/quant.sf"
## [10] "./data/final/S3292-3/salmon/quant.sf"
## [11] "./data/final/S3372-1/salmon/quant.sf"
## [12] "./data/final/S3374-2/salmon/quant.sf"
## [13] "./data/final/S3404-1/salmon/quant.sf"
## [14] "./data/final/S3424-1/salmon/quant.sf"
## [15] "./data/final/S3474-3/salmon/quant.sf"
## [16] "./data/final/S3477-1/salmon/quant.sf"
## [17] "./data/final/S3563-3/salmon/quant.sf"
## [18] "./data/final/S3582-4/salmon/quant.sf"
## [19] "./data/final/S3644-1/salmon/quant.sf"
## [20] "./data/final/S3652-1/salmon/quant.sf"
## [21] "./data/final/S3688-2/salmon/quant.sf"
## [22] "./data/final/S3697-3/salmon/quant.sf"
## [23] "./data/final/S3713-1/salmon/quant.sf"
## [24] "./data/final/S3715-2/salmon/quant.sf"
## [25] "./data/final/S3723-1/salmon/quant.sf"
## [26] "./data/final/S3728-3/salmon/quant.sf"
## [27] "./data/final/S3732-1/salmon/quant.sf"
## [28] "./data/final/S3741-3/salmon/quant.sf"
## [29] "./data/final/S3816-1/salmon/quant.sf"
## [30] "./data/final/S3822-1/salmon/quant.sf"
```

```
## [31] "./data/final/S3825-1/salmon/quant.sf"
## [32] "./data/final/S3837-2/salmon/quant.sf"
## [33] "./data/final/S4047-1/salmon/quant.sf"
## [34] "./data/final/S4056-1/salmon/quant.sf"
## [35] "./data/final/S4089-1/salmon/quant.sf"
## [36] "./data/final/S4101-3/salmon/quant.sf"
## [37] "./data/final/S4136-1/salmon/quant.sf"
## [38] "./data/final/S4144-2/salmon/quant.sf"
## [39] "./data/final/S4172-1/salmon/quant.sf"
## [40] "./data/final/S4176-3/salmon/quant.sf"
## [41] "./data/final/S4237-1/salmon/quant.sf"
## [42] "./data/final/S4249-1/salmon/quant.sf"
## [43] "./data/final/S4261-1/salmon/quant.sf"
## [44] "./data/final/S4295-5/salmon/quant.sf"

## Since all quant files have the same name it is useful to have names for each element
### change the string in str_replace so the pattern matches your filenames
names(files) <- str_replace(samples, "./data/final/", "")
```

```
# Load the data and metadata
meta <- read_csv("tables/metadata_corrected.csv") %>%
  column_to_rownames(var = "samplename") %>%
  dplyr::filter(treatment == "pre") %>%
  drop_na(response)
protein_coding_genes <- read_csv("tables/ensembl_w_description.protein_coding.csv")
```

```
# Connect to AnnotationHub
ah <- AnnotationHub()

# Query AnnotationHub
hs_ens <- query(ah, c("Homo sapiens", "EnsDb"))

# Get Ensembl94 - used in bcbio
hs_ens <- hs_ens[["AH64923"]]

# Extract gene-level information
txdb <- transcripts(hs_ens,
  return.type = "data.frame") %>%
  dplyr::select(tx_id, gene_id)

genedb <- genes(hs_ens,
  return.type = "data.frame") %>%
  dplyr::select(gene_id, gene_name, symbol)

gene_symbol <- genedb %>% dplyr::select(gene_id, symbol)

hsdb <- inner_join(txdb, genedb)
write.table(hsdb,
  file = "data/ensembl94_hg38_annotations.txt",
  sep = "\t",
  row.names = F,
  quote = F)
```

```
# Read in a tx2gene file with transcript identifiers in the first column and gene identifiers in the second
#wormdb <- read.table("ensembl94_WBcel235_annotations.txt", sep="\t", header=T)
```

```
tx2gene <- hsdb[, c("tx_id", "gene_id")]

# Run tximport
files <- files[rownames(meta)]
txi_file <- "data/txi.day1.RDS"
if (file.exists(txi_file)){
  txi <- readRDS(txi_file)
}else{
  txi <- tximport(files,
    type = "salmon",
    tx2gene = tx2gene,
    countsFromAbundance = "lengthScaledTPM",
    ignoreTxVersion = FALSE)
  saveRDS(txi, txi_file)
}

# Look at the counts
class(txi)

## [1] "list"
attributes(txi)

## $names
## [1] "abundance"          "counts"              "length"
## [4] "countsFromAbundance"

txi$counts %>% View()
```

## Checking to see that the transcript to gene mapping is correct

When you have annotations that are from a different source from your reference you can run into problems (i.e lose genes). Some checks you can do before proceeding:

1. Look at the dimensions of your count matrix. Do you have ~20k genes present? `dim(txi$counts)`
2. When running `tximport()` you will get a message in your console. If you see something like `transcripts missing from tx2gene` start troubleshooting.

```
dim(txi$counts)
```

```
## [1] 58735    20
```

## Sanity check that metadata matches your expression

It is always a good idea to check if:

1. Do you have expression data for all samples listed in your metadata?
2. Are the samples in your expression data in the same order as your metadata?

```
### Check that sample names match in both files
all(colnames(txi$counts) %in% rownames(meta))
```

```
## [1] TRUE
```

```
# Not the same? Make them the same
### This will change depending on what names you have listed!
```

```
#paste0(meta$samplename, "_", meta$library)
#rownames(meta) <- paste0(meta$samplename, "_", meta$library)
#meta$genotype <- releval(meta$genotype, ref="Wildtype")
```

```
### Check that sample names match in both files
all(colnames(txi$counts) %in% rownames(meta))
```

```
## [1] TRUE
```

```
### Check that all samples are in the same order
meta <- meta[colnames(txi$counts),]
all(colnames(txi$counts) == rownames(meta))
```

```
## [1] TRUE
```

## Run DESeq2

estimating size factors  
 estimating dispersions  
 gene-wise dispersion estimates  
 mean-dispersion relationship  
 final dispersion estimates  
 fitting model and testing

- Estimating size factors and count normalization
- Gene-wise dispersions
- Mean-dispersion(variance) relationship and the Negative Binomial Model
- Model fitting and hypothesis testing

## Wald test

*Here we subset protein coding genes.*

```
## Create DESeq2Dataset object
dds_file <- "data/dds.day1.RDS"
meta$treatment <- as.factor(meta$treatment)
meta$response <- as.factor(meta$response)
meta$er <- as.factor(meta$er)
meta$date_of <- as.factor(meta$date_of)
meta$tumor_percentage <- as.factor(meta$tumor_percentage)
meta$tumor_percentage_high <- as.factor(meta$tumor_percentage_high)

non_responders <- meta %>% dplyr::filter(study_id %in% c(2, 19)) %>% row.names()

if (file.exists(dds_file)){
  dds <- readRDS(dds_file)
}else{
  dds <- DESeqDataSetFromTximport(txi,
                                colData = meta,
                                design = ~response)

  #dds <- dds[,!colnames(dds) %in% non_responders]
  design(dds) <- formula(~response + er + tumor_percentage_high + date_of)

  # subset protein-coding genes
```



```

pc_genes <- intersect(protein_coding_genes$ensembl_gene_id, row.names(dds))
dds <- dds[pc_genes,]
# 100 reads / 20 samples
keep <- rowSums(counts(dds)) >= 100
dds <- dds[keep,]

# Run DESeq2
dds <- DESeq(dds)
saveRDS(dds, dds_file)
}

```

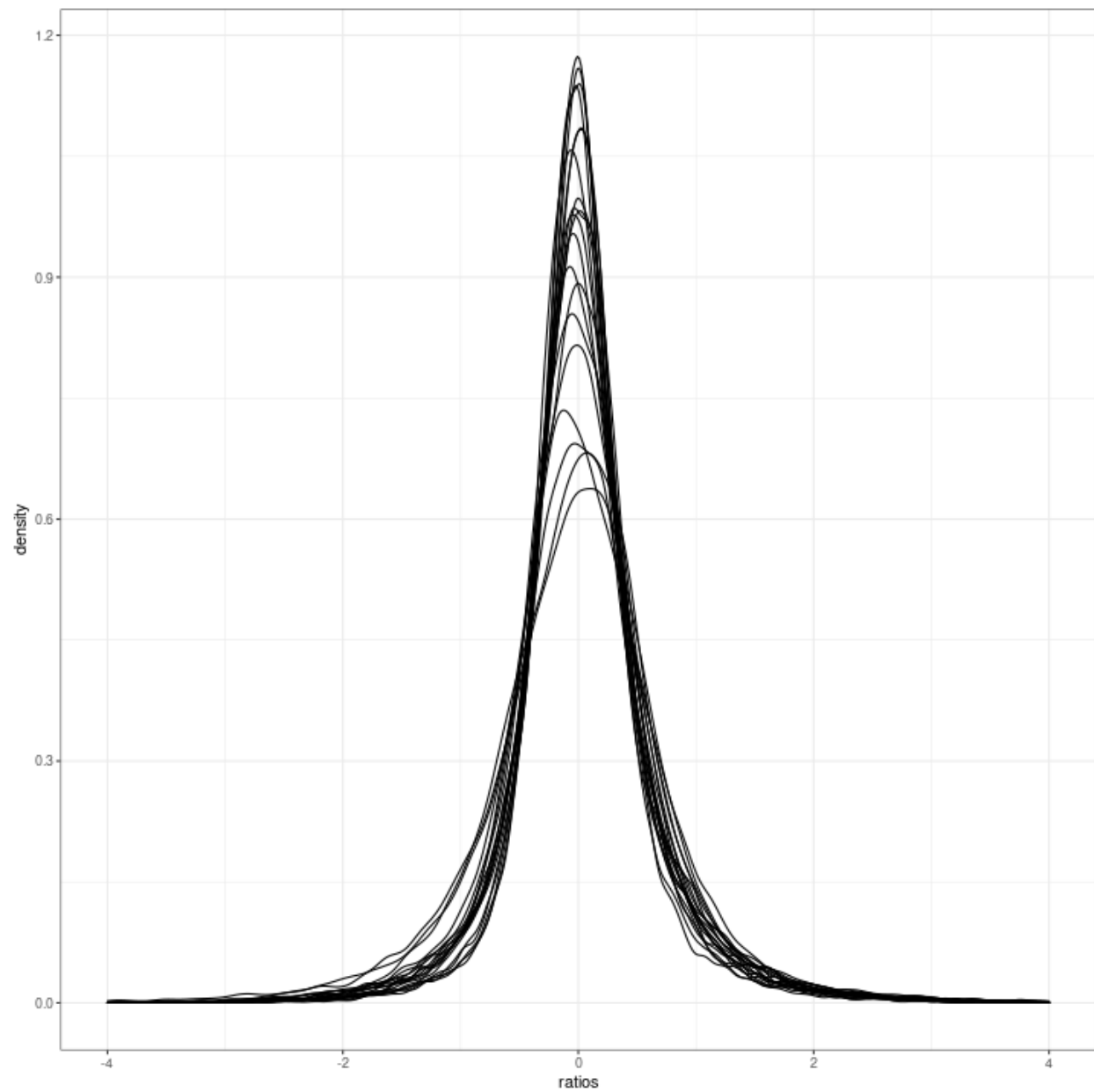
## DEGreport QC

### Size factor QC - samples 1-20

```

counts <- counts(dds, normalized = TRUE)
design <- as.data.frame(colData(dds))
degCheckFactors(counts[, 1:20])

