


```
head (annotation_col)
```

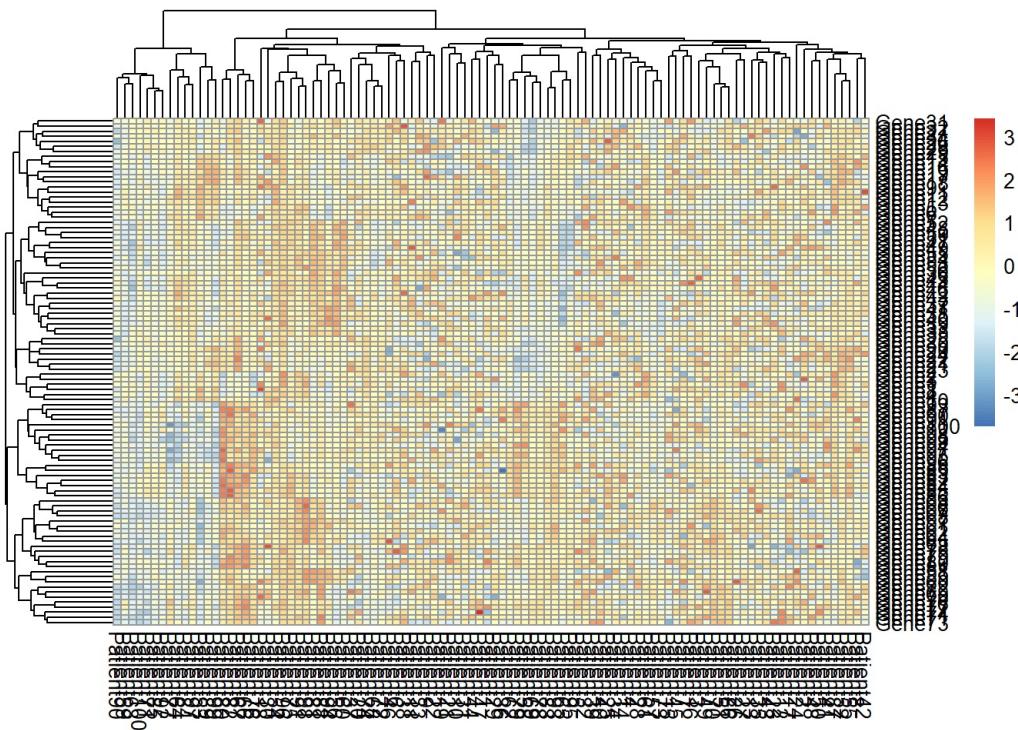
```
##      Exposure Type
## Patient1    X=0 T-cell
## Patient2    X=0 T-cell
## Patient3    X=0 B-cell
## Patient4    X=0 B-cell
## Patient5    X=0 B-cell
## Patient6    X=0 T-cell
```

```
head (annotation_row)
```

```
##      Pathway
## Gene1     1
## Gene2     1
## Gene3     1
## Gene4     1
## Gene5     1
## Gene6     1
```

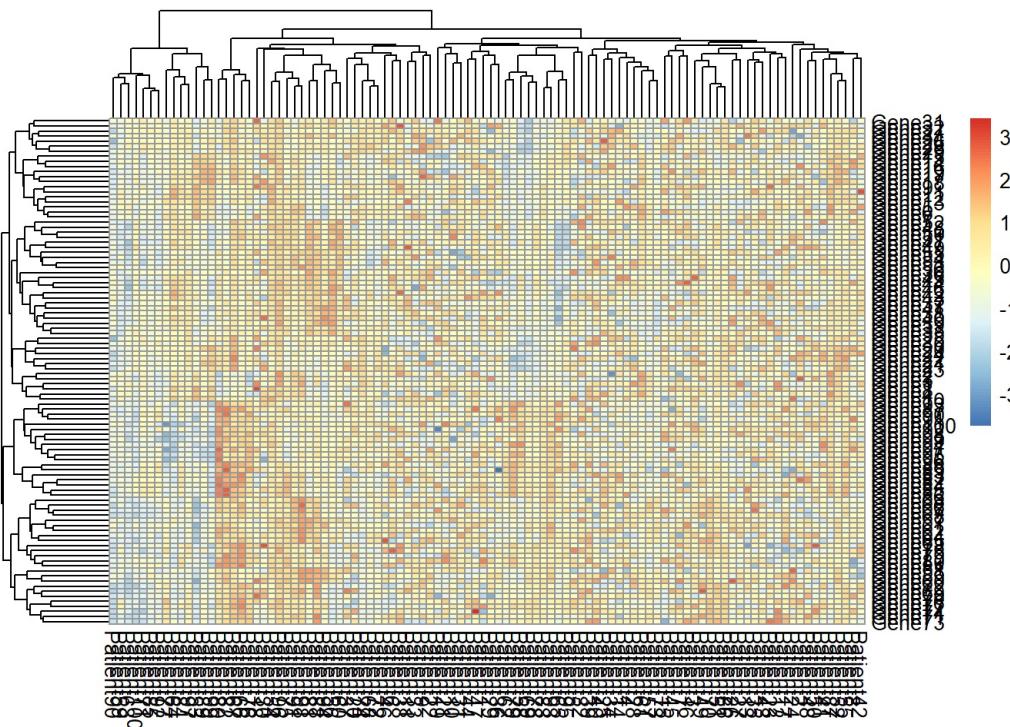
CREAMOS MAPA DE CALOR. Plotting with pheatmap!

```
pheatmap(genes)
```



