



**UNIVERSIDAD AUTÓNOMA DEL ESTADO DE HIDALGO**

**INSTITUTO DE CIENCIAS ECONÓMICO ADMINISTRATIVAS**

**DOCTORADO EN CIENCIAS ECONÓMICO ADMINISTRATIVAS**

**MATERIA: TEMAS SELECTOS 1 “ESTADÍSTICA PARA LAS CIENCIAS  
ECONÓMICO ADMINISTRATIVAS”**

**TERCER SEMESTRE**

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**LAB 34**  
**PRETTY HEAT MAPS CON R**

# Lab34 (Markdown)

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Alumna: Alejandra Guzmán Dimas PRETTYHEATMAP EN R

Prerrequisitos: Instalar paquetería “pheatmap”: install.packages(“pheatmap”) Llamar a la biblioteca “pheatmap”

```
library(pheatmap)
```

Convertir archivo de datos a matriz

```
genes=as.matrix(  
  read.csv("/Users/alejandraguzmandimas/Desktop/heatmap_data.csv",  
    sep=",",  
    header=T,  
    row.names = 1))
```

Importar archivo columnas

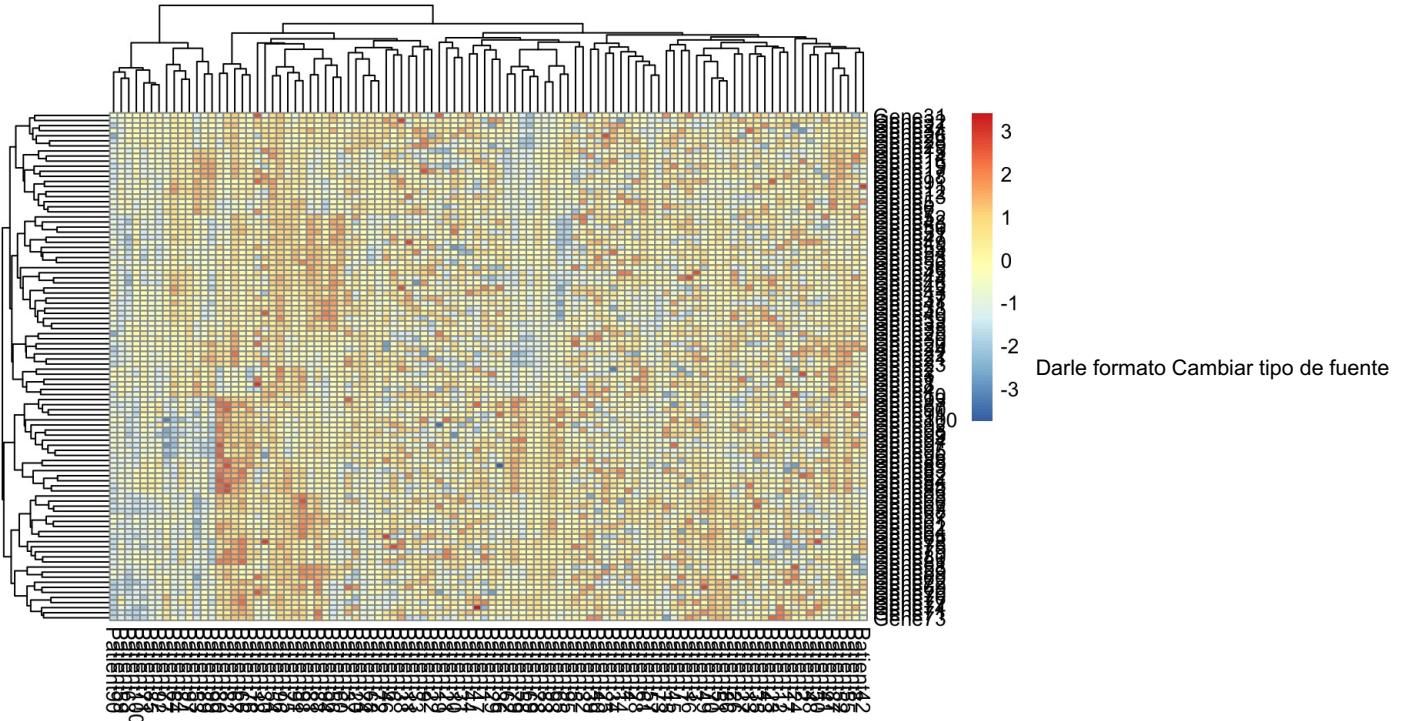
```
annotation_col=read.csv("/Users/alejandraguzmandimas/Desktop/annotation_col.csv", header=T, row.names = 1)
```

Importar archivo filas

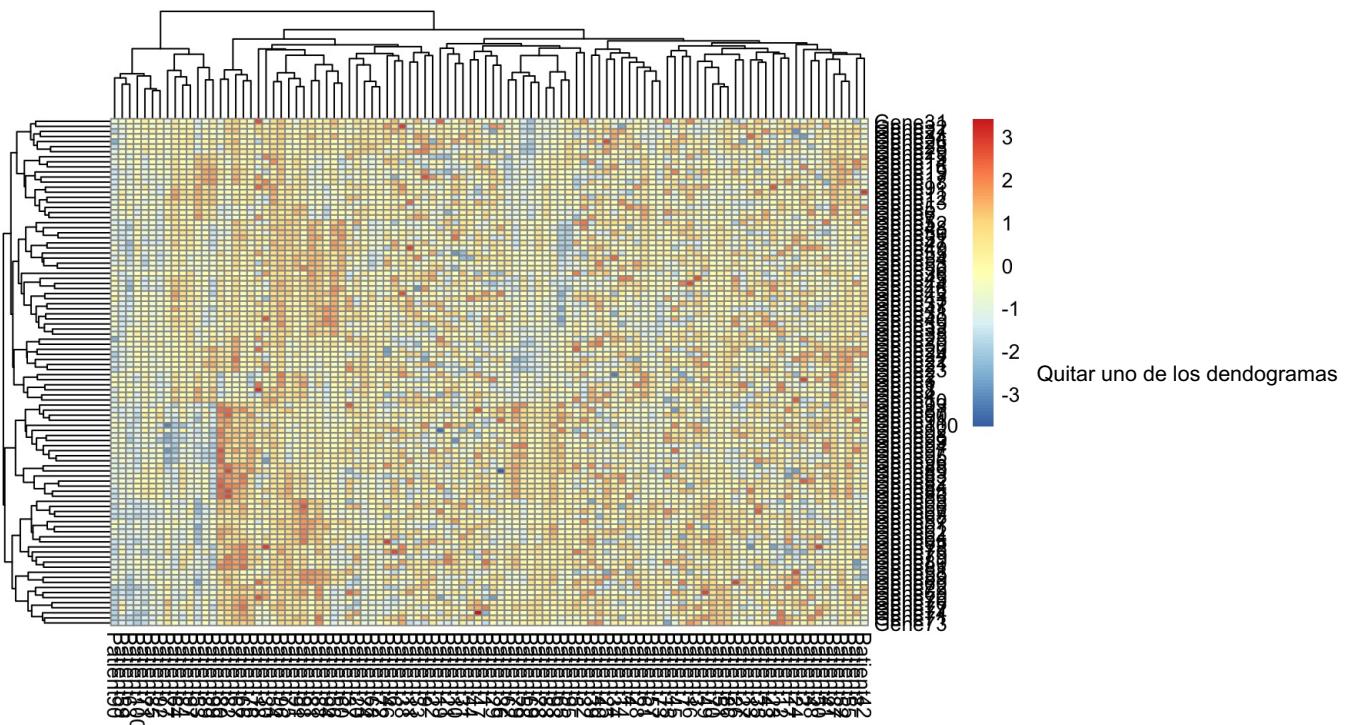
```
annotation_rows=read.csv("/Users/alejandraguzmandimas/Desktop/annotation_row.csv", header=T, row.names = 1)
```