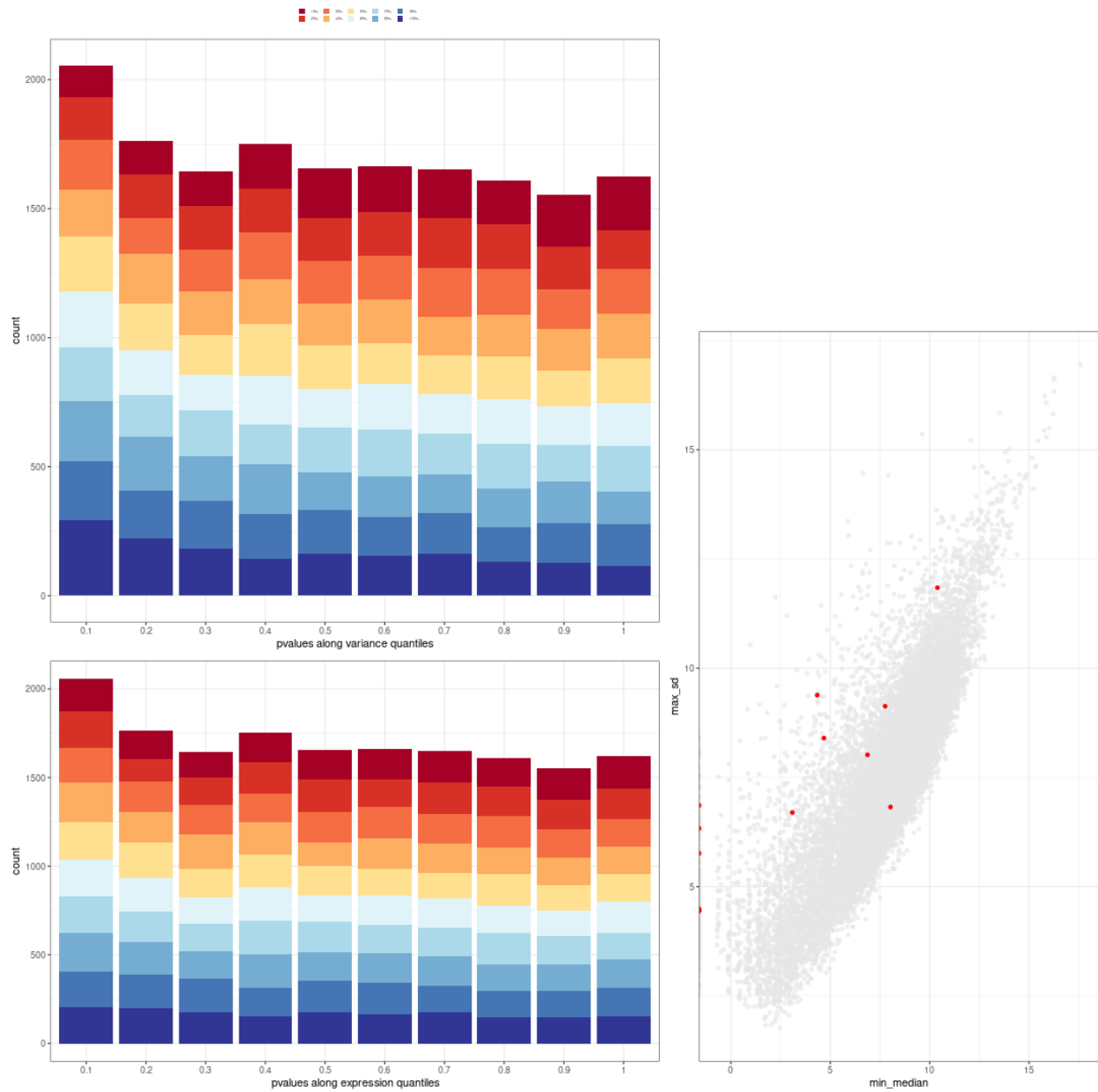
```



## Mean-Variance QC plots

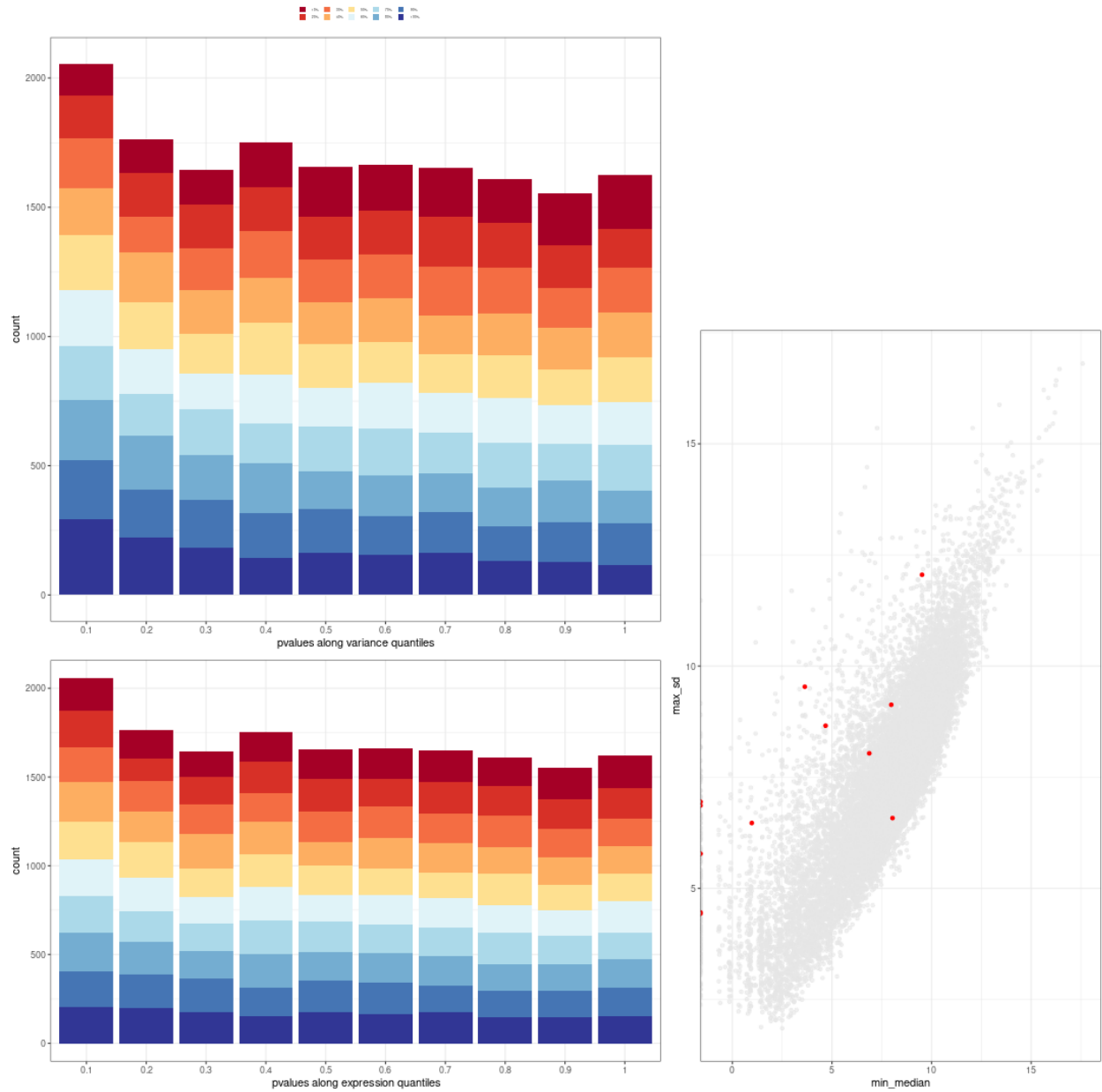
response

```
res <- results(dds)
degQC(counts, design[["response"]], pvalue = res[["pvalue"]])
```



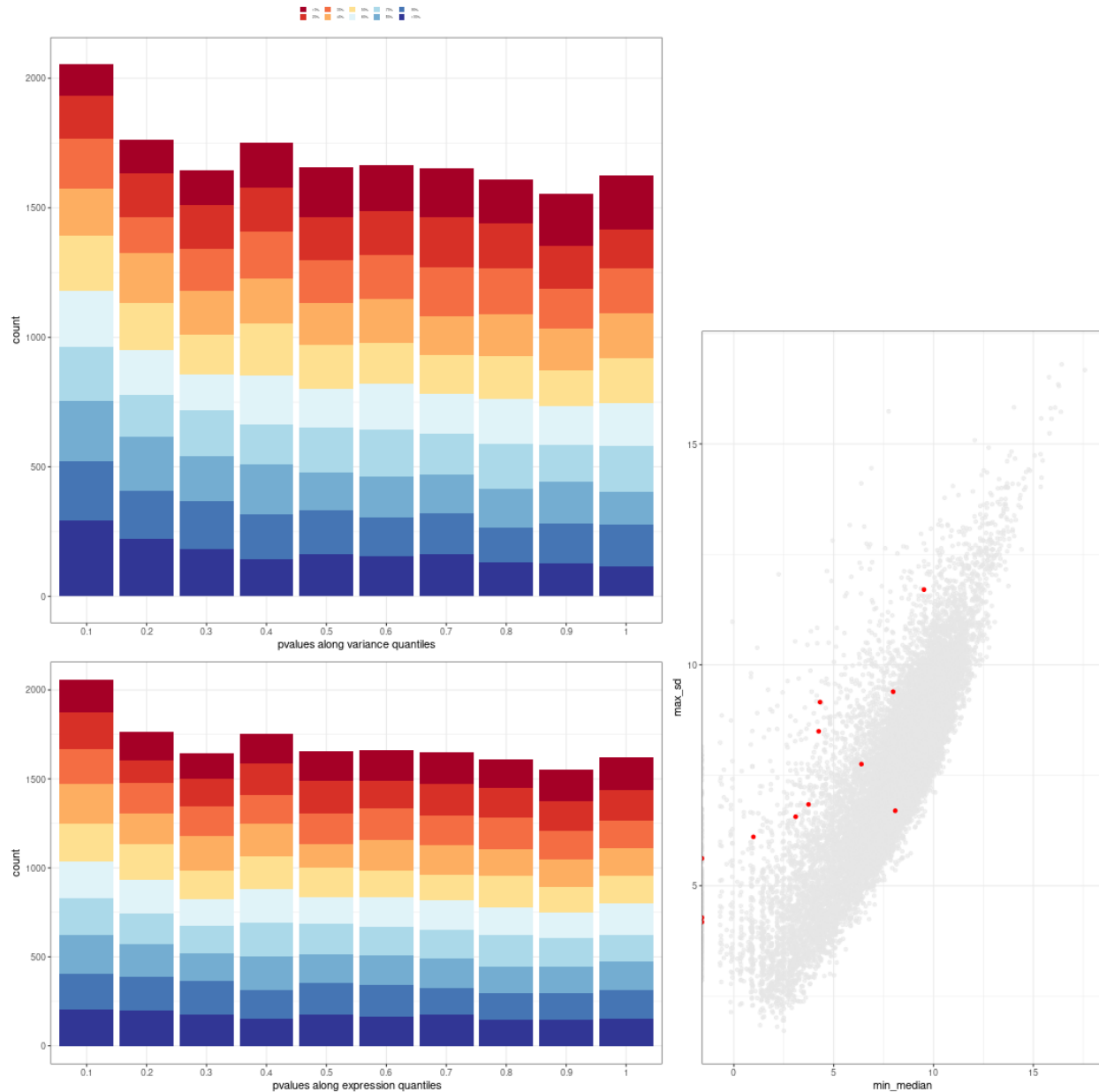
ER

```
degQC(counts, design[["er"]], pvalue = res[["pvalue"]])
```



tumor\_percentage\_high

```
degQC(counts, design[["tumor_percentage_high"]], pvalue = res[["pvalue"]])
```



## Covariates effect on count data

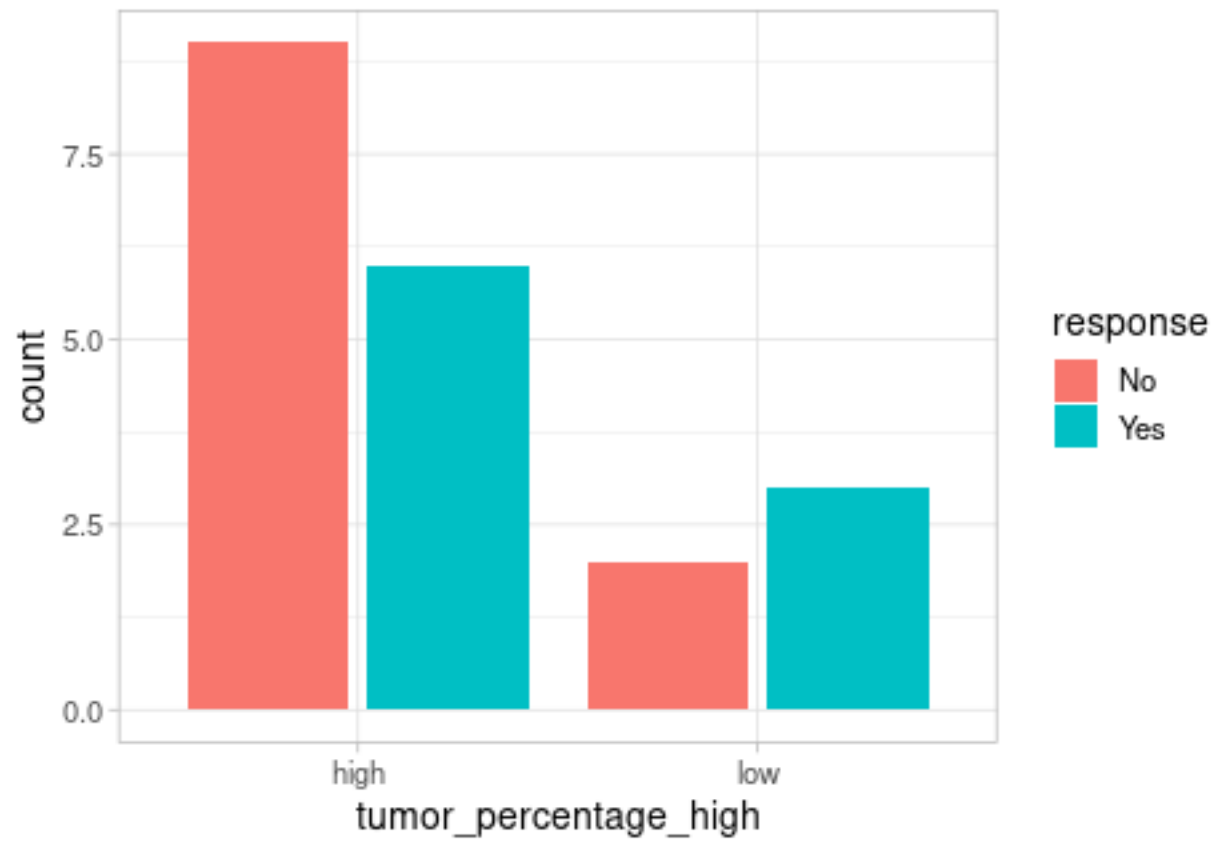
```

mdata <- colData(dds) %>% as.data.frame() %>%
  dplyr::select(response, er, date_of, tumor_percentage_high)