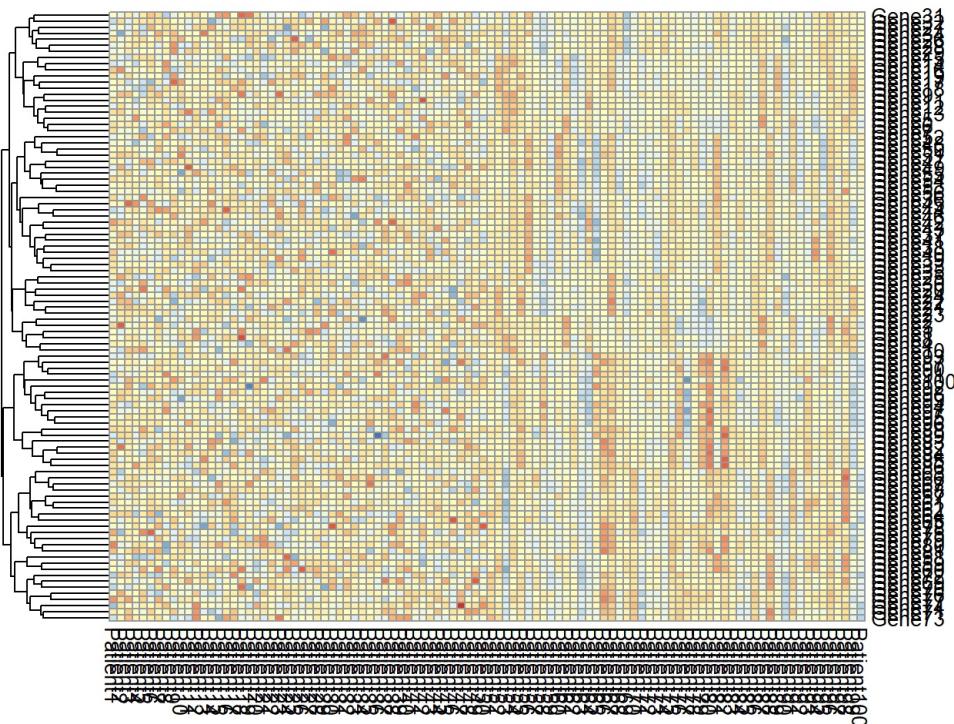
MODIFICAMOS MAPA DE CALOR. change font. Default is clustering rows and columns

```
pheatmap(genes, fontsize=6)
```



