Graphs for Amita's paper

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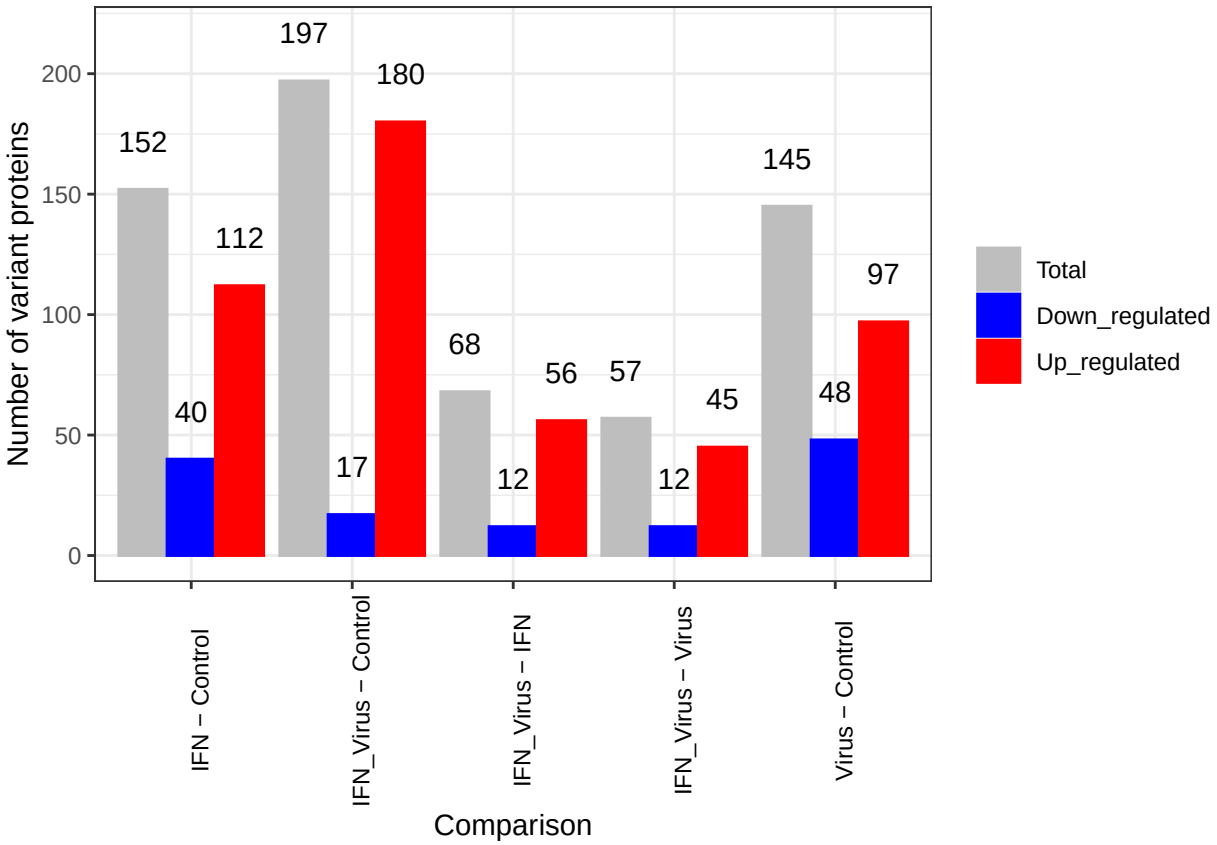
Using same qValue and just transforming the zscore ratio

I tried transforming the zscore ratio with this formula:

$$log_2(1/(2^{OZR}))$$

where OZR is the orignal log_2 zscore ratio. There problem is that I got no proteins deregulated for 3 of the 4 comparisons. So for the following graph, I transformed the OZR like this:

$$-1 * OZR$$



Re-calculating qvalue

For the two following graphs, I log_2-transformed the normalized abundances and used those to calculate the qvalue (with the following sequence of "limma" functions: "lmFit", "contrasts.fit", "eBayes" and "topTable" - this last one using adjust.method = "BH")

