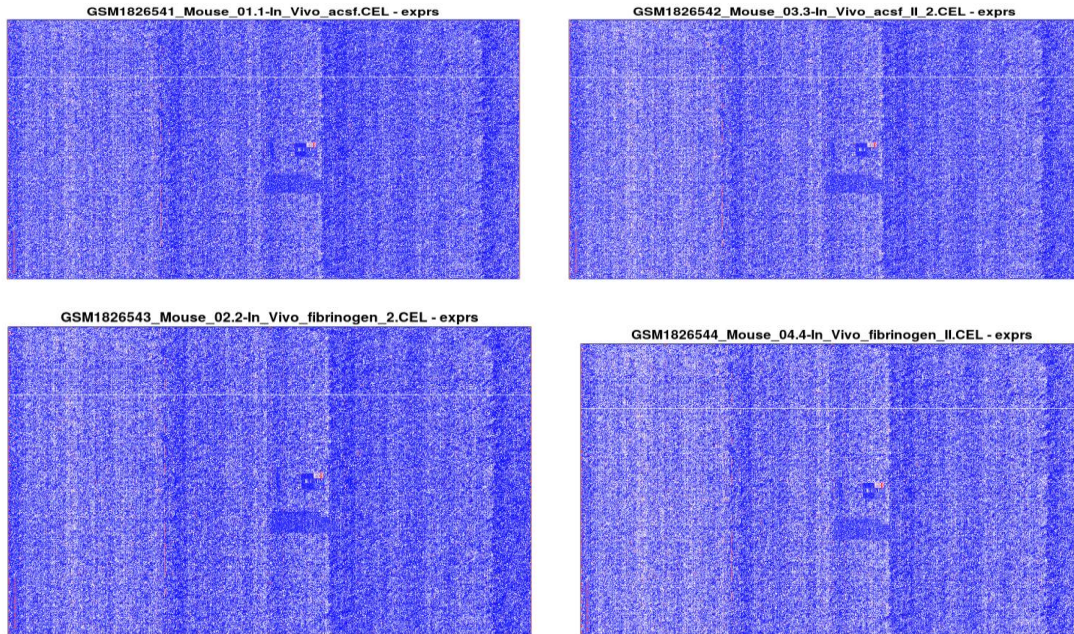# Microarrays. Transcriptomics Practise
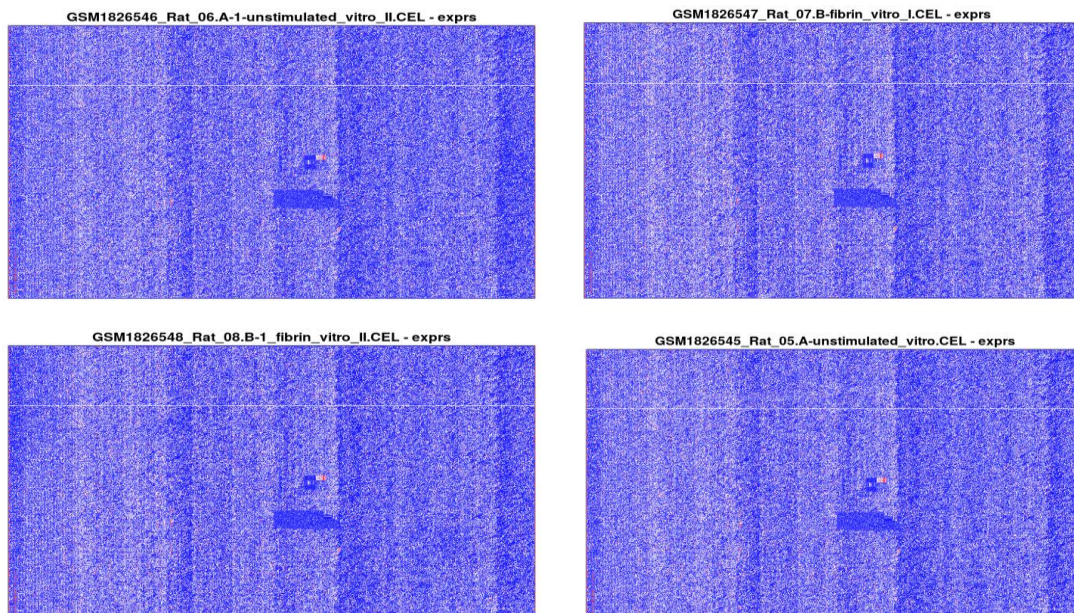
Álvaro Ponce Cabrera

