

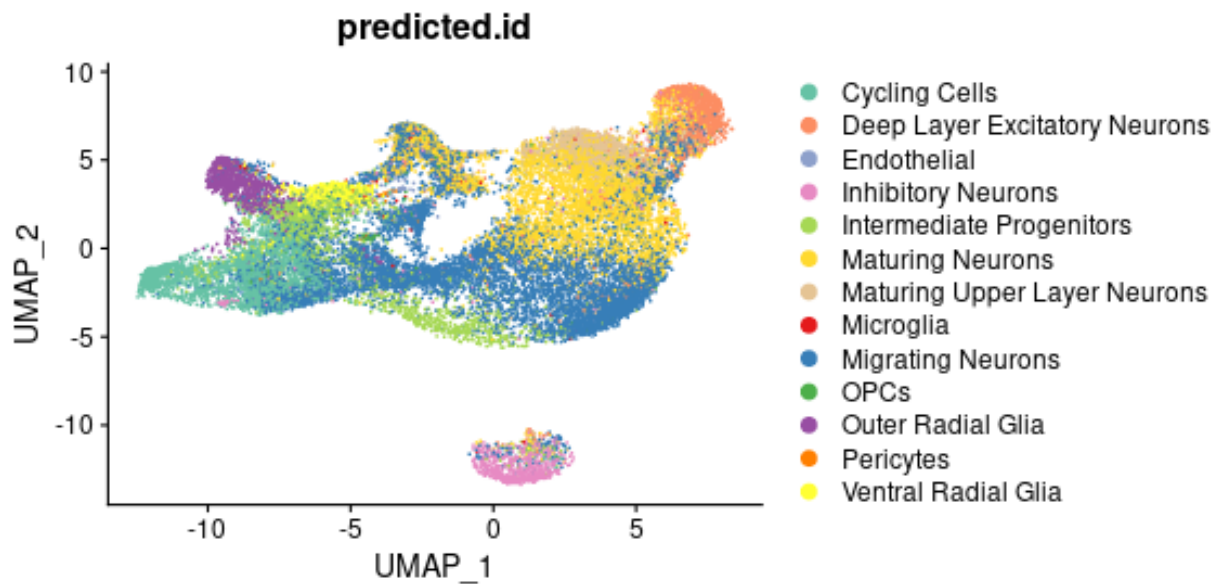
## Figure 2

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Figure 2B

```
dataset$age <- factor(dataset$age, levels = c('30', '90', '166'))  
UMAPPlot(dataset, group.by = 'predicted.id', cols = colors)
```



```
UMAPPlot(dataset, group.by = 'age', cols = colors)
```

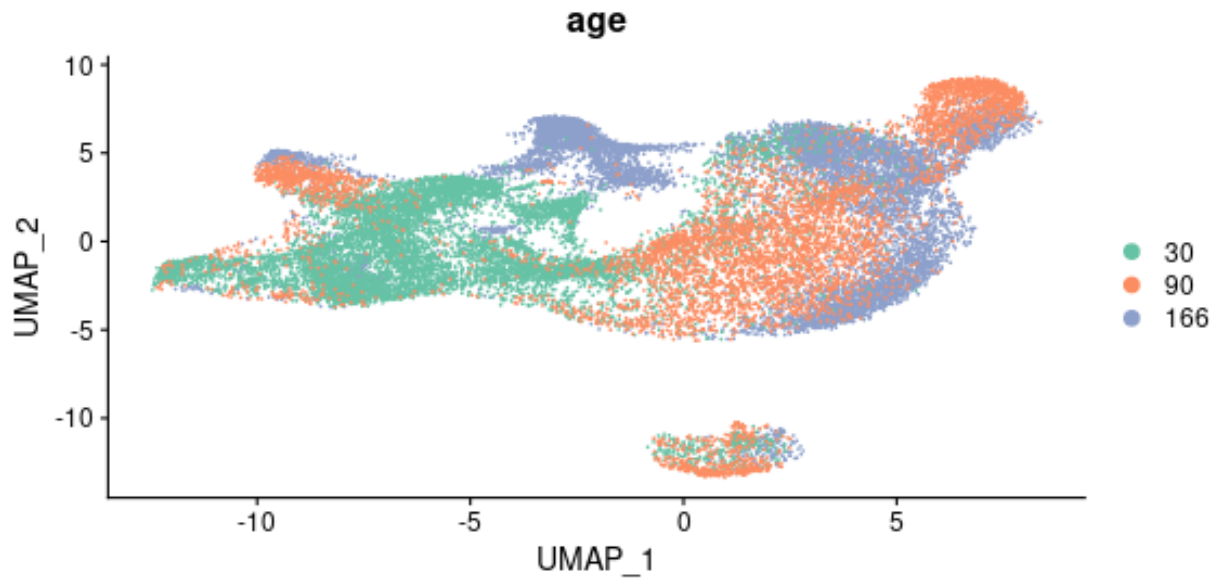


Figure 2C

```
stack.order <- c('Ventral Radial Glia', 'Outer Radial Glia', 'OPCs',
  'Migrating Neurons', 'Microglia', 'Maturing Upper Layer Neurons',
  'Maturing Neurons', 'Intermediate Progenitors', 'Inhibitory Neurons',
