Shank3 Modulates Sleep and Expression of Circadian Transcription Factors differential expression

November 03, 2018

Contents

Description

This is the report of the analysis made for the paper *Shank3 Modulates Sleep and Expression of Circadian Transcription Factors* by *Ashley M. Ingiosi, Taylor Wintler, Hannah Schoch, Kristan G. Singletary, Dario Righelli, Leandro G. Roser, Davide Risso, Marcos G. Frank and Lucia Peixoto.*

Autism Spectrum Disorder (ASD) is the most prevalent neurodevelopmental disorder in the US that often co-presents with sleep problems. Sleep impairments in ASD predict the severity of ASD core diagnostic symptoms and have a considerable impact on the quality of life of caregivers. However, little is known about the underlying molecular mechanism(s) of sleep impairments in ASD. In this study we investigated the role of Shank3, a high confidence ASD gene candidate, in the regulation of sleep. We show that Shank3 mutant mice have problems falling asleep despite accumulating sleep pressure. Using RNA-seq we show that sleep deprivation doubles the differences in gene expression between mutants and wild types and downregulates

circadian transcription factors Per3, Dec2, and Rev-erbα. Shank3 mutants also have trouble regulating locomotor activity in the absence of light. Overall, our study shows that Shank3 is an important modulator of sleep and circadian activity. # Differential Expression Analysis

Importing data

Importing data and filtering out those genes with cpm lesser than 1. We use the *filtered.data* method in *NOISeq* package.

```
countMatrix <- ReadDataFrameFromTsv(file.name.path="./data/refSEQ_countMatrix.txt")
```

```
## ./data/refSEQ_countMatrix.txt read from disk!
```

```
# head(countMatrix)

designMatrix <- ReadDataFrameFromTsv(file.name.path="./design/all_samples_short_names.tsv")
```

```
## ./design/all_samples_short_names.tsv read from disk!
```

```
# head(designMatrix)

filteredCountsProp <- filterLowCounts(counts.dataframe=countMatrix,
                                      is.normalized=FALSE,
                                      design.dataframe=designMatrix,
                                      cond.col.name="gcondition",
                                      method.type="Proportion")
```

```
## features dimensions before normalization: 27179
```

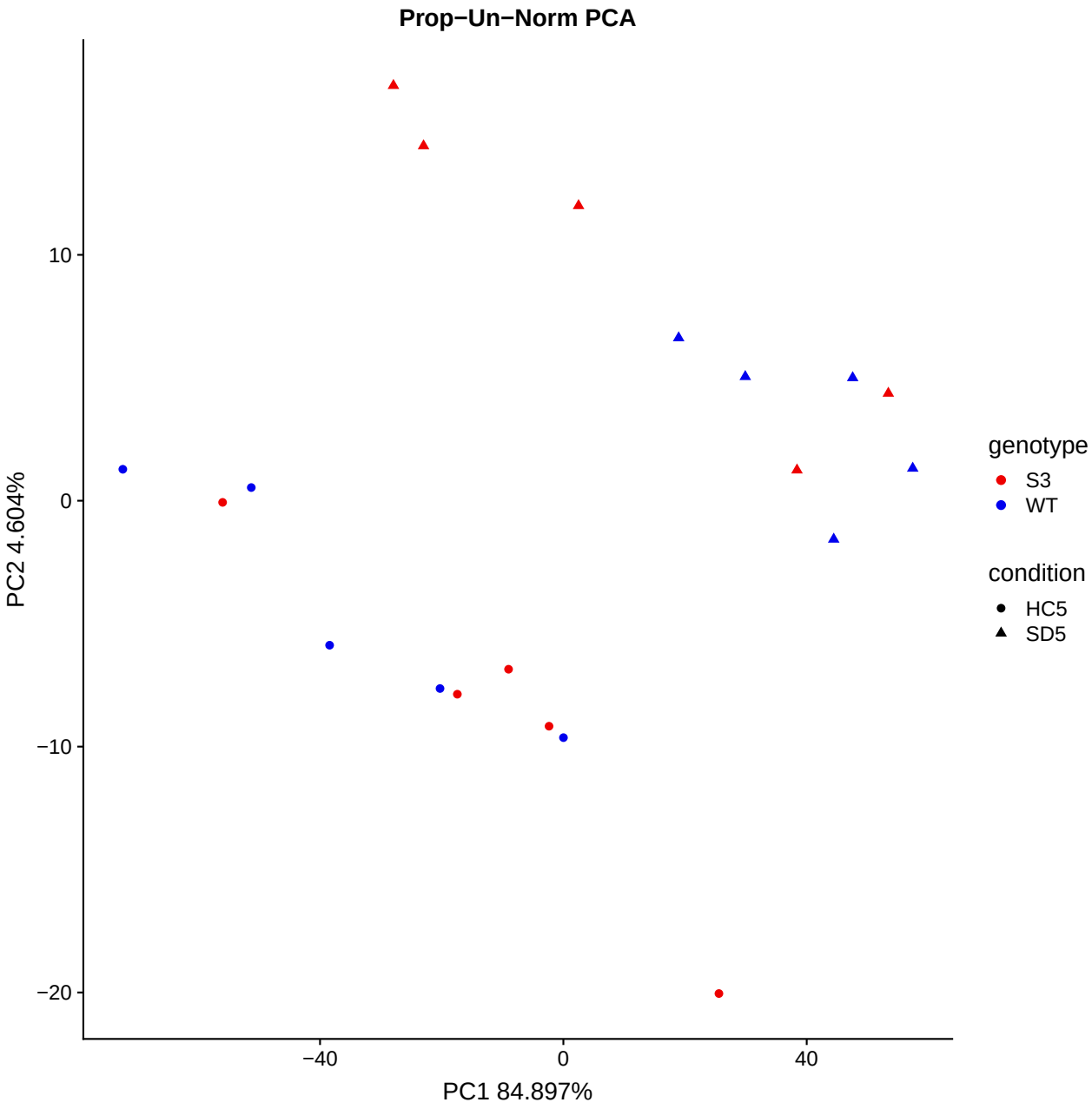
```
## Filtering out low count features...
## 14454 features are to be kept for differential expression analysis with filtering method 3
```

Plot PCA of log unnormalized data

PCA Plot of filtered not-normalized data.

```
PlotPCAPlotlyFunction(counts.data.frame=log1p(filteredCountsProp),
    design.matrix=designMatrix,
    shapeColname="condition", colorColname="genotype", xPCA="PC1", yPCA="PC2",
    plotly.flag=FALSE, show.plot.flag=TRUE, prefix.plot="Prop-Un-Norm")
```

```
## [1] FALSE
```



Control Genes

Negative control genes

Loading Negative Control Genes to normalize data

```
library(readxl)

sd.ctrls <- read_excel(path="./data/controls/Additional File 4 full list of BMC genomics SD&RS2.xlsx", s
sd.ctrls <- sd.ctrls[order(sd.ctrls$adj.P.Val),]

sd.neg.ctrls <- sd.ctrls[sd.ctrls$adj.P.Val > 0.9, ]
```

```
sd.neg.ctrls <- sd.neg.ctrls$`MGI Symbol`
sd.neg.ctrls <- sd.neg.ctrls[-which(is.na(sd.neg.ctrls))]

int.neg.ctrls <- sd.neg.ctrls
int.neg.ctrls <- unique(int.neg.ctrls)
neg.map <- convertGenesViaMouseDb(gene.list=int.neg.ctrls, fromType="SYMBOL",
                                  "ENTREZID")
# sum(is.na(neg.map$ENTREZID))
neg.ctrls.entrez <- as.character(neg.map$ENTREZID)


ind.ctrls <- which(rownames(filteredCountsProp) %in% neg.ctrls.entrez)
counts.neg.ctrls <- filteredCountsProp[ind.ctrls,]
```

positive control genes

Loading Positive Control Genes to detect them during the differential expression step.

```
## sleep deprivation
sd.lit.pos.ctrls <- read_excel("./data/controls/SD_RS_PosControls_final.xlsx",
                        sheet=1)
colnames(sd.lit.pos.ctrls) <- sd.lit.pos.ctrls[1,]
sd.lit.pos.ctrls <- sd.lit.pos.ctrls[-1,]


sd.est.pos.ctrls <- read_excel("./data/controls/SD_RS_PosControls_final.xlsx",
                        sheet=3)

sd.pos.ctrls <- cbind(sd.est.pos.ctrls$`MGI Symbol`, "est")
sd.pos.ctrls <- rbind(sd.pos.ctrls, cbind(sd.lit.pos.ctrls$Gene, "lit"))

sd.pos.ctrls <- sd.pos.ctrls[-which(duplicated(sd.pos.ctrls[,1])),]
sd.pos.ctrls <- sd.pos.ctrls[-which(is.na(sd.pos.ctrls[,1])),]
```