1. Quality assessment

First of all, we use the **image** function to see the microarrays and check for physical damage. We obtain the following 8 images:
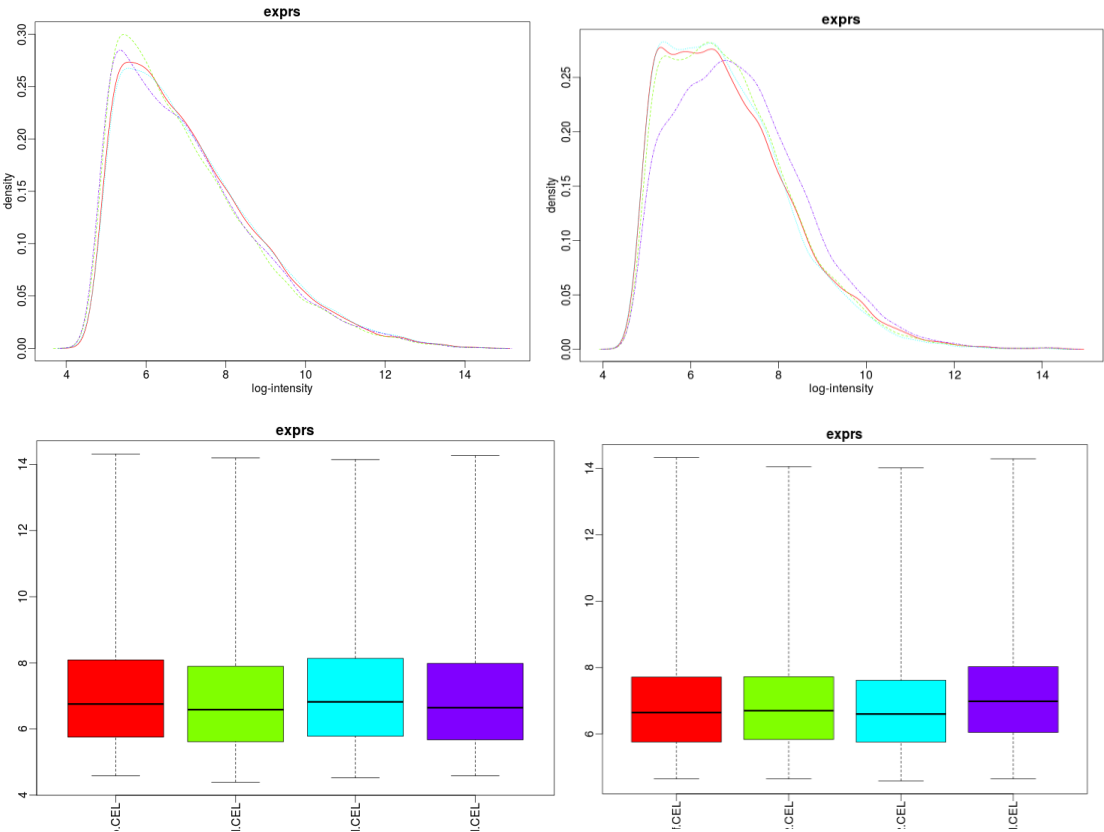
- Mouse

