

Figure 3

This notebook reproduces the main analyses from figure 2 of the manuscript. First we import the necessary packages.

```
library(tidyverse)
library(patchwork)
library(Seurat)
library(voxhunt)
```

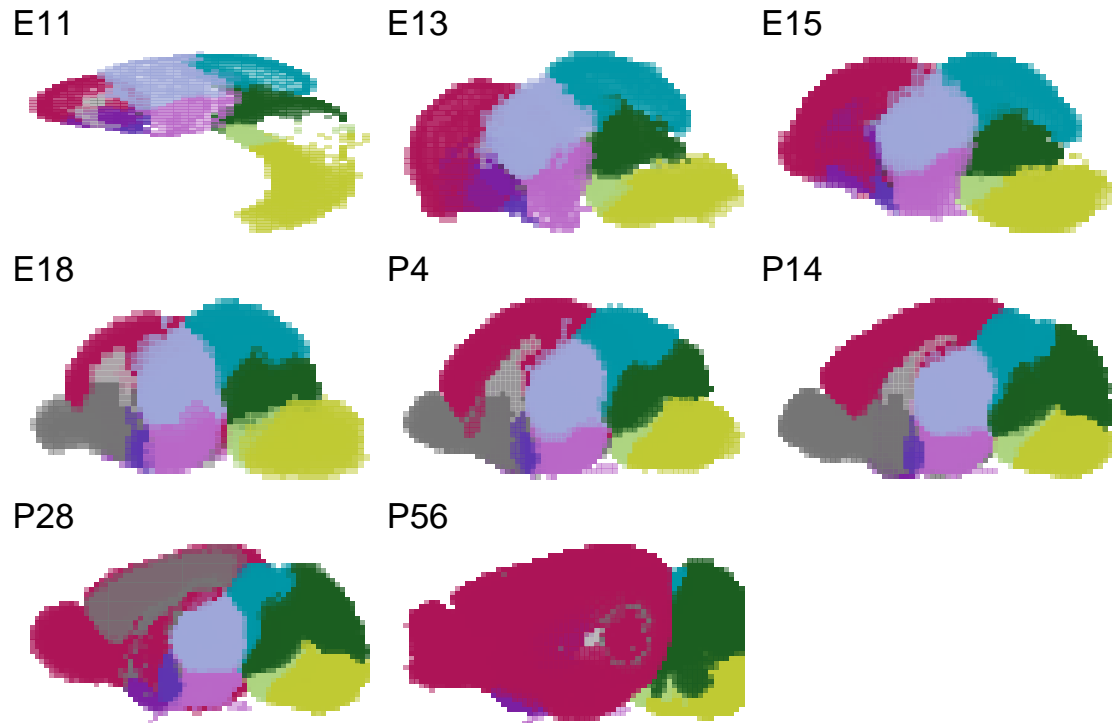
Now we load the data. The loaded seurat object contains the neuronal populations of the datasets shown in the manuscript. We further subset the ones shown in figure 2.

```
load_abi_data('voxhunt_data/')
```

We can plot annotations of the mouse brain at different timepoints with the `plot_annotation()` function:

```
e11 <- voxhunt::plot_annotation('E11')
e13 <- voxhunt::plot_annotation('E13')
e15 <- voxhunt::plot_annotation('E15')
e18 <- voxhunt::plot_annotation('E18')
p4 <- voxhunt::plot_annotation('P4')
p14 <- voxhunt::plot_annotation('P14')
p28 <- voxhunt::plot_annotation('P28')
p56 <- voxhunt::plot_annotation('P56')

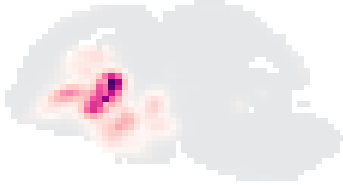
e11 + e13 + e15 + e18 + p4 + p14 + p28 + p56
```



Since for each voxel, the expression of almost 2000 genes is registered, we can plot some common markers:

```
marker_genes <- c('NEUROD6', 'EOMES', 'DCN', 'DLX1', 'DLX2',
                  'GBX2', 'OTX2', 'GATA3', 'PAX8')
voxhunt::plot_expression('E15', marker_genes, slices=8:12) & no_legend()
```

DLX1



OTX2



GATA3



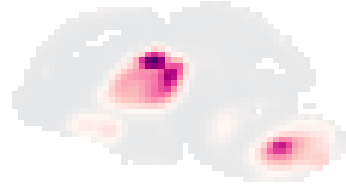
EOMES



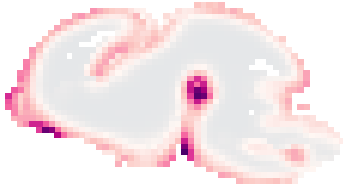
NEUROD6



GBX2



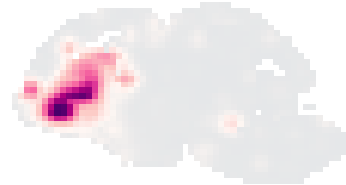
DCN



PAX8



DLX2



We can also look for markers of specific brain structures:

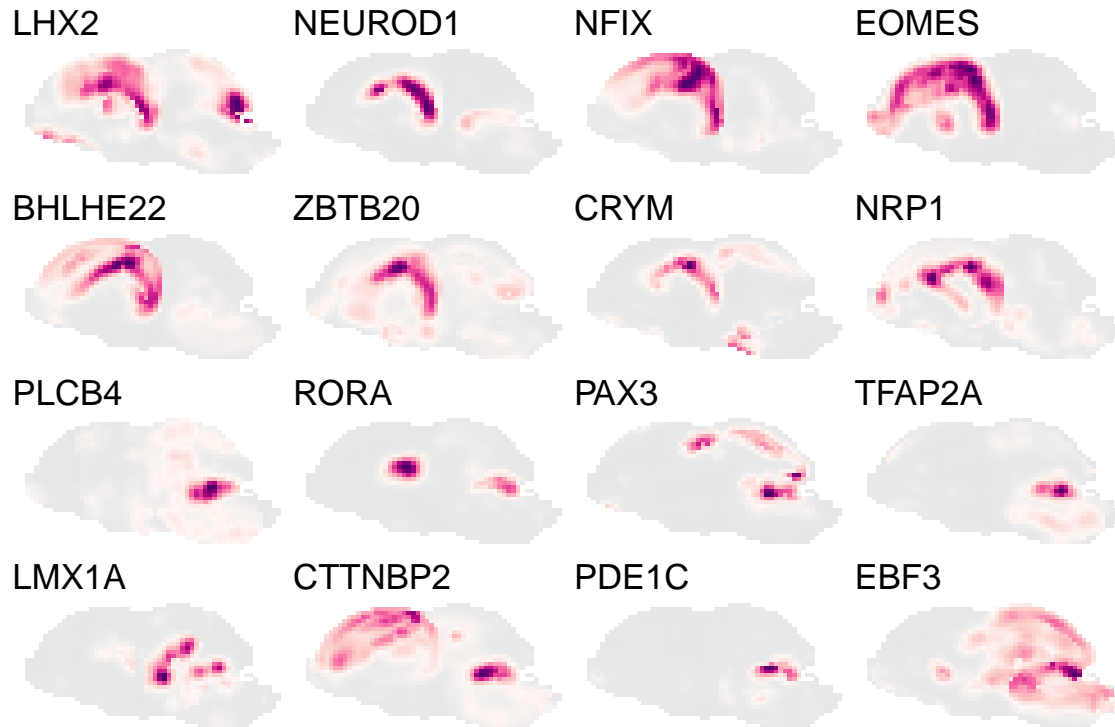
```
c4_markers <- structure_markers('E15', 'custom_4')
hipp_markers <- c4_markers %>%
  filter(group=='hippocampus') %>%
  top_n(8, auc) %>% pull(gene)

cb_markers <- c4_markers %>%
  filter(group=='cerebellar hemisphere') %>%
  top_n(8, auc) %>% pull(gene)

p1 <- voxhunt::plot_expression(
  'E15',
  hipp_markers,
  nrow=2
) & no_legend()

p2 <- voxhunt::plot_expression(
  'E15',
  cb_markers,
  nrow=2
) & no_legend()

p1 / p2
```



As shown in figure 2e), we can do this DE analysis on different levels of annotation at all available developmental stages:

```
c2_markers <- structure_markers('P4', 'custom_2')
top_markers <- c2_markers %>%
  group_by(group) %>%
  top_n(1, auc) %>%
  pull(gene)

voxhunt::plot_expression('P4', top_markers) & no_legend()
```

TCF4



TCF7L2



GPR88



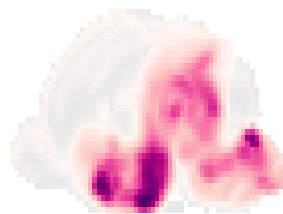
NEFH



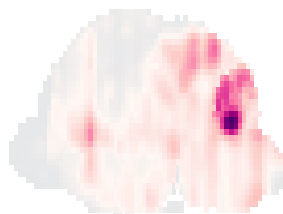
ZIC5



BAIAP3



PLCB4



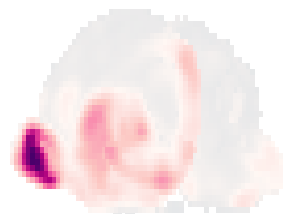
MEST



CNP



EGR1



SOX14

