GSE100924

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Contents

1 Exploring microarray data. A naïve (simple) approach

Summary

Zbtb7b is a zinc finger and BTB domain containing transcription factor that activates the thermogenic gene program during brown and beige adipocyte differentiation. Zbtb7b interacts with the long noncoding RNA Blnc1 and hnRNPU to form a ribonucleoprotein transcriptional complex We used microarray to determine how Zbtb7b regulates brown fat gene expression at ambient room temperature and following cold exposure

Overall design

Wild type and Zbtb7b knockout mice of 10 weeks of age were kept at ambient room temperature (22C) or following cold exposure at 4C for 4 hrs. Brown adipose tissue was harvested for total RNA isolation and microarray analysis. ## Loading the data

1.1 Exploratory analysis with univariate statistics

A boxplot of the data shows that values are assymetrically distributed

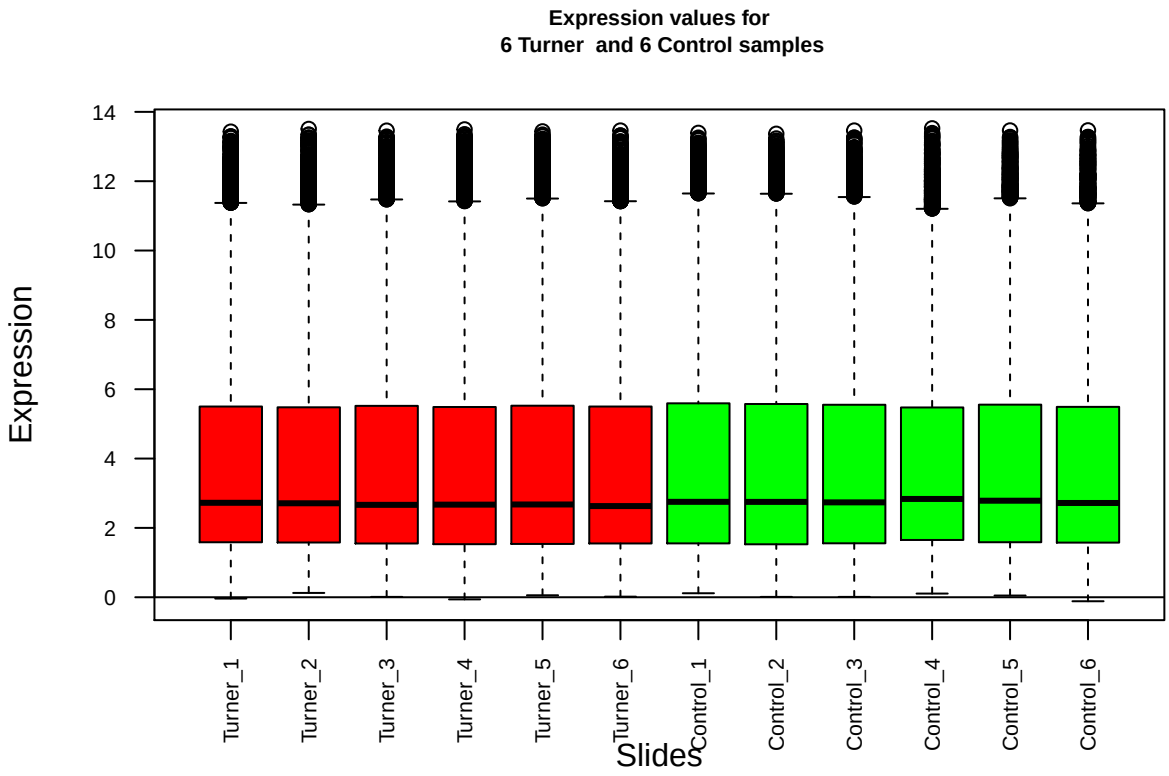
```
## Loading required package: knitr
```

```
## Warning: package 'knitr' was built under R version 4.0.4
```

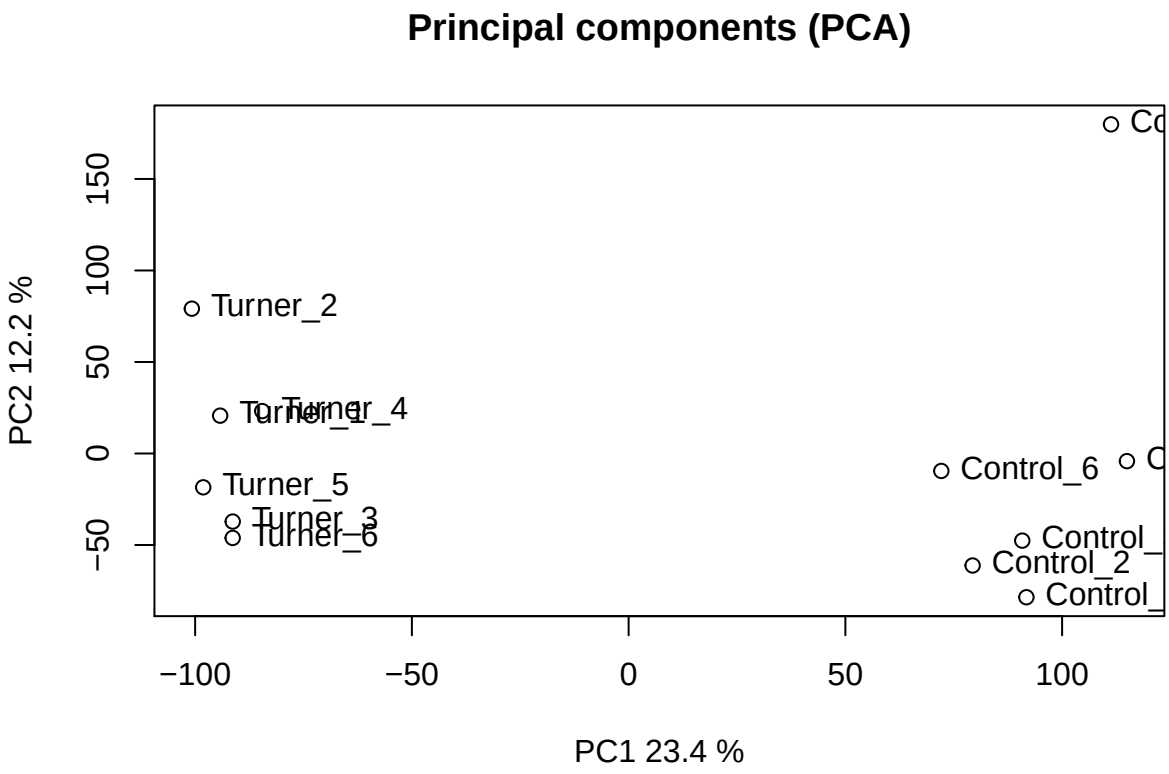
1.2 Data visualization using unsupervised techniques (PCA, Clustering)

