Graphs for Amita's paper - with data from U Laval

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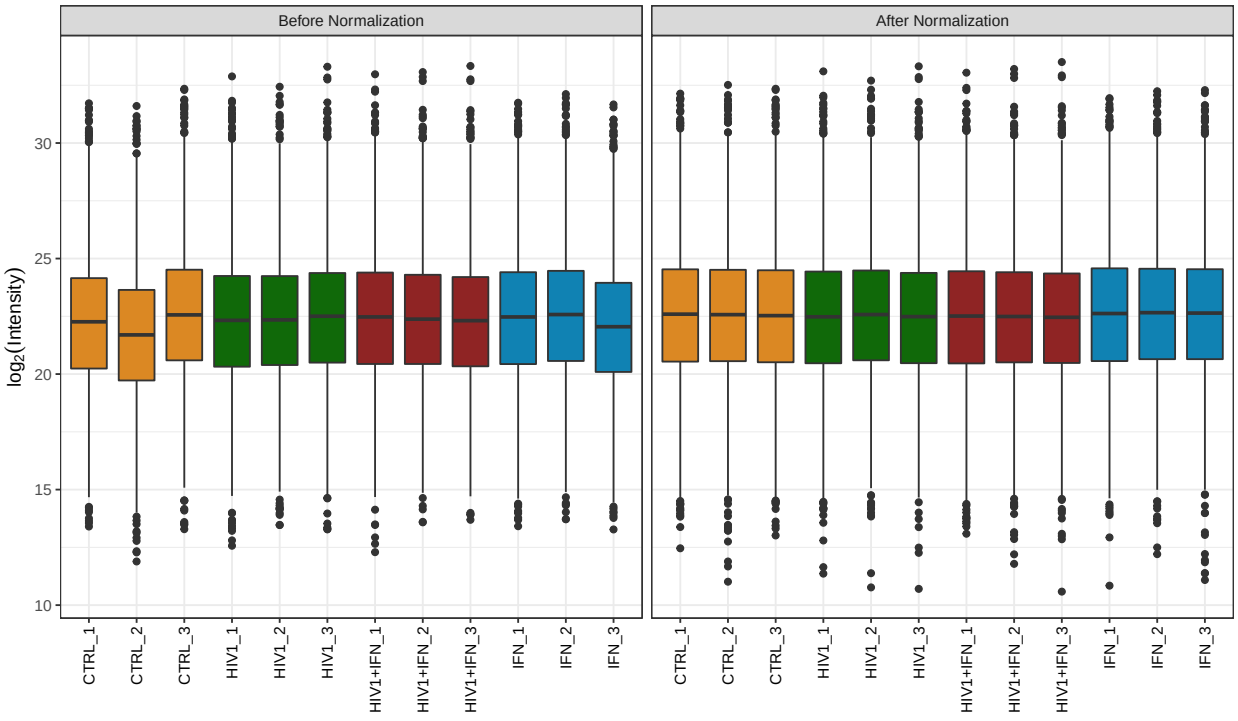
