sc-org figures (AB) to pdf

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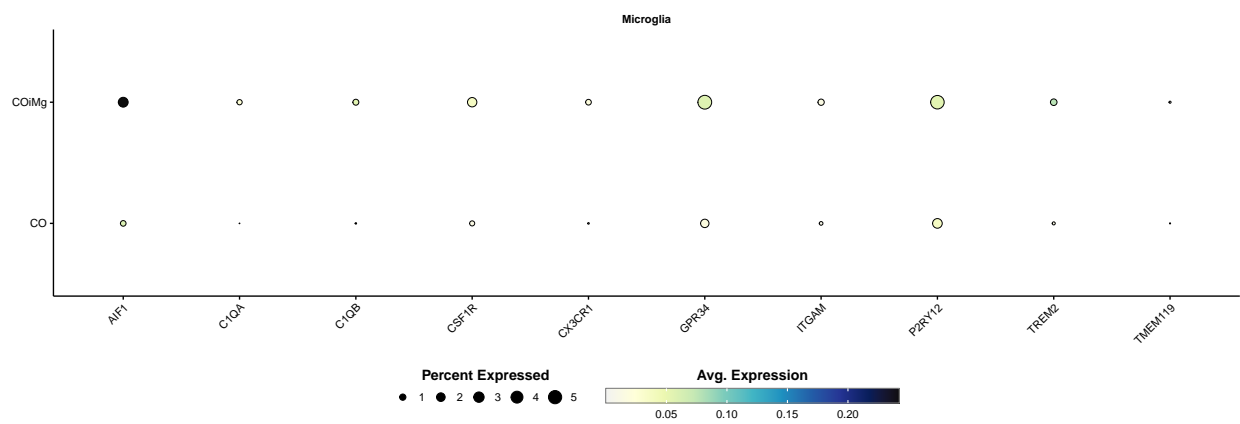
Contents

Single-cell RNA-seq analysis of COs vs COiMG

UMAP

```
SCpubr::do_DotPlot(PV_filt,features=list('Microglia'=AB_markers_curated$Microglia),
                   group.by = "Organoids") +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1))
```



```
SCpubr::do_DotPlot(PV_filt, features=list('Epithelial'=AB_markers$`Epithelial Cells`,
                                          'Radial Glia'=AB_markers$`Radial Glia`,
                                          'NPCs'=AB_markers$NPCs,
                                        'Neurons'=AB_markers$Neurons,
                                        'Exc. neurons'=AB_markers$`Excitatory neurons`,