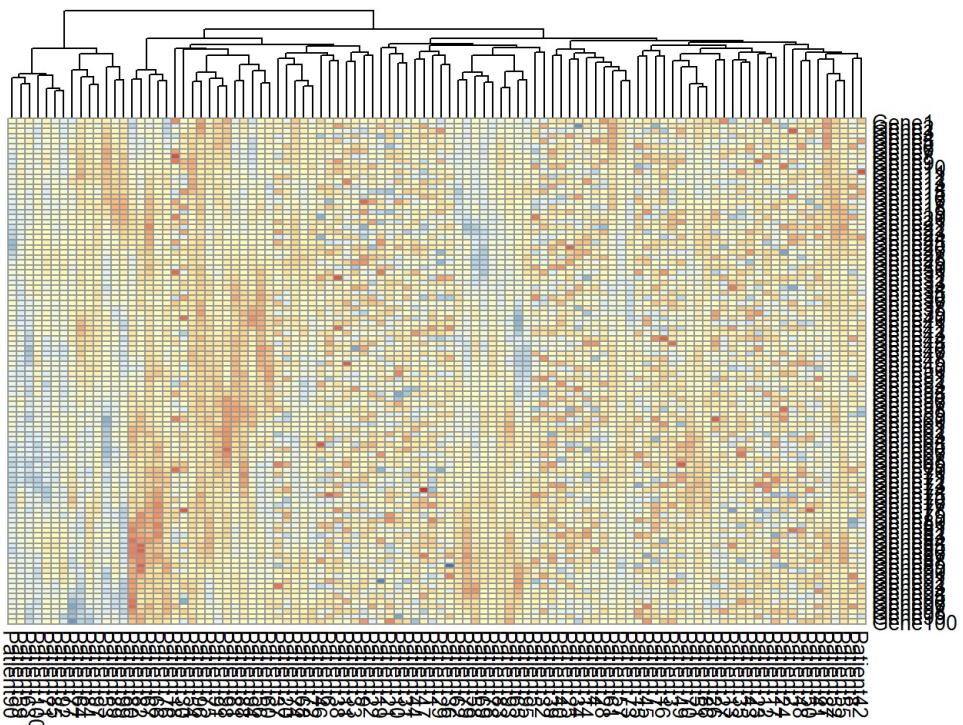
QUITAMOS ENDOGRAMA DEL EJE DE LAS X. cluster by gene - groups of similar genes—LOS GENES ESTAN EN LOS RENGLONES. POR DEFAULT CLUSTEA LOS RENGLONES

```
pheatmap(genes, frontsize=6, cluster_rows = T, cluster_cols = F)
```



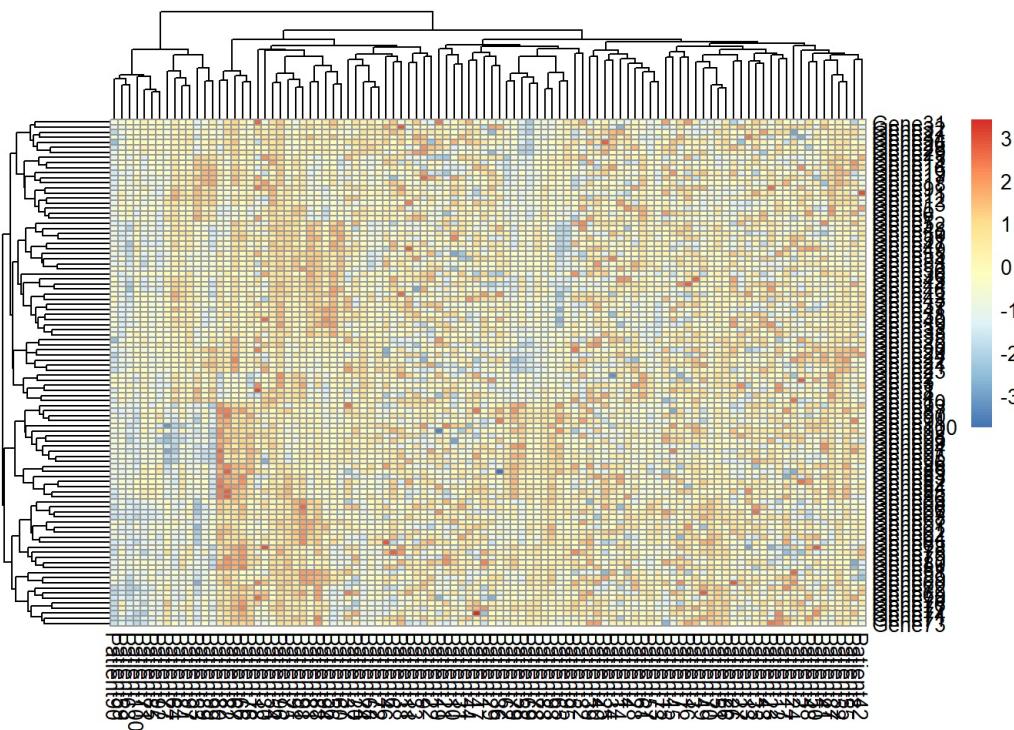
ENDOGRAMA DEL EJE DE LAS Y- cluster by patient - groups of similar patients.DEBES HACER QUE LAS COLUMNAS SE TRANFORMEN A RENGLONES

```
pheatmap(genes, frontsize=6, cluster_rows = F, cluster_cols = T)
```