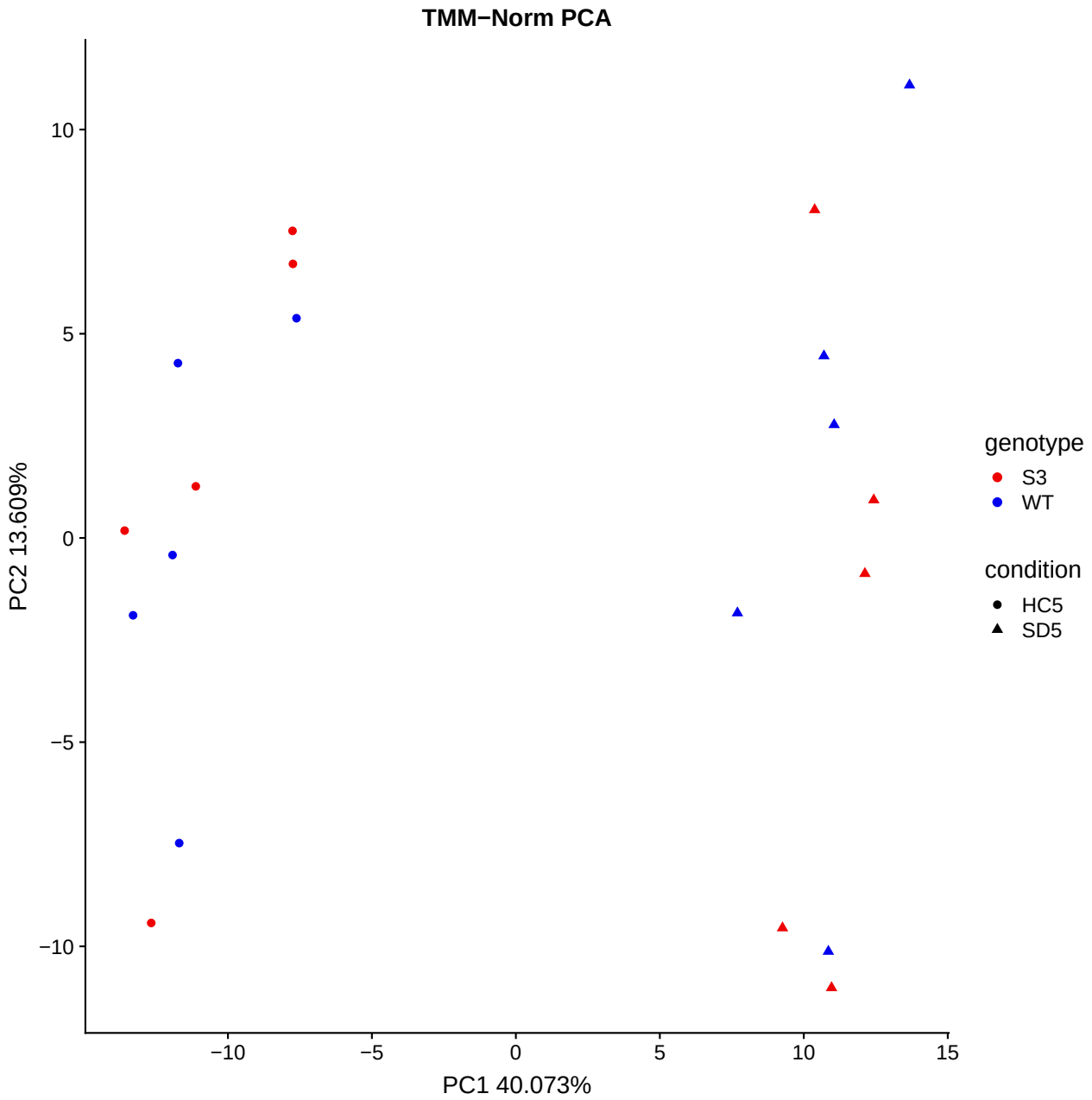
Normalizations

TMM Normalization

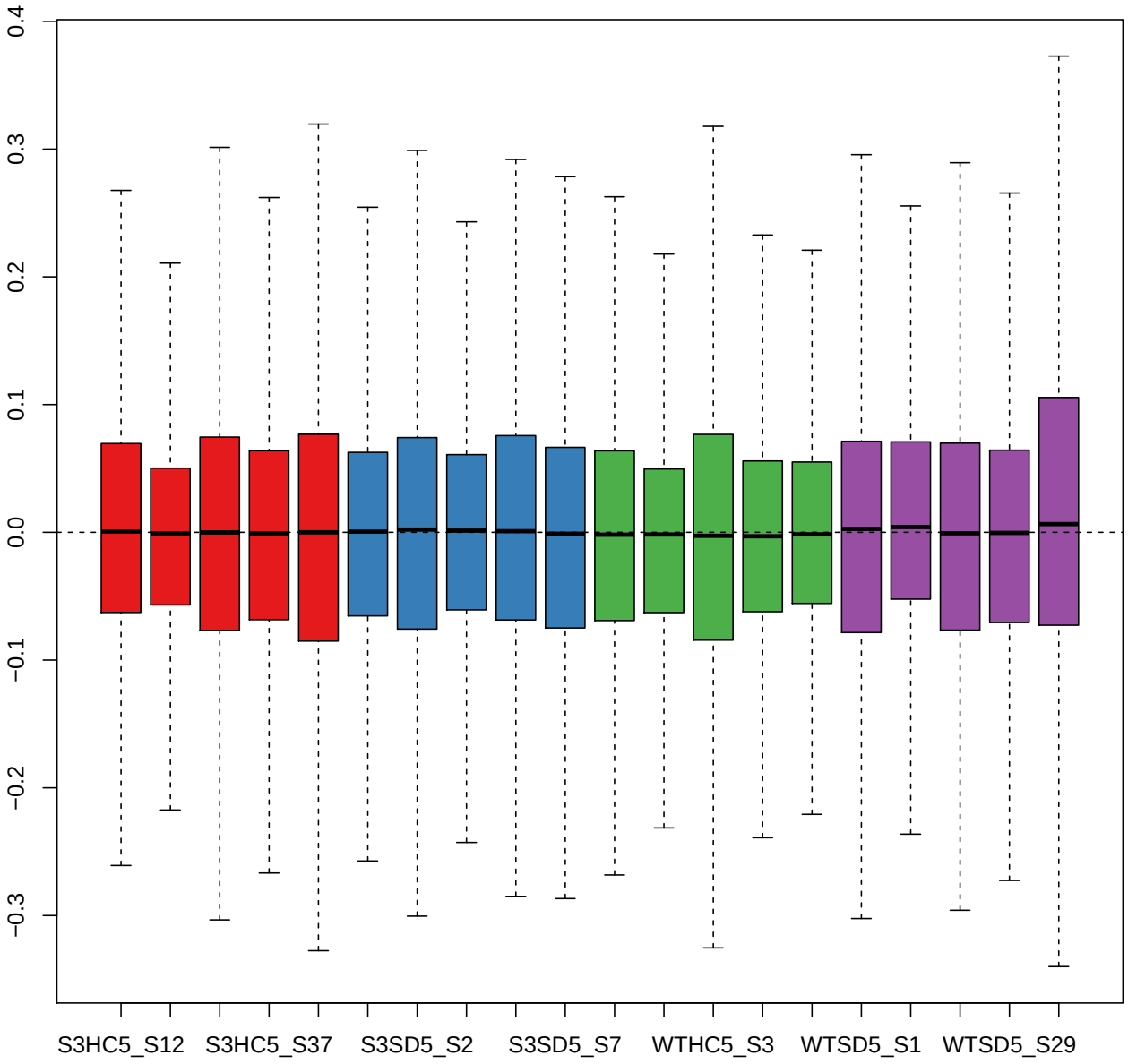
Normalizing data with *TMM*, as implemented in *edgeR* package, and plotting a PCA and an RLE plot of them.

```
normPropCountsUqua <- NormalizeData(data.to.normalize=filteredCountsProp,
                                    norm.type="tmm",
                                    design.matrix=designMatrix)

PlotPCAPlotlyFunction(counts.data.frame=log1p(normPropCountsUqua),
                      design.matrix=designMatrix, shapeColname="condition",
                      colorColname="genotype", xPCA="PC1", yPCA="PC2",
                      plotly.flag=FALSE, show.plot.flag=TRUE,
                      prefix.plot="TMM-Norm")
```

```
## [1] FALSE
```




```
pal <- RColorBrewer::brewer.pal(9, "Set1")
plotRLE(as.matrix(normPropCountsUqua), outline=FALSE, col=pal[designMatrix$gcondition])
```



TMM + RUVs Normalization

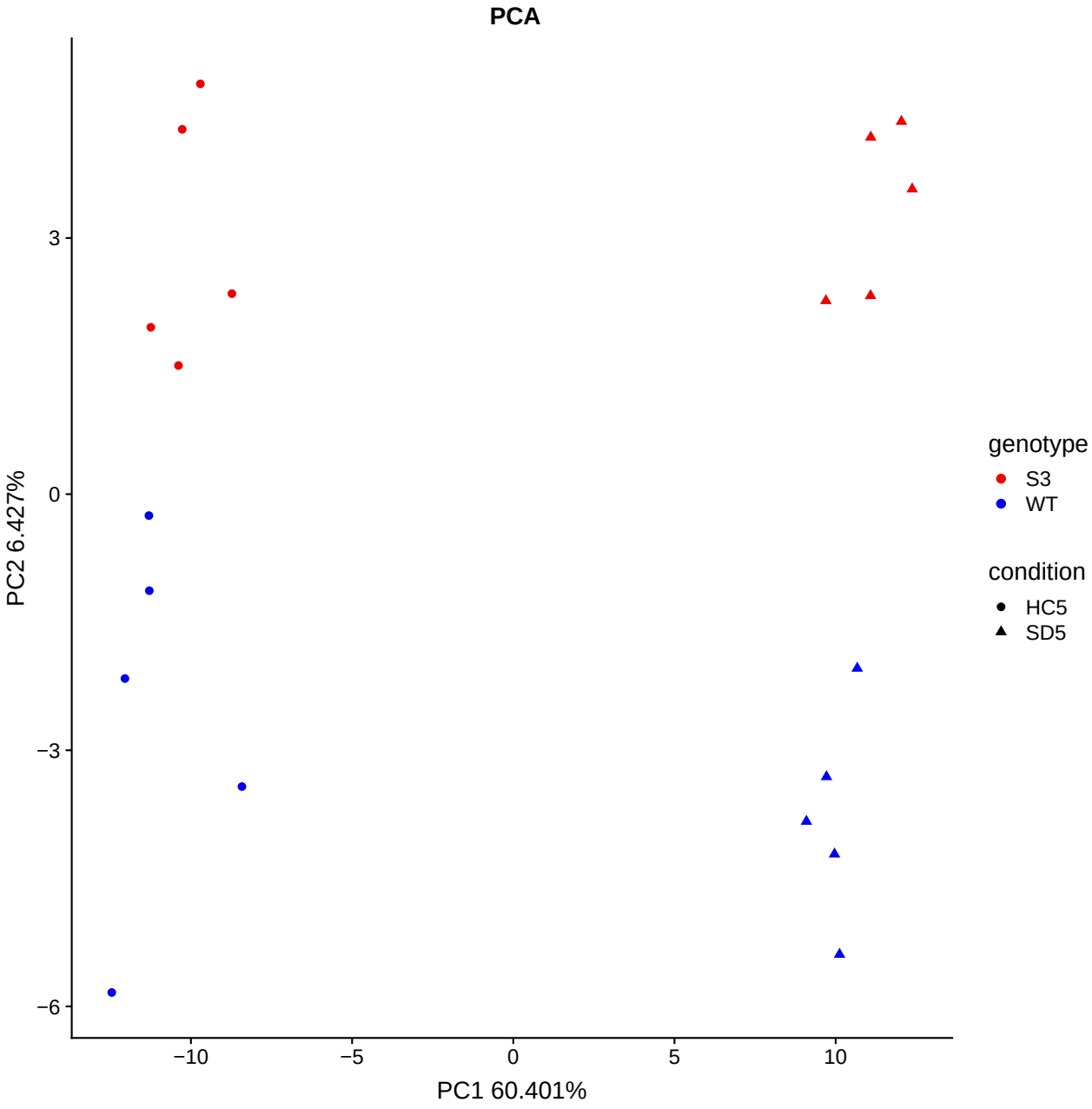
Applying a *RUVs* method of *RUVSeq* package on normalized data, in order to adjust the counts for the unwanted variation. And of corse we plot a PCA and an RLE plot on these data.

```
library(RUVSeq)
neg.ctrl.list <- rownames(counts.neg.ctrls)
groups <- makeGroups(designMatrix$gcondition)
ruvedSExprData <- RUVs(as.matrix(round(normPropCountsUqua)), cIdx=neg.ctrl.list,
                       scIdx=groups, k=5)

normExprData <- ruvedSExprData$normalizedCounts

ggp <- PlotPCAPlotlyFunction(counts.data.frame=log1p(normExprData),
                    design.matrix=designMatrix, shapeColname="condition",
                    colorColname="genotype", xPCA="PC1", yPCA="PC2",
```

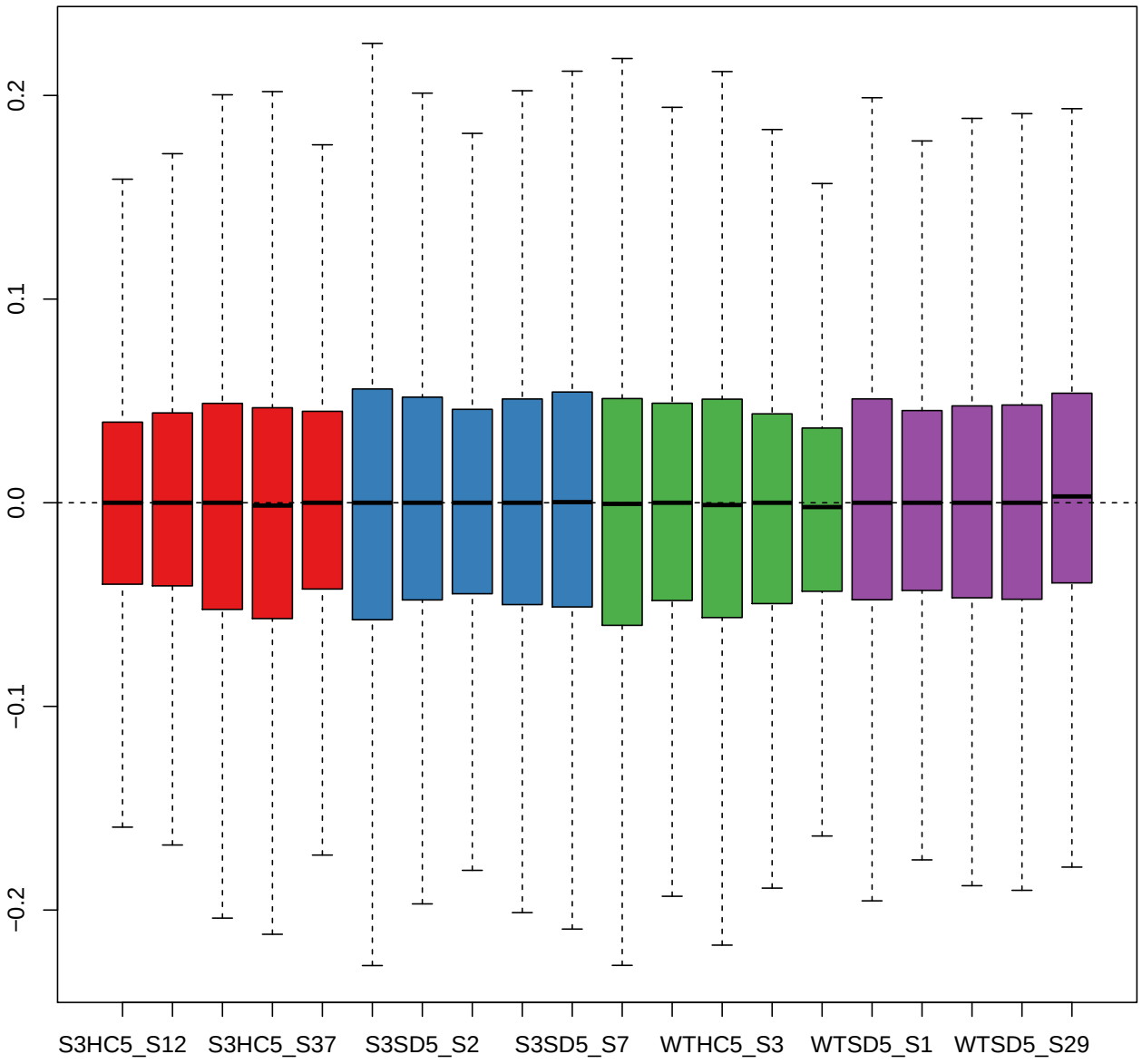
```
                    plotly.flag=FALSE, show.plot.flag=FALSE, save.plot=FALSE,
                    prefix.plot=NULL)
```

```
## [1] FALSE
```

```
print(ggp)
```




```
dir.create("plots")
save_plot(filename="plots/PCA.pdf", plot=ggp)

pal <- RColorBrewer::brewer.pal(9, "Set1")
plotRLE(normExprData, outline=FALSE, col=pal[designMatrix$gcondition])
```



edgeR Differential Expression Analysis

Making differential expression analysis with *edgeR* package on four different contrasts.