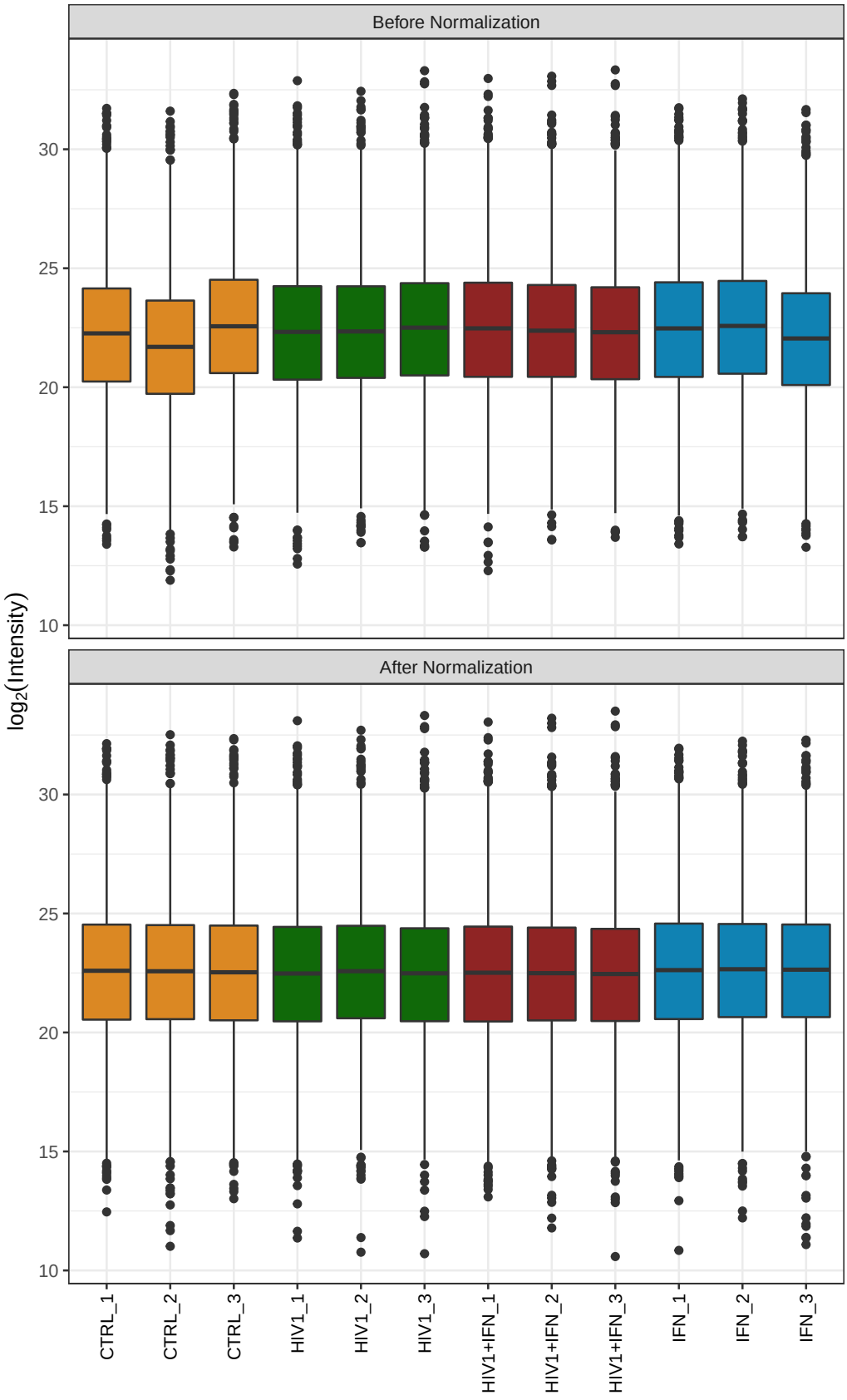
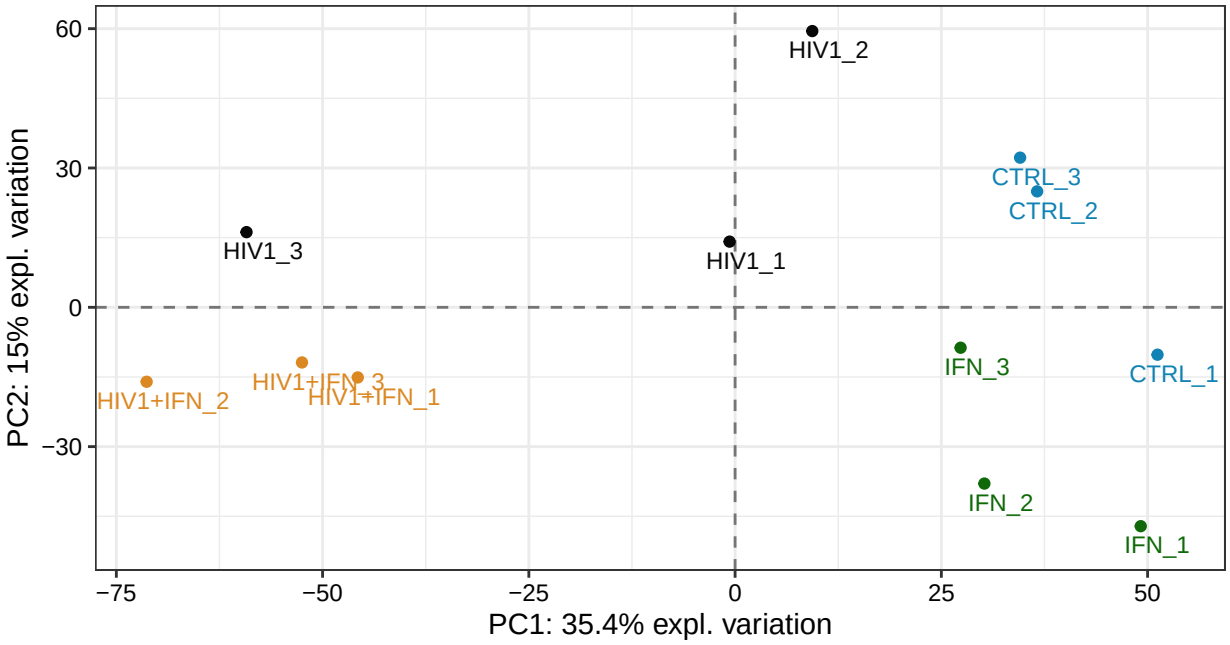
2) BoxPlot before and after normalization.