Dibujar heatmap

```
pheatmap(genes)
```

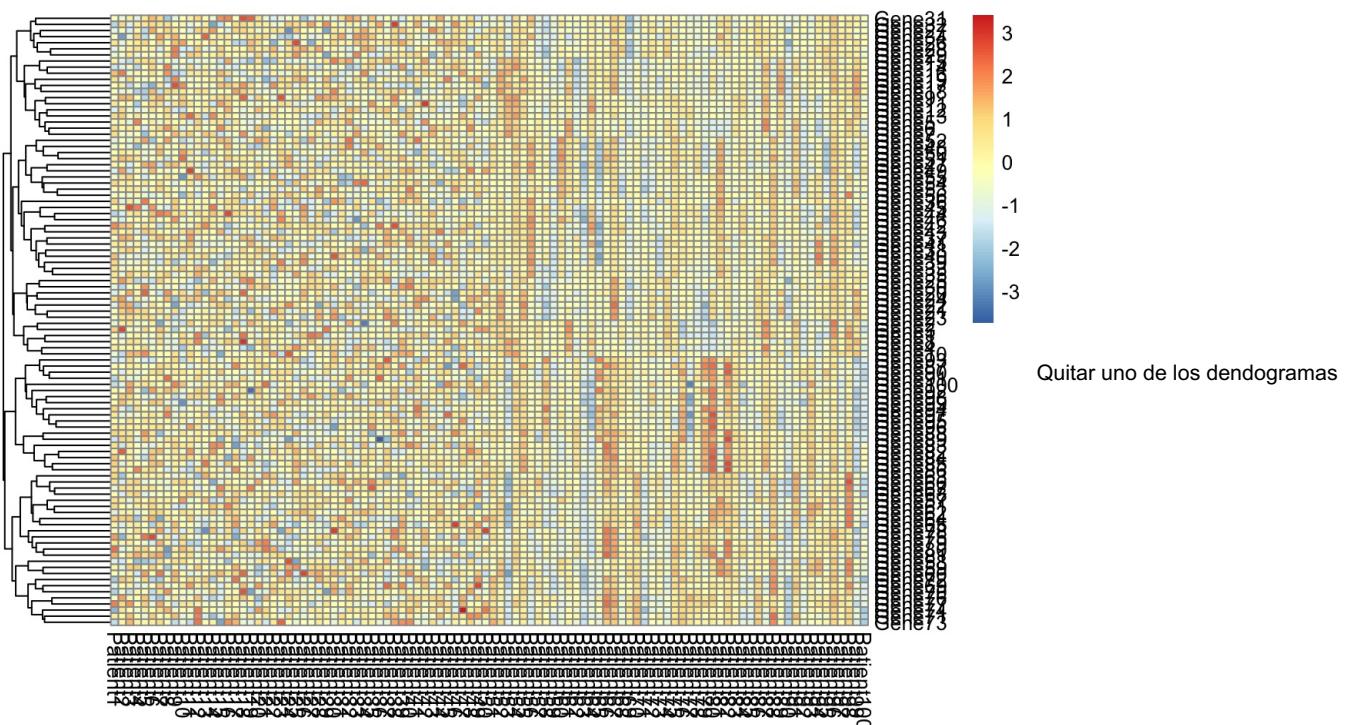


```
pheatmap(genes, fontsize=6)
```



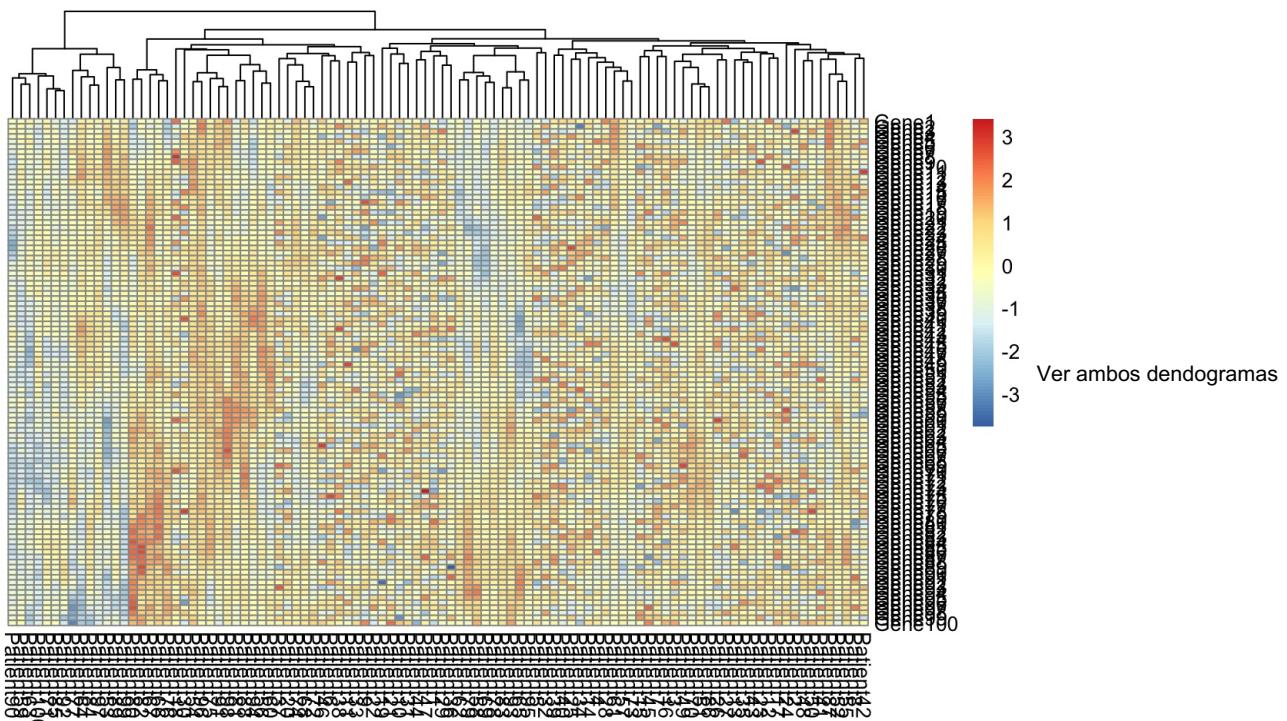
(pacientes)