#resCov <- degCovariates(log2(counts(dds)+0.5), mdata)

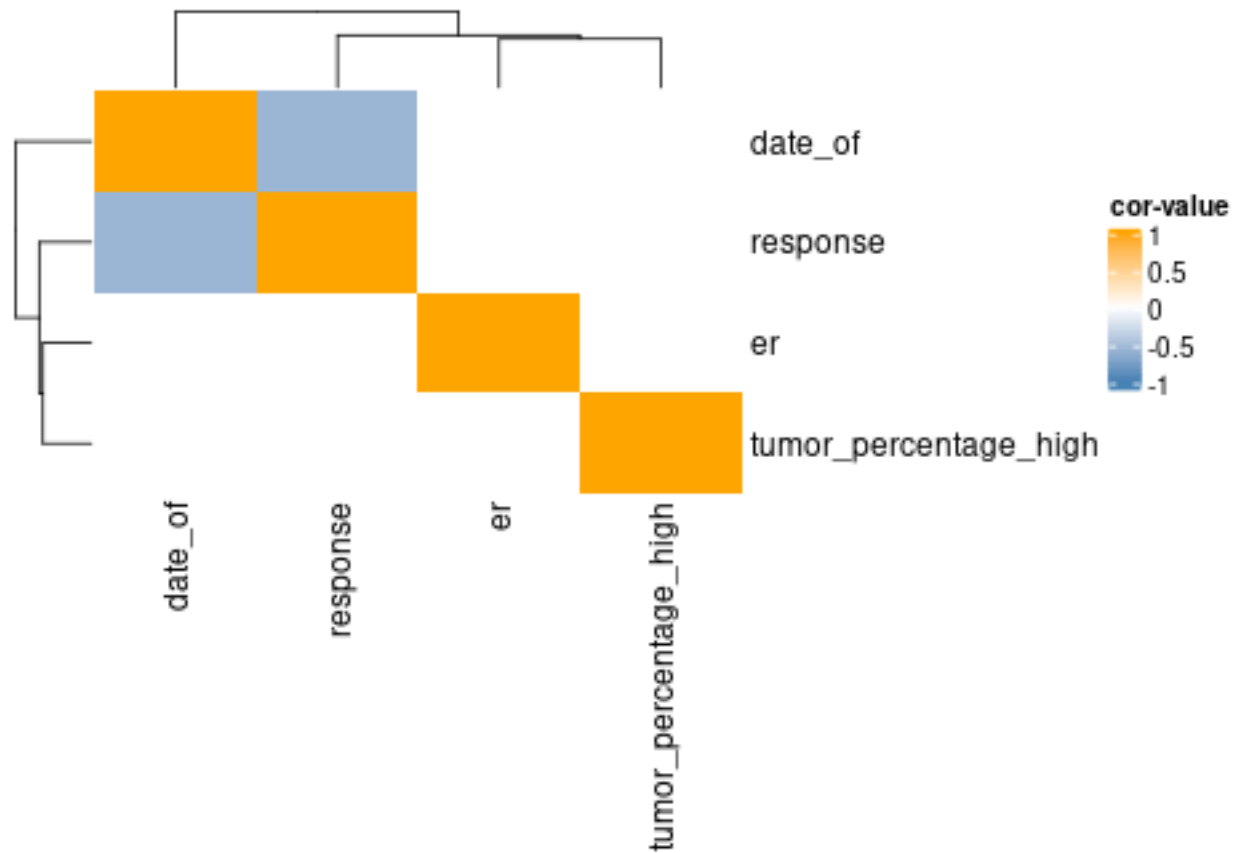
mdata %>% ggplot(aes(tumor_percentage_high, fill = response)) + geom_bar(position = "dodge2")

```

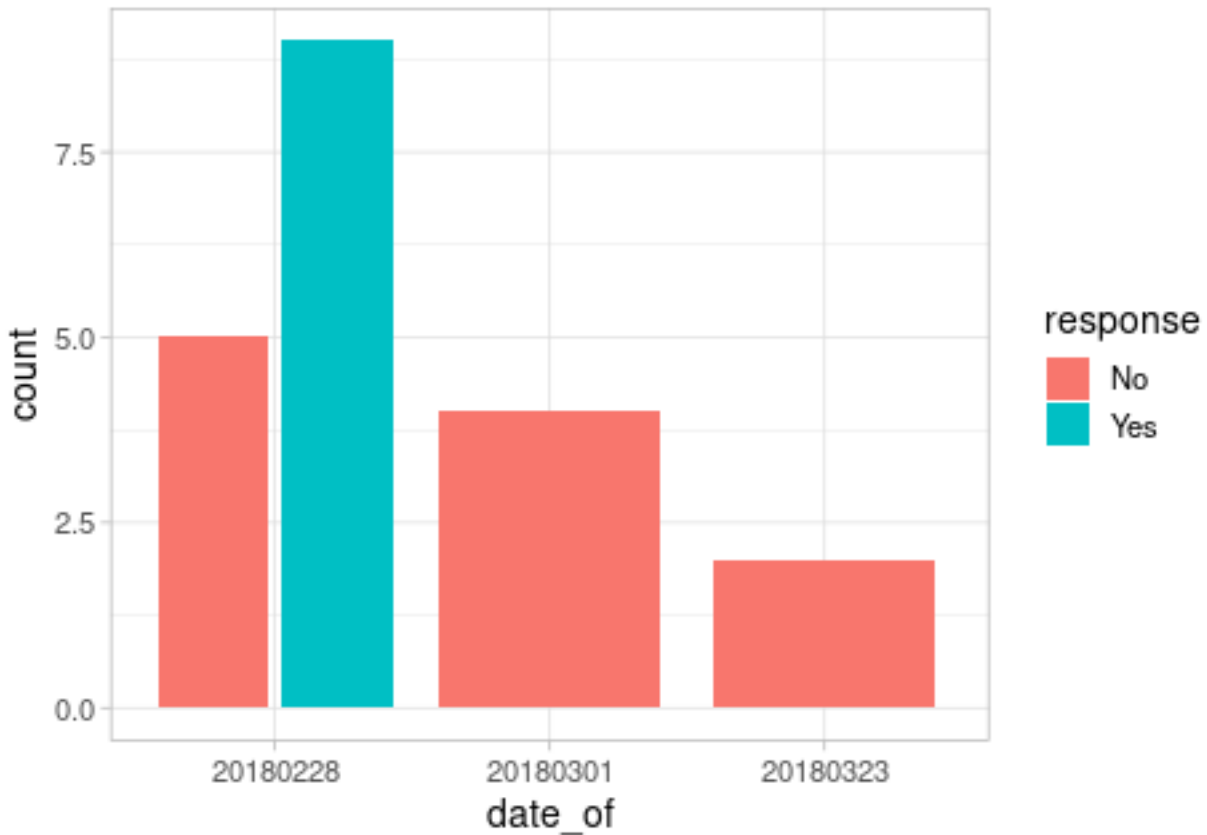


## Covariates correlation with metrics

```
cor <- degCorCov(mdata)
```



```
mdata %>% ggplot(aes(date_of, fill = response)) + geom_bar(position = "dodge2")
```



## Sample-level QC analysis

```
### Transform counts for data visualization (unsupervised analysis)
rld_file <- "data/rld.day1.RDS"
if (file.exists(rld_file)){
  rld <- readRDS(rld_file)
}else{
  rld <- rlog(dds, blind = TRUE)
  saveRDS(rld, rld_file)
}
class(rld) # what type of object is this
```

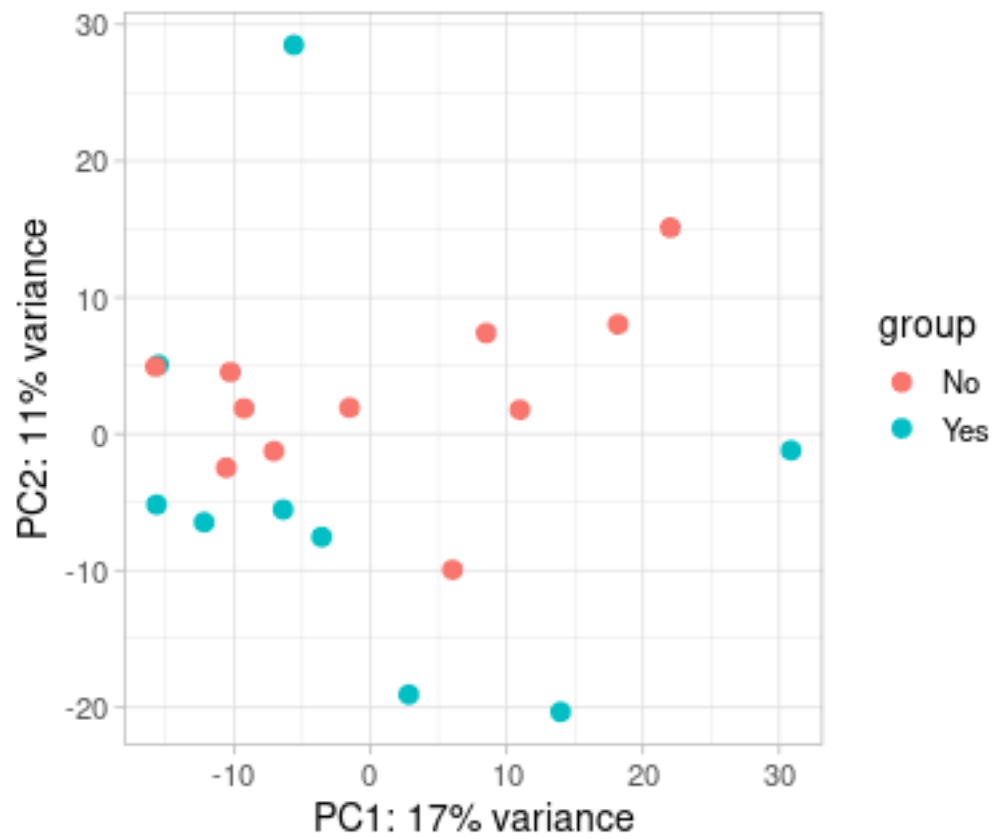
```
## [1] "DESeqTransform"
## attr(,"package")
## [1] "DESeq2"
```