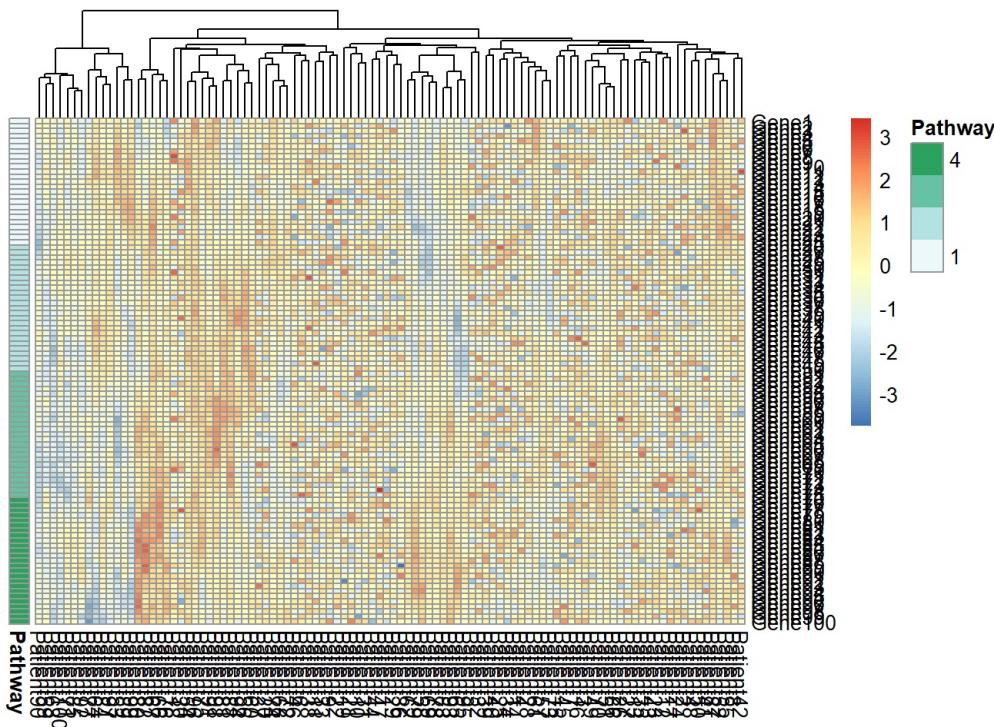
AMBOS ENDOGRAMAS COMO LA VERSIÓN ORIGINAL usually order by both

```
pheatmap(genes, frontsize=6, cluster_rows = T, cluster_cols = T)
```



seeing some patterns emerge - but what do they mean? Great time to add annotation to our plot

```
pheatmap(genes, frontsize=6, cluster_rows = F, cluster_cols = T, annotation_row = annotation_row)
```



add to row first, see that genes are clustering according to the pathways they belong to

```
pheatmap(genes, frontsize=6, cluster_rows = F, cluster_cols = T, annotation_row = annotation_row, annotation_col=annotation_col)
```