                                        'Inh. neurons'=AB_markers$`Inhibitory neurons`,
                                        'Interneurons'=AB_markers$Interneurons,
```
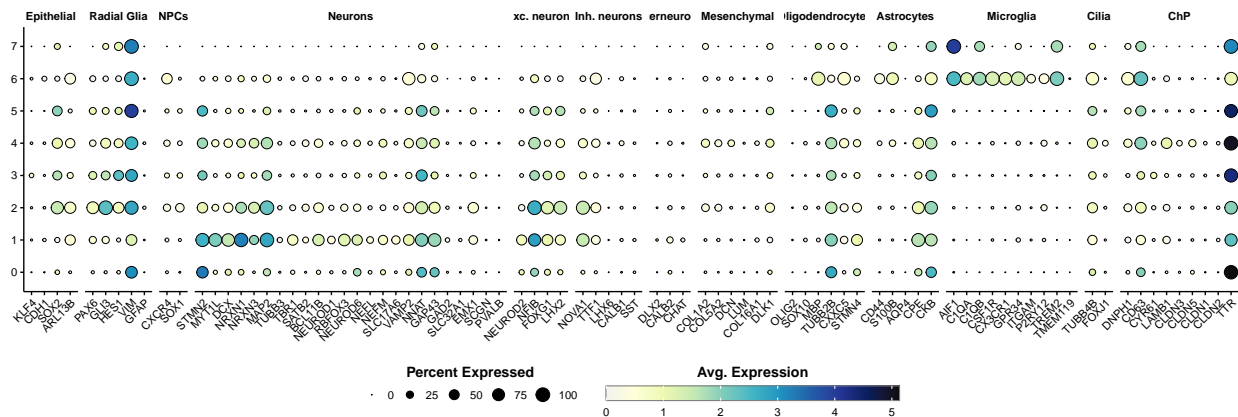
```
                                          'Cortical neurons'=AB_markers$`Cortical neurons`,
                                          'Mesenchymal'=AB_markers$`Mesenchymal cells`,
                                          'Oligodendrocytes'=AB_markers$Oligodendrocytes,
                                          'Astrocytes'=AB_markers$Astrocytes,
                                          'Microglia'=AB_markers$Microglia,
                                          'Cilia'=AB_markers$Cilia,
                                          'ChP'=AB_markers$ChP),