```
# we also need just a matrix of transformed counts
rld_mat <- assay(rld)
```

## PCA - response

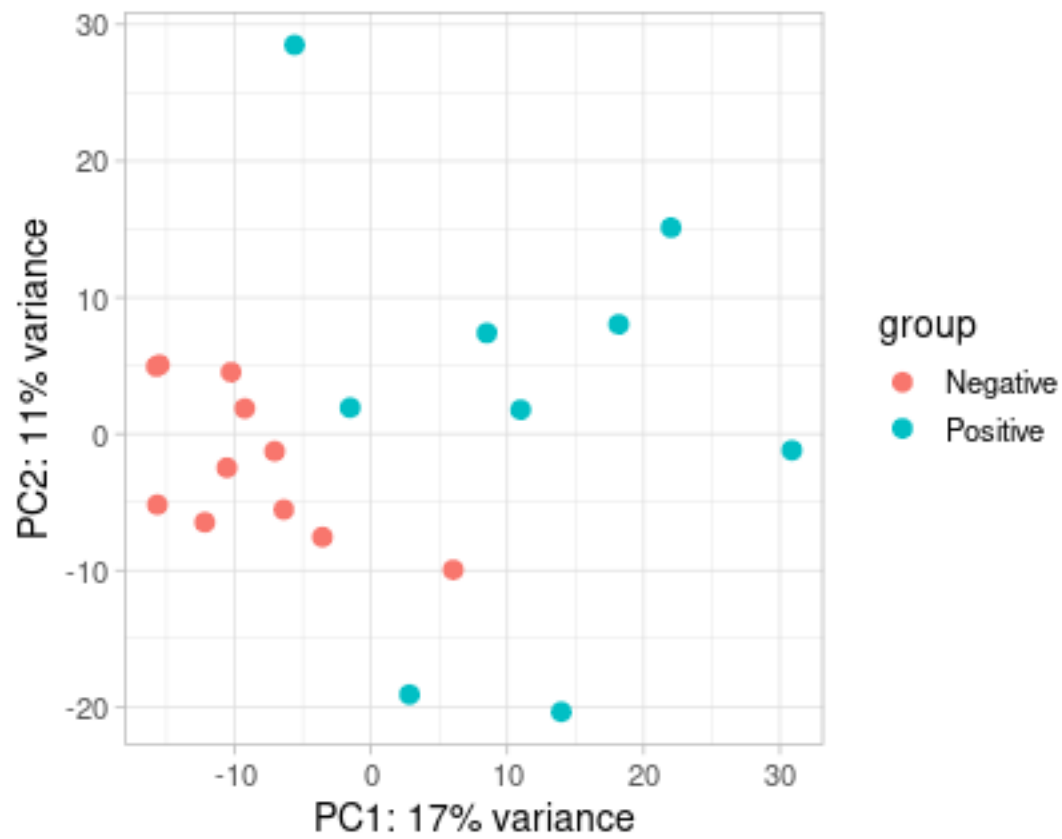
```
# Use the DESeq2 function
plotPCA(rld, intgroup = c("response"))
```





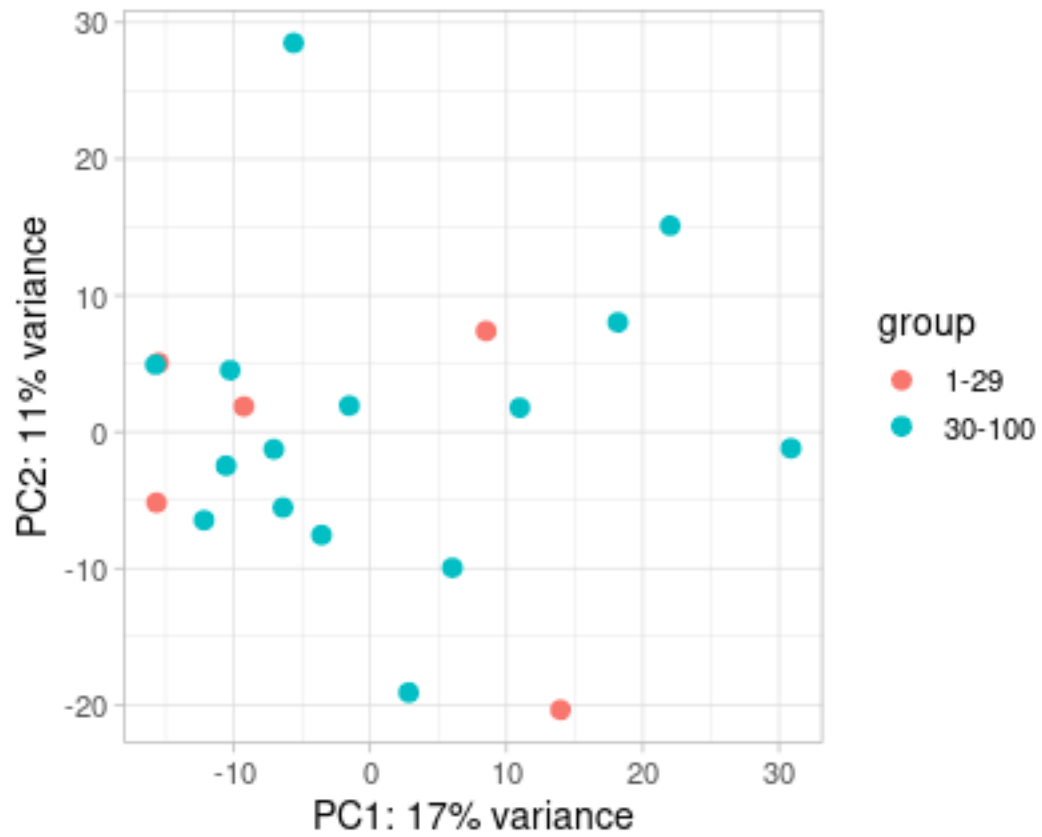
## PCA - ER

```
# Use the DESeq2 function  
plotPCA(rld, intgroup = c("er"))
```



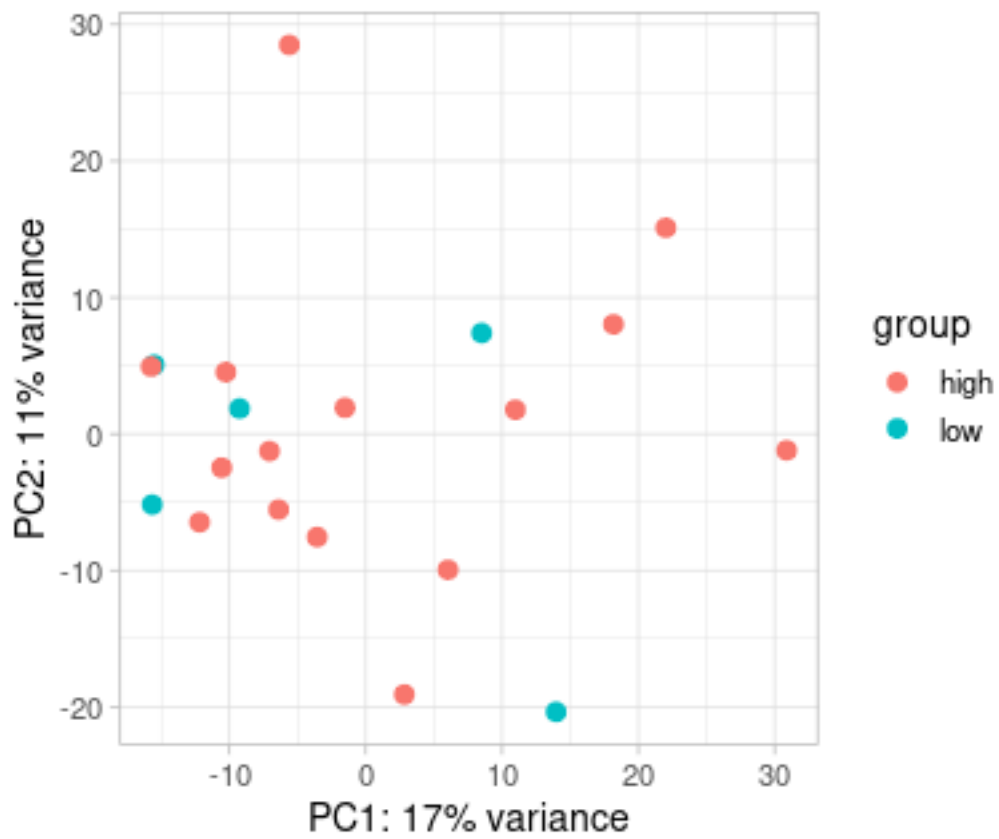
### PCA - tumor\_percentage

```
# Use the DESeq2 function  
plotPCA(rld, intgroup = c("tumor_percentage"))
```



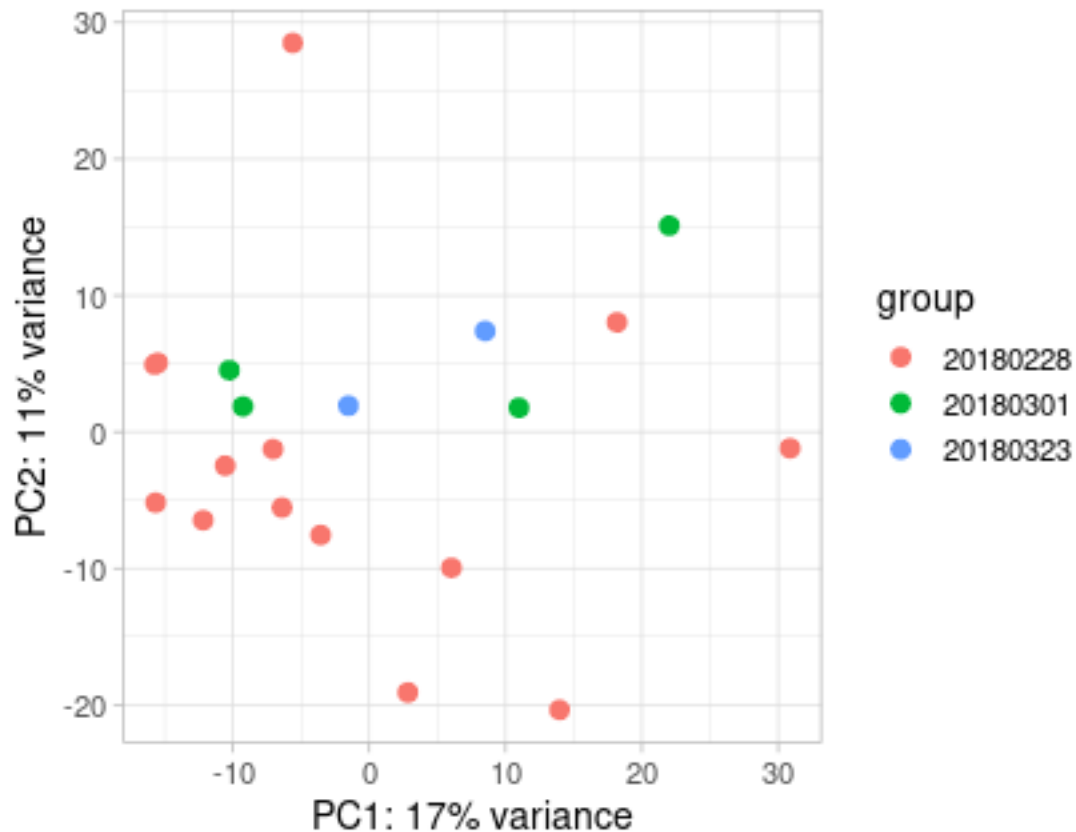
### PCA - tumor\_percentage\_high

```
# Use the DESeq2 function  
plotPCA(rld, intgroup = c("tumor_percentage_high"))
```



## PCA - date\_of

```
# Use the DESeq2 function  
plotPCA(rld, intgroup = c("date_of"))
```



## Inter-correlation analysis

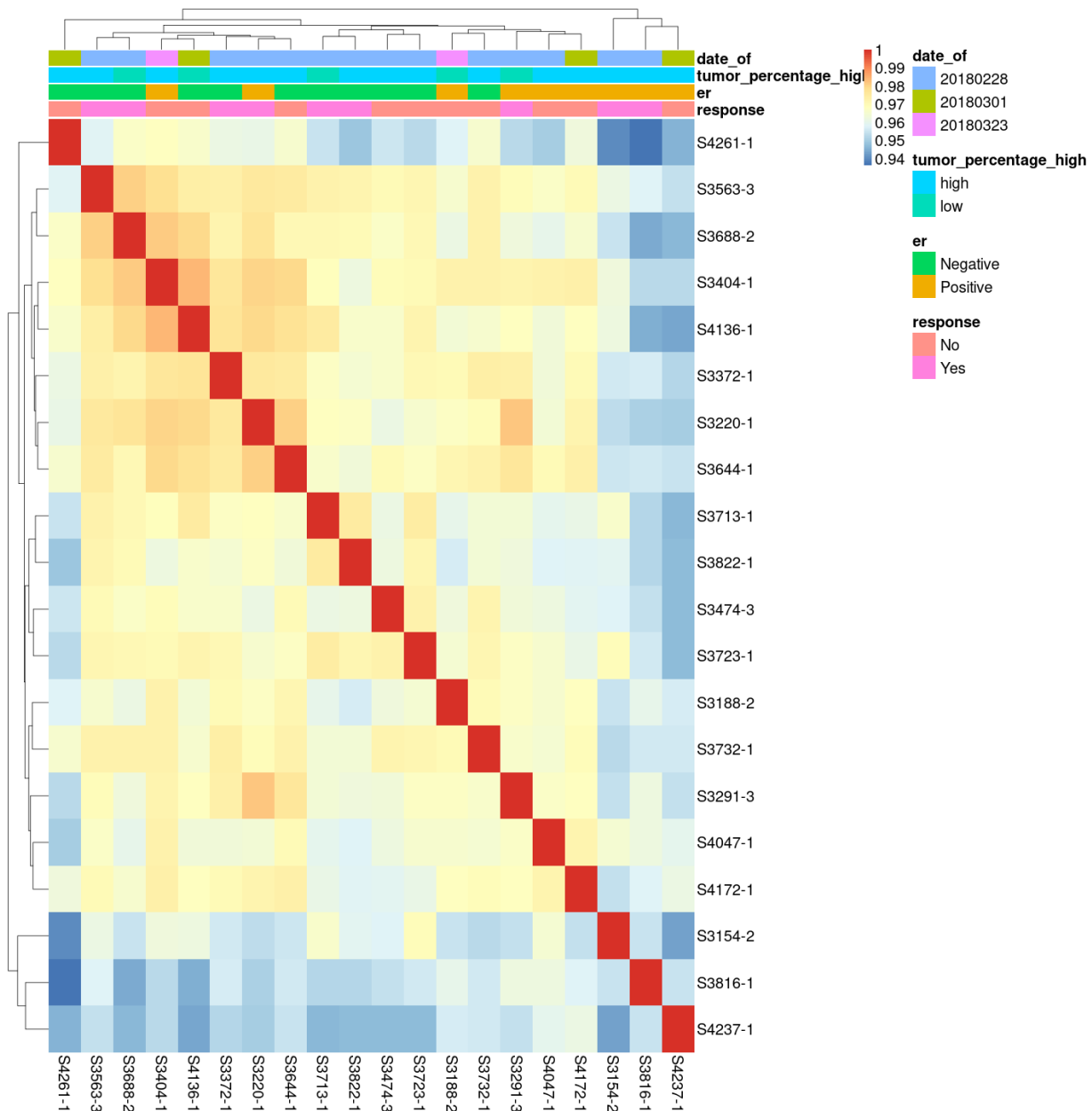
### Without study\_id

```
# Correlation matrix
rld_cor <- cor(rld_mat)

meta$study_id <- as.factor(meta$study_id)
# Create annotation file for samples
annotation <- meta[, c("response", "er", "tumor_percentage_high", "date_of")]

