# DE plot

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```r
suppressMessages(library(readxl))
suppressMessages(library(tidyr))
suppressMessages(library(ggplot2))
suppressMessages(library(dplyr))
suppressMessages(library(EnhancedVolcano))
suppressMessages(library(pheatmap))
```

## loading function to save pheatmap as pdf
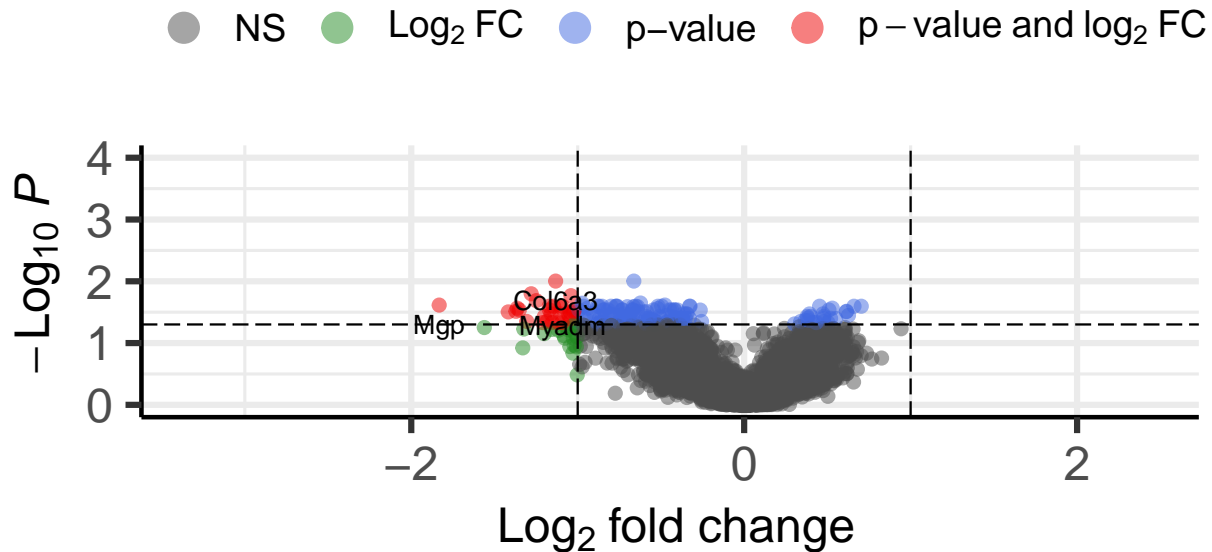
```r
source("save_pheatmap_pdf.R")
```

## Loading perilesional vs intralesional

### making volcano plot

```r
DE_perivsintra$padj <- as.numeric(DE_perivsintra$`Adjusted pvalue`)

EnhancedVolcano(DE_perivsintra, DE_perivsintra$`Target name`, x = "Log2", y = "padj", title= "DE-periles
```

# DE–perilesional vs intralesional

*EnhancedVolcano*



total = 19962 variables

```
#ggsave("volcanoplot/Volcano_perivsintra.pdf", width = 15, height = 10)
```

## Gene for Heatmap (in red in the volcanoplot)

```
gene_significant <- subset(DE_perivsintra, (Log2 > 1 | Log2< -1) & padj <=0.05)
gene_significant <- gene_significant$`Target name`
```

## load the annotation file from Q3 - publications

```
colData <- read_excel("../Data_Thomas/Q3 - publication.xlsx", sheet = "SegmentProperties")
colData <- as.data.frame(colData)
rownames(colData) <- colData$SegmentDisplayName
```

## Load the normalised count matrix and making the heatmap

```
Q3_publication <- read_excel("../Data_Thomas/Q3 - publication.xlsx", sheet = "TargetCountMatrix")
Q3_publication <- as.data.frame(Q3_publication)
rownames(Q3_publication) <- Q3_publication$TargetName
Q3_publication$TargetName <- NULL

rld <- log2(Q3_publication)