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

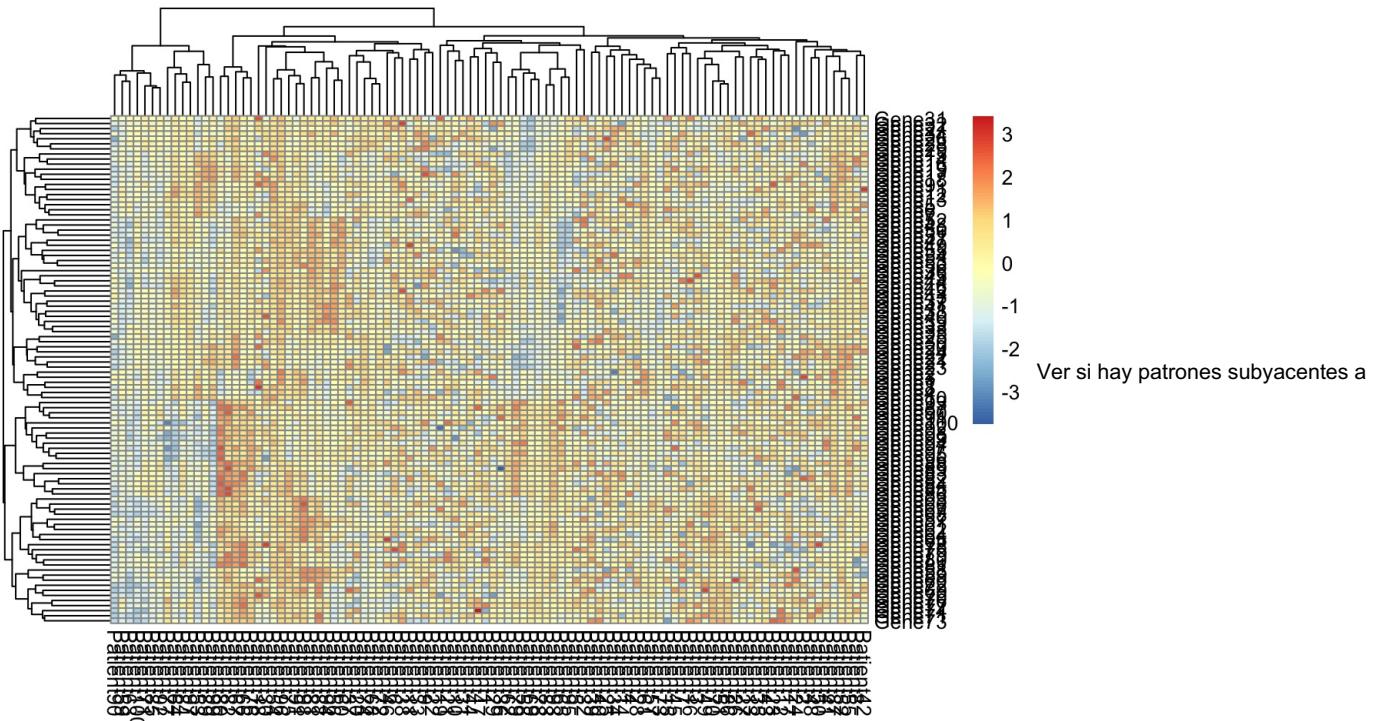


(vertical)

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

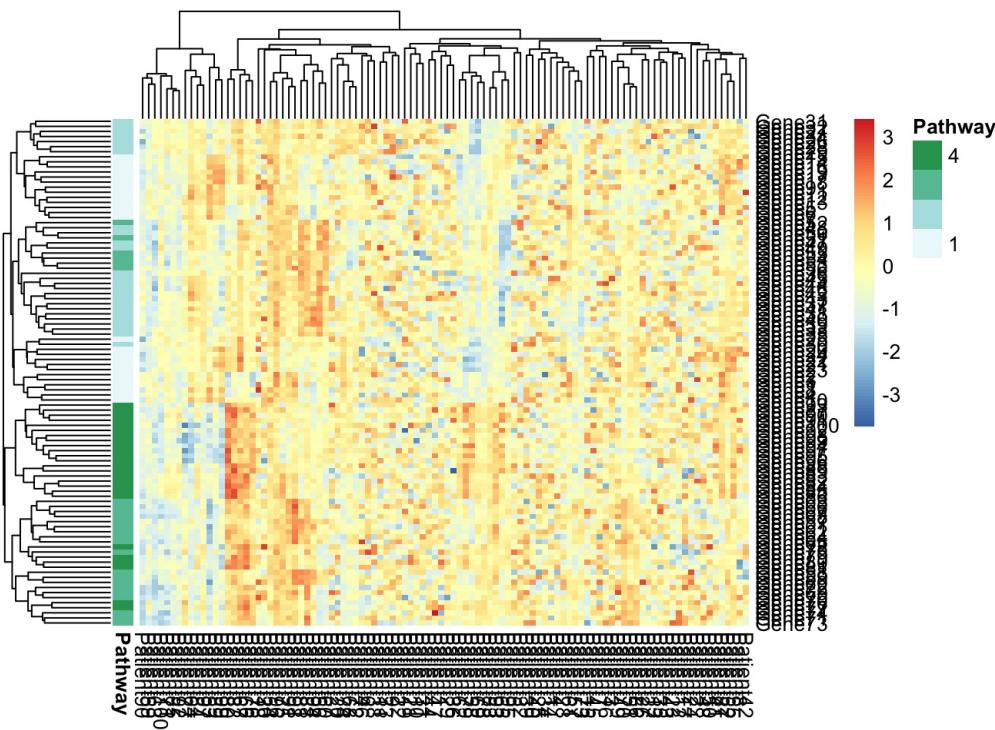


```
pheatmap(genes, frontsize=6, cluster_rows=T, cluster_cols = T)
```



