

# WholeBrain tutorials

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# Chapter 1

## Preface

TBA



## Chapter 2

# Introduction



# **Chapter 3**

## **Segment**

Segmentation.



## **Chapter 4**

# **Registration**

TBA.



# Chapter 5

## Make web map

### 5.1 Static web maps.



# Chapter 6

## 3D reconstruction

Once you have processed more than one section you can collapse them into a single tidy data frame that can be used for 3D reconstruction..



# Chapter 7

## Statistical analysis

7.1 Handling data.

7.2 Plotting.

7.3 Modeling.



## Chapter 8

# Colocalization

TBA.



# Chapter 9

## smFISH

TBA.



# Chapter 10

## Spatial transcriptomics.

### 10.1 Load in the preprocessed WholeBrain/ST-data.

First lets load the segmentation of individual spots (with polygon contours) as well as their centroid (seg.spots list object) together with segmentation of individual cell nuclei (cells) and the registration object to the reference atlas (regi).

```
#load registration and segmentation output into R workspace
load('./data/spatial_transcriptomics/170605/D2_S4_seg_and_reg.RData')
```

With this you will have the following list objects in your working space:

- seg.spots output from `segmentation(image, get.contour=TRUE)` on the Cy3 spot image.
- cells output from `segmentation(image)` on the H&E image (individual nuclei and tissue contour).
- regi output from `registration(image, coordinate=X)`

Check that this is true by typing `ls()` in the R console to check objects in your working space.

```
ls()
```

```
## [1] "cells"      "regi"       "seg.spots"
```

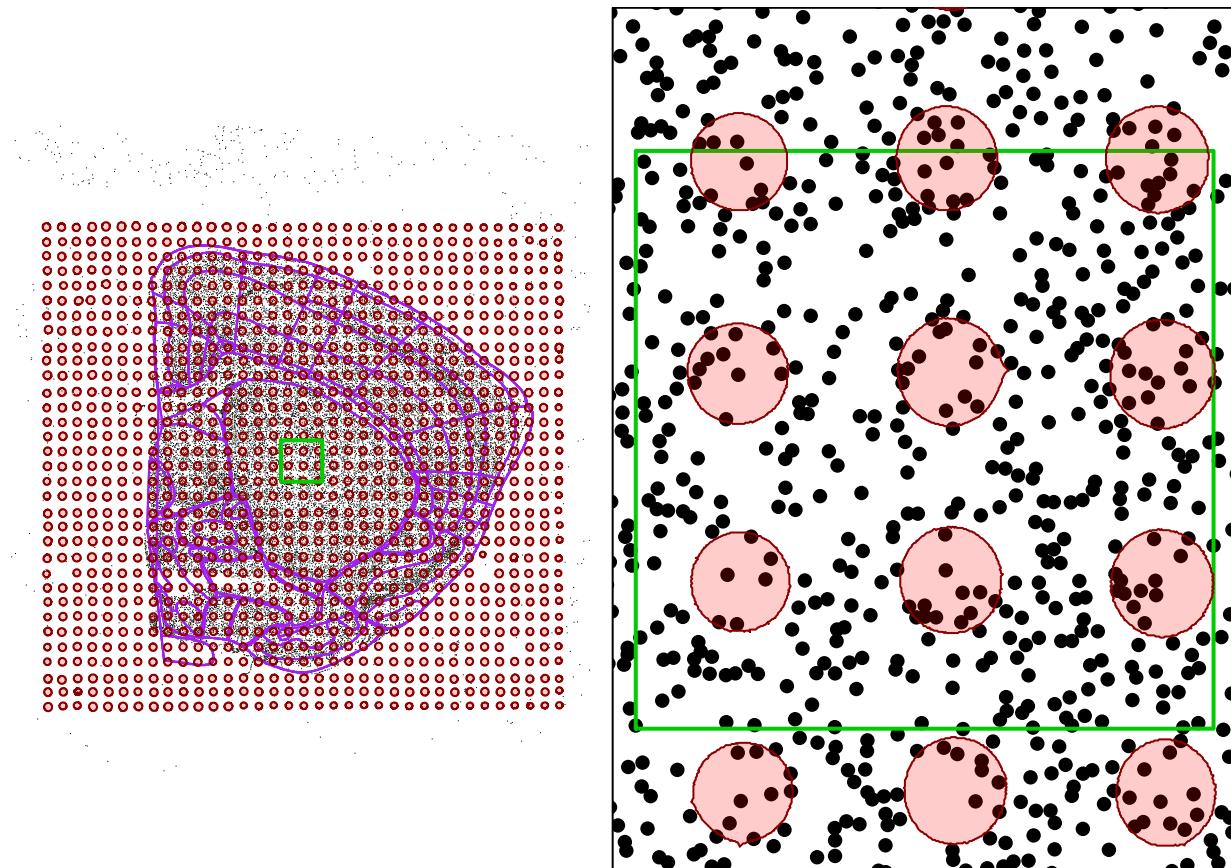
You can try to plot all individual cell nuclei and all segmented spots by the following commands:

```
#helper function to plot spots as polygons
polygon.spot<-function(contour.ID, alpha=0.2){
  x<-seg.spots$soma$contour.x[which(seg.spots$soma$contour.ID==contour.ID)]
  y<-seg.spots$soma$contour.y[which(seg.spots$soma$contour.ID==contour.ID)]
  polygon(x,y, border='darkred', col=rgb(1,0,0, alpha))
}

#helper function to plot atlas regions in the tissue
polygon.atlas<-function(contour.ID){
  #scale fatcor to upsample to original image
  scale.factor<-mean(c(regi$transformationgrid$height, regi$transformationgrid$width)/dim(regi$transformationgrid))
  for(i in 1:2){
    region<-regi$atlas$outlines[[contour.ID]][c(2*i-1, 2*i)+4]
    names(region)<-c('x', 'y')
    polygon(region$x*scale.factor, region$y*scale.factor, border='purple')
  }
}
```

Then lets plot this with:

```
#do some plotting
par(mfrow=c(1,2), mar=c(0,0,0,0))
#plot cell nuclei as black small spots
plot(cells$soma$x, cells$soma$y, cex=0.08, pch=16, ylim=c(max(cells$soma$y),0), asp=1, ylab='', xlab='')
#plot region outlines
invisible(lapply(1:regi$atlas$numRegions, polygon.atlas))
#plot spots as polygons
invisible(lapply(unique(seg.spots$soma$contour.ID), polygon.spot))
#make a ROI for closeup
roi<-list(x=median(cells$soma$x)+c(-1000,1000), y=median(cells$soma$y)+c(-1000,1000))
polygon(c(roi$x, rev(roi$x)), rep(roi$y, each=2), border='green3', lwd=2)
#plot closeup
#plot cell nuclei as black small spots
plot(cells$soma$x, cells$soma$y, cex=1, pch=16, ylim=roi$y, xlim=roi$x, asp=1, ylab='', xlab='', axes=)
polygon(c(roi$x, rev(roi$x)), rep(roi$y, each=2), border='green3', lwd=2)
box()
#plot spots as polygons
invisible(lapply(unique(seg.spots$soma$contour.ID), polygon.spot))
```



Then load in the integrated ST-data and WholeBrain dataset as a list object called dataset with the following members:

- dataset\$spots data.frame object from get.cells.ids(regi, seg.spots, forward.warps=TRUE)
- dataset\$genes data.frame object with transcript count where each row corresponds to the same row (spot) in dataset\$spots and each column is a gene.
- dataset\$nuclei data.frame object from get.cells.ids(regi, cells, forward.warps=TRUE) con-

tains all nuclei as rows and each nuclei is assigned to a spot.id (`dataset$nuclei$spot.id`) corresponding to spot.id in `dataset$spots$spot.id`

```
#load combined ST-data and WholeBrain output as a list object called dataset with members
# dataset$spots (row= individual spots, col= region acronyms etc), dataset$genes (row = spots, col=genes)
# dataset$nuclei individually segmented nuclei with parent spot indicated by spot.id
# which have corresponding vector in dataset$spots$spot.id.
load('./data/spatial_transcriptomics/170605/D2_S4_p1_0_mapped.RData')
```

Your working space should now look like:

```
ls()
```

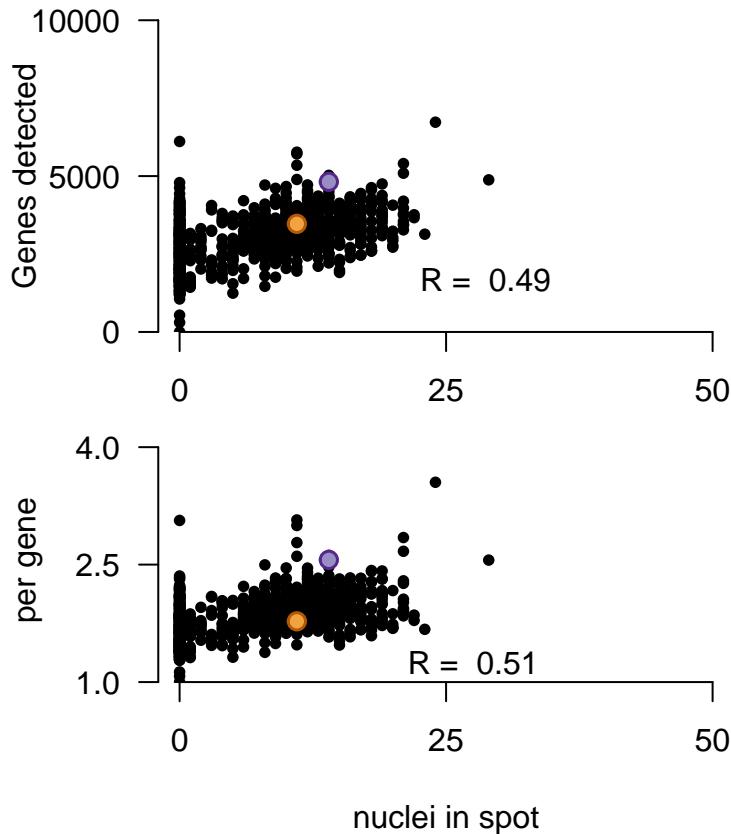
```
## [1] "cells"          "dataset"        "polygon.atlas" "polygon.spot"
## [5] "regi"           "roi"            "seg.spots"
```

We can for example see that there is a good correlation between number of nuclei inside a spot and number of detected genes:

```
genecount<-apply(dataset$genes, 1, function(x)sum(x>0))
gene.expression<-apply(dataset$genes, 1, function(x)mean(x[x>0]))

#Place Pearson correlation coefficient in quadrant.
get.quadrant<-function(x,y, lim=c(0.75,0.85),col='black'){
  text(max(x, na.rm=TRUE)*lim[1],
       max(y, na.rm=TRUE)*lim[2],
       paste('R = ', round(cor(na.omit(cbind(x, y)))[1,2],2)),
       col=col
     )
}

#plot
par(mfrow=c(1,2))
par(yaxs='i', xaxs='r', mar=c(2,4,1,2), mfrow=c(2,1))
plot(dataset$spots$nuclei, genecount, pch=16, cex=0.8, xlab='nuclei in spot', ylab='Genes detected', xlim=c(0,25), ylim=c(0,10000))
get.quadrant(dataset$spots$nuclei, genecount, lim=c(0.99,0.25))
points(data.frame(dataset$spots$nuclei, genecount)[which(dataset$spots$spot.id%in%c(693,706)),], pch=21, col='red')
axis(1, at=c(0,25,50))
axis(2, at=c(0,5000,10000), las=1)
par(mar=c(4,4,1,2))
plot(dataset$spots$nuclei, gene.expression, pch=16, cex=0.8, xlab='nuclei in spot', ylab='Avg. molecules per nucleus', xlim=c(0,25), ylim=c(0,10000))
get.quadrant(dataset$spots$nuclei, gene.expression, lim=c(0.95,0.35))
points(data.frame(dataset$spots$nuclei, gene.expression)[which(dataset$spots$spot.id%in%c(693,706)),], pch=21, col='red')
axis(1, at=c(0,25,50))
axis(2, at=c(1,2.5,4), las=1)
```



Let us now load in a custom plotting function for plotting gene expression for individual genes using **base R**.

## 10.2 Plotting gene expressions

The function to display gene expression with base R is the following load it into working space by running this code chunk:

```
plot.atlas<-function(regi, main='', xlim=c(0,4), ylim=c(-7, -1)){
  scale.factor<-mean(c(regi$transformationgrid$height, regi$transformationgrid$width)/dim(regi$transformationgrid))
  regi<-get.forward.warpRCP(regi)
  region<-regi$atlas$outlines[[1]][c(2*1-1,2*1)]
  names(region)<-c('x', 'y')
  index<-round(cbind(region$y, region$x))*scale.factor
  #region$x<-regi$transformationgrid$mxF[index]
  #region$y<-regi$transformationgrid$myF[index]
  region<-list(x=index[,2], y=index[,1])
  region<-stereotactic.coordinates(region$x, region$y, regi, inverse=FALSE)
  plot(region, asp=1, type='n', axes=FALSE, main = main, ylab='Dorso-ventral (mm)', xlab='Medio-lateral (mm)')

  for(j in 1:regi$atlas$numRegions){
    for(i in 1:2){
      region<-regi$atlas$outlines[[j]][c(2*1-1,2*1)]
      names(region)<-c('x', 'y')
      index<-round(cbind(region$y, region$x))*scale.factor
      #region$x<-regi$transformationgrid$mxF[index]
      #region$y<-regi$transformationgrid$myF[index]
```

```

#region$y<-regi$transformationgrid$myF[index]
region<-list(x=index[,2], y=index[,1])
region<-stereotactic.coordinates(region$x, region$y, regi, inverse=FALSE)
polygon(region$x, region$y, border='black', col=gray(0.95))
}
}
xlim<-sort(xlim, decreasing=TRUE)
ylim<-sort(ylim, decreasing=TRUE)

axis(2, at = seq(ylim[1], ylim[2], by=-0.1), labels = FALSE, las = 1, col = "orange", tck = -0.0125)
axis(2, at = seq(ylim[1], ylim[2], by=-0.5), labels = FALSE, las = 1, col = "darkblue", tck = -0.025)
axis(2, at = ylim[1]:ylim[2], las = 1)

axis(1, at = seq(xlim[1], -xlim[2], by=-0.1), labels = FALSE, las = 1, col = "orange", tck = -0.0125)
axis(1, at = seq(xlim[1], -xlim[2], by=-0.5), labels = FALSE, las = 1, col = "darkblue", tck = -0.025)
axis(1, at = xlim[1]:xlim[2], las = 1)

}

plot.gene<-function(dataset, regi, gene, colorfunc = heat.colors, atlas=TRUE){
  if(atlas)
    plot.atlas(regi, main=gene)

  gene<-dataset$genes[,gene]
  colors <- mapply(function(col, i) adjustcolor(col, alpha.f = (gene/max(gene))[i]),
                  colorfunc(length(unique(gene)))[gene+1], seq_along(gene))

  inside.tissue<-!is.na(dataset$spots$acronym)
  points(dataset$spots$ML[inside.tissue], dataset$spots$DV[inside.tissue], pch=16, col=colors[inside.tissue])
}

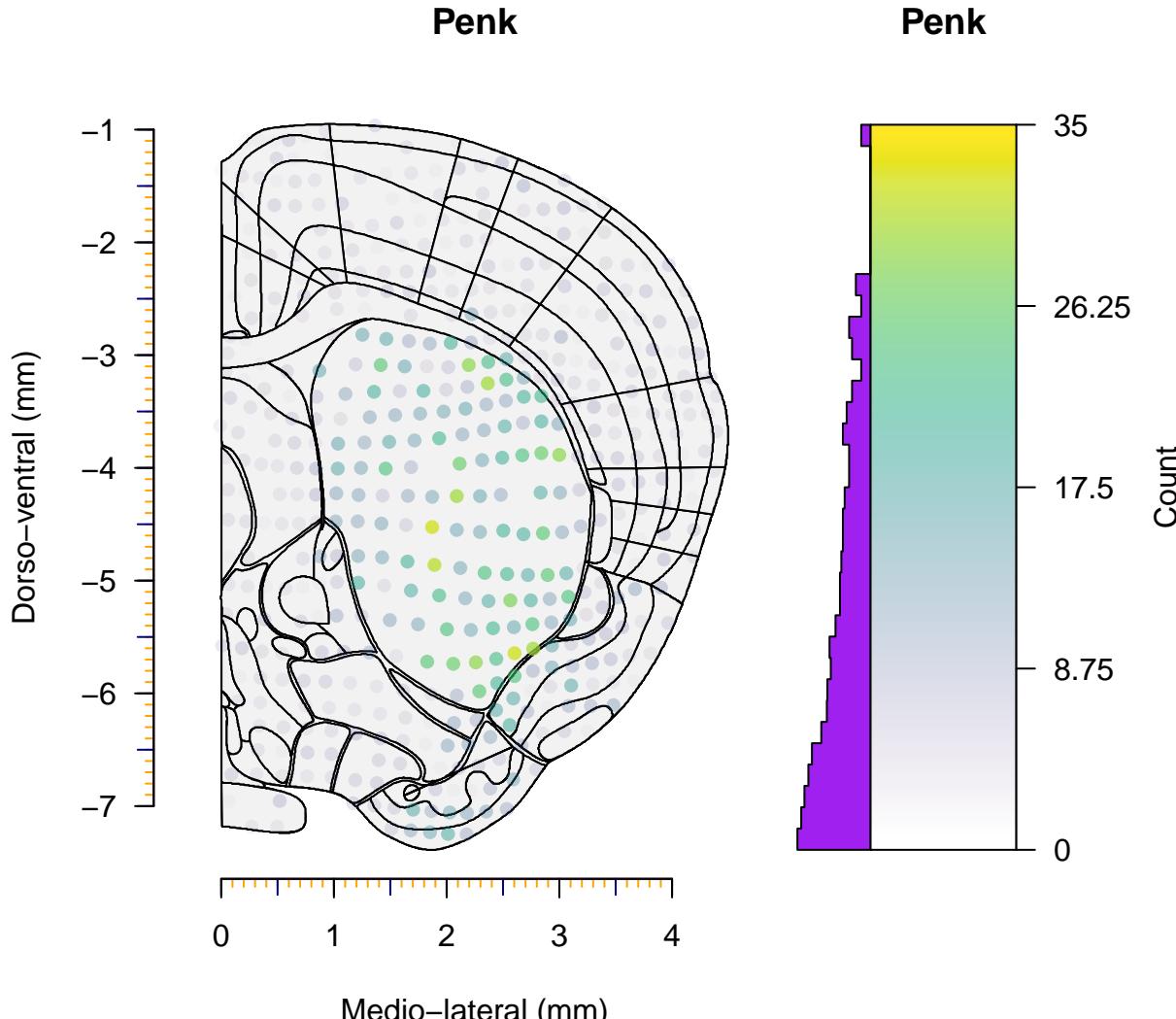
legend.gene<-function(dataset, gene, colorfunc = heat.colors){
  par(xaxs='i')
  plot(c(0,1),c(0,1),type = 'n', axes = F,xlab = '', ylab = '', main = gene, xlim=c(0,1))
  gene<-dataset$genes[,gene]
  color<-sapply(seq_along(unique(gene)), function(x){adjustcolor(colorfunc(length(unique(gene)))[x], alpha=0.5)})
  legend_image <- as.raster(matrix(rev(color), ncol=1))
  axis(4, at = seq(0,1,l=5), labels = seq(0,max(gene),l=5), las=1)
  rasterImage(legend_image, 0, 0, 1,1)
  polygon(c(0,1,1,0), c(0, 0, 1,1))
  mtext('Count',4,3.5)
  histogram<-hist(gene, breaks=seq(0,max(gene)), plot=FALSE)
  y<-histogram$counts
  y<-log2(y+1)
  y<-0.5*(y/max(y))
  x<-(histogram$mids-0.5)/max(histogram$mids-0.5)
  y<-c(0, -rep(y, each=2)[-length(rep(y, each=2))])
  x<-rep(x, each=2)
  par(xpd=T)
  polygon(c(y, rep(0, length(y))), c(x, rev(x)), col='purple')
  par(xpd=F)
}

```

```
#viridis for color scale
library(viridis)
```

Now we can plot any gene like this:

```
layout(matrix(1:2,ncol=2), width = c(4,3),height = c(1,1))
par(mar=c(4,4,4,0))
plot.gene(dataset, regi, gene='Penk', colorfunc=viridis)
par(mar=c(4,2,4,10))
legend.gene(dataset, gene='Penk', colorfunc=viridis)
```



Now lets declare a plotting function for plotting all genes we throw at it in a vector:

```
plot.these.genes<-function(geneList){
non.detected<-character()
striatum<-character()
somatosensory<-character()
for(i in geneList){

if(sum(i%in%names(dataset$genes)) ) {
  layout(matrix(1:2,ncol=2), width = c(2,1),height = c(1,1))
```

```

par(mar=c(4,4,4,0))
plot.gene(dataset, regi, gene=i, colorfunc=viridis)
par(mar=c(4,2,4,5))
legend.gene(dataset, gene=i, colorfunc=viridis)

cat(i)
region.index<-substr(dataset$spots$acronym, 1,2)
CP<-dataset$genes[which(region.index=='CP'), i]
SS<-dataset$genes[which(region.index=='SS'), i]
ttest<-t.test(CP, SS)
if(!is.nan(ttest$p.value)){
  if(ttest$p.value<0.05){
    cat('          ')
    if(ttest$statistic<0){
      cat(' MARKER FOR SOMATOSENSORY!')
      somatosensory<-append(somatosensory, i)
    }else{
      cat(' MARKER FOR CAUDATE PUTAMEN!')
      striatum<-append(striatum, i)
    }
  }
}

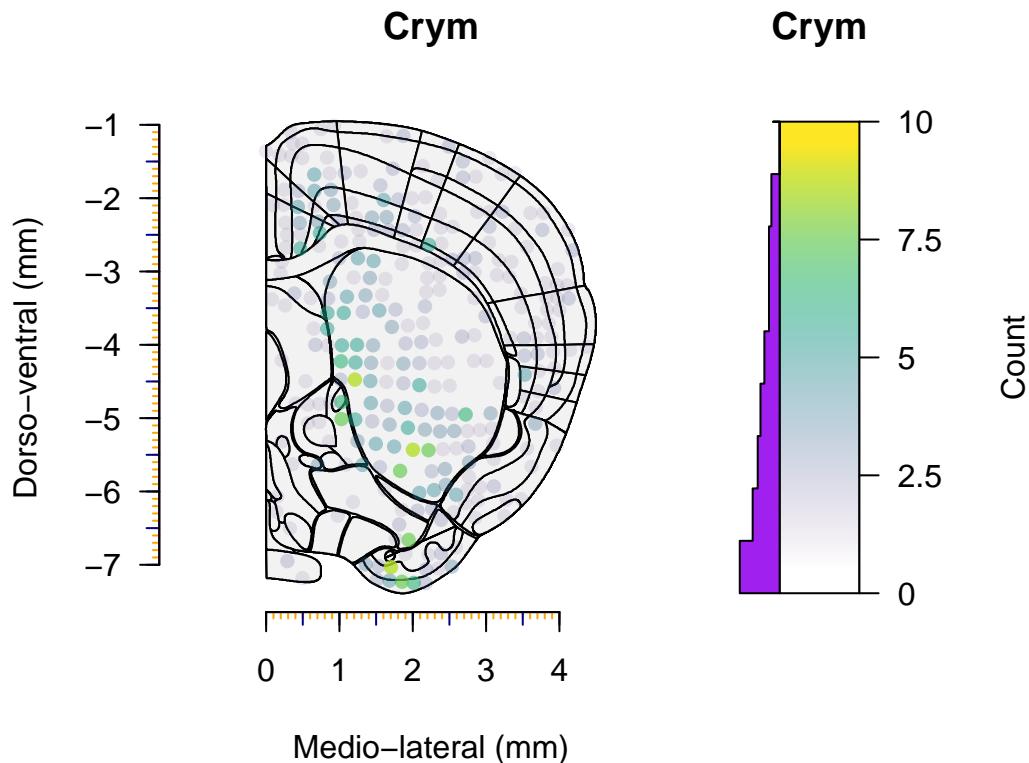
cat(paste('\n ----- \n Average number of', i, 'transcripts detected:\n CPu : M =', round(mean(CP), 2),
print(ttest)
}else{
  non.detected<-append(non.detected, i)
}
}
cat(paste0('\n Nondetected genes: \n', paste0(non.detected, collapse=', ')))
return(list(non.detected = non.detected, striatum = striatum, somatosensory = somatosensory))
}

```

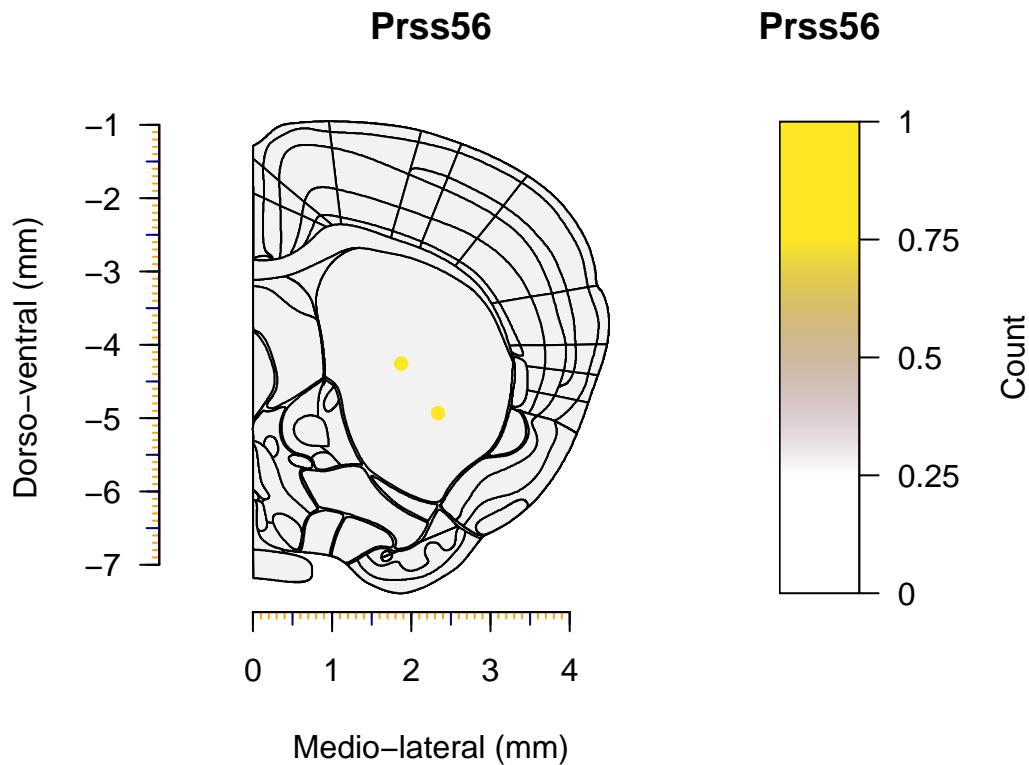
## 10.3 Confirmatory analysis

Running `plot.these.genes()` with a character vector of genes that we are interested will plot all of them:

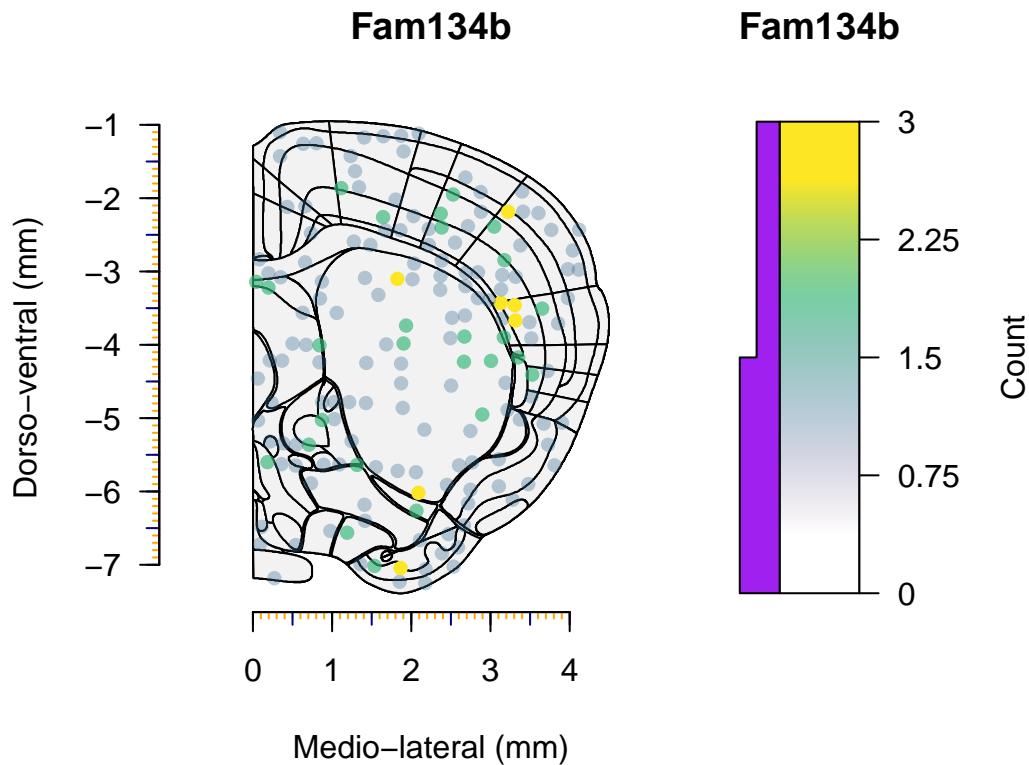
*#Genes that are differentially expressed between striatal and somatosensory cortical astrocytes:*  
`astrocytes<-c("Crym", "6330403K07Rik", "Prss56", "Fam134b", "Sntb1", "Rcn1", "Nme6", "Bex2", "Hey2", "S`  
`conf.analysis<-plot.these.genes(astrocytes)`



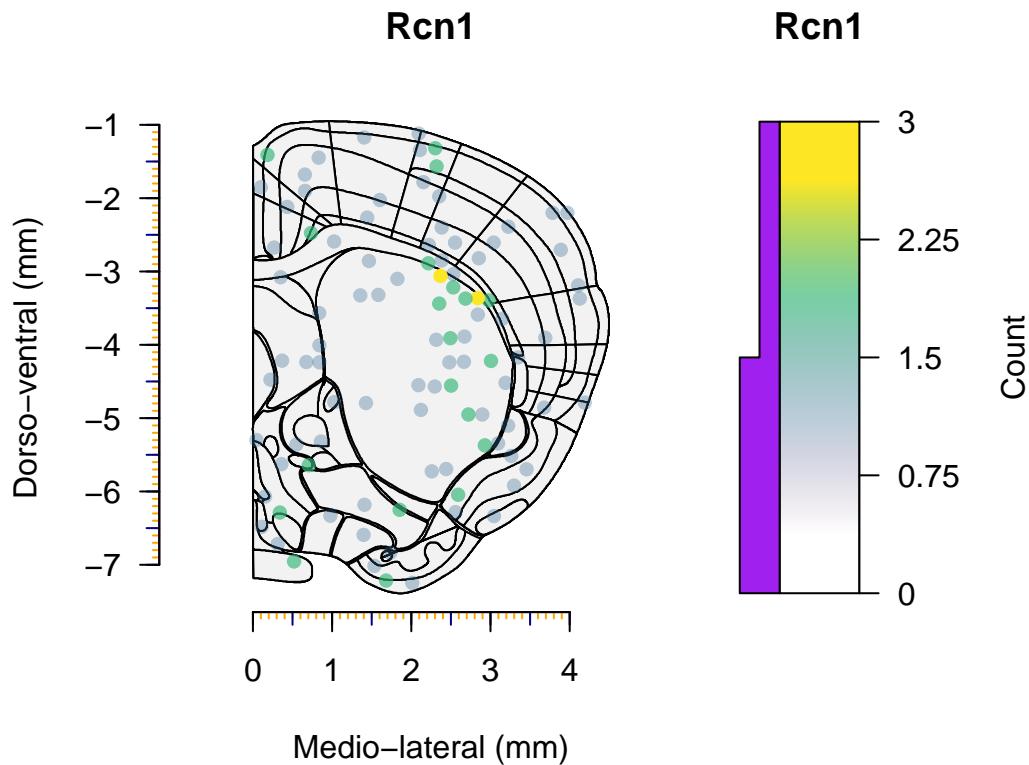
```
## Crym                         MARKER FOR CAUDATE PUTAMEN!
## -----
## Average number of Crym transcripts detected:
## CPu : M = 2.17 ( SD = 2.19 ) molecules
## SS : M = 0.63 ( SD = 0.8 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = 7.1829, df = 145.34, p-value = 3.274e-11
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  1.119830 1.970018
## sample estimates:
## mean of x mean of y
## 2.1709402 0.6260163
```



```
## Prss56
## -----
## Average number of Prss56 transcripts detected:
## CPu : M = 0.02 ( SD = 0.13 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = 1.4203, df = 116, p-value = 0.1582
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.00674298 0.04093101
## sample estimates:
## mean of x mean of y
## 0.01709402 0.00000000
```



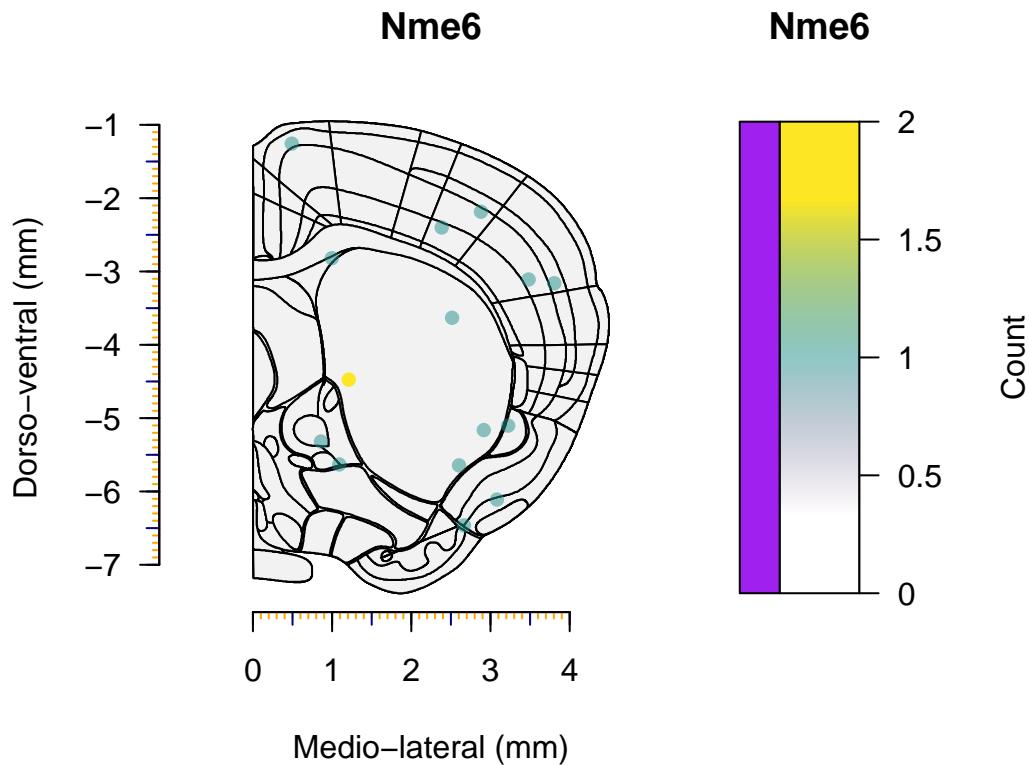
```
## Fam134b
## -----
## Average number of Fam134b transcripts detected:
## CPu : M = 0.41 ( SD = 0.67 ) molecules
## SS : M = 0.42 ( SD = 0.74 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = -0.13768, df = 237.6, p-value = 0.8906
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.1914788 0.1664632
## sample estimates:
## mean of x mean of y
## 0.4102564 0.4227642
```



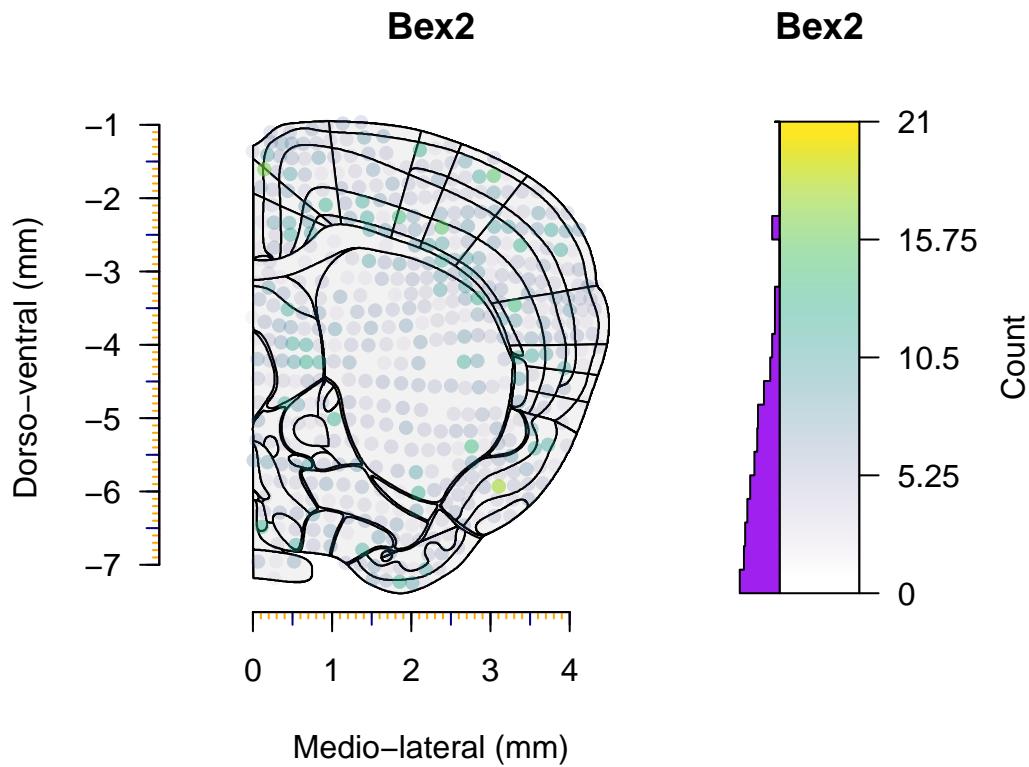
```

## Rcn1          MARKER FOR CAUDATE PUTAMEN!
## -----
## Average number of Rcn1 transcripts detected:
## CPu : M = 0.34 ( SD = 0.68 ) molecules
## SS : M = 0.16 ( SD = 0.41 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = 2.443, df = 188.58, p-value = 0.01549
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.03451781 0.32403962
## sample estimates:
## mean of x mean of y
## 0.3418803 0.1626016

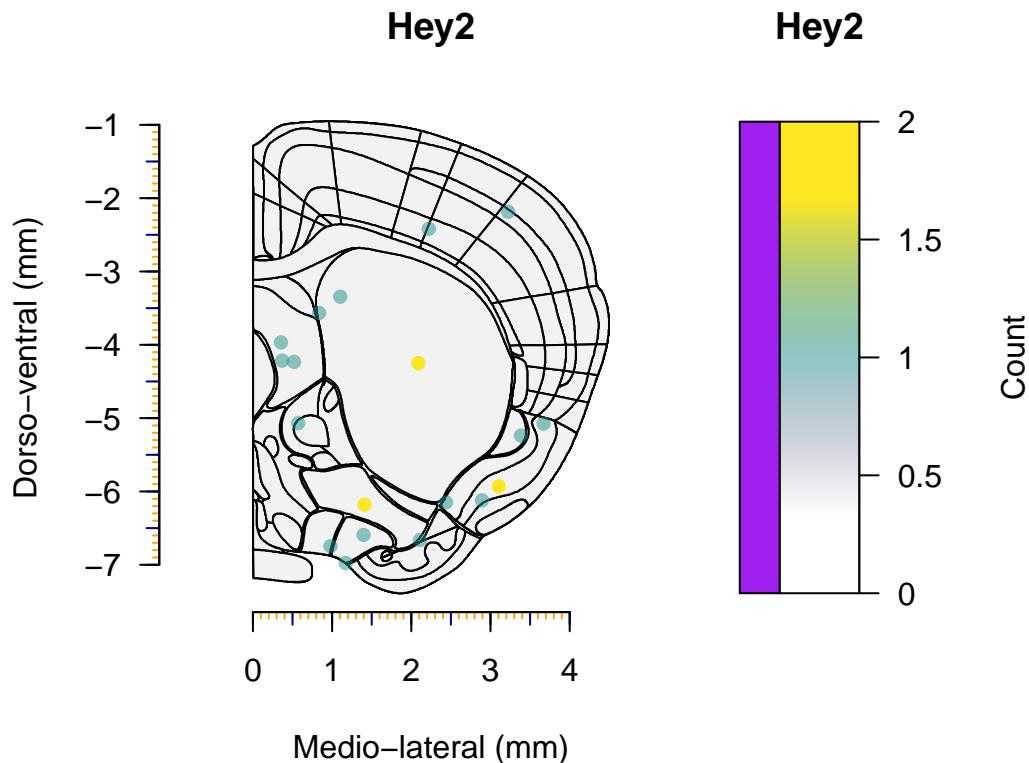
```



