Untitled

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```
##
## Attaching package: 'BBmisc'

## The following object is masked from 'package:base':
##
##     isFALSE
```

SPECIFIC ANALYSIS

In this part of the data analysis, the focus will be effect of Vorinostat on gene expression levels of genes found commonly in 59 different cell lines.

The genes who respond to Vorinostat are considered biomarkers.

We will try to define biomarkers in 2 different ways;

- Overall biomarkers present in many cancerogenic cell lines

- Cancer-type specific biomarkers (Biomarkers as genes highly expressed in some specific cancerogenic cell lines)

1- Finding Overall Biomarkers

Firstly, we tried to find out biomarkers using a two-tailed paired t-test (Treated vs. Untreated)

```
##            p_values significance
## A4GALT 1.001496e-03         TRUE
## AAAS   4.656829e-02         TRUE
## AAGAB  2.212806e-09         TRUE
## AAK1   2.991843e-08         TRUE
## AAMDC  2.614942e-18         TRUE
## AAMP   2.703757e-07         TRUE
## AAR2   2.908756e-03         TRUE
```

Histogram of p_values_Vorinostat[, 1]
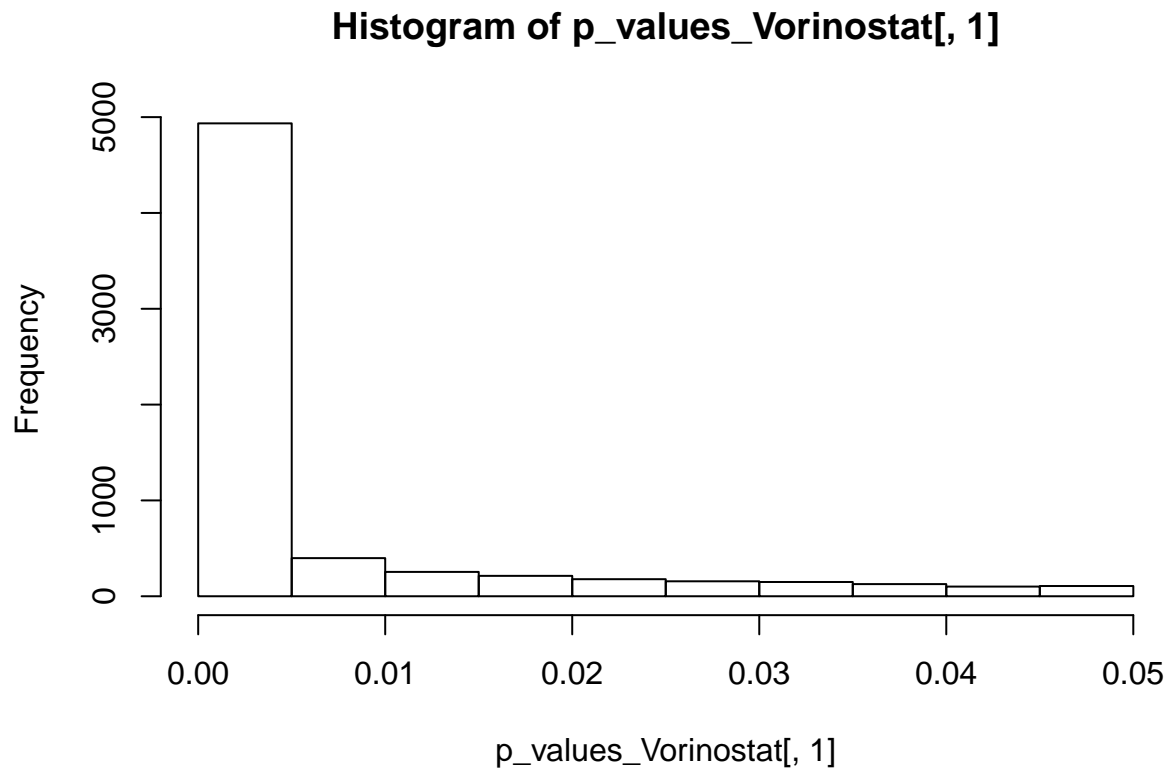
A lot of values were essentially zero.

Second, we used a two-tailed independent t-test on Expression Change (= FC =Treated - Untreated)