Here is a brief legend:

- WTHC5: Wild Type Home Cage Control 5 days
- WTSD5: Wild Type Sleep Deprivation 5 days.
- KOHC5: Knock Out Home Cage Control 5 days.
- KOSD5: Knock Out Sleep Deprivation 5 days.

```
padj.thr <- 0.05
venn.padgj.thr <- 0.1
desMat <- cbind(designMatrix, ruvedSExprData$W)
colnames(desMat) <- c(colnames(designMatrix), colnames(ruvedSExprData$W))

cc <- c("S3HC5 - WTHC5", "S3SD5 - WTSD5")
```

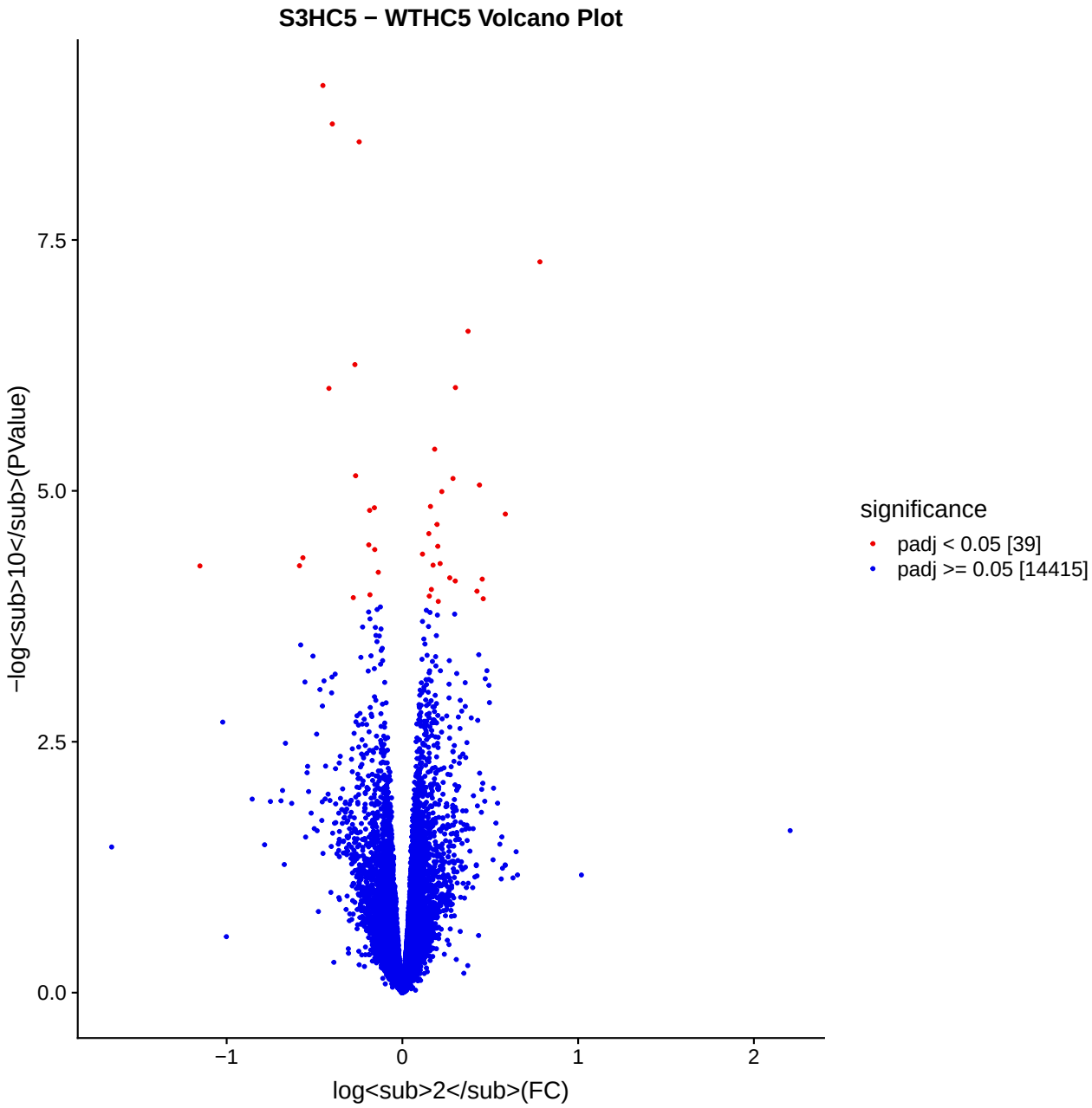
```
rescList1 <- applyEdgeR(counts=filteredCountsProp, design.matrix=desMat,
                        factors.column="gcondition",
                        weight.columns=c("W_1", "W_2", "W_3", "W_4", "W_5"),
                        contrasts=cc, useIntercept=FALSE, p.threshold=1,
                        is.normalized=FALSE, verbose=TRUE)
names <- names(rescList1)
rescList1 <- lapply(seq_along(rescList1), function(i)
{
    attachMeans(normalized.counts=normExprData, design.matrix=desMat,
                factor.column="gcondition", contrast.name=names(rescList1)[i],
                de.results=rescList1[[i]])
})
names(rescList1) <- names
```

Shank3 Home Cage control VS Wild Type Home Cage Controls

volcano plot

A volcano plot of differential expressed genes.

```
res.o.map1 <- convertGenesViaMouseDb(gene.list=rownames(rescList1[[1]]),
                             fromType="ENTREZID")

res.o <- attachGeneColumnToDf(mainDf=rescList1[[1]],
                                genesMap=res.o.map1,
                                rowNamesIdentifier="ENTREZID",
                                mapFromIdentifier="ENTREZID",
                                mapToIdentifier="SYMBOL")
WriteDataFrameAsTsv(data.frame.to.save=res.o,
                    file.name.path=paste0(names(rescList1)[1], "_edgeR"))

vp <- luciaVolcanoPlot(res.o, prefix=names(rescList1)[1],
                        positive.controls.df=NULL,
                        threshold=padj.thr)
print(vp)
```




```
de <- sum(res.o$FDR < padj.thr)
nde <- sum(res.o$FDR >= padj.thr)
detable <- cbind(de,nde)
rownames(detable) <- names(rescList1)[1]
ddetable <- detable

tot.ctrls <- dim(sd.pos.ctrls)[1]
idx.pc <- which(tolower(res.o$gene) %in% tolower(sd.pos.ctrls[,1]))
tot.pc.de <- sum(res.o$FDR[idx.pc] < padj.thr)
tot.pc.nde <- length(idx.pc) - tot.pc.de

wt <- res.o[which(res.o$FDR < padj.thr),]
wt.sign.genes.entrez <- rownames(res.o)[which(res.o$FDR < venn.padgj.thr)]
```

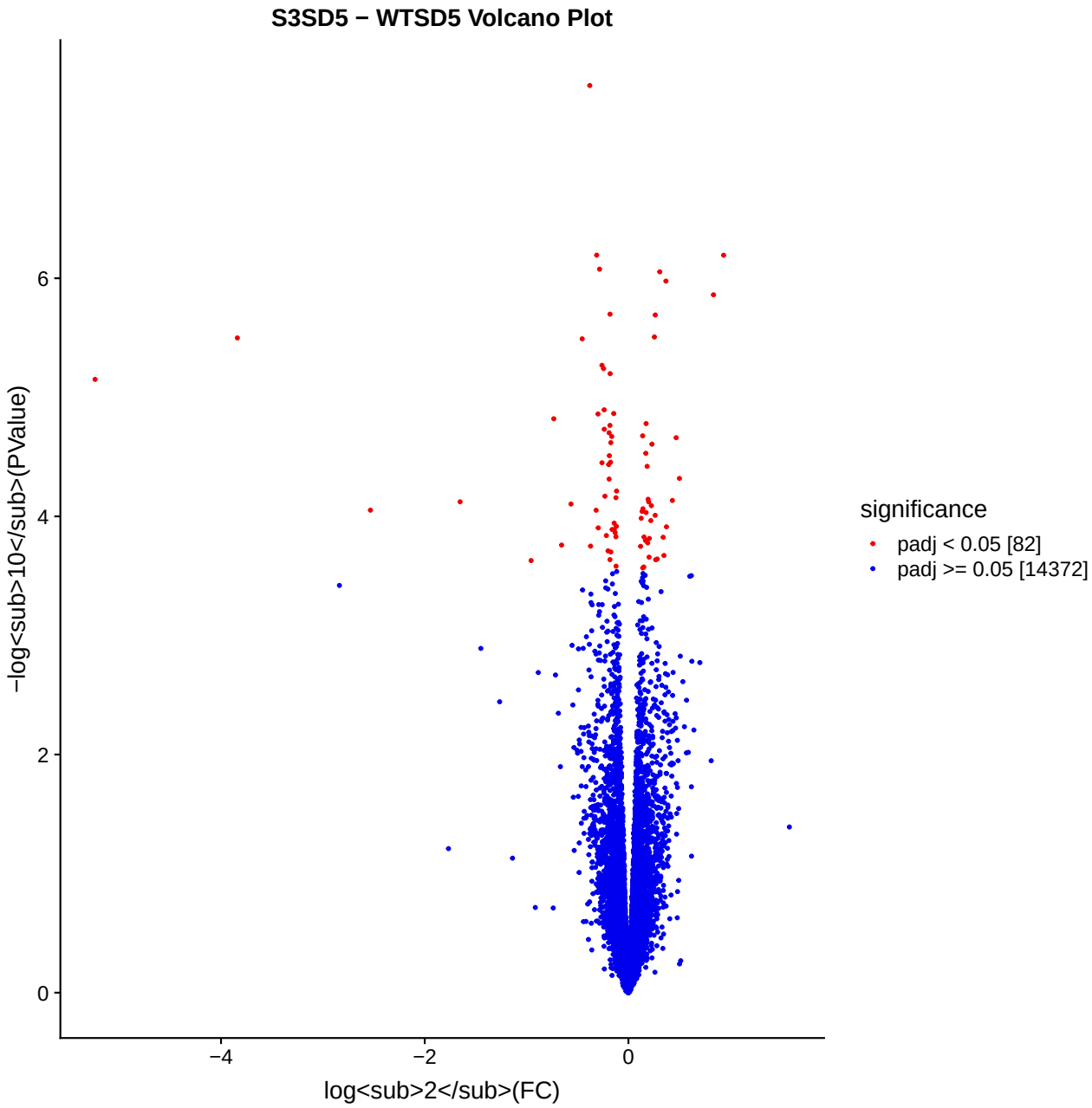
```
kowthc5 <- res.o[which(res.o$FDR < padj.thr),]
kowthc5.sign.genes.entrez <- rownames(res.o)[which(res.o$FDR < venn.padgj.thr)]
```