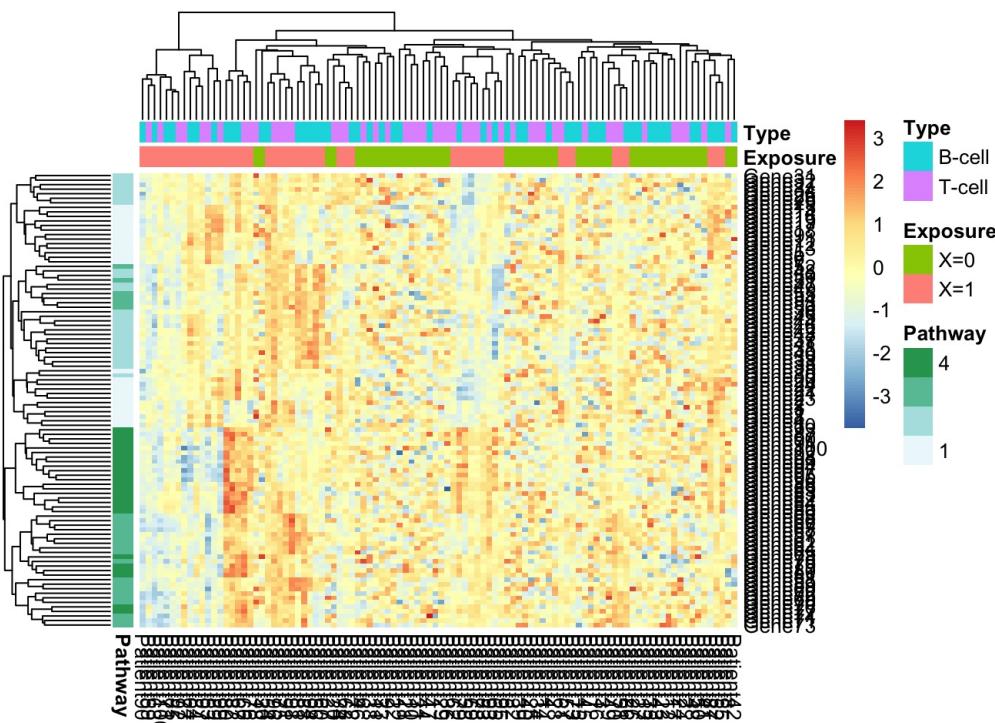
las anotaciones de las columnas o renglones

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

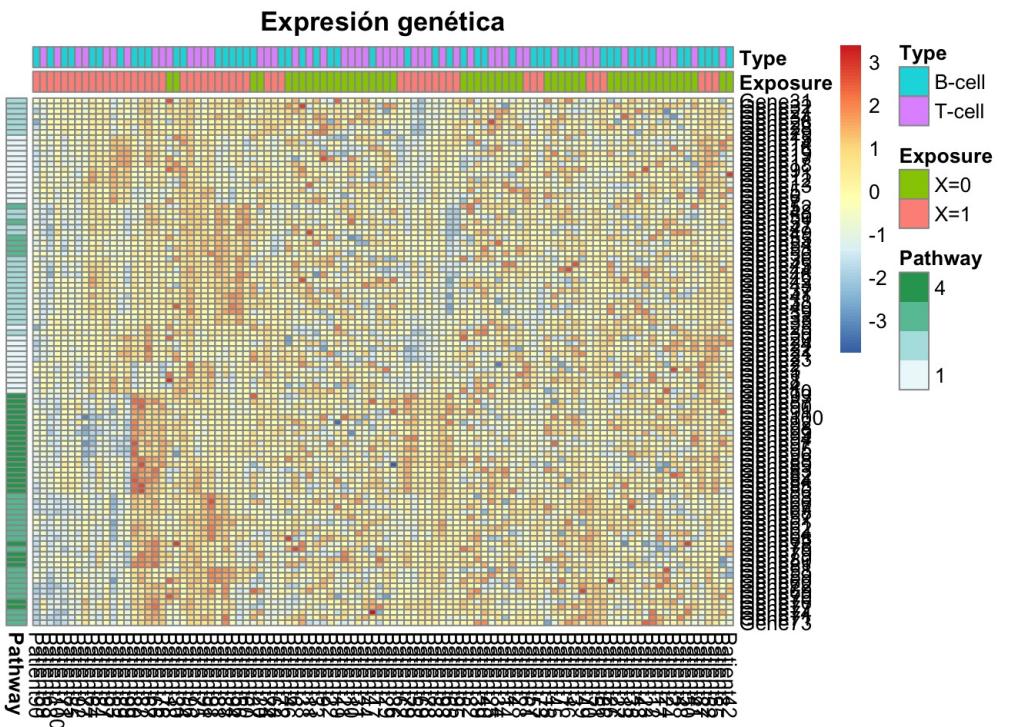


columnas

```
heatmap(genes, fontsize=6, cluster_rows=T, cluster_cols = T, annotation_row = annotation_rows, annotation_col=annotation_col)
```



