

My first Rmarkdown

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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

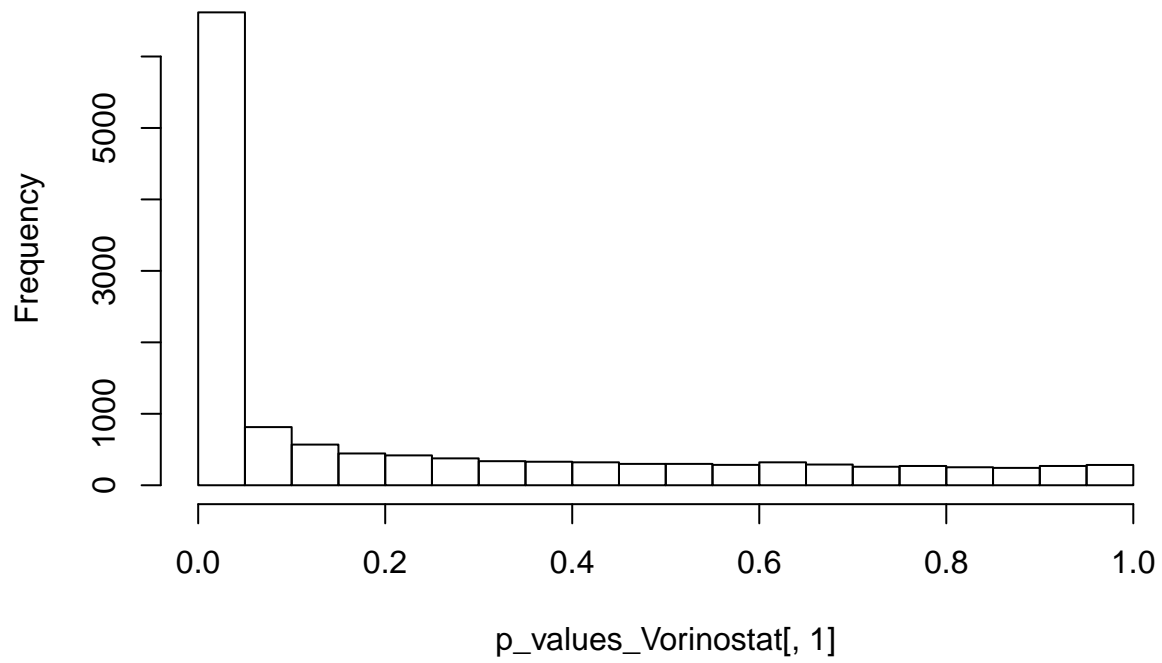
Firstly, we tried to find out biomarkers using a two-tailed paired t-test (Treated vs. Untreated)

```
##
## The downloaded binary packages are in
## /var/folders/gv/mlkc7mx97qn_x33b5rty20440000gn/T//Rtmpe1HFjh/downloaded_packages

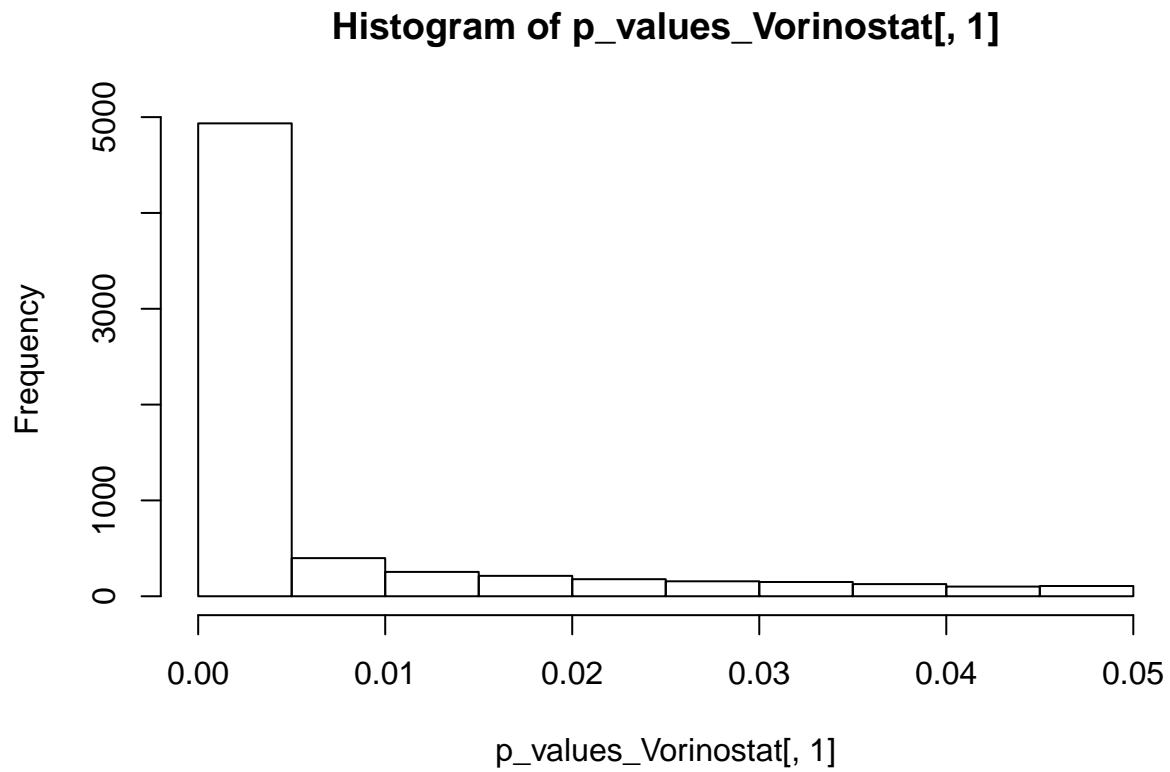