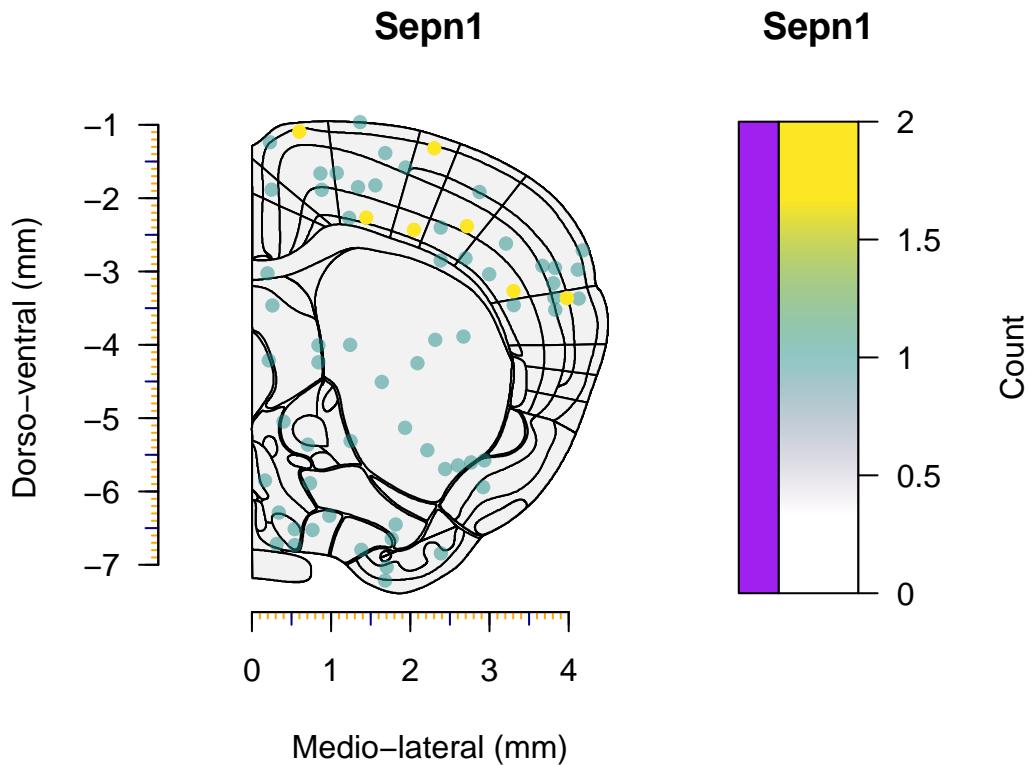
```
## Nme6
## -----
## Average number of Nme6 transcripts detected:
## CPu : M = 0.04 ( SD = 0.24 ) molecules
## SS : M = 0.03 ( SD = 0.18 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = 0.37104, df = 212.71, p-value = 0.711
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.04405236 0.06448180
## sample estimates:
## mean of x mean of y
## 0.04273504 0.03252033
```



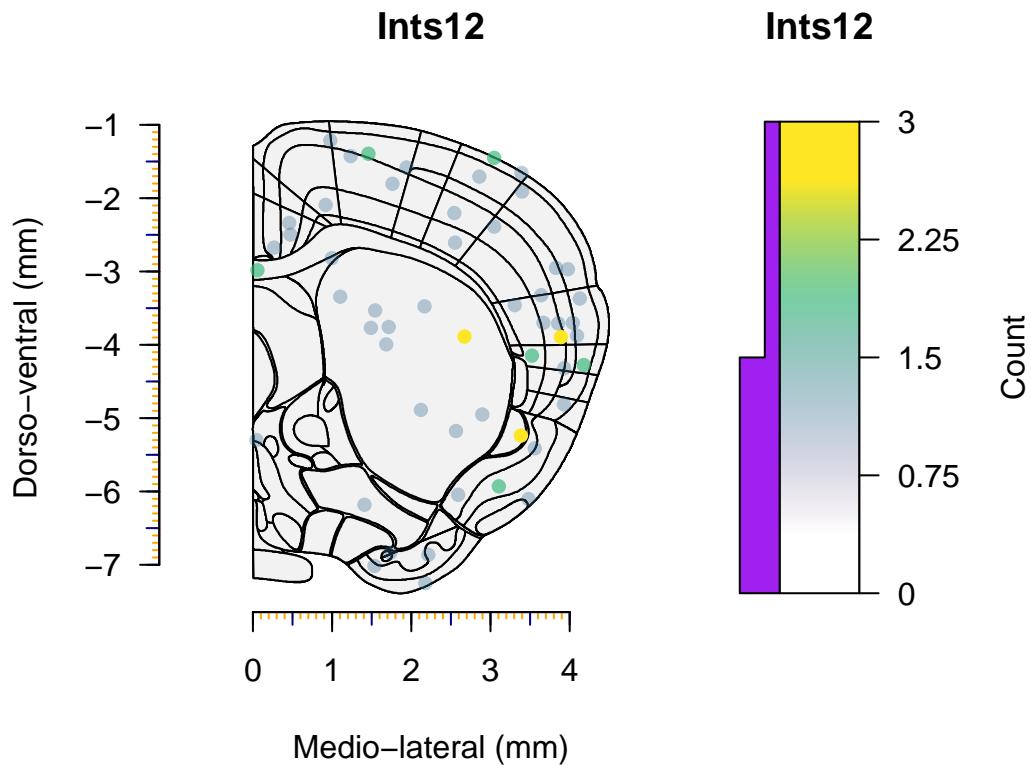
```
## Bex2
## -----
## Average number of Bex2 transcripts detected:
## CPu : M = 3.17 ( SD = 2.02 ) molecules
## SS : M = 3.67 ( SD = 2.48 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = -1.7041, df = 232.63, p-value = 0.08969
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.06886101 0.07740801
## sample estimates:
## mean of x mean of y
## 3.170940 3.666667
```



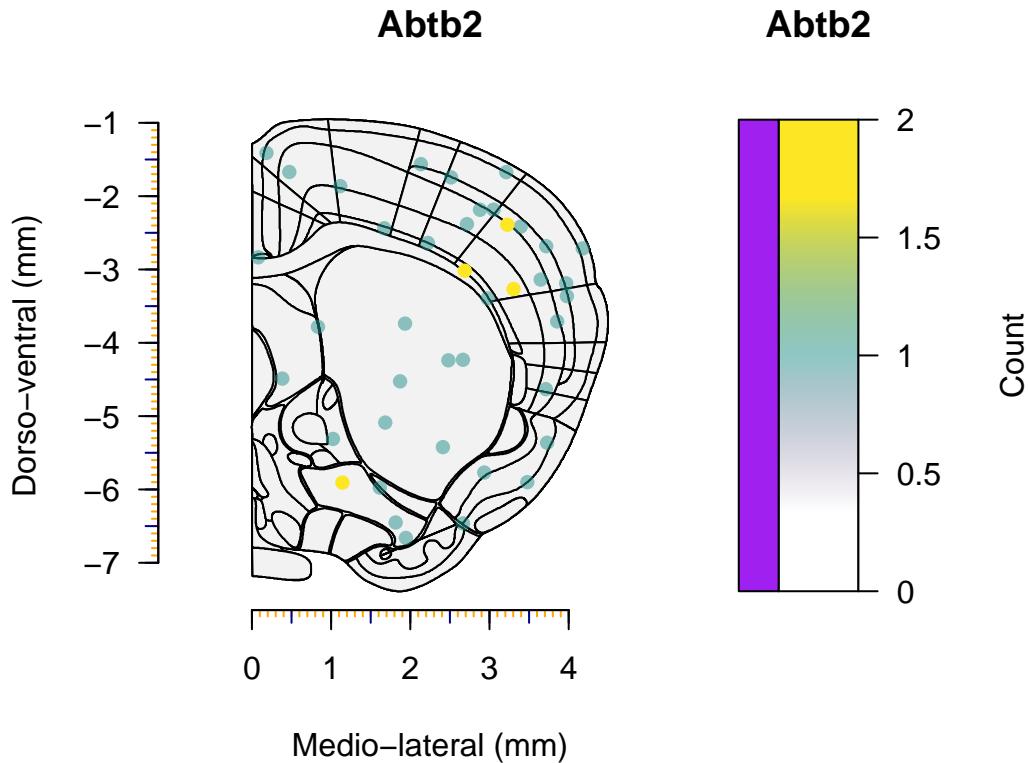
```
## Hey2
## -----
## Average number of Hey2 transcripts detected:
## CPu : M = 0.03 ( SD = 0.22 ) molecules
## SS : M = 0.02 ( SD = 0.13 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = 0.75549, df = 181.22, p-value = 0.4509
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.02889519  0.06475094
## sample estimates:
## mean of x mean of y
## 0.03418803 0.01626016
```



```
## Sepn1          MARKER FOR SOMATOSENSORY!
## -----
## Average number of Sepn1 transcripts detected:
## CPu : M = 0.08 ( SD = 0.27 ) molecules
## SS : M = 0.2 ( SD = 0.49 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = -2.3335, df = 190.73, p-value = 0.02067
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.21811251 -0.01828524
## sample estimates:
## mean of x mean of y
## 0.07692308 0.19512195
```



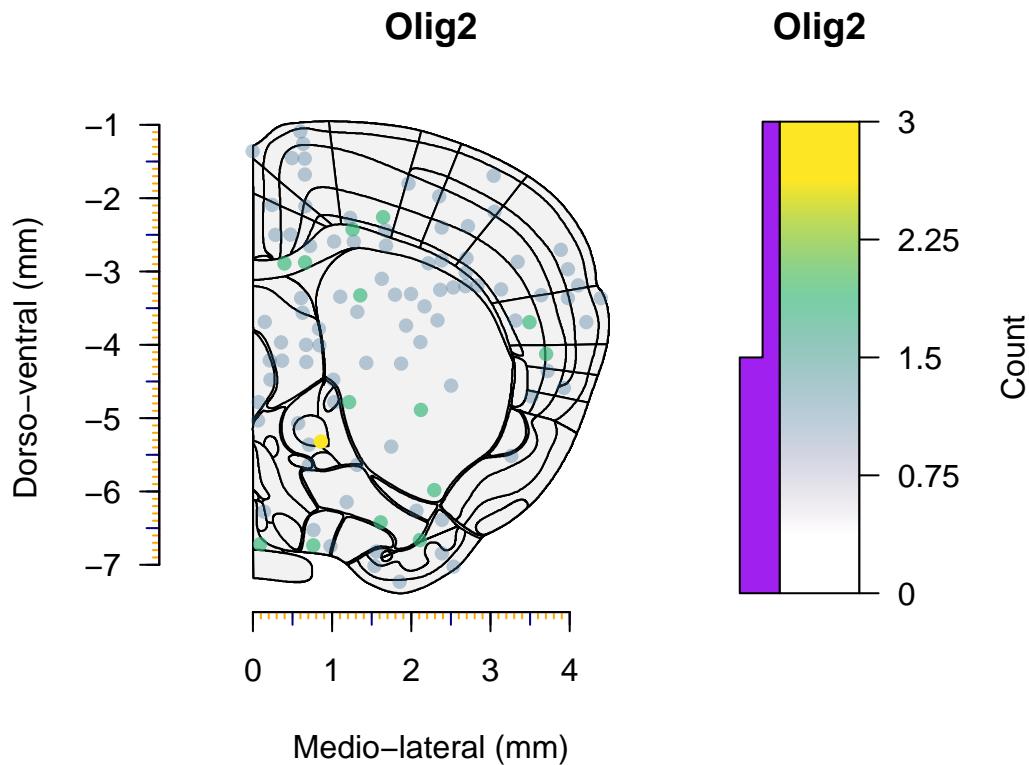
```
## Ints12
## -----
## Average number of Ints12 transcripts detected:
## CPu : M = 0.1 ( SD = 0.38 ) molecules
## SS : M = 0.16 ( SD = 0.45 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = -1.1178, df = 234.72, p-value = 0.2648
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.16585309  0.04577804
## sample estimates:
## mean of x mean of y
## 0.1025641  0.1626016
```



```

## Abtb2          MARKER FOR SOMATOSENSORY!
## -----
## Average number of Abtb2 transcripts detected:
## CPu : M = 0.05 ( SD = 0.22 ) molecules
## SS : M = 0.16 ( SD = 0.43 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = -2.5304, df = 184.03, p-value = 0.01223
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.19811407 -0.02452508
## sample estimates:
## mean of x mean of y
## 0.05128205 0.16260163

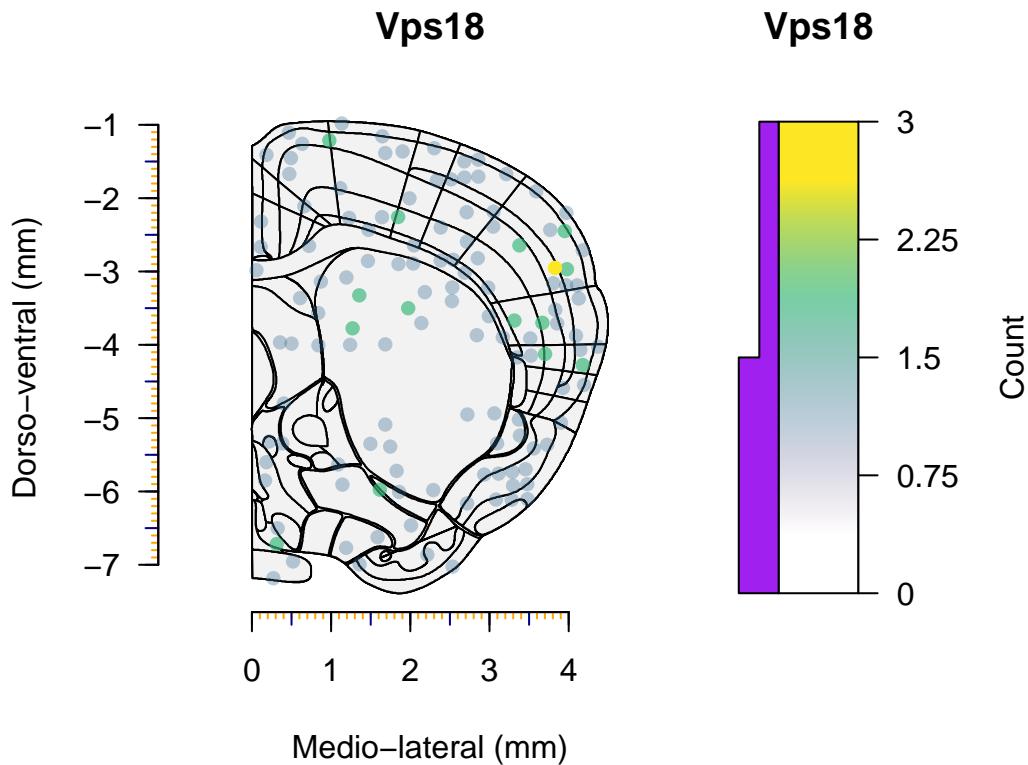
```



```

## Olig2
## -----
## Average number of Olig2 transcripts detected:
## CPu : M = 0.21 ( SD = 0.49 ) molecules
## SS : M = 0.16 ( SD = 0.39 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = 0.8908, df = 222.36, p-value = 0.374
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.06191493 0.16406211
## sample estimates:
## mean of x mean of y
## 0.2136752 0.1626016

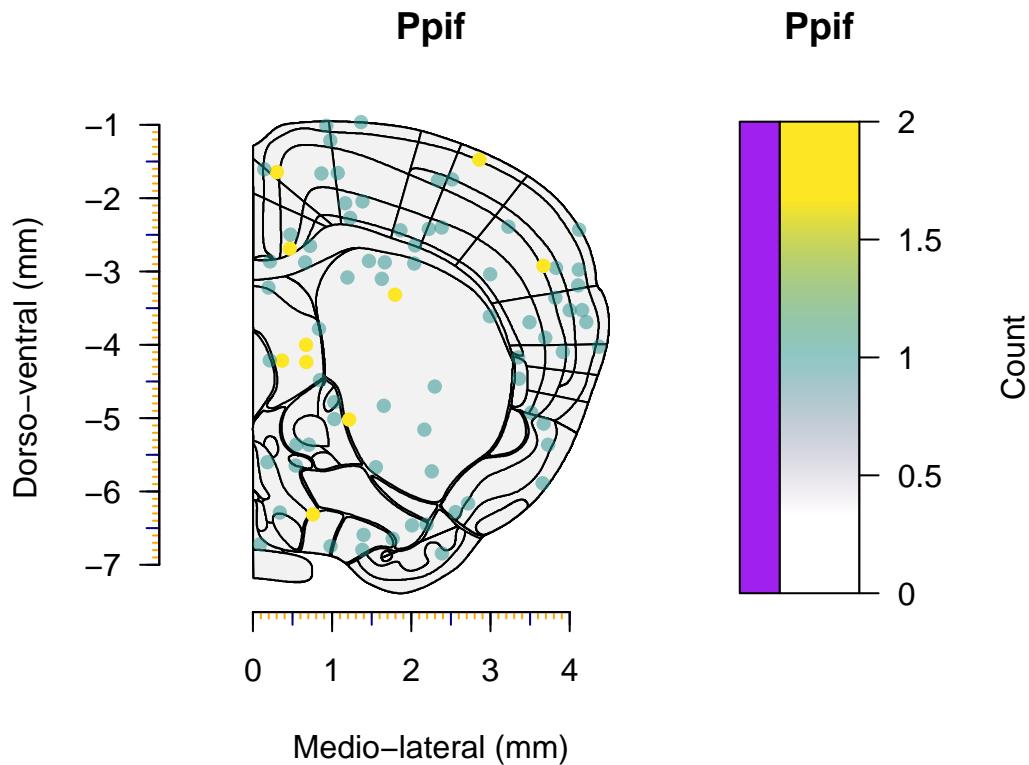
```



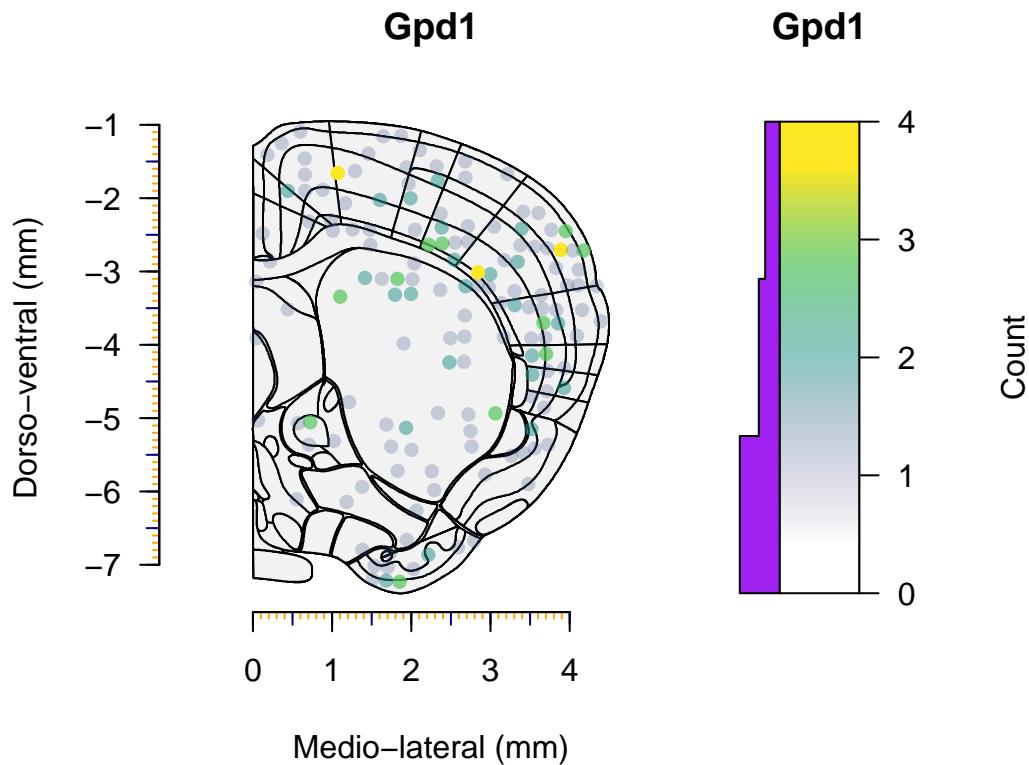
```

## Vps18          MARKER FOR SOMATOSENSORY!
## -----
## Average number of Vps18 transcripts detected:
## CPu : M = 0.23 ( SD = 0.48 ) molecules
## SS : M = 0.37 ( SD = 0.62 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = -2.0072, df = 228.85, p-value = 0.04591
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.283802806 -0.002626212
## sample estimates:
## mean of x mean of y
## 0.2307692 0.3739837

```



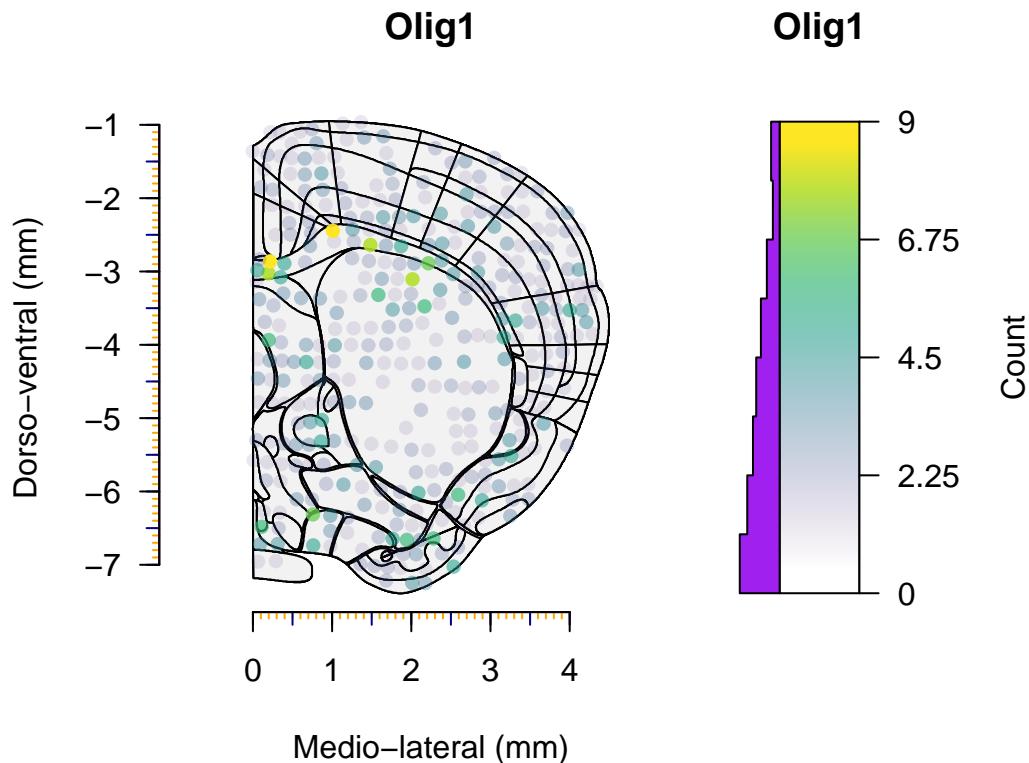
```
## Ppif
## -----
## Average number of Ppif transcripts detected:
## CPu : M = 0.13 ( SD = 0.38 ) molecules
## SS : M = 0.18 ( SD = 0.43 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = -0.96975, df = 237.34, p-value = 0.3332
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.15356323  0.05224991
## sample estimates:
## mean of x mean of y
## 0.1282051  0.1788618
```



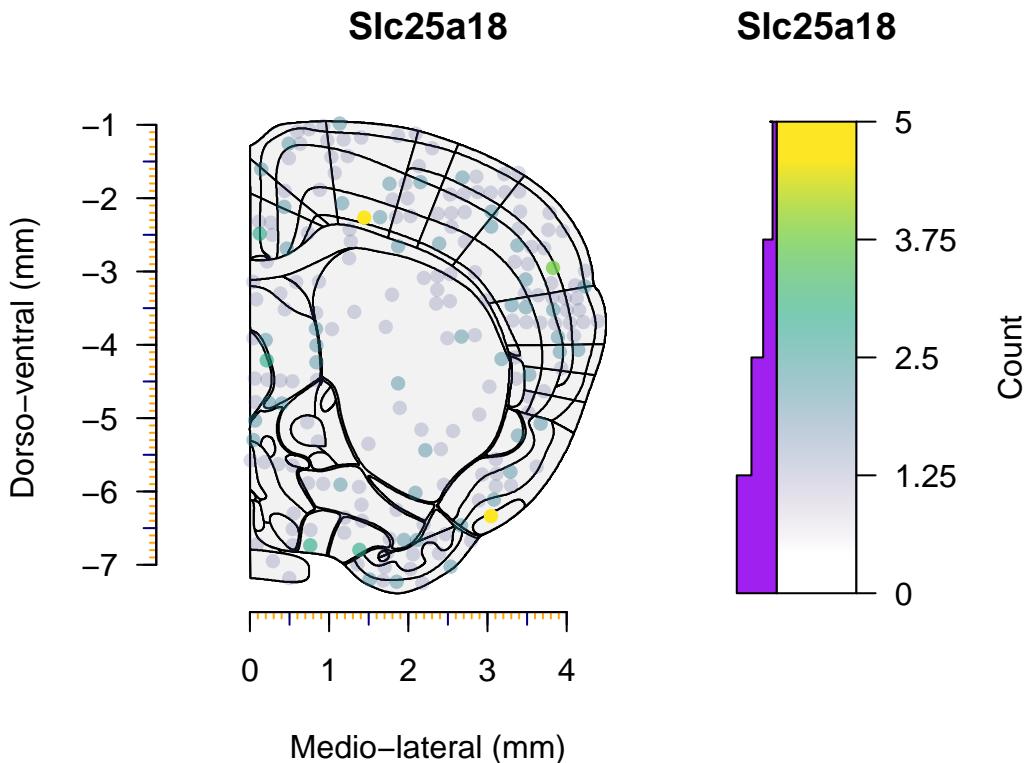
```

## Gpd1          MARKER FOR SOMATOSENSORY!
## -----
## Average number of Gpd1 transcripts detected:
## CPu : M = 0.35 ( SD = 0.7 ) molecules
## SS : M = 0.63 ( SD = 0.91 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data:  CP and SS
## t = -2.721, df = 228.2, p-value = 0.007011
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.48917663 -0.07826135
## sample estimates:
## mean of x mean of y
## 0.3504274 0.6341463

```



```
## Olig1
## -----
## Average number of Olig1 transcripts detected:
## CPu : M = 1.38 ( SD = 1.49 ) molecules
## SS : M = 1.29 ( SD = 1.34 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = 0.45585, df = 232.13, p-value = 0.6489
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.2770180 0.4437889
## sample estimates:
## mean of x mean of y
## 1.376068 1.292683
```



```
## Slc25a18          MARKER FOR SOMATOSENSORY!
## -----
## Average number of Slc25a18 transcripts detected:
## CPu : M = 0.27 ( SD = 0.54 ) molecules
## SS : M = 0.62 ( SD = 0.73 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = -4.1812, df = 223.72, p-value = 4.164e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.5066931 -0.1820708
## sample estimates:
## mean of x mean of y
## 0.2735043 0.6178862
## 
## 
## Nondetected genes:
## 6330403K07Rik, Sntb1
```

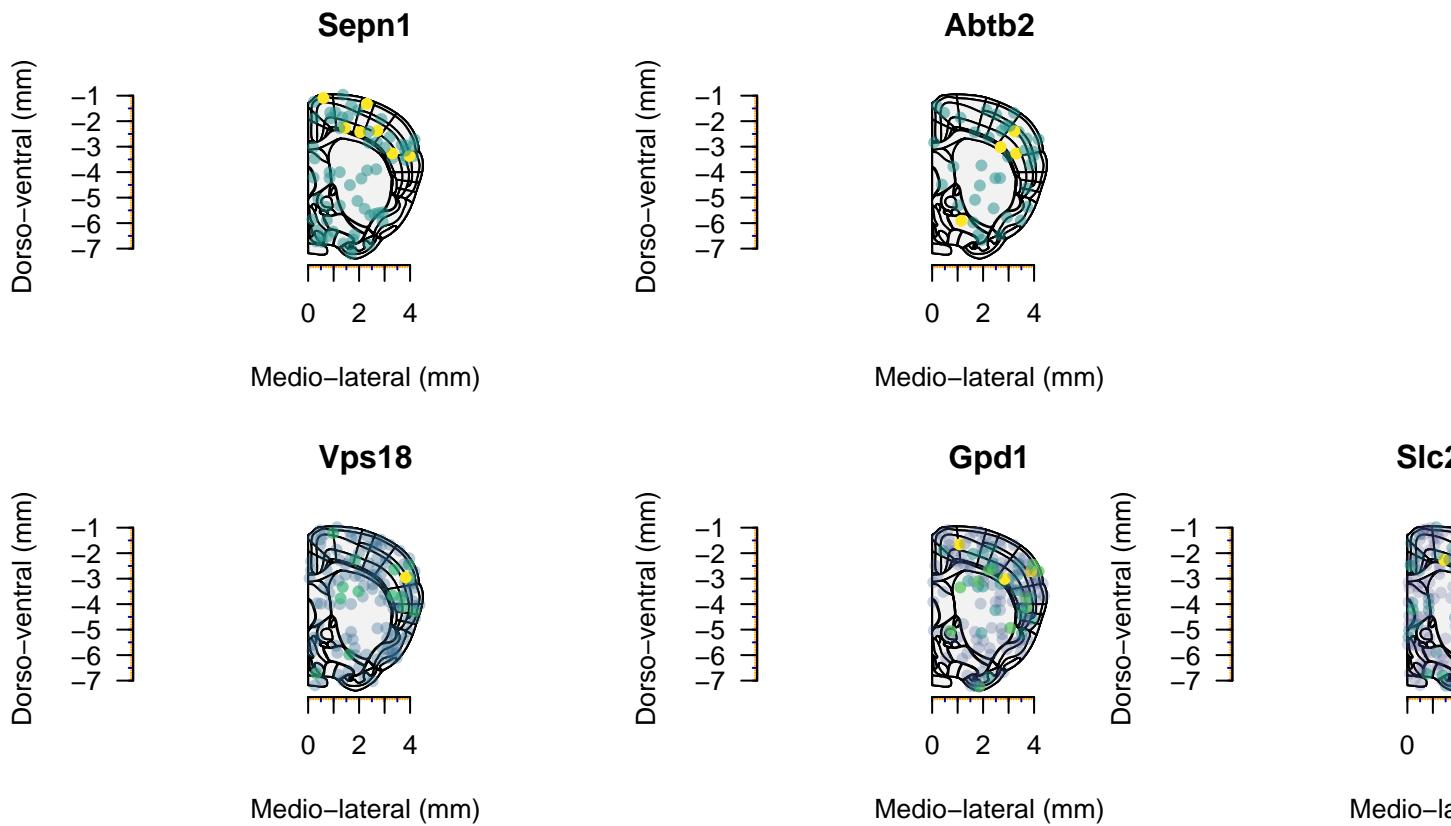
### 10.3.1 Confirmatory conclusion:

- Somatosensory:
- {r} cat(paste(conf.analysis\$somatosensory , collapse=' ,'))
- Striatal:
- {r} cat(paste(conf.analysis\$striatum , collapse=' ,'))
- Non detected:

- {r} cat(paste(conf.analysis\$non.detected , collapse=' '))

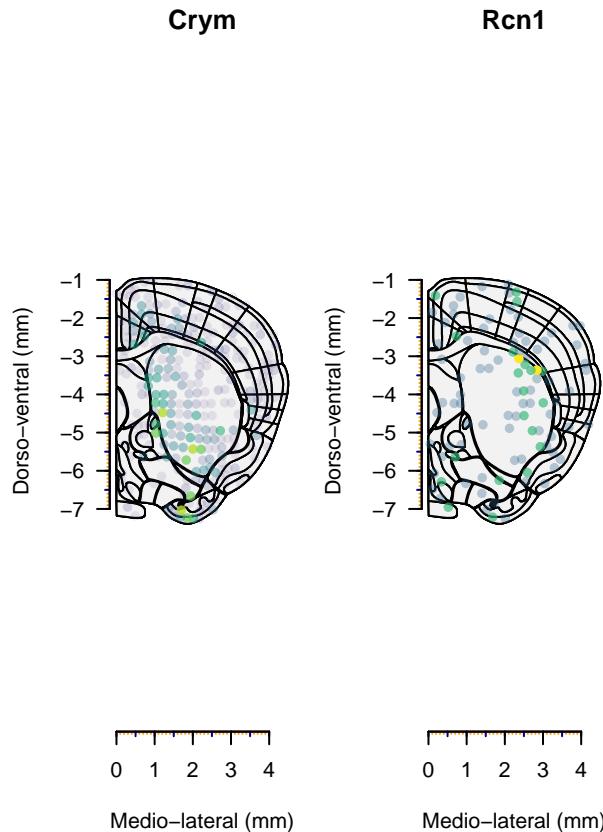
### 10.3.2 Somatosensory:

```
par(mfrow=c(length(conf.analysis$somatosensory)%/%4+1,4%/%4+1), mar=c(4,4,4,1))
invisible(sapply(conf.analysis$somatosensory, function(x)plot.gene(dataset, regi, gene=x, colorfunc=viridis)))
```



### 10.3.3 Striatal:

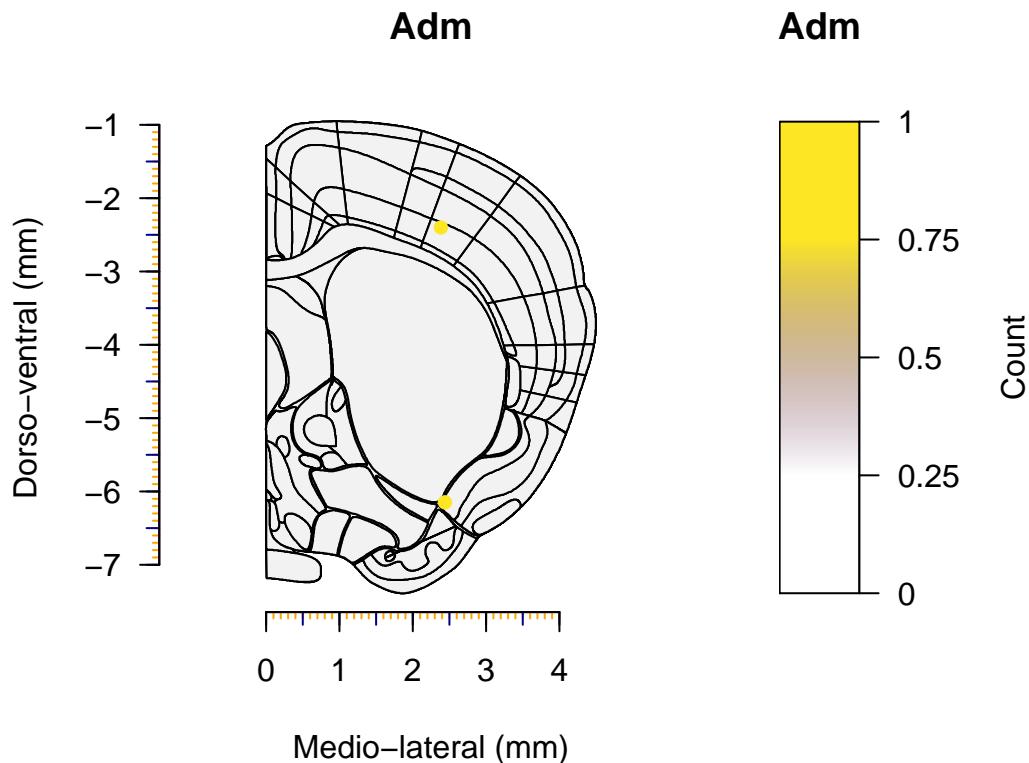
```
par(mfrow=c(length(conf.analysis$striatum)%/%4+1,4), mar=c(4,4,4,1))
invisible(sapply(conf.analysis$striatum, function(x)plot.gene(dataset, regi, gene=x, colorfunc=viridis)))
```



## 10.4 Exploratory analysis

Now lets run for some other genes:

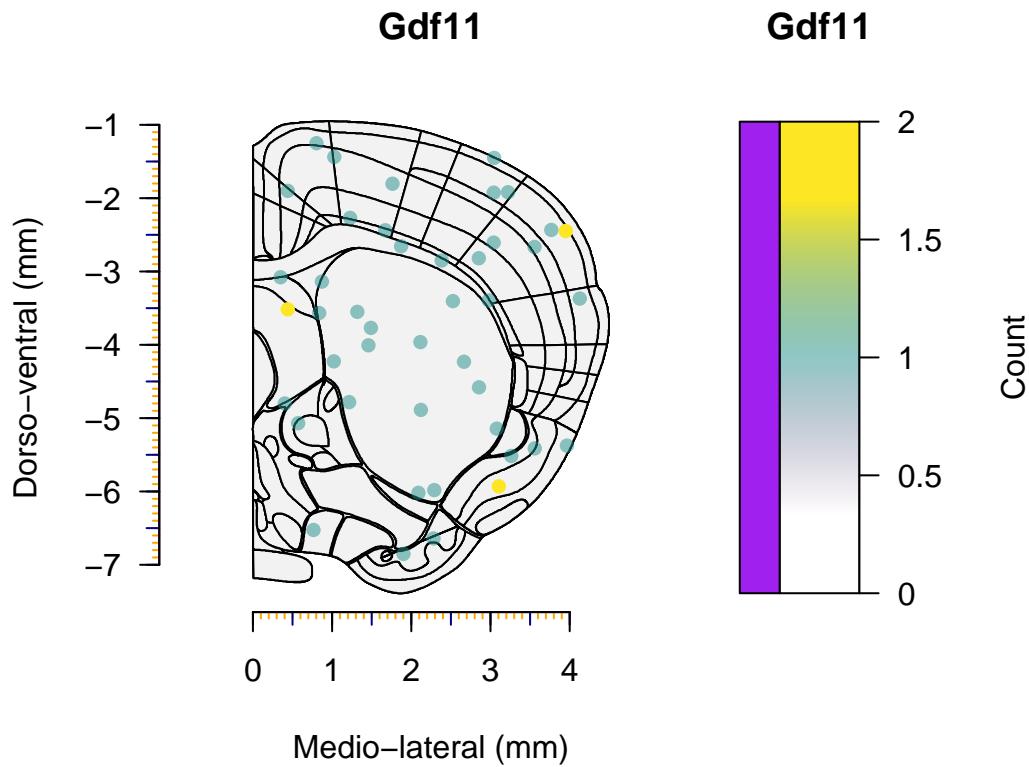
```
#Genes that are differentially expressed between striatal and somatosensory cortical astrocytes:  
genes.of.interest<-c("Adm", "Gdf11", "Mstn", "Bmp3", "Gdf10", "Gdf2", "Bmp10", "Gdf6", "Gdf5", "Gdf7",  
expl.analysis<-plot.these.genes(genes.of.interest)
```



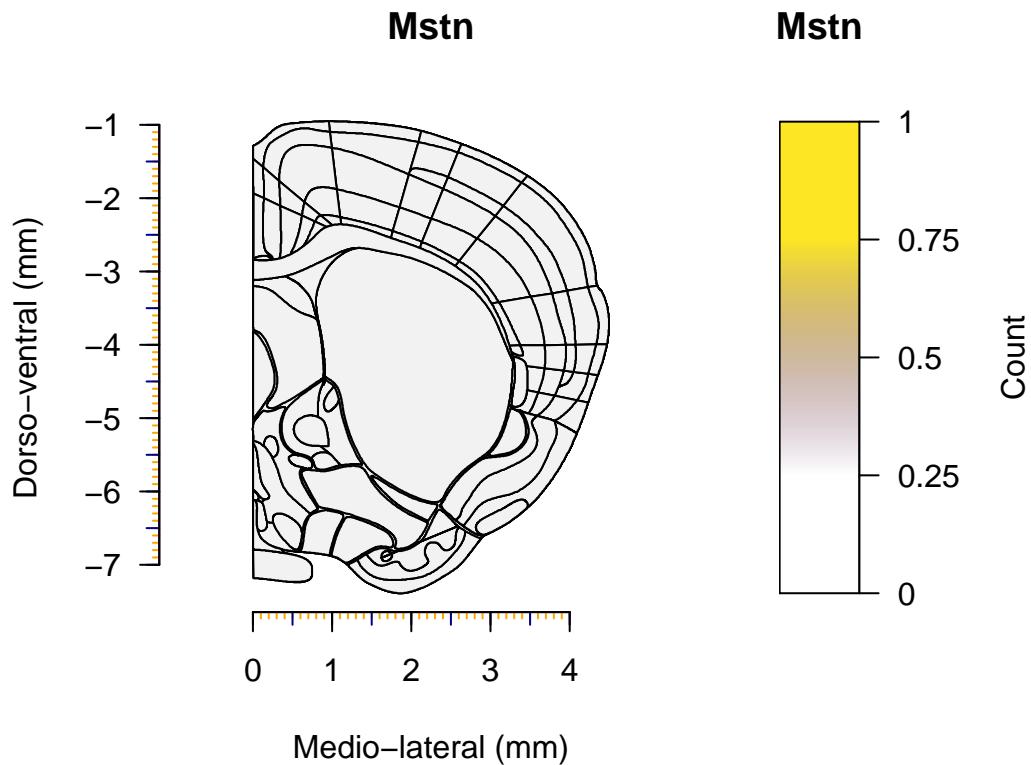
```

## Adm
## -----
## Average number of Adm transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0.01 ( SD = 0.09 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = -1, df = 122, p-value = 0.3193
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.024224389 0.007964227
## sample estimates:
## mean of x mean of y
## 0.000000000 0.008130081

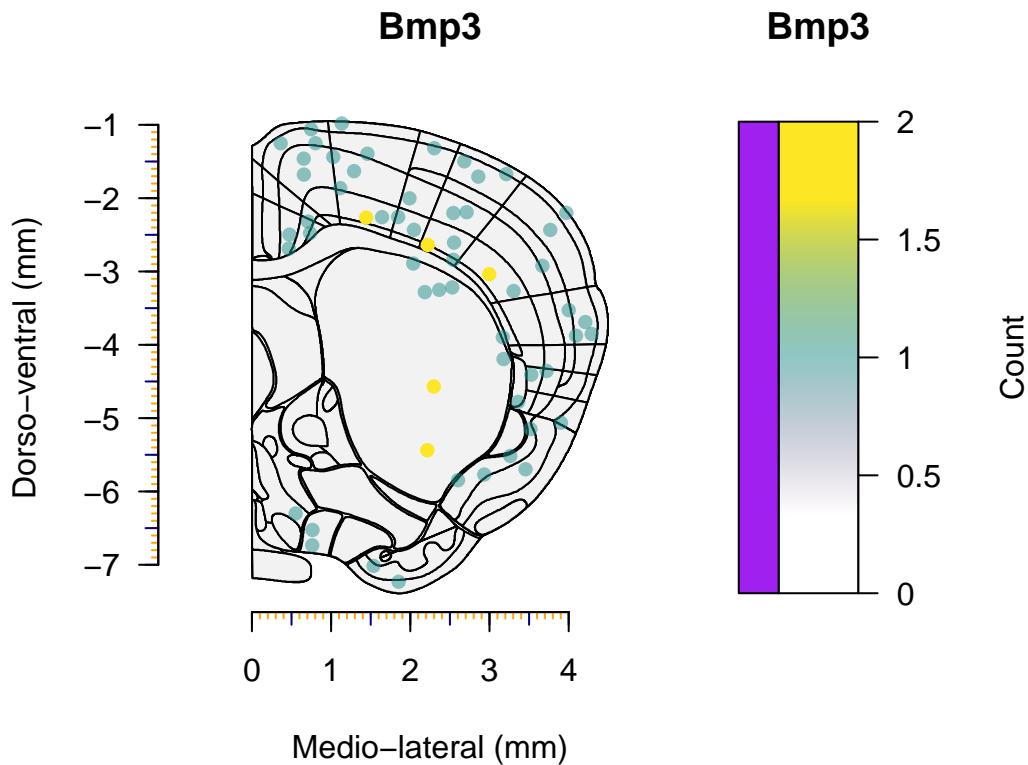
```



```
## Gdf11
## -----
## Average number of Gdf11 transcripts detected:
## CPu : M = 0.13 ( SD = 0.34 ) molecules
## SS : M = 0.08 ( SD = 0.3 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = 1.1346, df = 232.57, p-value = 0.2577
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.03454511 0.12835374
## sample estimates:
## mean of x mean of y
## 0.12820513 0.08130081
```



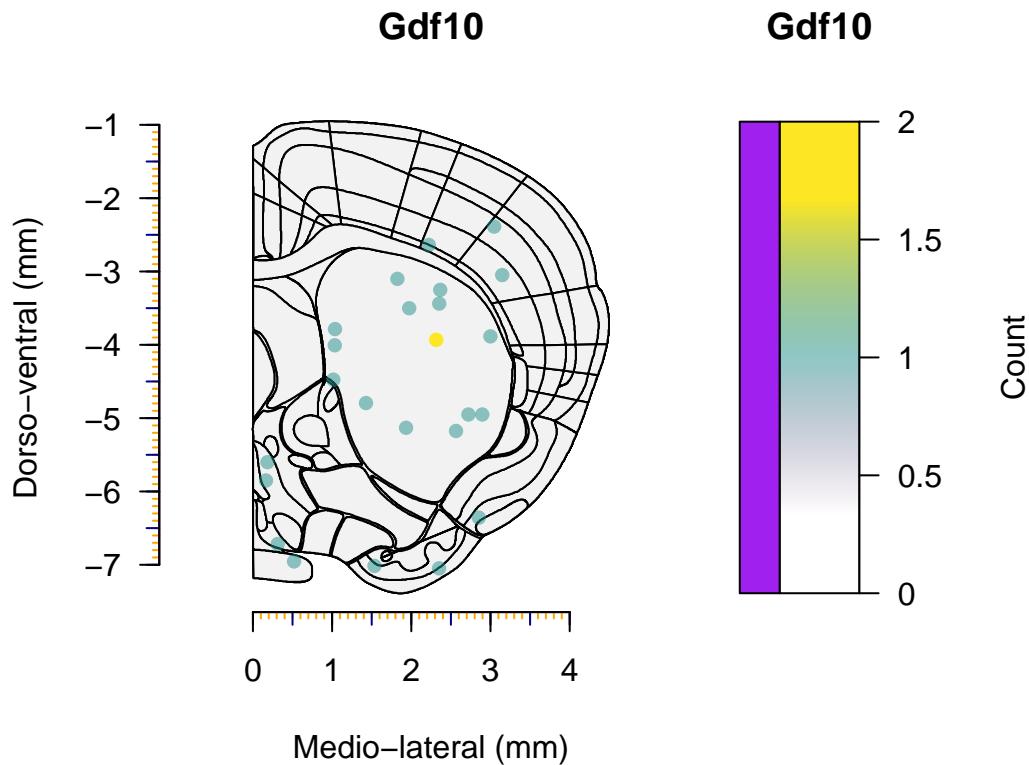
```
## Mstn
## -----
## Average number of Mstn transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = NaN, df = NaN, p-value = NA
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   NaN NaN
## sample estimates:
## mean of x mean of y
##          0          0
```



```

## Bmp3          MARKER FOR SOMATOSENSORY!
## -----
## Average number of Bmp3 transcripts detected:
## CPu : M = 0.08 ( SD = 0.33 ) molecules
## SS  : M = 0.19 ( SD = 0.43 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = -2.2377, df = 226.51, p-value = 0.02621
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.20699456 -0.01314302
## sample estimates:
## mean of x  mean of y
## 0.07692308 0.18699187

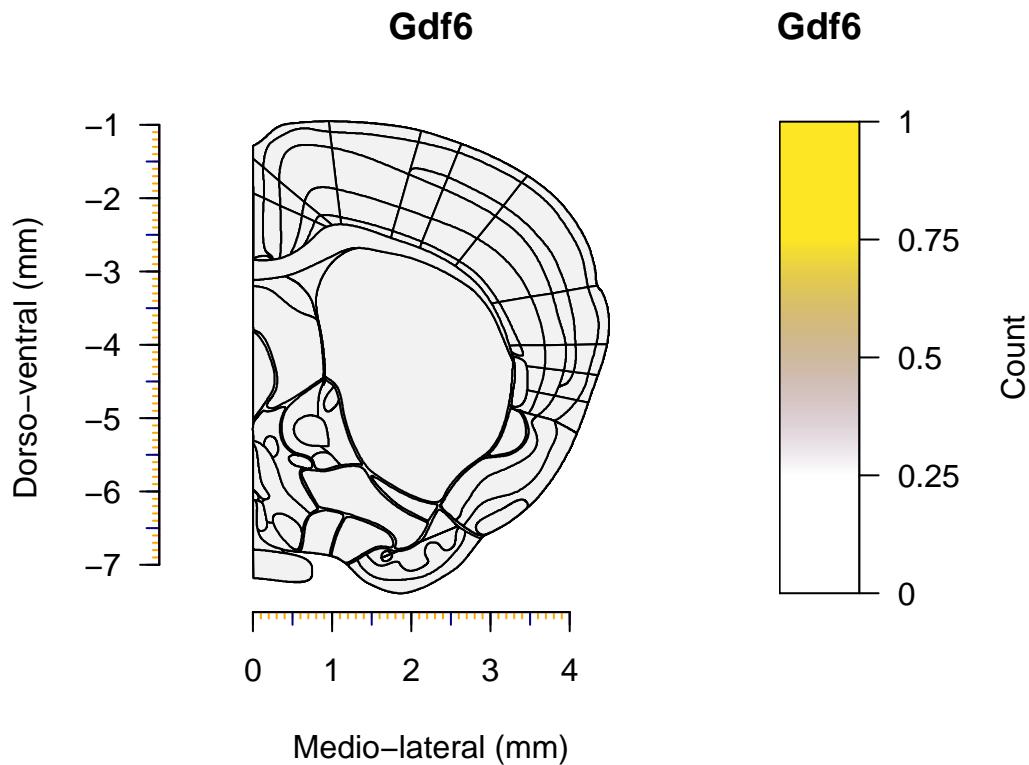
```



```

## Gdf10          MARKER FOR CAUDATE PUTAMEN!
## -----
## Average number of Gdf10 transcripts detected:
## CPu : M = 0.13 ( SD = 0.36 ) molecules
## SS  : M = 0.02 ( SD = 0.15 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = 2.8728, df = 155.74, p-value = 0.004637
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.03243176 0.17519801
## sample estimates:
## mean of x  mean of y
## 0.12820513 0.02439024

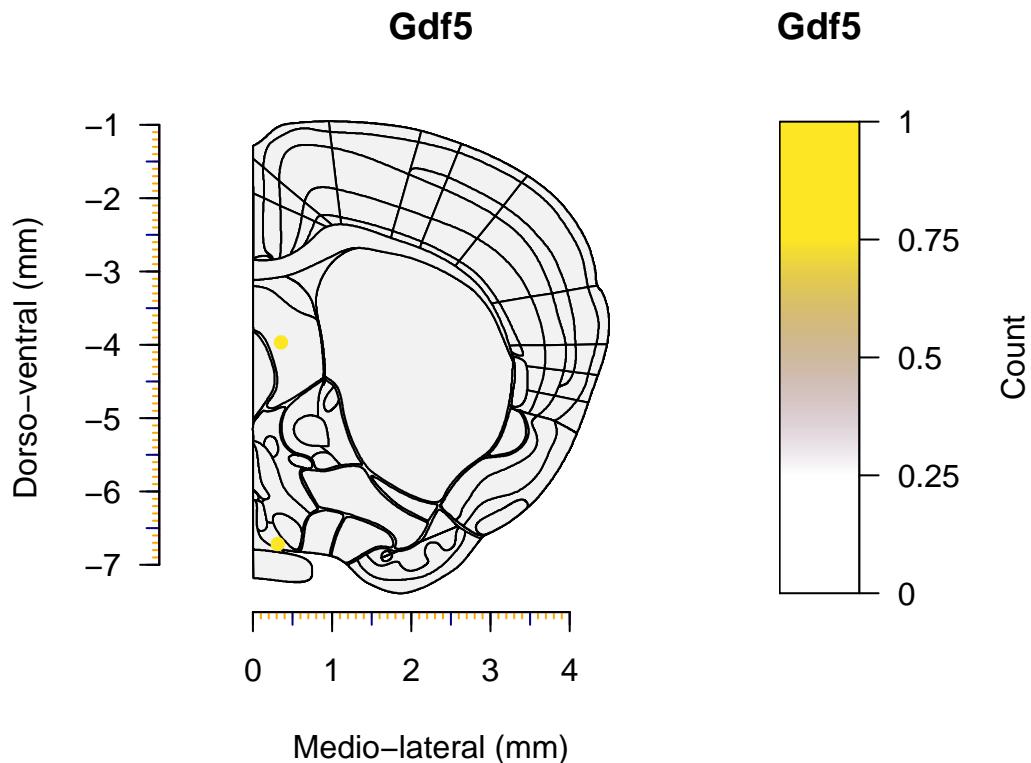
```



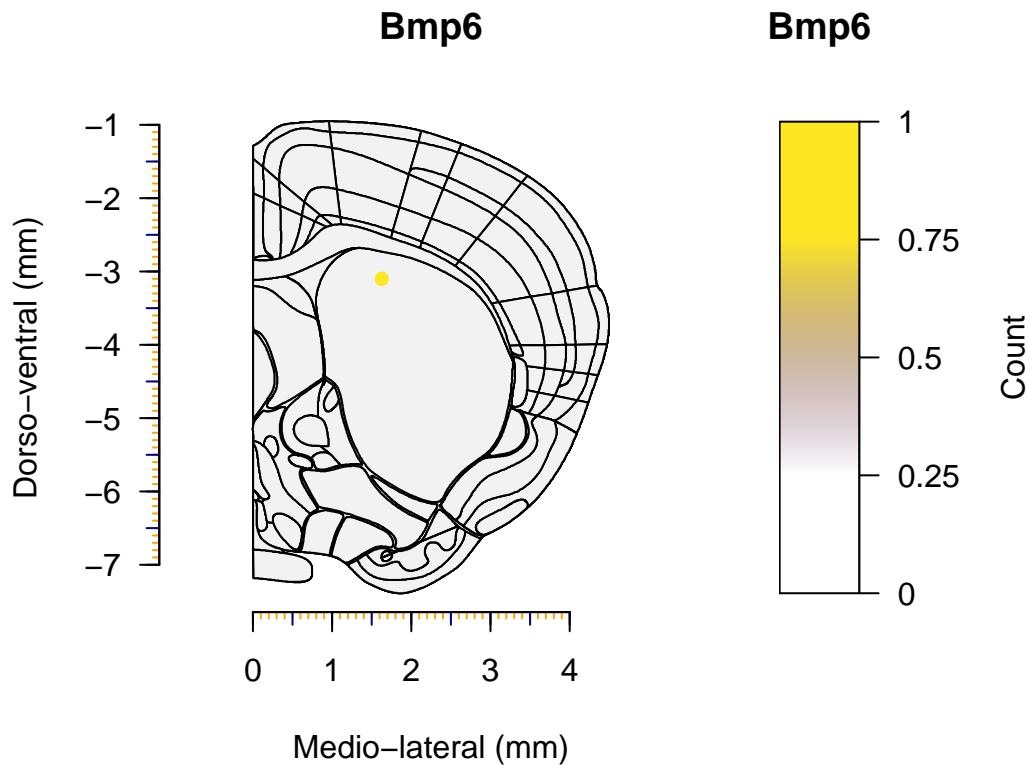
```

## Gdf6
## -----
## Average number of Gdf6 transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = NaN, df = NaN, p-value = NA
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   NaN NaN
## sample estimates:
## mean of x mean of y
##          0          0

```



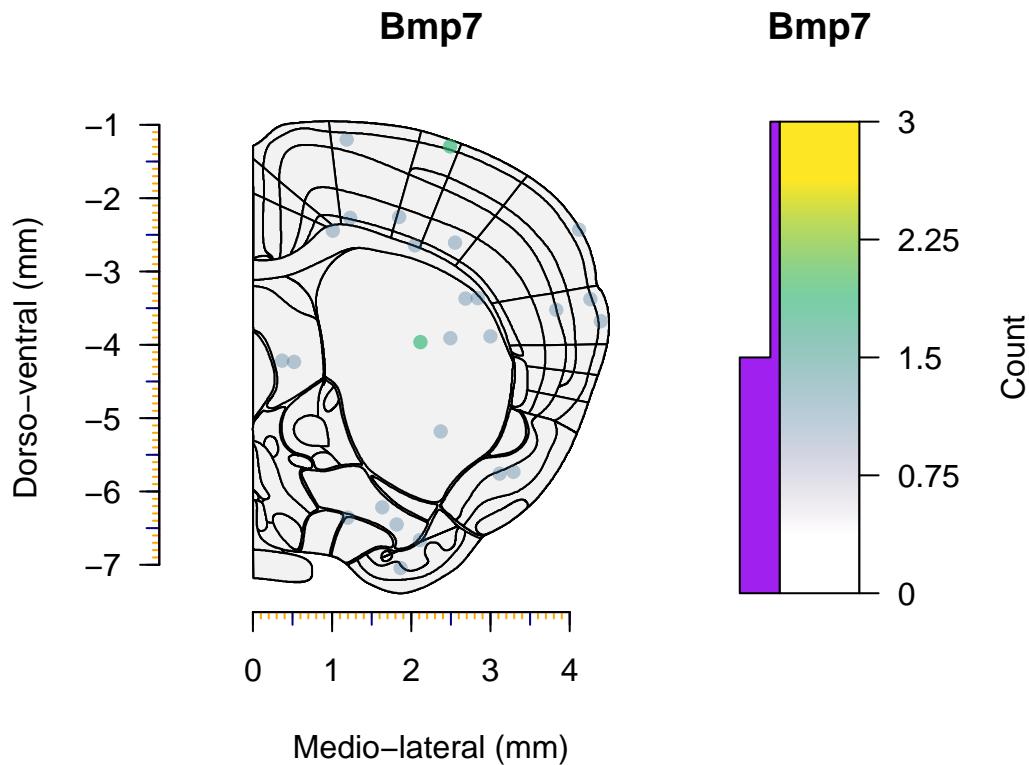
```
## Gdf5
## -----
## Average number of Gdf5 transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = NaN, df = NaN, p-value = NA
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   NaN NaN
## sample estimates:
## mean of x mean of y
##          0          0
```



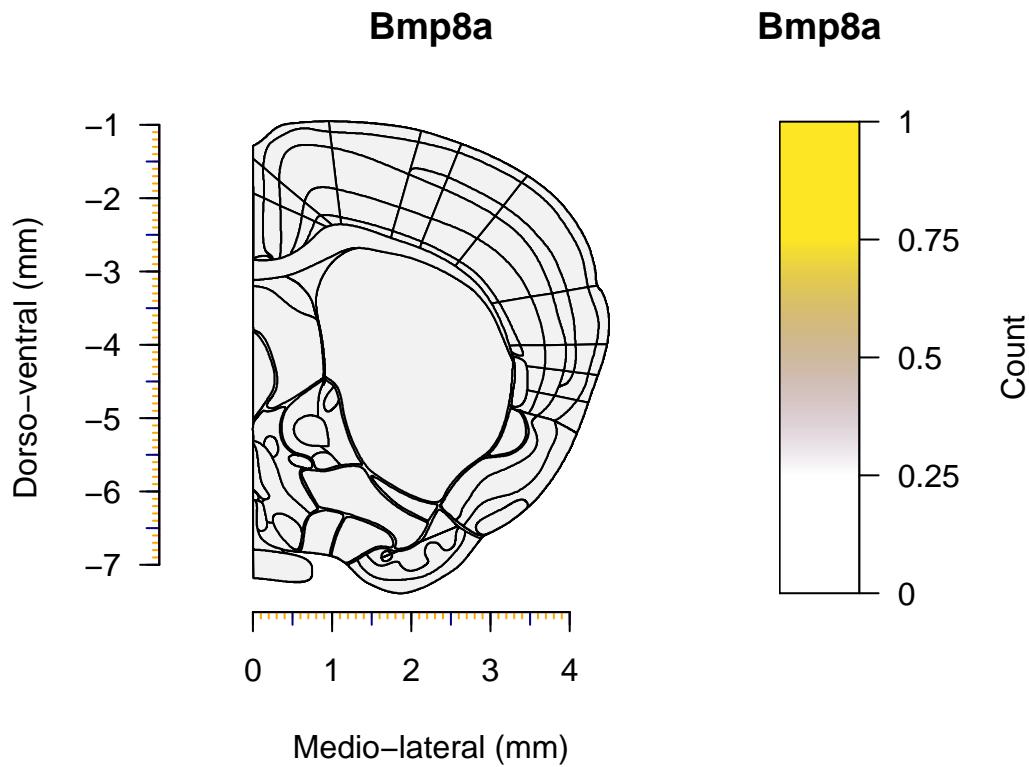
```

## Bmp6
## -----
## Average number of Bmp6 transcripts detected:
## CPu : M = 0.01 ( SD = 0.09 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = 1, df = 116, p-value = 0.3194
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.008381419 0.025475436
## sample estimates:
## mean of x mean of y
## 0.008547009 0.000000000

```



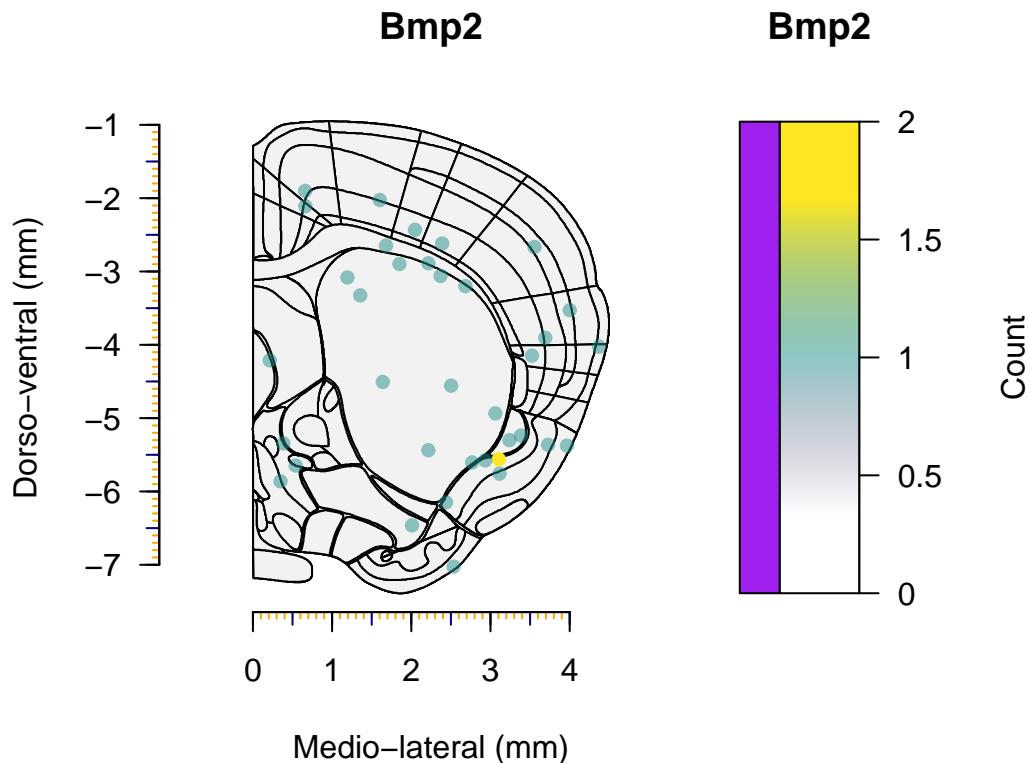
```
## Bmp7
## -----
## Average number of Bmp7 transcripts detected:
## CPu : M = 0.06 ( SD = 0.27 ) molecules
## SS : M = 0.07 ( SD = 0.29 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = -0.36702, df = 237.92, p-value = 0.7139
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.08495346  0.05827011
## sample estimates:
## mean of x  mean of y
## 0.05982906 0.07317073
```



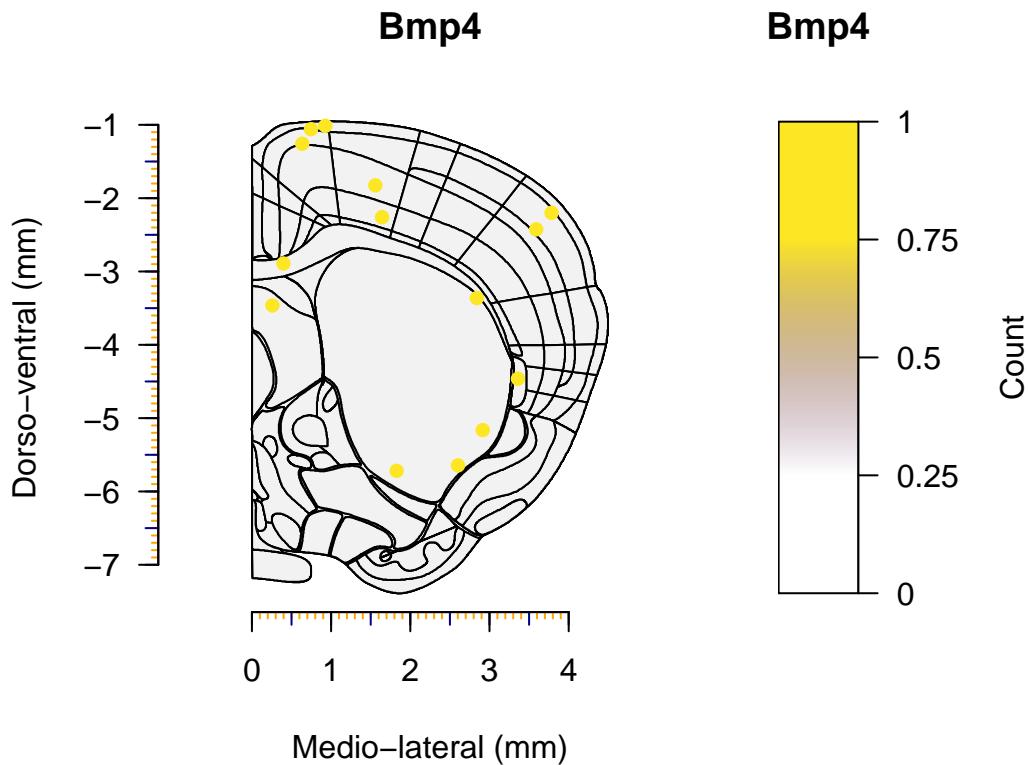
```

## Bmp8a
## -----
## Average number of Bmp8a transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = NaN, df = NaN, p-value = NA
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   NaN NaN
## sample estimates:
## mean of x mean of y
##          0          0

```



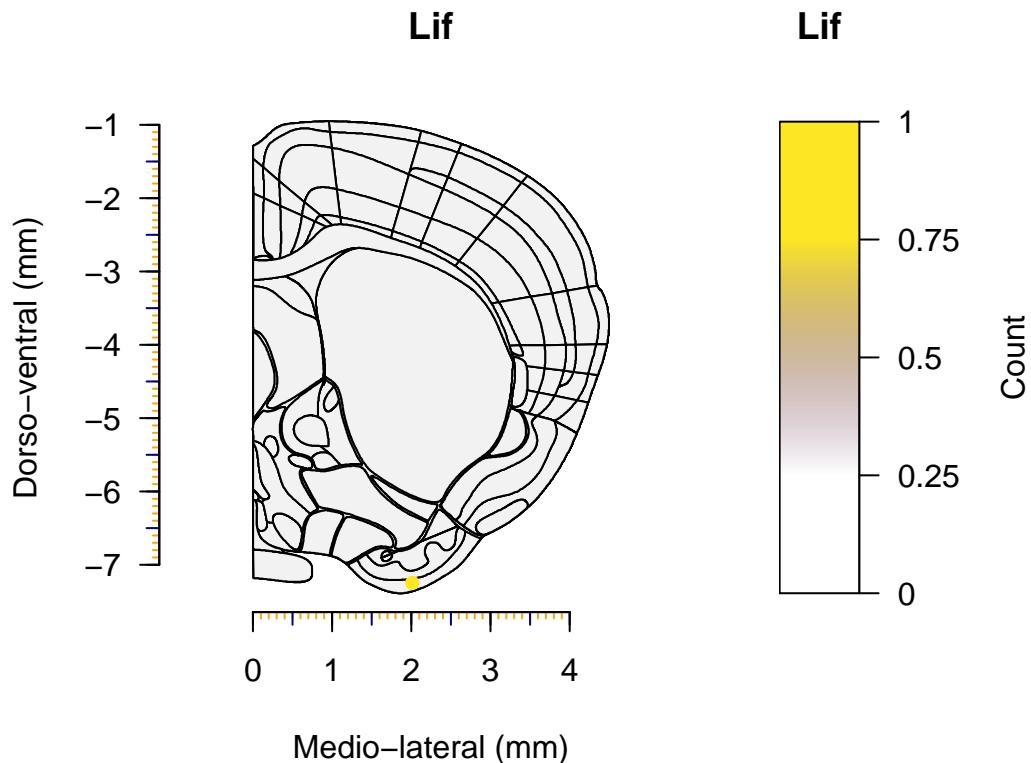
```
## Bmp2
## -----
## Average number of Bmp2 transcripts detected:
## CPu : M = 0.08 ( SD = 0.27 ) molecules
## SS : M = 0.04 ( SD = 0.2 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = 1.1883, df = 213.44, p-value = 0.236
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.02389638 0.09644173
## sample estimates:
## mean of x mean of y
## 0.07692308 0.04065041
```



```

## Bmp4
## -----
## Average number of Bmp4 transcripts detected:
## CPu : M = 0.03 ( SD = 0.18 ) molecules
## SS : M = 0.02 ( SD = 0.13 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = 0.87924, df = 205.93, p-value = 0.3803
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.02227249 0.05812823
## sample estimates:
## mean of x mean of y
## 0.03418803 0.01626016

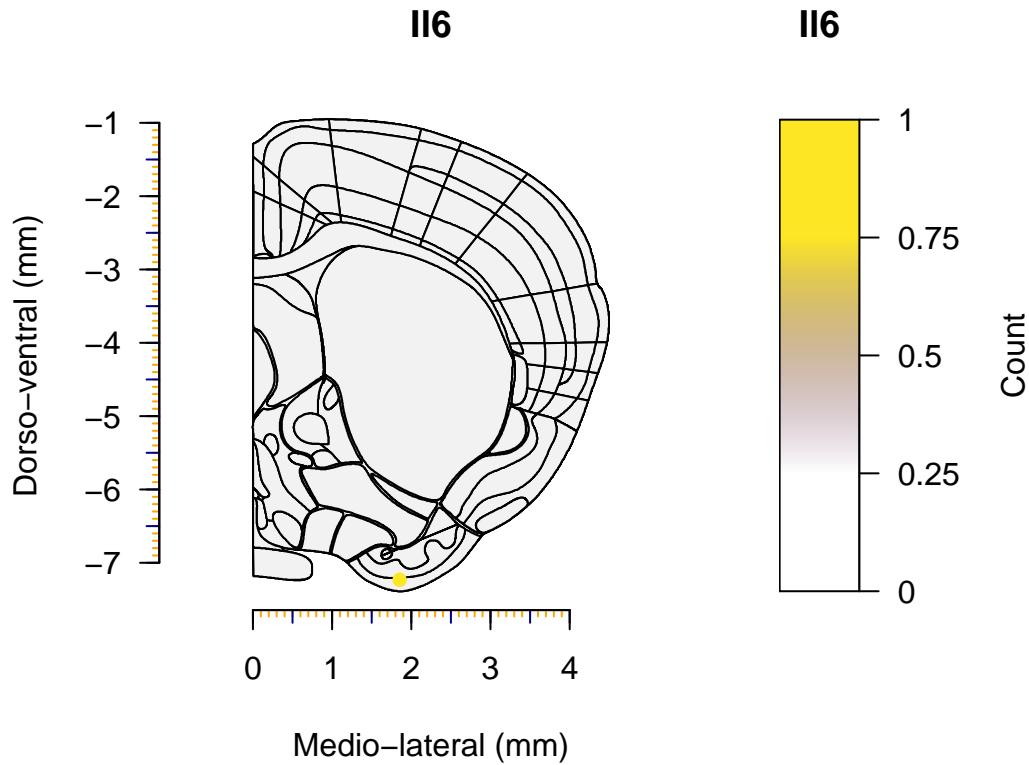
```



```

## Lif
## -----
## Average number of Lif transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = NaN, df = NaN, p-value = NA
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   NaN NaN
## sample estimates:
## mean of x mean of y
##          0          0

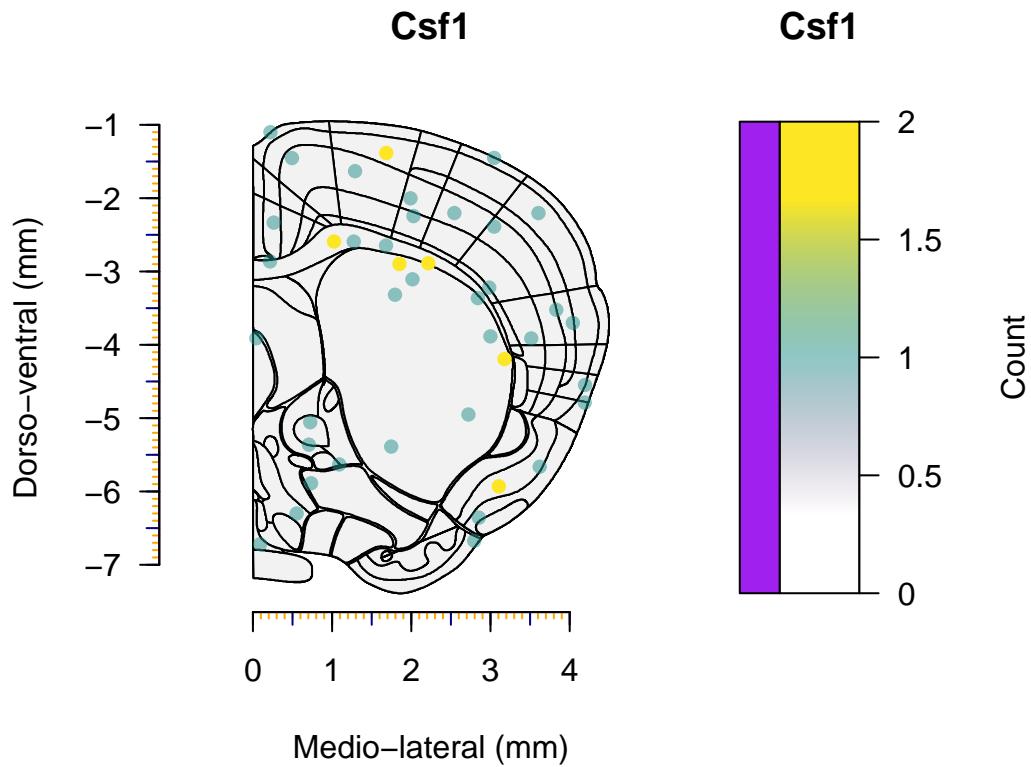
```



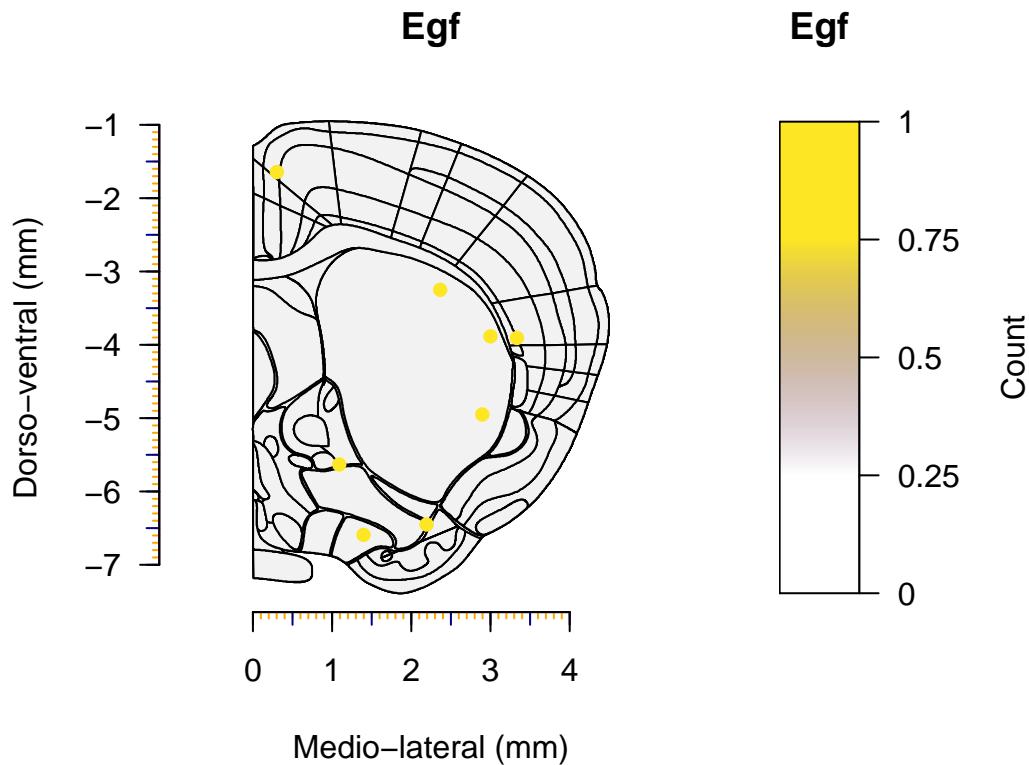
```

## I16
## -----
## Average number of I16 transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = NaN, df = NaN, p-value = NA
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   NaN NaN
## sample estimates:
## mean of x mean of y
##          0          0