# Change colors
heat.colors <- brewer.pal(6, "Blues")

# Plot heatmap
pheatmap(rld_cor,
  annotation = annotation,
  border = NA,
  fontsize = 20)
```



## With study\_id

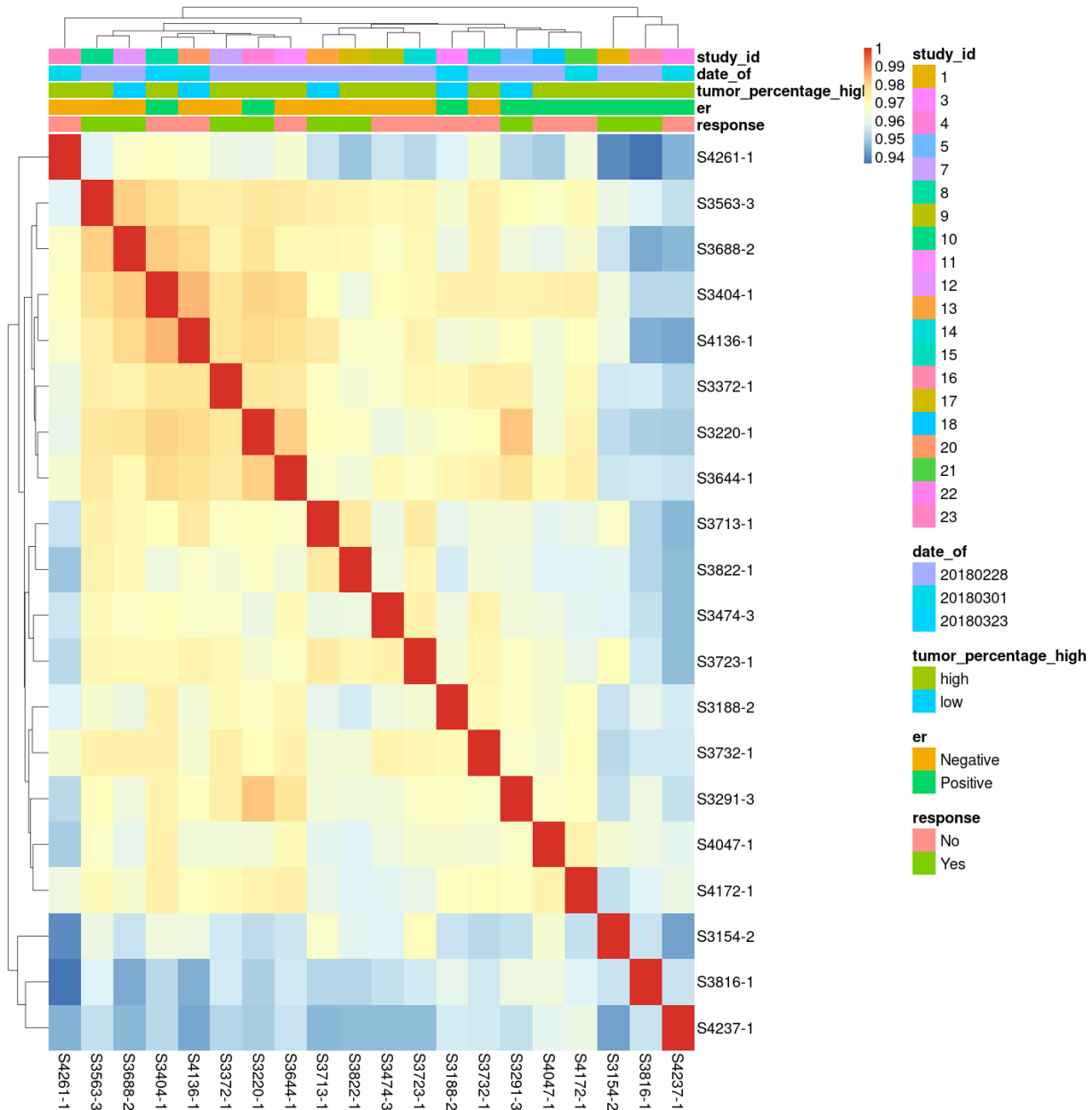
```
# Correlation matrix
rld_cor <- cor(rld_mat)

meta$study_id <- as.factor(meta$study_id)
# Create annotation file for samples
annotation <- meta[, c("response", "er", "tumor_percentage_high", "date_of", "study_id")]

# Change colors
heat.colors <- brewer.pal(6, "Blues")

# Plot heatmap
```

```
pheatmap(rld_cor,
  annotation = annotation,
  border = NA,
  fontsize = 20)
```



## Response Yes vs No for Day 1- see Table9

```
# Get results for rescue vs wt
contrast <- c("response", "Yes", "No")
resResponse <- results(dds, contrast = contrast, alpha = 0.05)
length(which(resResponse$padj < 0.05))
```

```
## [1] 15
```

```

# Add annotations
resResponse_tb <- resResponse %>%
  data.frame() %>%
  rownames_to_column(var = "gene") %>%
  as_tibble() %>%
  left_join(gene_symbol, by = c("gene" = "gene_id"))

resResponse_tb_significant <- dplyr::filter(resResponse_tb, padj < 0.05)

samples_no <- meta %>% dplyr::filter(response == "No") %>% row.names()

counts_no <- txi$abundance %>%
  as.data.frame() %>%
  dplyr::select(any_of(samples_no)) %>%
  rowSums() %>%
  as.data.frame() %>%
  rownames_to_column(var = "ensembl_gene_id")
colnames(counts_no) <- c("ensembl_gene_id", "no_expression_mean_tpm")

samples_yes <- meta %>% dplyr::filter(response == "Yes") %>% row.names()

counts_yes <- txi$abundance %>%
  as.data.frame() %>%
  dplyr::select(any_of(samples_yes)) %>%
  rowSums() %>%
  as.data.frame() %>%
  rownames_to_column(var = "ensembl_gene_id")

colnames(counts_yes) <- c("ensembl_gene_id", "yes_expression_mean_tpm")

counts_yes <- counts_yes %>%
  left_join(counts_no,
    by = c("ensembl_gene_id" = "ensembl_gene_id"))

resResponse_tb_significant <- resResponse_tb_significant %>%
  left_join(counts_yes, by = c("gene" = "ensembl_gene_id"))

write_csv(resResponse_tb_significant,
  "tables/T9.DE_response_day1.csv")

# Separate into up and down-regulated gene sets
sigResponse_up <- rownames(resResponse)[which(resResponse$padj < 0.01 & resResponse$log2FoldChange > 0)]
sigResponse_down <- rownames(resResponse)[which(resResponse$padj < 0.01 & resResponse$log2FoldChange < 0)]

```

## ER : Positive vs Negative for Day1 - Table 10

```

contrast <- c("er", "Positive", "Negative")
resER <- results(dds, contrast = contrast, alpha = 0.05)
length(which(resER$padj < 0.05))

```

```
## [1] 571
```



```

# Add annotations
resER_tb <- resER %>%
  data.frame() %>%
  rownames_to_column(var = "gene") %>%
  as_tibble() %>%
  left_join(gene_symbol, by = c("gene" = "gene_id"))

resER_tb_significant <- dplyr::filter(resER_tb, padj < 0.05)

samples_pos <- meta %>% dplyr::filter(er == "Positive") %>% row.names()

counts_pos <- txi$abundance %>%
  as.data.frame() %>%
  dplyr::select(any_of(samples_pos)) %>%
  rowMeans() %>%
  as.data.frame() %>%
  rownames_to_column(var = "ensembl_gene_id")
colnames(counts_pos) <- c("ensembl_gene_id", "Positive_expression_mean_tpm")

samples_neg <- meta %>% dplyr::filter(er == "Negative") %>% row.names()

counts_neg <- txi$abundance %>%
  as.data.frame() %>%
  dplyr::select(any_of(samples_neg)) %>%
  rowMeans() %>%
  as.data.frame() %>%
  rownames_to_column(var = "ensembl_gene_id")

colnames(counts_neg) <- c("ensembl_gene_id", "Negative_expression_mean_tpm")

counts_pos <- counts_pos %>%
  left_join(counts_neg,
    by = c("ensembl_gene_id" = "ensembl_gene_id"))

resER_tb_significant <- resER_tb_significant %>%
  left_join(counts_pos, by = c("gene" = "ensembl_gene_id"))

write_csv(resER_tb_significant,
  "tables/T10.DE_ER.day1.csv")

# Separate into up and down-regulated gene sets
sigER_up <- rownames(resER)[which(resER$padj < 0.01 & resER$log2FoldChange > 0)]
sigER_down <- rownames(resER)[which(resER$padj < 0.01 & resER$log2FoldChange < 0)]

```

## tumor\_percentage\_high : High vs Low for Day1- Table 11

```

contrast <- c("tumor_percentage_high", "high", "low")
resTP <- results(dds, contrast = contrast, alpha = 0.05)
length(which(resTP$padj < 0.05))

```

```
## [1] 7
```

```

# Add annotations
resTP_tb <- resTP %>%
  data.frame() %>%
  rownames_to_column(var = "gene") %>%
  as_tibble() %>%
  left_join(gene_symbol, by = c("gene" = "gene_id"))

resTP_tb_significant <- dplyr::filter(resTP_tb, padj < 0.05)

samples_high <- meta %>% dplyr::filter(tumor_percentage_high == "high") %>% row.names()

counts_high <- txi$abundance %>%
  as.data.frame() %>%
  dplyr::select(any_of(samples_high)) %>%
  rowMeans() %>%
  as.data.frame() %>%
  rownames_to_column(var = "ensembl_gene_id")
colnames(counts_high) <- c("ensembl_gene_id", "High_expression_mean_tpm")

samples_low <- meta %>% dplyr::filter(tumor_percentage_high == "low") %>% row.names()

counts_low <- txi$abundance %>%
  as.data.frame() %>%
  dplyr::select(any_of(samples_low)) %>%
  rowMeans() %>%
  as.data.frame() %>%
  rownames_to_column(var = "ensembl_gene_id")

colnames(counts_low) <- c("ensembl_gene_id", "Low_expression_mean_tpm")

counts_high <- counts_high %>%
  left_join(counts_low,
    by = c("ensembl_gene_id" = "ensembl_gene_id"))

resTP_tb_significant <- resTP_tb_significant %>%
  left_join(counts_high, by = c("gene" = "ensembl_gene_id"))

write_csv(resTP_tb_significant,
  "tables/T11.DE_tumor_percentage_high.day1.csv")

# Separate into up and down-regulated gene sets
sigTP_up <- rownames(resTP)[which(resTP$padj < 0.01 & resTP$log2FoldChange > 0)]
sigTP_down <- rownames(resTP)[which(resTP$padj < 0.01 & resTP$log2FoldChange < 0)]

```

## date\_of: 20180323 vs 20180228 - for Day1: Table 12

```

contrast <- c("date_of", "20180323", "20180228")
resD0 <- results(dds, contrast = contrast, alpha = 0.05)
length(which(resD0$padj < 0.05))

```

```
## [1] 30
```

```

# Add annotations
resD0_tb <- resD0 %>%
  data.frame() %>%
  rownames_to_column(var = "gene") %>%
  as_tibble() %>%
  left_join(gene_symbol, by = c("gene" = "gene_id"))

resD0_tb_significant <- dplyr::filter(resD0_tb, padj < 0.05)

samples_23 <- meta %>% dplyr::filter(date_of == "20180323") %>% row.names()

counts_23 <- txi$abundance %>%
  as.data.frame() %>%
  dplyr::select(any_of(samples_23)) %>%
  rowMeans() %>%
  as.data.frame() %>%
  rownames_to_column(var = "ensembl_gene_id")
colnames(counts_23) <- c("ensembl_gene_id", "20180323_expression_mean_tpm")

samples_28 <- meta %>% dplyr::filter(date_of == "20180228") %>% row.names()

counts_28 <- txi$abundance %>%
  as.data.frame() %>%
  dplyr::select(any_of(samples_28)) %>%
  rowMeans() %>%
  as.data.frame() %>%
  rownames_to_column(var = "ensembl_gene_id")

colnames(counts_28) <- c("ensembl_gene_id", "20180228_expression_mean_tpm")

counts_23 <- counts_23 %>%
  left_join(counts_28,
    by = c("ensembl_gene_id" = "ensembl_gene_id"))

resD0_tb_significant <- resD0_tb_significant %>%
  left_join(counts_23, by = c("gene" = "ensembl_gene_id"))

write_csv(resD0_tb_significant,
  "tables/T12.DE_date_of.day1.csv")