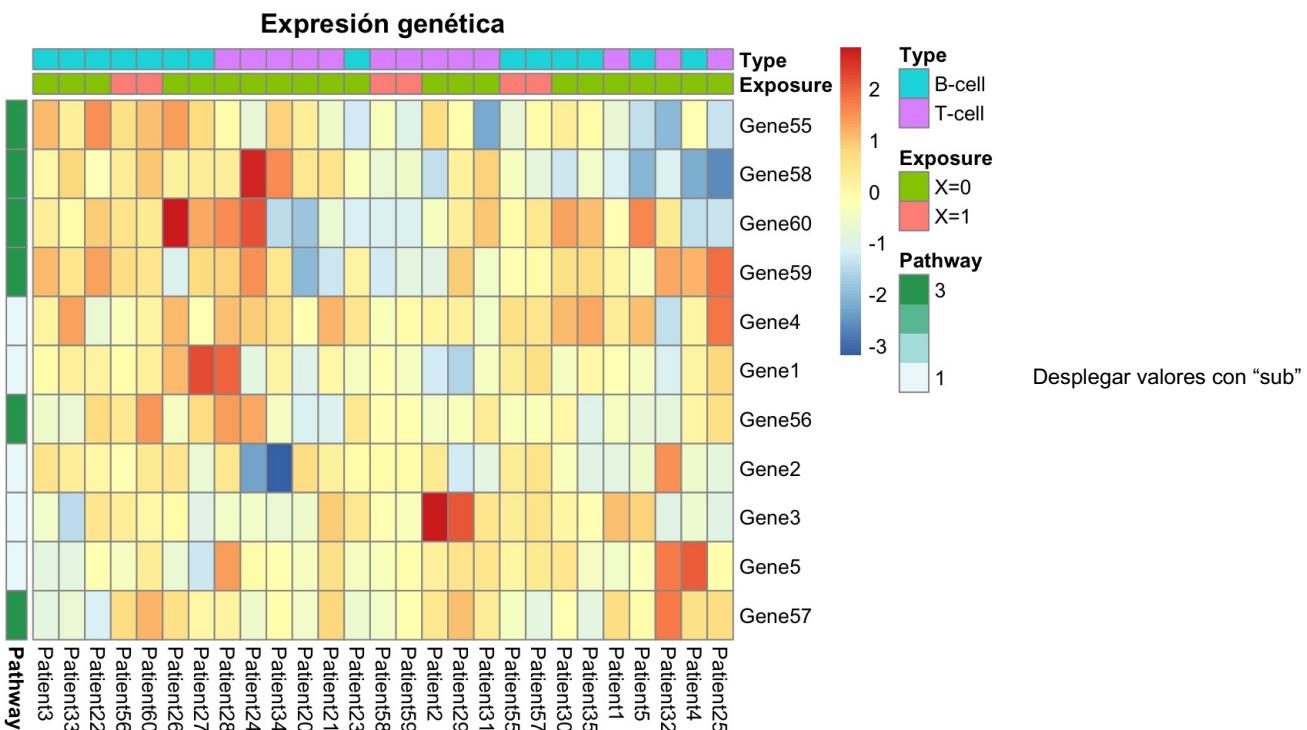
```
heatmap(genes, fontsize=6, cluster_rows=T, cluster_cols = T, annotation_row = annotation_rows, annotation_col=annotation_col, treeheight_row = 0, treeheight_col = 0, main="Expresión genética")
```



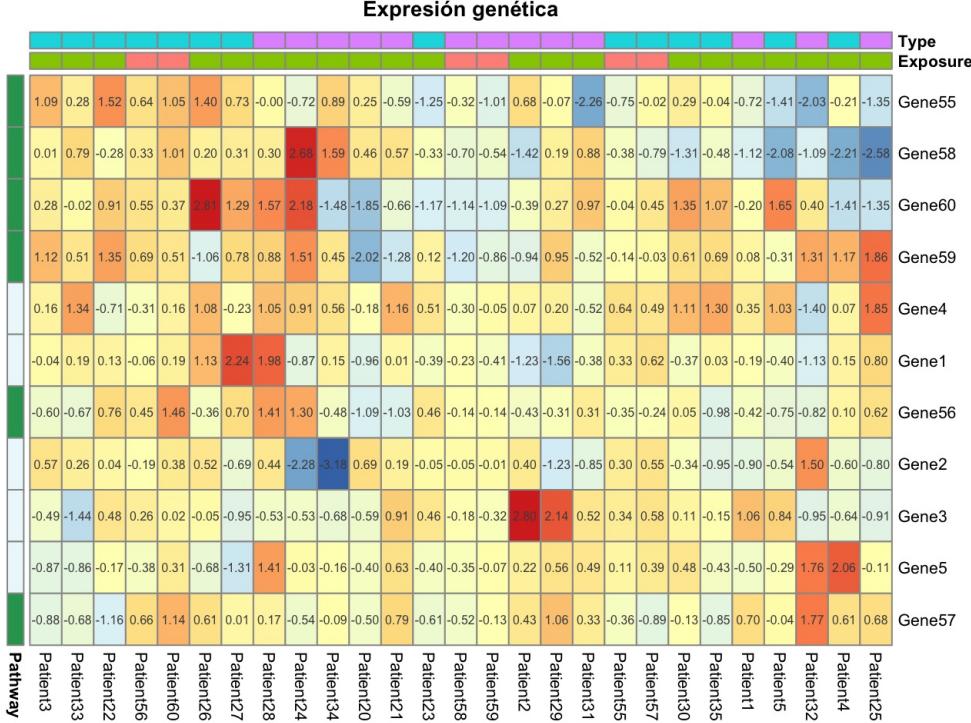
```
sub=genes[c(1:5, 55:60), c(1:5,20:35, 55:60)]
```

Generar mapa de calor del subconjunto llamado "sub"

```
pheatmap(sub, frontsize=6, cluster_rows=T, cluster_cols = T, annotation_row = annotation_rows, annotation_col=annotation_col, treeheight_row = 0, treeheight_col = 0, main="Expresión genética")
```



```
pheatmap(sub, frontsize=6, cluster_rows=T, cluster_cols = T, annotation_row = annotation_rows, annotation_col=annotation_col, treeheight_row = 0, treeheight_col = 0, main="Expresión genética", fontsize = 8, annotation_legend = FALSE, display_numbers = T, fontsize_number = 6)
```



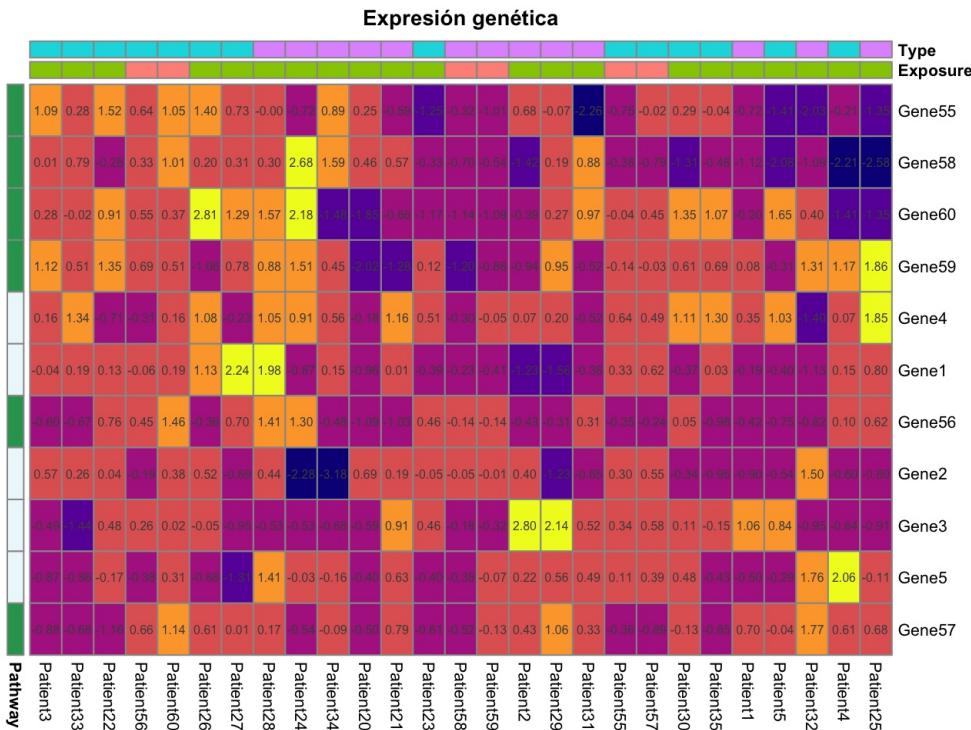
`install.packages("viridis")` Llamar a la biblioteca "viridis"

```
library(viridis)
```