                    group.by = "seurat_clusters")+
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1))
```



```
Idents(PV_filt) <- PV_filt$seurat_clusters
identity <- c('0'='NPC',
              '1'='Cortical neurons',
              '2'='NPC',
              '3'='NPC',
              '4'='Mesenchymal/ChP (Cilia-associated)',
              '5'='NPC',
              '6'='Microglia',
              '7'='Microglia')
PV_filt <- RenameIdents(object = PV_filt, identity)
PV_filt@meta.data$identity <- Idents(PV_filt)
table(PV_filt$identity)
```

```
##
##                              NPC              Cortical neurons
##                            79480                         22070
## Mesenchymal/ChP (Cilia-associated)                   Microglia
##                             5588                           282
```
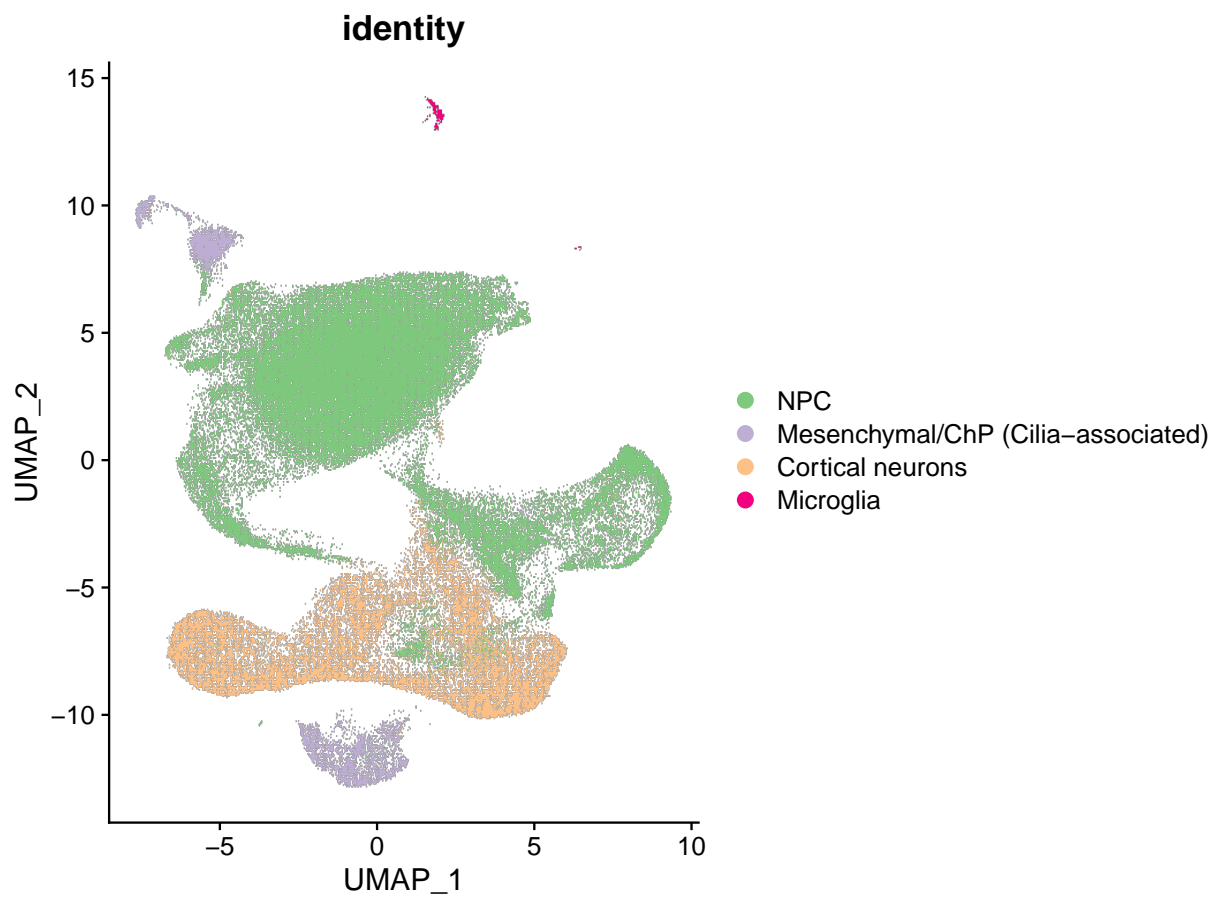
```
PV_filt$identity <- factor(PV_filt$identity, levels=unique(PV_filt$identity))

DimPlot(PV_filt, reduction = 'umap', group.by='identity', cols = RColorBrewer::brewer.pal(7,'Accent')[c
```
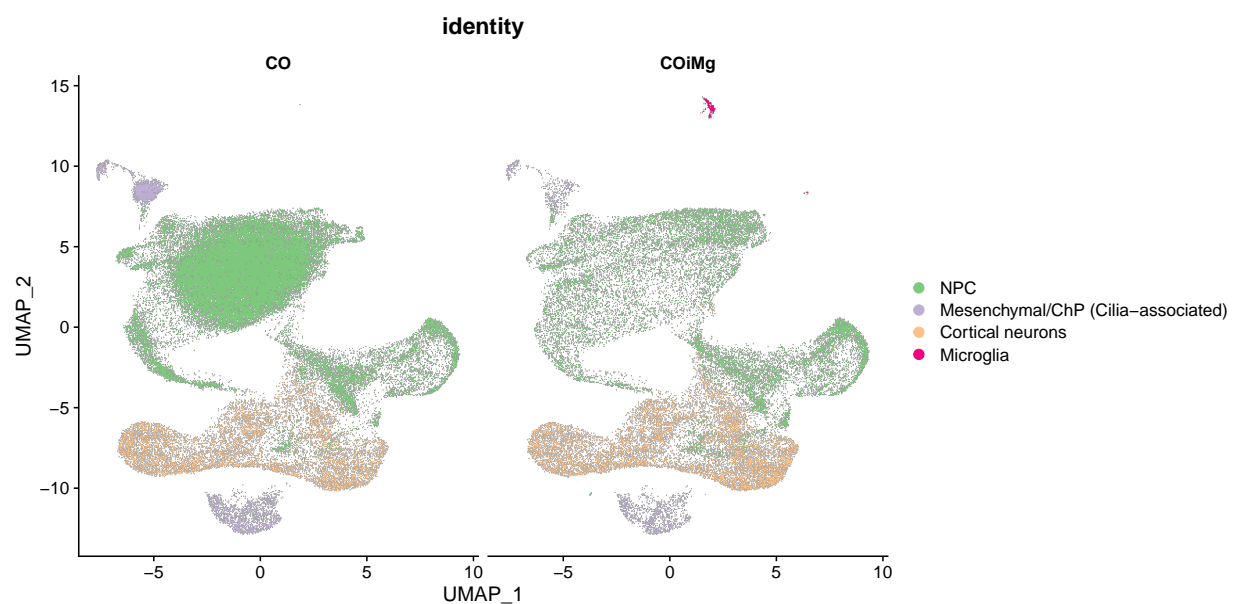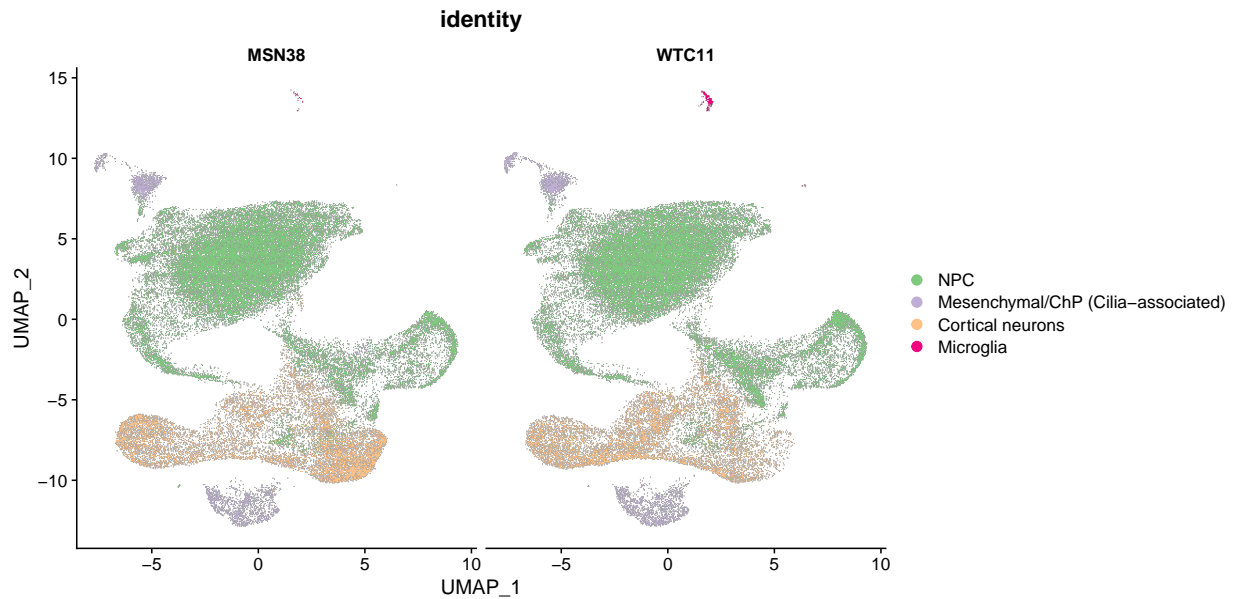
identity

Legend:
- NPC
- Mesenchymal/ChP (Cilia−associated)
- Cortical neurons
- Microglia

```
DimPlot(PV_filt, reduction = 'umap', group.by='identity', split.by = 'Organoids', cols = RColorBrewer::
```


identity

CO   COiMg

Legend:
- NPC
- Mesenchymal/ChP (Cilia−associated)
- Cortical neurons
- Microglia

```
DimPlot(PV_filt, reduction = 'umap', group.by='identity', split.by = 'cell.line', cols = RColorBrewer::