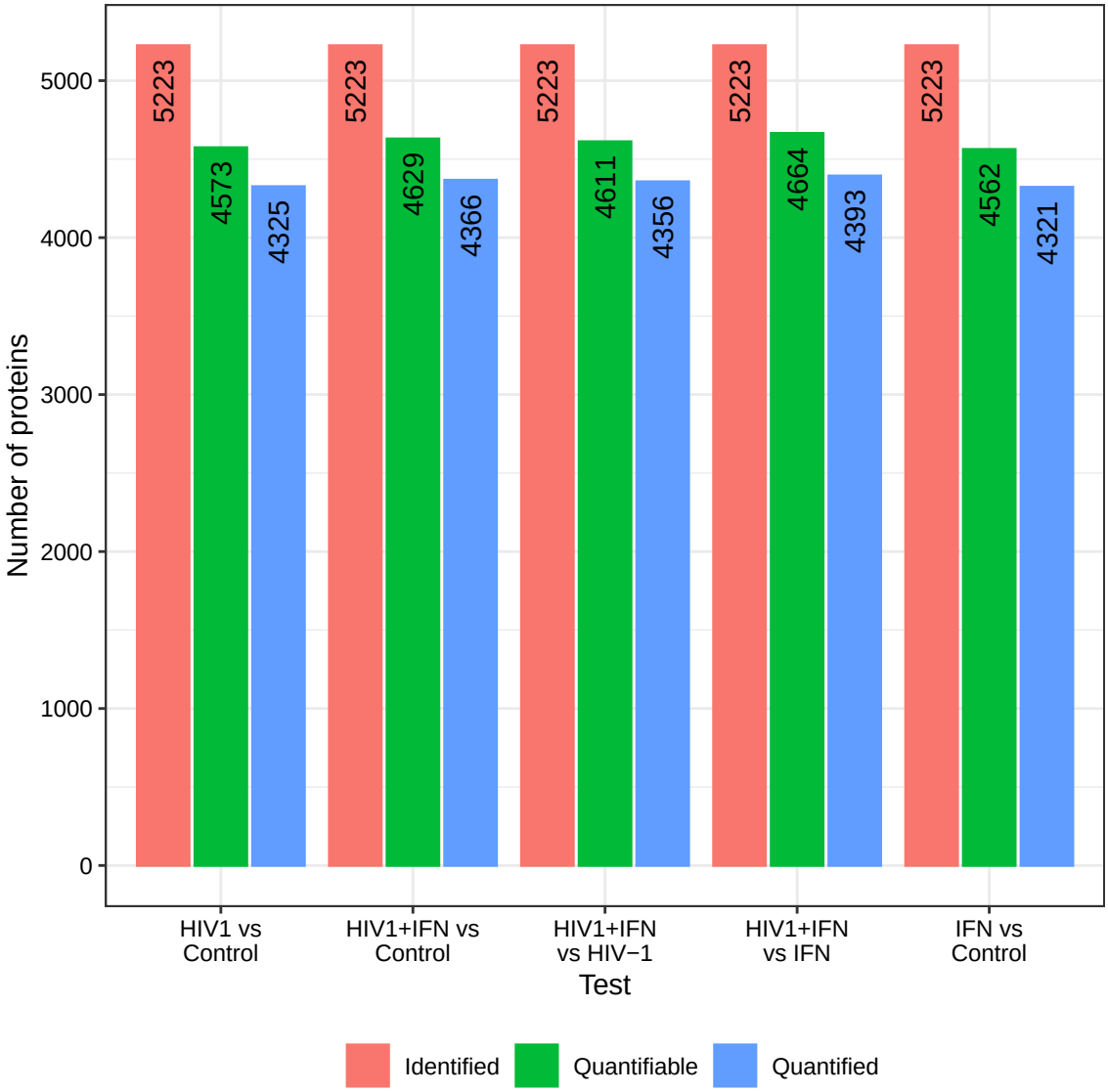



Before Normalization
After Normalization
log2(Intensity)
30
25
20
15
10
CTRL_1
CTRL_2
CTRL_3
HIV1_1
HIV1_2
HIV1_3
HIV1+IFN_1
HIV1+IFN_2
HIV1+IFN_3
IFN_1
IFN_2
IFN_3