##
## Attaching package: 'BBmisc'

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

Histogram of p_values_Vorinostat[, 1]

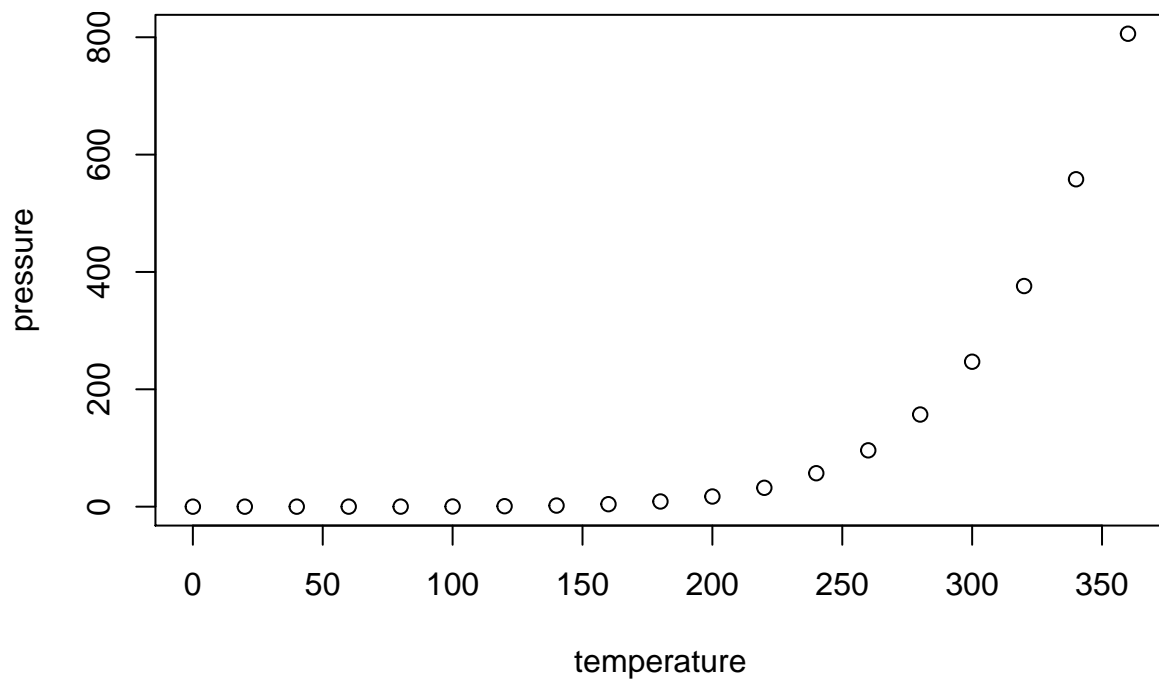


##		p_values	significance
##	A4GALT	1.001496e-03	TRUE
##	AAAS	4.656829e-02	TRUE
##	AAGAB	2.212806e-09	TRUE
##	AAK1	2.991843e-08	TRUE
##	AAMDC	2.614942e-18	TRUE
##	AAMP	2.703757e-07	TRUE
##	AAR2	2.908756e-03	TRUE



Including Plots

You can also embed plots, for example:



Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.