Shank3 Sleed Deprivation VS Wild Type Sleep Deprivation

volcano plot

A volcano plot of differential expressed genes.

```
rs2.o.map <- convertGenesViaMouseDb(gene.list=rownames(rescList1[[2]]),
                            fromType="ENTREZID")

res.rs2.o <- attachGeneColumnToDf(mainDf=rescList1[[2]],
                                  genesMap=rs2.o.map,
                                  rowNamesIdentifier="ENTREZID",
                                  mapFromIdentifier="ENTREZID",
                                  mapToIdentifier="SYMBOL")
WriteDataFrameAsTsv(data.frame.to.save=res.rs2.o,
                    file.name.path=paste0(names(rescList1)[2], "_edgeR"))

vp <- luciaVolcanoPlot(res.rs2.o, positive.controls.df=NULL,
                       prefix=names(rescList1)[2],
                       threshold=padj.thr)
print(vp)
```




```
de <- sum(res.rs2.o$FDR < padj.thr)
nde <- sum(res.rs2.o$FDR >= padj.thr)
detable <- cbind(de,nde)
rownames(detable) <- names(rescList1)[2]
ddetable <- rbind(ddetable, detable)
pos.df <- cbind(tot.ctrls, tot.pc.de, tot.pc.nde)
colnames(pos.df) <- c("total_p.ctrl", "p.ctrl_de_mapped",
                      "p.ctrl_notde_mapped")
rownames(pos.df) <- names(rescList1)[2]

kowtsd5 <- res.rs2.o[which(res.rs2.o$FDR < padj.thr),]
kowtsd5.sign.genes.entrez <- rownames(res.rs2.o)[which(res.rs2.o$FDR < venn.padgj.thr)]
```

DE TABLE + Positive Controls table

We present a summarization of the results. The first table is a summarization on how many genes are Differentially Expressed. The second table explains on the first column how many positive controls we have, on the second column how many positive controls have been identified over the differentially expressed genes, and, finally, on the third column how many positive controls have beed identified on the NOT differentially expressed genes.

```
ddetable
```

```
##                de   nde
## S3HC5 - WTHC5 39 14415
## S3SD5 - WTSD5 82 14372
```

```
pos.df
```

```
##                total_p.ctrl p.ctrl_de_mapped p.ctrl_notde_mapped
## S3SD5 - WTSD5           579                3                 553
```

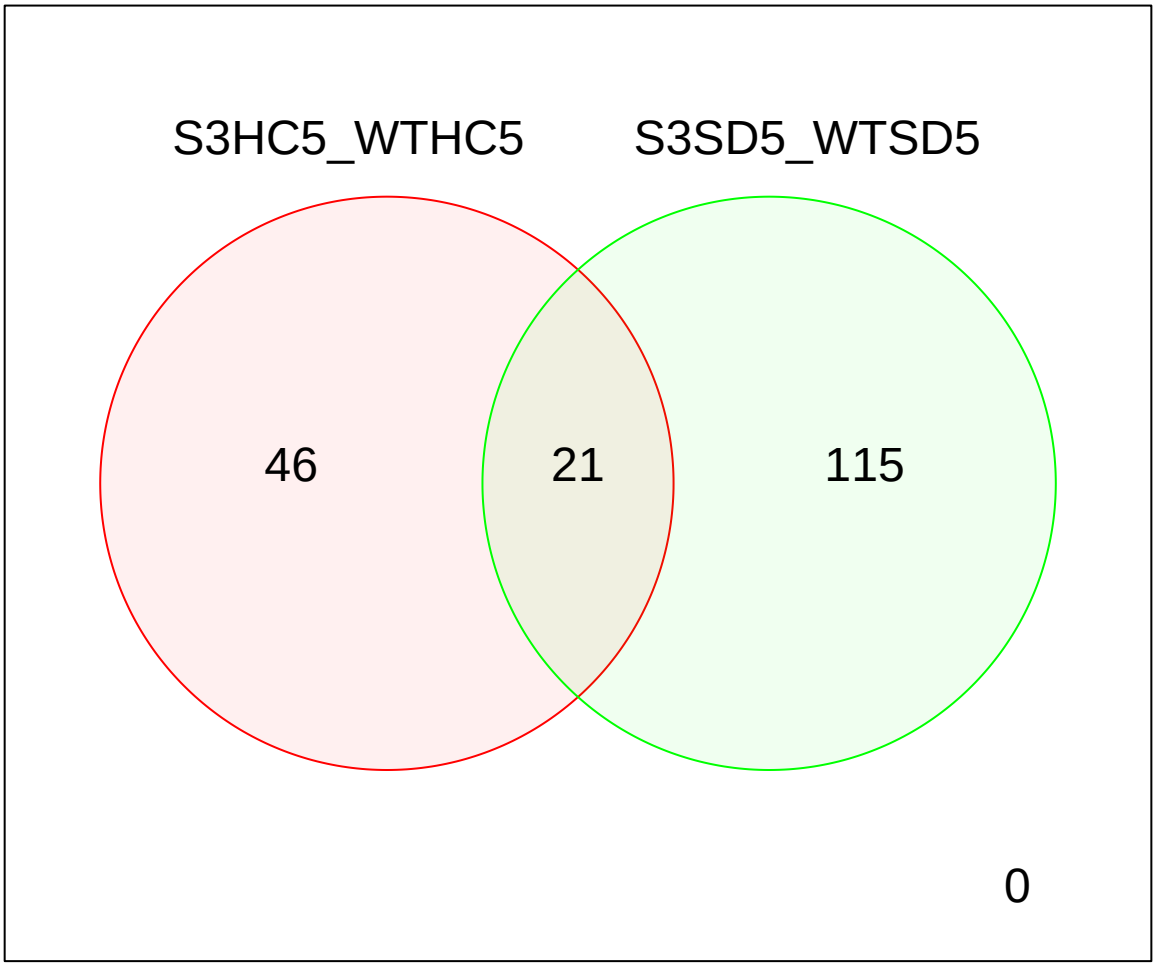
Venn Diagram

KOHC5-WTHC5 vs KOSD5-WTSD5

We take the results of the two contrasts. *Knock Out Sleed Deprivation VS Wild Type Sleep Deprivation* and *Knock Out Home Cage control VS Wild Type Home Cage Controls* . And plot the results in a Venn Diagram

```
source("./R/venn2.R")

gene.map <- convertGenesViaMouseDb(gene.list=rownames(normExprData),
                                   fromType="ENTREZID", toType="SYMBOL")
venn <- Venn2de(x=kowthc5.sign.genes.entrez, y=kowtsd5.sign.genes.entrez,
        label1="S3HC5_WTHC5", label2="S3SD5_WTSD5",
        title="S3HC5_WTHC5 venn S3SD5_WTSD5", plot.dir="./",
        conversion.map=gene.map)
```

S3HC5_WTHC5 venn S3SD5_WTSD5



Heatmaps

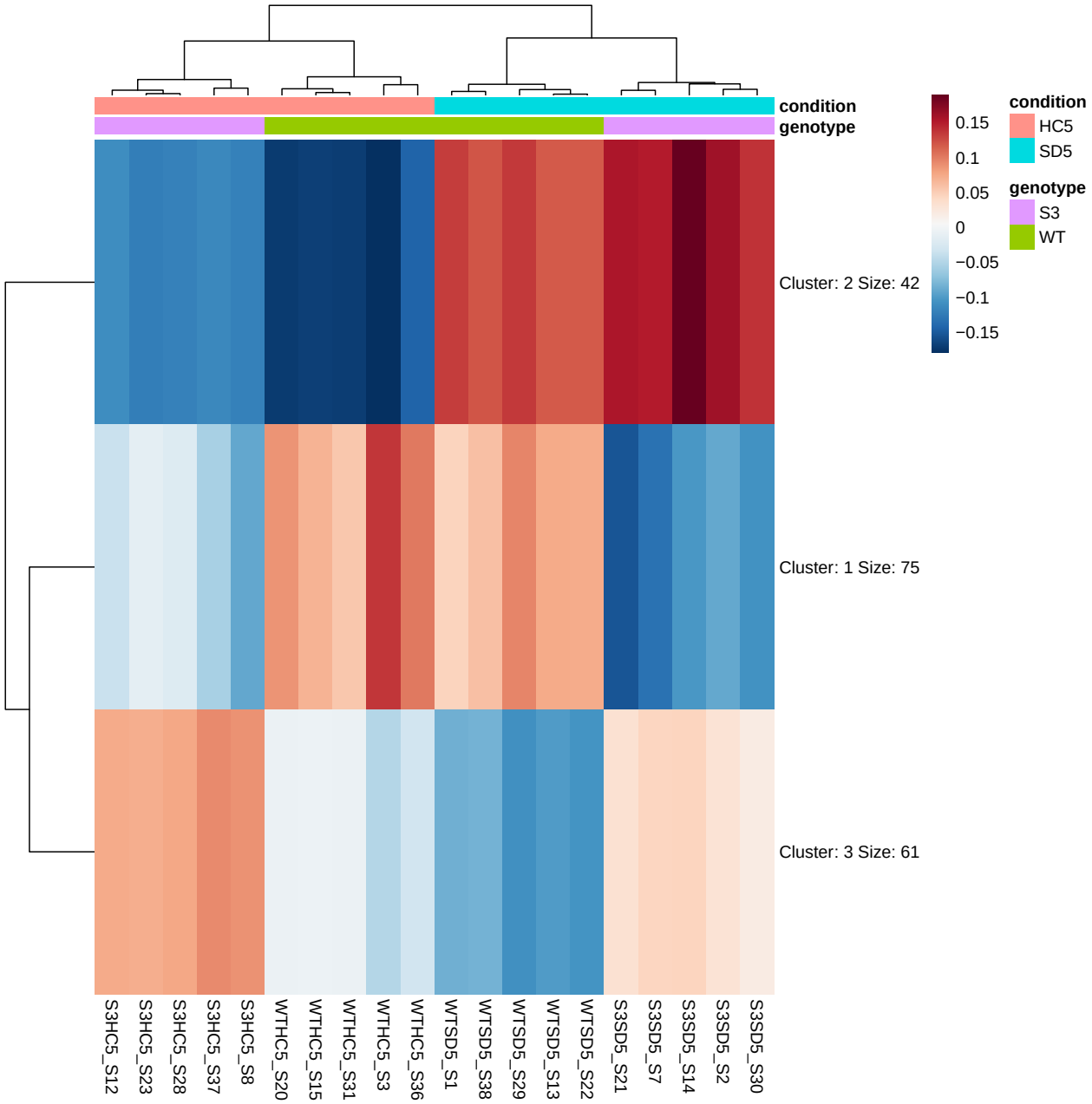
Setting up the data structures for the heatmps.

```
source("./R/heatmapFunctions.R")
de.genes.entr <- union(rownames(venn$int), rownames(venn$XnoY))
de.genes.entr <- union(de.genes.entr, rownames(venn$YnoX))

gene.map <- convertGenesViaMouseDb(gene.list=de.genes.entr,
                            fromType="ENTREZID")
```

```
de.genes.symb <- attachGeneColumnToDf(as.data.frame(de.genes.entr,
                                                    row.names=de.genes.entr),
                                      genesMap=gene.map,
                                      rowNamesIdentifier="ENTREZID",
                                      mapFromIdentifier="ENTREZID",
                                      mapToIdentifier="SYMBOL")

# de.genes.symb[which(is.na(de.genes.symb$gene)),]
de.genes.symb$gene[which(de.genes.symb$de.genes.entr=="100039826")]  <- "Gm2444" ## not annotated in nc
de.genes.symb$gene[which(de.genes.symb$de.genes.entr=="210541")]  <- "Entrez:210541" ## not annotated i


de.genes.counts <- normExprData[match(de.genes.symb$de.genes.entr, rownames(normExprData)),]
rownames(de.genes.counts) <- de.genes.symb$gene

de.gene.means <- computeGeneMeansOverGroups(counts=de.genes.counts,
                            design=designMatrix, groupColumn="gcondition")

library(gplots)
library(clusterExperiment)
color.palette = clusterExperiment::seqPal3#c("black", "yellow")
pal <- colorRampPalette(color.palette)(n = 1000)


library(pheatmap)
filter2 <- rowMeans(de.gene.means)>0
filter <- apply(de.gene.means, 1, function(x) log(x[4]/x[3]) * log(x[2]/x[1]) < 0)
filter[is.na(filter)] <- FALSE
```