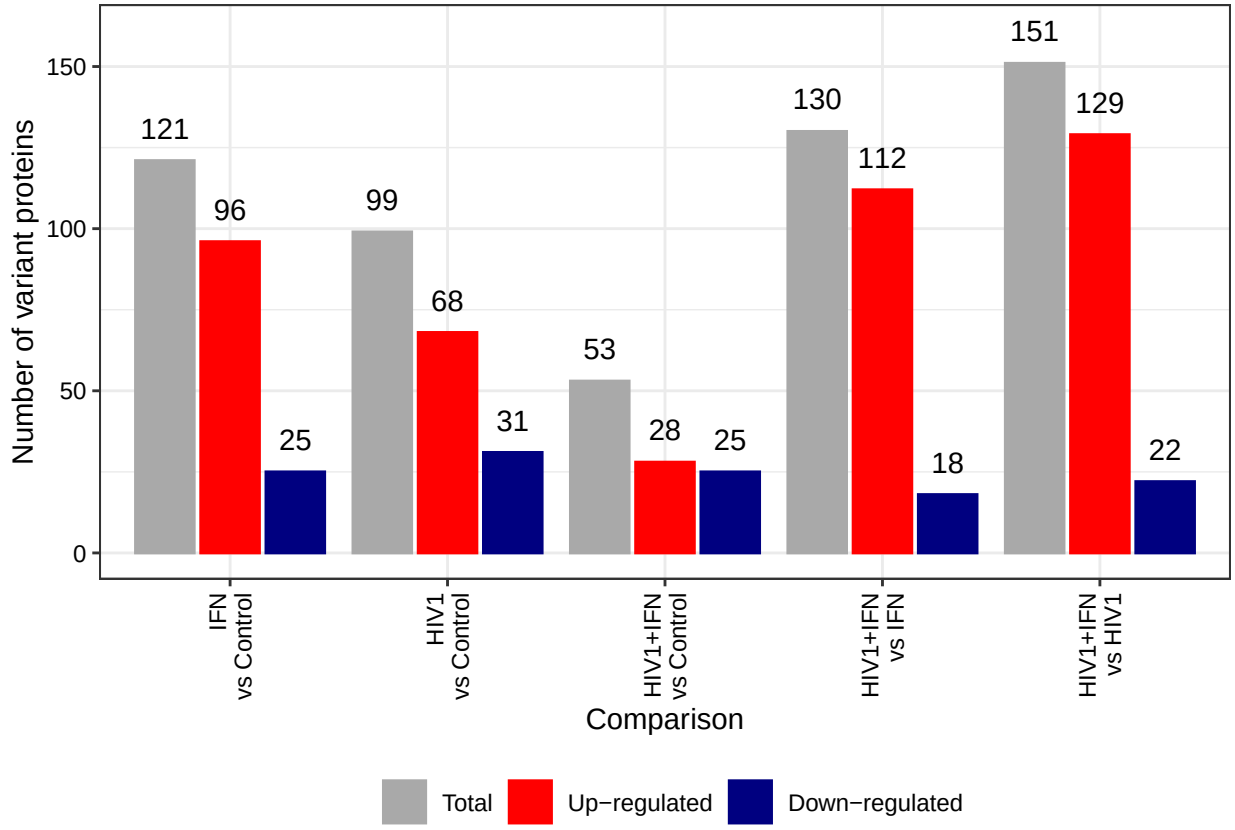
3) PCA analysis



4) Number of quantifications for each sample