```



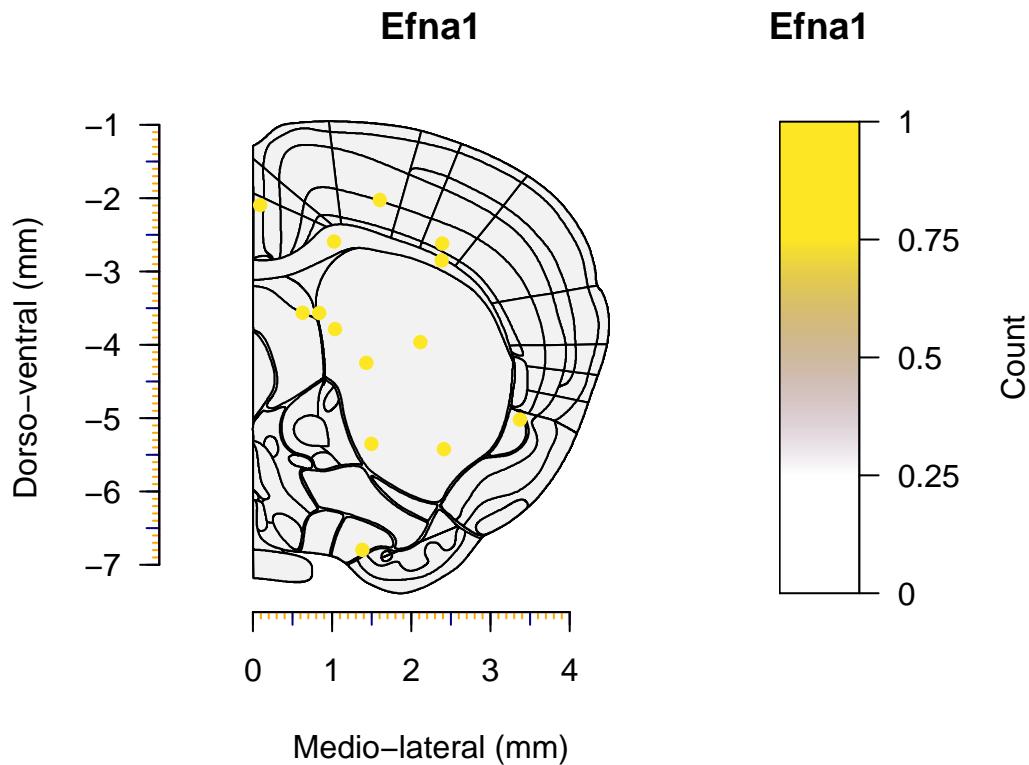
```
## Csf1
## -----
## Average number of Csf1 transcripts detected:
## CPu : M = 0.09 ( SD = 0.34 ) molecules
## SS : M = 0.08 ( SD = 0.27 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = 0.10486, df = 223.93, p-value = 0.9166
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.07418047 0.08251902
## sample estimates:
## mean of x mean of y
## 0.08547009 0.08130081
```



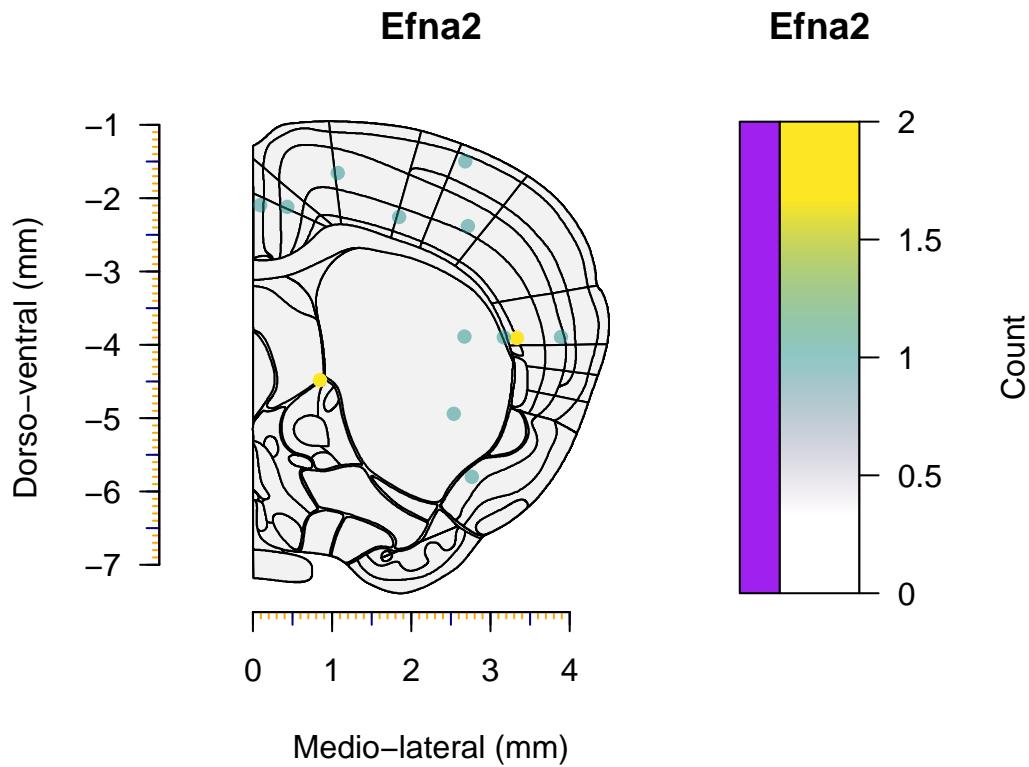
```

## Egf
## -----
## Average number of Egf transcripts detected:
## CPu : M = 0.03 ( SD = 0.16 ) molecules
## SS : M = 0.01 ( SD = 0.09 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = 1.0437, df = 181.84, p-value = 0.298
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.01559204 0.05061392
## sample estimates:
## mean of x mean of y
## 0.025641026 0.008130081

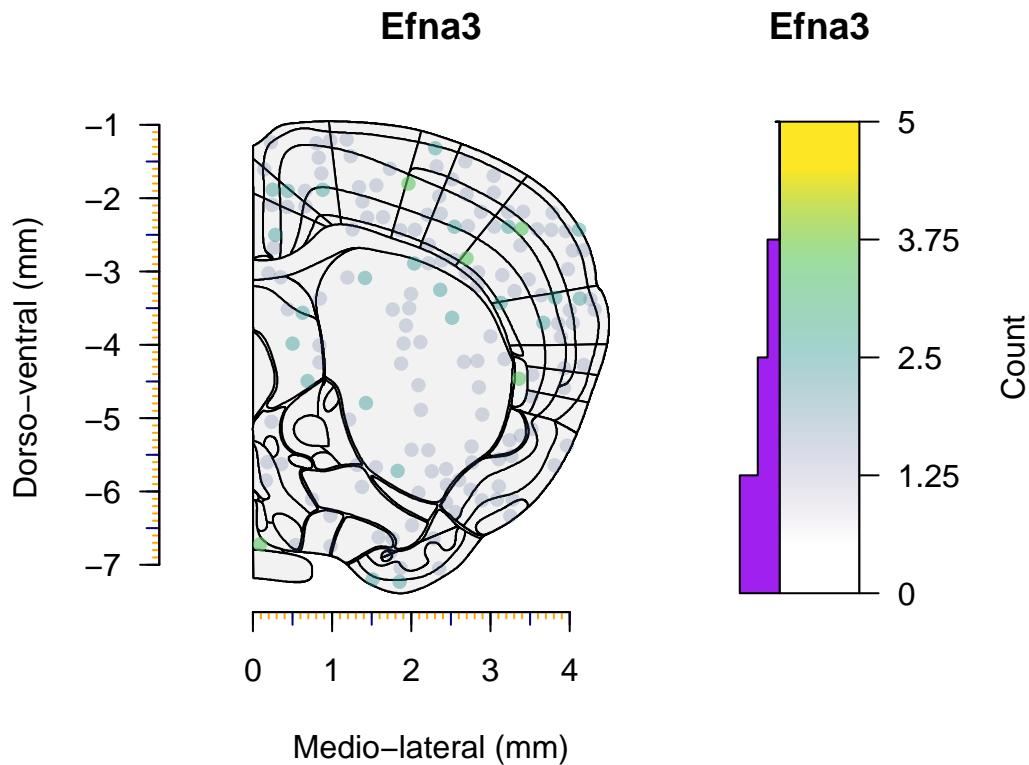
```



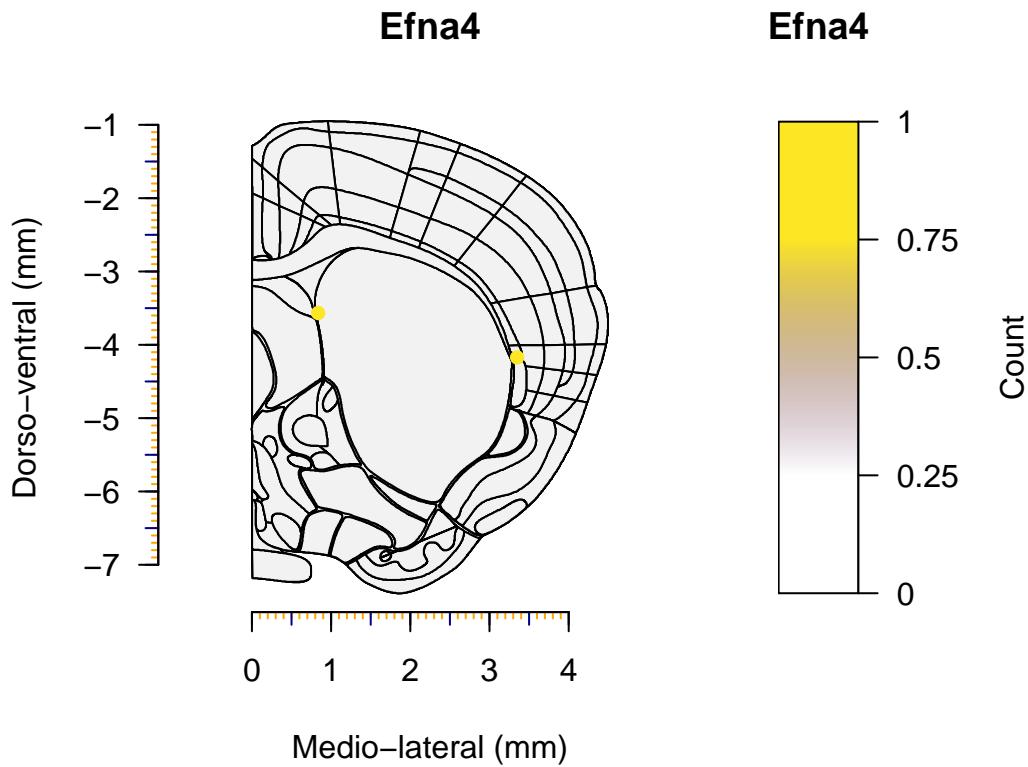
```
## Efna1
## -----
## Average number of Efna1 transcripts detected:
## CPu : M = 0.05 ( SD = 0.22 ) molecules
## SS : M = 0.01 ( SD = 0.09 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = 1.9584, df = 151.86, p-value = 0.05202
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.0003815429 0.0866854829
## sample estimates:
## mean of x mean of y
## 0.051282051 0.008130081
```



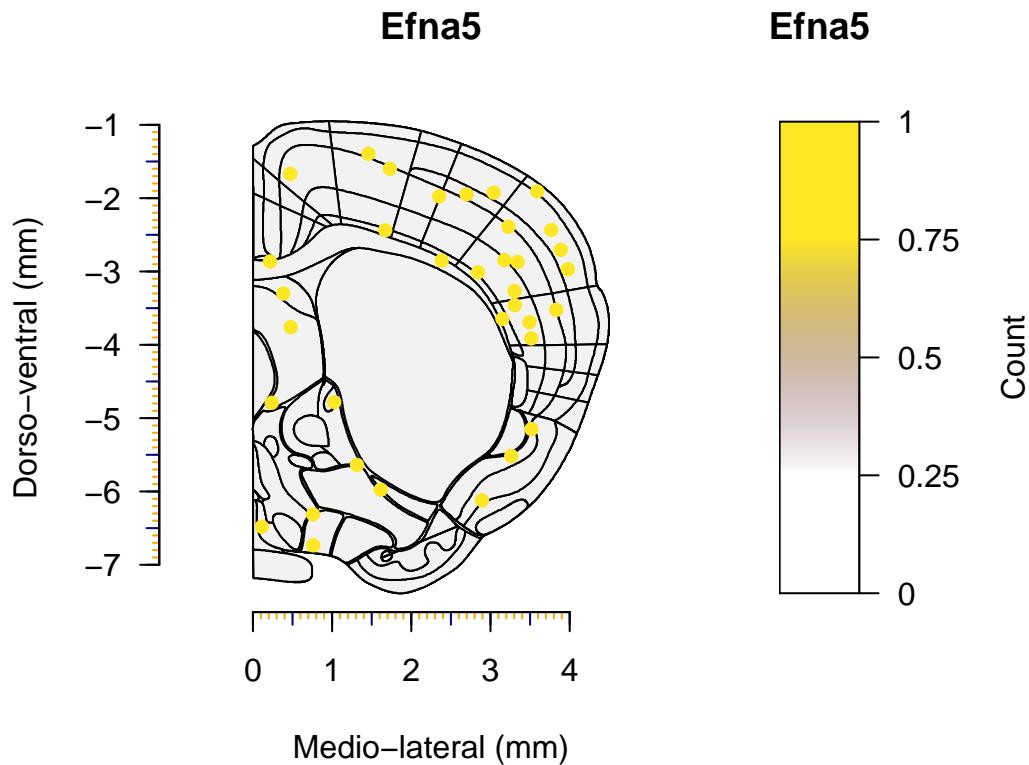
```
## Efna2
## -----
## Average number of Efna2 transcripts detected:
## CPu : M = 0.02 ( SD = 0.13 ) molecules
## SS : M = 0.05 ( SD = 0.25 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = -1.2348, df = 185.04, p-value = 0.2185
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.08231115 0.01893820
## sample estimates:
## mean of x mean of y
## 0.01709402 0.04878049
```



```
## Efna3          MARKER FOR SOMATOSENSORY!
## -----
## Average number of Efna3 transcripts detected:
## CPu : M = 0.32 ( SD = 0.57 ) molecules
## SS  : M = 0.51 ( SD = 0.73 ) molecules
## -----
## Welch Two Sample t-test
##
## data:  CP and SS
## t = -2.226, df = 229.54, p-value = 0.02699
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.35329814 -0.02151946
## sample estimates:
## mean of x mean of y
## 0.3247863 0.5121951
```



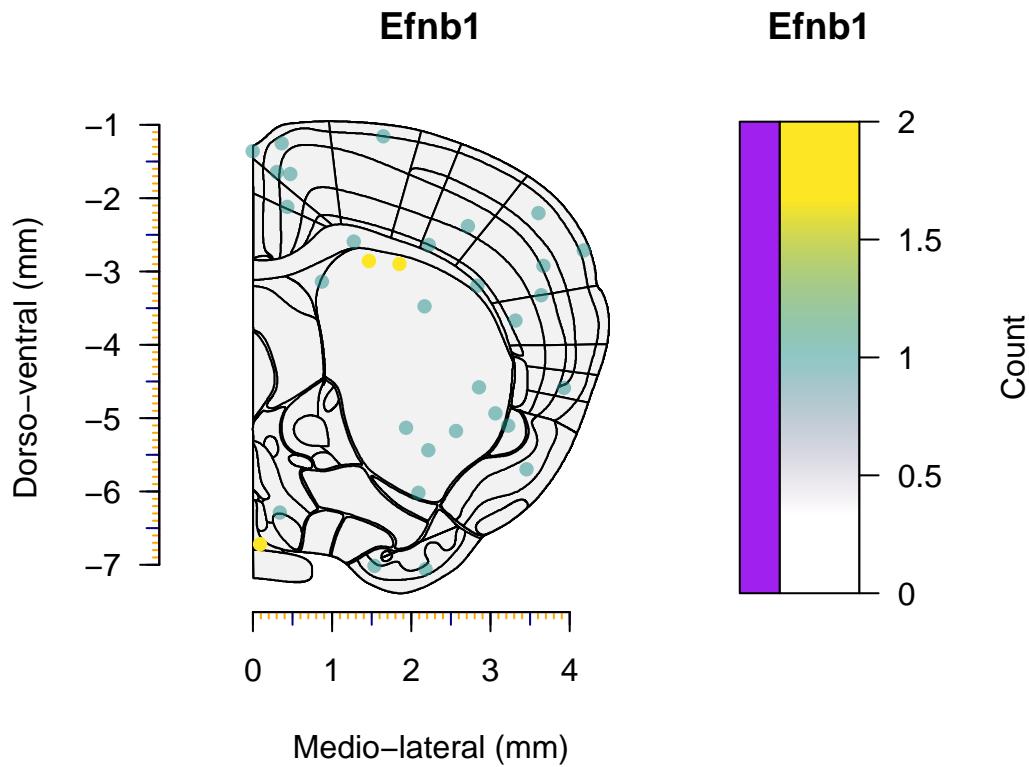
```
## Efna4
## -----
## Average number of Efna4 transcripts detected:
## CPu : M = 0.01 ( SD = 0.09 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = 1, df = 116, p-value = 0.3194
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.008381419 0.025475436
## sample estimates:
## mean of x mean of y
## 0.008547009 0.000000000
```



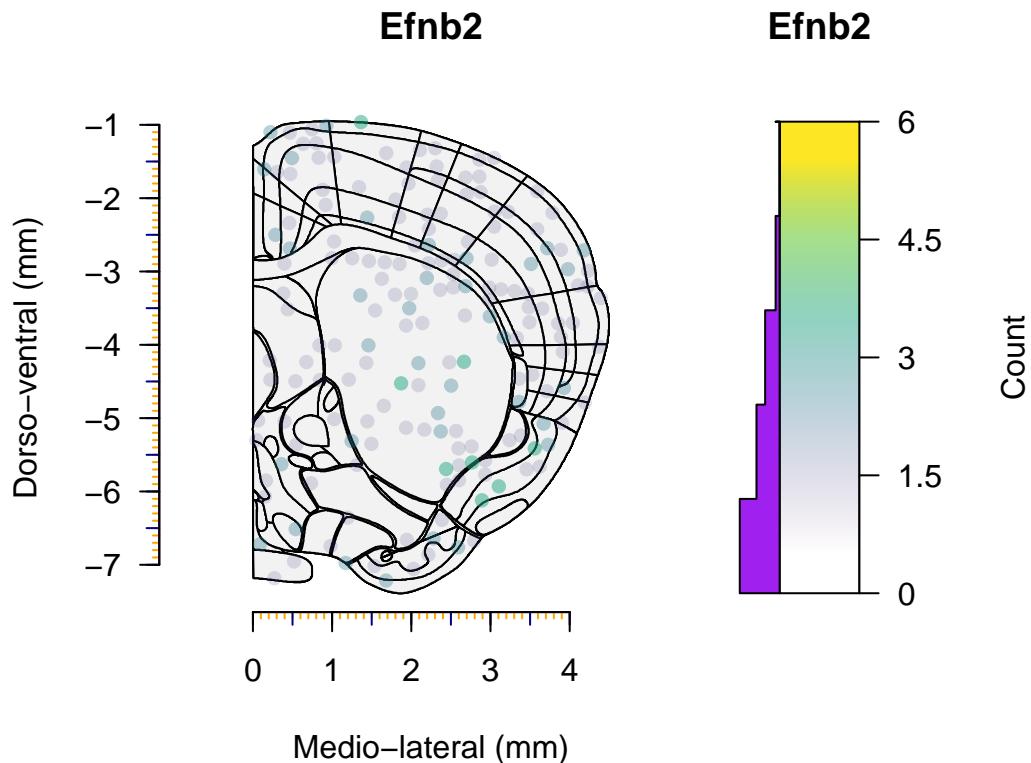
```

## Efna5          MARKER FOR SOMATOSENSORY!
## -----
## Average number of Efna5 transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0.14 ( SD = 0.35 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = -4.4234, df = 122, p-value = 2.125e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.2000657 -0.0763571
## sample estimates:
## mean of x mean of y
## 0.0000000 0.1382114

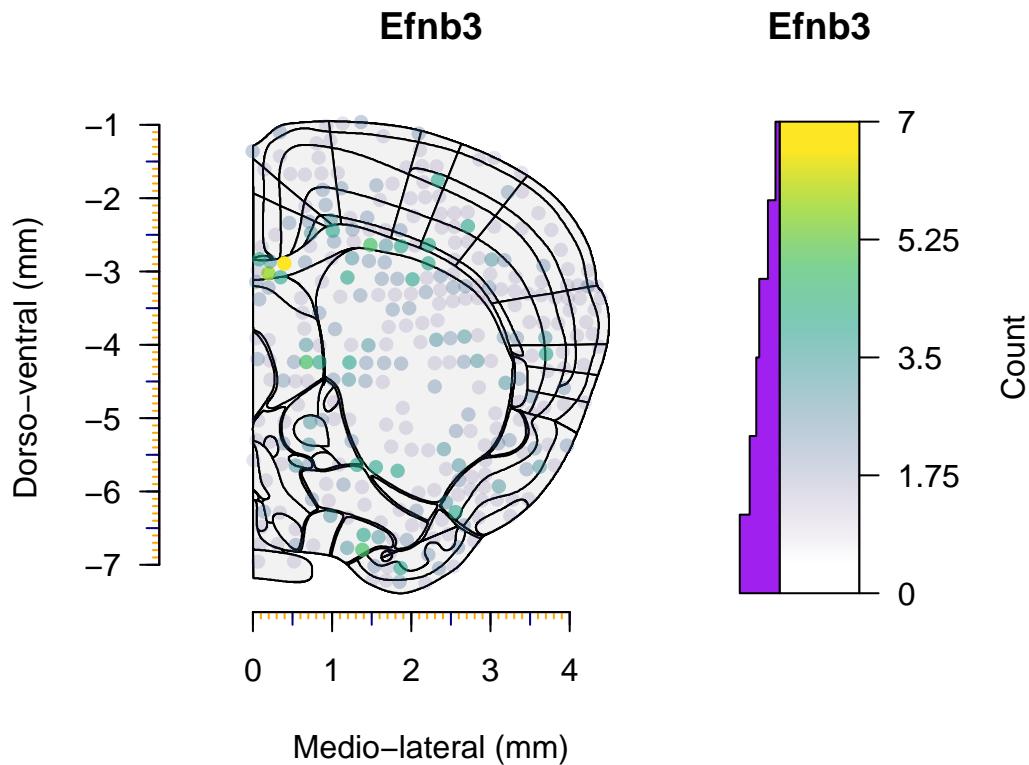
```



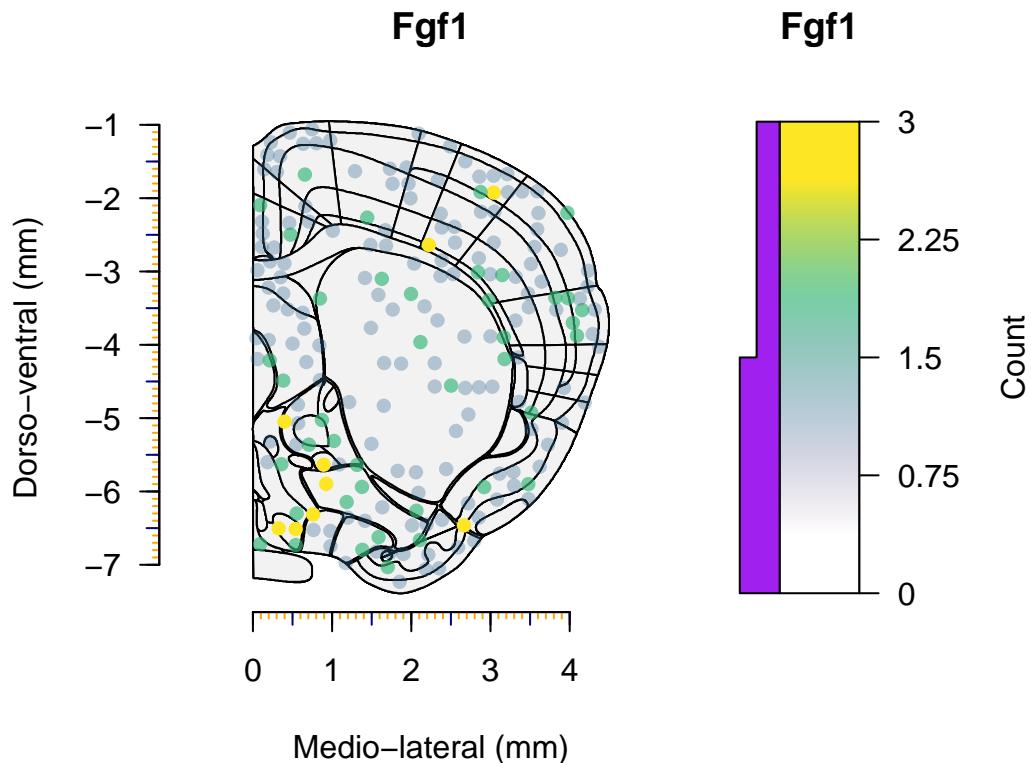
```
## Efnb1
## -----
## Average number of Efnb1 transcripts detected:
## CPu : M = 0.1 ( SD = 0.36 ) molecules
## SS : M = 0.06 ( SD = 0.23 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = 1.1679, df = 197.98, p-value = 0.2443
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.03143564 0.12274270
## sample estimates:
## mean of x mean of y
## 0.10256410 0.05691057
```



```
## Efnb2
## -----
## Average number of Efnb2 transcripts detected:
## CPu : M = 0.49 ( SD = 0.76 ) molecules
## SS : M = 0.43 ( SD = 0.59 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = 0.63881, df = 218.17, p-value = 0.5236
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.1173703 0.2299407
## sample estimates:
## mean of x mean of y
## 0.4871795 0.4308943
```



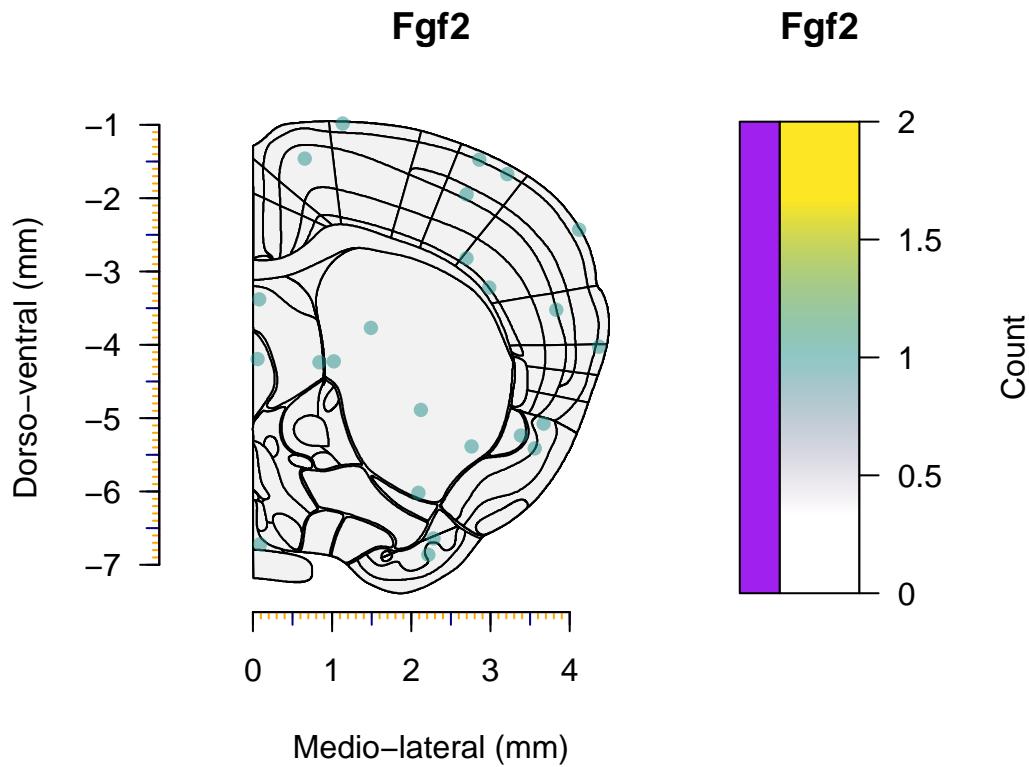
```
## Efnb3          MARKER FOR CAUDATE PUTAMEN!
## -----
## Average number of Efnb3 transcripts detected:
## CPu : M = 1.12 ( SD = 1.12 ) molecules
## SS  : M = 0.68 ( SD = 0.85 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = 3.3958, df = 217, p-value = 0.0008138
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.1832461 0.6902165
## sample estimates:
## mean of x mean of y
## 1.1196581 0.6829268
```



```

## Fgf1          MARKER FOR SOMATOSENSORY!
## -----
## Average number of Fgf1 transcripts detected:
## CPu : M = 0.32 ( SD = 0.57 ) molecules
## SS : M = 0.49 ( SD = 0.71 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = -1.9737, df = 231.96, p-value = 0.0496
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.3257498750 -0.0002872315
## sample estimates:
## mean of x mean of y
## 0.3247863 0.4878049

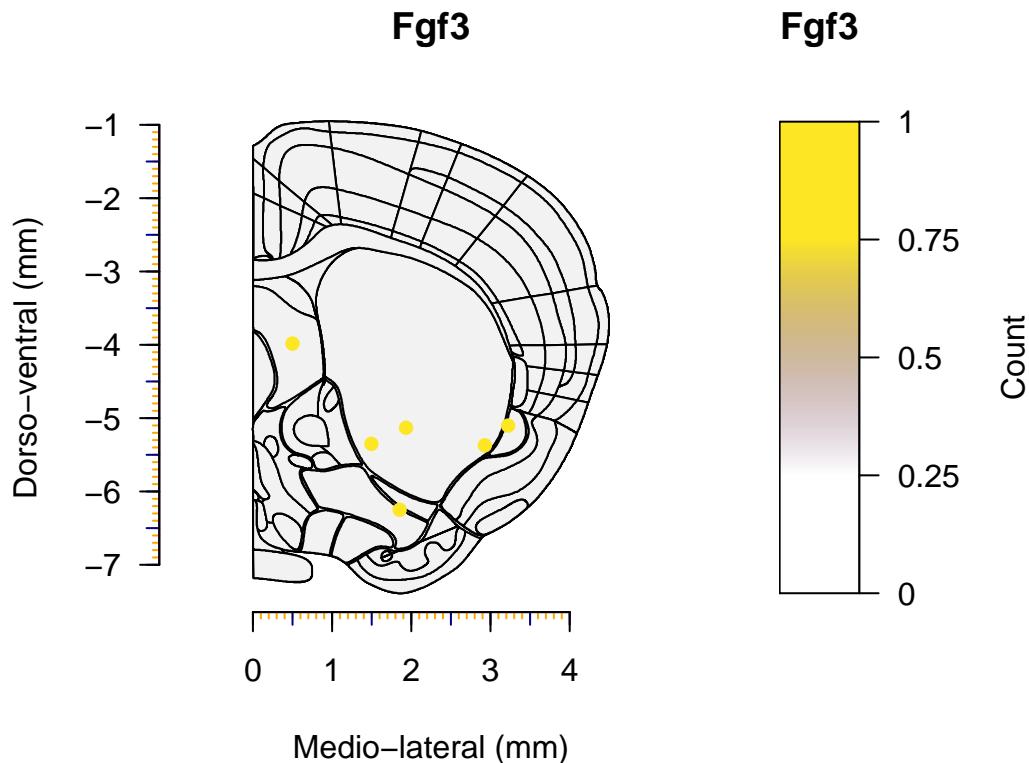
```



```

## Fgf2
## -----
## Average number of Fgf2 transcripts detected:
## CPu : M = 0.04 ( SD = 0.2 ) molecules
## SS : M = 0.06 ( SD = 0.23 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = -0.50352, df = 236.3, p-value = 0.6151
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.06963856 0.04128750
## sample estimates:
## mean of x mean of y
## 0.04273504 0.05691057

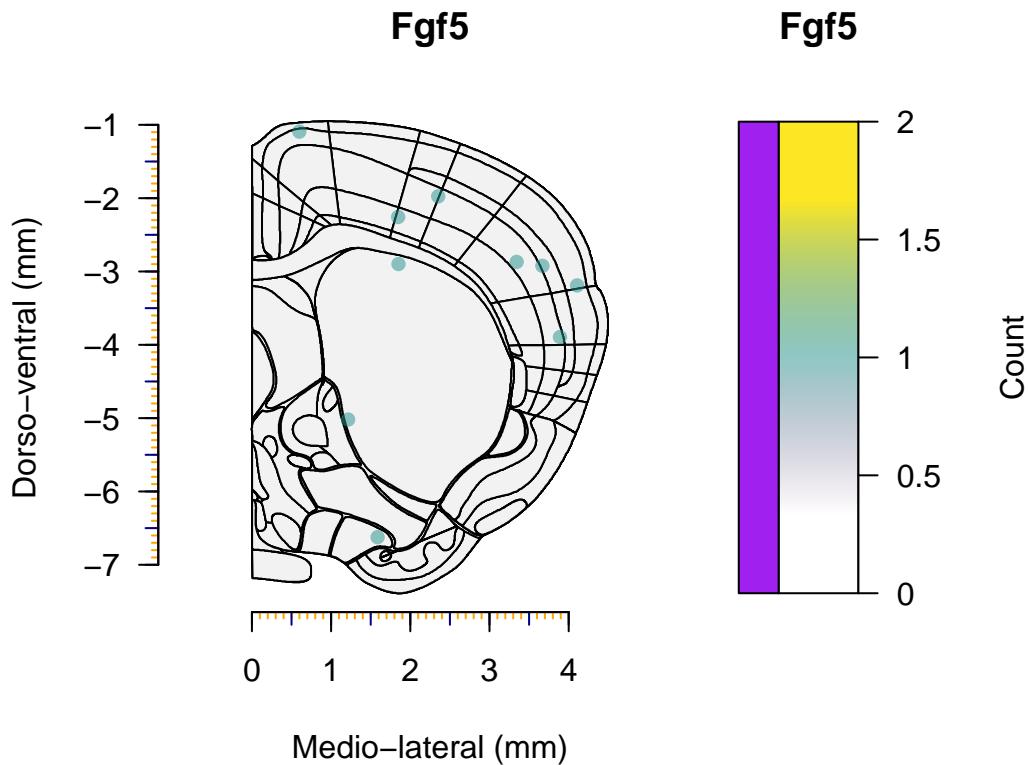
```



```

## Fgf3
## -----
## Average number of Fgf3 transcripts detected:
## CPu : M = 0.03 ( SD = 0.16 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = 1.7472, df = 116, p-value = 0.08325
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.003426005 0.054708057
## sample estimates:
## mean of x mean of y
## 0.02564103 0.00000000

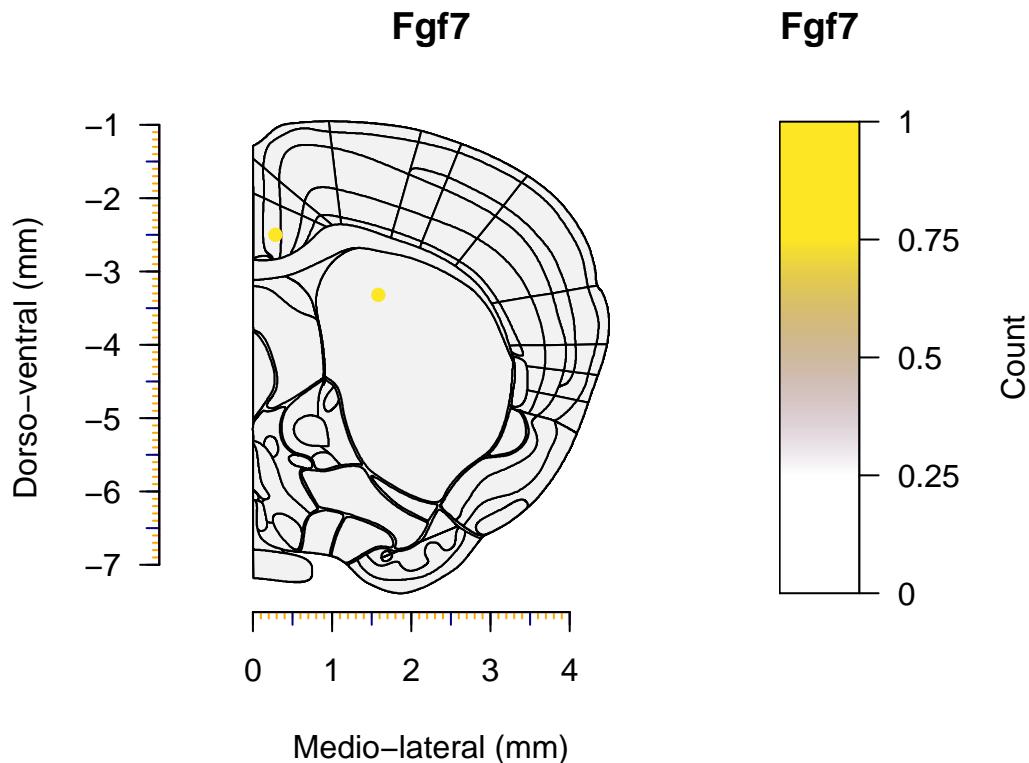
```