df <- as.data.frame(colData[,c("SlideName","Group")])
Heatmap_perivsintra <- pheatmap(rld[gene_significant,], cluster_rows=FALSE, show_rownames=T,
         cluster_cols=T, annotation_col=df, scale = "row", main = "Genes differentially expressed in Per
```

# fferentially expressed in Perilesional over intralesionnal
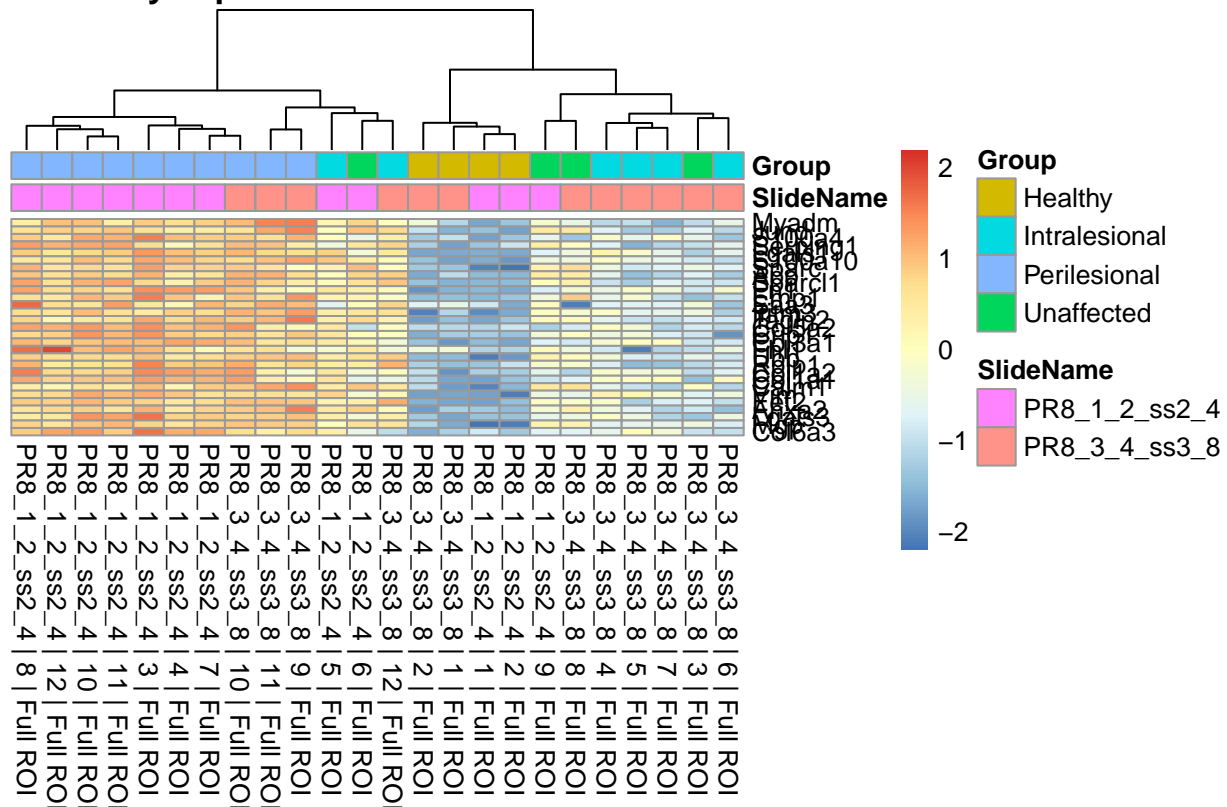


```
#save_pheatmap_pdf(Heatmap_perivsintra, "Heatmap/Heatmap_perivsintra.pdf", width = 10, height = 10)
```
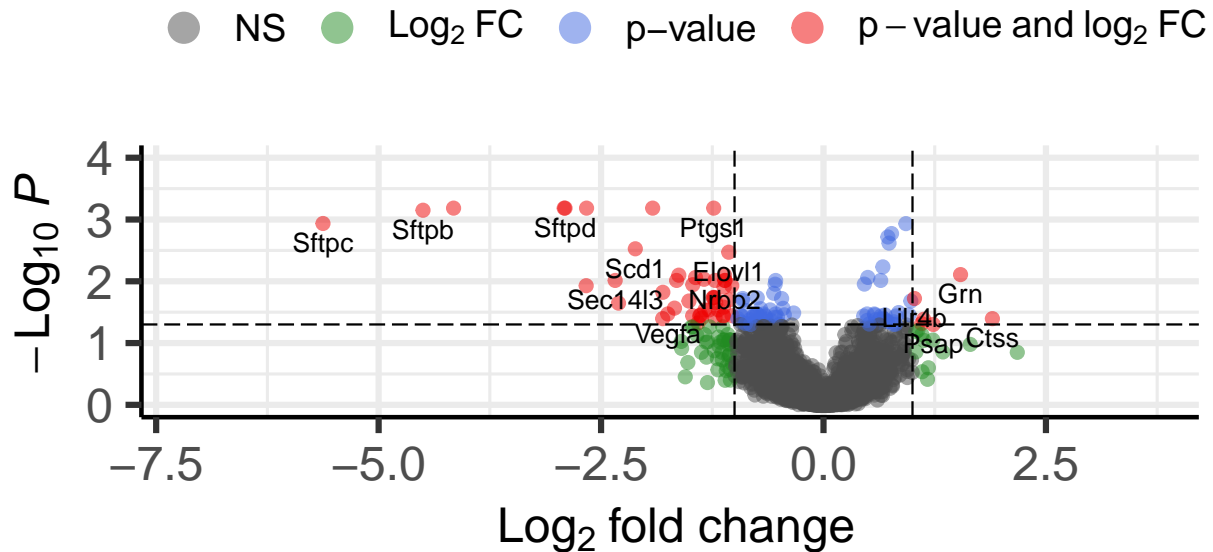
## Loading unaffected vs intralesionnal