```
##             p_values significance
## CLP1     1.481879e-30        TRUE
## MAP1LC3B 7.610927e-30        TRUE
## OSER1    3.216898e-29        TRUE
## ZNF277   7.395399e-29        TRUE
## TOE1     1.617893e-28        TRUE
## SPAG9    2.171353e-28        TRUE
## NME6     3.545470e-28        TRUE
```

Histogram of p_values_EC[, 1]
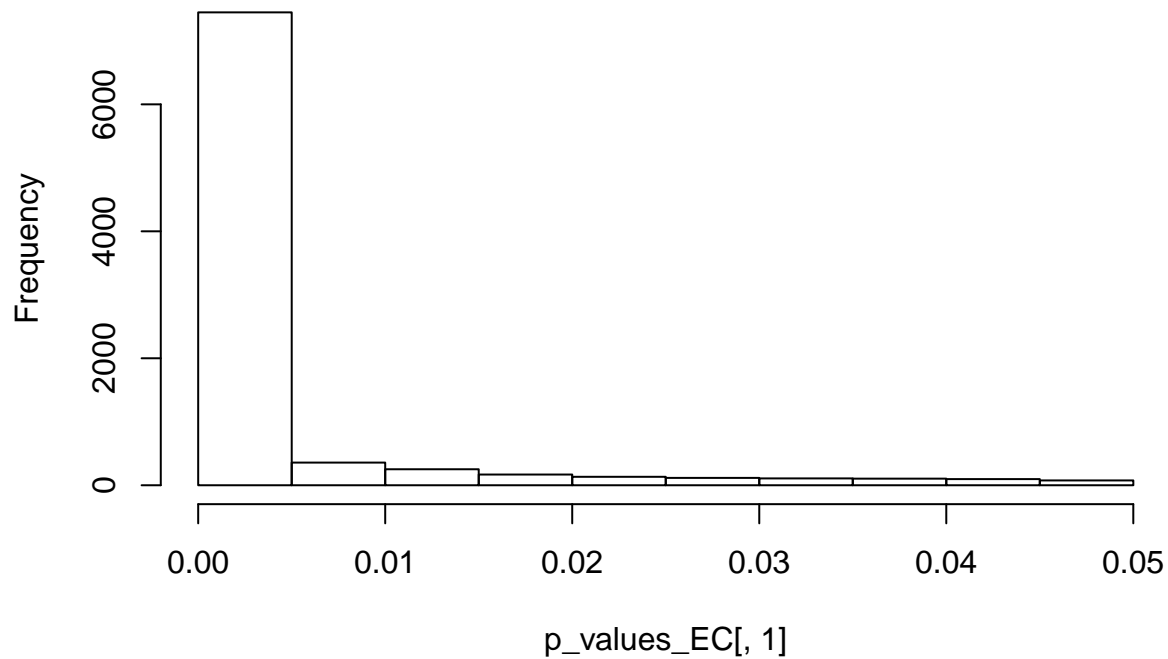
The problem has been that, when comparing very small values e.g. drug responses, small changes result in a low p value without actually being significant.

Therefore, we opted for taking mean values of gen expression changes after treatment in absolute numbers.