Heatmap gene by bene

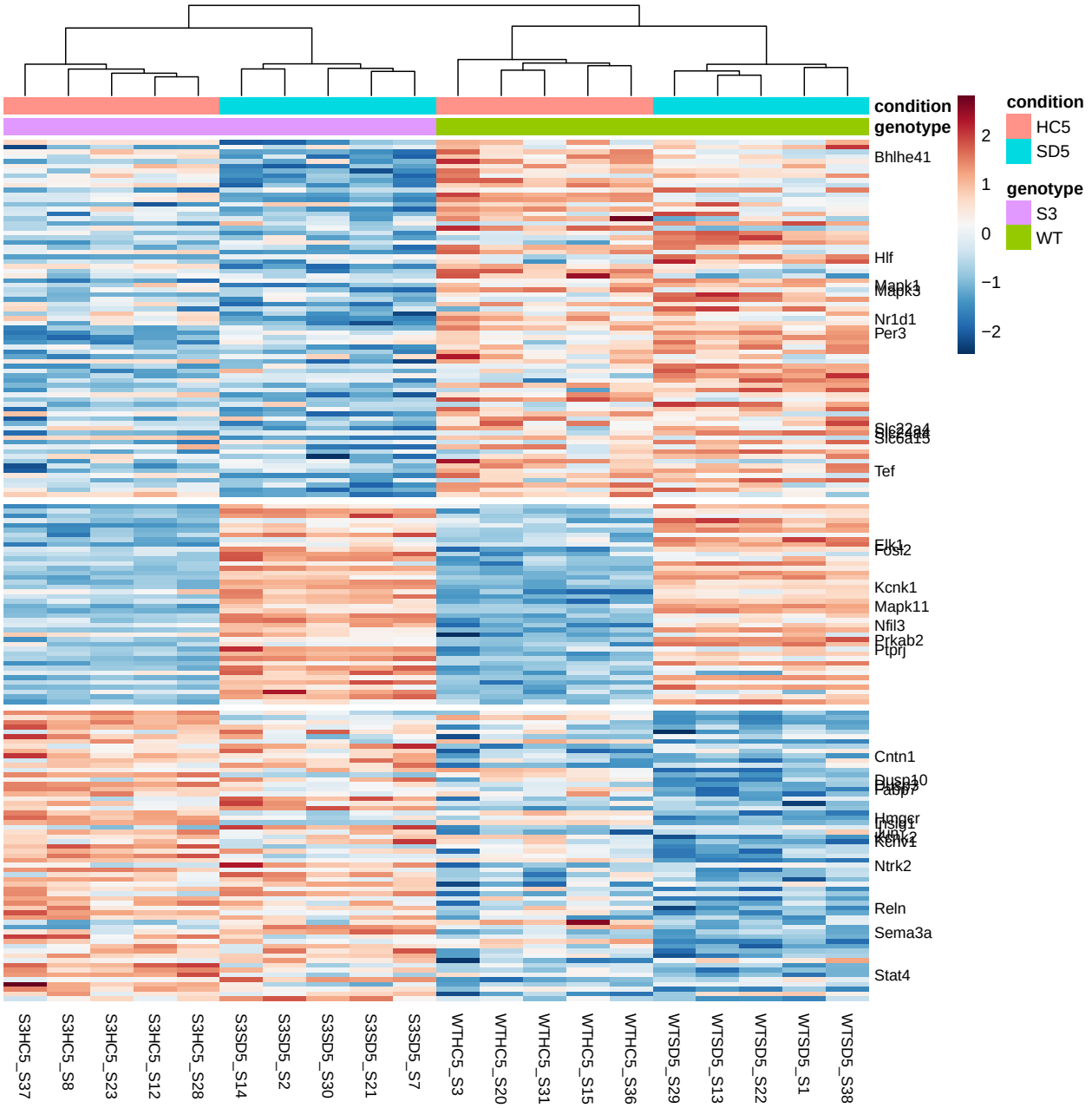
```
gene_names <- c("Nr1d1", "Fabp7", "Per3", "Jun", "Elk1", "Fosl2", "Mapk1",
                "Mapk3", "Mapk11", "Hmgcr", "Insig1", "Nfil3", "Stat4",
                "Kcnv1", "Kcnk1", "Kcnk2", "Dusp10", "Dusp3", "Ptprj",
                "Cntn1", "Ntrk2", "Reln", "Sema3a", "Tef", "Hlf", "Nr1d1",
                "Prkab2", "Bhlhe41", "Slc6a15", "Slc22a4", "Slc24a4")
idx <- which(!(rownames(de.genes.counts) %in% gene_names))
de.genes.counts1 <- de.genes.counts
rownames(de.genes.counts1)[idx] <- ""
ann.col <- desMat[, c(1:2)]
de.heatmap <- de.genes.counts[filter2,]
set.seed(0)
heatmap_data <- t(scale(t(log(de.heatmap+1)), center = TRUE, scale = FALSE))
ph1 <- pheatmap(heatmap_data, cluster_cols=TRUE, scale="none",
            color=pal, border_color=NA, fontsize_row=10, kmeans_k=3, annotation_col=ann.col)
```




```
clusterized.genes <- as.data.frame(ph1$kmeans$cluster)

gene.map <- convertGenesViaMouseDb(gene.list=rownames(clusterized.genes), fromType="SYMBOL")
converted.clusterized.gens <- attachGeneColumnToDf(mainDf=clusterized.genes, genesMap=gene.map,
                  rowNamesIdentifier="SYMBOL", mapFromIdentifier="SYMBOL", mapToIdentifier="ENTREZID")

converted.clusterized.gens$gene[which(rownames(converted.clusterized.gens)=="Gm2444")]  <- "100039826" #
converted.clusterized.gens$gene[which(rownames(converted.clusterized.gens)=="Entrez:210541")]  <- "2105
converted.clusterized.gens <- converted.clusterized.gens[order(converted.clusterized.gens$`ph1$kmeans$cl

save_pheatmap_pdf(filename="plots/heatmap_kmeans_k3.pdf", plot=ph1, width=20, height=20)
```

```
## pdf
##   2
```

```
WriteDataFrameAsTsv(data.frame.to.save=converted.clusterized.gens, file.name.path="plots/clustered_genes

ord.de.genes.counts <- de.heatmap[match(rownames(converted.clusterized.gens), rownames(de.heatmap)),]
idx <- which(!(rownames(ord.de.genes.counts) %in% gene_names))

rownames(ord.de.genes.counts)[idx] <- ""
gaps.row <- c()
for(i in c(1:3))
{
    li <- length(which(converted.clusterized.gens$`ph1$kmeans$cluster`==i))
    l <- ifelse(i!=1, gaps.row[i-1]+li, li)
    gaps.row <- c(gaps.row, l)
}

heatmap_data_scaled <- t(scale(t(log(ord.de.genes.counts+1)), center = TRUE, scale = TRUE))

library(dendextend)
column_dend <- as.dendrogram(hclust(dist(t(heatmap_data_scaled))))
ord <- labels(column_dend)
ord[11:15] <- labels(column_dend)[16:20]
ord[16:20] <- labels(column_dend)[11:15]
column_dend <- rotate(column_dend, ord)

ph1 <- pheatmap(heatmap_data_scaled, cluster_cols=as.hclust(column_dend), scale="none",
            color=pal, border_color=NA, fontsize_row=9, fontsize_col=9, cluster_rows=FALSE,
            annotation_col=ann.col, gaps_row=gaps.row)
```



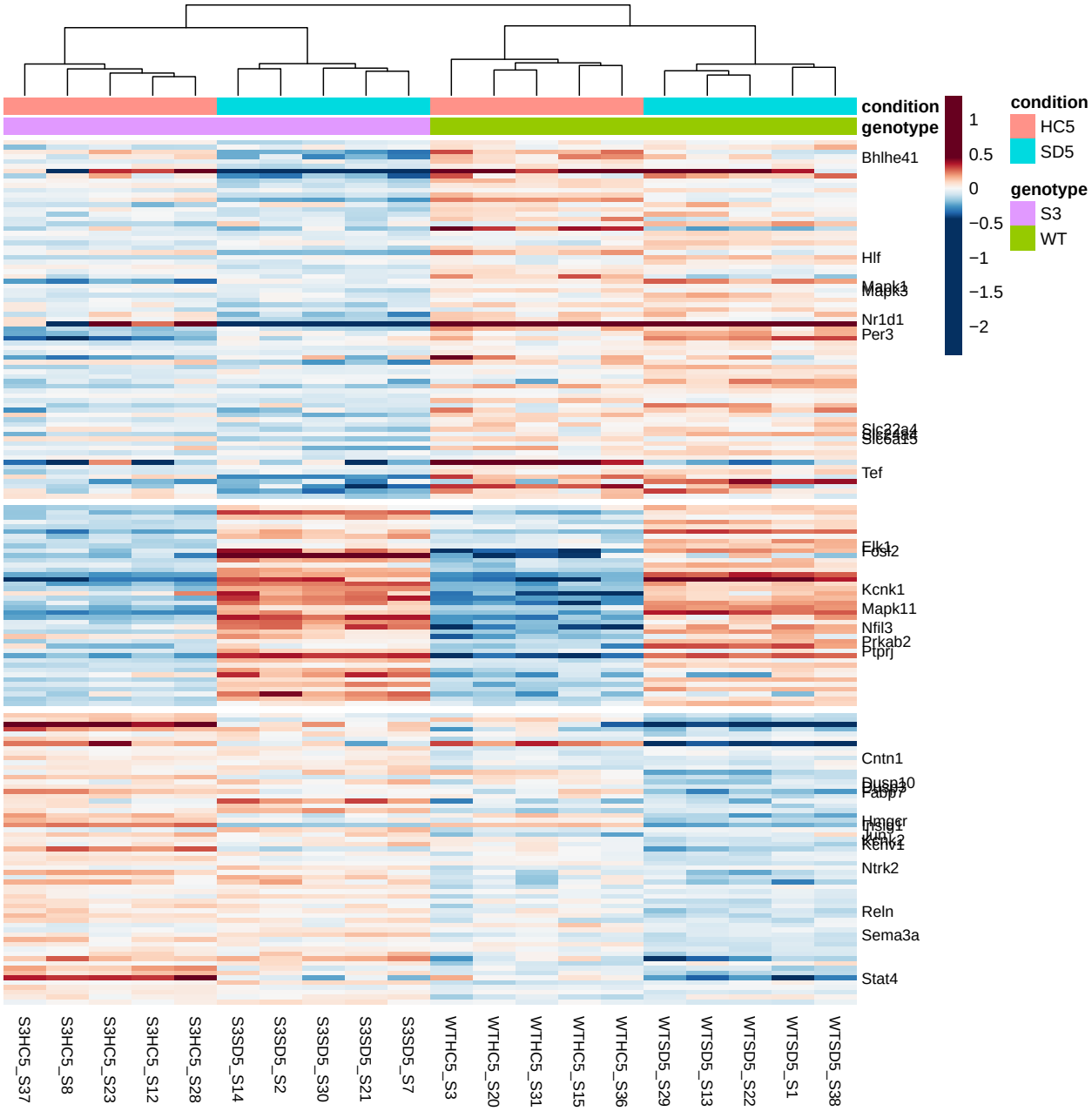

```
save_pheatmap_pdf(filename="plots/heatmap_gg_k3.pdf", plot=ph1, width=20, height=20)
```

```
## pdf
##   2
```

other heatmaps

```
heatmap_data <- t(scale(t(log(ord.de.genes.counts+1)), center = TRUE, scale = FALSE))

ph1 <- pheatmap(heatmap_data, cluster_cols=as.hclust(column_dend), scale="none",
            color=pal, border_color=NA, fontsize_row=9, fontsize_col=9, cluster_rows=FALSE,
            annotation_col=ann.col, gaps_row=gaps.row,
```