Re-calculating zscore ratio

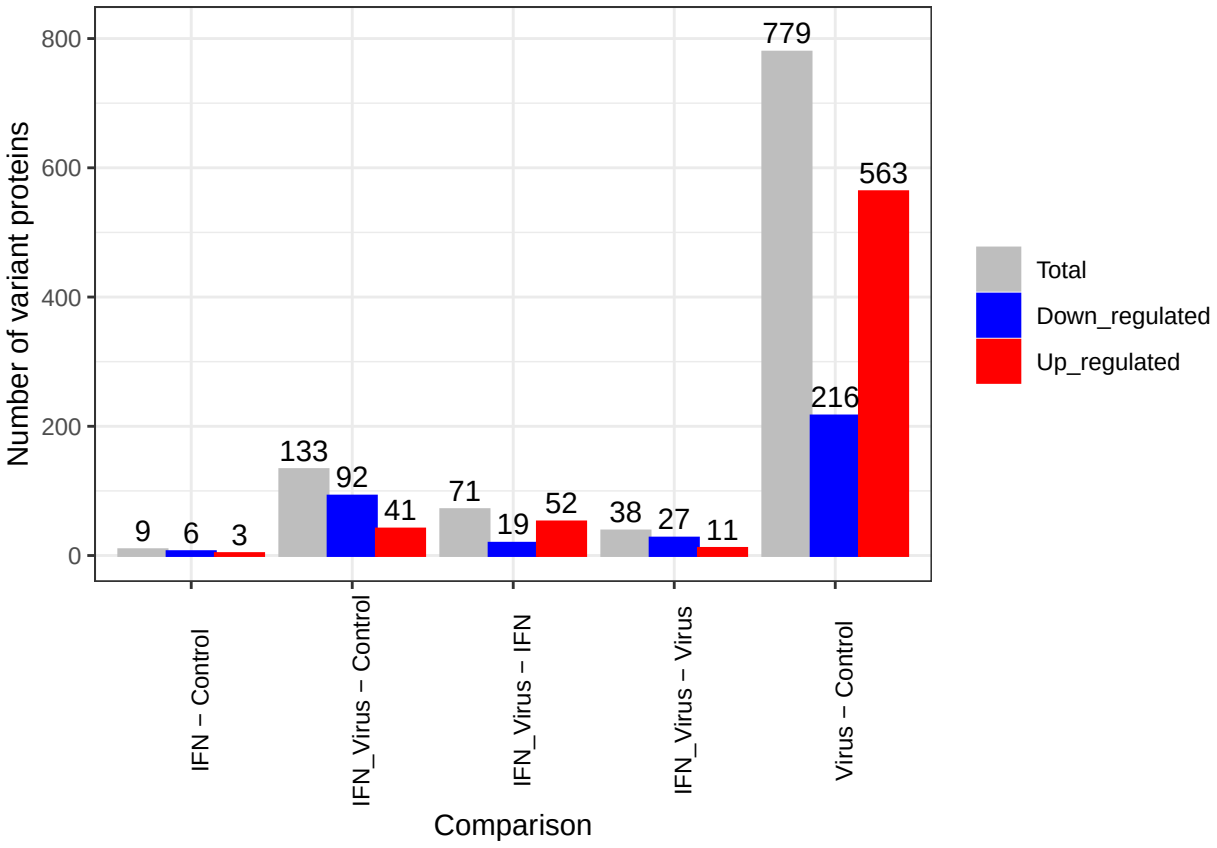
I calculated the zscore with the formula:

$$zscore = (X - MEAN)/STDEV$$

Where X is the average abundance of each protein in a sample, MEAN and STDEV are the average and the standard deviation, respectively, of the abundance of each protein accross the experiment.