```



```
table(PV_filt$cell.line,PV_filt$identity)
```

```
##
##           NPC Mesenchymal/ChP (Cilia-associated) Cortical neurons Microglia
##    MSN38 38690                              2603            11712        26
##    WTC11 40790                              2985            10358       256
```
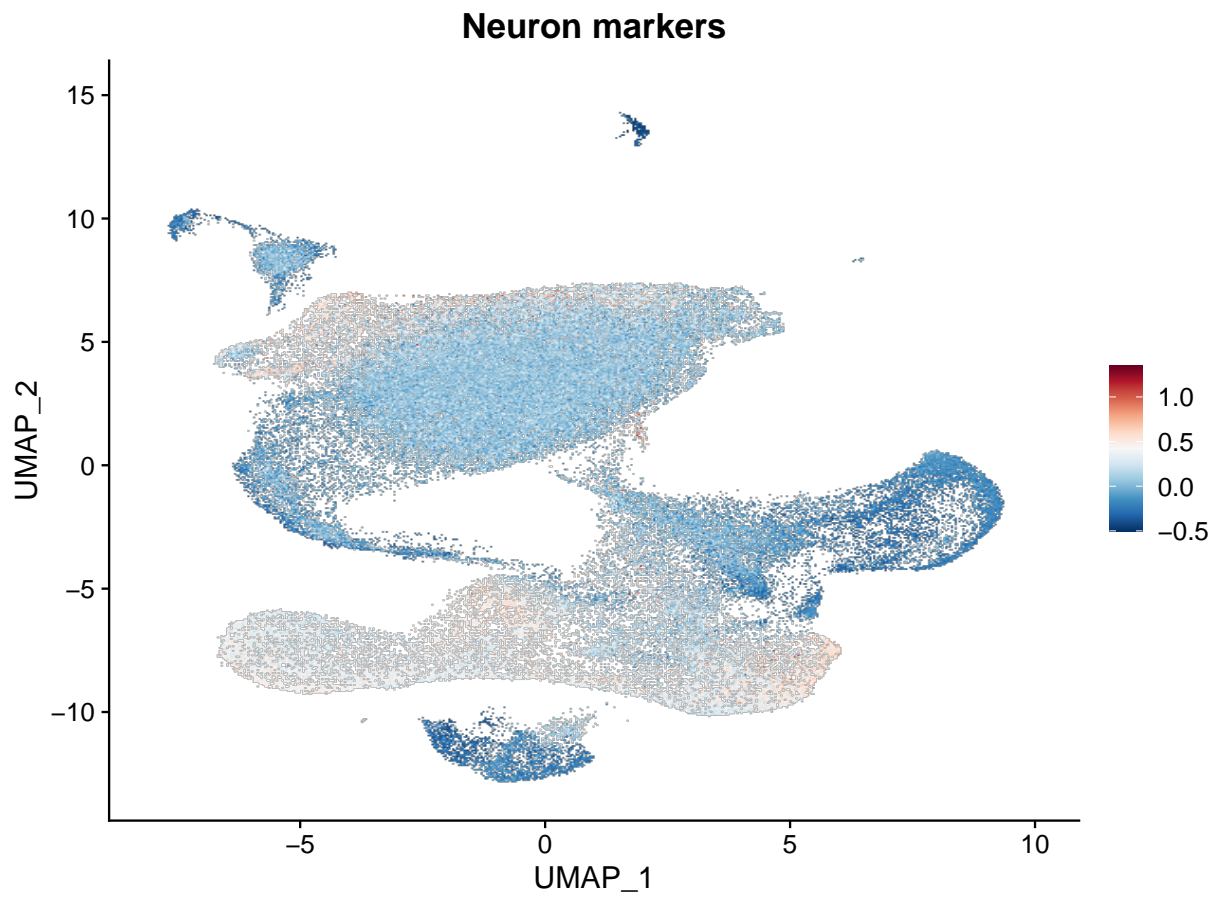
```
FeaturePlot(PV_filt,features = 'Cluster1',reduction = 'umap') +
  scale_colour_gradientn(colours = rev(brewer.pal(n = 11, name = "RdBu"))) +
  ggtitle('Microglia markers')
```
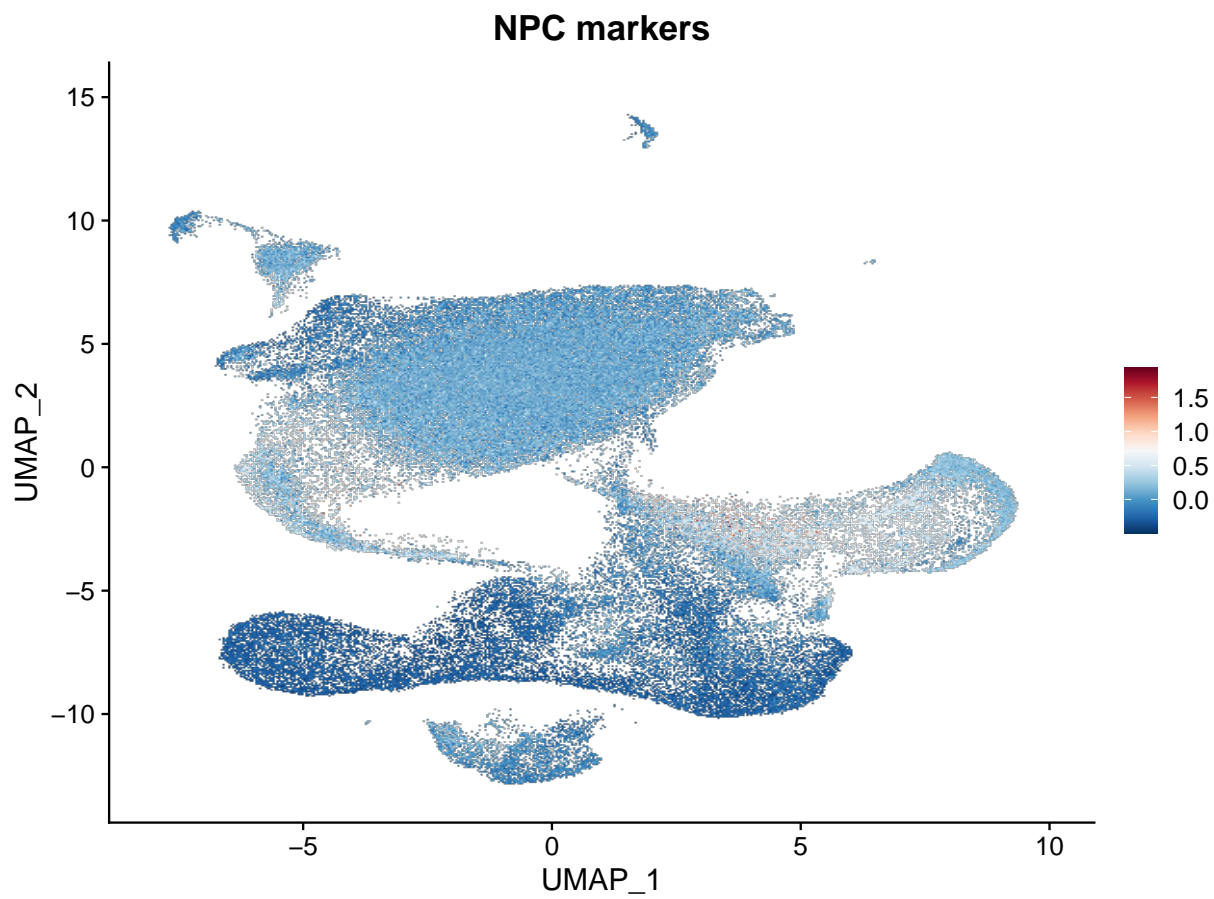
Microglia markers
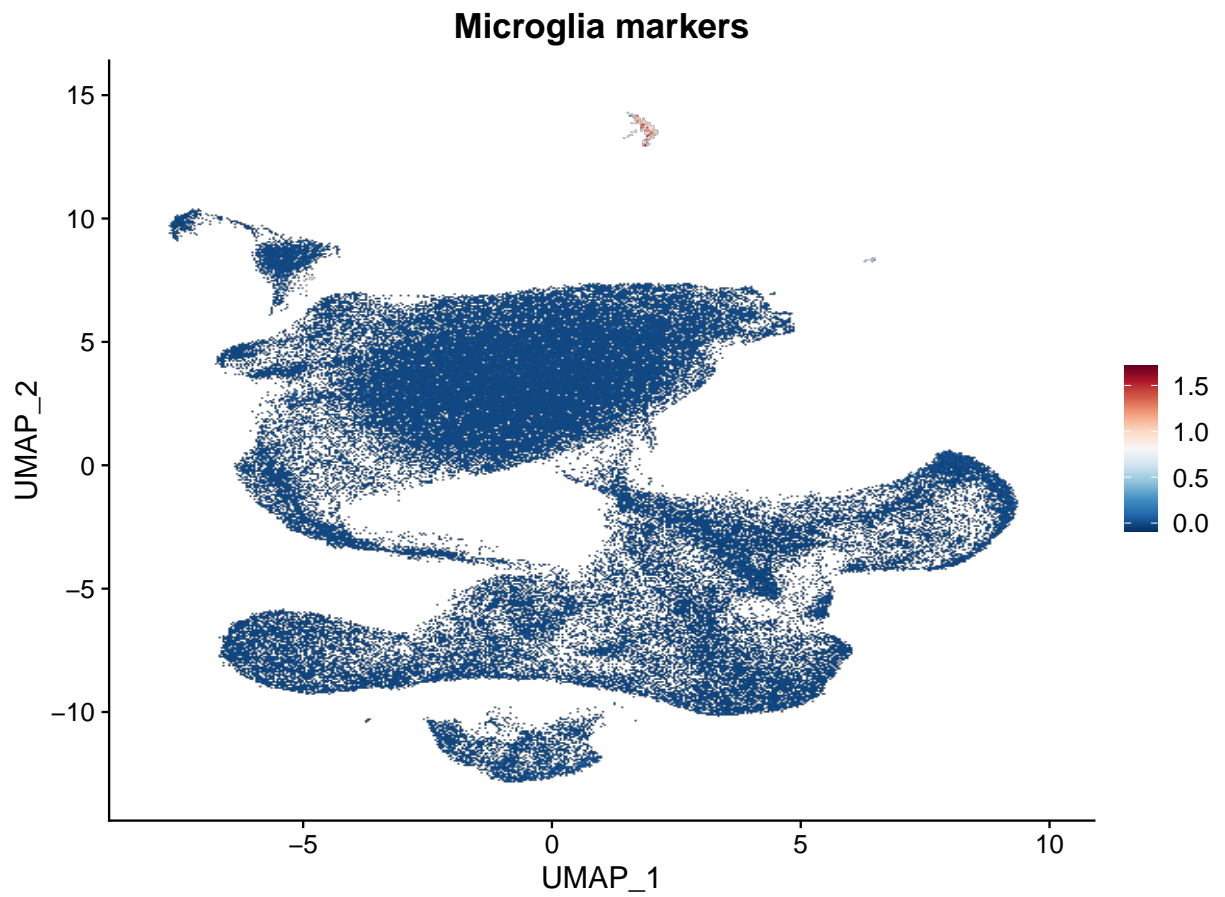

```
FeaturePlot(PV_filt,features = 'Cluster2',reduction = 'umap') +
  scale_colour_gradientn(colours = rev(brewer.pal(n = 11, name = "RdBu"))) +