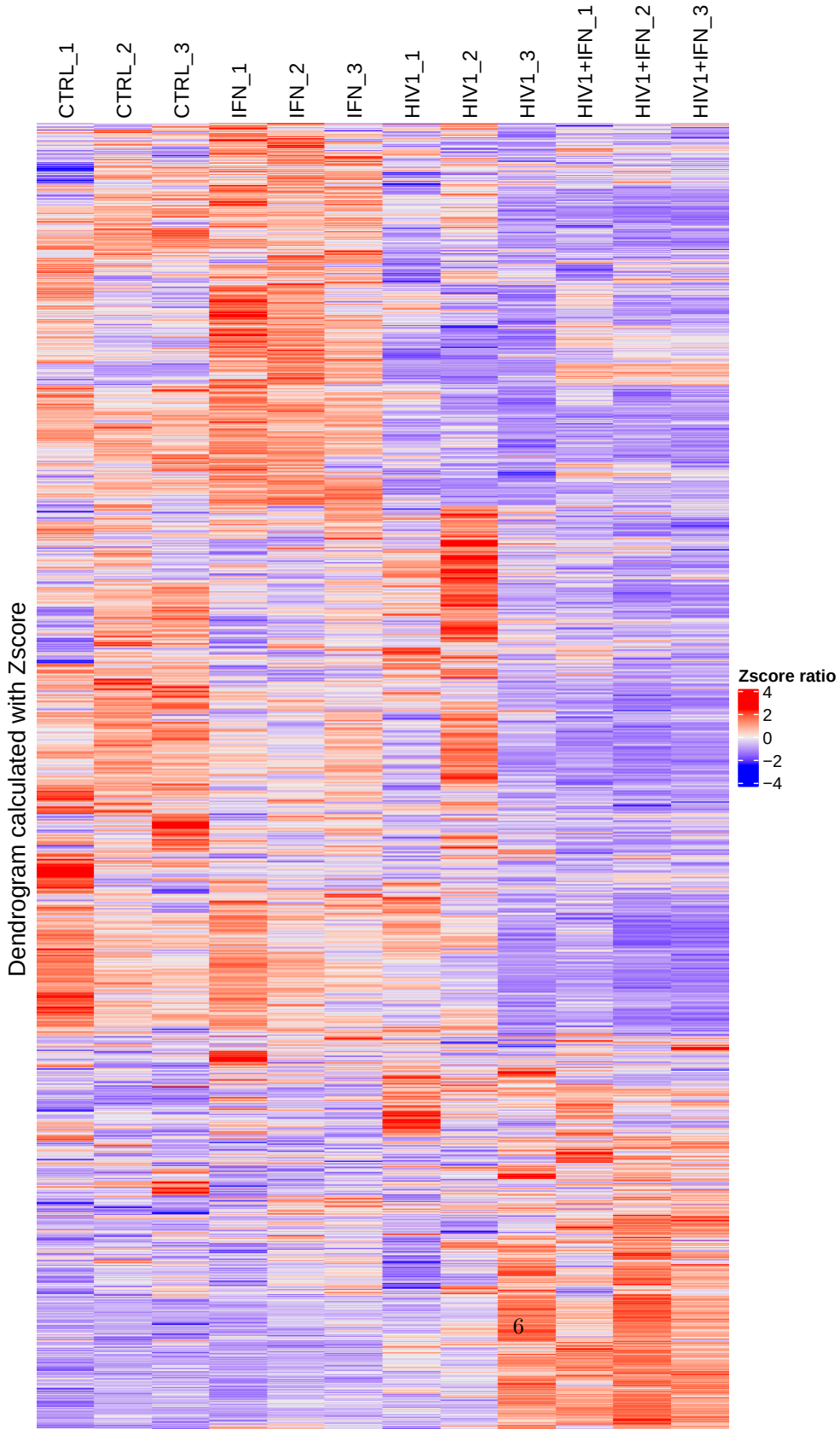
5) Number of variant proteins for each comparison