```
##                 Mean_of_abs_DR
## DHRS2                 1.776307
## ABAT                  1.335351
## SERPINI1              1.261878
## MIR612///NEAT1        1.238418
## CLU                   1.071682
## HBA2///HBA1           1.063014
```

The following heatmap shows the expression changes of the selected biomarkers.
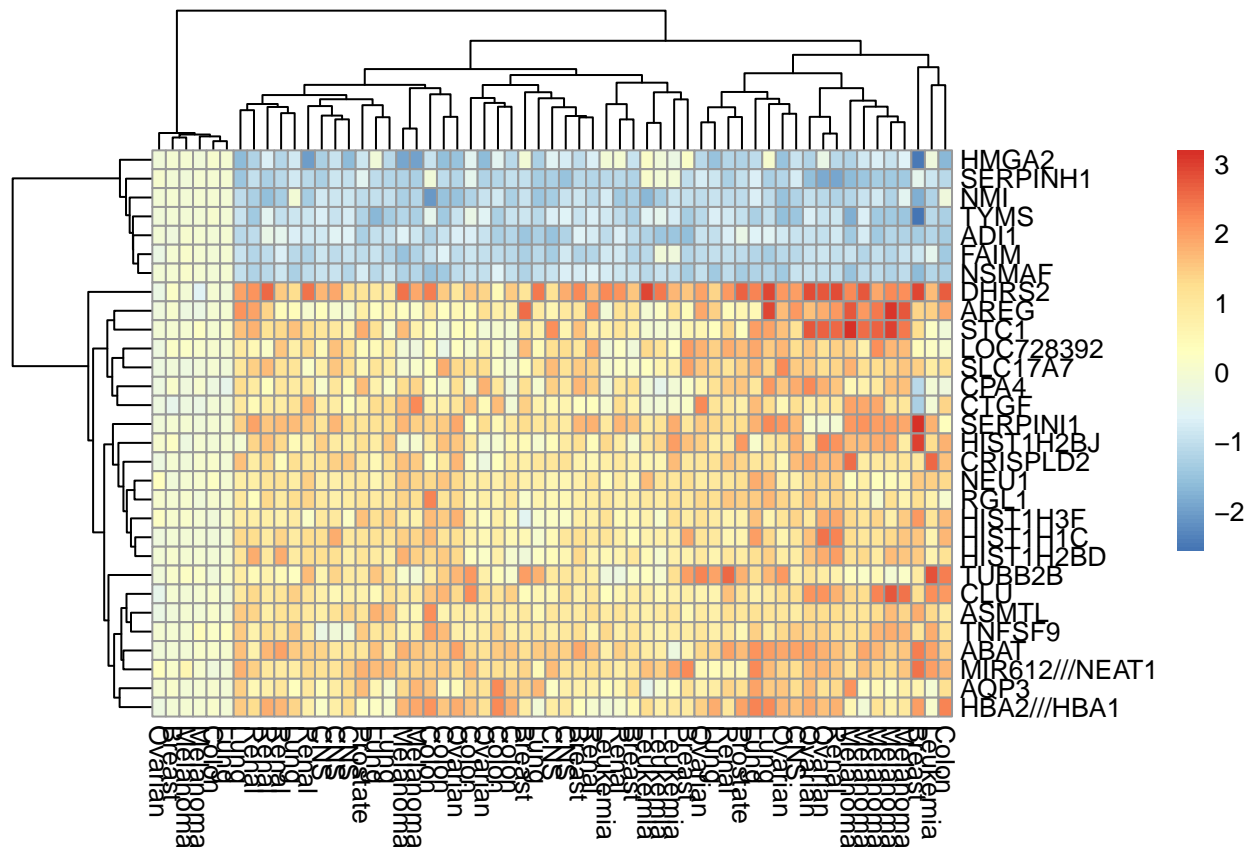
It can be seen that melanoma cell lines reacted strongly to Vorinostat treatment.

2- Finding Cancer-type specific biomarkers

In this part, we firstly took a look at the highly variant genes.

We regarded these as: - either cell line specific - or, of cancerogenic character

Then we compared, which of these changes showed a high change in their variance.

2.1 - Selecting genes with a variance above 95% quartile of variances before treatment

2.2 - Selecting genes which showed a significant decrease in their high variances

2.3 - Depicting the drug responses of these genes with a heatmap
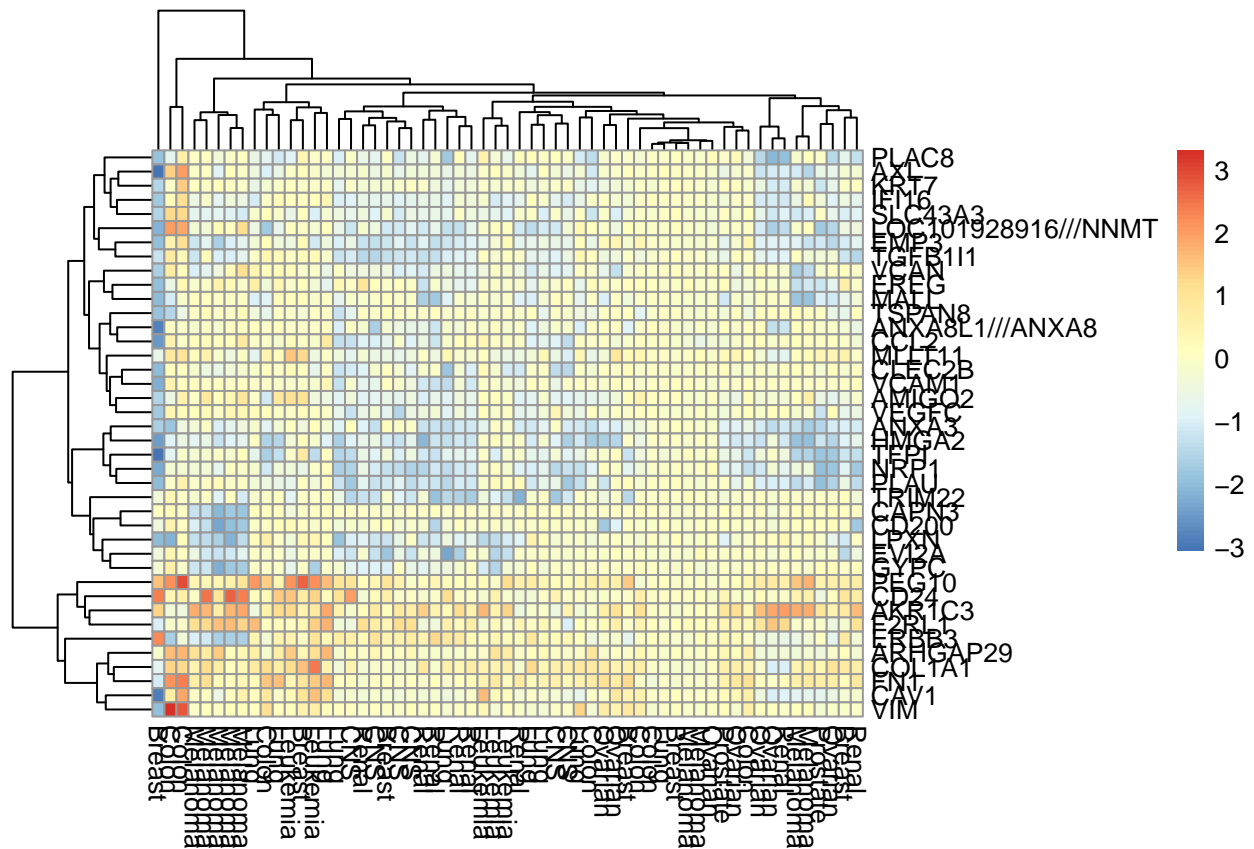
Clearly, in most of the cell lines, not a real change can be observed.

However, an overall downregulation in a breast cell line and high upregulation of some genes of two colon cell lines stand out.