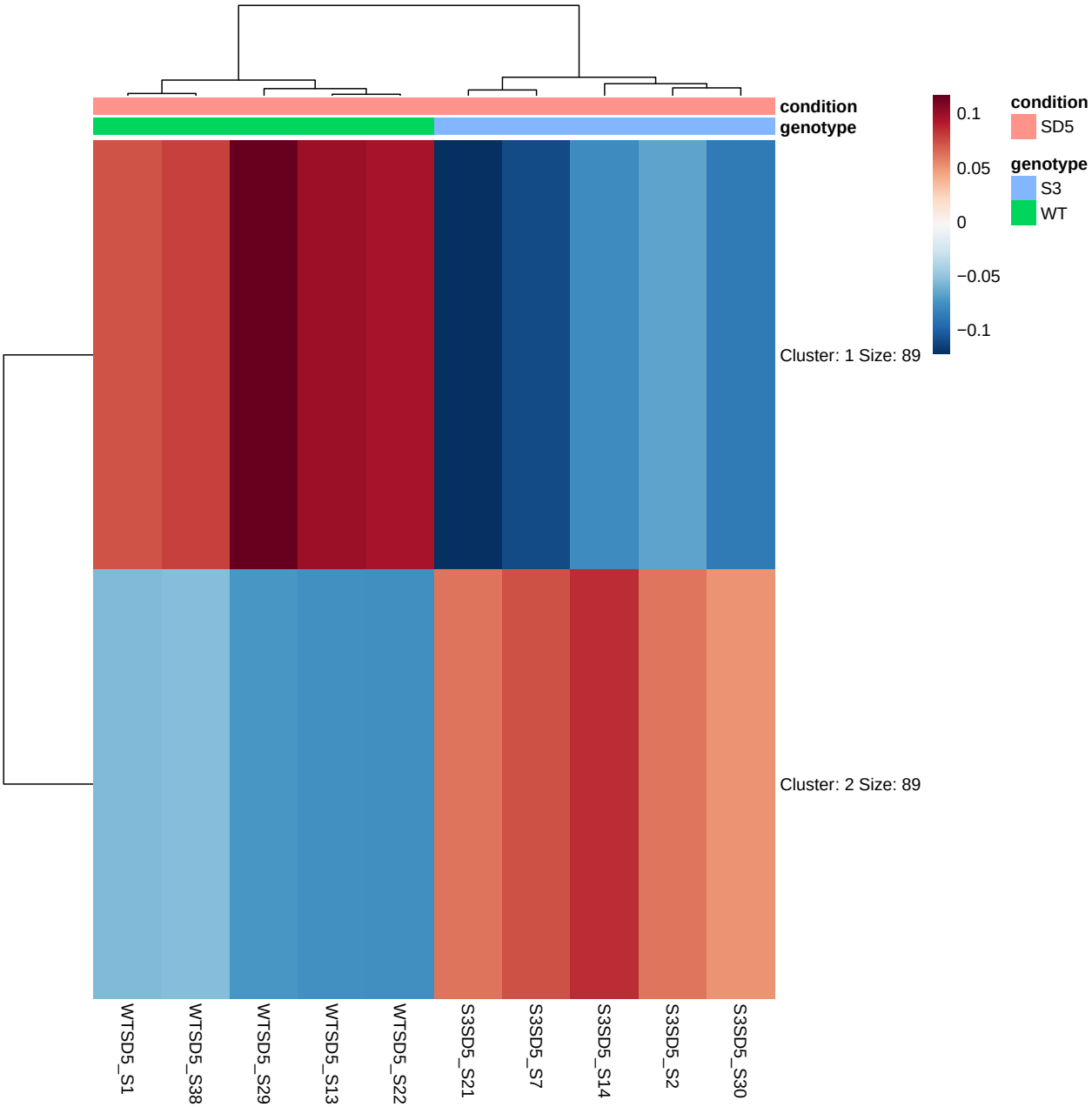
```
            breaks = c(min(heatmap_data), seq(quantile(as.vector(heatmap_data), .01), quantile(as.vecto
```




```
save_pheatmap_pdf(filename="plots/heatmap_gg_k3_no_scale.pdf", plot=ph1, width=20, height=20)
```

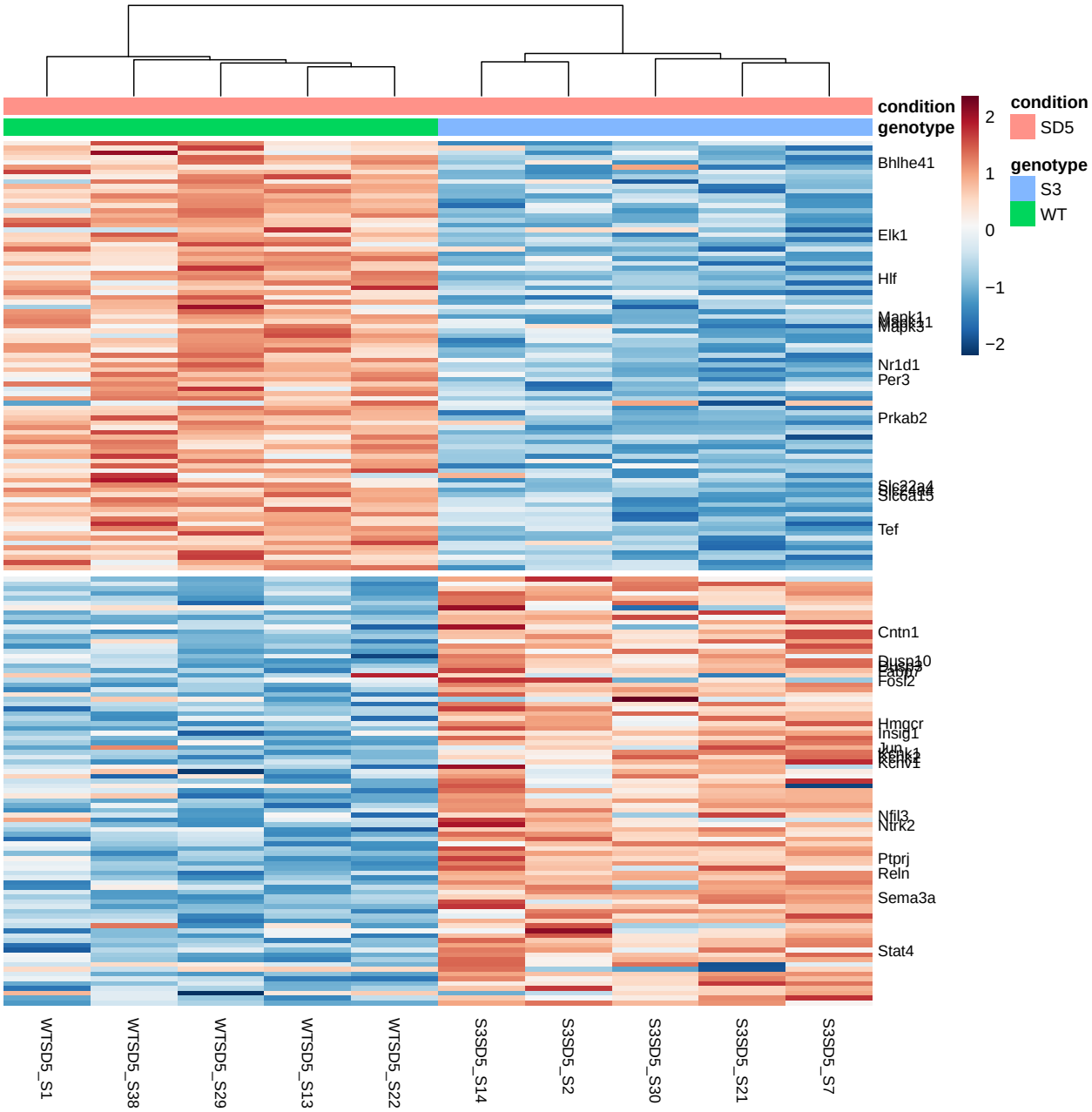
```
## pdf
##   2
```

```
## Only SD samples
heatmap_data <- t(scale(t(log(de.heatmap[, grep("^SD", desMat[,2])]+1)), center = TRUE, scale = FALSE))
ph1 <- pheatmap(heatmap_data, cluster_cols=TRUE, scale="none",
            color=pal, border_color=NA, fontsize_row=10, kmeans_k=2, annotation_col=ann.col)
```




```
clusterized.genes <- as.data.frame(ph1$kmeans$cluster)

gene.map <- convertGenesViaMouseDb(gene.list=rownames(clusterized.genes), fromType="SYMBOL")
converted.clusterized.gens <- attachGeneColumnToDf(mainDf=clusterized.genes, genesMap=gene.map,
                    rowNamesIdentifier="SYMBOL", mapFromIdentifier="SYMBOL", mapToIdentifier="ENTREZID")

converted.clusterized.gens$gene[which(rownames(converted.clusterized.gens)=="Gm2444")]  <- "100039826" #
converted.clusterized.gens$gene[which(rownames(converted.clusterized.gens)=="Entrez:210541")]  <- "2105
converted.clusterized.gens <- converted.clusterized.gens[order(converted.clusterized.gens$`ph1$kmeans$cl

ord.de.genes.counts <- de.heatmap[match(rownames(converted.clusterized.gens), rownames(de.heatmap)),]
idx <- which(!(rownames(ord.de.genes.counts) %in% gene_names))
```

```
rownames(ord.de.genes.counts)[idx] <- ""
gaps.row <- c()
for(i in c(1:2))
{
    li <- length(which(converted.clusterized.gens$`ph1$kmeans$cluster`==i))
    l <- ifelse(i!=1, gaps.row[i-1]+li, li)
    gaps.row <- c(gaps.row, l)
}

heatmap_data <- t(scale(t(log(ord.de.genes.counts[, grep("^SD", desMat[,2])]+1)), center = TRUE, scale =

ph1 <- pheatmap(heatmap_data, cluster_cols=TRUE, scale="none",
            color=pal, border_color=NA, fontsize_row=9, fontsize_col=9, cluster_rows=FALSE,
            annotation_col=ann.col, gaps_row=gaps.row)
```




```
save_pheatmap_pdf(filename="plots/heatmap_gg_sd_only.pdf", plot=ph1, width=20, height=20)
```

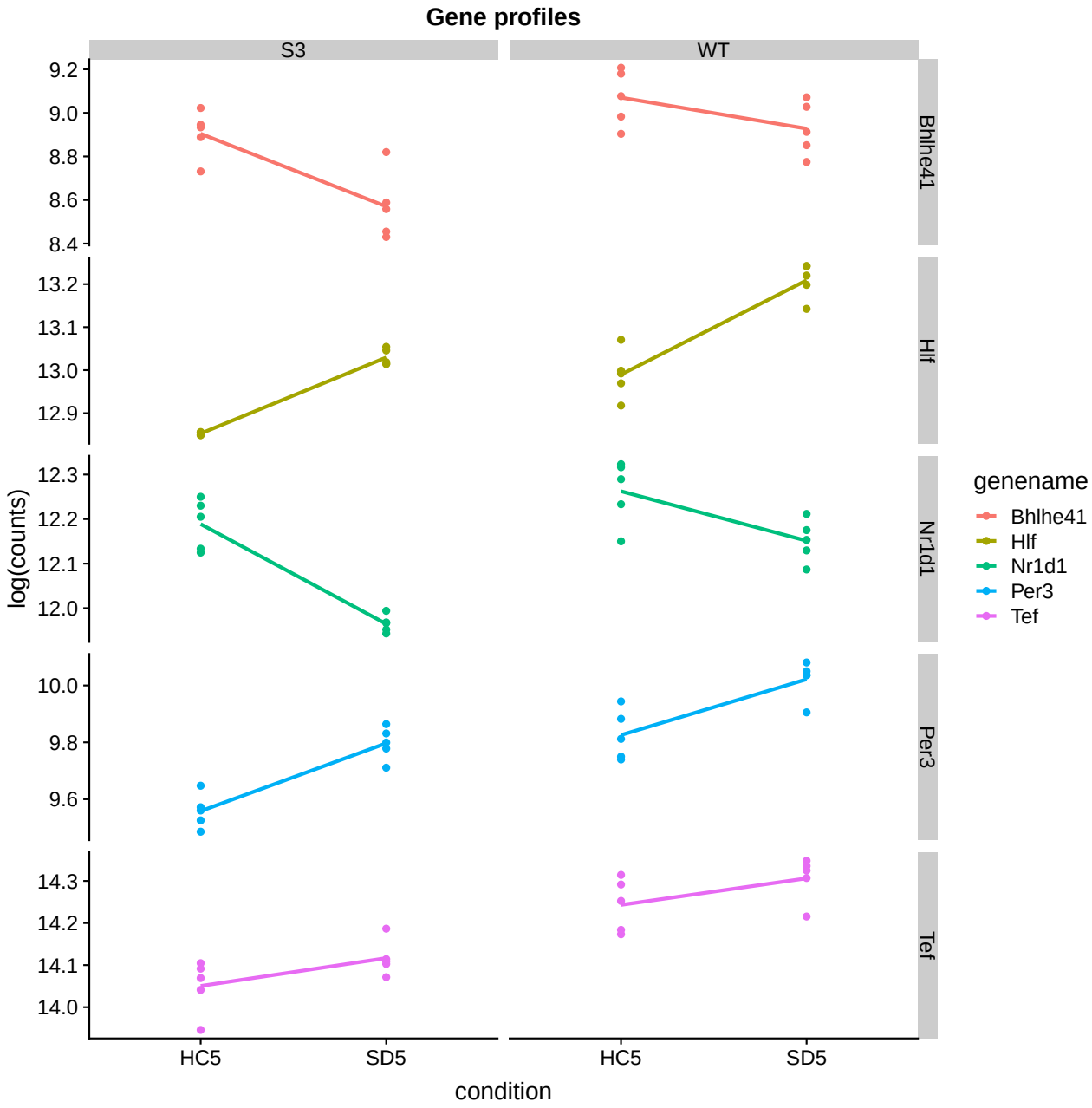
```
## pdf
##   2
```

Group gene profiles

Group gene profiles by genotype

```
g <- geneGroupProfileRows(normalized.counts=normExprData, design.matrix=designMatrix,
            gene.names=c("Nr1d1", "Hlf", "Per3", "Bhlhe41", "Tef"),
            res.o=de.genes.symb, show.plot=TRUE, plotly.flag=FALSE, log.flag=TRUE)
```