Start by computing prncipal components and loadings.

```
pcX<-prcomp(t(ex), scale=TRUE)
loads<- round(pcX$sdev^2/sum(pcX$sdev^2)*100,1)
```



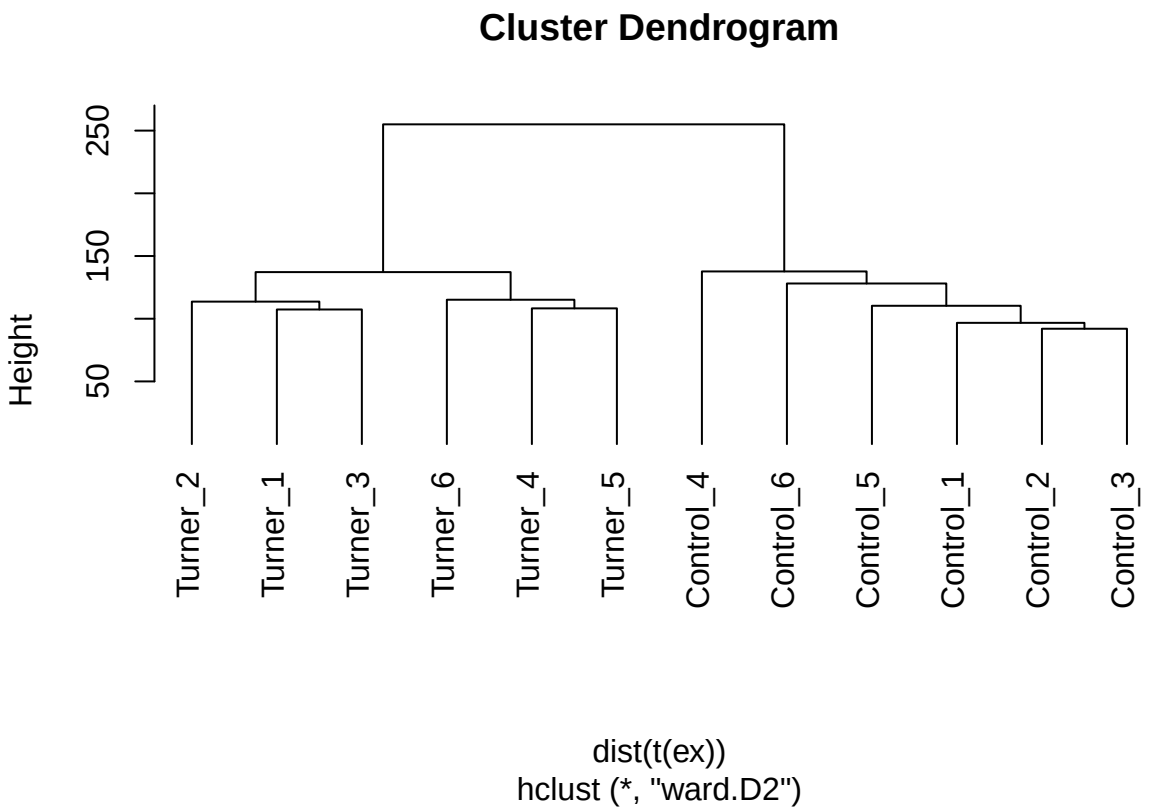

```
xlab<-c(paste("PC1",loads[1],"%"))
ylab<-c(paste("PC2",loads[2],"%"))
plot(pcX$x[,1:2],xlab=xlab,ylab=ylab)
title("Principal components (PCA)")
text(pcX$x[,1],pcX$x[,2],colnames(ex), pos=4)
```



Alternatively a hierarchichal clustering can be applied to detect any expected (or unexpected grouping of the samples).

```
clust.euclid.average <- hclust(dist(t(ex)),method="ward.D2")
```

```
plot(clust.euclid.average, hang=-1)
```


Cluster Dendrogram
Height
250
150
50
Turner_2
Turner_1
Turner_3
Turner_6
Turner_4
Turner_5
Control_4
Control_6
Control_5
Control_1
Control_2
Control_3
dist(t(ex))
hclust (*, "ward.D2")