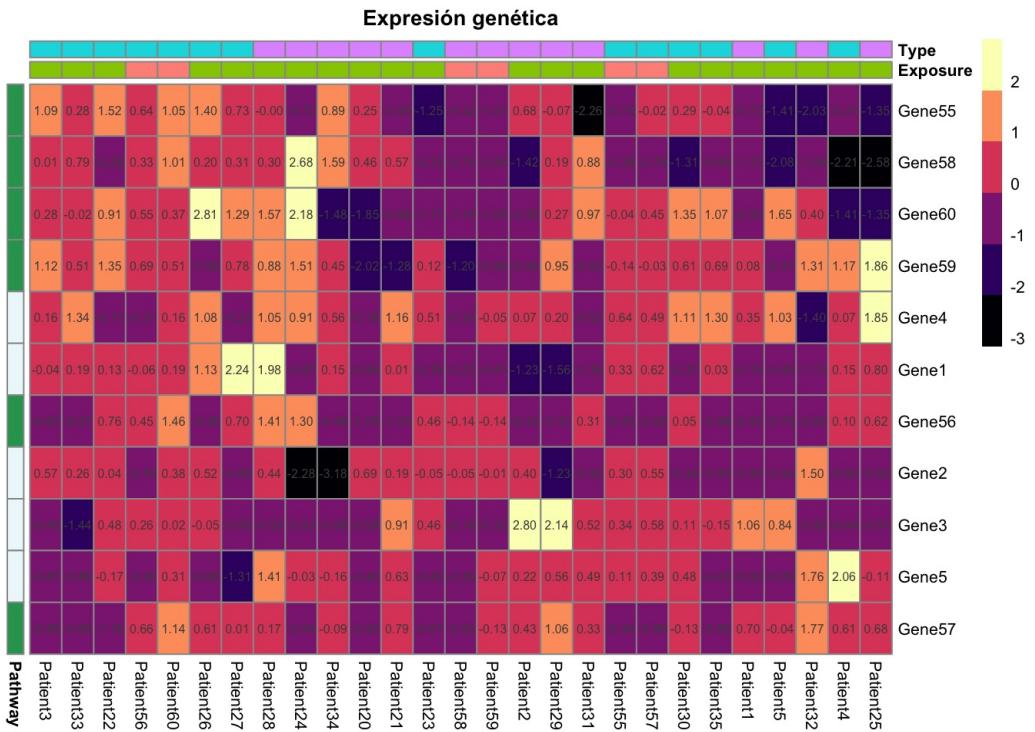
```
## Loading required package: viridisLite
```

Ocupar paletas para visualizar cómo cambia nuestro mapa de calor

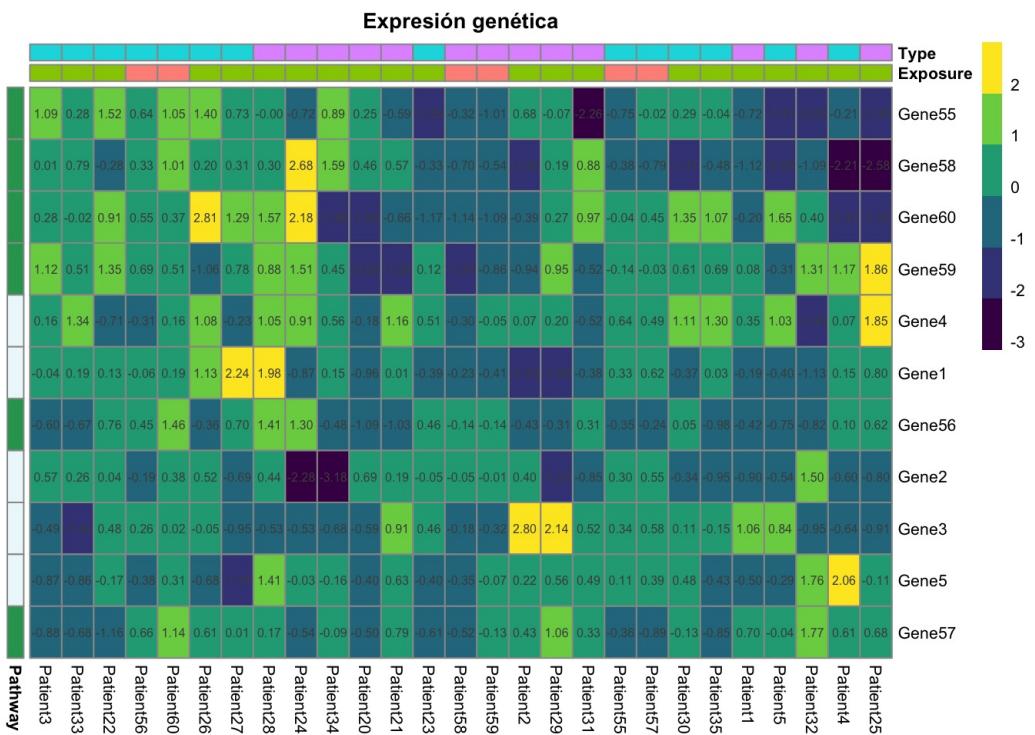
```
heatmap(sub, frontsize=6, cluster_rows=T, cluster_cols = T, annotation_row = annotation_rows, annotation_col=annotation_col, treeheight_row = 0, treeheight_col = 0, main="Expresión genética", fontsize = 8, annotation_legend = FALSE, display_numbers = T, fontsize_number = 6, col=viridis_pal(option= "plasma")(6))
```