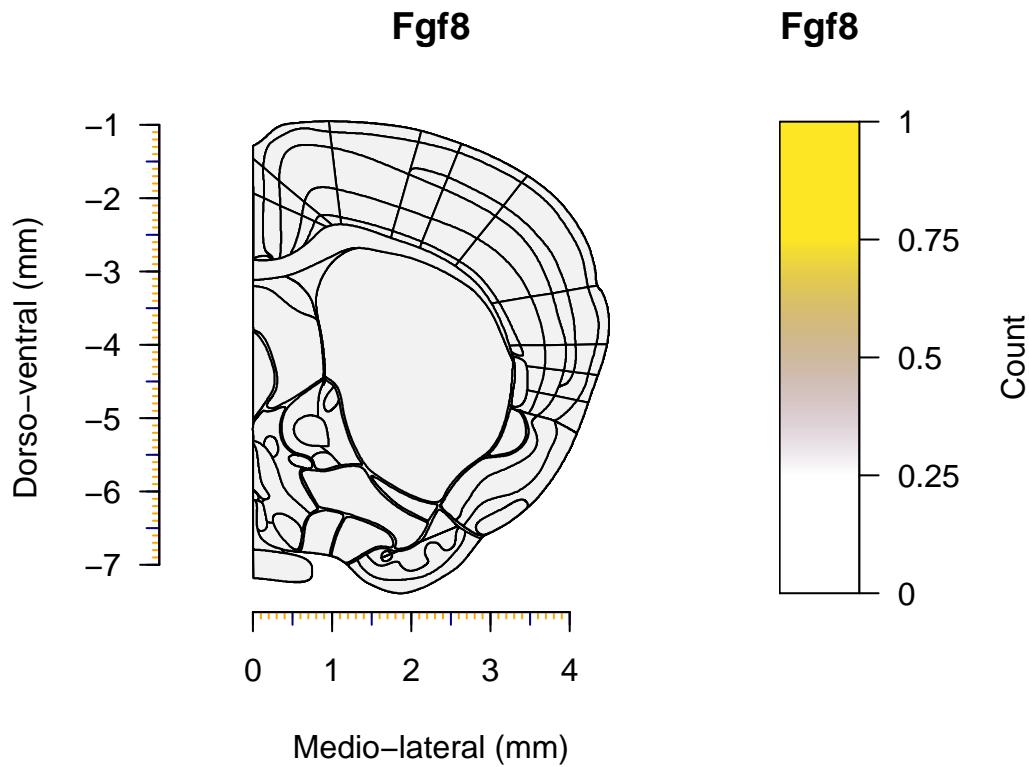
```

## Fgf5
## -----
## Average number of Fgf5 transcripts detected:
## CPu : M = 0.02 ( SD = 0.13 ) molecules
## SS : M = 0.05 ( SD = 0.22 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = -1.3827, df = 201.83, p-value = 0.1683
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.07687349 0.01350055
## sample estimates:
## mean of x mean of y
## 0.01709402 0.04878049

```



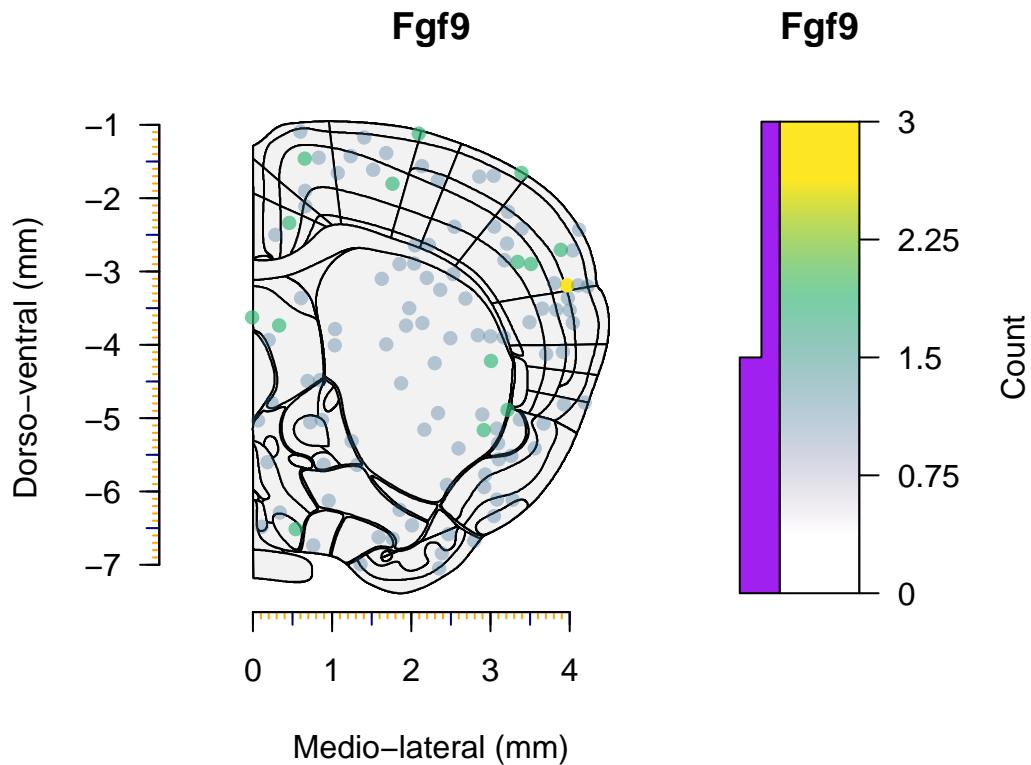
```
## Fgf7
## -----
## Average number of Fgf7 transcripts detected:
## CPu : M = 0.01 ( SD = 0.09 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = 1, df = 116, p-value = 0.3194
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.008381419 0.025475436
## sample estimates:
## mean of x mean of y
## 0.008547009 0.000000000
```



```

## Fgf8
## -----
## Average number of Fgf8 transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = NaN, df = NaN, p-value = NA
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   NaN NaN
## sample estimates:
## mean of x mean of y
##          0          0

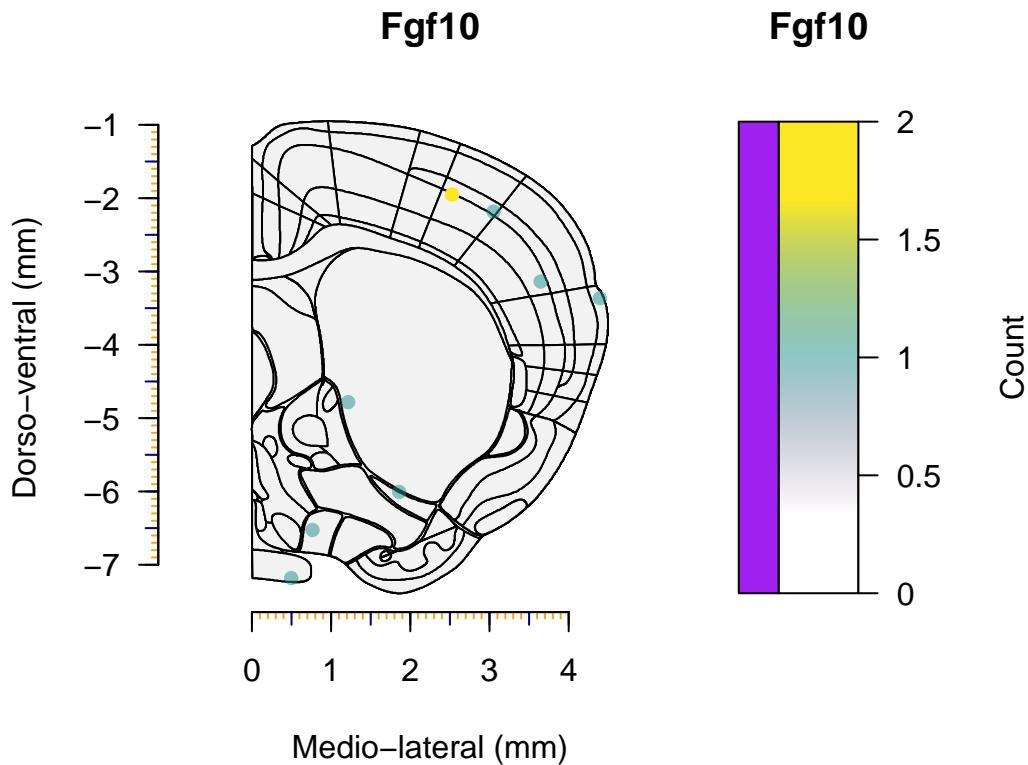
```



```

## Fgf9
## -----
## Average number of Fgf9 transcripts detected:
## CPu : M = 0.23 ( SD = 0.46 ) molecules
## SS : M = 0.28 ( SD = 0.56 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = -0.68845, df = 233.11, p-value = 0.4919
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.17630326  0.08499619
## sample estimates:
## mean of x mean of y
## 0.2307692  0.2764228

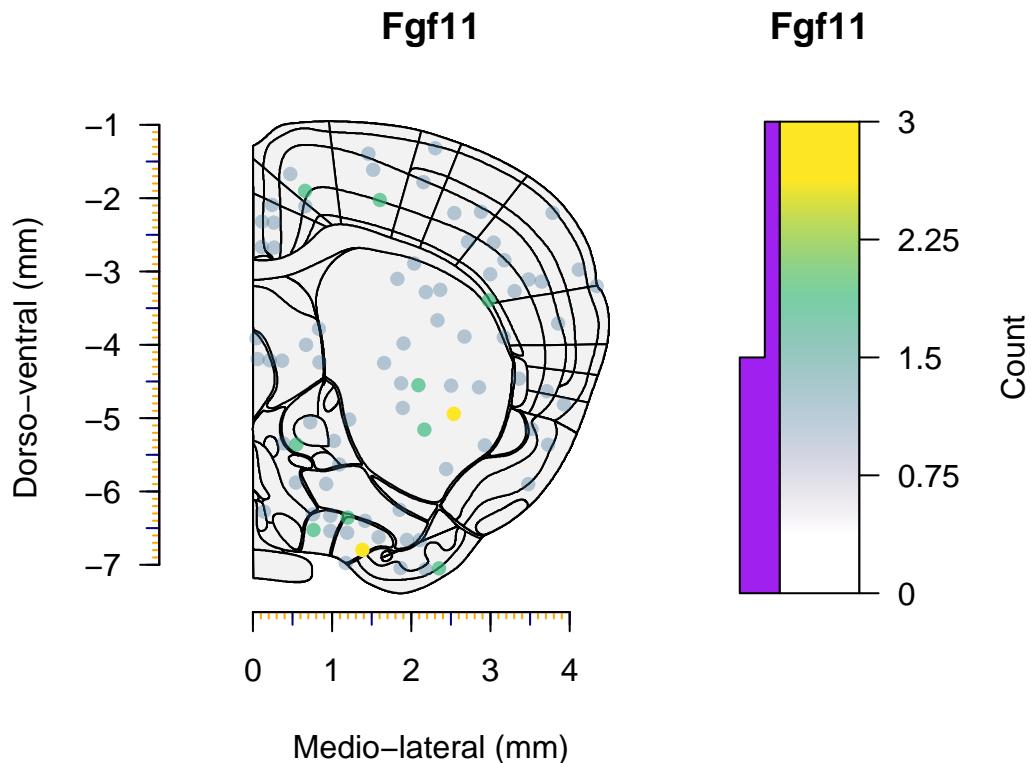
```



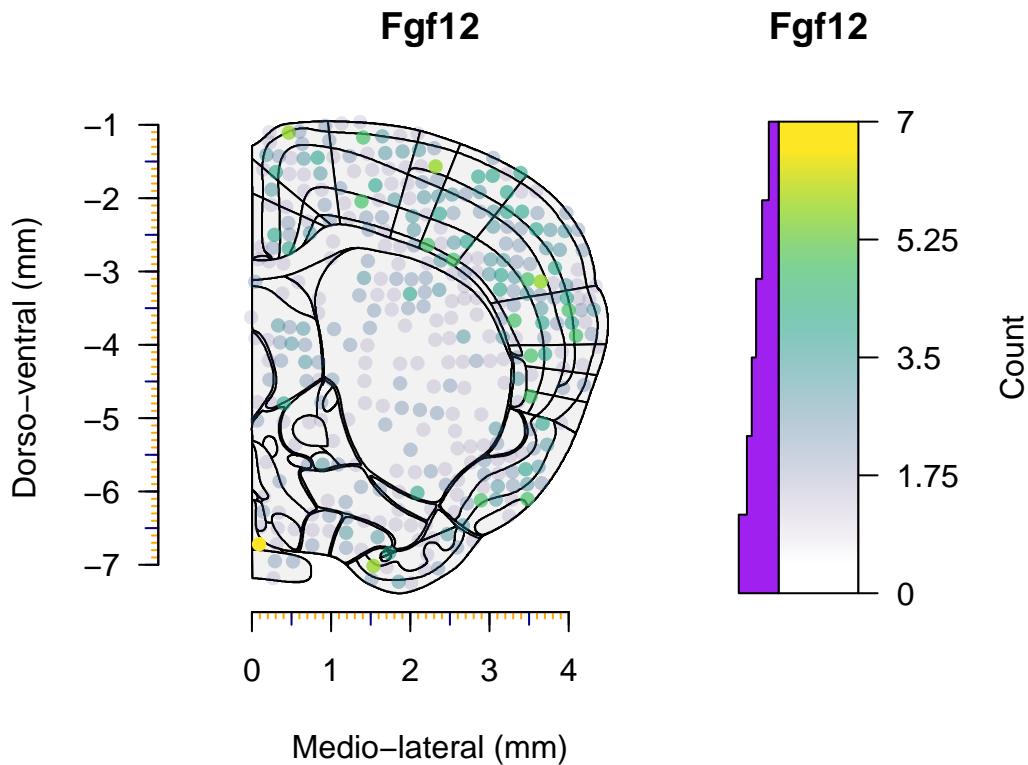
```

## Fgf10
## -----
## Average number of Fgf10 transcripts detected:
## CPu : M = 0.01 ( SD = 0.09 ) molecules
## SS : M = 0.04 ( SD = 0.24 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = -1.3998, df = 160.15, p-value = 0.1635
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.07739627 0.01318947
## sample estimates:
## mean of x mean of y
## 0.008547009 0.040650407

```



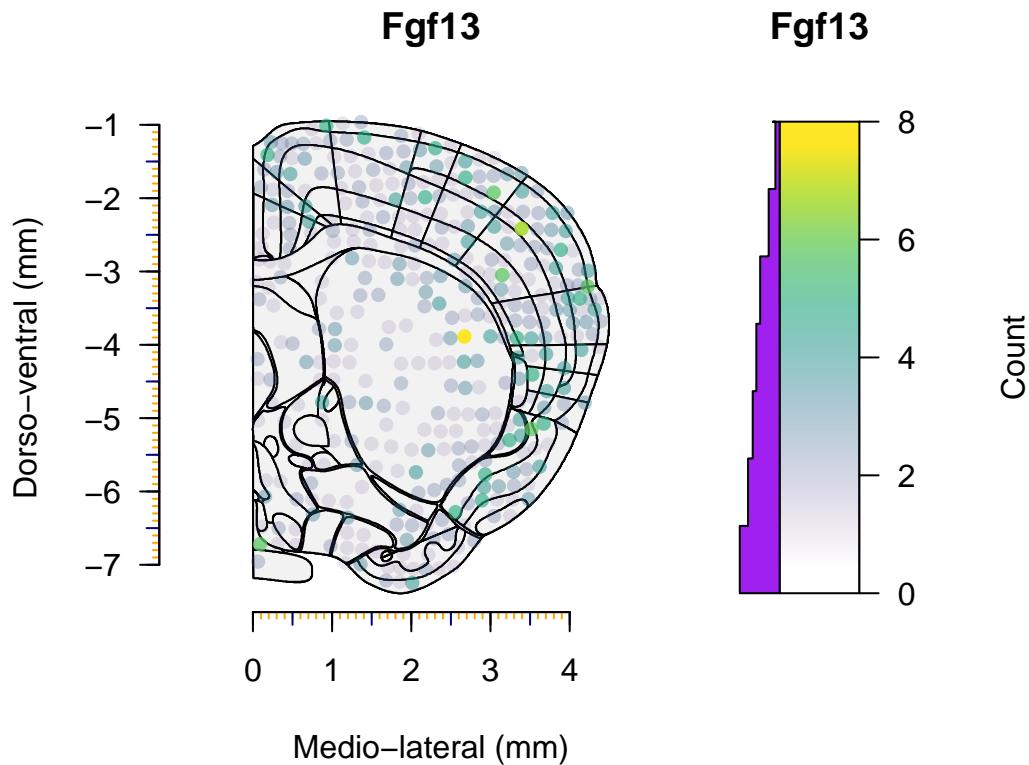
```
## Fgf11
## -----
## Average number of Fgf11 transcripts detected:
## CPu : M = 0.19 ( SD = 0.49 ) molecules
## SS : M = 0.12 ( SD = 0.33 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = 1.2207, df = 201.39, p-value = 0.2236
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.04066287 0.17282881
## sample estimates:
## mean of x mean of y
## 0.1880342 0.1219512
```



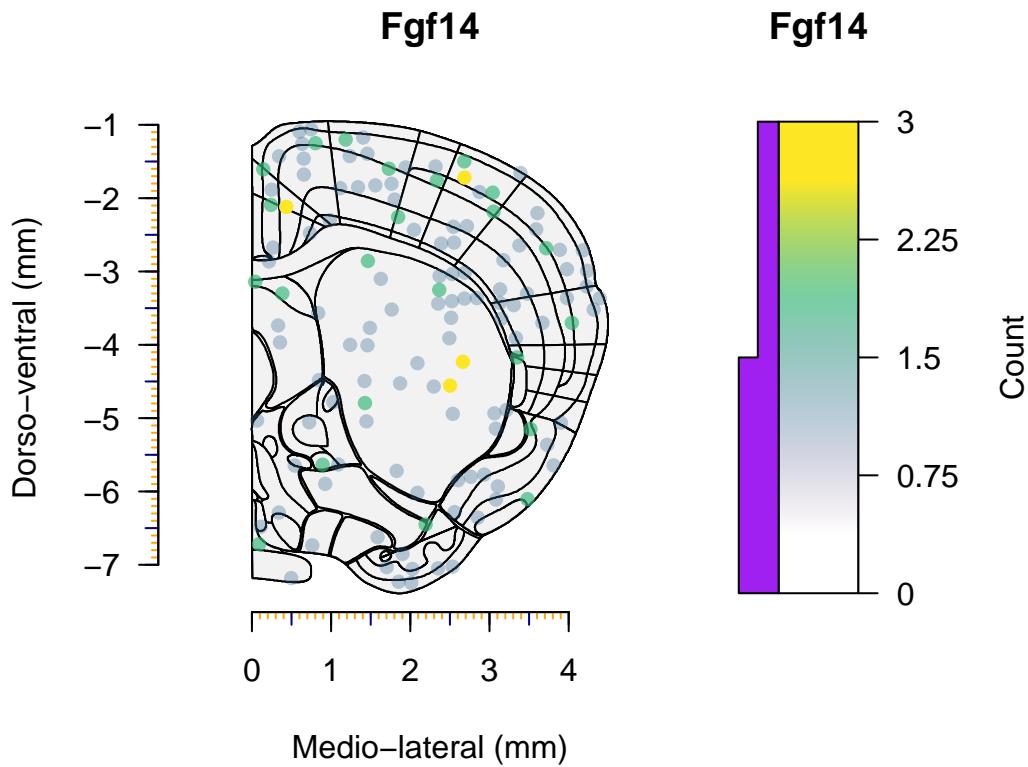
```

## Fgf12          MARKER FOR SOMATOSENSORY!
## -----
## Average number of Fgf12 transcripts detected:
## CPu : M = 0.93 ( SD = 0.94 ) molecules
## SS : M = 1.99 ( SD = 1.58 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = -6.359, df = 199.82, p-value = 1.354e-09
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.3890276 -0.7314643
## sample estimates:
## mean of x mean of y
## 0.9316239 1.9918699

```



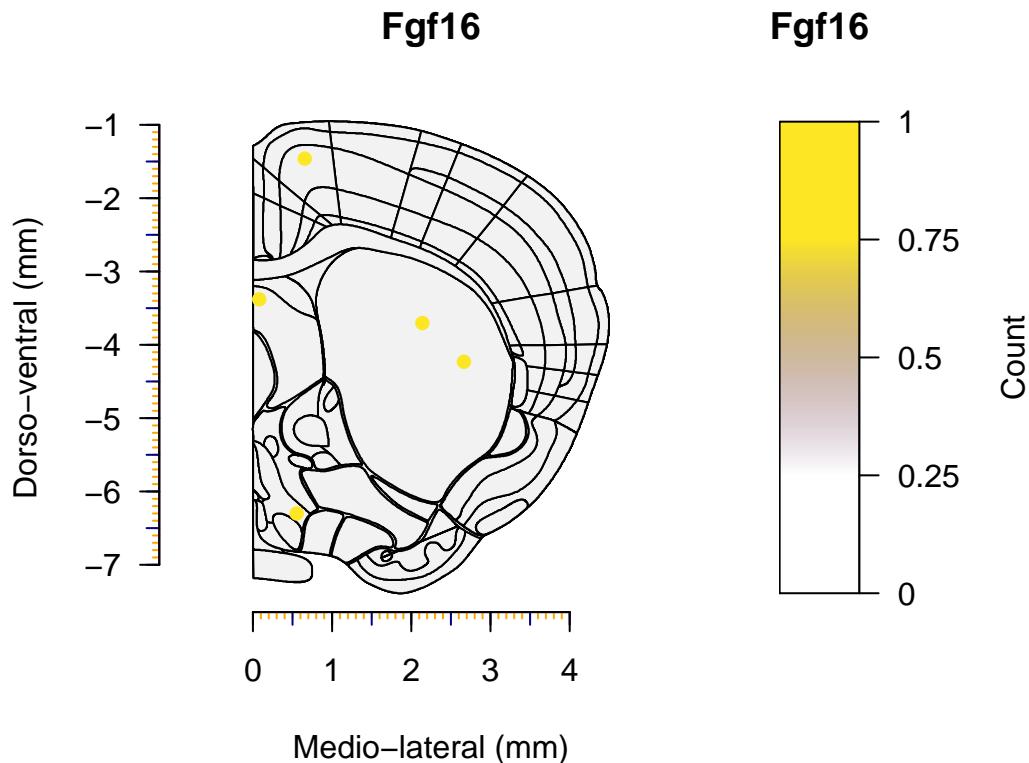
```
## Fgf13          MARKER FOR SOMATOSENSORY!
## -----
## Average number of Fgf13 transcripts detected:
## CPu : M = 1.26 ( SD = 1.27 ) molecules
## SS  : M = 2.02 ( SD = 1.55 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = -4.2025, df = 233.17, p-value = 3.762e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.1280204 -0.4079396
## sample estimates:
## mean of x mean of y
## 1.25641   2.02439
```



```

## Fgf14
## -----
## Average number of Fgf14 transcripts detected:
## CPu : M = 0.3 ( SD = 0.61 ) molecules
## SS : M = 0.37 ( SD = 0.63 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = -0.83594, df = 237.98, p-value = 0.404
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.22391406 0.09049735
## sample estimates:
## mean of x mean of y
## 0.2991453 0.3658537

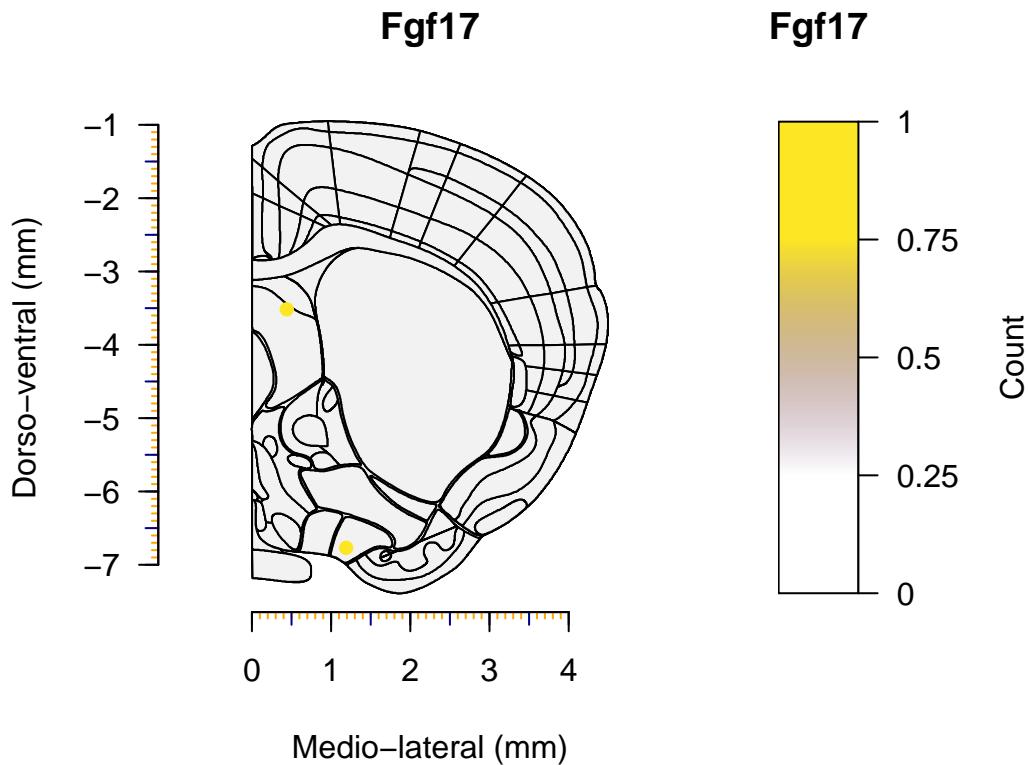
```



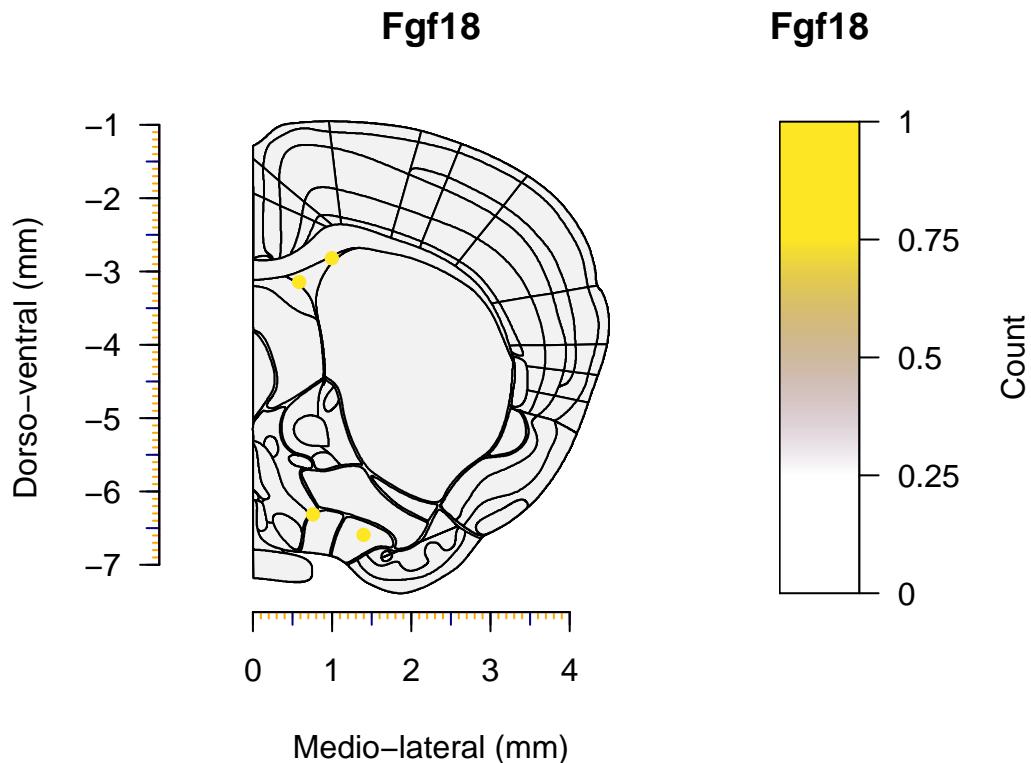
```

## Fgf16
## -----
## Average number of Fgf16 transcripts detected:
## CPu : M = 0.02 ( SD = 0.13 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = 1.4203, df = 116, p-value = 0.1582
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.00674298  0.04093101
## sample estimates:
## mean of x  mean of y
## 0.01709402 0.00000000

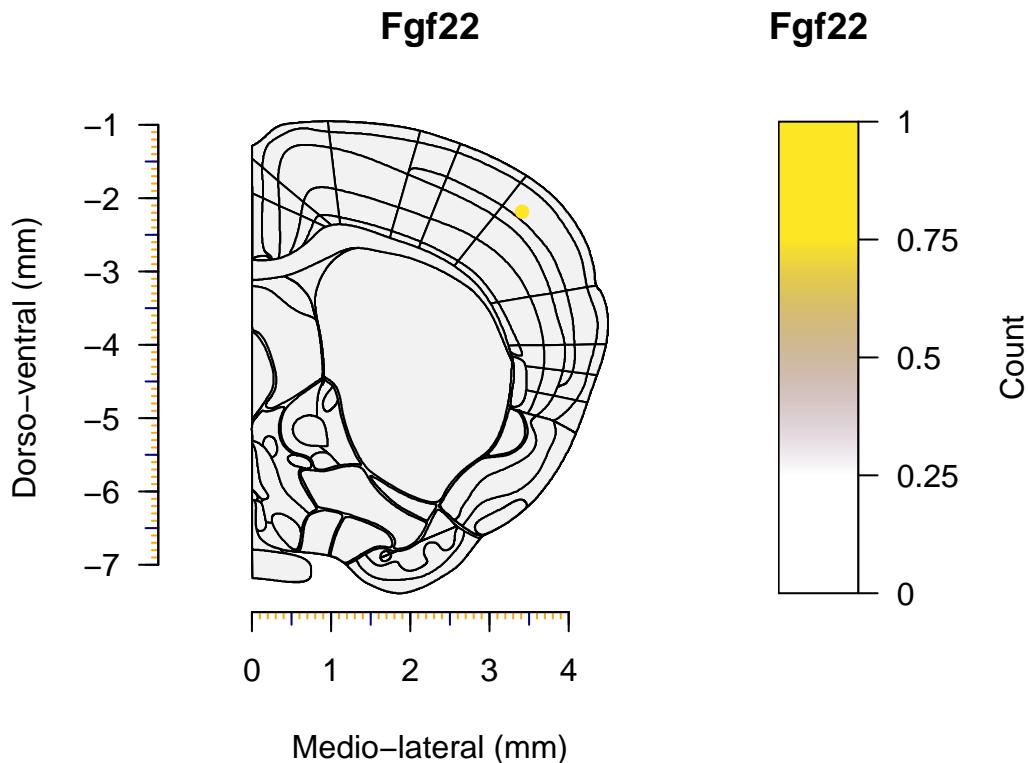
```



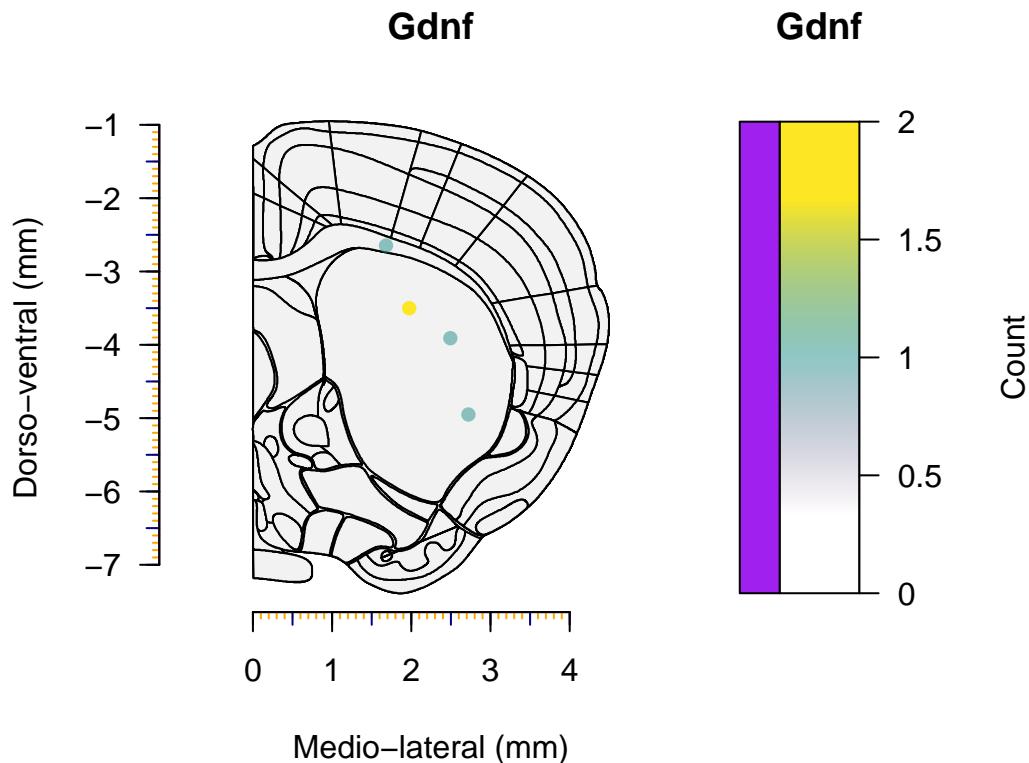
```
## Fgf17
## -----
## Average number of Fgf17 transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = NaN, df = NaN, p-value = NA
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   NaN NaN
## sample estimates:
## mean of x mean of y
##           0          0
```



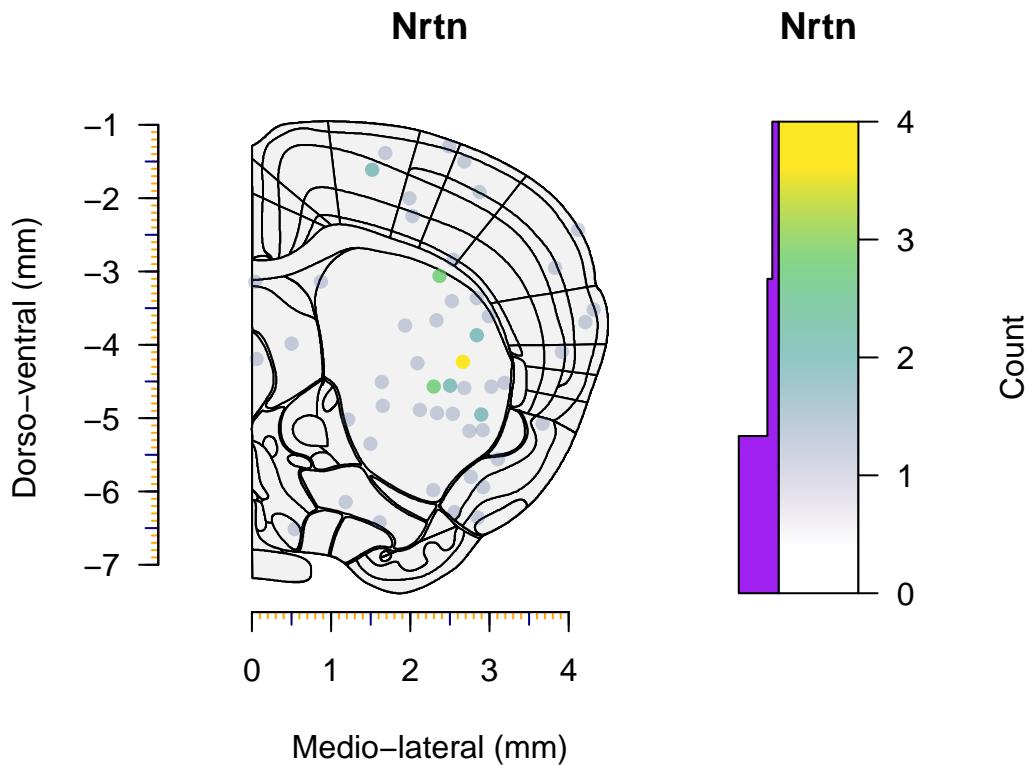
```
## Fgf18
## -----
## Average number of Fgf18 transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = NaN, df = NaN, p-value = NA
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   NaN NaN
## sample estimates:
## mean of x mean of y
##          0          0
```



```
## Fgf22
## -----
## Average number of Fgf22 transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0.01 ( SD = 0.09 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = -1, df = 122, p-value = 0.3193
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.024224389 0.007964227
## sample estimates:
## mean of x mean of y
## 0.000000000 0.008130081
```



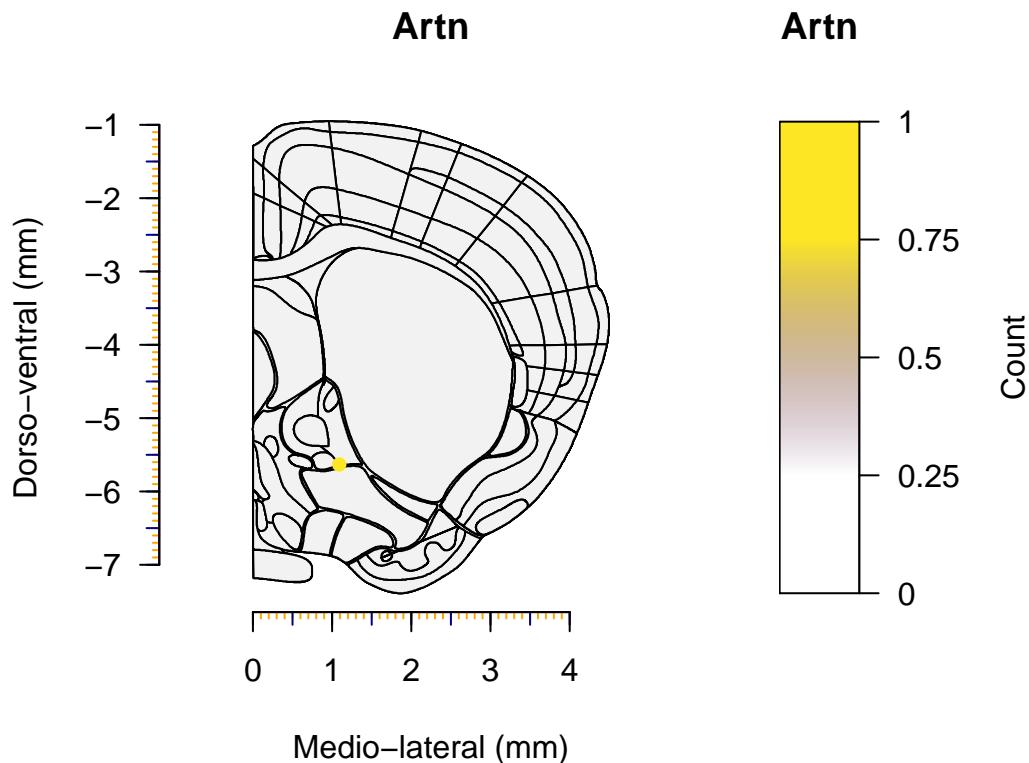
```
## Gdnf
## -----
## Average number of Gdnf transcripts detected:
## CPu : M = 0.03 ( SD = 0.22 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = 1.6449, df = 116, p-value = 0.1027
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.006979009 0.075355078
## sample estimates:
## mean of x mean of y
## 0.03418803 0.00000000
```