GSM1826541_Mouse_01.1-In_Vivo_acsf.CEL - exprs

GSM1826542_Mouse_03.3-In_Vivo_acsf_II_2.CEL - exprs

GSM1826543_Mouse_02.2-In_Vivo_fibrinogen_2.CEL - exprs

GSM1826544_Mouse_04.4-In_Vivo_fibrinogen_II.CEL - exprs

- Rat

GSM1826546_Rat_06.A-1-unstimulated_vitro_II.CEL - exprs

GSM1826547_Rat_07.B-fibrin_vitro_I.CEL - exprs

GSM1826548_Rat_08.B-1_fibrin_vitro_II.CEL - exprs

GSM1826545_Rat_05.A-unstimulated_vitro.CEL - exprs

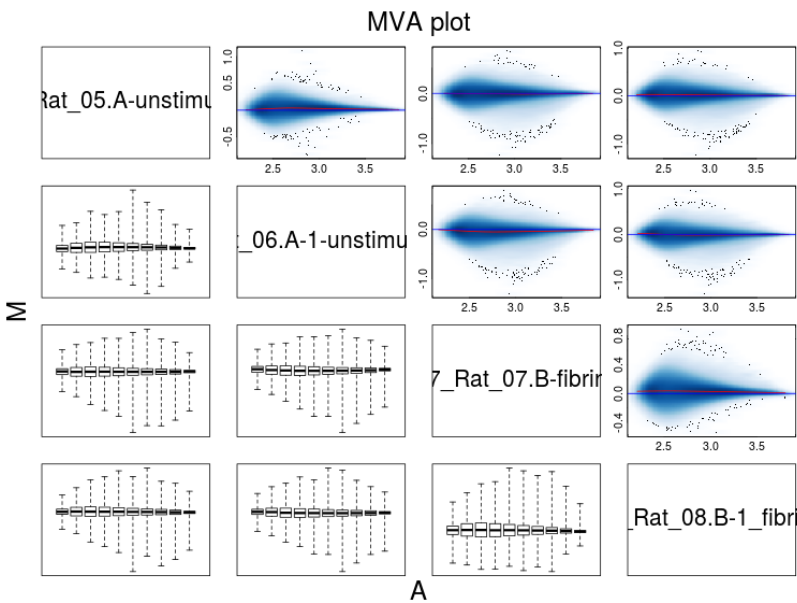The microarrays are ok and with no physical damage.

Following with the quality assessment, we can plot histograms and boxplots of fluorescence level of the samples:
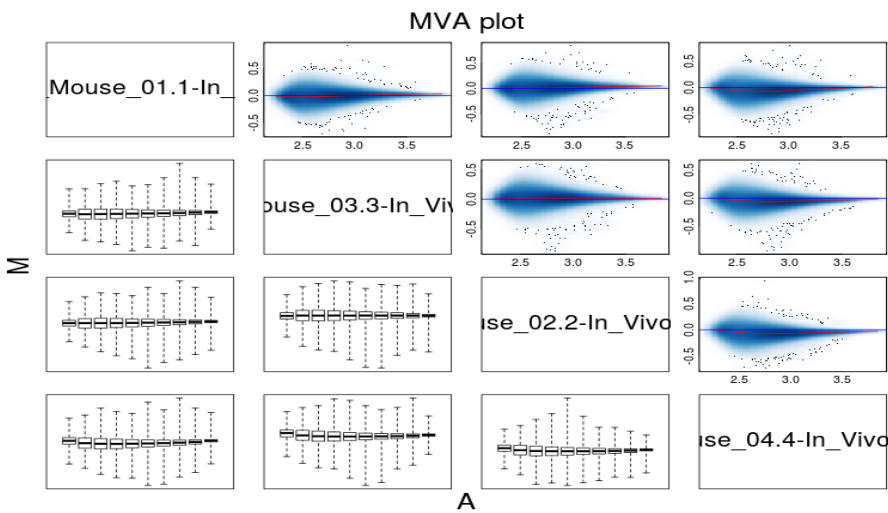
Rat vs Mouse.
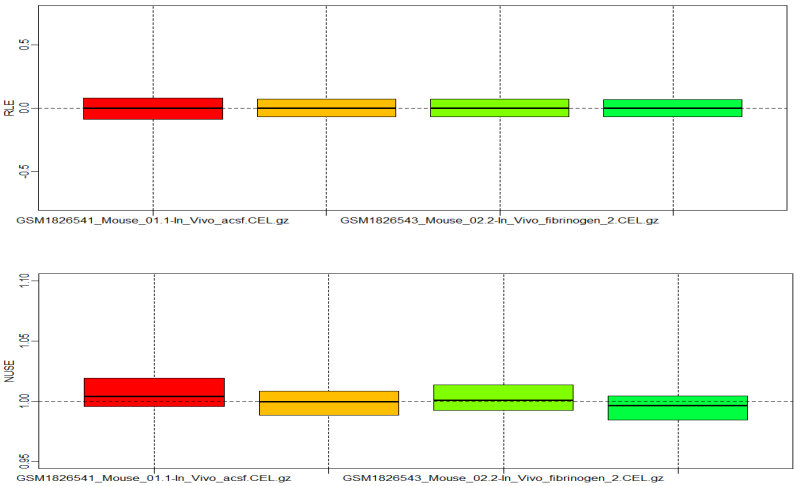