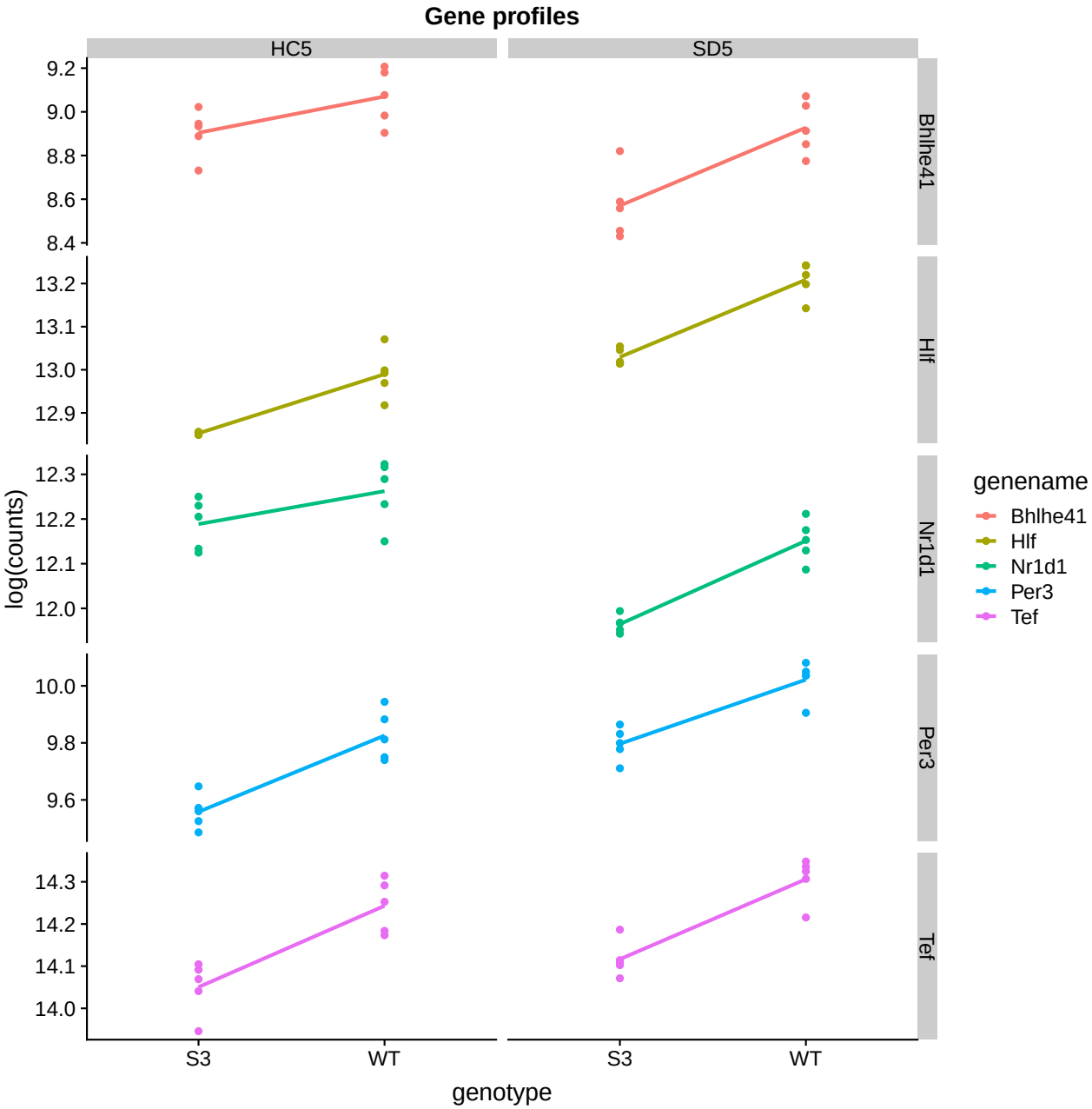
```
print(g)
```




```
save_plot(filename=paste0("plots/", "Nr1d1_Hlf_Per3_Bhlhe41_Tef", "_log_gene_profile_genotype.pdf"), pl
        base_height=15, base_width=15)
```

Group gene profiles by condition

```
g <- geneGroupProfileRowsRev(normalized.counts=normExprData, design.matrix=designMatrix,
            gene.names=c("Nr1d1", "Hlf", "Per3", "Bhlhe41", "Tef"),
            res.o=de.genes.symb, show.plot=TRUE, plotly.flag=FALSE, log.flag=TRUE)
print(g)
```




```
save_plot(filename=paste0("plots/", "Nr1d1_Hlf_Per3_Bhlhe41_Tef", "_log_gene_profile_condition.pdf"), pl
        base_height=15, base_width=15)
```

Circadian Analysis

Analysis for activity

```
wt <- read_xlsx("data/Activity_analysis_4_R.xlsx", sheet = 1)
mut <- read_xlsx("data/Activity_analysis_4_R.xlsx", sheet = 2)

wt <- wt %>%
```

```
  bind_cols(WT.M=rep("WT", nrow(wt)), time = decimal_date(ymd(wt$`Total_revolutions/day`)), .) %>%
  gather(mice, activity, -c(1:5))  %>%
  mutate(time = time-min(time)) %>%
  dplyr::select(-`Total_revolutions/day`)

mut <- mut %>%
  bind_cols(WT.M=rep("M", nrow(mut)), time = decimal_date(ymd(mut$`Total_revolutions/day`)), .) %>%
  gather(mice, activity, -c(1:5))  %>%
  mutate(time = time-min(time)) %>%
  dplyr::select(-`Total_revolutions/day`)

data <- wt %>% bind_rows(mut)

data <- data %>% filter(week>=3)

data$mice <- factor(data$mice, levels= unique(data$mice))
data$time_scaled <- scale(data$time, scale=FALSE)
data$period <- factor(data$period, levels= unique(data$period))
data$WT.M <-factor(data$WT.M, levels=c("WT", "M"))

mod <- lme(activity ~ time_scaled * WT.M, random=~1|mice, data = data)

cat("Estimates, errors and the significance")
```

```
## Estimates, errors and the significance
```

```
summary(mod)
```

```
## Linear mixed-effects model fit by REML
##  Data: data
##        AIC      BIC   logLik
##   8681.339 8705.303 -4334.67
##
## Random effects:
##  Formula: ~1 | mice
##         (Intercept) Residual
## StdDev:    14936.81 11161.46
##
## Fixed effects: activity ~ time_scaled * WT.M
##                         Value Std.Error  DF   t-value p-value
## (Intercept)          38778.45   5335.29 388  7.268296  0.0000
## time_scaled         -20486.52  35588.68 388 -0.575647  0.5652
## WT.MM               -20324.26   7810.06  13 -2.602317  0.0219
## time_scaled:WT.MM -289880.69  52096.49 388 -5.564304  0.0000
##  Correlation:
##                    (Intr) tm_scl WT.MM
## time_scaled         0.000
## WT.MM              -0.683  0.000
## time_scaled:WT.MM  0.000 -0.683  0.000
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -2.69133816 -0.63470177  0.03277689  0.63109234  3.19701990
##
```

```
## Number of Observations: 405
## Number of Groups: 15
```

```
cat("Bootstrap confidence intervals for the estimates")
```

```
## Bootstrap confidence intervals for the estimates
```

```
mod_lmer <- lmer(activity ~ time_scaled * WT.M + (1|mice), data = data)
confint.merMod(mod_lmer, method = "boot", nsim = 999)
```

```
##                            2.5 %      97.5 %
## .sig01                  8955.95   20503.825
## .sigma                 10389.64   12032.640
## (Intercept)            28479.16   48421.280
## time_scaled           -87582.69   48954.982
## WT.MM                 -36065.65   -4532.543
## time_scaled:WT.MM -384418.16 -187596.734
```

```
cat("ANOVA table")
```

```
## ANOVA table
```

```
anova.lme(mod, type = "marginal", adjustSigma = F)
```

```
##                   numDF denDF  F-value p-value
## (Intercept)           1   388 52.82812  <.0001
## time_scaled           1   388  0.33137  0.5652
## WT.M                  1    13  6.77206  0.0219
## time_scaled:WT.M      1   388 30.96148  <.0001
```

Analysis for alpha

```
wt <- read_xlsx("data/Alpha_Activity_analysis_4_R.xlsx", sheet = 1, na = "NA")
mut <- read_xlsx("data/Alpha_Activity_analysis_4_R.xlsx", sheet = 2, na = "NA")

wt <- wt %>%
  bind_cols(WT.M = rep("WT", nrow(wt)), time = decimal_date(ymd(wt$`Total_revolutions/day`)), .)%>%
  gather(mice, alpha, -c(1:5))  %>%
  mutate(time = time-min(time)) %>%
  dplyr::select(-`Total_revolutions/day`)

mut <- mut %>%
  bind_cols(WT.M=rep("M", nrow(mut)), time = decimal_date(ymd(mut$`Total_revolutions/day`)), .)%>%
  gather(mice, alpha, -c(1:5))  %>%
  mutate(time = time-min(time)) %>%
  dplyr::select(-`Total_revolutions/day`)

alpha_data <- wt %>% bind_rows(mut)

alpha_data <- alpha_data %>% filter(week>=3)
alpha_data<- na.omit(alpha_data)

alpha_data$mice <- factor(alpha_data$mice, levels= unique(alpha_data$mice))
alpha_data$time_scaled <- scale(alpha_data$time, scale=FALSE)
alpha_data$period <- factor(alpha_data$period, levels= unique(alpha_data$period))
alpha_data$WT.M <- factor(alpha_data$WT.M, levels=c("WT", "M"))
```

```r
alpha_data$alpha <-  as.numeric(alpha_data$alpha)

mod1 <- lme(alpha ~ time_scaled * WT.M, random=~1|mice, data = alpha_data, na.action = na.omit)

cat("Estimates, errors and the significance")
```

```
## Estimates, errors and the significance
```

```r
summary(mod1)
```

```
## Linear mixed-effects model fit by REML
##  Data: alpha_data
##        AIC      BIC    logLik
##   2068.243 2091.978 -1028.121
##
## Random effects:
##  Formula: ~1 | mice
##         (Intercept) Residual
## StdDev:   0.6720236 3.405597
##
## Fixed effects: alpha ~ time_scaled * WT.M
##                        Value Std.Error  DF   t-value p-value
## (Intercept)        10.101010  0.334981 373 30.154013  0.0000
## time_scaled       -16.267322 11.031558 373 -1.474617  0.1412
## WT.MM              -0.714526  0.490361  13 -1.457142  0.1688
## time_scaled:WT.MM   2.360361 16.148547 373  0.146166  0.8839
##  Correlation:
##                   (Intr) tm_scl WT.MM
## time_scaled        0.000
## WT.MM             -0.683  0.000
## time_scaled:WT.MM  0.000 -0.683  0.000
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -2.73631345 -0.48276146  0.06646042  0.49709145  3.94949030
##
## Number of Observations: 390
## Number of Groups: 15
```

```r
cat("Bootstrap confidence intervals for the estimates")
```

```
## Bootstrap confidence intervals for the estimates
```

```r
mod1_lmer <- lmer(alpha ~ time_scaled * WT.M + (1|mice), data = alpha_data)
confint.merMod(mod1_lmer, method = "boot", nsim = 999)
```

```
##                         2.5 %    97.5 %
## .sig01              0.000000  1.126553
## .sigma              3.147126  3.655970
## (Intercept)         9.461287 10.763733
## time_scaled       -38.593893  4.970986
## WT.MM              -1.680165  0.235239
## time_scaled:WT.MM -29.410802 34.100068
```

```r
cat("ANOVA table")
```

```
## ANOVA table
```

```
anova.lme(mod1, type = "marginal", adjustSigma = F)
```

```
##                   numDF denDF  F-value p-value
## (Intercept)           1   373 909.2645  <.0001
## time_scaled           1   373   2.1745  0.1412
## WT.M                  1    13   2.1233  0.1688
## time_scaled:WT.M      1   373   0.0214  0.8839
```