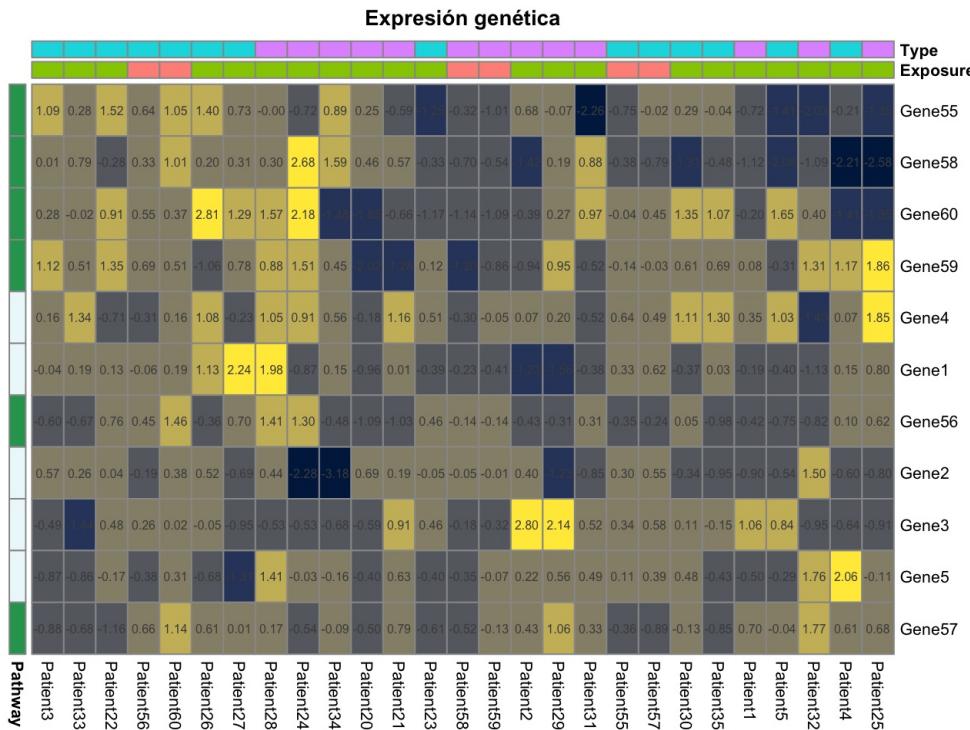
```
heatmap(sub, frontsize=6, cluster_rows=T, cluster_cols = T, annotation_row = annotation_rows, annotation_col=annotation_col, treeheight_row = 0, treeheight_col = 0, main="Expresión genética", fontsize = 8, annotation_legend = FALSE, display_numbers = T, fontsize_number = 6, col=viridis_pal(option= "magma")(6))
```



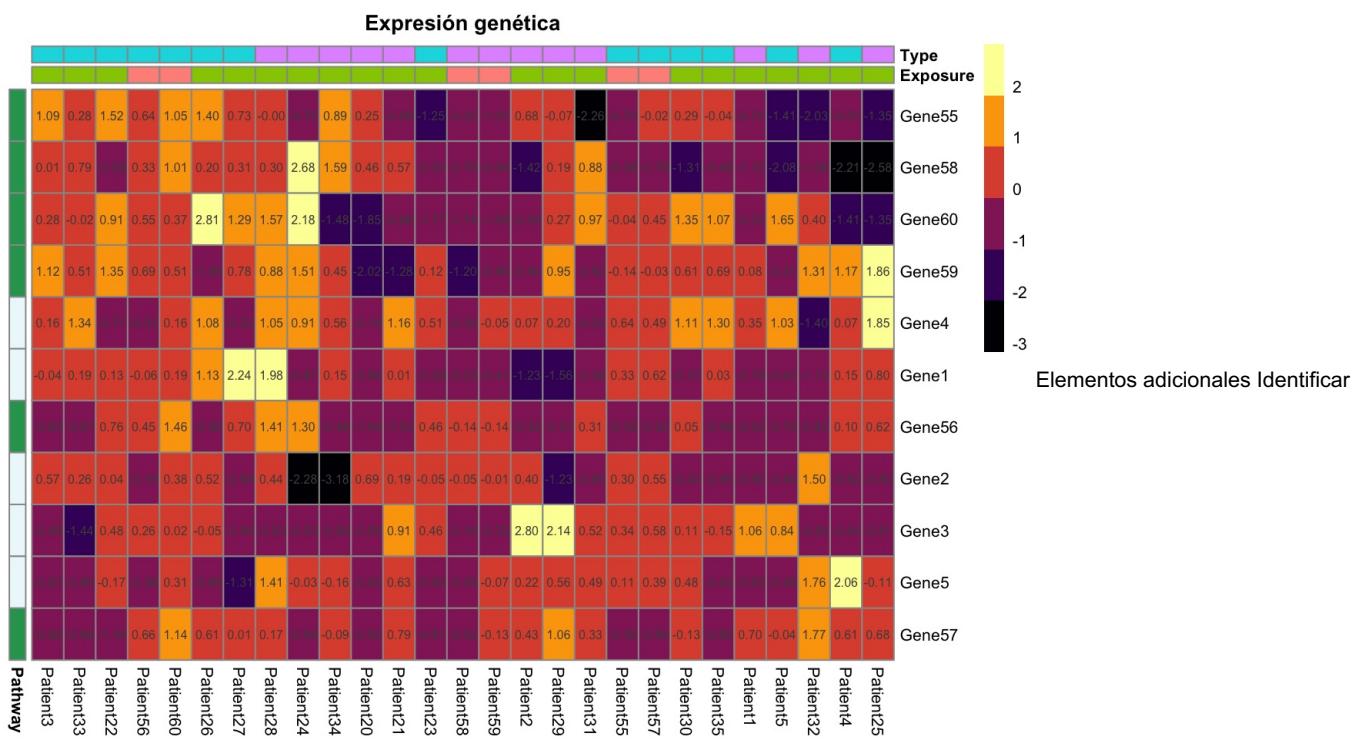
```
pheatmap(sub, frontsize=6, cluster_rows=T, cluster_cols = T, annotation_row = annotation_rows, annotation_col=annotation_col, treeheight_row = 0, treeheight_col = 0, main="Expresión genética", fontsize = 8, annotation_legend = FALSE, display_numbers = T, fontsize_number = 6, col=viridis_pal(option= "viridis")(6))
```



```
pheatmap(sub, frontsize=6, cluster_rows=T, cluster_cols = T, annotation_row = annotation_rows, annotation_col=annotation_col, treeheight_row = 0, treeheight_col = 0, main="Expresión genética", fontsize = 8, annotation_legend = FALSE, display_numbers = T, fontsize_number = 6, col=viridis_pal(option= "cividis")(6))
```



```
heatmap(sub, fontsize=6, cluster_rows=T, cluster_cols = T, annotation_row = annotation_rows, annotation_col=annotation_col, treeheight_row = 0, treeheight_col = 0, main="Expresión genética", fontsize = 8, annotation_legend = FALSE, display_numbers = T, fontsize_number = 6, col=viridis_pal(option= "inferno")(6))
```



Elementos adicionales Identificar

distancias entre genes

```
dist(sub)
```

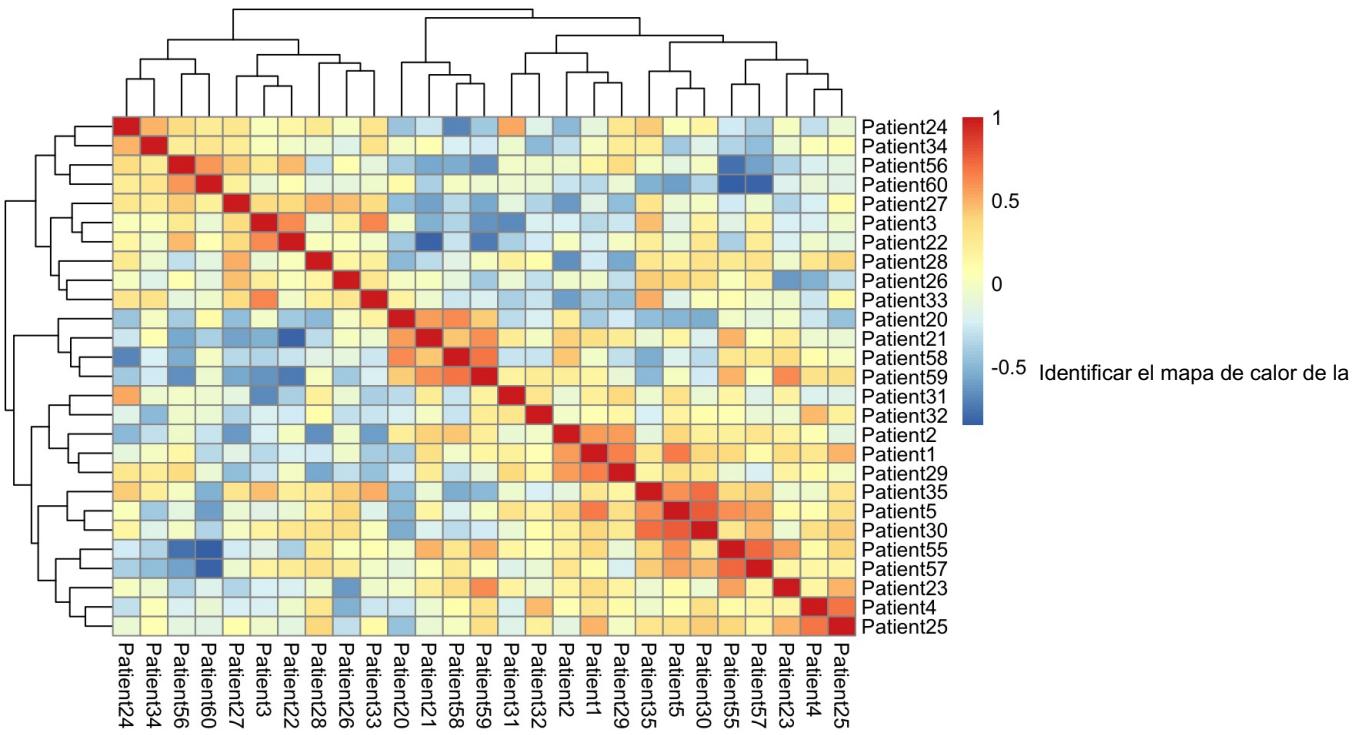
```

##          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

```

Identificar el mapa de calor de la correlación de datos

```
pheatmap(cor(sub))
```

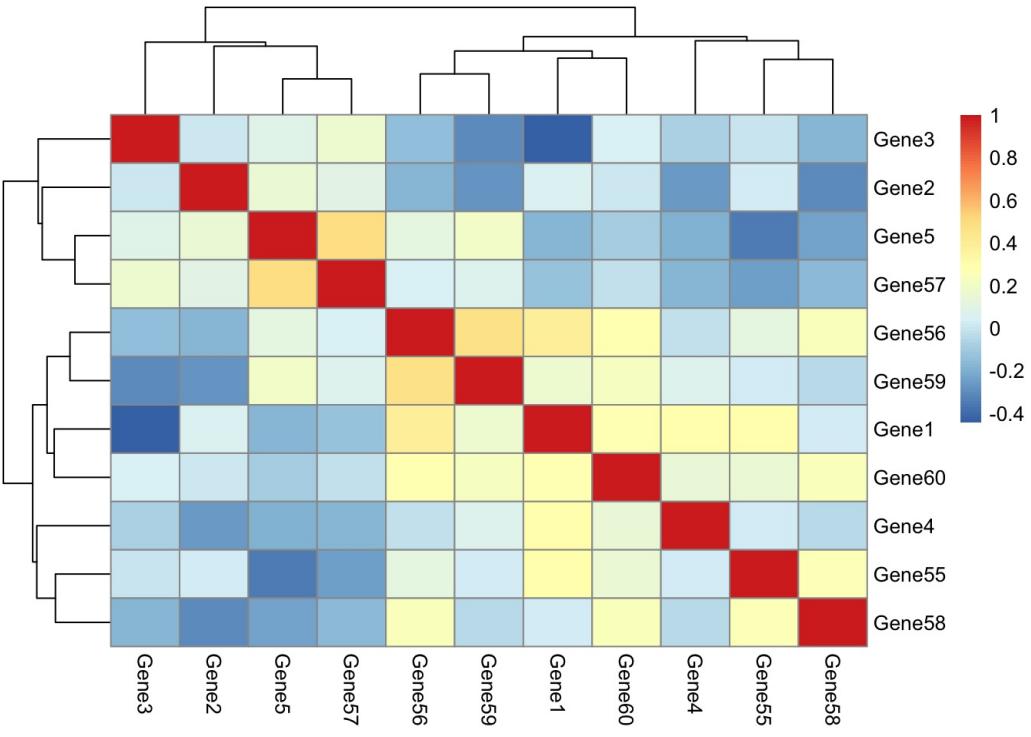


correlación de los genes Matriz transpuesta

```
trans=t(sub)
```

Correlación de la matriz transpuesta

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



```
pheatmap(cor(sub))
```