6) Volcano plots

7) Heatmaps

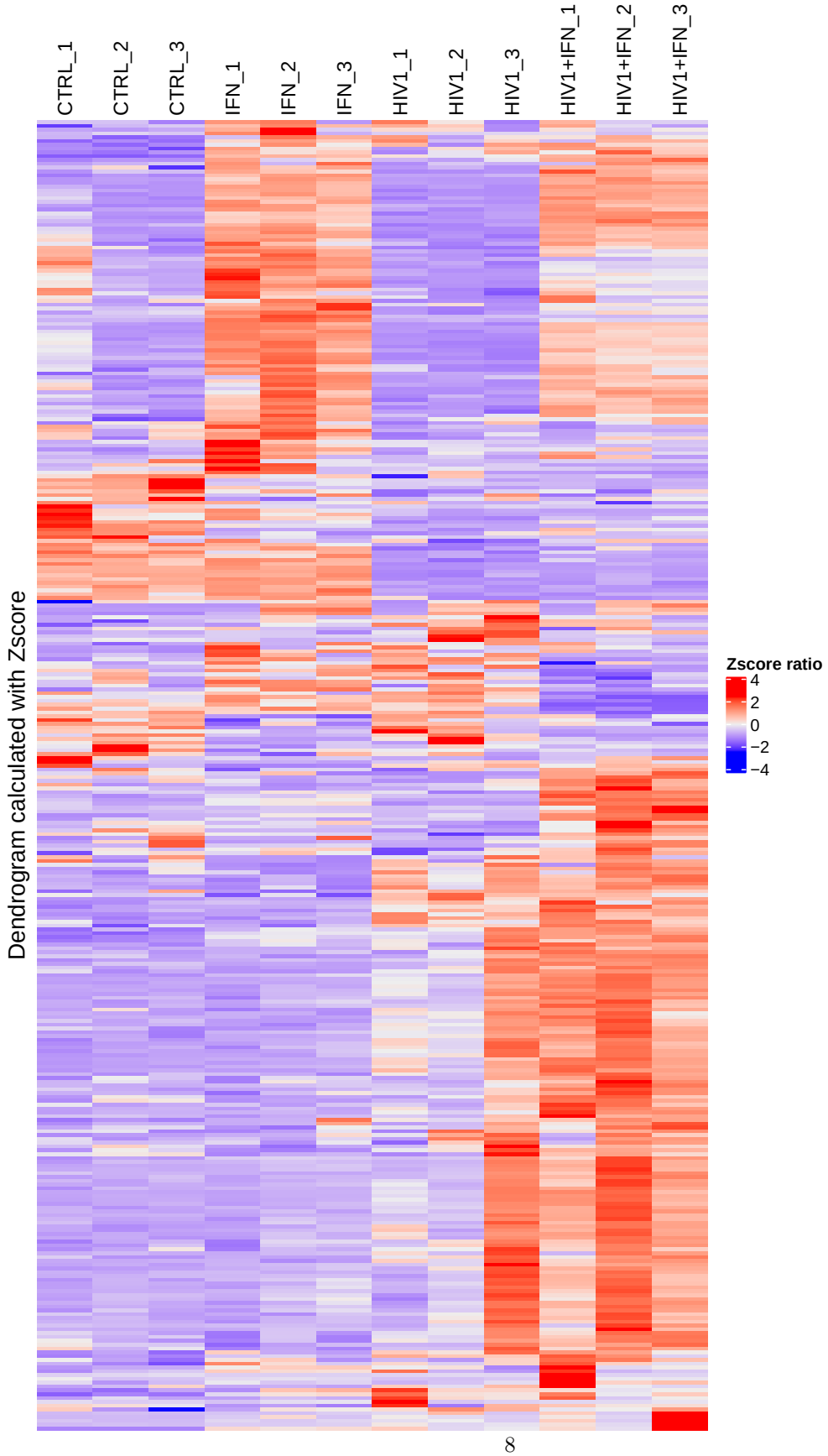
Single heatmap with all proteins (deregulated or not)



```
## pdf
##   2
```

```
## pdf
##   2
```