  'Endothelial', 'Deep Layer Excitatory Neurons', 'Cycling Cells')
meta <- dataset@meta.data[dataset@meta.data$predicted.id %in% stack.order,]
gg <- JR.bar.plot(meta = meta, grouping = 'predicted.id',
  x.axis = 'age', grouping.order = rev(stack.order),
  cols = c(colors[1:11], colors[13]), grouping_style = 'stack')
gg + xlab('Age (days)') + ylab('Fraction Cells within Sample')
```

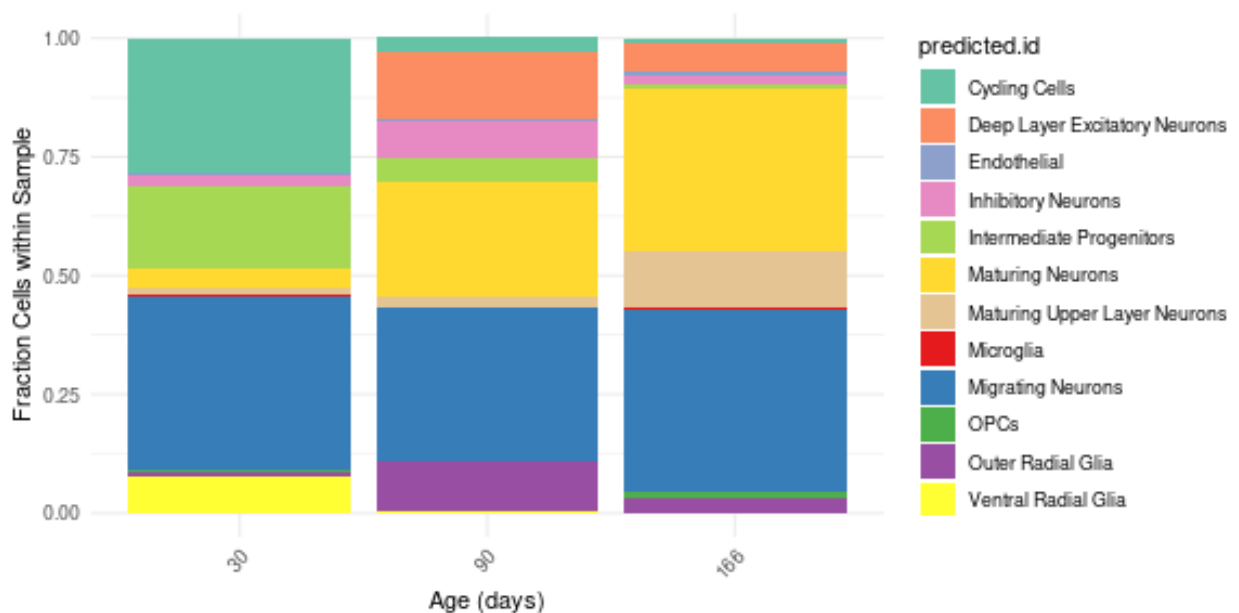
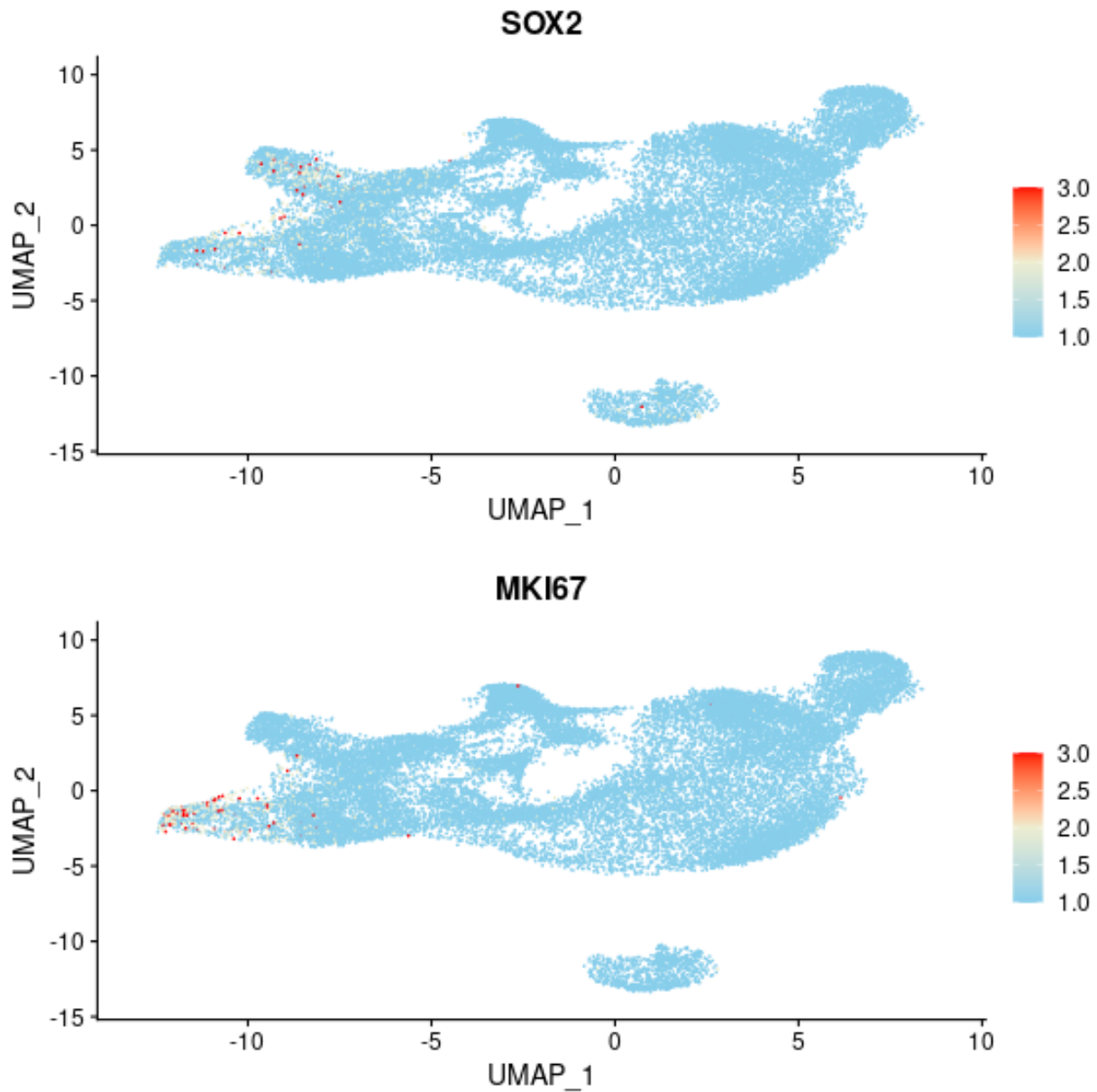
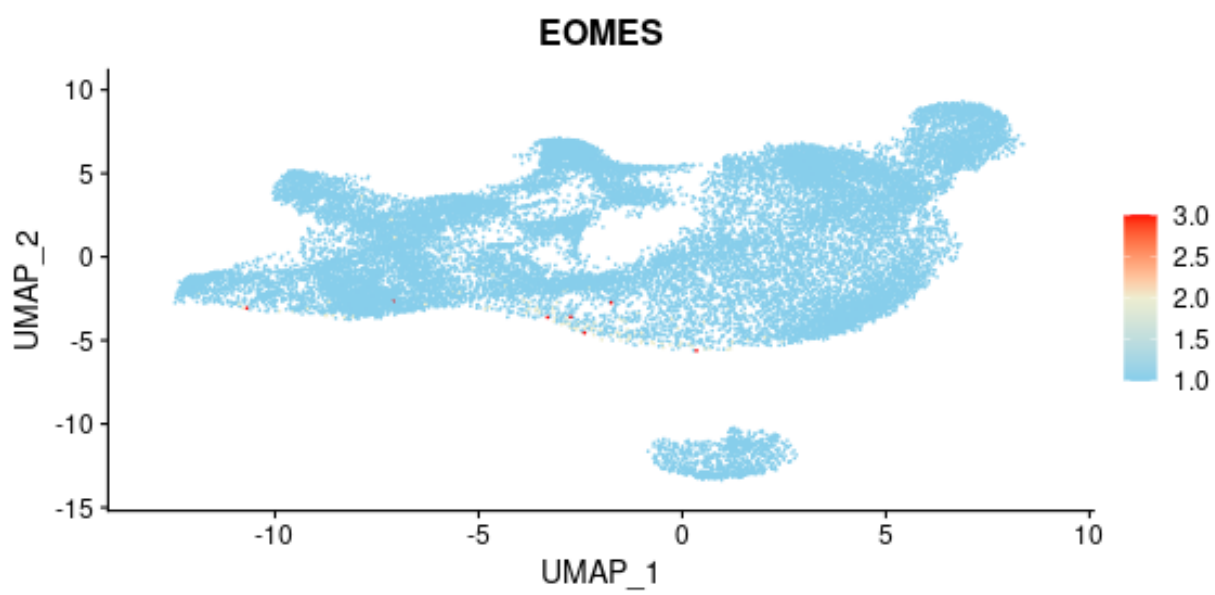