# Separate into up and down-regulated gene sets
sigD0_up <- rownames(resD0)[which(resD0$padj < 0.01 & resD0$log2FoldChange > 0)]
sigD0_down <- rownames(resD0)[which(resD0$padj < 0.01 & resD0$log2FoldChange < 0)]

```

## Visualization

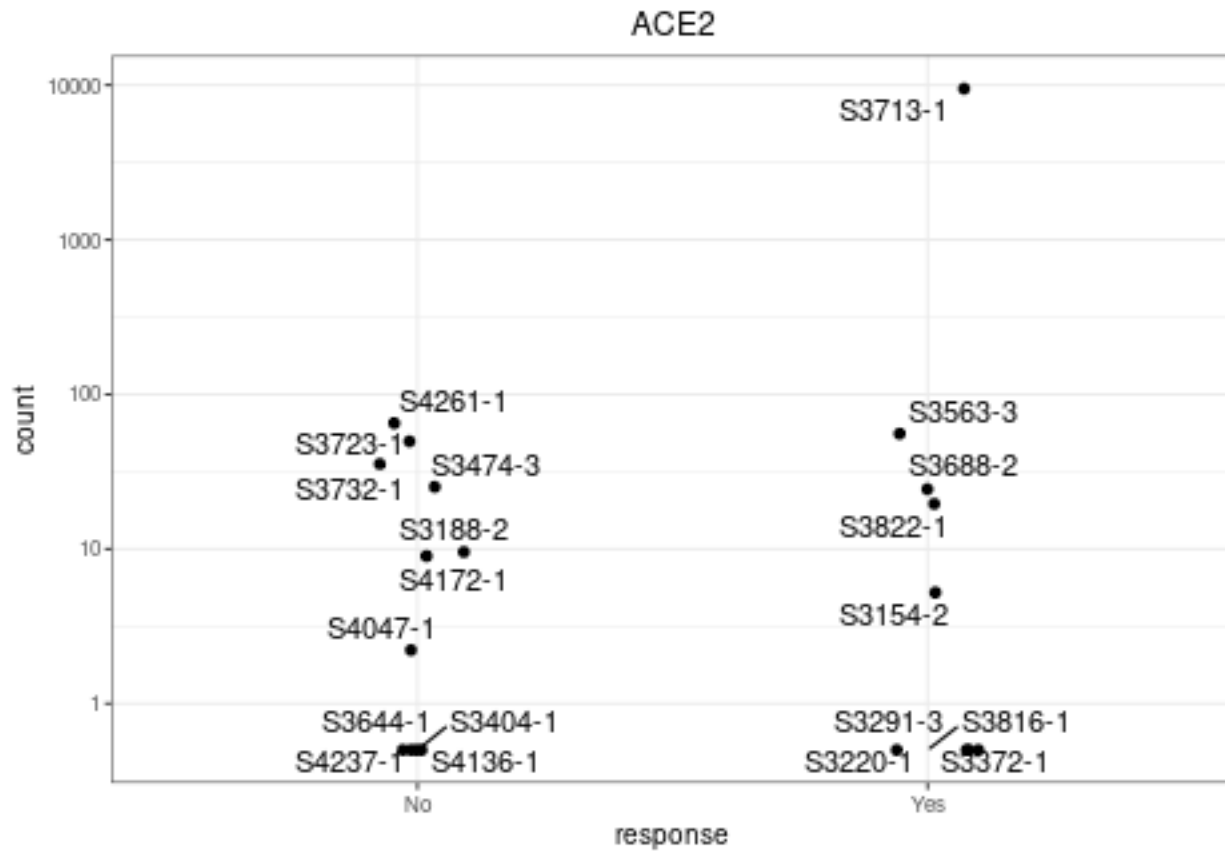
### Gene example

```

d <- plotCounts(dds,
  gene = "ENSG00000130234",
  intgroup = "response",
  returnData = TRUE)

```

```
ggplot(d, aes(x = response, y = count)) +
  geom_point(position = position_jitter(w = 0.1, h = 0)) +
  geom_text_repel(aes(label = rownames(d))) +
  theme_bw(base_size = 10) +
  ggtitle("ACE2") +
  theme(plot.title = element_text(hjust = 0.5)) +
  scale_y_log10()
```



```
# Add a column for significant genes
resResponse_tb <- resResponse_tb %>% mutate(threshold = padj < 0.01)

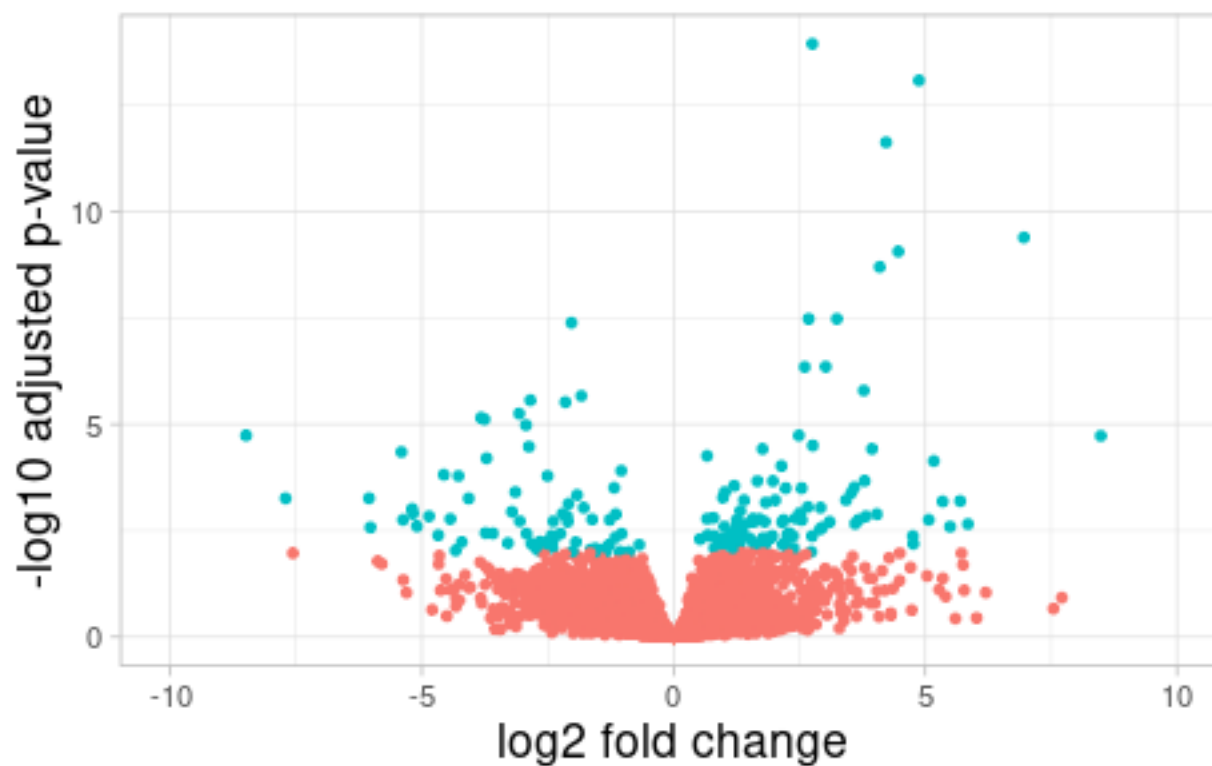
ggplot(resResponse_tb) +
  geom_point(aes(x = log2FoldChange, y = -log10(padj), colour = threshold)) +
  ggtitle("Response Yes vs No") +
  xlab("log2 fold change") +
  ylab("-log10 adjusted p-value") +
  scale_x_continuous(limits = c(-10,10)) +
  scale_y_continuous(limits = c(0, 7.5))+
  theme(legend.position = "none",
        plot.title = element_text(size = rel(1.5), hjust = 0.5),
        axis.title = element_text(size = rel(1.25)))
```



```
# Add a column for significant genes
resER_tb <- resER_tb %>% mutate(threshold = padj < 0.01)

ggplot(resER_tb) +
  geom_point(aes(x = log2FoldChange, y = -log10(padj), colour = threshold)) +
  ggtitle("ER: Positive vs Negative") +
  xlab("log2 fold change") +
  ylab("-log10 adjusted p-value") +
  scale_x_continuous(limits = c(-10,10)) +
  theme(legend.position = "none",
        plot.title = element_text(size = rel(1.5), hjust = 0.5),
        axis.title = element_text(size = rel(1.25)))
```

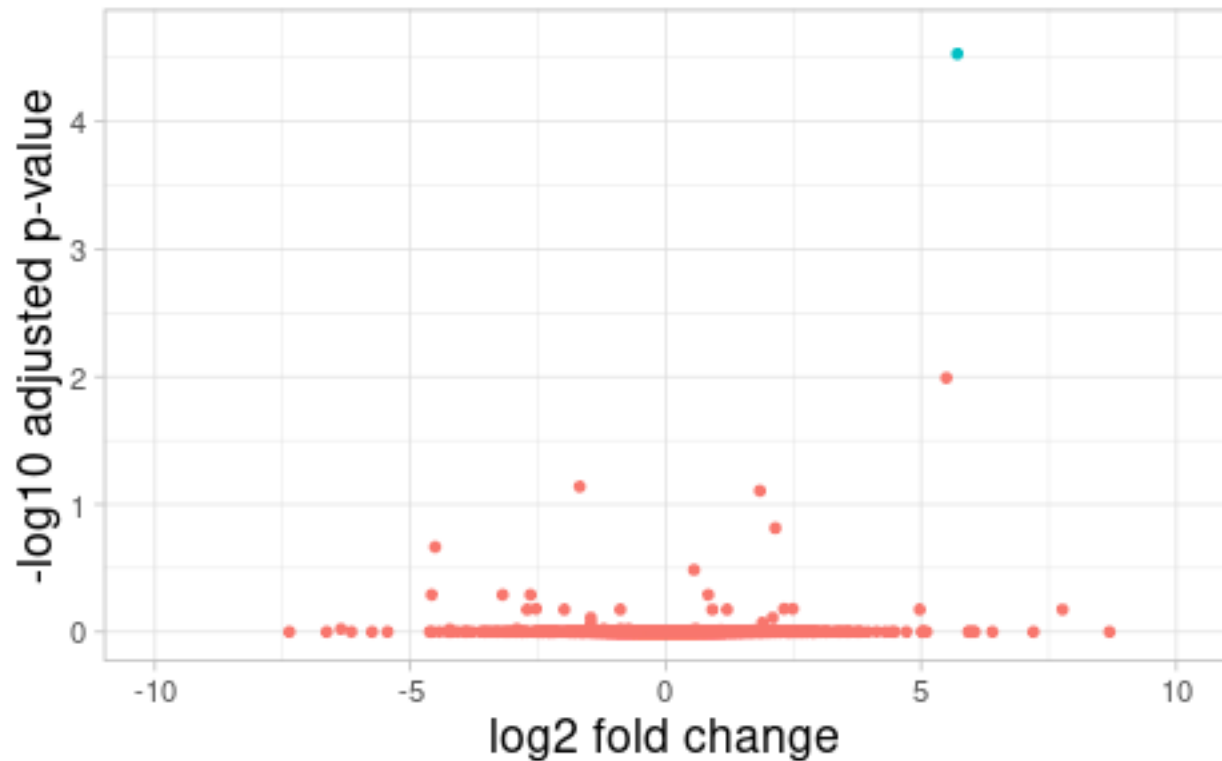
## ER: Positive vs Negative



```
# Add a column for significant genes
resTP_tb <- resTP_tb %>% mutate(threshold = padj < 0.01)

ggplot(resTP_tb) +
  geom_point(aes(x = log2FoldChange, y = -log10(padj), colour = threshold)) +
  ggtitle("Tumor_percentage_high: High vs Low") +
  xlab("log2 fold change") +
  ylab("-log10 adjusted p-value") +
  scale_x_continuous(limits = c(-10,10)) +
  theme(legend.position = "none",
        plot.title = element_text(size = rel(1.5), hjust = 0.5),
        axis.title = element_text(size = rel(1.25)))
```

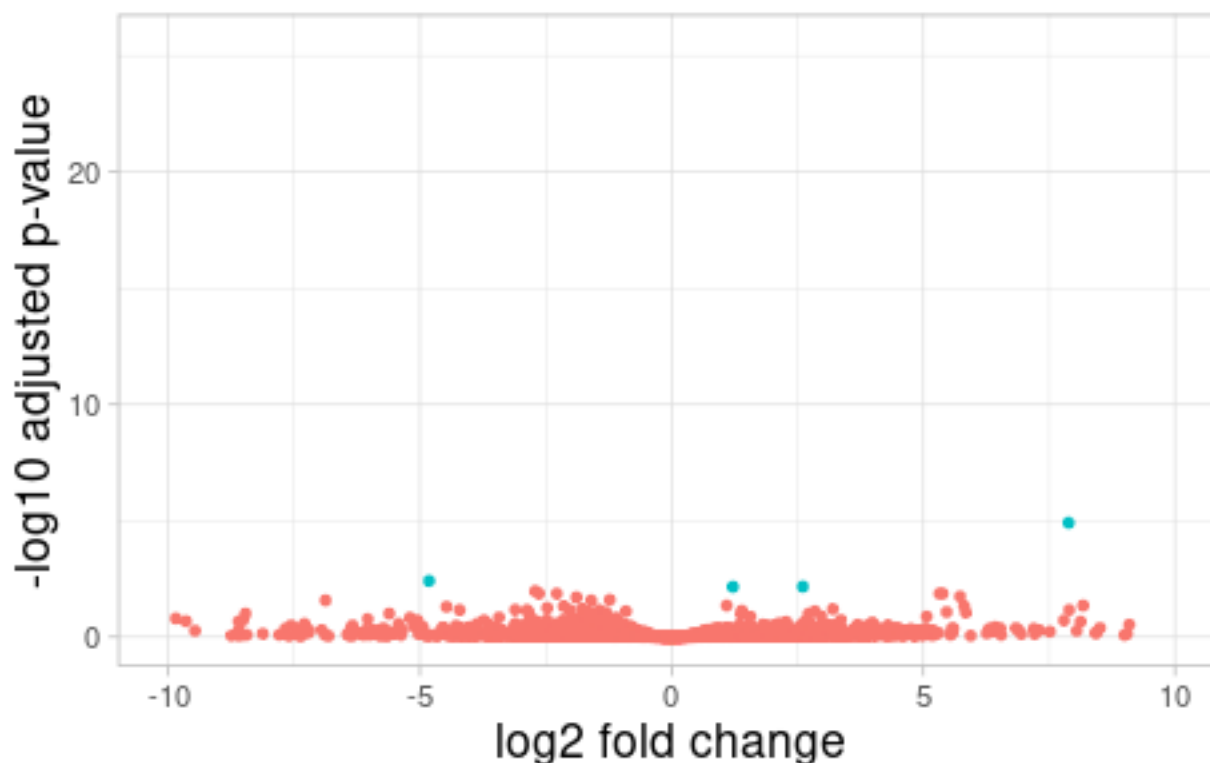
## Tumor\_percentage\_high: High vs Low