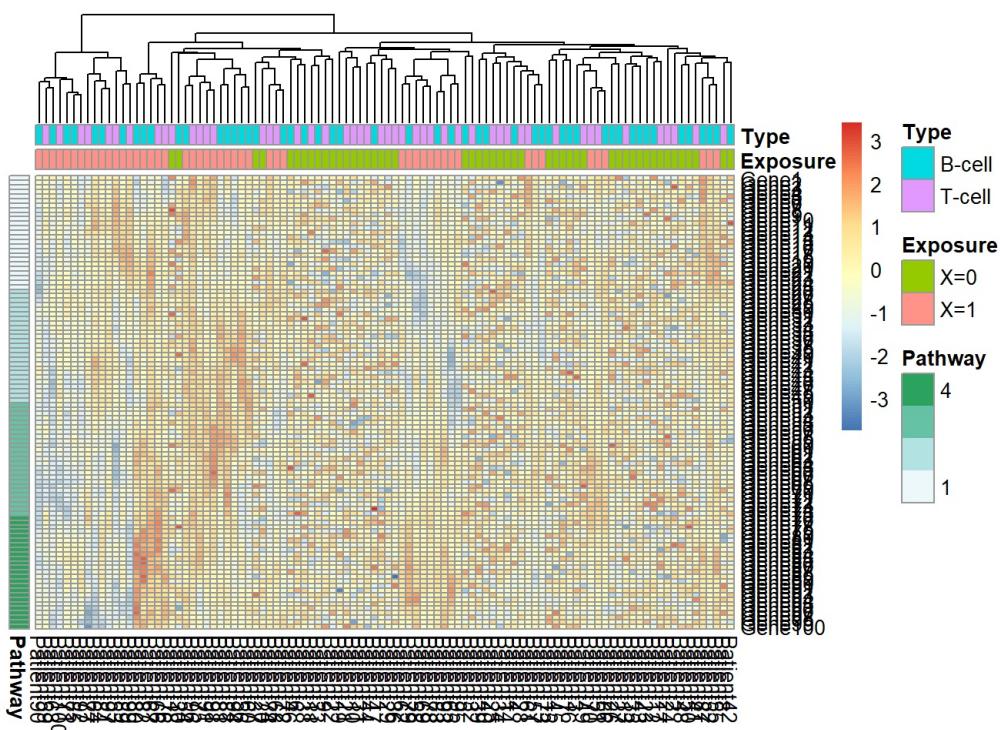
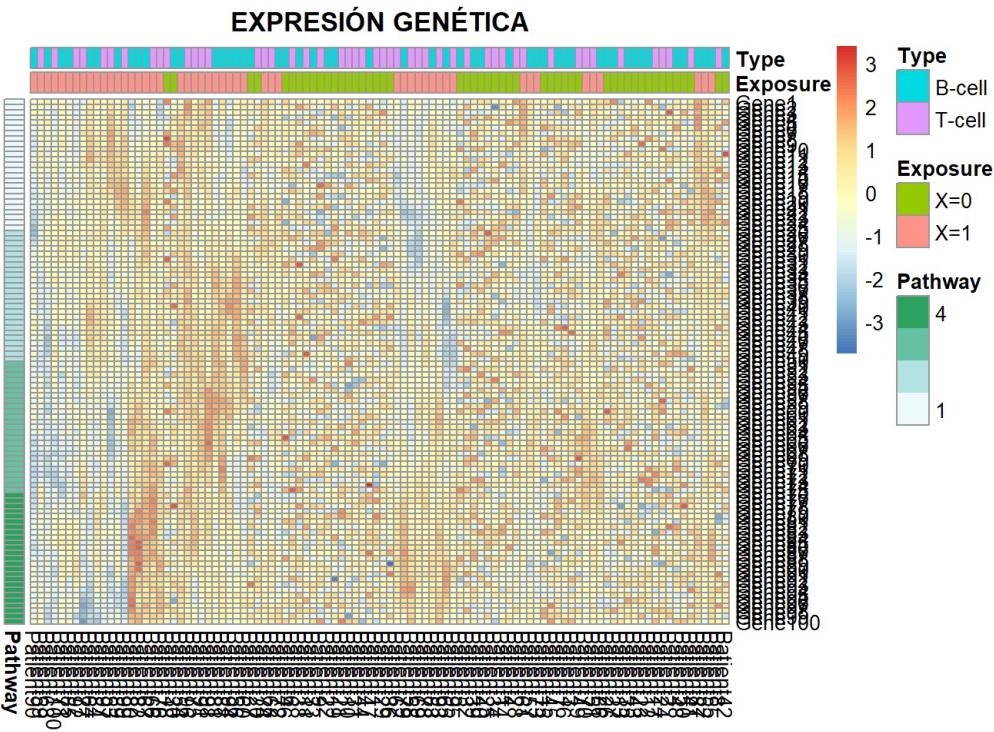


GRAFICO COMPLETO G1 AGREGANDO UN TITULO

```
pheatmap(genes, frontsize=6, cluster_rows = F, cluster_cols = T, annotation_row = annotation_row, annotation_col=annotation_col, treeheight_row = 0, treeheight_col = 0, main = "EXPRESIÓN GENÉTICA")
```