  ggtitle('Mesenchymal/ChP markers')
```

Mesenchymal/ChP markers
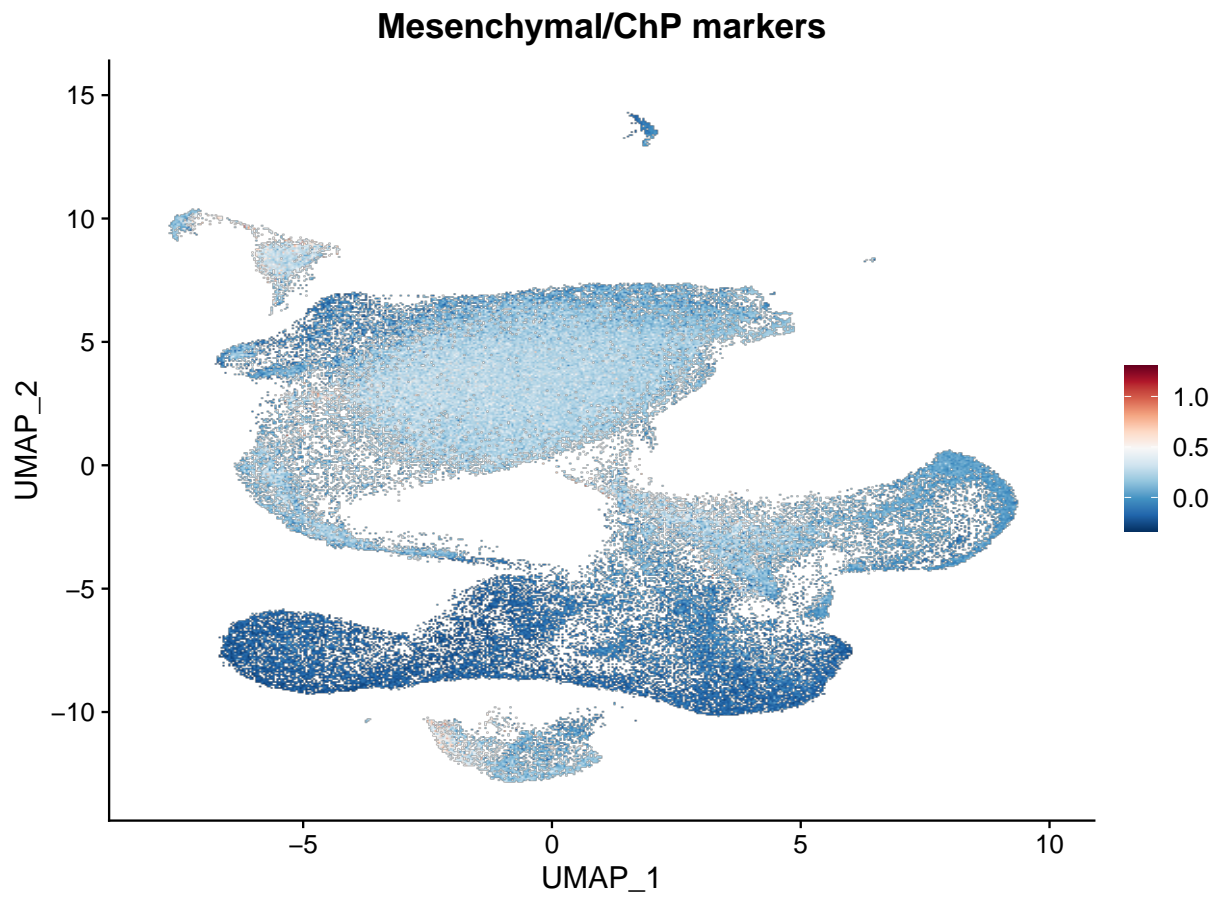

```
FeaturePlot(PV_filt,features = 'Cluster3',reduction = 'umap') +
  scale_colour_gradientn(colours = rev(brewer.pal(n = 11, name = "RdBu"))) +
  ggtitle('Neuron markers')
```
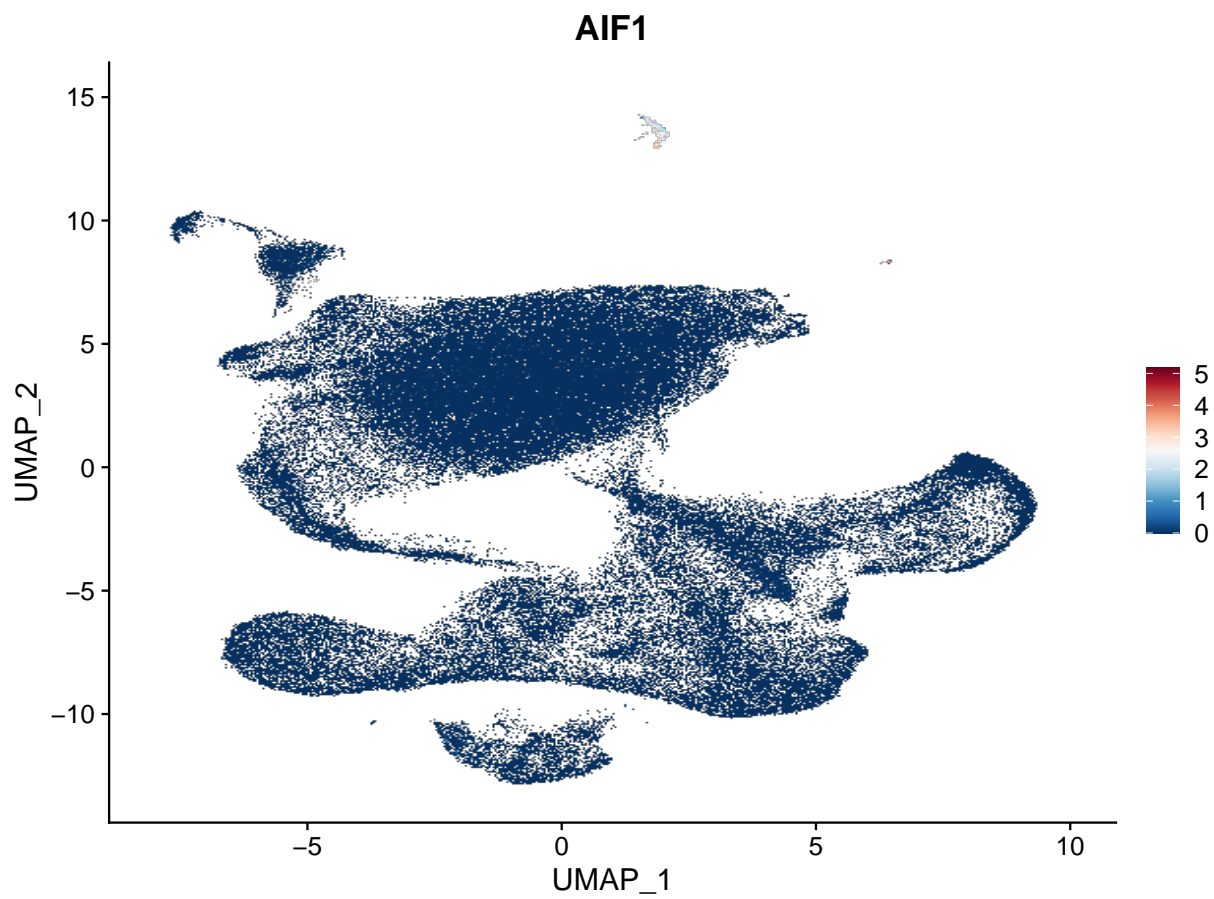
Neuron markers


```r
FeaturePlot(PV_filt,features = 'Cluster4',reduction = 'umap') +
  scale_colour_gradientn(colours = rev(brewer.pal(n = 11, name = "RdBu"))) +
  ggtitle('NPC markers')
```
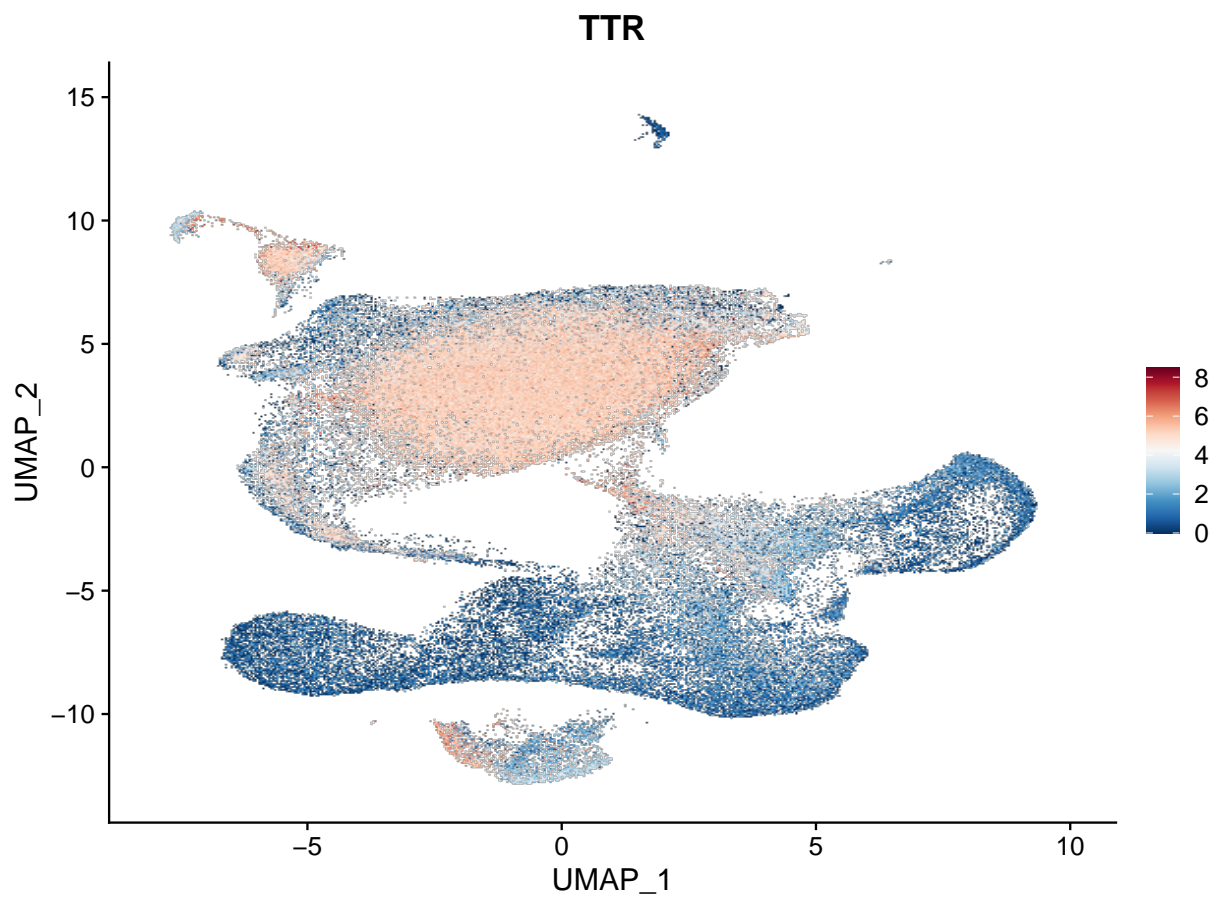
NPC markers


```
FeaturePlot(PV_filt,features = 'AIF1',reduction = 'umap') +
  scale_colour_gradientn(colours = rev(brewer.pal(n = 11, name = "RdBu")))
```
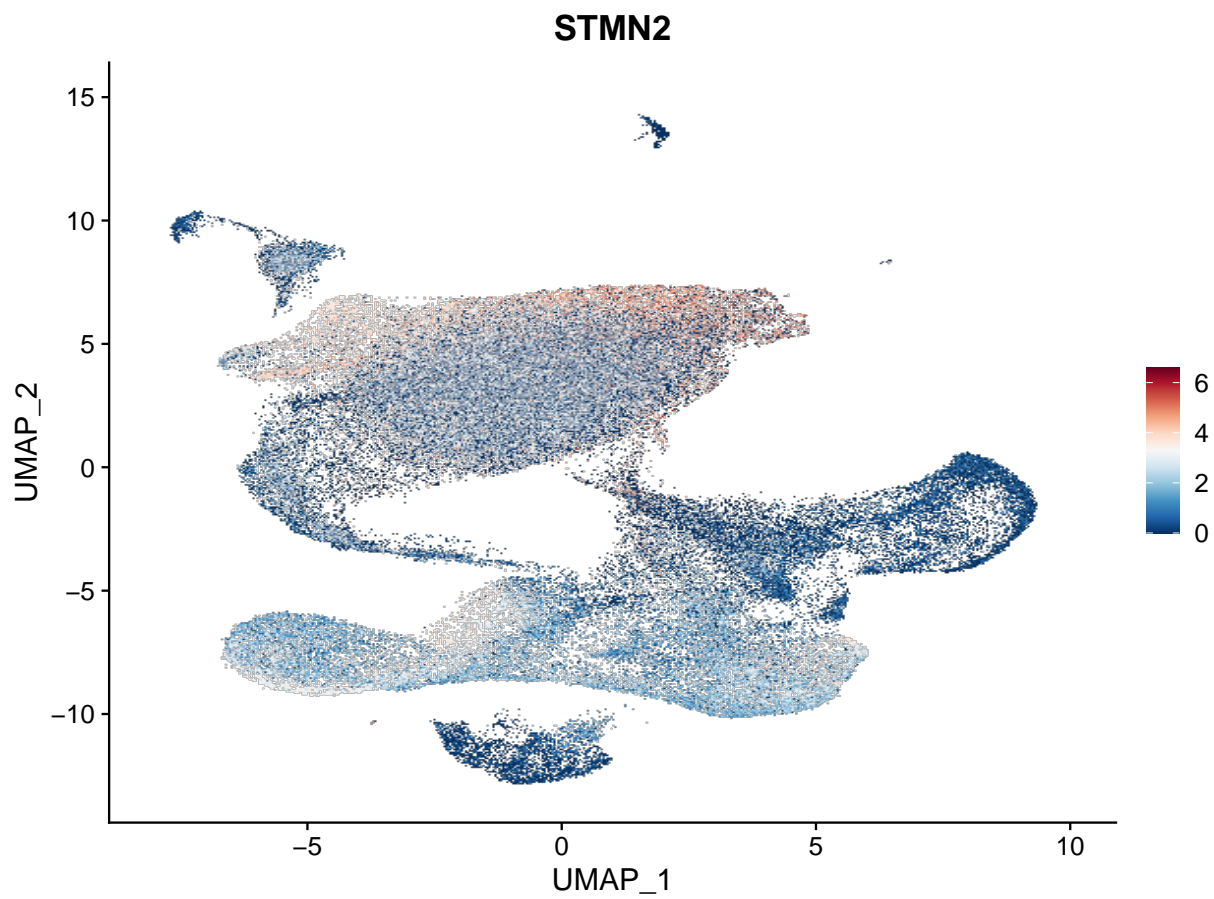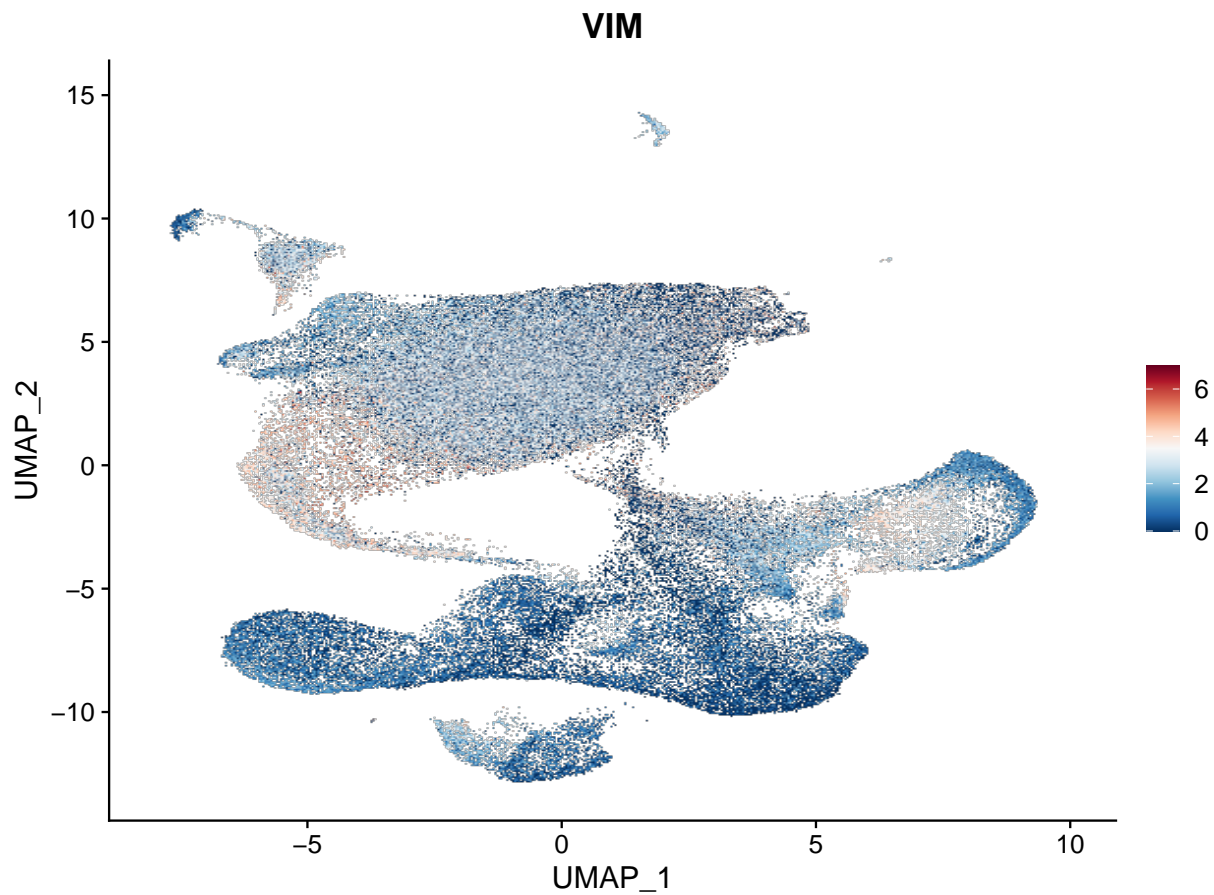
AIF1


```
FeaturePlot(PV_filt,features = 'TTR',reduction = 'umap') +
  scale_colour_gradientn(colours = rev(brewer.pal(n = 11, name = "RdBu")))
```

TTR

```
FeaturePlot(PV_filt,features = 'STMN2',reduction = 'umap') +
  scale_colour_gradientn(colours = rev(brewer.pal(n = 11, name = "RdBu")))
```

STMN2

```
FeaturePlot(PV_filt,features = 'VIM',reduction = 'umap') +
  scale_colour_gradientn(colours = rev(brewer.pal(n = 11, name = "RdBu")))
```

VIM


```
prop <- data.frame('CO'=prop.table(table(PV_filt$identity,PV_filt$Organoids)[,1]),'COiMg'=prop.table(tal

df <- data.frame('Cell Type'=rep(rownames(prop),2),'Organoids'=c(rep('CO',4),rep('COiMg',4)),'Percentage

ggplot(df, aes(x = Organoids, y = Percentage, fill = `Cell.Type`))+
  geom_bar(stat = "identity")+
  geom_text(aes(label = paste(Percentage,"%")), position = position_stack(vjust = 0.5)) +
  scale_fill_manual(values=RColorBrewer::brewer.pal(7,'Accent')[c(2,6,3,1)]) +
  theme_minimal()
```
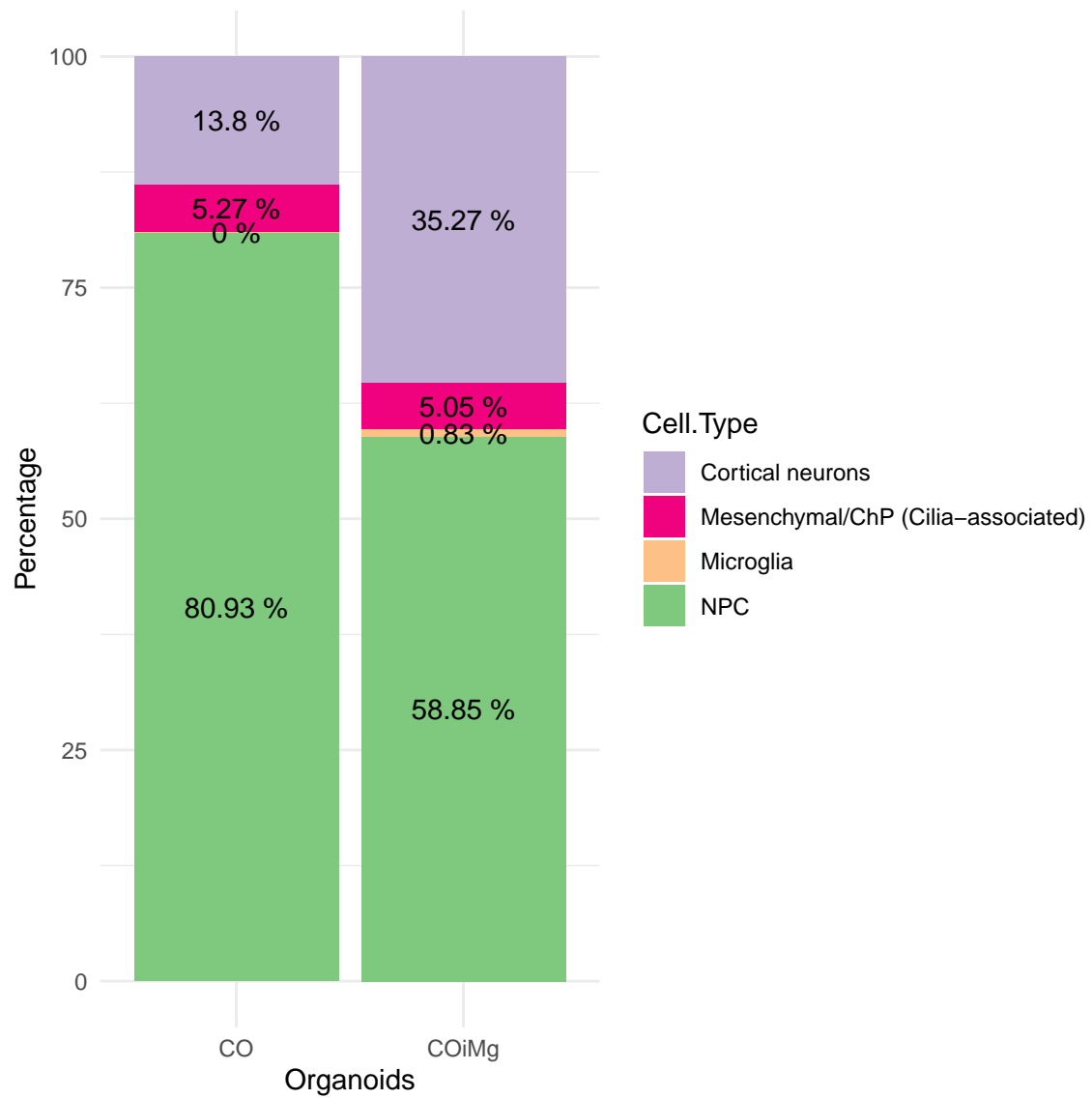
```
SCpubr::do_DotPlot(PV_filt, features=list('Microglia'=AB_markers$Microglia,'Cilia'=AB_markers$Cilia,
                                          'ChP'=AB_markers$ChP),group.by = 'Organoids')+
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1))
```
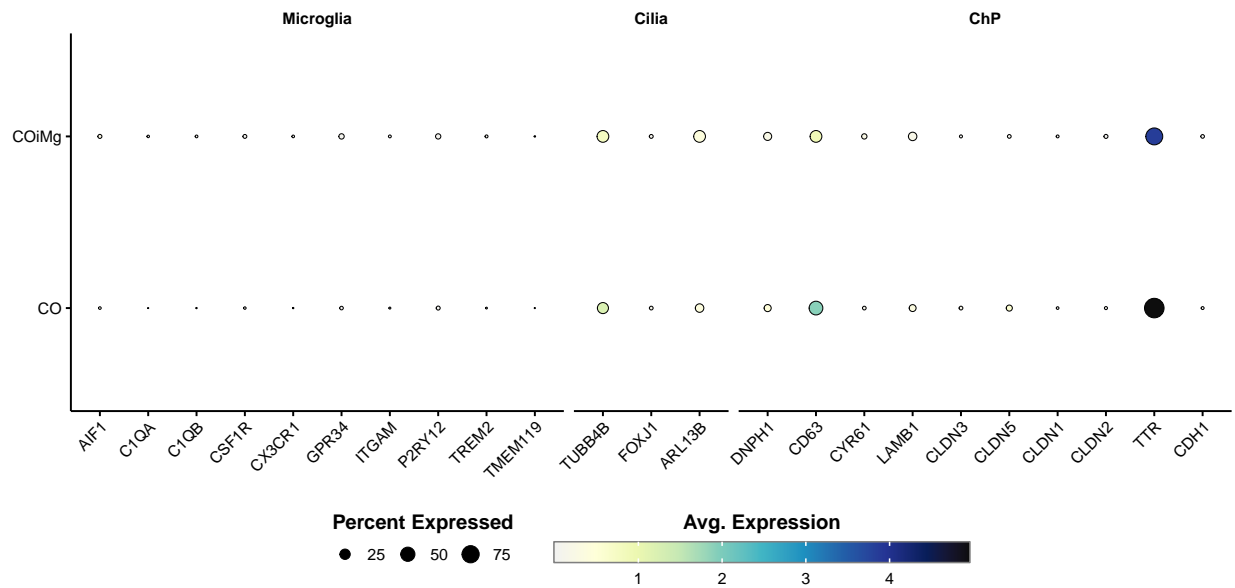
```
SCpubr::do_DotPlot(PV_filt, features=list('COiMg DEGs'=coimg_degs[[2]][coimg_degs[[2]] %in% rownames(PV_
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust=1))
```