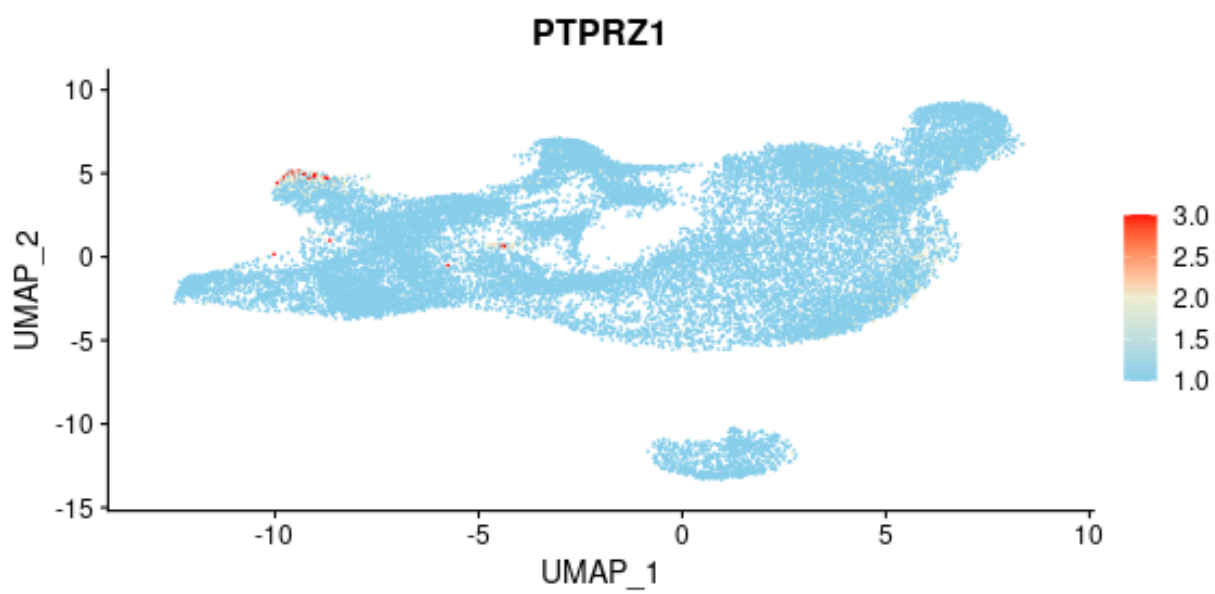
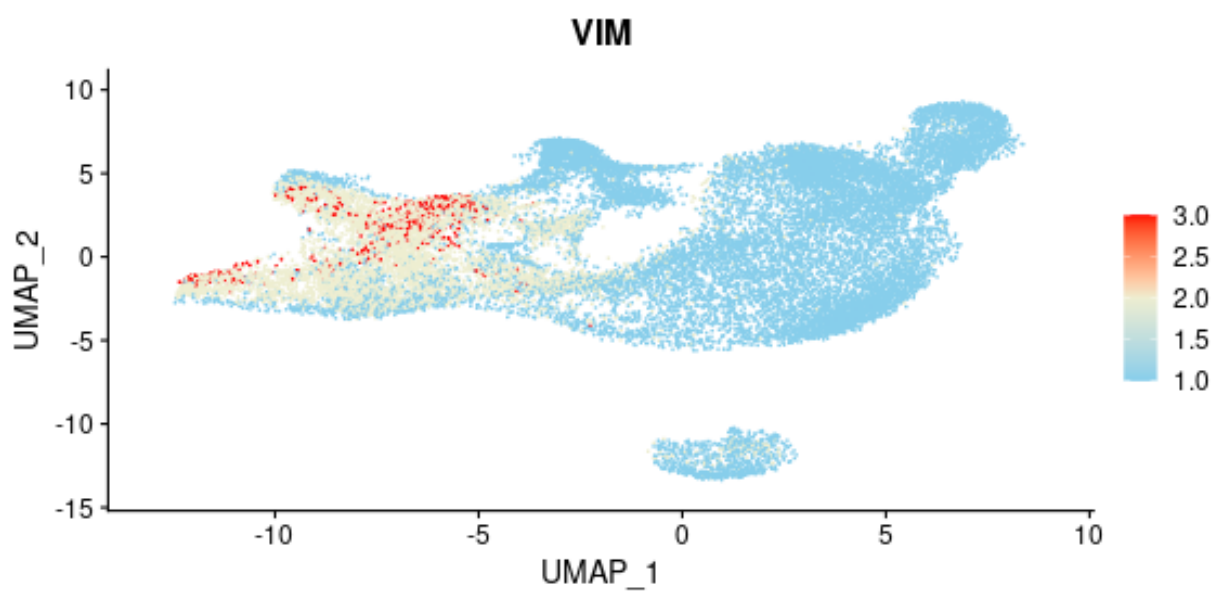
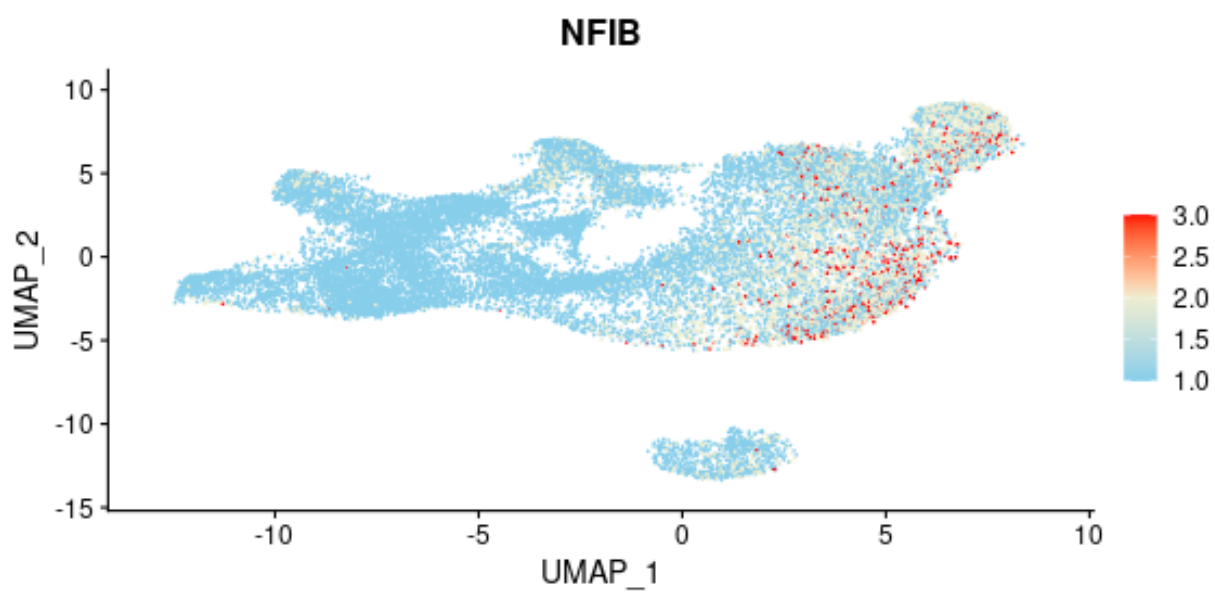


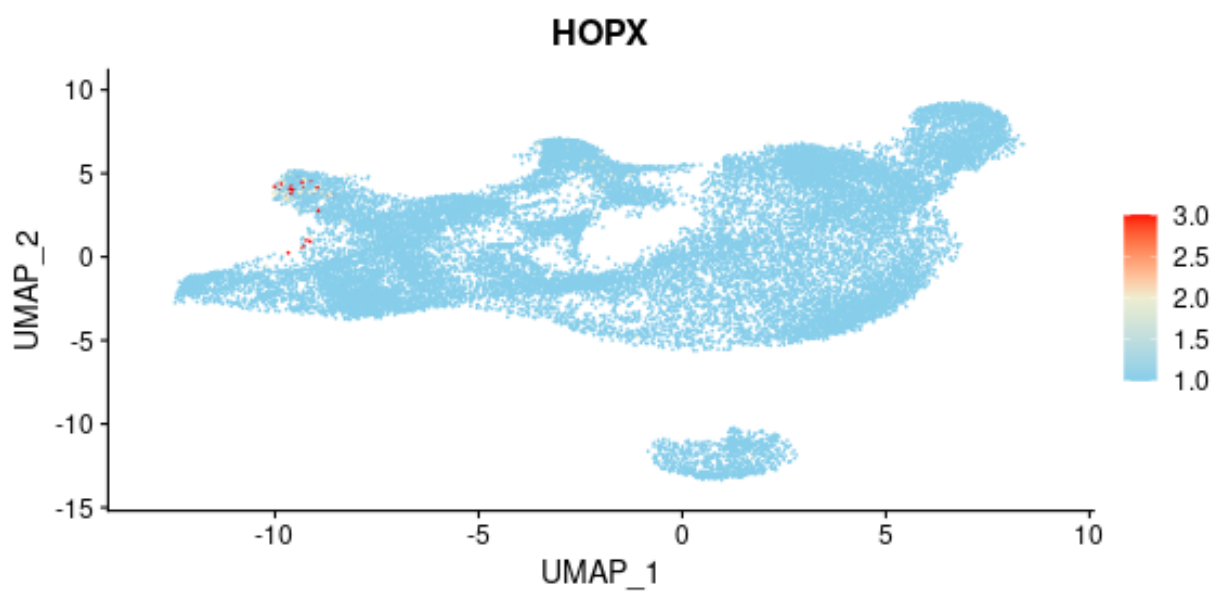
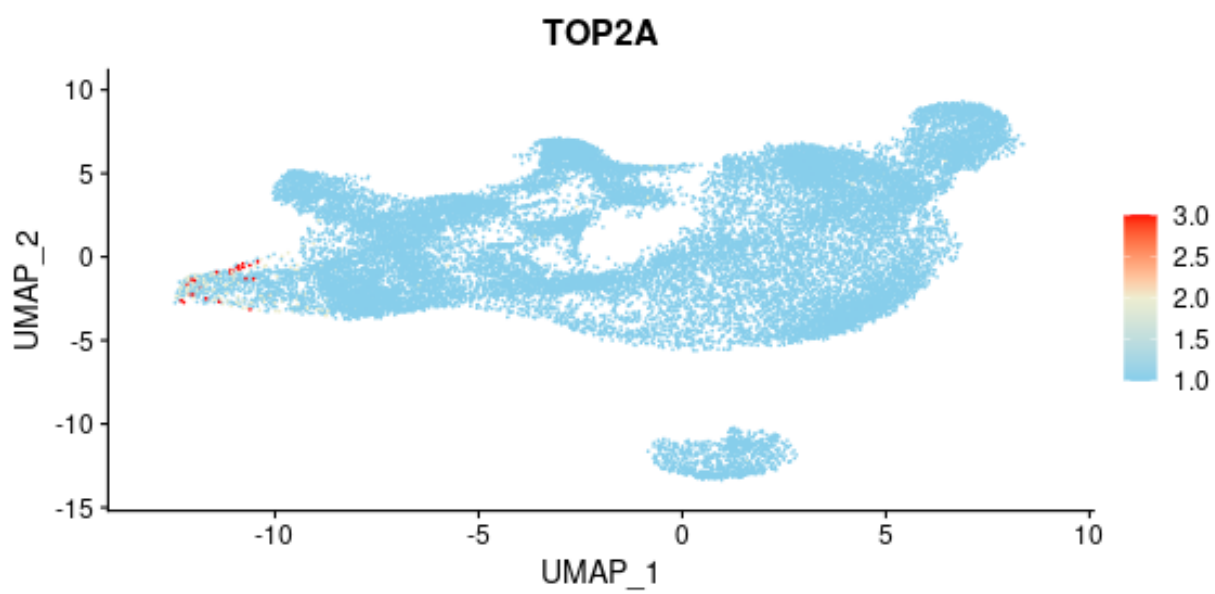
Figure 2D

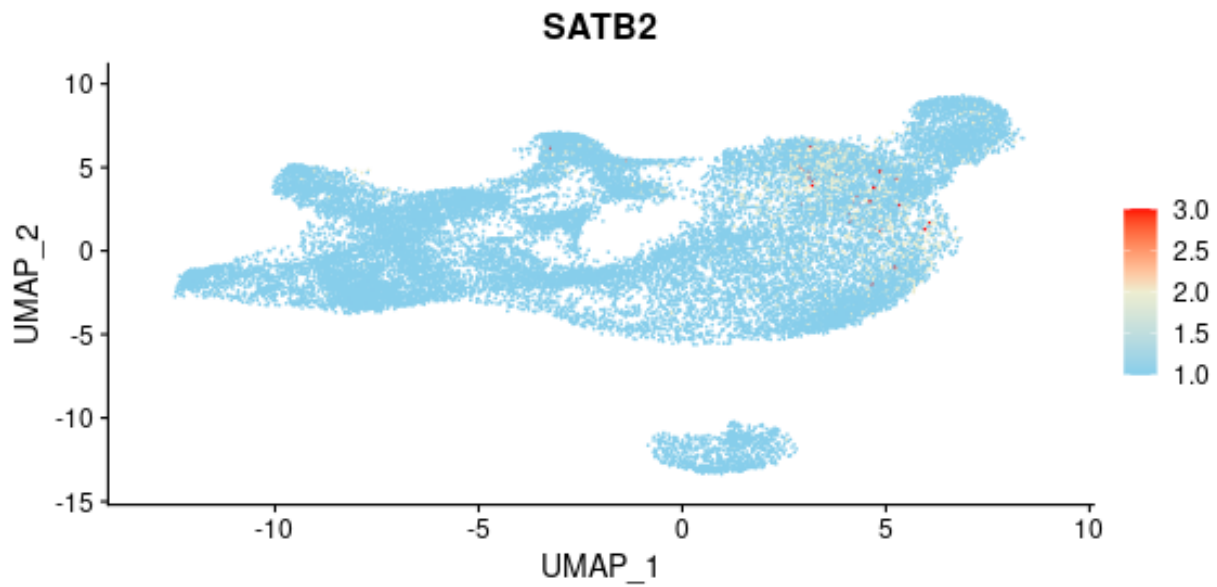
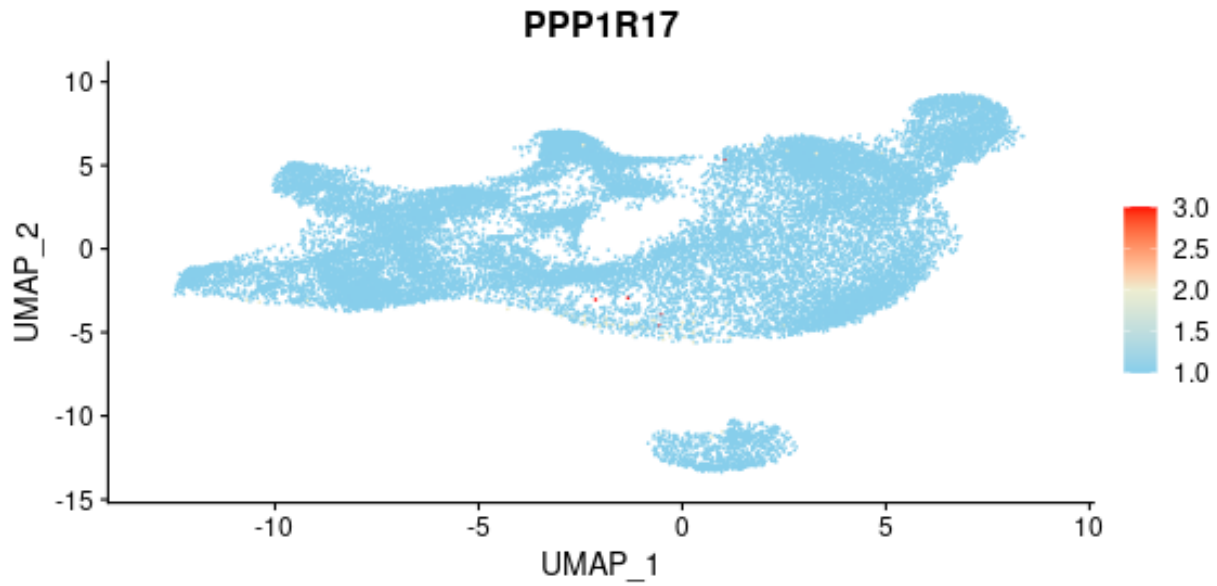
```
genes <- c('SOX2', 'MKI67', 'PTPRZ1', 'EOMES', 'NFIB', 'VIM', 'TOP2A', 'HOPX',  
           'PPP1R17', 'SATB2')  
for(i in genes){  
  print(FeaturePlot(dataset, features = i, cols = heat))  
}
```











```
sessionInfo()
```

```