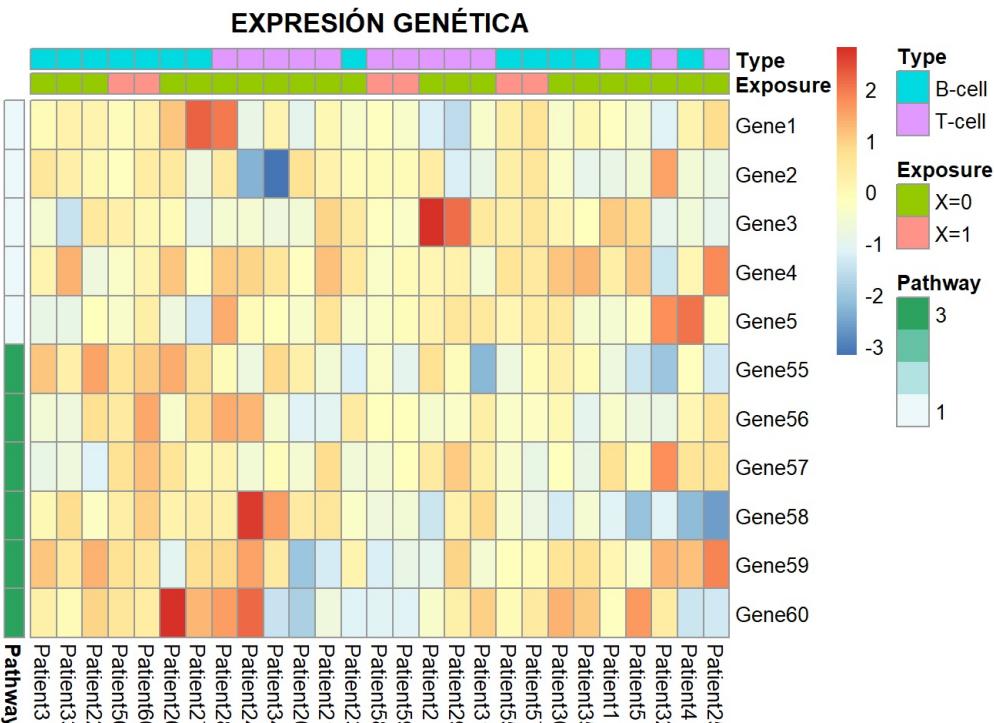


TOMANDO UNA PARTE DE LA MUESTRA ORIGINAL GRAFICO QUITANDO CLUSTERS (ARBOLES DE AGRUPACIÓN-DENDROGRAMAS)
take a smaller subset

```
SUB <- genes [c(1:5, 55:60), c(1:5, 20:35, 55:60)]
```

con subset 1 (COPIAR G1)

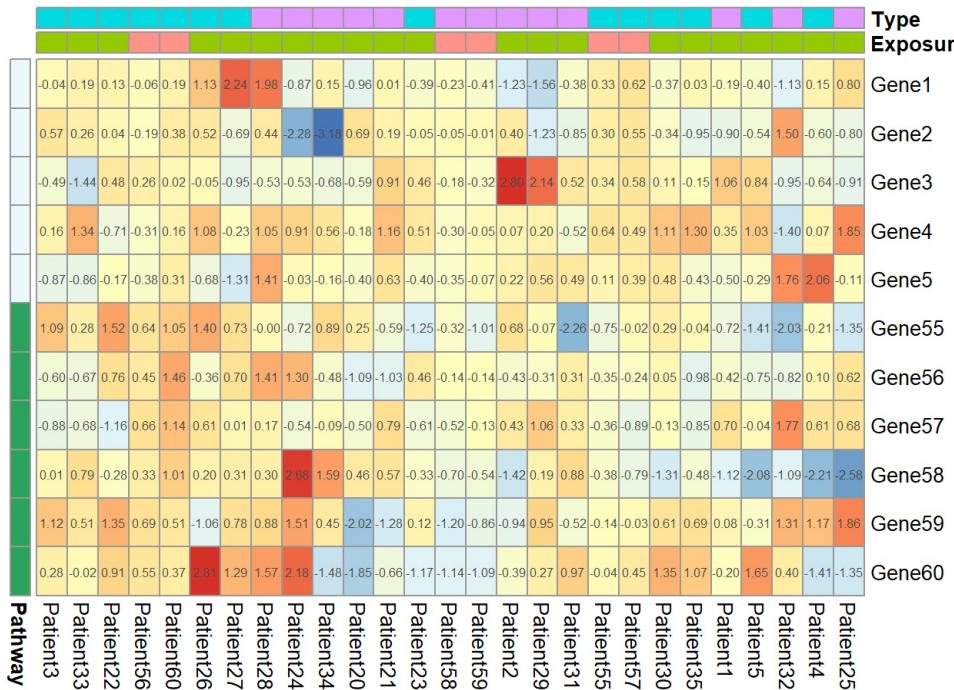
```
heatmap(SUB, frontsize=6, cluster_rows = F, cluster_cols = T, annotation_row = annotation_row, annotation_col=annotation_col, treeheight_row = 0, treeheight_col = 0, main = "EXPRESIÓN GENÉTICA")
```



con subset 2 – DESPLEGAR VALORES

```
heatmap(SUB, frontsize=6, cluster_rows = F, cluster_cols = T, annotation_row = annotation_row, annotation_col=annotation_col, treeheight_row = 0, treeheight_col = 0, main = "EXPRESIÓN GENÉTICA", frontsize=8, annotation_legend = F, display_numbers = T, fontsize_number = 6)
```