I calculated the ratios and then I did the filtering that the people from U Laval did

$$|log_2(zScoreRatio)| > 1.96 \cap qValue < 0.05$$



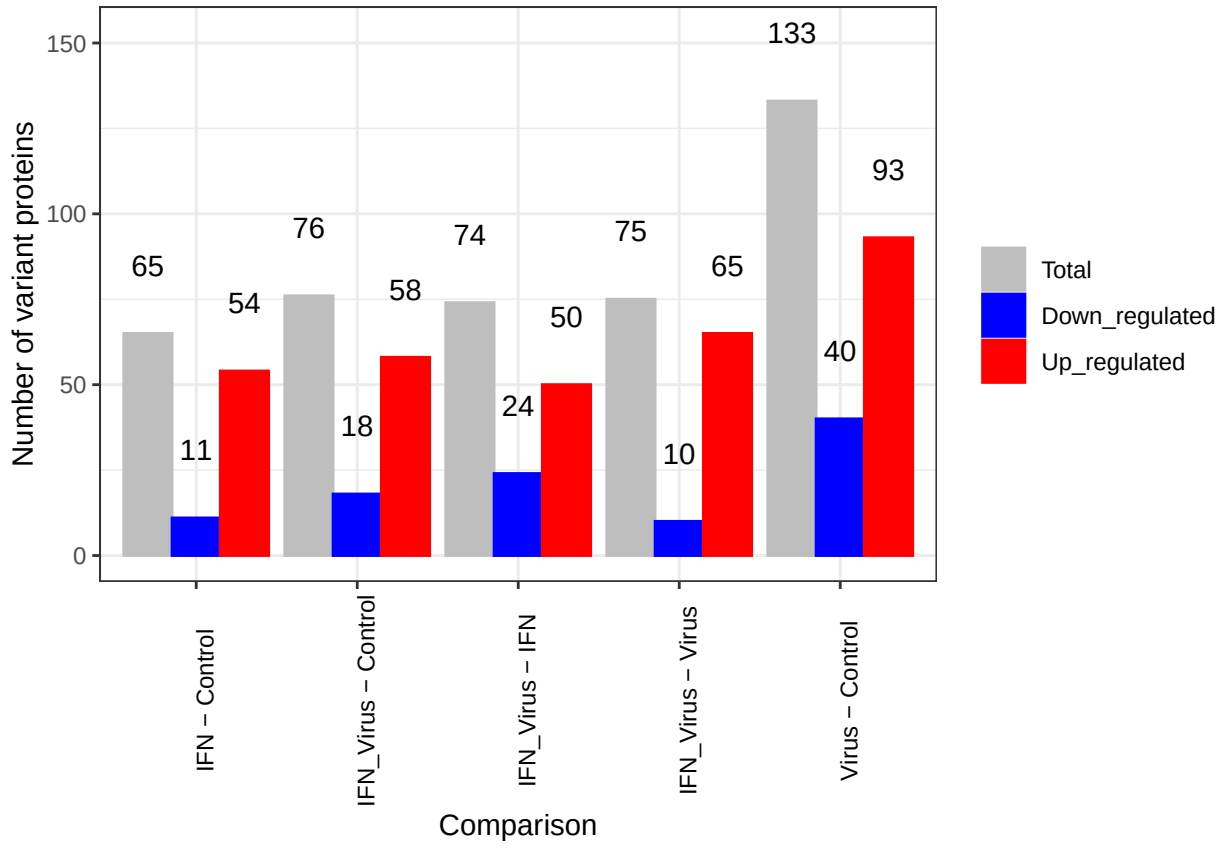
Transforming the zscore ratio from ULaval

Here I took the log_2 transformed zscore ratios from the excel sheet, de-transformed the values, inverted them and re-transformed to log_2:

$$log_2(1/(2^{OZR}))$$

Then I did the filtering that the people from U Laval did:

$$|log_2(zScoreRatio)| > 1.96 \cap qValue < 0.05$$



Overall

Basically I cannot get the same results either using the original zScore ratio and transforming with $log_2(1/(2^{OZR}))$ or with $-1 * OZR$ and using the original qValues, recalculating the qValue and transforming the original zscore or reca