```
# Add a column for significant genes
resD0_tb <- resD0_tb %>% mutate(threshold = padj < 0.01)

ggplot(resD0_tb) +
  geom_point(aes(x = log2FoldChange, y = -log10(padj), colour = threshold)) +
  ggtitle("Dafe of: 20180323 vs 20180228") +
  xlab("log2 fold change") +
  ylab("-log10 adjusted p-value") +
  scale_x_continuous(limits = c(-10,10)) +
  theme(legend.position = "none",
        plot.title = element_text(size = rel(1.5), hjust = 0.5),
        axis.title = element_text(size = rel(1.25)))
```

Date of: 20180323 vs 20180228



# Heatmaps

*# Create a matrix of normalized expression*

```
sig_up <- resResponse_tb_significant %>% arrange(-log2FoldChange) %>% head(50) %>% pull(gene)
sig_down <- resResponse_tb_significant %>% arrange(log2FoldChange) %>% head(50) %>% pull(gene)
sig <- c(sig_up, sig_down)
```

```
row_annotation <- gene_symbol %>%
  as_tibble() %>%
  dplyr::filter(gene_id %in% sig)
```

```
plotmat <- txi$abundance[c(sig_up, sig_down),] %>% as.data.frame() %>%
  rownames_to_column(var = "ensembl_gene_id") %>%
  left_join(gene_symbol, by = c("ensembl_gene_id" = "gene_id")) %>%
  drop_na(symbol)
```

```
plotmat$ensembl_gene_id <- NULL
```

```
plotmat <- plotmat %>% column_to_rownames(var = "symbol") %>% as.matrix()
```

*# Color palette*

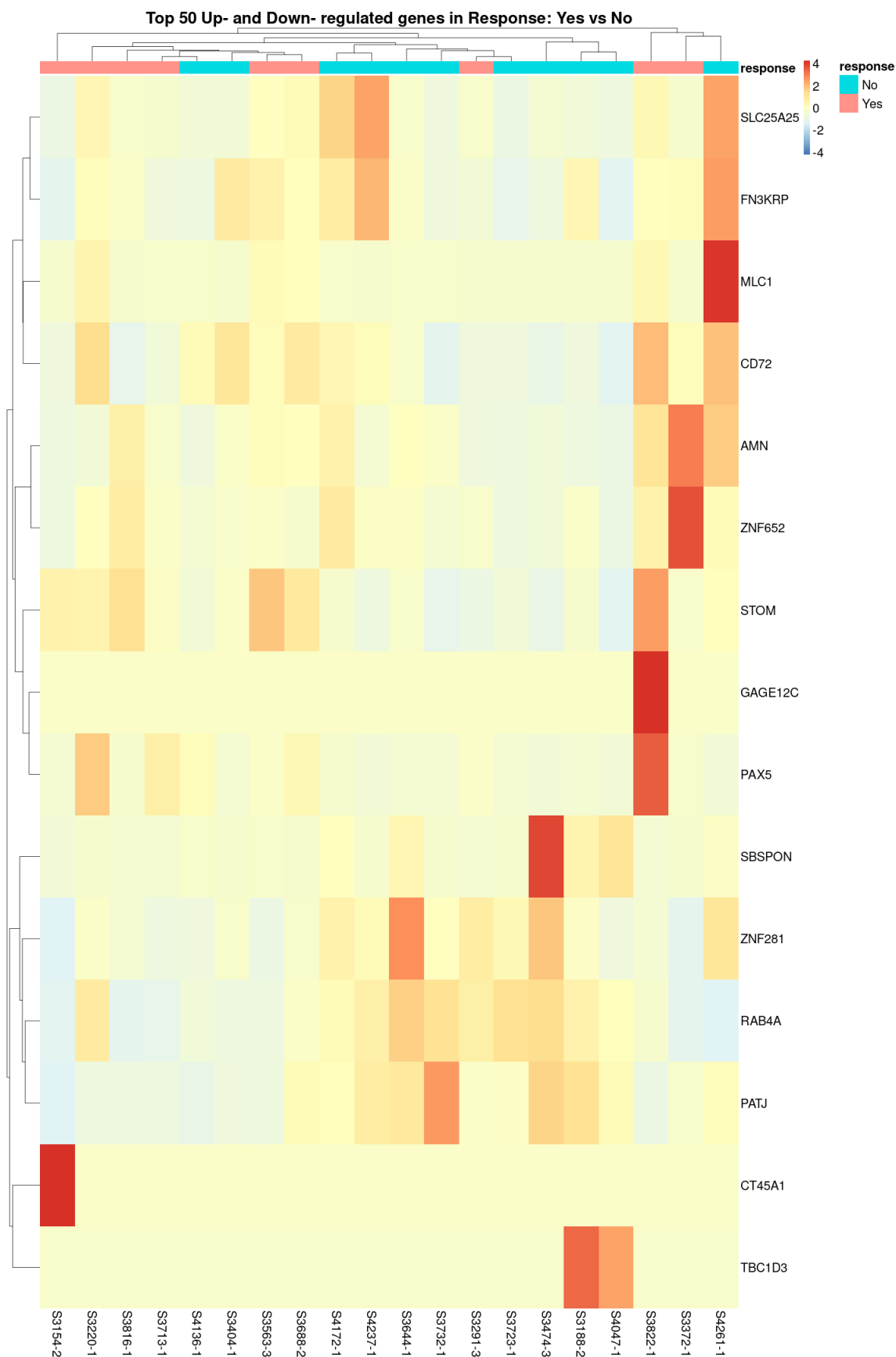
```
heat.colors <- brewer.pal(6, "YlOrRd")
```

*# Plot heatmap*

```
pheatmap(plotmat,
  scale = "row",
  show_rownames = TRUE,
```



```
border = FALSE,  
annotation = meta[, c("response"), drop = FALSE],  
main = "Top 50 Up- and Down- regulated genes in Response: Yes vs No",  
fontsize = 20)
```



```

# Create a matrix of normalized expression
sig_up <- resER_tb_significant %>% arrange(-log2FoldChange) %>% head(50) %>% pull(gene)
sig_down <- resER_tb_significant %>% arrange(log2FoldChange) %>% head(50) %>% pull(gene)
sig <- c(sig_up, sig_down)

row_annotation <- gene_symbol %>%
  as_tibble() %>%
  dplyr::filter(gene_id %in% sig)

plotmat <- txi$abundance[c(sig_up, sig_down),] %>% as.data.frame() %>%
  rownames_to_column(var = "ensembl_gene_id") %>%
  left_join(gene_symbol, by = c("ensembl_gene_id" = "gene_id")) %>%
  drop_na(symbol)

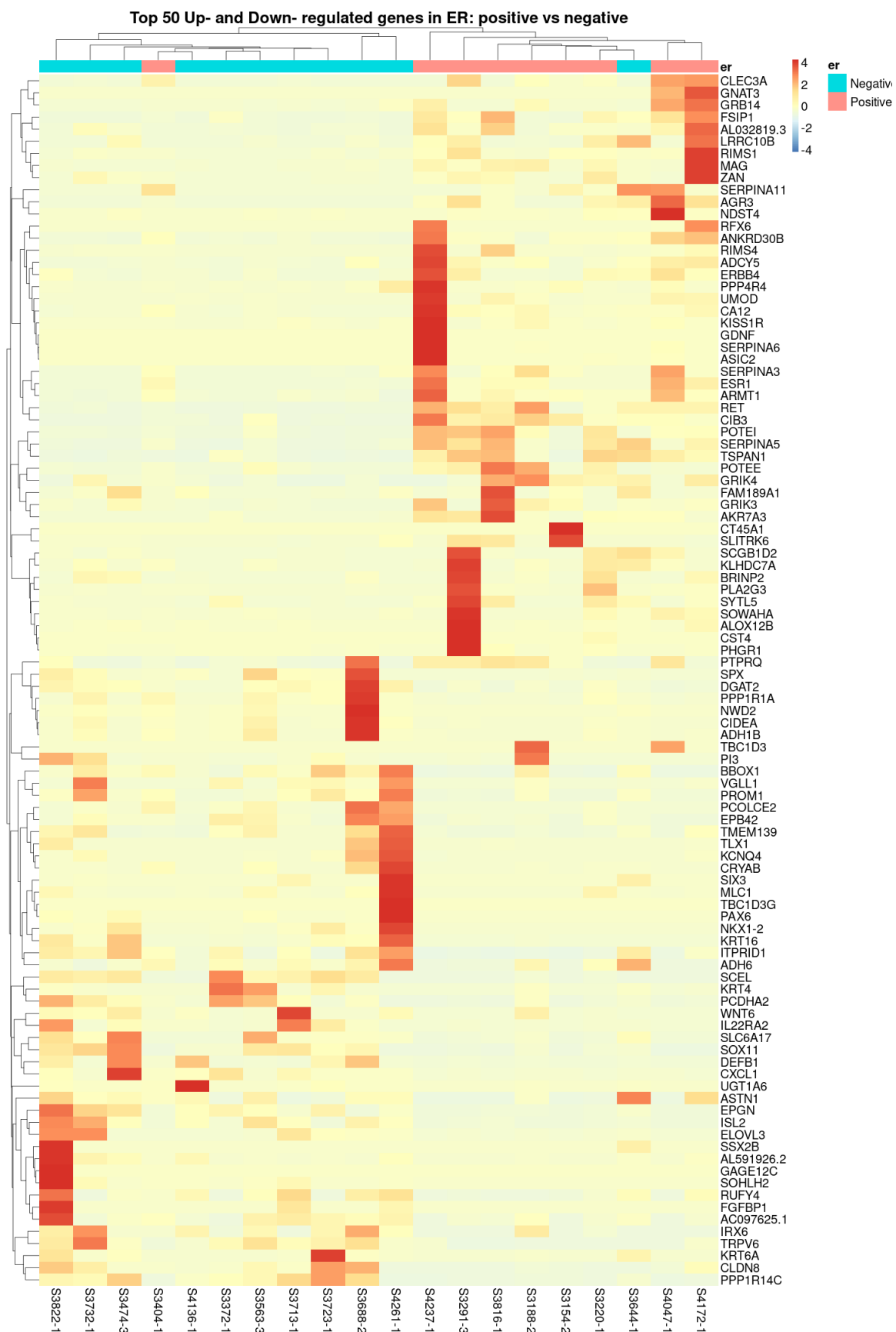
plotmat$ensembl_gene_id <- NULL

plotmat <- plotmat %>% column_to_rownames(var = "symbol") %>% as.matrix()

# Color palette
heat.colors <- brewer.pal(6, "YlOrRd")

# Plot heatmap
pheatmap(plotmat,
  scale = "row",
  show_rownames = TRUE,
  border = FALSE,
  annotation = meta[, c("er"), drop = FALSE],
  main = "Top 50 Up- and Down- regulated genes in ER: positive vs negative",
  fontsize = 20)

```



```

# Create a matrix of normalized expression
sig_up <- resTP_tb_significant %>% arrange(-log2FoldChange) %>% head(50) %>% pull(gene)
sig_down <- resTP_tb_significant %>% arrange(log2FoldChange) %>% head(50) %>% pull(gene)
sig <- c(sig_up, sig_down)

row_annotation <- gene_symbol %>%
  as_tibble() %>%
  dplyr::filter(gene_id %in% sig)

plotmat <- txi$abundance[c(sig_up, sig_down),] %>% as.data.frame() %>%
  rownames_to_column(var = "ensembl_gene_id") %>%
  left_join(gene_symbol, by = c("ensembl_gene_id" = "gene_id")) %>%
  drop_na(symbol)