```
DE_UnaffectedvsIntra <- read_excel("DE-Unaffected-Intra.xlsx", sheet = "VolcanoPlot", range = "C7:H1996)
DE_UnaffectedvsIntra$padj <- as.numeric(DE_UnaffectedvsIntra$`Adjusted pvalue`)

EnhancedVolcano(DE_UnaffectedvsIntra, DE_UnaffectedvsIntra$`Target name`, x = "Log2", y = "padj", title=
```

# DE−unaffected vs intralesionnal

*EnhancedVolcano*



total = 19962 variables

```
#ggsave("volcanoplot/Volcano_UnaffectedvsIntra.pdf", width = 15, height = 10)
```

## Heatmap !! je ne prends pas tous les gènes significatif

```
gene_significant <- subset(DE_UnaffectedvsIntra, (Log2 > 1 | Log2< -1) & padj <=0.05)
gene_significant_pos <- gene_significant[gene_significant$Log2 >=1,]
gene_significant_neg <- gene_significant[gene_significant$Log2 <= -1,]
gene_significant_neg <- gene_significant_neg[order(gene_significant_neg$Log2),]
gene_toplot <- c(gene_significant_neg$`Target name`[1:20], gene_significant_pos$`Target name`)


Heatmap_UnaffectedvsIntra <- pheatmap(rld[gene_toplot,], cluster_rows=FALSE, show_rownames=T,
        cluster_cols=T, annotation_col=df, scale = "row", main = "Genes differentially expressed in una
```

# ifferentially expressed in unaffected over intralesionnal



```
#save_pheatmap_pdf(Heatmap_UnaffectedvsIntra, "Heatmap/Heatmap_UnaffectedvsIntra.pdf", width = 10, heig
```

## DE unaffected vs perilesional

```
DE_UnaffectedvsPeri <- read_excel("DE-Unaffected-Peri.xlsx", sheet = "VolcanoPlot", range = "C7:H19969")
DE_UnaffectedvsPeri$padj <- as.numeric(DE_UnaffectedvsPeri$`Adjusted pvalue`)

EnhancedVolcano(DE_UnaffectedvsPeri, DE_UnaffectedvsPeri$`Target name`, x = "Log2", y = "padj", title= "
```

# DE−unaffected vs perilesional

*EnhancedVolcano*
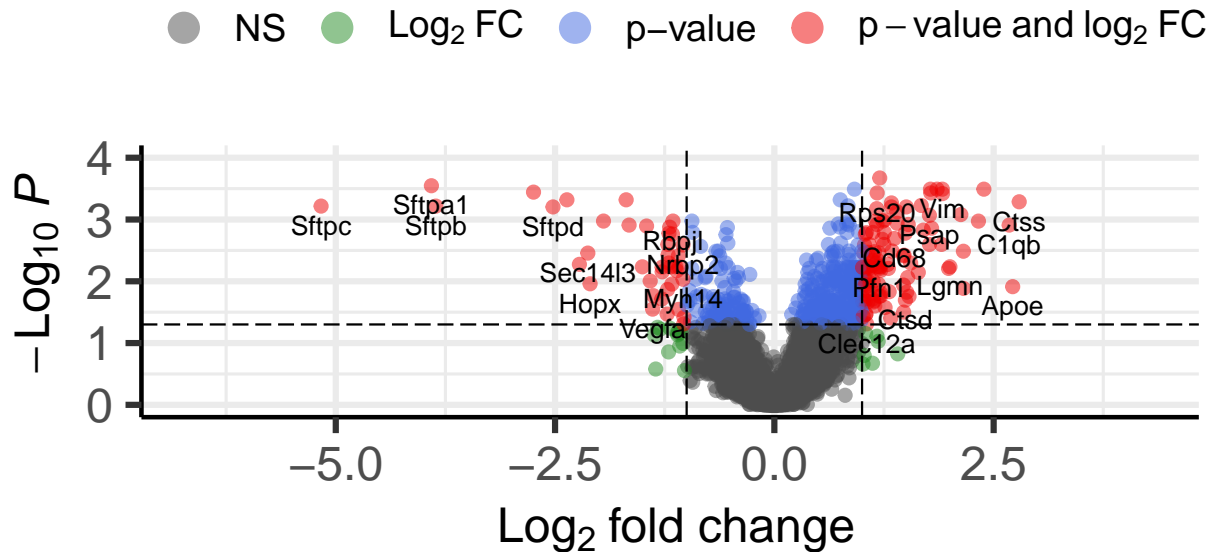


total = 19962 variables