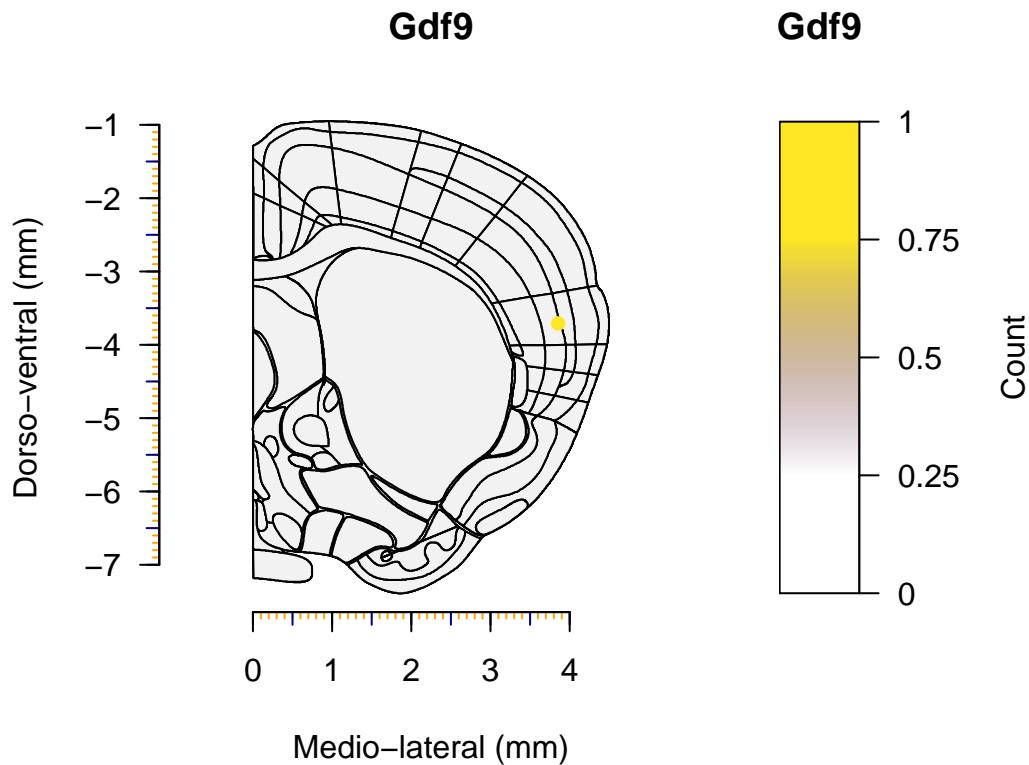
```

## Nrtn                         MARKER FOR CAUDATE PUTAMEN!
## -----
## Average number of Nrtn transcripts detected:
## CPu : M = 0.31 ( SD = 0.69 ) molecules
## SS : M = 0.08 ( SD = 0.27 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = 3.3168, df = 150.48, p-value = 0.001142
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.09152566 0.36125732
## sample estimates:
## mean of x  mean of y
## 0.30769231 0.08130081

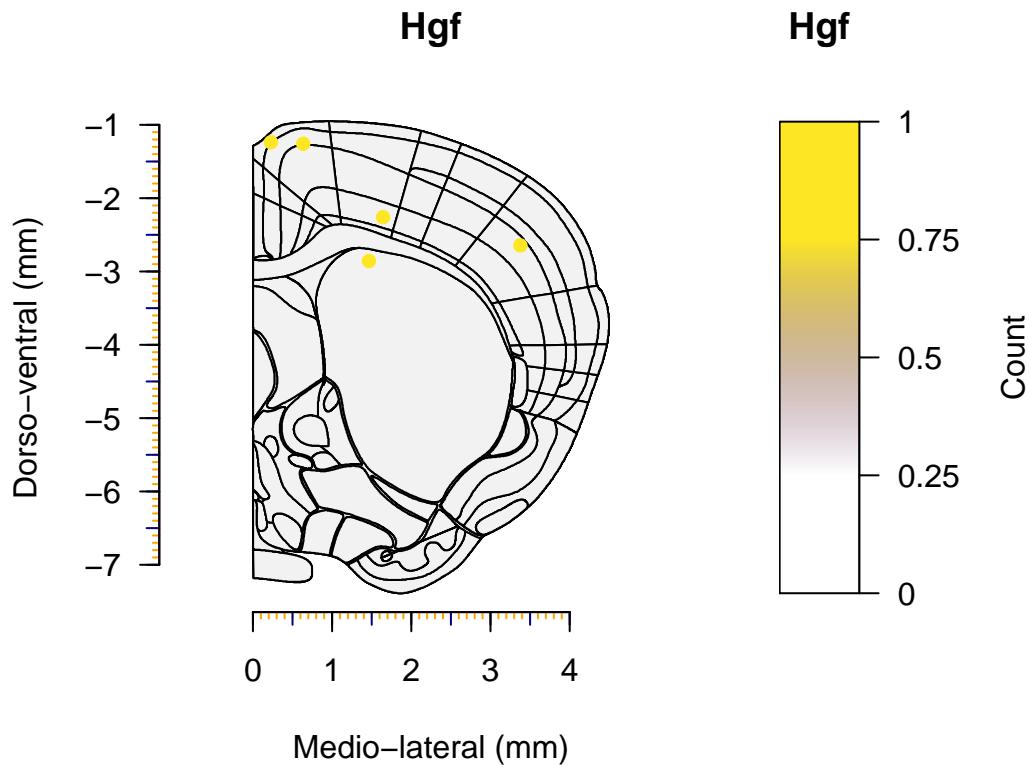
```



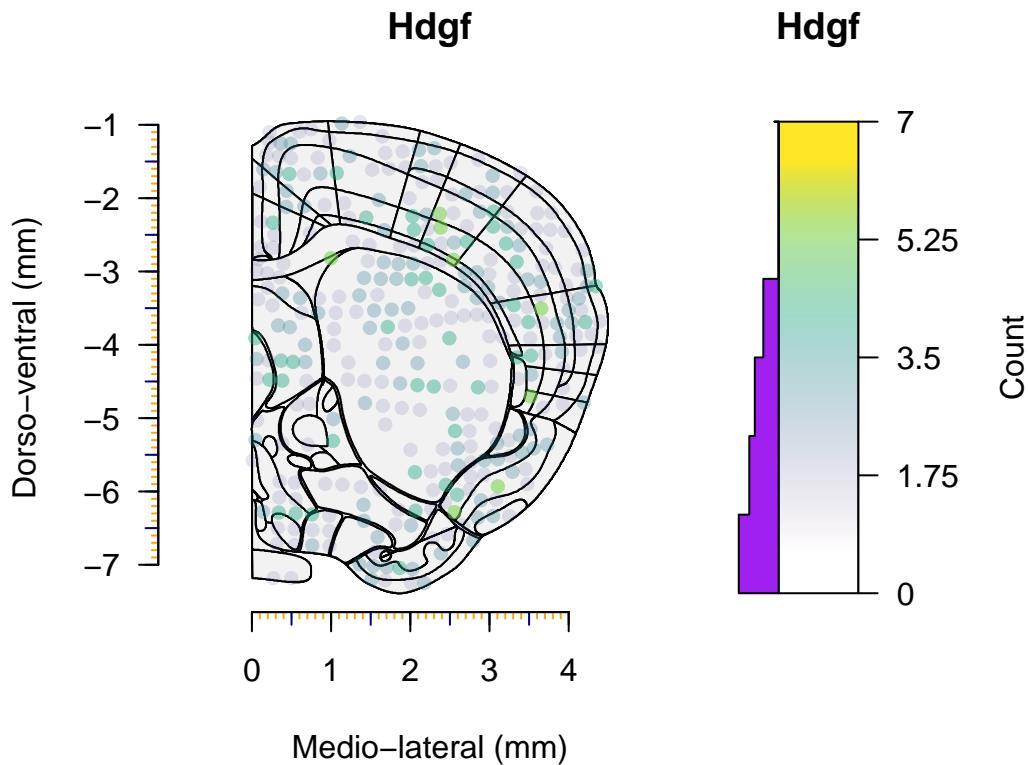
```
## Artn
## -----
## Average number of Artn transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = NaN, df = NaN, p-value = NA
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   NaN NaN
## sample estimates:
## mean of x mean of y
##          0          0
```



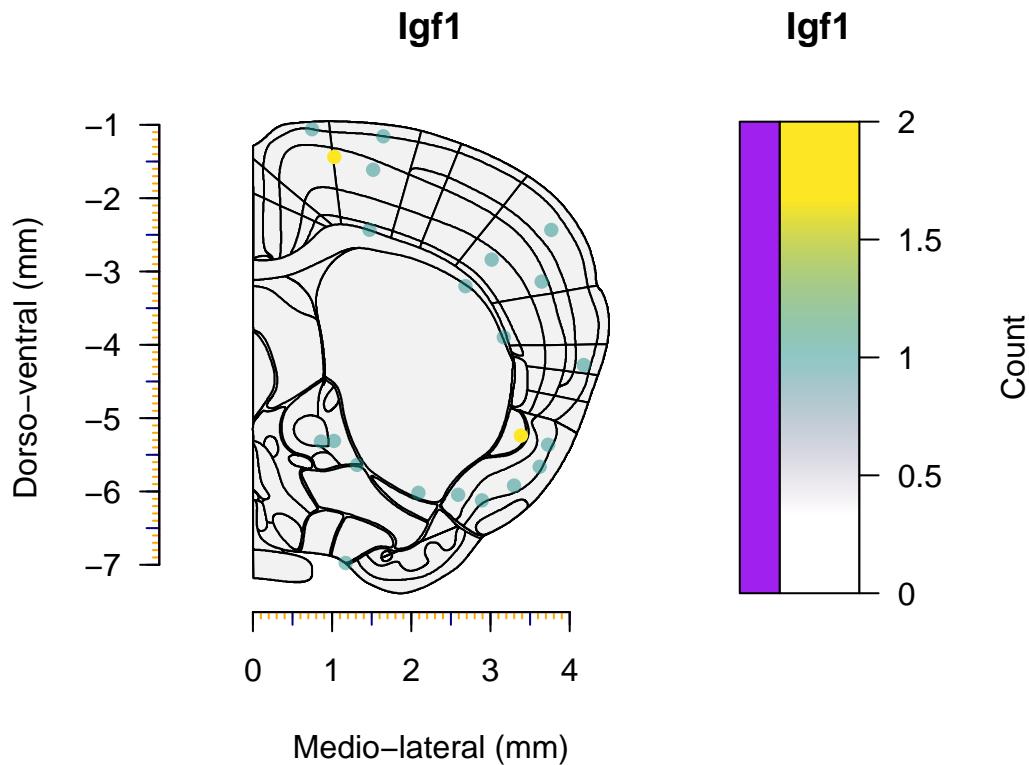
```
## Gdf9
## -----
## Average number of Gdf9 transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0.01 ( SD = 0.09 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = -1, df = 122, p-value = 0.3193
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.024224389 0.007964227
## sample estimates:
## mean of x mean of y
## 0.000000000 0.008130081
```



```
## Hgf
## -----
## Average number of Hgf transcripts detected:
## CPu : M = 0.01 ( SD = 0.09 ) molecules
## SS : M = 0.01 ( SD = 0.09 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = 0.035344, df = 236.66, p-value = 0.9718
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.02282198 0.02365583
## sample estimates:
## mean of x mean of y
## 0.008547009 0.008130081
```



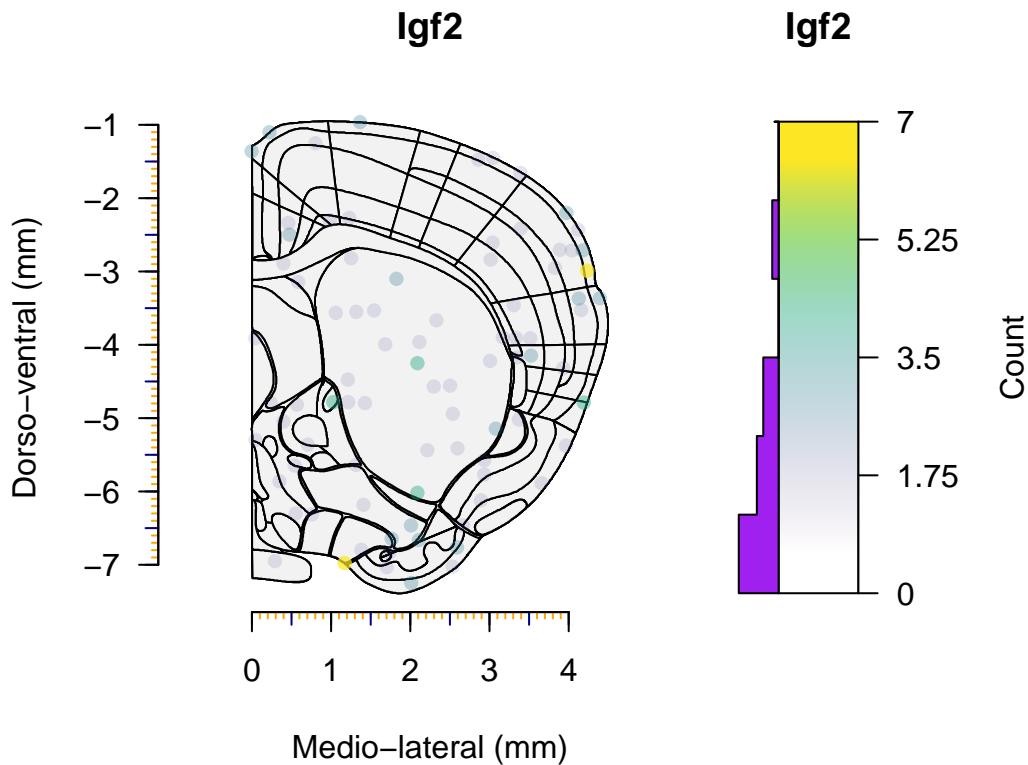
```
## Hdgf
## -----
## Average number of Hdgf transcripts detected:
## CPu : M = 1.03 ( SD = 0.97 ) molecules
## SS : M = 1.16 ( SD = 1.09 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = -1.0303, df = 236.95, p-value = 0.3039
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.3988450  0.1249238
## sample estimates:
## mean of x mean of y
## 1.025641  1.162602
```



```

## Igf1
## -----
## Average number of Igf1 transcripts detected:
## CPu : M = 0.02 ( SD = 0.13 ) molecules
## SS : M = 0.02 ( SD = 0.15 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = -0.39576, df = 234.48, p-value = 0.6926
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.04361765 0.02902520
## sample estimates:
## mean of x mean of y
## 0.01709402 0.02439024

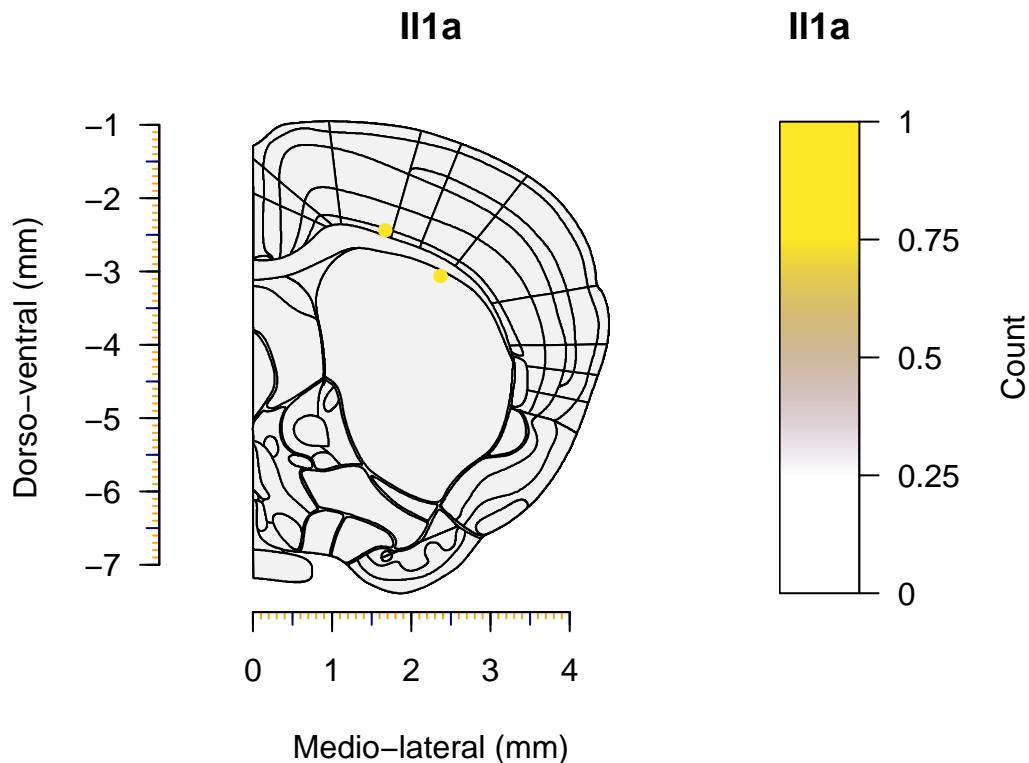
```



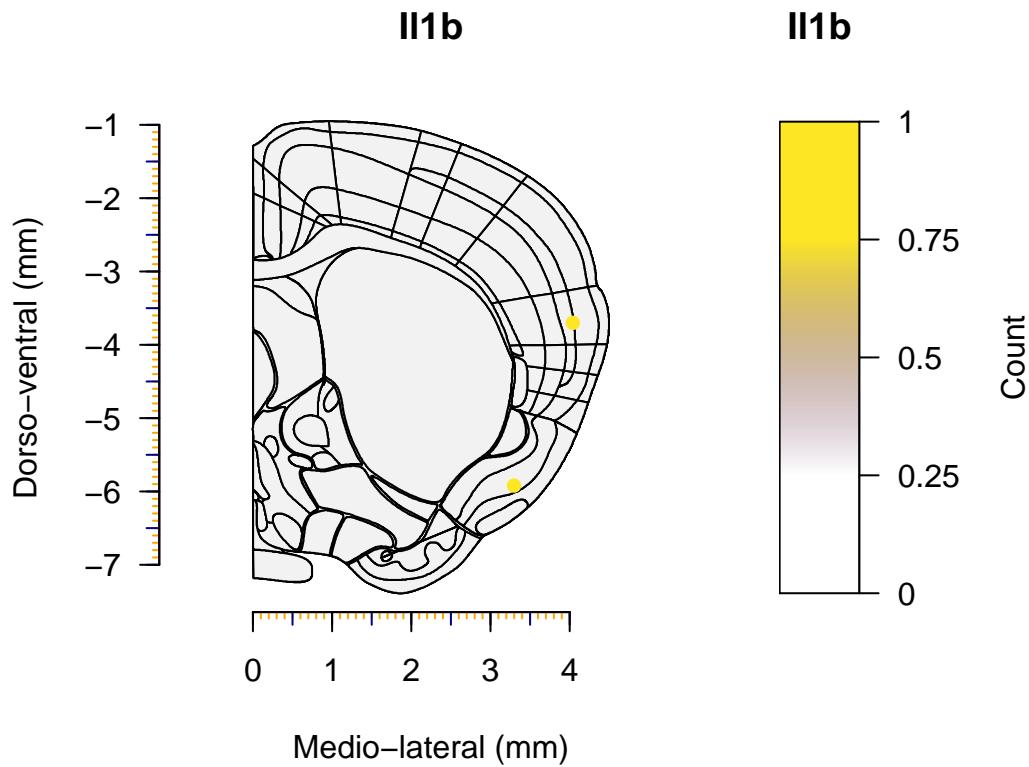
```

## Igf2
## -----
## Average number of Igf2 transcripts detected:
## CPu : M = 0.22 ( SD = 0.56 ) molecules
## SS : M = 0.22 ( SD = 0.63 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = 0.035165, df = 236.63, p-value = 0.972
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.1491126  0.1545326
## sample estimates:
## mean of x mean of y
## 0.2222222 0.2195122

```



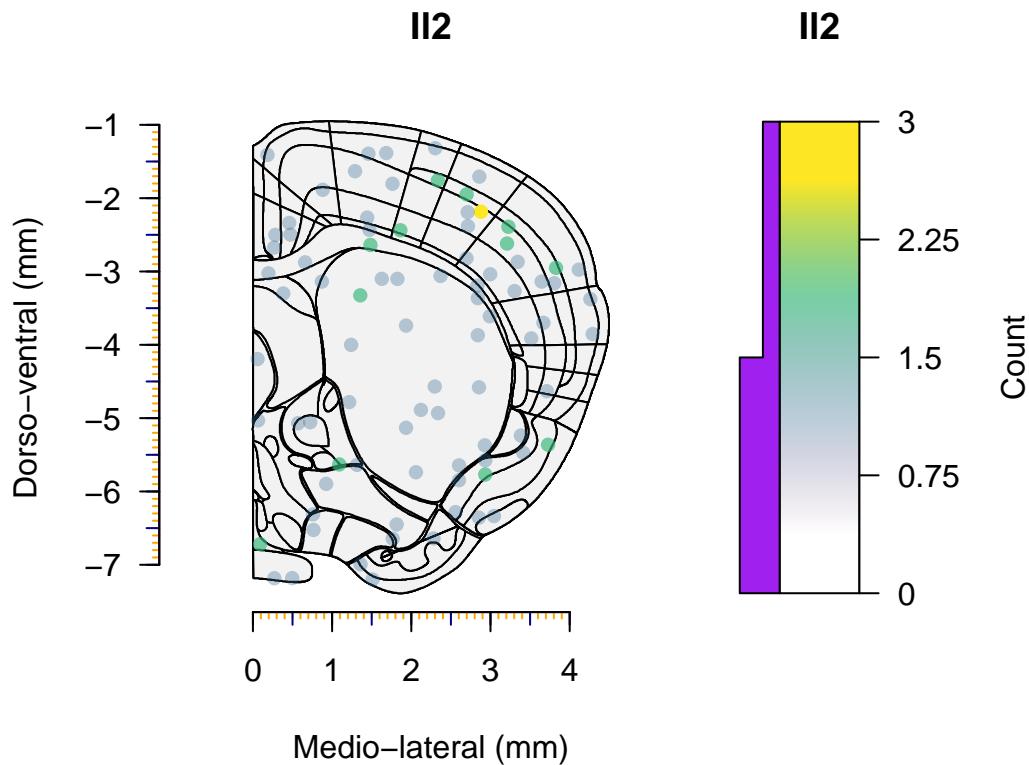
```
## Il1a
## -----
## Average number of Il1a transcripts detected:
## CPu : M = 0.01 ( SD = 0.09 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = 1, df = 116, p-value = 0.3194
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.008381419 0.025475436
## sample estimates:
## mean of x mean of y
## 0.008547009 0.000000000
```



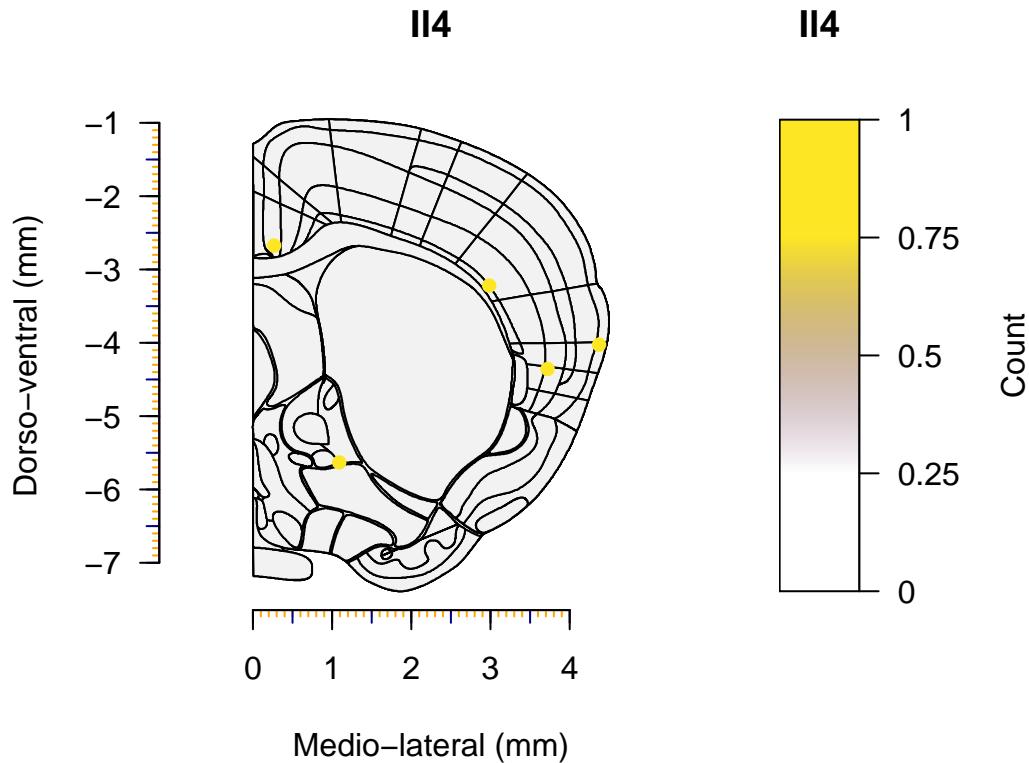
```

## Il1b
## -----
## Average number of Il1b transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0.01 ( SD = 0.09 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = -1, df = 122, p-value = 0.3193
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.024224389 0.007964227
## sample estimates:
## mean of x mean of y
## 0.000000000 0.008130081

```



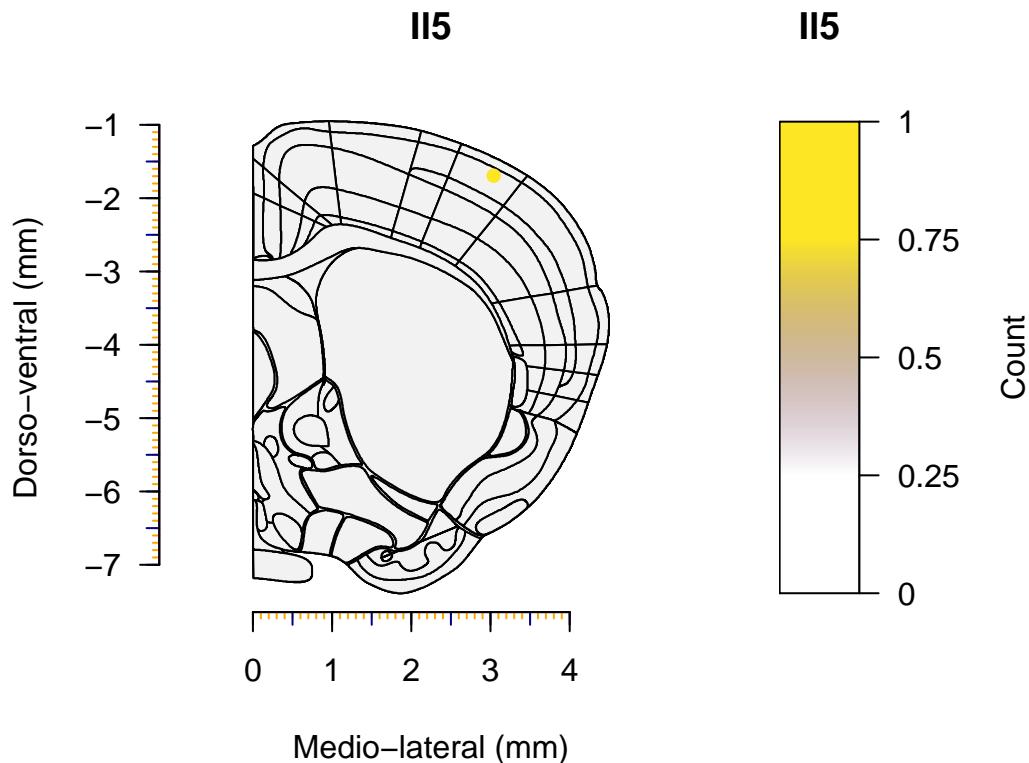
```
## I12
## -----
## Average number of I12 transcripts detected:
## CPu : M = 0.17 ( SD = 0.4 ) molecules
## SS : M = 0.24 ( SD = 0.58 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = -1.1422, df = 217.89, p-value = 0.2546
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.19885697  0.05293243
## sample estimates:
## mean of x mean of y
## 0.1709402  0.2439024
```



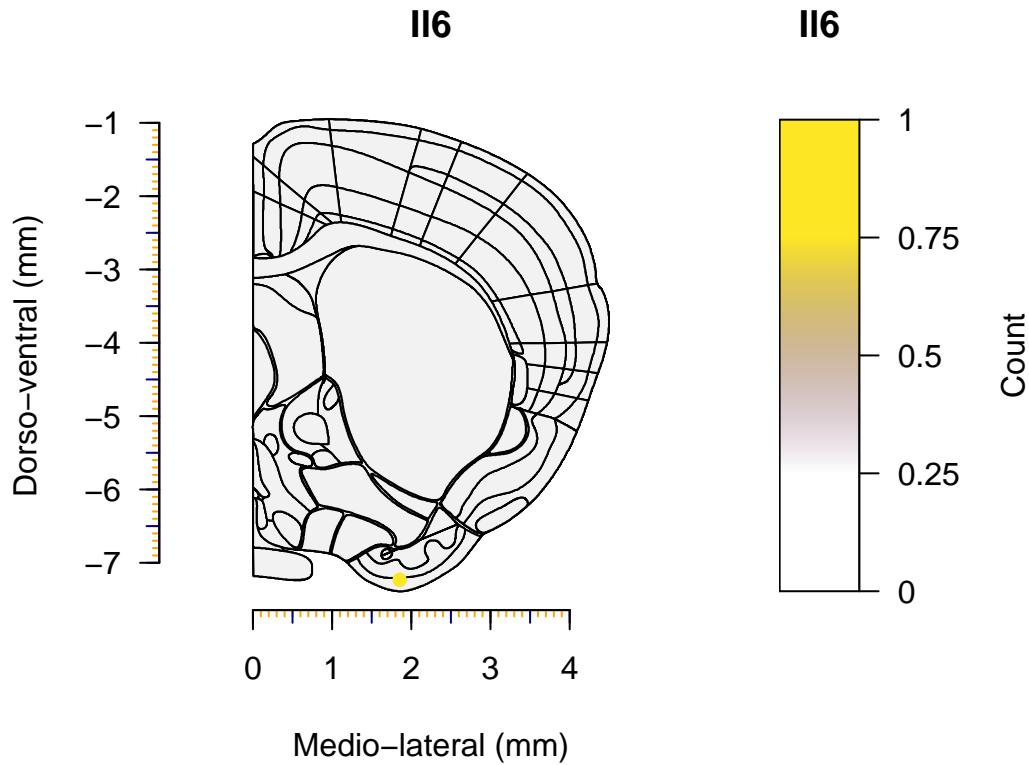
```

## II4
## -----
## Average number of II4 transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0.01 ( SD = 0.09 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = -1, df = 122, p-value = 0.3193
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.024224389 0.007964227
## sample estimates:
## mean of x mean of y
## 0.000000000 0.008130081

```



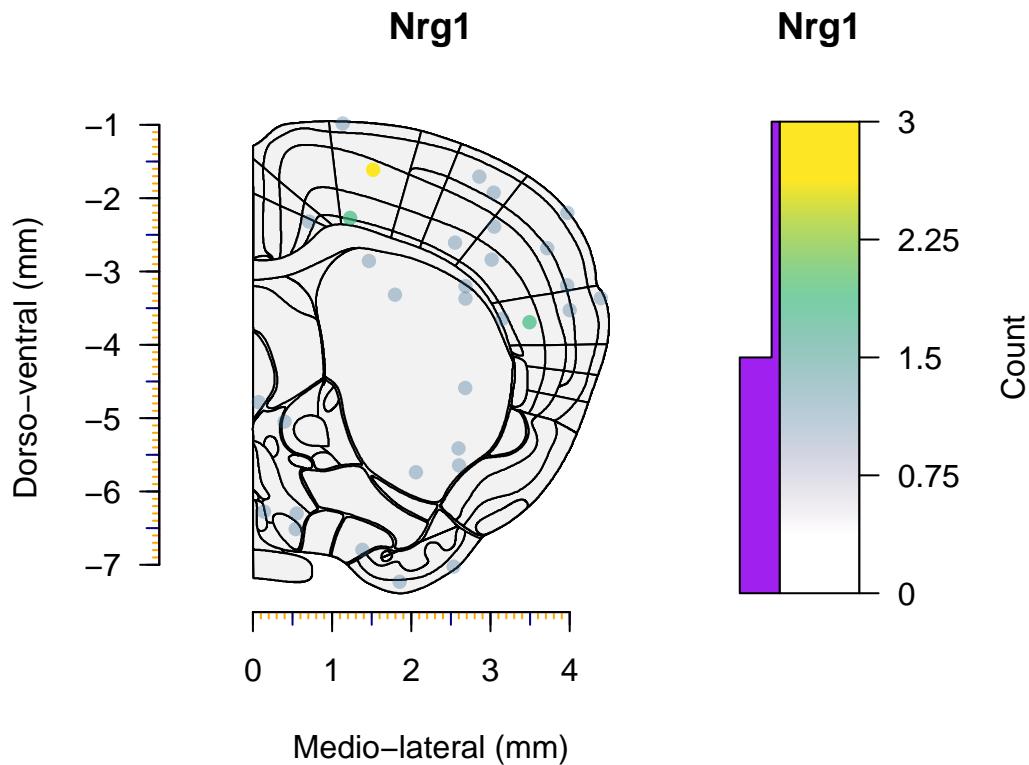
```
## II5
## -----
## Average number of II5 transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0.01 ( SD = 0.09 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = -1, df = 122, p-value = 0.3193
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.024224389 0.007964227
## sample estimates:
## mean of x mean of y
## 0.000000000 0.008130081
```



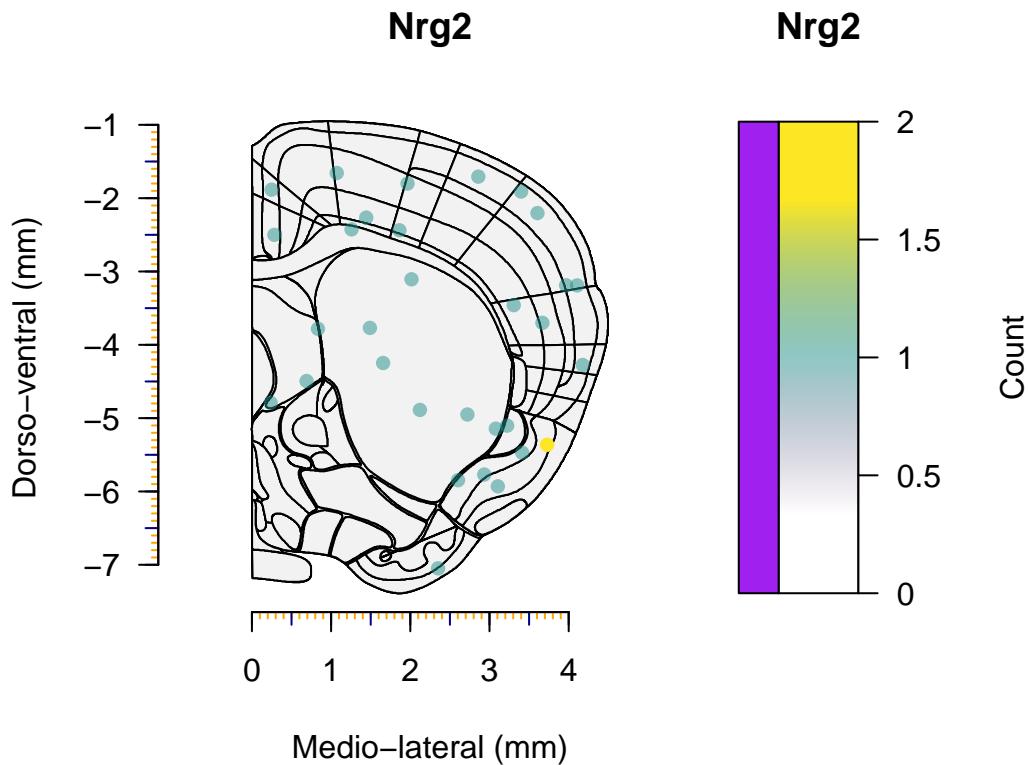
```

## II6
## -----
## Average number of II6 transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = NaN, df = NaN, p-value = NA
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   NaN NaN
## sample estimates:
## mean of x mean of y
##          0          0

```



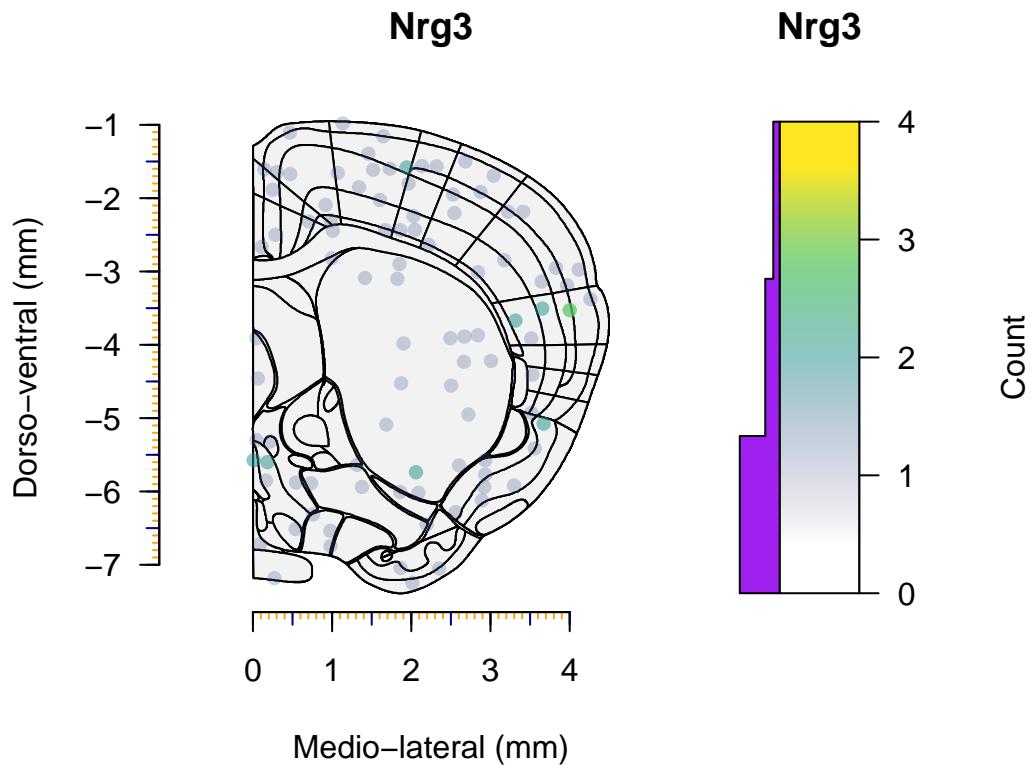
```
## Nrg1
## -----
## Average number of Nrg1 transcripts detected:
## CPu : M = 0.07 ( SD = 0.25 ) molecules
## SS : M = 0.11 ( SD = 0.33 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = -0.97752, df = 226.9, p-value = 0.3294
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.11253401  0.03790404
## sample estimates:
## mean of x  mean of y
## 0.06837607 0.10569106
```