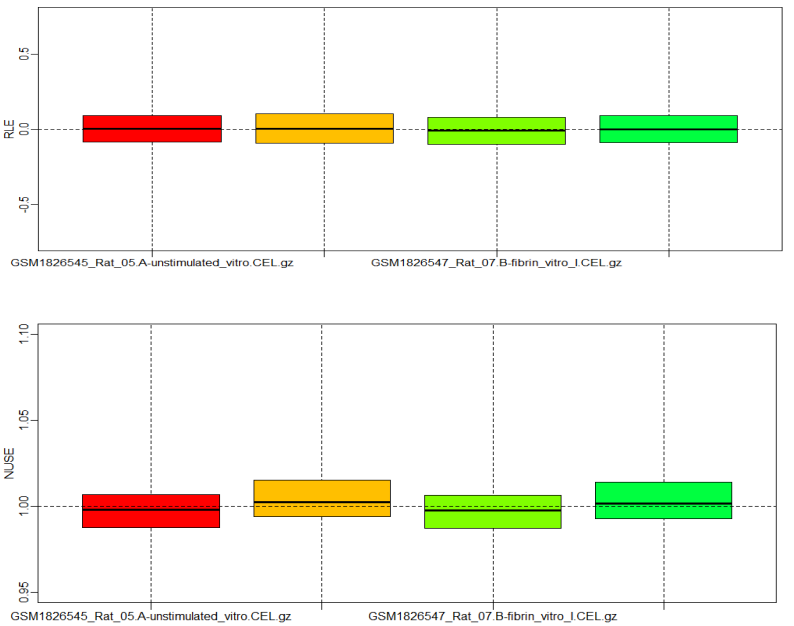Also we can see the MA-plots:

Rat:

Mouse:

MVA plot

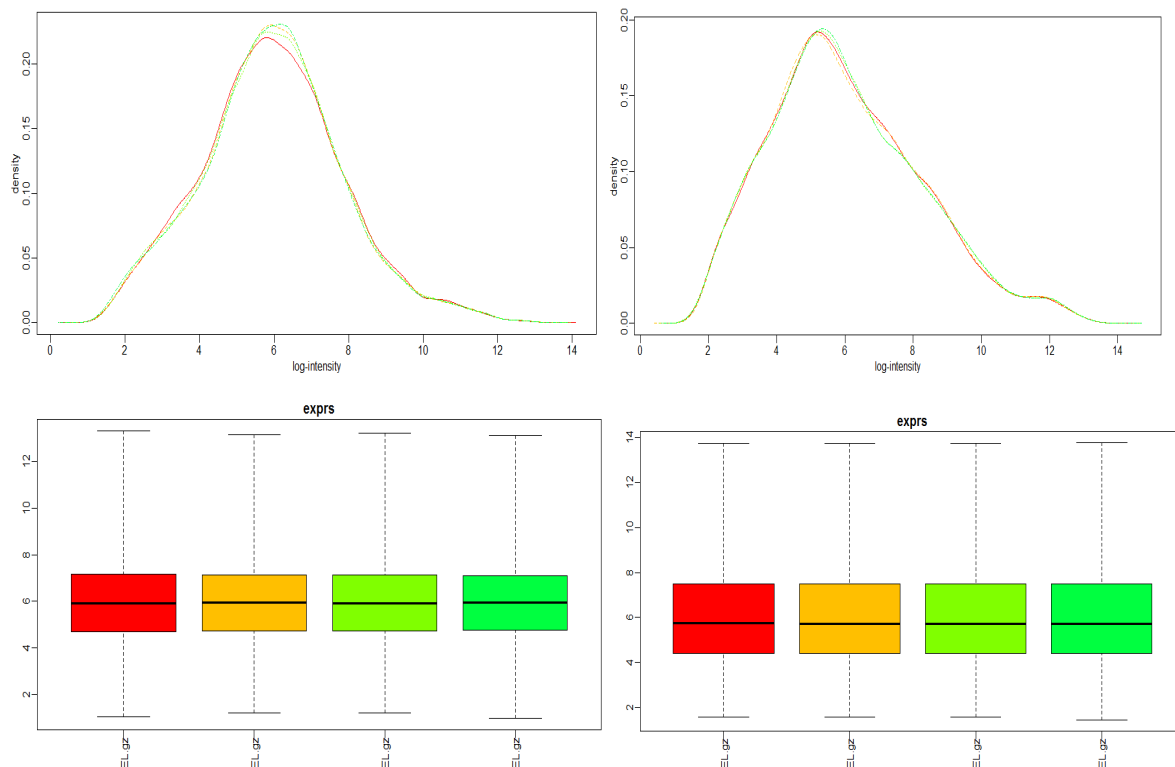Finally, we plot the RLE and NUSE.
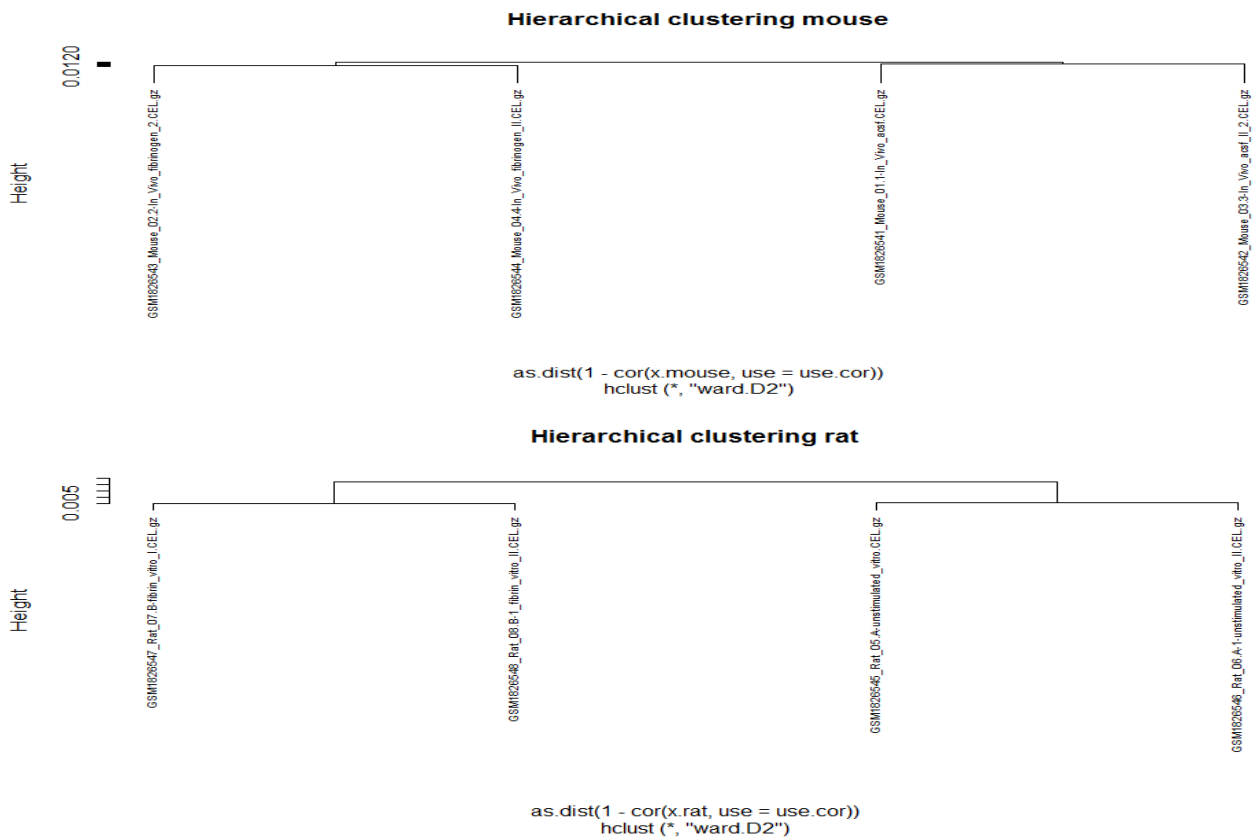
Mouse (RLE vs NUSE):