```
#ggsave("volcanoplot/Volcano_UnaffectedvsPeri.pdf", width = 15, height = 10)
```

**Heatmap !! je ne prends pas tous les gènes significatif**

```
gene_significant <- subset(DE_UnaffectedvsPeri, (Log2 > 1 | Log2< -1) & padj <=0.05)
gene_significant_pos <- gene_significant[gene_significant$Log2 >=1,]
gene_significant_pos <- gene_significant_pos[order(gene_significant_pos$Log2, decreasing = T),]
gene_significant_neg <- gene_significant[gene_significant$Log2 <= -1,]
gene_significant_neg <- gene_significant_neg[order(gene_significant_neg$Log2),]

gene_toplot <- c(gene_significant_neg$`Target name`[1:20], gene_significant_pos$`Target name`[1:20])


Heatmap_UnaffectedvsPeri <- pheatmap(rld[gene_toplot,], cluster_rows=FALSE, show_rownames=T,
        cluster_cols=T, annotation_col=df, scale = "row", main = "Genes differentially expressed in una
```

# differentially expressed in unaffected over perilesional
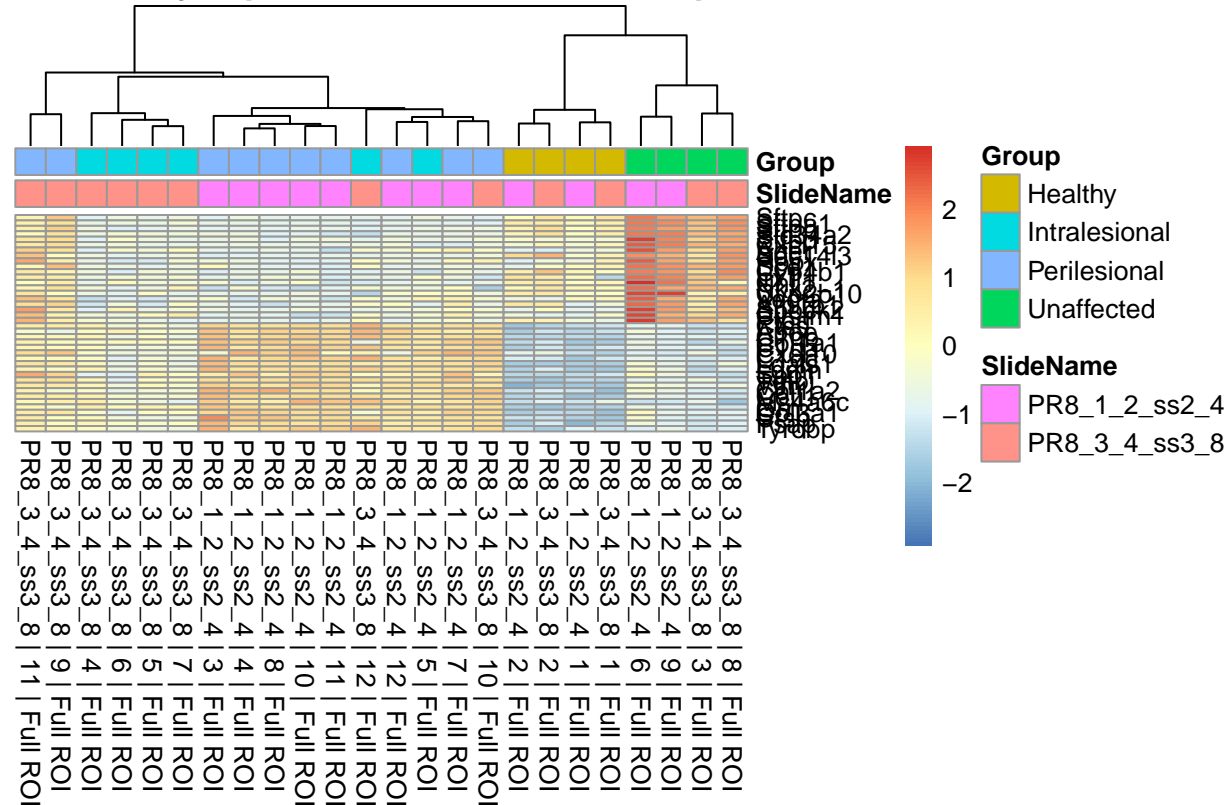


```
#save_pheatmap_pdf(Heatmap_UnaffectedvsPeri, "Heatmap/Heatmap_UnaffectedvsPeri.pdf", width = 10, height
```