Single heatmap with only deregulated proteins



```
## pdf
##   2
```

```
## pdf
##   2
```

Heatmap of deregulated proteins in test *IFN vs Control*

```
## pdf
##   2
```

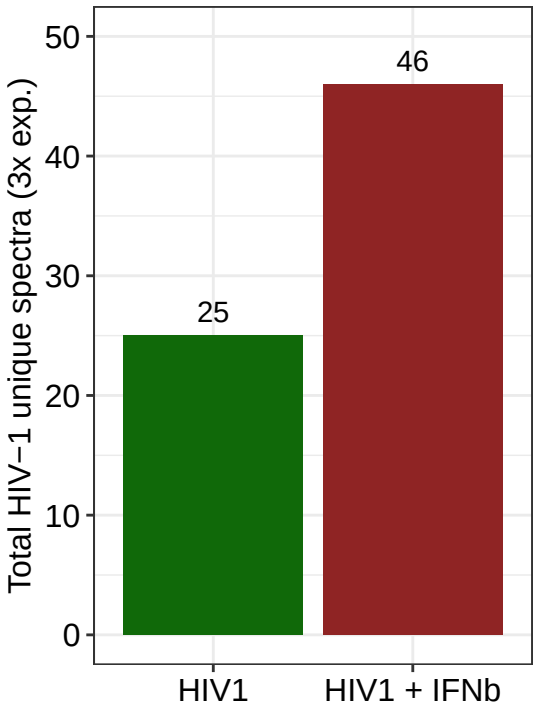
```
## pdf
##   2
```

Heatmap of deregulated proteins in test *HIV-1 vs Control*

```
## pdf
##   2
```

```
## pdf
##   2
```

10) HIV-1 peptides in the nuclear membrane



```r
interaction_hiv <- read.delim("Karen vs ULaval and inetraction with HIV-1 protein.txt", header = T, row
interactions <- interaction_hiv[interaction_hiv$X == "", -c(1, 3, 4)]

for (j in 2:ncol(interactions)) {
  for (i in 1:nrow(interactions)) {
    interactions[i, j] <- ifelse(is.na(interactions[i, j]), 0,
                                 ifelse(interactions[i, j] == "", 0, 1))
  }
  interactions[, j] <- as.numeric(interactions[, j])
}

melt_interactions <- melt(interactions, id = "U.laval.Accession")
melt_interactions <- melt_interactions[melt_interactions$value == 1,-3]
nodes <- data.frame(Protein_ID = c(levels(melt_interactions$variable), unique(melt_interactions$U.laval
                    Origin = c(rep("HIV-1", levels(melt_interactions$variable) %>% length),
                               rep("Human", unique(melt_interactions$U.laval.Accession) %>% length)),
                    Protein_name = c(levels(melt_interactions$variable),
                                     gene_names[gene_names$uniprot_id %in% melt_interactions$U.laval.Ac
names(melt_interactions) <- c("Human", "HIV-1")

write.table(nodes, "nodes_interactions.txt", quote = F, sep = "\t", eol = "\n", row.names = F, col.name
write.table(melt_interactions, "edges_interactions.txt", quote = F, sep = "\t", eol = "\n", row.names =
```