## R version 4.0.2 (2020-06-22)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: CentOS Linux 7 (Core)
##
## Matrix products: default
## BLAS/LAPACK: /usr/prog/OpenBLAS/0.2.20-GCC-6.4.0-2.28/lib/libopenblas_haswellp-r0.2.20.so
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8      LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
```

```

## [7] LC_PAPER=en_US.UTF-8      LC_NAME=C
## [9] LC_ADDRESS=C                LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods    base
##
## other attached packages:
## [1] ggplot2_3.3.3      reshape2_1.4.4      RColorBrewer_1.1-2 dplyr_1.0.5
## [5] SeuratObject_4.0.0 Seurat_4.0.0
##
## loaded via a namespace (and not attached):
## [1] nlme_3.1-152      matrixStats_0.58.0  RcppAnnoy_0.0.18
## [4] httr_1.4.2        sctransform_0.3.2   tools_4.0.2
## [7] utf8_1.1.4        R6_2.5.0            irlba_2.3.3
## [10] rpart_4.1-15      KernSmooth_2.23-18  uwot_0.1.10
## [13] mgcv_1.8-34       DBI_1.1.1           lazyeval_0.2.2
## [16] colorspace_2.0-0  withr_2.4.1         tidyselect_1.1.0
## [19] gridExtra_2.3     compiler_4.0.2      plotly_4.9.3
## [22] labeling_0.4.2    