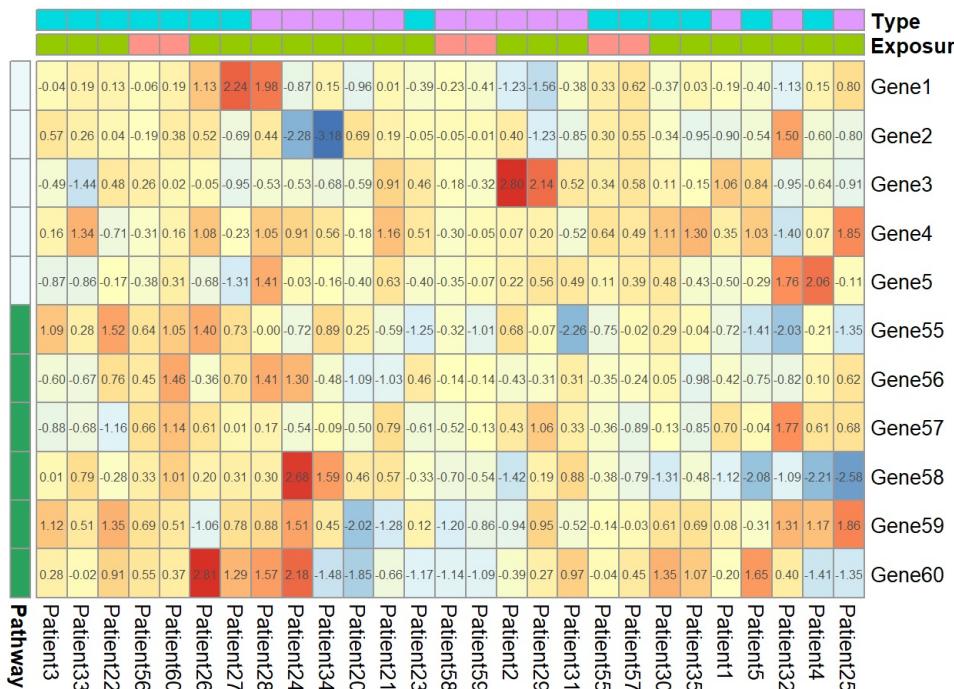
EXPRESIÓN GENÉTICA



con color

```
pheatmap(SUB, frontsize=6, cluster_rows = F, cluster_cols = T, annotation_row = annotation_row, annotation_col= annotation_col, treeheight_row = 0, treeheight_col = 0, main = "EXPRESIÓN GENÉTICA", frontsize=8, annotation_legend = F, display_numbers = T, fontsize_number = 6)
```

EXPRESIÓN GENÉTICA



```
viridis, library(viridis) pheatmap(SUB, frontsize=6, cluster_rows = F, cluster_cols = T, annotation_row = annotation_row, annotation_col= annotation_col, treeheight_row = 0, treeheight_col = 0, main = "EXPRESIÓN GENÉTICA", frontsize=8, annotation_legend = F, display_numbers = T, fontsize_number = 6, col= viridis(option = "plasma")) (6)
```