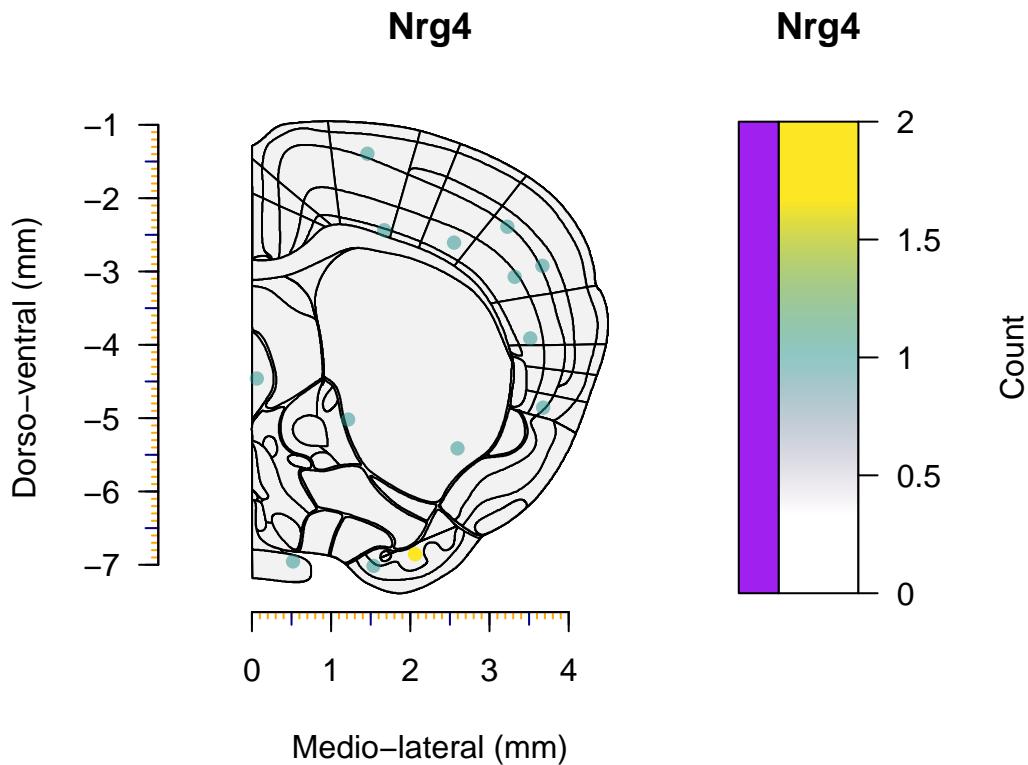
```

## Nrg2
## -----
## Average number of Nrg2 transcripts detected:
## CPu : M = 0.05 ( SD = 0.22 ) molecules
## SS : M = 0.07 ( SD = 0.26 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = -0.70089, df = 234.91, p-value = 0.4841
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.08341464 0.03963728
## sample estimates:
## mean of x mean of y
## 0.05128205 0.07317073

```



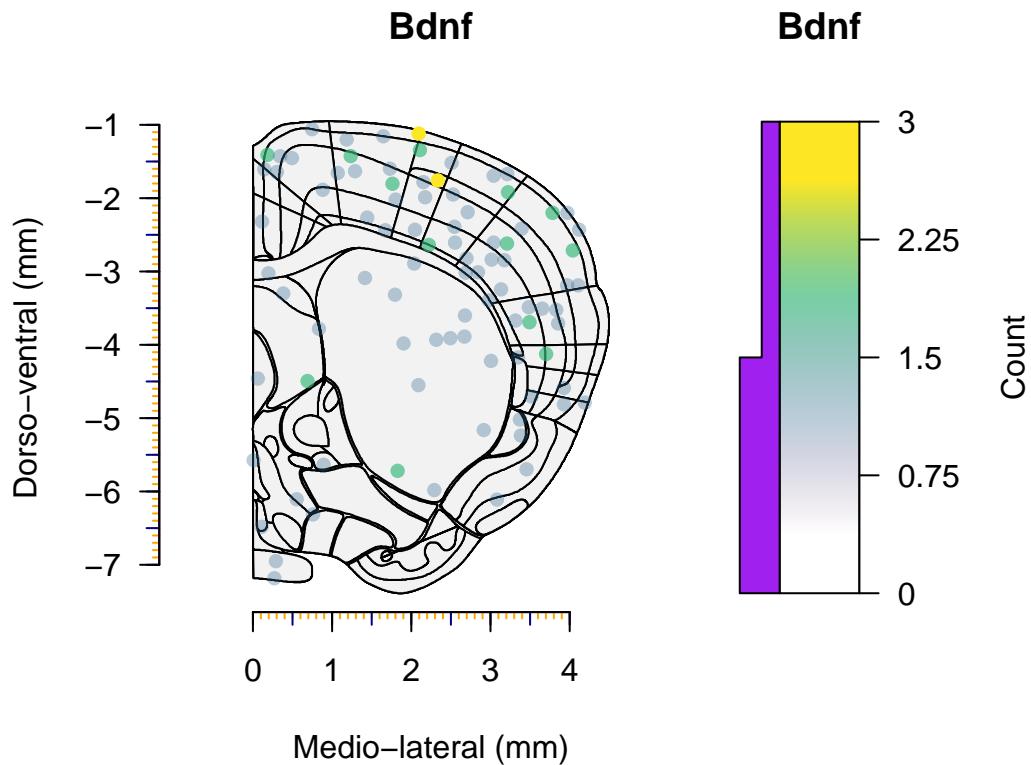
```
## Nrg3
## -----
## Average number of Nrg3 transcripts detected:
## CPu : M = 0.15 ( SD = 0.38 ) molecules
## SS : M = 0.24 ( SD = 0.51 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = -1.5605, df = 223.98, p-value = 0.12
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.20472212 0.02377569
## sample estimates:
## mean of x mean of y
## 0.1452991 0.2357724
```



```

## Nrg4
## -----
## Average number of Nrg4 transcripts detected:
## CPu : M = 0.02 ( SD = 0.13 ) molecules
## SS : M = 0.04 ( SD = 0.2 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = -1.093, df = 211.86, p-value = 0.2756
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.06604067 0.01892789
## sample estimates:
## mean of x mean of y
## 0.01709402 0.04065041

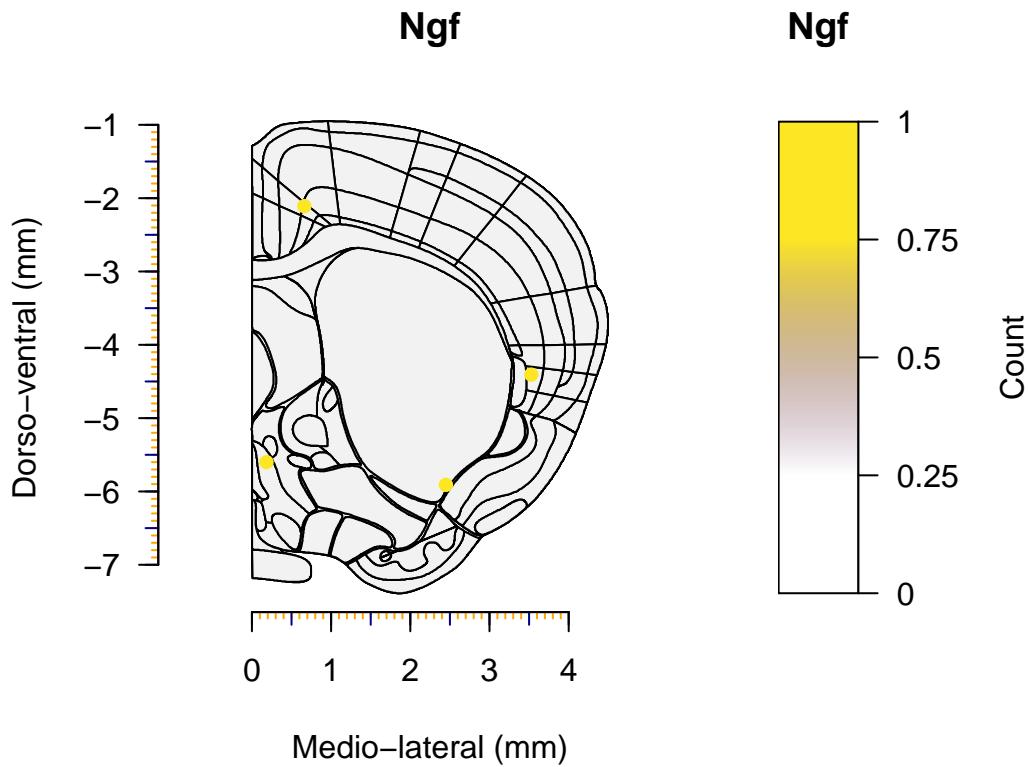
```



```

## Bdnf          MARKER FOR SOMATOSENSORY!
## -----
## Average number of Bdnf transcripts detected:
## CPu : M = 0.12 ( SD = 0.35 ) molecules
## SS : M = 0.36 ( SD = 0.63 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = -3.6425, df = 193.32, p-value = 0.0003467
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.3669696 -0.1091613
## sample estimates:
## mean of x mean of y
## 0.1196581 0.3577236

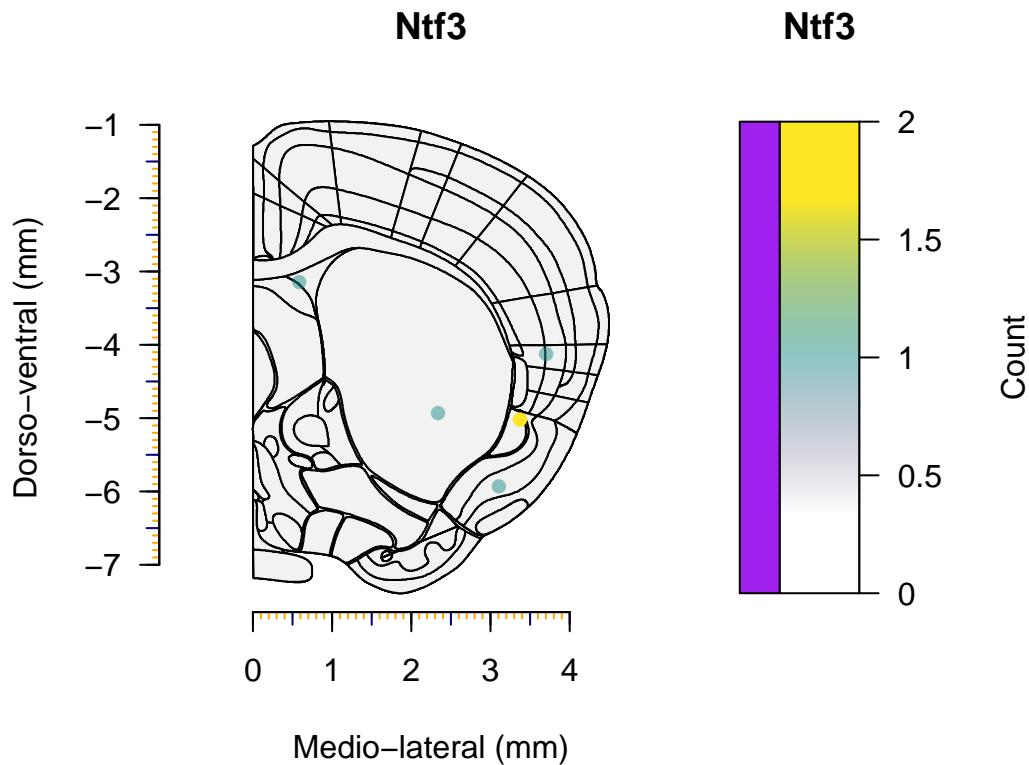
```



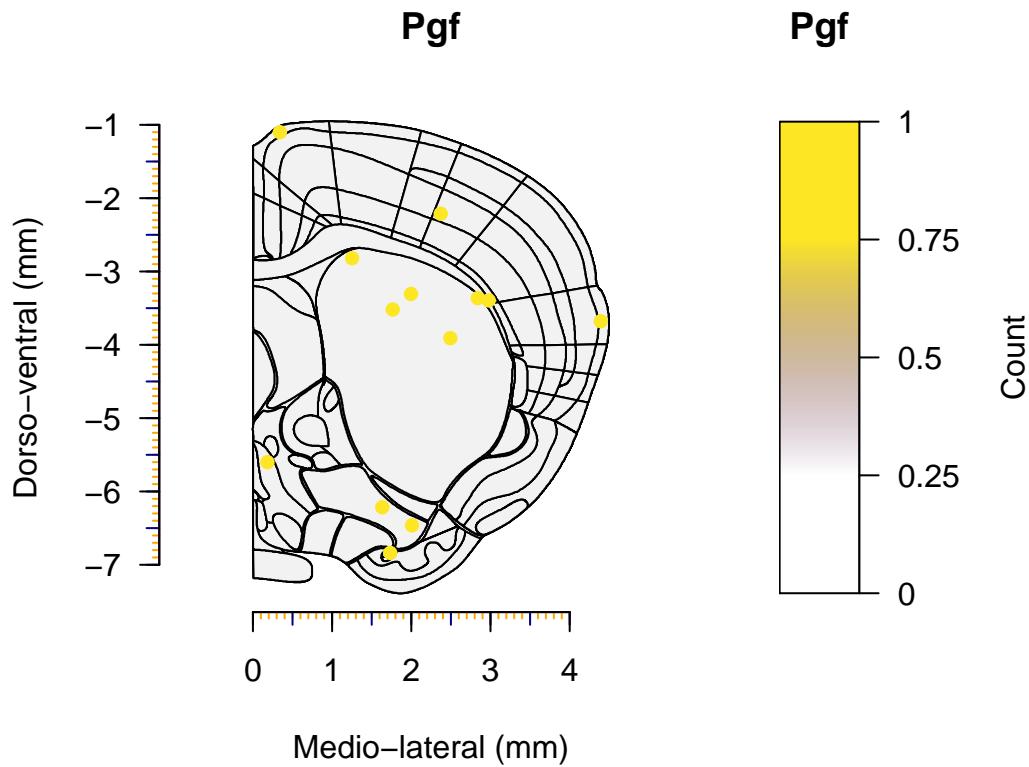
```

## Ngf
## -----
## Average number of Ngf transcripts detected:
## CPu : M = 0.01 ( SD = 0.09 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = 1, df = 116, p-value = 0.3194
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.008381419 0.025475436
## sample estimates:
## mean of x mean of y
## 0.008547009 0.000000000

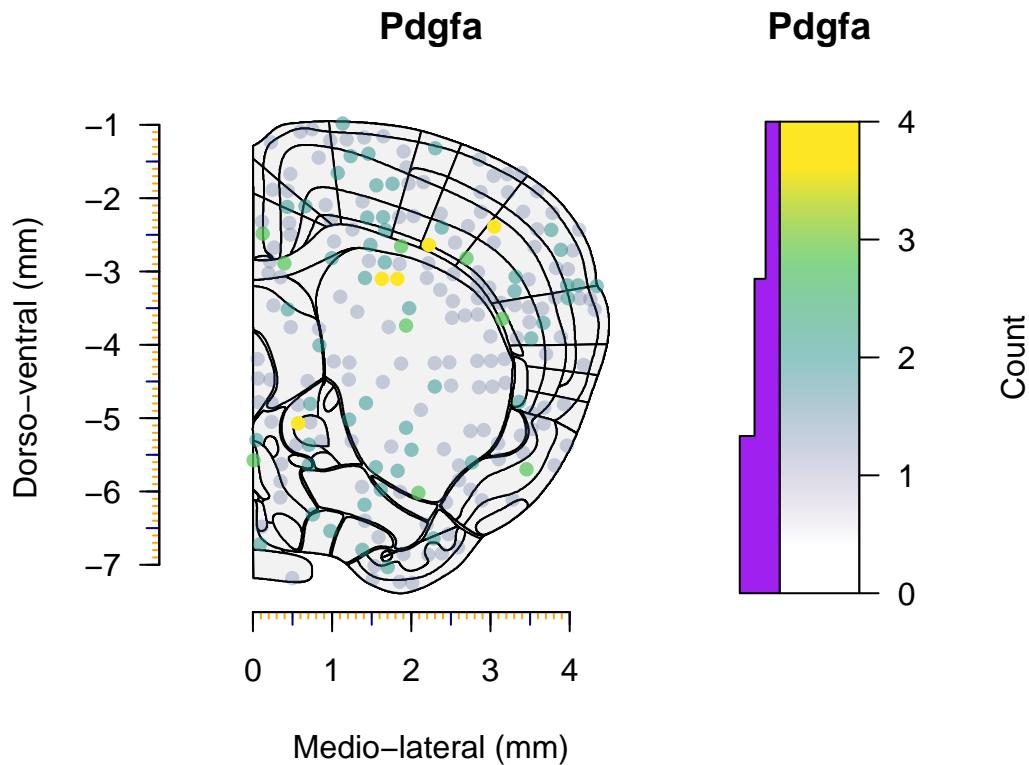
```



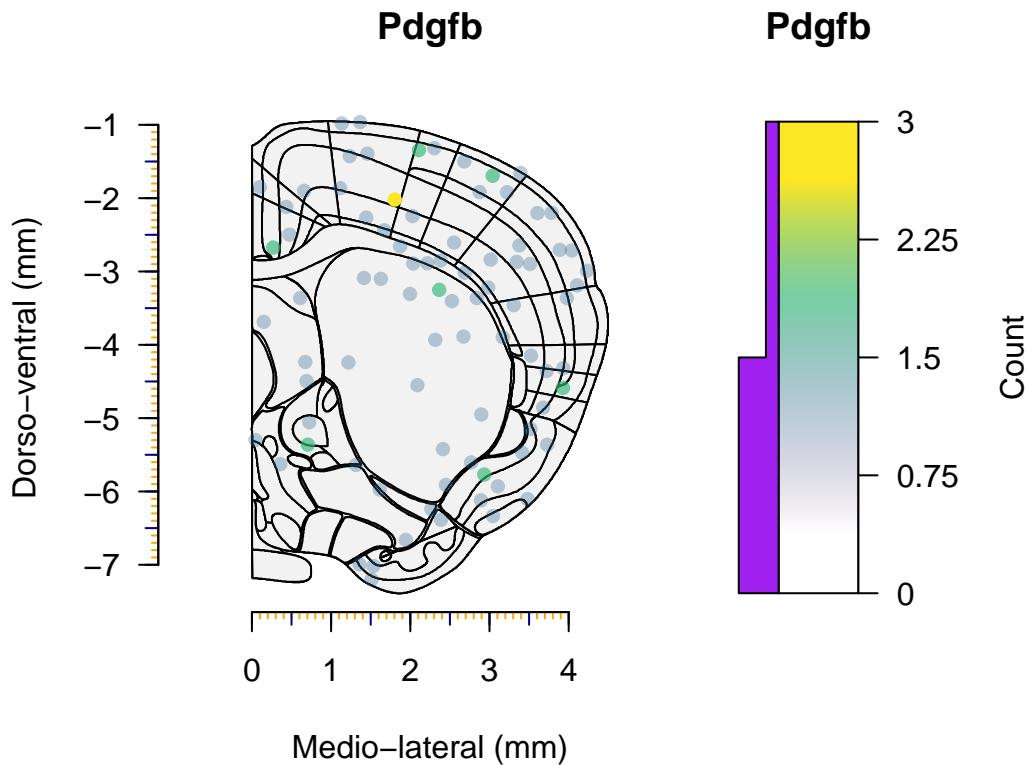
```
## Ntf3
## -----
## Average number of Ntf3 transcripts detected:
## CPu : M = 0.01 ( SD = 0.09 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = 1, df = 116, p-value = 0.3194
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.008381419 0.025475436
## sample estimates:
## mean of x mean of y
## 0.008547009 0.000000000
```



```
## Pgf
## -----
## Average number of Pgf transcripts detected:
## CPu : M = 0.04 ( SD = 0.2 ) molecules
## SS : M = 0.02 ( SD = 0.13 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = 1.2037, df = 192.93, p-value = 0.2302
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.01690641 0.06985617
## sample estimates:
## mean of x mean of y
## 0.04273504 0.01626016
```



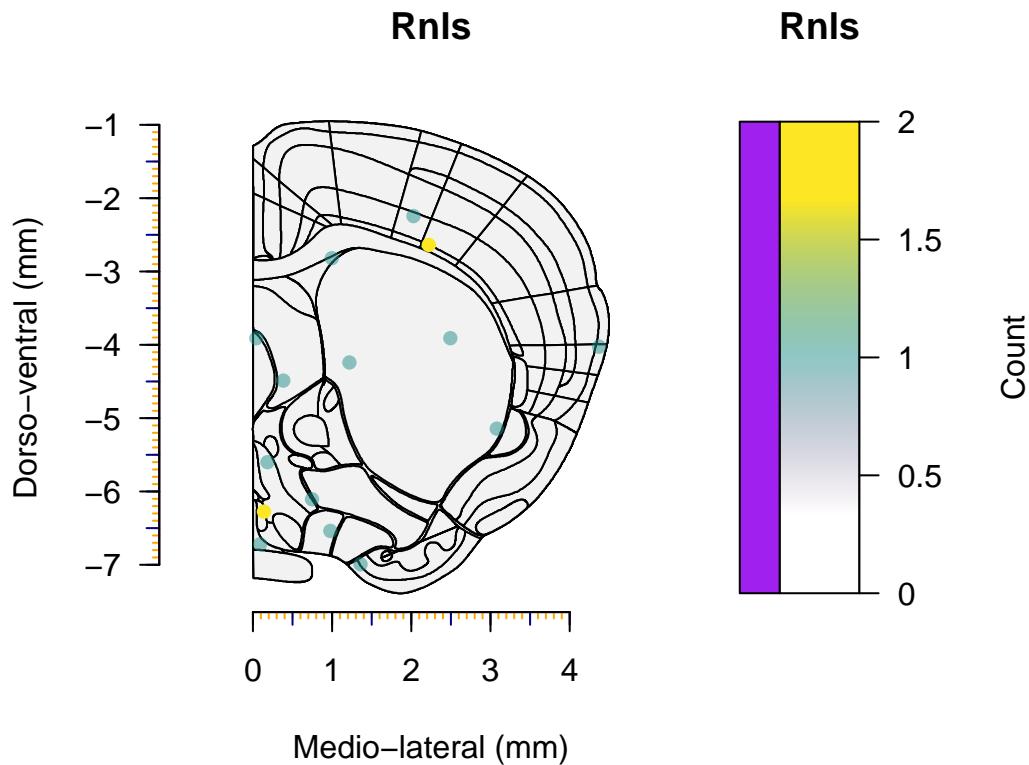
```
## Pdgfa
## -----
## Average number of Pdgfa transcripts detected:
## CPu : M = 0.57 ( SD = 0.85 ) molecules
## SS : M = 0.62 ( SD = 0.85 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = -0.41007, df = 237.41, p-value = 0.6821
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.2625587 0.1720855
## sample estimates:
## mean of x mean of y
## 0.5726496 0.6178862
```



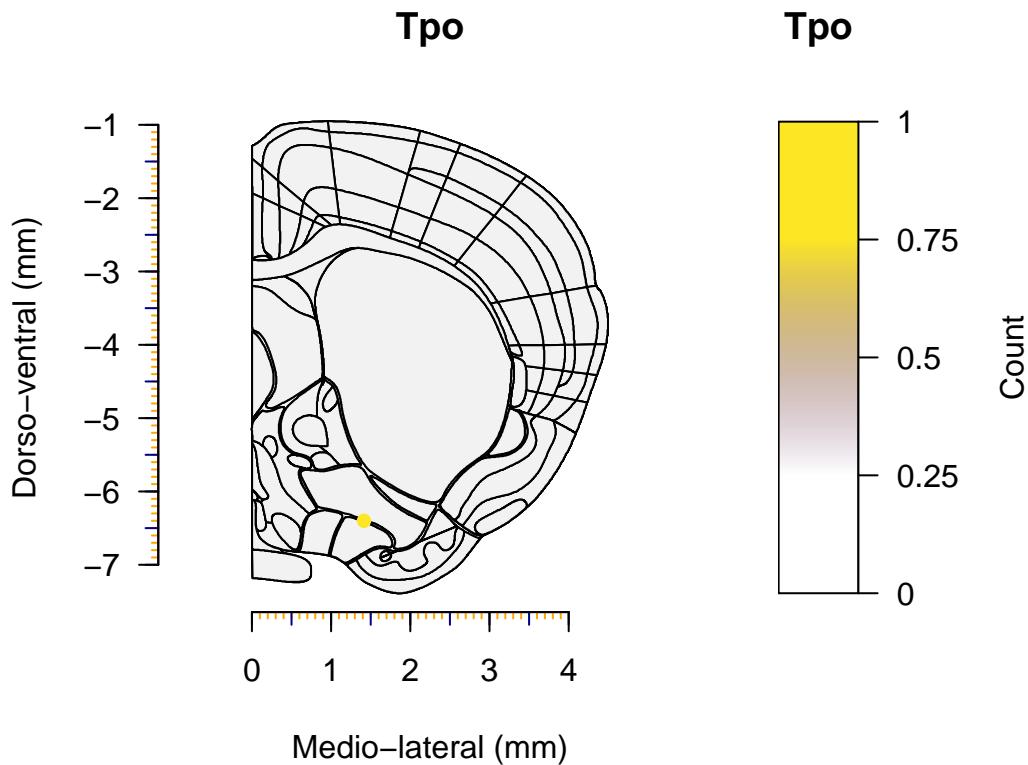
```

## Pdgfb
## -----
## Average number of Pdgfb transcripts detected:
## CPu : M = 0.13 ( SD = 0.36 ) molecules
## SS : M = 0.2 ( SD = 0.44 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = -1.443, df = 232.53, p-value = 0.1504
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.17751393 0.02742012
## sample estimates:
## mean of x mean of y
## 0.1282051 0.2032520

```



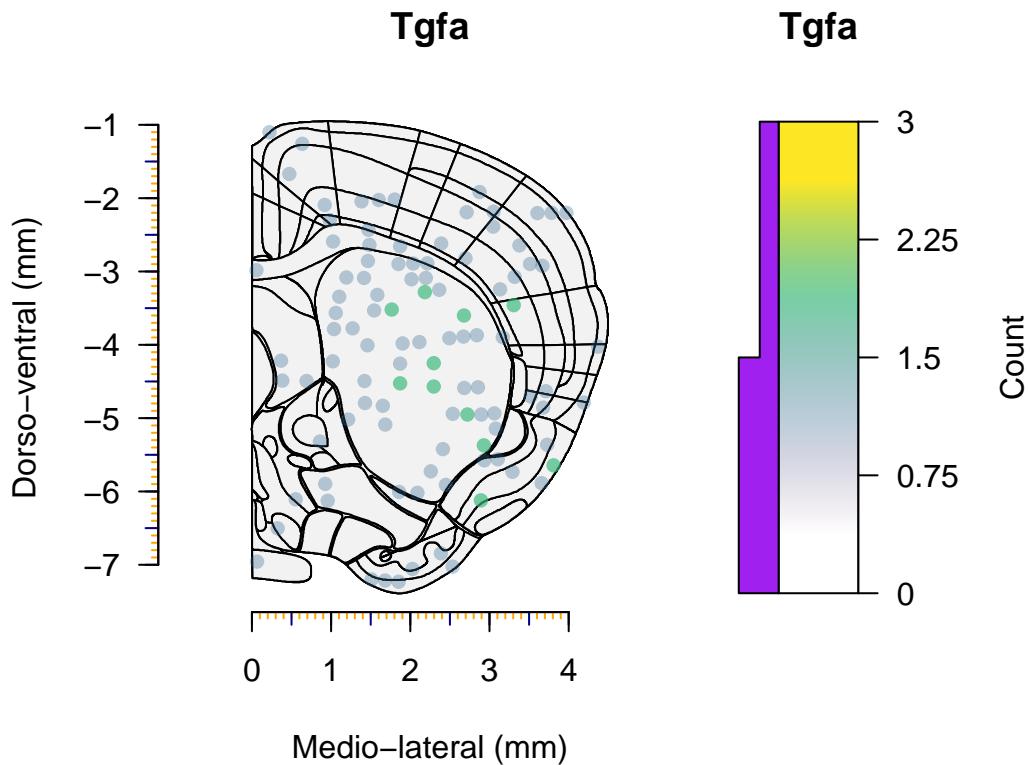
```
## Rnls
## -----
## Average number of Rnls transcripts detected:
## CPu : M = 0.03 ( SD = 0.16 ) molecules
## SS : M = 0.02 ( SD = 0.2 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = 0.053642, df = 230.32, p-value = 0.9573
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.04469182 0.04719339
## sample estimates:
## mean of x mean of y
## 0.02564103 0.02439024
```



```

## Tpo
## -----
## Average number of Tpo transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = NaN, df = NaN, p-value = NA
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   NaN NaN
## sample estimates:
## mean of x mean of y
##          0          0

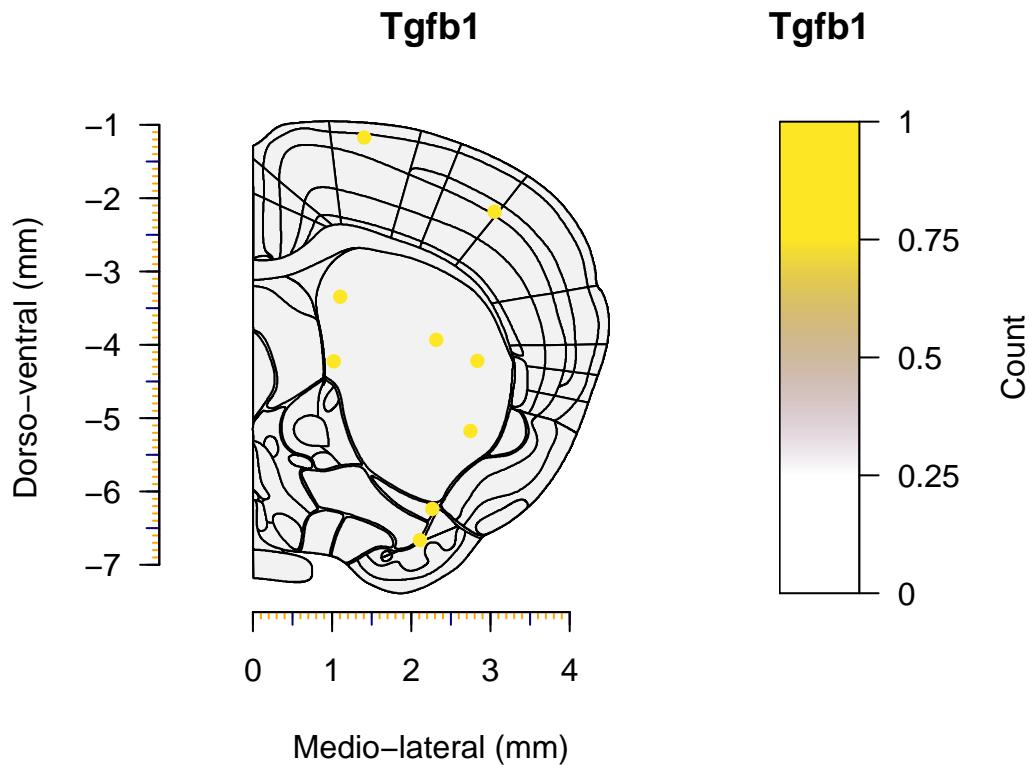
```



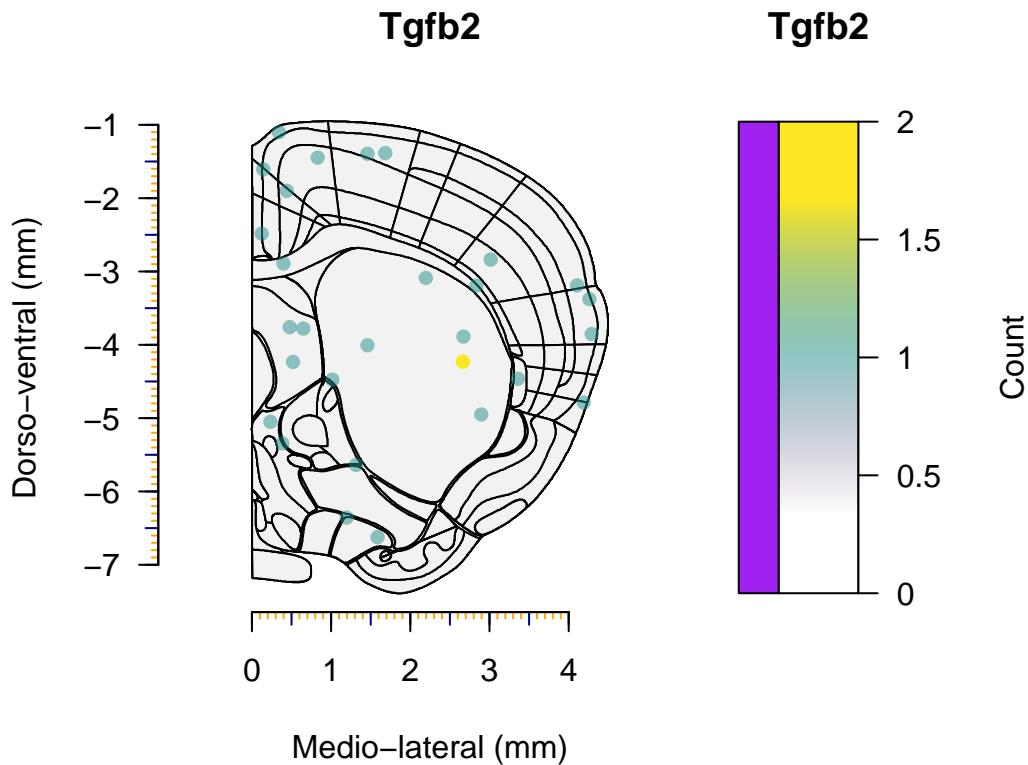
```

## Tgfa          MARKER FOR CAUDATE PUTAMEN!
## -----
## Average number of Tgfa transcripts detected:
## CPu : M = 0.45 ( SD = 0.62 ) molecules
## SS : M = 0.13 ( SD = 0.36 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = 4.8815, df = 184.19, p-value = 2.274e-06
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.1924007 0.4534196
## sample estimates:
## mean of x mean of y
## 0.4529915 0.1300813

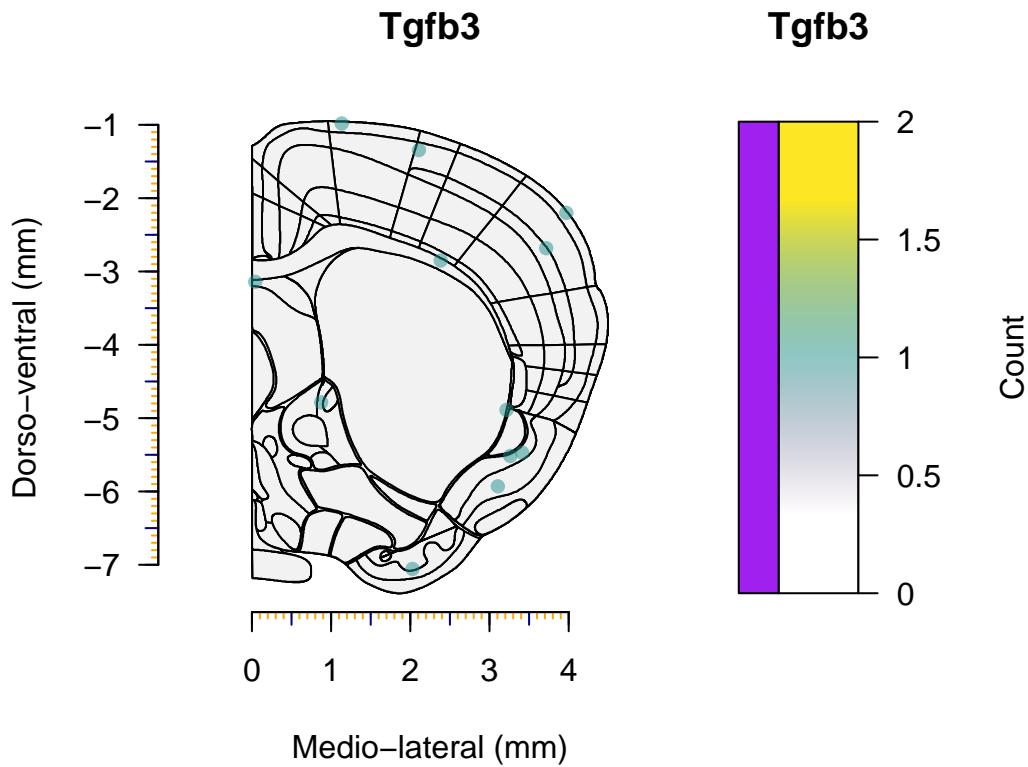
```



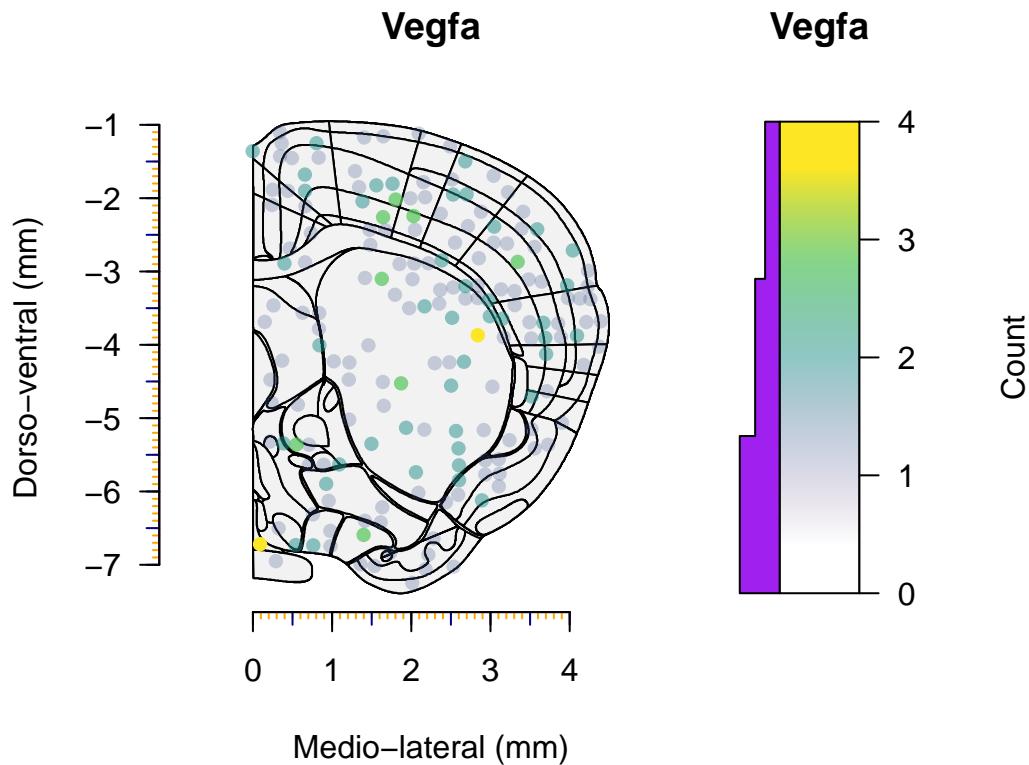
```
## Tgfb1
## -----
## Average number of Tgfb1 transcripts detected:
## CPu : M = 0.04 ( SD = 0.2 ) molecules
## SS : M = 0.01 ( SD = 0.09 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = 1.691, df = 158.27, p-value = 0.0928
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.005812046 0.075021969
## sample estimates:
## mean of x mean of y
## 0.042735043 0.008130081
```