scales_1.1.1        spatstat.data_2.0-0
## [25] lmtest_0.9-38     ggribes_0.5.3       pbapply_1.4-3
## [28] goftest_1.2-2     spatstat_1.64-1     stringr_1.4.0
## [31] digest_0.6.27     spatstat.utils_2.0-0 rmarkdown_2.7
## [34] pkgconfig_2.0.3   htmltools_0.5.1.1   parallelly_1.23.0
## [37] highr_0.8         fastmap_1.1.0       htmlwidgets_1.5.3
## [40] rlang_0.4.10      shiny_1.6.0         farver_2.1.0
## [43] generics_0.1.0    zoo_1.8-8           jsonlite_1.7.2
## [46] ica_1.0-2         magrittr_2.0.1      patchwork_1.1.1
## [49] Matrix_1.3-2      Rcpp_1.0.6          munsell_0.5.0
## [52] fansi_0.4.2       abind_1.4-5         reticulate_1.18
## [55] lifecycle_1.0.0   stringi_1.5.3       yaml_2.2.1
## [58] MASS_7.3-53.1     Rtsne_0.15          plyr_1.8.6
## [61] grid_4.0.2        parallel_4.0.2      listenv_0.8.0
## [64] promises_1.2.0.1  ggrepel_0.9.1       crayon_1.4.1
## [67] deldir_0.2-10     miniUI_0.1.1.1      lattice_0.20-41
## [70] cowplot_1.1.1     splines_4.0.2       tensor_1.5
## [73] knitr_1.31        pillar_1.5.1        igraph_1.2.6
## [76] future.apply_1.7.0 codetools_0.2-18     leiden_0.3.7
## [79] glue_1.4.2        evaluate_0.14        data.table_1.14.0
## [82] vctrs_0.3.6       png_0.1-7           httpuv_1.5.5
## [85] polyclip_1.10-0   gtable_0.3.0        RANN_2.6.1
## [88] purrr_0.3.4       tidyr_1.1.3         scattermore_0.7
## [91] future_1.21.0     assertthat_0.2.1     xfun_0.21
## [94] mime_0.10         xtable_1.8-4         later_1.1.0.1
## [97] survival_3.2-7    viridisLite_0.3.0    tibble_3.1.0
## [100] cluster_2.1.1     globals_0.14.0       fitdistrplus_1.1-3
## [103] ellipsis_0.3.1    ROCR_1.0-11

```