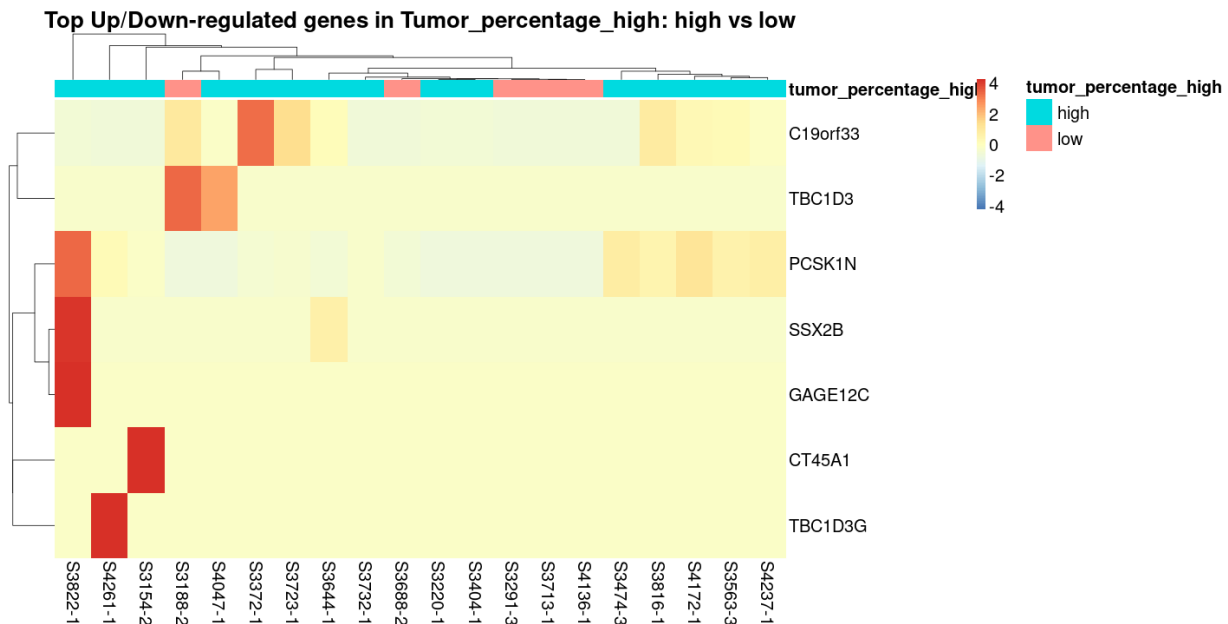
plotmat$ensembl_gene_id <- NULL

plotmat <- plotmat %>% column_to_rownames(var = "symbol") %>% as.matrix()

# Color palette
heat.colors <- brewer.pal(6, "YlOrRd")

# Plot heatmap
pheatmap(plotmat,
  scale = "row",
  show_rownames = TRUE,
  border = FALSE,
  annotation = meta[, c("tumor_percentage_high"), drop = FALSE],
  main = "Top Up/Down-regulated genes in Tumor_percentage_high: high vs low",
  fontsize = 20)

```



```

# Create a matrix of normalized expression
sig_up <- resD0_tb_significant %>% arrange(-log2FoldChange) %>% head(50) %>% pull(gene)
sig_down <- resD0_tb_significant %>% arrange(log2FoldChange) %>% head(50) %>% pull(gene)
sig <- c(sig_up, sig_down)

```

```

row_annotation <- gene_symbol %>%
  as_tibble() %>%
  dplyr::filter(gene_id %in% sig)

plotmat <- txi$abundance[c(sig_up, sig_down),] %>% as.data.frame() %>%
  rownames_to_column(var = "ensembl_gene_id") %>%
  left_join(gene_symbol, by = c("ensembl_gene_id" = "gene_id")) %>%
  drop_na(symbol)

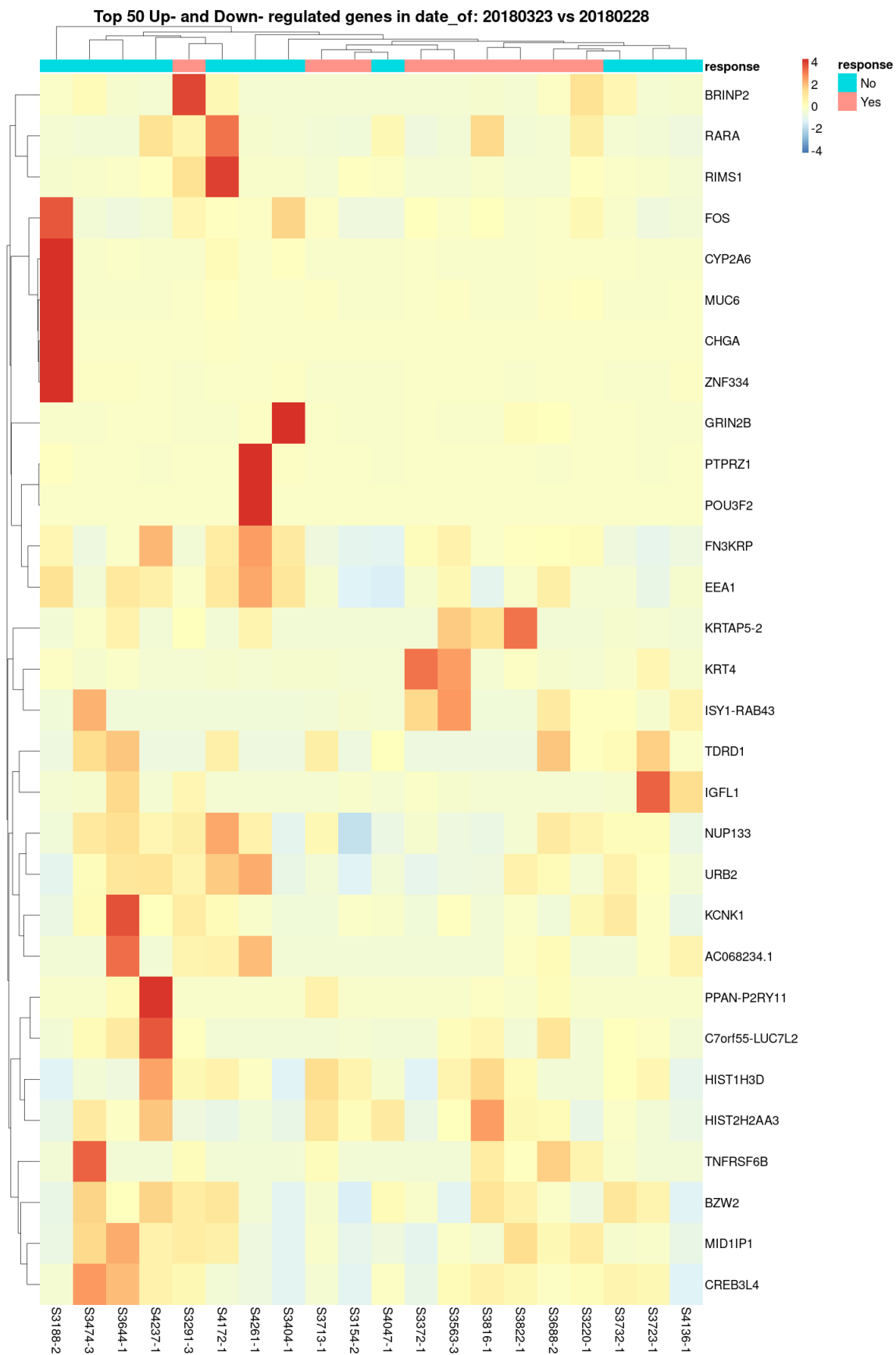
plotmat$ensembl_gene_id <- NULL

plotmat <- plotmat %>% column_to_rownames(var = "symbol") %>% as.matrix()

# Color palette
heat.colors <- brewer.pal(6, "YlOrRd")

# Plot heatmap
pheatmap(plotmat,
  scale = "row",
  show_rownames = TRUE,
  border = FALSE,
  annotation = meta[, c("response"), drop = FALSE],
  main = "Top 50 Up- and Down- regulated genes in date_of: 20180323 vs 20180228",
  fontsize = 20)

```



## R session

```
sessionInfo()
```

```
## R version 4.0.3 (2020-10-10)
## Platform: x86_64-redhat-linux-gnu (64-bit)
## Running under: Fedora 32 (Workstation Edition)
##
## Matrix products: default
## BLAS/LAPACK: /usr/lib64/libopenblas-r0.3.12.so
##
## locale:
##  [1] LC_CTYPE=en_CA.UTF-8      LC_NUMERIC=C
##  [3] LC_TIME=en_CA.UTF-8      LC_COLLATE=en_CA.UTF-8
##  [5] LC_MONETARY=en_CA.UTF-8  LC_MESSAGES=en_CA.UTF-8
##  [7] LC_PAPER=en_CA.UTF-8     LC_NAME=C
##  [9] LC_ADDRESS=C             LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_CA.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] parallel stats4      stats      graphics  grDevices  utils      datasets
## [8] methods   base
##
## other attached packages:
##  [1] ensemblDb_2.14.0      AnnotationFilter_1.14.0
##  [3] GenomicFeatures_1.42.1 AnnotationDbi_1.52.0
##  [5] AnnotationHub_2.22.0  BiocFileCache_1.14.0
##  [7] dbplyr_2.1.0          knitr_1.30
##  [9] ggrepel_0.9.1         tximport_1.18.0
## [11] DEGreport_1.26.0      pheatmap_1.0.12
## [13] RColorBrewer_1.1-2    forcats_0.5.1
## [15] stringr_1.4.0         dplyr_1.0.5
## [17] purrr_0.3.4           readr_1.4.0
## [19] tidyr_1.1.3           tibble_3.1.0
## [21] ggplot2_3.3.3         tidyverse_1.3.0
## [23] DESeq2_1.30.1         SummarizedExperiment_1.20.0
## [25] Biobase_2.50.0        MatrixGenerics_1.2.1
## [27] matrixStats_0.58.0    GenomicRanges_1.42.0
## [29] GenomeInfoDb_1.26.2   IRanges_2.24.1
## [31] S4Vectors_0.28.1     BiocGenerics_0.36.0
##
## loaded via a namespace (and not attached):
##  [1] readxl_1.3.1          backports_1.2.1
##  [3] circlize_0.4.12       plyr_1.8.6
##  [5] lazyeval_0.2.2        ConsensusClusterPlus_1.54.0
##  [7] splines_4.0.3         BiocParallel_1.24.1
##  [9] digest_0.6.27         htmltools_0.5.1.1
## [11] fansi_0.4.2           magrittr_2.0.1
## [13] memoise_2.0.0         cluster_2.1.0
## [15] limma_3.46.0          ComplexHeatmap_2.6.2
## [17] Biostrings_2.58.0     annotate_1.68.0
## [19] Nozzle.R1_1.1-1       modelr_0.1.8
## [21] askpass_1.1           prettyunits_1.1.1
## [23] colorspace_2.0-0      blob_1.2.1
```



## [25] rvest_1.0.0	rappdirs_0.3.3
## [27] haven_2.3.1	xfun_0.19
## [29] crayon_1.4.1	RCurl_1.98-1.2
## [31] jsonlite_1.7.1	genefilter_1.72.1
## [33] survival_3.2-7	glue_1.4.2
## [35] gtable_0.3.0	zlibbioc_1.36.0
## [37] XVector_0.30.0	GetoptLong_1.0.5
## [39] DelayedArray_0.16.2	shape_1.4.5
## [41] scales_1.1.1	DBI_1.1.1
## [43] edgeR_3.32.1	Rcpp_1.0.6
## [45] progress_1.2.2	xtable_1.8-4
## [47] lasso2_1.2-21.1	tmvnsim_1.0-2
## [49] clue_0.3-58	bit_4.0.4
## [51] httr_1.4.2	ellipsis_0.3.1
## [53] farver_2.1.0	pkgconfig_2.0.3
## [55] reshape_0.8.8	XML_3.99-0.5
## [57] locfit_1.5-9.4	utf8_1.1.4
## [59] labeling_0.4.2	tidyselect_1.1.0
## [61] rlang_0.4.10	later_1.1.0.1
## [63] munsell_0.5.0	BiocVersion_3.12.0
## [65] cellranger_1.1.0	tools_4.0.3
## [67] cachem_1.0.4	cli_2.3.1
## [69] generics_0.1.0	RSQLite_2.2.3
## [71] broom_0.7.5	evaluate_0.14
## [73] fastmap_1.1.0	ggdendro_0.1.22
## [75] yaml_2.2.1	bit64_4.0.5
## [77] fs_1.5.0	nlme_3.1-149
## [79] mime_0.9	xml2_1.3.2
## [81] biomaRt_2.46.3	compiler_4.0.3
## [83] rstudioapi_0.13	curl_4.3
## [85] png_0.1-7	interactiveDisplayBase_1.28.0
## [87] reprex_1.0.0	geneplotter_1.68.0
## [89] stringi_1.5.3	lattice_0.20-41
## [91] ProtGenerics_1.22.0	Matrix_1.2-18
## [93] psych_2.0.12	vctrs_0.3.6
## [95] pillar_1.5.1	lifecycle_1.0.0
## [97] BiocManager_1.30.10	GlobalOptions_0.1.2
## [99] cowplot_1.1.1	bitops_1.0-6
## [101] rtracklayer_1.50.0	httpuv_1.5.5
## [103] R6_2.5.0	promises_1.2.0.1
## [105] MASS_7.3-53	assertthat_0.2.1
## [107] openssl_1.4.3	rjson_0.2.20
## [109] withr_2.4.1	GenomicAlignments_1.26.0
## [111] Rsamtools_2.6.0	mnormt_2.0.2
## [113] GenomeInfoDbData_1.2.4	hms_1.0.0
## [115] grid_4.0.3	rmarkdown_2.5
## [117] Cairo_1.5-12.2	logging_0.10-108
## [119] shiny_1.6.0	lubridate_1.7.10