Rat (RLE vs NUSE):

2. Normalization.

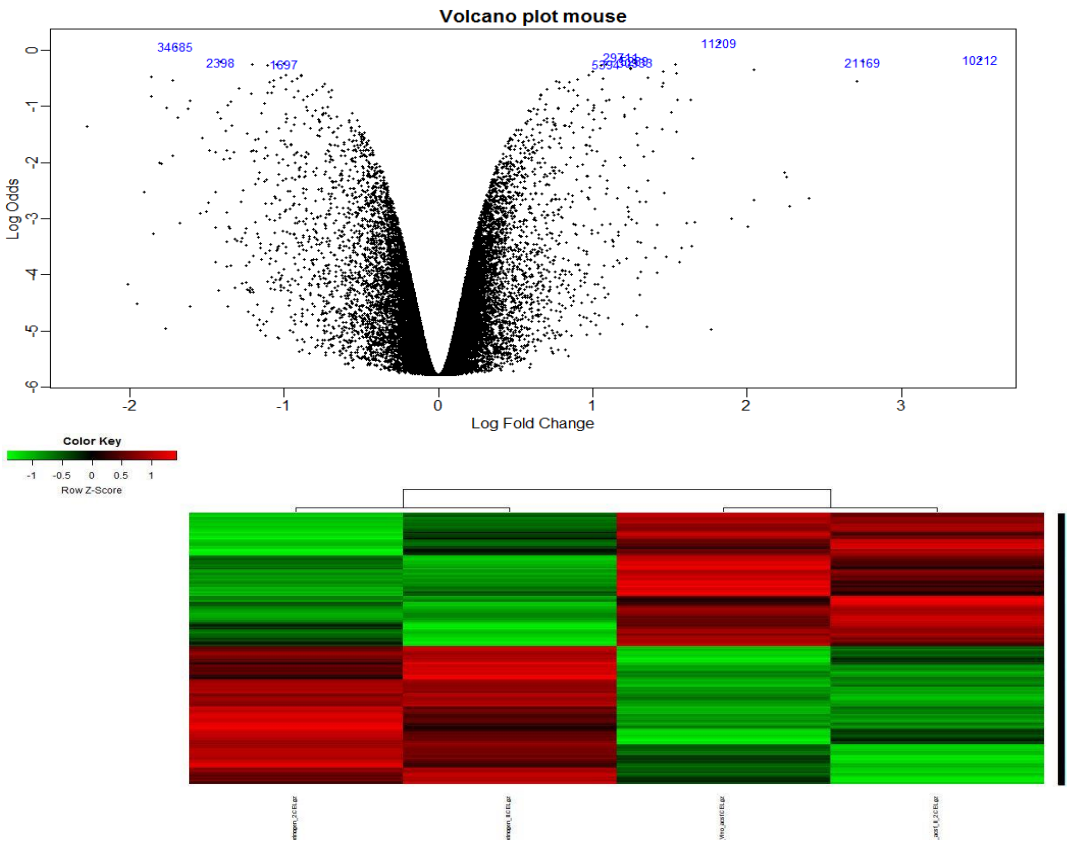We can check the boxplot and histogram after normalization too (Mouse vs Rat):

We can also see data aggregation in order to check for Batch effect:

Everything seems to be ok.

3. Generation of volcano plot and heat map.

Volcano plot and heat map of mouse:

Volcano plot and heat map for Rat: