

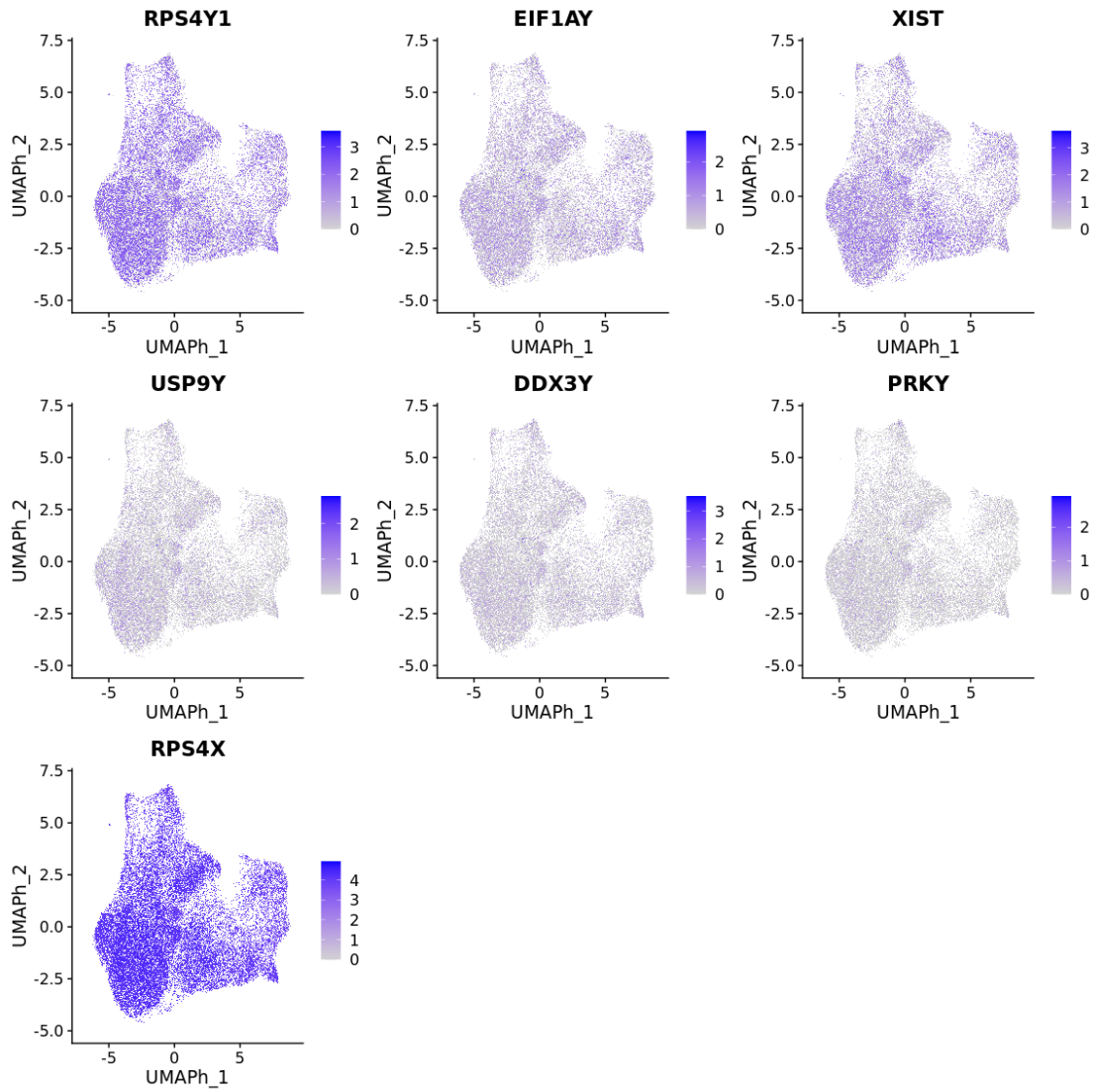
Check donor bias in new full object

Check donor genes expression in full object - Dimplot (female/male)

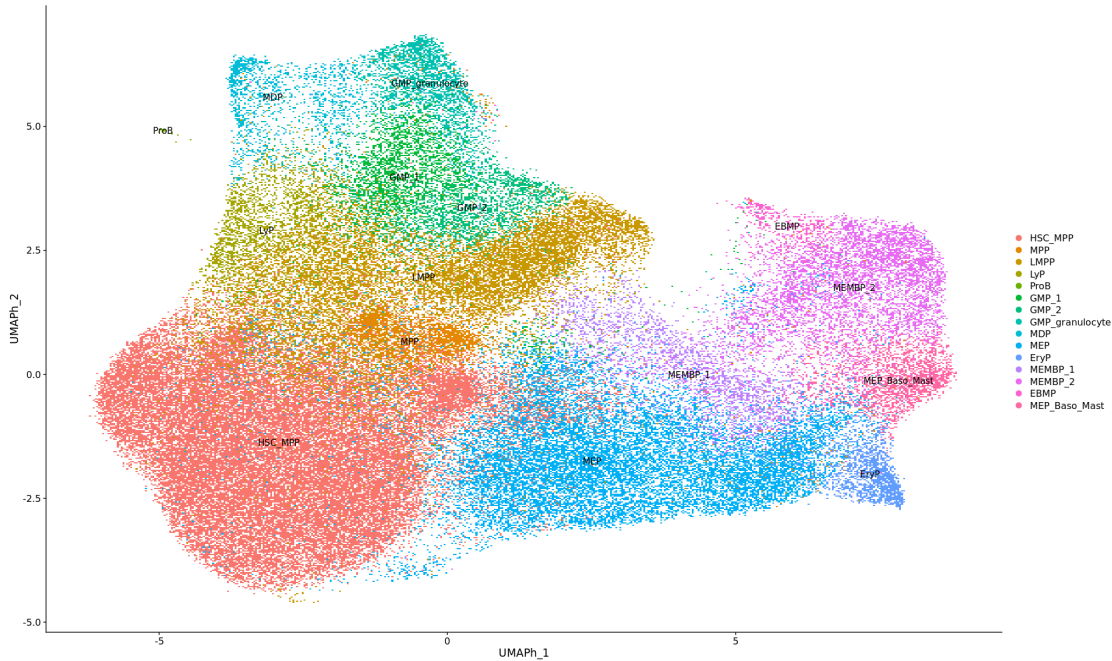
```
library(Seurat)
library(clusterProfiler)
library(dplyr)
library(viridis)
library(ggplot2)
library(grid)
library(gridExtra)
library(reshape2)
library(scales)
library(RColorBrewer)
library(ComplexHeatmap)
library(circlize)
library(stringr)
library(ggrepel)
library(openxlsx)
library(cowplot)

full_new <- readRDS(paste(wdir,"Full_final.rds", sep = "/"))

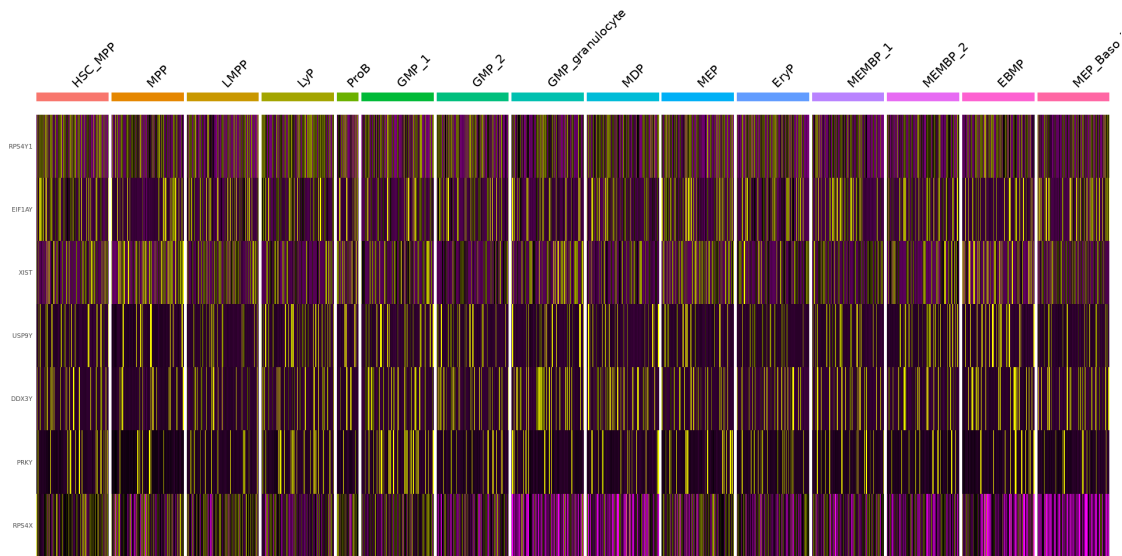
dnew <- FeaturePlot(object = full_new, features =
c('RPS4Y1', 'EIF1AY', 'XIST', 'USP9Y', 'DDX3Y', 'PRKY', 'RPS4X'), order=T)
# ggsave(filename = paste(out_dir, 'Donor_plots', "donor_composition.png", sep =
"/"),
# plot = d, width = 20, height = 20, dpi = 150)
dnew
```



```
DimPlot(full_new, label = T)
```

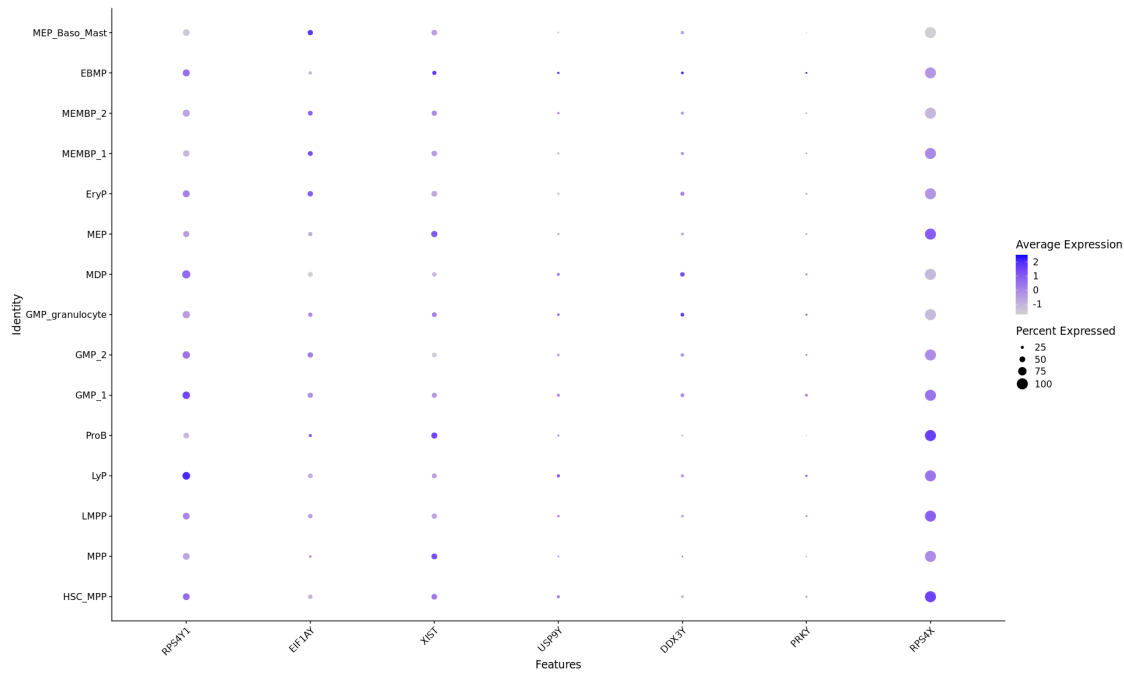


```
DoHeatmap(subset(full_new, downsample = 100), features =
c('RPS4Y1', 'EIF1AY', 'XIST', 'USP9Y', 'DDX3Y', 'PRKY', 'RPS4X')) + NoLegend()+
theme(axis.text = element_text(size = 8))
```



```
g <- c('RPS4Y1', 'EIF1AY', 'XIST', 'USP9Y', 'DDX3Y', 'PRKY', 'RPS4X')
a <- DotPlot(object = full_new, features = g)+
theme(axis.text.x = element_text(angle = 45, hjust=1))

plot(a)
```



VlnPlot(full_new, features = g, pt.size = 0)