Analysis for period

```
wt <- read_xlsx("data/Period_analysis_4_R.xlsx", sheet = 1)  %>% gather(mice, value, -1)
wt <- data.frame(WT.M=rep("WT", nrow(wt))) %>% bind_cols(wt)
mut <- read_xlsx("data/Period_analysis_4_R.xlsx", sheet = 2)  %>% gather(mice, value, -1)
mut <- data.frame(WT.M=rep("M", nrow(mut))) %>% bind_cols(mut)

period_data <- wt %>% bind_rows(mut)
period_data$value <- as.numeric(period_data$value)

mod2 <- lme(value~ week * WT.M, random = ~1|mice, data = period_data)

cat("Estimates, errors and the significance")
```

```
## Estimates, errors and the significance
```

```
summary(mod2)
```

```
## Linear mixed-effects model fit by REML
##  Data: period_data
##        AIC   BIC    logLik
##   309.1875 328.7 -144.5938
##
## Random effects:
##  Formula: ~1 | mice
##         (Intercept) Residual
## StdDev:   0.7251103 3.268825
##
## Fixed effects: value ~ week * WT.M
##                            Value Std.Error DF   t-value p-value
## (Intercept)           23.721429  1.265532 39 18.744234  0.0000
## weekDD_Week_2         -3.381429  1.747260 39 -1.935275  0.0602
## weekDD_Week_3          2.055714  1.747260 39  1.176536  0.2465
## weekLD_Week_3          0.208571  1.747260 39  0.119371  0.9056
## WT.MWT                 0.137321  1.732901 13  0.079244  0.9380
## weekDD_Week_2:WT.MWT   3.251429  2.392535 39  1.358989  0.1820
## weekDD_Week_3:WT.MWT -2.426964  2.392535 39 -1.014390  0.3166
## weekLD_Week_3:WT.MWT -0.063571  2.392535 39 -0.026571  0.9789
##  Correlation:
##                       (Intr) wkDD_W_2 wkDD_W_3 wkLD_W_3 WT.MWT wDD_W_2:
## weekDD_Week_2         -0.690
## weekDD_Week_3         -0.690  0.500
## weekLD_Week_3         -0.690  0.500    0.500
## WT.MWT                -0.730  0.504    0.504    0.504
## weekDD_Week_2:WT.MWT  0.504 -0.730   -0.365   -0.365   -0.690
```

```
## weekDD_Week_3:WT.MWT  0.504 -0.365   -0.730   -0.365   -0.690  0.500
## weekLD_Week_3:WT.MWT  0.504 -0.365   -0.365   -0.730   -0.690  0.500
##                      wDD_W_3:
## weekDD_Week_2
## weekDD_Week_3
## weekLD_Week_3
## WT.MWT
## weekDD_Week_2:WT.MWT
## weekDD_Week_3:WT.MWT
## weekLD_Week_3:WT.MWT  0.500
##
## Standardized Within-Group Residuals:
##          Min           Q1          Med           Q3          Max
## -5.938352181 -0.067963537 -0.001414478  0.093674882  1.778532447
##
## Number of Observations: 60
## Number of Groups: 15
```

```
cat("Bootstrap confidence intervals for the estimates")
```

```
## Bootstrap confidence intervals for the estimates
```

```
mod2_lmer <- lmer(value ~ week * WT.M + (1|mice), data = period_data)
confint.merMod(mod2_lmer, method = "boot", nsim = 999)
```

```
##                           2.5 %      97.5 %
## .sig01                 0.000000  2.14316485
## .sigma                 2.513938  3.84935166
## (Intercept)           21.295014 26.08264006
## weekDD_Week_2         -6.777346  0.06162009
## weekDD_Week_3         -1.202367  5.34826111
## weekLD_Week_3         -3.176616  3.68604026
## WT.MWT                -3.217573  3.26535504
## weekDD_Week_2:WT.MWT -1.222345  8.16487237
## weekDD_Week_3:WT.MWT -6.663714  1.92943012
## weekLD_Week_3:WT.MWT -4.658113  4.21914440
```

```
cat("ANOVA table")
```

```
## ANOVA table
```

```
anova.lme(mod2, type = "marginal", adjustSigma = F)
```

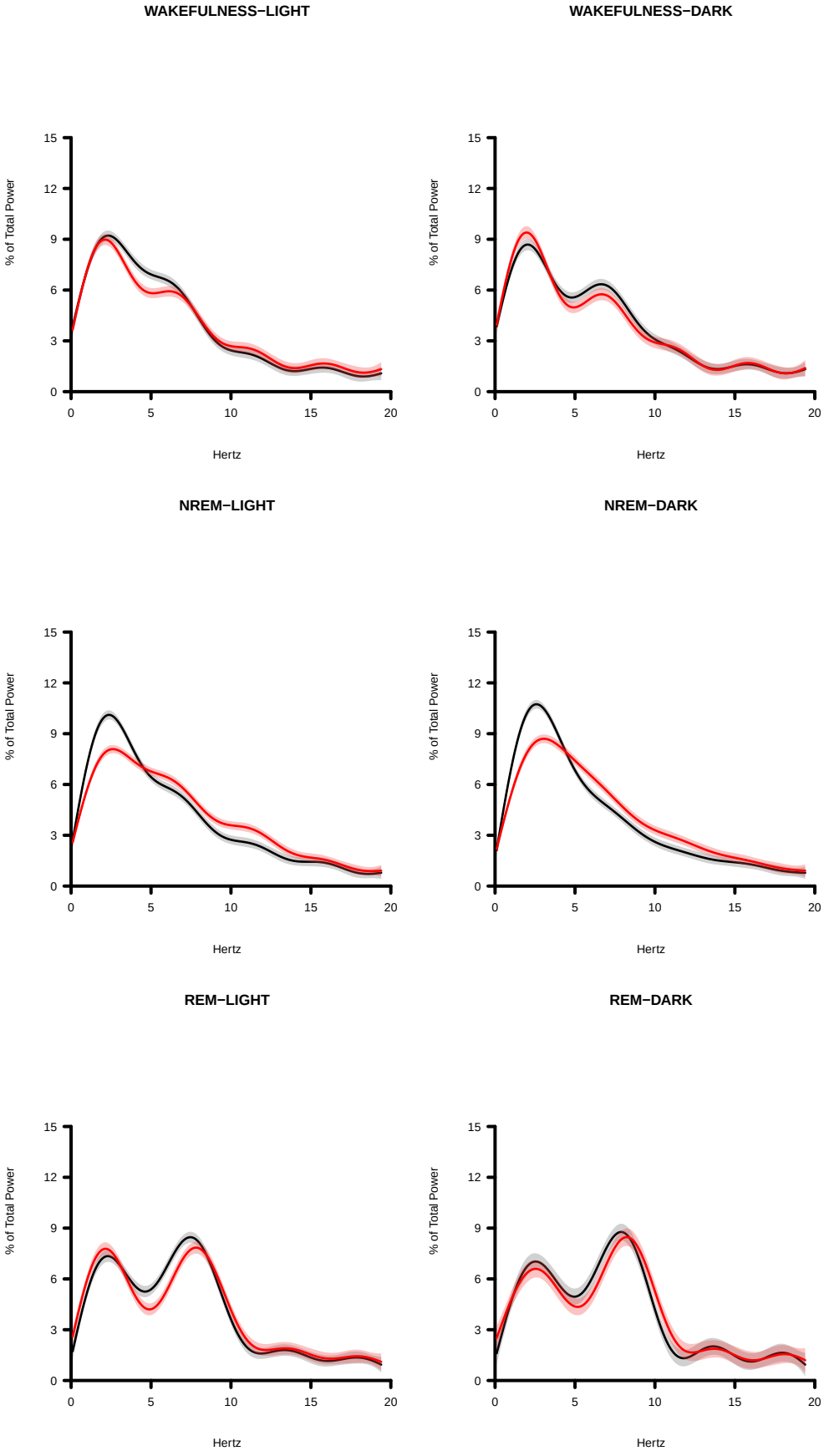
```
##             numDF denDF  F-value p-value
## (Intercept)     1    39 351.3463  <.0001
## week            3    39   3.3611  0.0282
## WT.M            1    13   0.0063  0.9380
## week:WT.M       3    39   1.9008  0.1454
```

Analysis for Spectral Data

```
# GAM plots
library(mgcv)

data<-read_xlsx("data/BL_spectral.xlsx")
```

```r
data <- data %>% gather(Hertz, value,  -c(1:3))
data <- data %>%
  mutate(GT=replace(GT,GT == 1, "WT")) %>%
  mutate(GT=replace(GT,GT == 2, "MT")) %>%
  mutate(LD=replace(LD,LD == 1, "LIGHT")) %>%
  mutate(LD=replace(LD,LD == 2, "DARK")) %>%
  mutate(hz= as.numeric(Hertz)) %>%
  mutate(STATE = factor(STATE, levels = unique(STATE))) %>%
  mutate(GT = factor(GT, levels = unique(GT))) %>%
  mutate(LD  = factor(LD, levels = unique(LD))) %>%
  mutate(value = replace(value,value == -99, NA))

temp<-data %>% filter(STATE == "WAKEFULNESS" & LD == "LIGHT")
index <-paste(data$STATE, data$LD, sep = "")
index_lev <- unique(index)

layout(matrix(seq_len(6), nrow = 3, ncol = 2, byrow = TRUE))
shadow_col <- c(rgb(109, 109, 109, max = 255, alpha = 80),
                rgb(244, 66, 66, max = 255, alpha = 80))

for(this_index in index_lev) {
  state <- unique(data[index == this_index, ][, 1])
  state <- as.character(unlist(state))
  light <- unique(data[index == this_index, ][, 3])
  light <- as.character(unlist(light))

  temp2 <- data[index == this_index, ]
  plot(x = temp2$hz, y = temp2$value, type = "n",
       ylab =  "% of Total Power", ylim = c(0,20),
       xlab = 'Hertz', lwd = 3, cex = 1.2,
       main = paste0(state, "-", light), axes = FALSE)
  axis(1, at = seq(0, 20, by = 5), las = 1, pos = 0, lwd = 3)
  axis(2, at = seq(0, 15, by = 3), las = 2, pos = 0, lwd = 3)

  mod <- list(wt = gam(value~s(hz), data = temp2[temp2$GT == "WT",]),
              mt = gam(value~s(hz), data = temp2[temp2$GT == "MT",]))

  for(i in seq_along(mod)) {
    ss <- seq(min(temp2$hz) + 0.1, max(temp2$hz) - 0.1, 0.1)
    pred <- predict(mod[[i]], data.frame(hz = ss), se = TRUE)
    fit <- pred$fit
    se <- pred$se.fit
    lower <- fit - 1.96 * se
    upper  <- fit + 1.96 * se
    to_plot <- data.frame(hz = ss, fit, lower, upper)

    polygon(c(to_plot$hz, rev(to_plot$hz)),
            c(to_plot$lower, rev(to_plot$upper)),
            col = shadow_col[i],
            border = NA)

    lines(to_plot$hz, fit,  lwd=2, col = c("black", "red")[i])
  }
```

```
  legend(x = "topright",horiz = TRUE, c("MT", "WT"),
         pch = c(NA, NA), col = c("black", "red"),
         inset = c(0, -0.08), cex = 1,  bty = 'n',
         box.lty = c('NA', 'NA'), lwd = 3 )

}
```


WAKEFULNESS−LIGHT
WAKEFULNESS−DARK
NREM−LIGHT
NREM−DARK
REM−LIGHT
REM−DARK
% of Total Power
Hertz
0
3
6
9
12
15
0
5
10
15
20