ELEMENTOS ADICIONALES DISTANCIA ENTRE LOS GENES

```
dist(SUB)
```

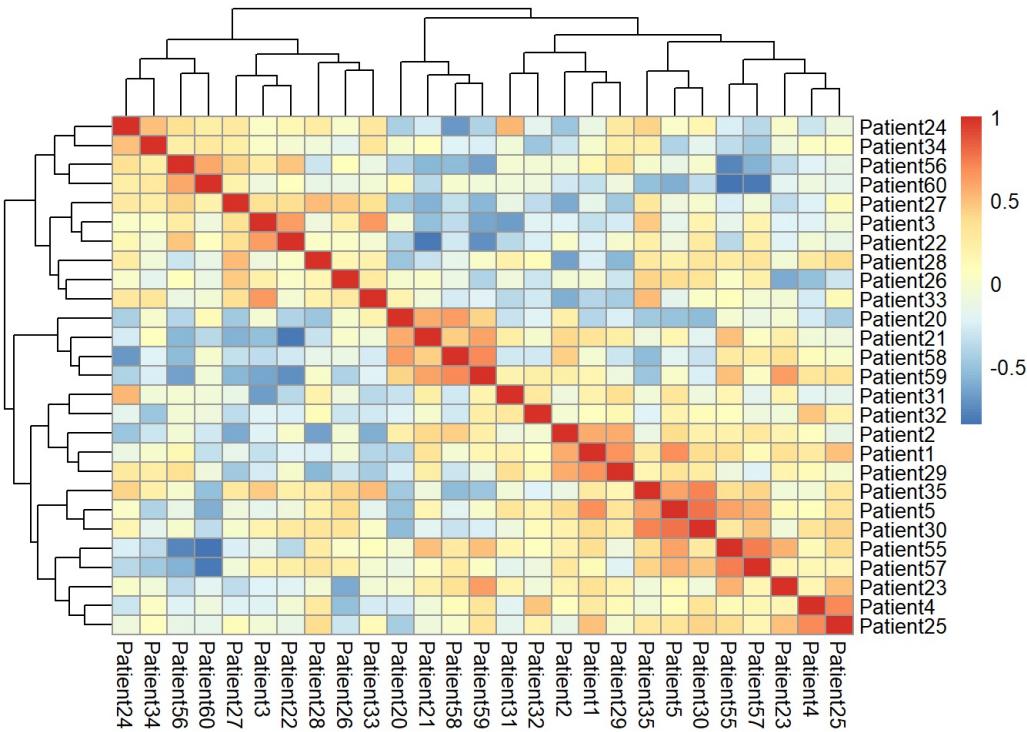
```

##          Gene1    Gene2    Gene3    Gene4    Gene5    Gene55   Gene56   Gene57
## Gene2  6.506125
## Gene3  7.823569 7.021725
## Gene4  5.253565 7.649124 6.516104
## Gene5  6.411847 5.977640 5.967513 6.184570
## Gene55 5.703940 6.969997 7.096321 6.837653 7.534618
## Gene56 4.544832 6.723925 6.542745 5.805165 5.150859 6.028094
## Gene57 6.124657 6.069362 5.550487 6.004035 3.881691 7.122986 5.209746
## Gene58 7.417422 8.796956 8.462521 7.874145 8.030439 6.777444 6.292359 7.669524
## Gene59 6.189649 8.293720 7.977707 6.115718 5.821355 7.317126 4.835770 6.104449
## Gene60 6.623226 8.133474 7.665999 6.837342 7.659167 7.569942 6.373711 7.296198
##           Gene58   Gene59
## Gene2
## Gene3
## Gene4
## Gene5
## Gene55
## Gene56
## Gene57
## Gene58
## Gene59 8.312043
## Gene60 7.813793 6.992657

```

CORRELACIÓN DE LOS DATOS DE PACIENTES

```
pheatmap(cor(SUB))
```



MATRIZ TRANSPUESTA Y MAPA NUEVO DE NO GENES

```

trans <- t(SUB)
head(trans)

```

```

##          Gene1    Gene2    Gene3    Gene4    Gene5    Gene55   Gene56   Gene57
## Patient1 -0.19141902 -0.8978632  1.0639177  0.35247721 -0.5016748 -0.7221485
## Patient2 -1.23415247  0.3954955  2.7956449  0.07475244  0.2161688  0.6753315
## Patient3 -0.04346178  0.5669153 -0.4903151  0.15824275 -0.8670291  1.0926214
## Patient4  0.14572108 -0.5960268 -0.6446058  0.06590853  2.0592507 -0.2133837
## Patient5 -0.40172052 -0.5403446  0.8419138  1.03019320 -0.2852306 -1.4104579
## Patient20 -0.95908196  0.6888356 -0.5930431 -0.18213253 -0.4013906  0.2480023
##           Gene56    Gene57    Gene58    Gene59    Gene60
## Patient1 -0.41944303  0.69780284 -1.12468089  0.08419999 -0.1987275
## Patient2 -0.43072699  0.42919602 -1.42110465 -0.94132773 -0.3889914
## Patient3 -0.59700018 -0.88436496  0.01066352  1.11876069  0.2811201
## Patient4  0.09977285  0.61070630 -2.20755068  1.17203816 -1.4117939
## Patient5 -0.74547611 -0.04041247 -2.07971045 -0.30758847  1.6546370
## Patient20 -1.09100971 -0.49770640  0.45695793 -2.01806030 -1.8450509

```

```
pheatmap(cor(trans))
```