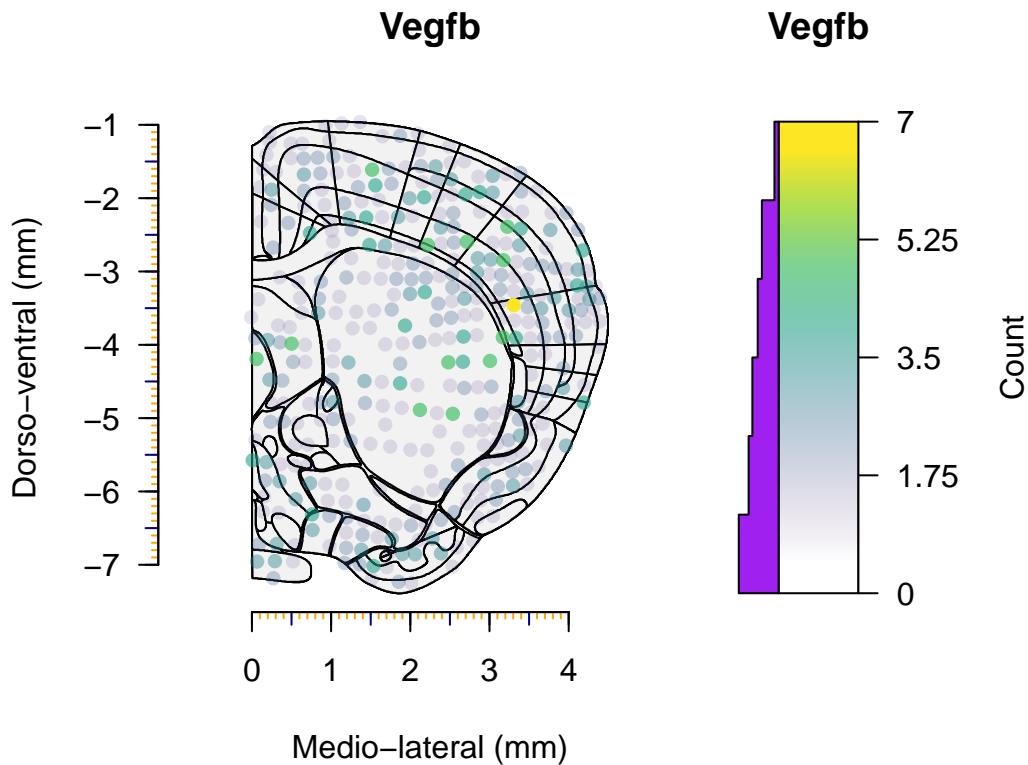
```
## Tgfb2
## -----
## Average number of Tgfb2 transcripts detected:
## CPu : M = 0.06 ( SD = 0.27 ) molecules
## SS : M = 0.03 ( SD = 0.18 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = 0.91531, df = 198.52, p-value = 0.3611
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.03152665  0.08614412
## sample estimates:
## mean of x  mean of y
## 0.05982906  0.03252033
```



```
## Tgfb3
## -----
## Average number of Tgfb3 transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0.02 ( SD = 0.15 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = -1.7464, df = 122, p-value = 0.08325
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.052036966 0.003256478
## sample estimates:
## mean of x mean of y
## 0.00000000 0.02439024
```



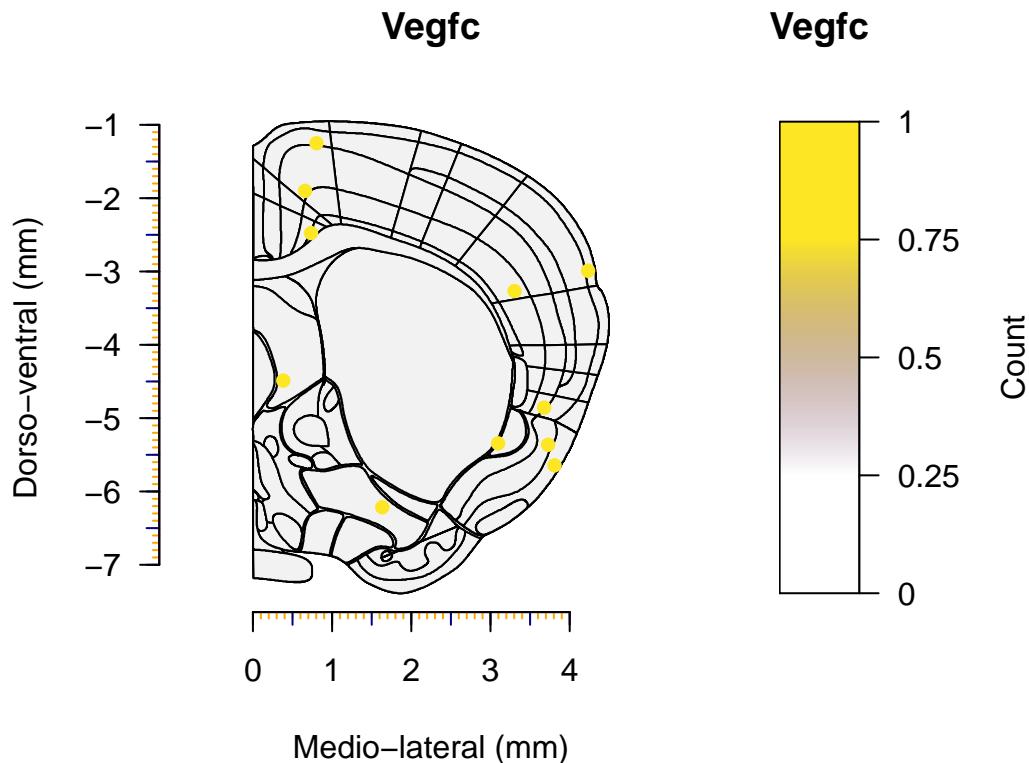
```
## Vegfa
## -----
## Average number of Vegfa transcripts detected:
## CPu : M = 0.5 ( SD = 0.82 ) molecules
## SS : M = 0.5 ( SD = 0.73 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = 0.002084, df = 231.85, p-value = 0.9983
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.1968806 0.1972975
## sample estimates:
## mean of x mean of y
## 0.5042735 0.5040650
```



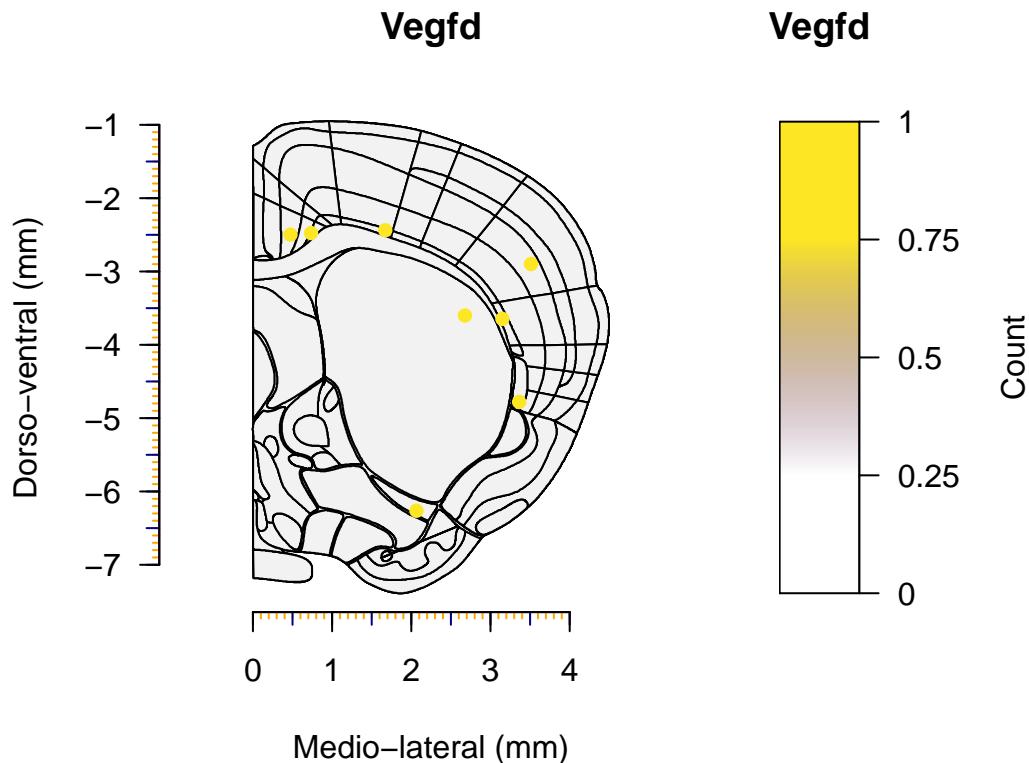
```

## Vegfb          MARKER FOR SOMATOSENSORY!
## -----
## Average number of Vegfb transcripts detected:
## CPu : M = 1.24 ( SD = 1.24 ) molecules
## SS : M = 1.59 ( SD = 1.42 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = -2.0644, df = 236.2, p-value = 0.04007
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.69217742 -0.01618197
## sample estimates:
## mean of x mean of y
## 1.239316 1.593496

```



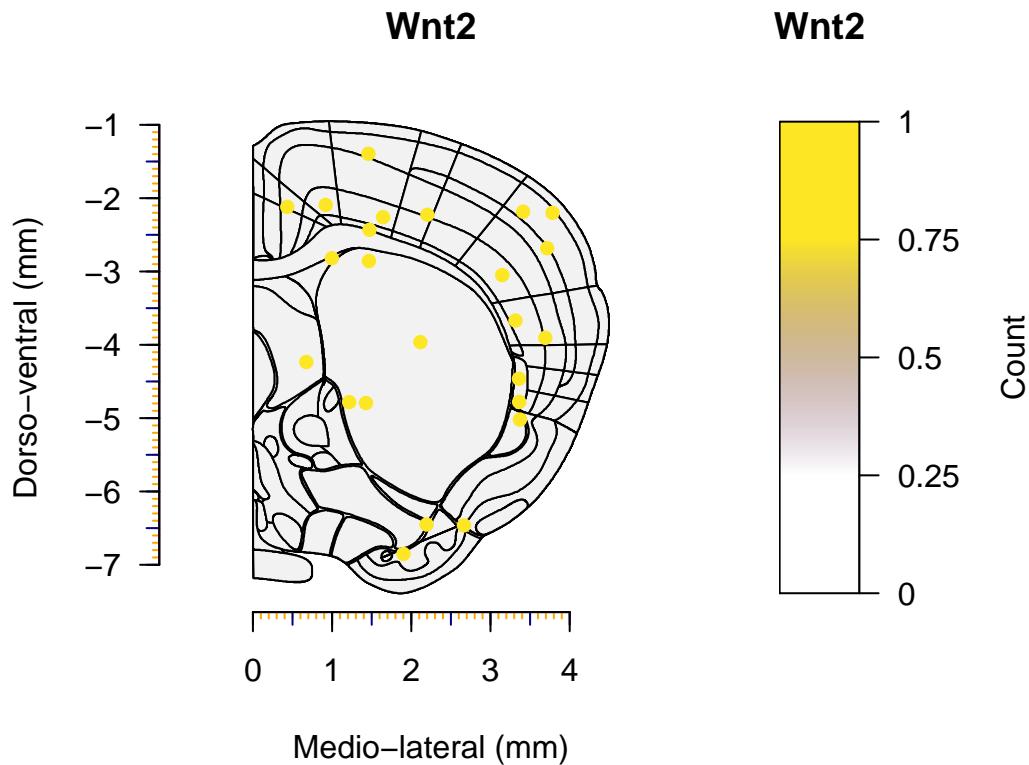
```
## Vegfc
## -----
## Average number of Vegfc transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0.02 ( SD = 0.13 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = -1.42, df = 122, p-value = 0.1581
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.038927477 0.006407152
## sample estimates:
## mean of x mean of y
## 0.00000000 0.01626016
```



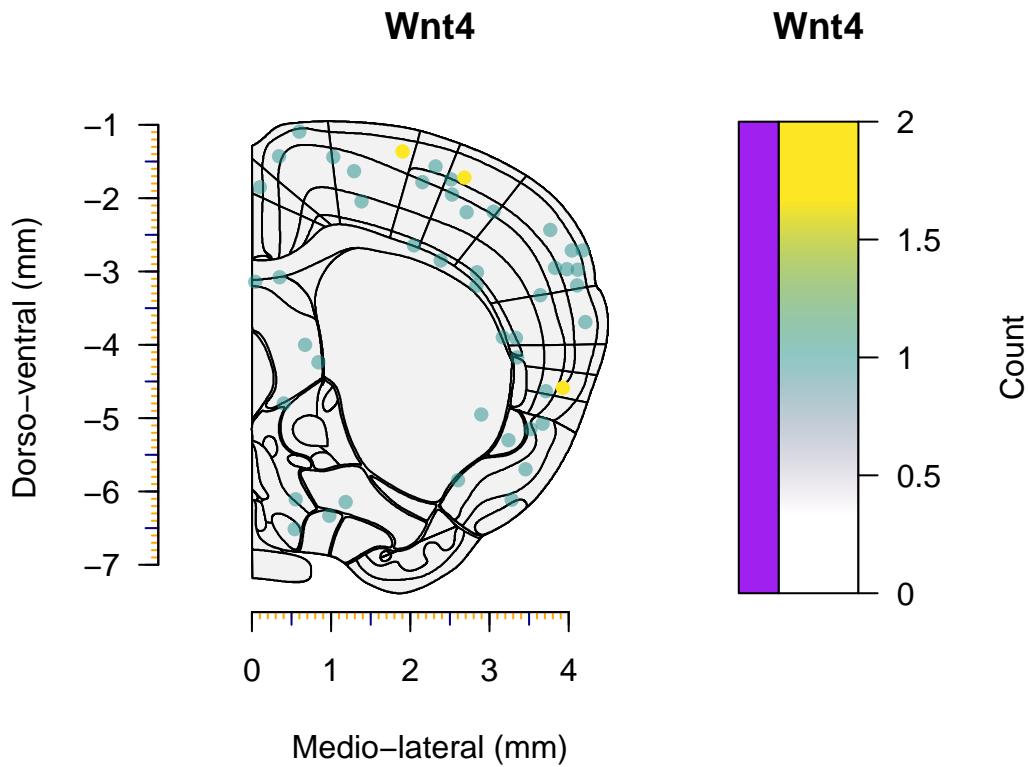
```

## Vegfd
## -----
## Average number of Vegfd transcripts detected:
## CPu : M = 0.01 ( SD = 0.09 ) molecules
## SS : M = 0.02 ( SD = 0.13 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = -0.53981, df = 223.01, p-value = 0.5899
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.03587111 0.02044481
## sample estimates:
## mean of x mean of y
## 0.008547009 0.016260163

```



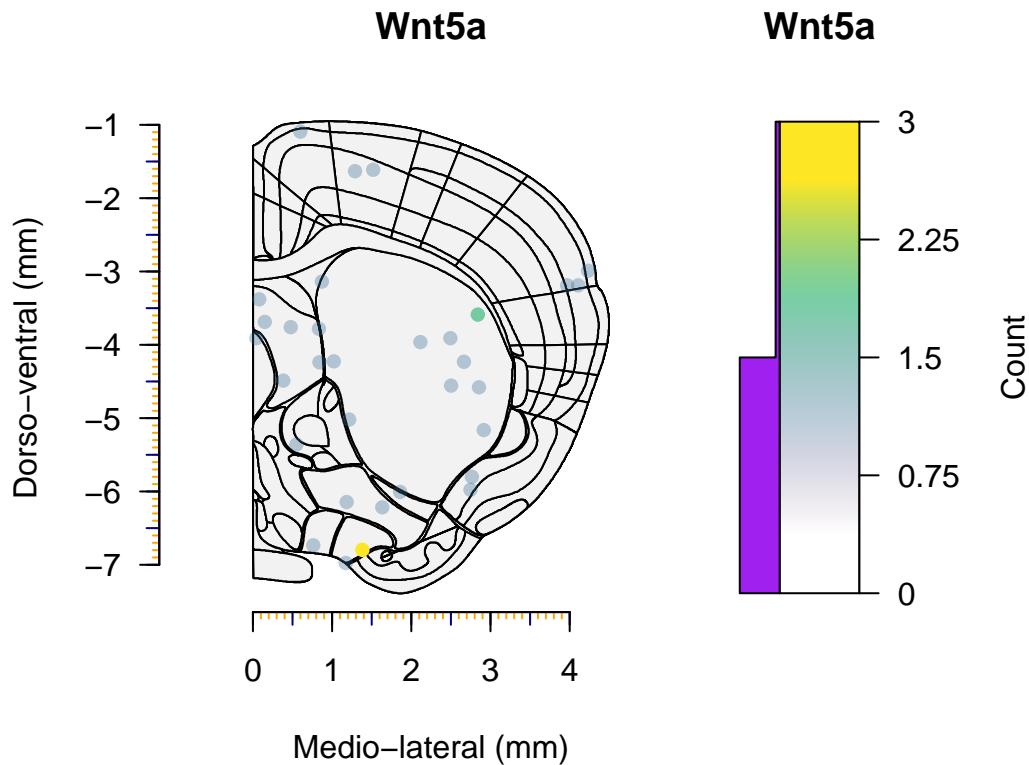
```
## Wnt2
## -----
## Average number of Wnt2 transcripts detected:
## CPu : M = 0.03 ( SD = 0.18 ) molecules
## SS : M = 0.06 ( SD = 0.23 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = -0.84414, df = 229.78, p-value = 0.3995
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.07576027 0.03031520
## sample estimates:
## mean of x mean of y
## 0.03418803 0.05691057
```



```

## Wnt4          MARKER FOR SOMATOSENSORY!
## -----
## Average number of Wnt4 transcripts detected:
## CPu : M = 0.01 ( SD = 0.09 ) molecules
## SS : M = 0.16 ( SD = 0.39 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = -4.2363, df = 136.19, p-value = 4.159e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.22596777 -0.08214146
## sample estimates:
## mean of x   mean of y
## 0.008547009 0.162601626

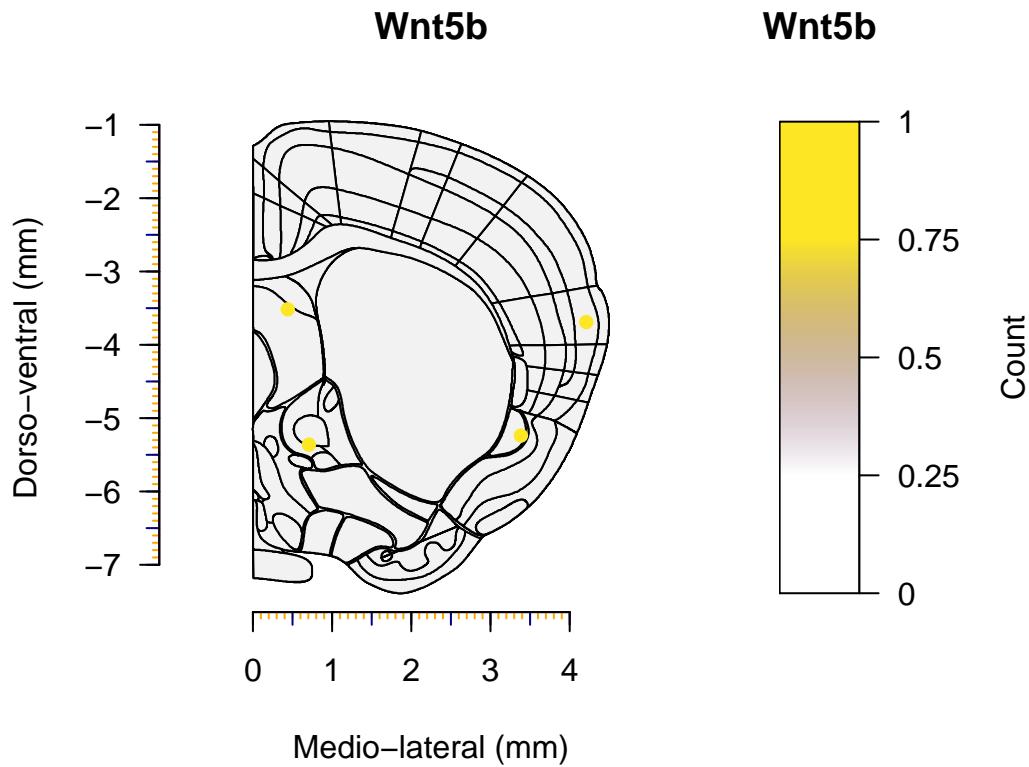
```



```

## Wnt5a          MARKER FOR CAUDATE PUTAMEN!
## -----
## Average number of Wnt5a transcripts detected:
## CPu : M = 0.09 ( SD = 0.32 ) molecules
## SS  : M = 0.02 ( SD = 0.15 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = 2.1219, df = 165.31, p-value = 0.03533
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.004840102 0.134413598
## sample estimates:
## mean of x  mean of y
## 0.09401709 0.02439024

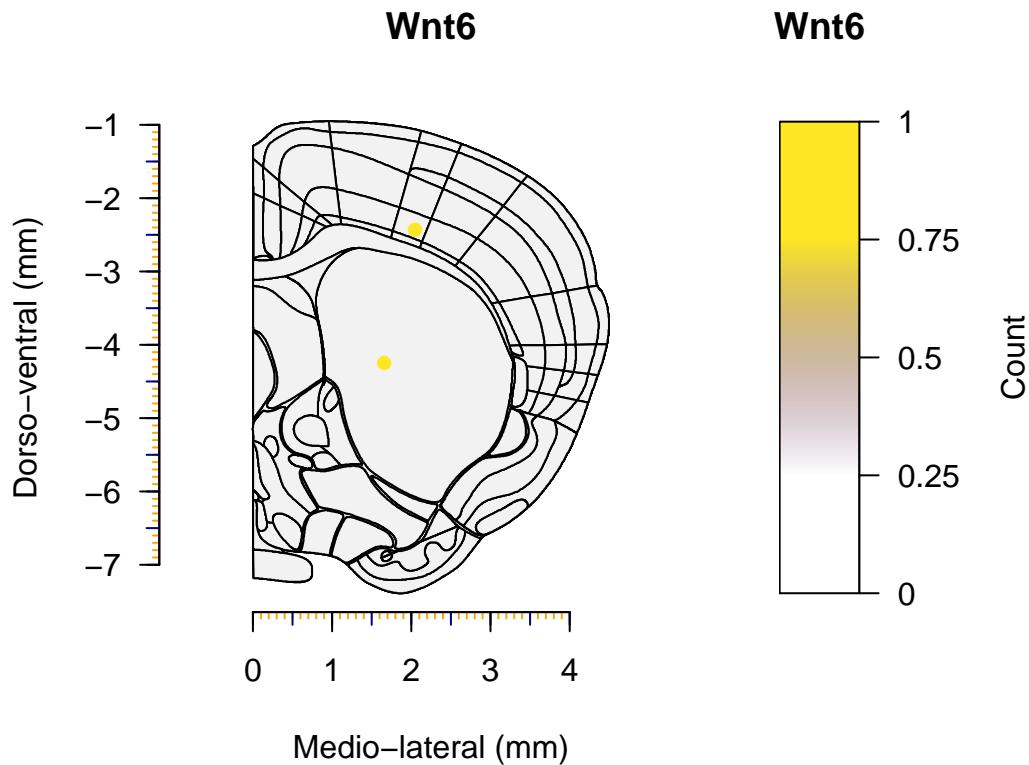
```



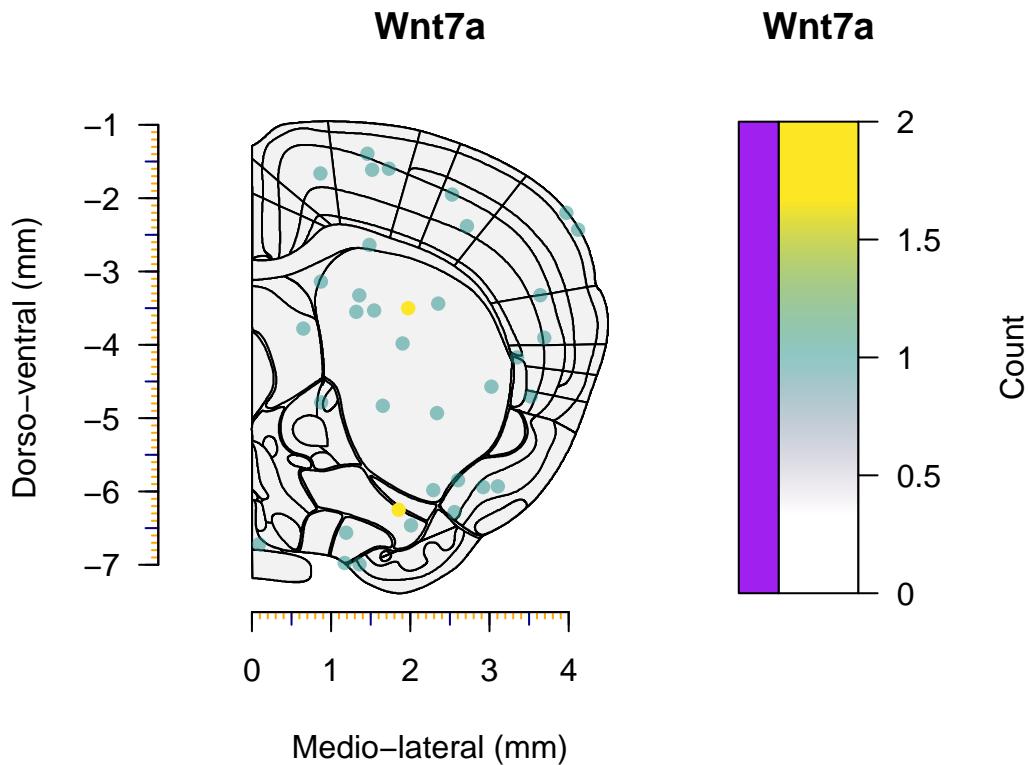
```

## Wnt5b
## -----
## Average number of Wnt5b transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0.01 ( SD = 0.09 ) molecules
## -----
## 
## Welch Two Sample t-test
## 
## data: CP and SS
## t = -1, df = 122, p-value = 0.3193
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.024224389 0.007964227
## sample estimates:
## mean of x mean of y
## 0.000000000 0.008130081

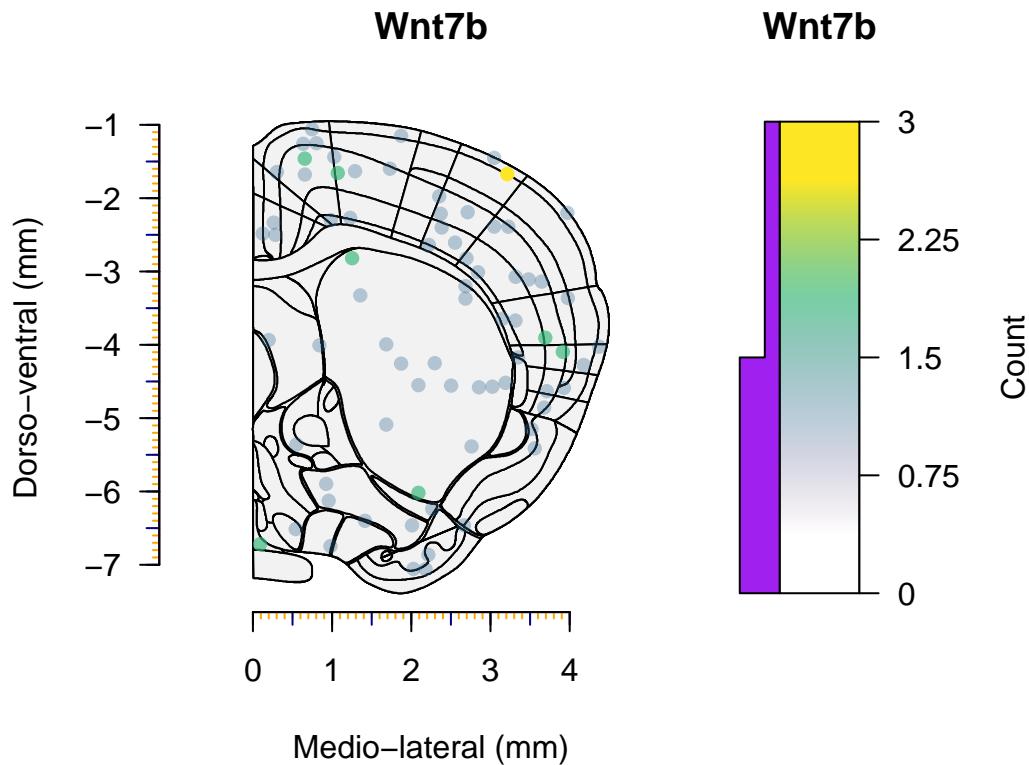
```



```
## Wnt6
## -----
## Average number of Wnt6 transcripts detected:
## CPu : M = 0.01 ( SD = 0.09 ) molecules
## SS : M = 0.01 ( SD = 0.09 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = 0.035344, df = 236.66, p-value = 0.9718
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.02282198 0.02365583
## sample estimates:
## mean of x mean of y
## 0.008547009 0.008130081
```



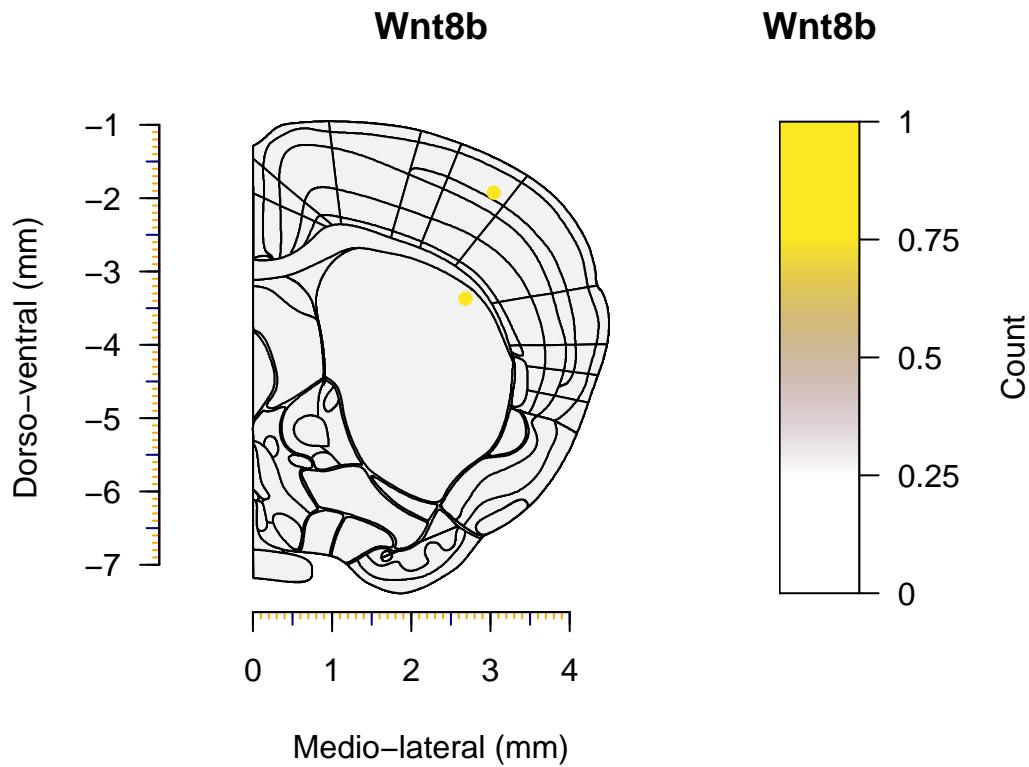
```
## Wnt7a
## -----
## Average number of Wnt7a transcripts detected:
## CPu : M = 0.1 ( SD = 0.33 ) molecules
## SS : M = 0.05 ( SD = 0.22 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = 1.4797, df = 197.98, p-value = 0.1405
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.01789558 0.12546281
## sample estimates:
## mean of x mean of y
## 0.10256410 0.04878049
```



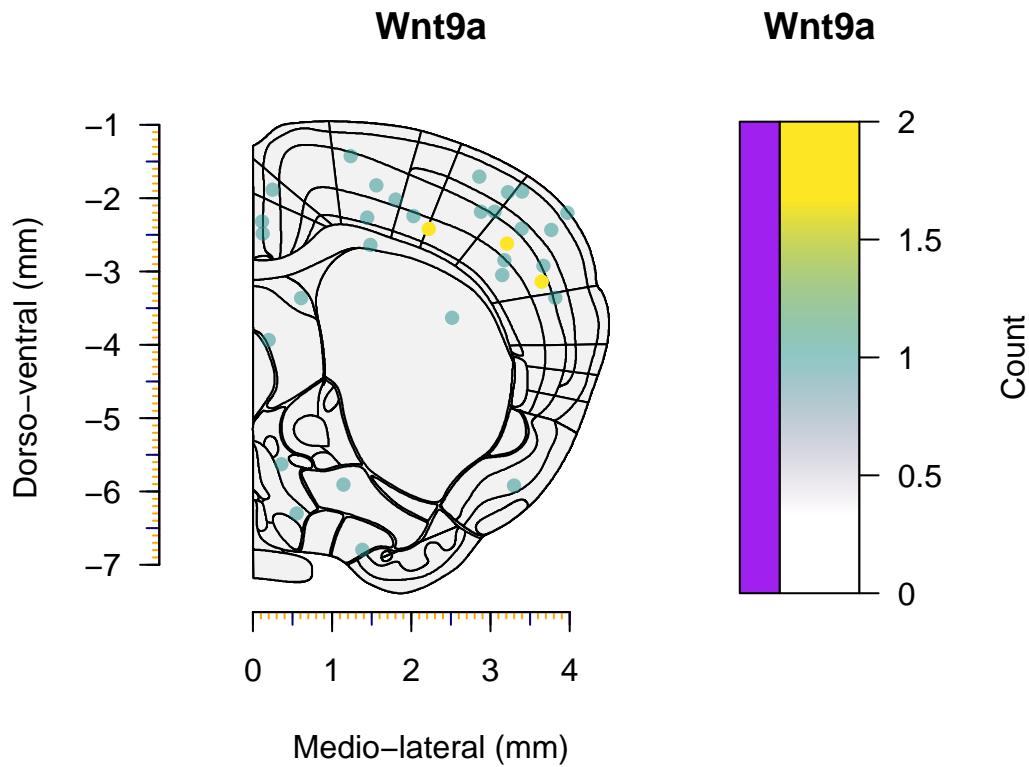
```

## Wnt7b
## -----
## Average number of Wnt7b transcripts detected:
## CPu : M = 0.15 ( SD = 0.4 ) molecules
## SS : M = 0.19 ( SD = 0.47 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = -0.7435, df = 235.33, p-value = 0.4579
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.15216818  0.06878273
## sample estimates:
## mean of x mean of y
## 0.1452991  0.1869919

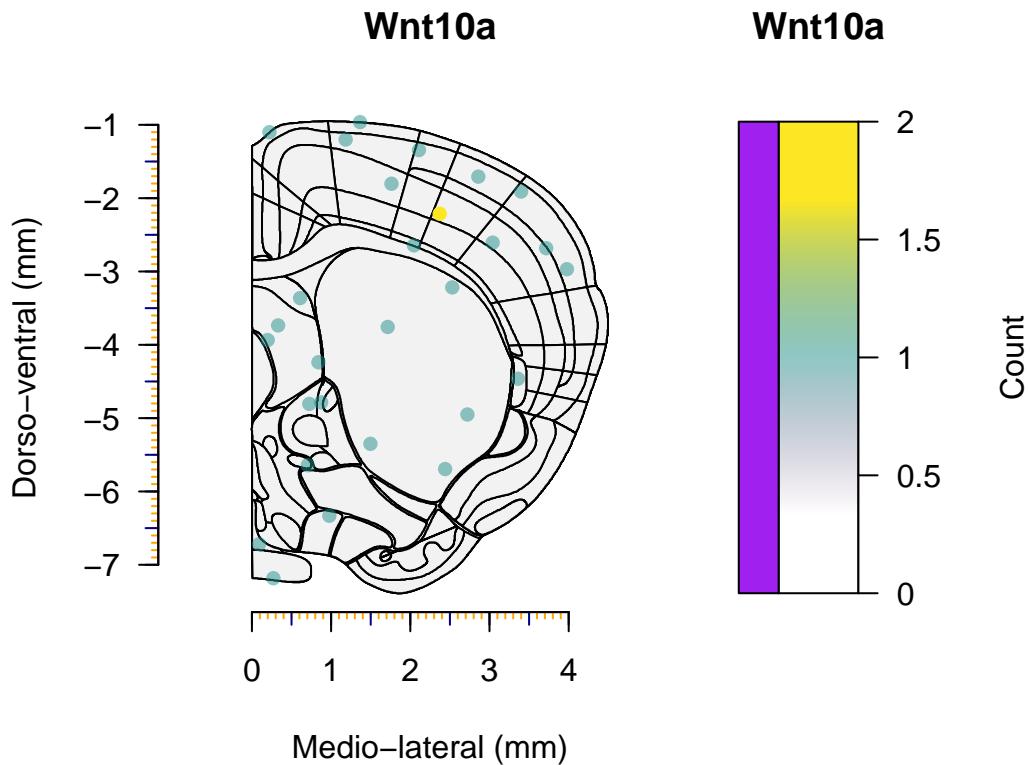
```



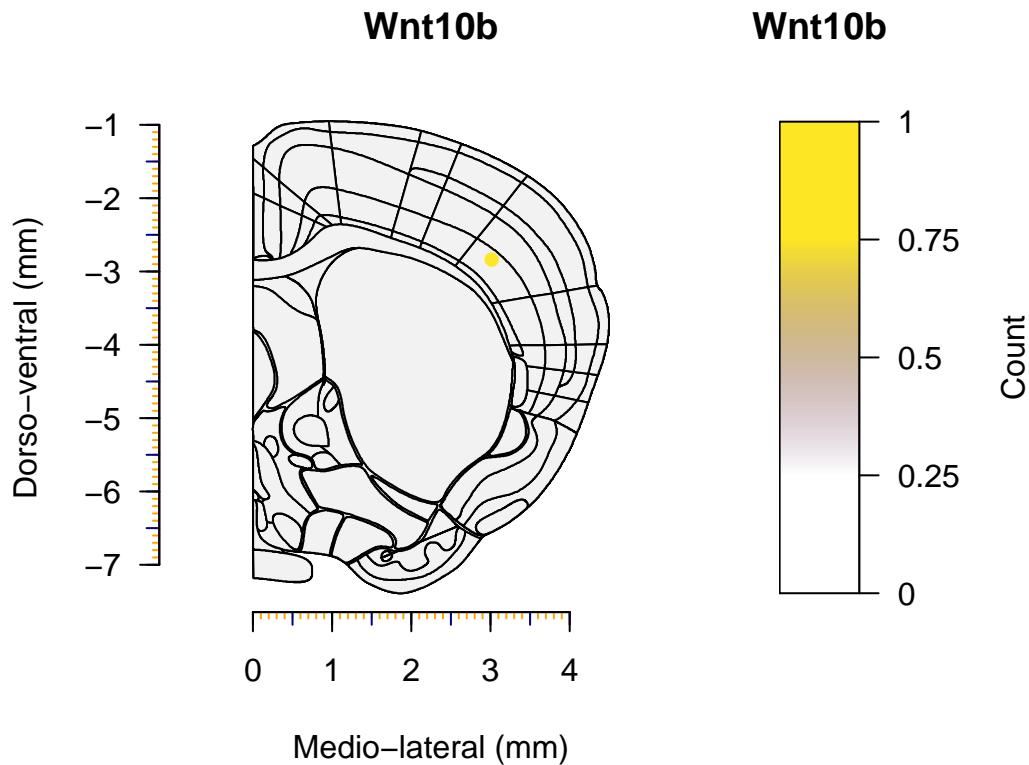
```
## Wnt8b
## -----
## Average number of Wnt8b transcripts detected:
## CPu : M = 0.01 ( SD = 0.09 ) molecules
## SS : M = 0.01 ( SD = 0.09 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = 0.035344, df = 236.66, p-value = 0.9718
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.02282198 0.02365583
## sample estimates:
## mean of x mean of y
## 0.008547009 0.008130081
```



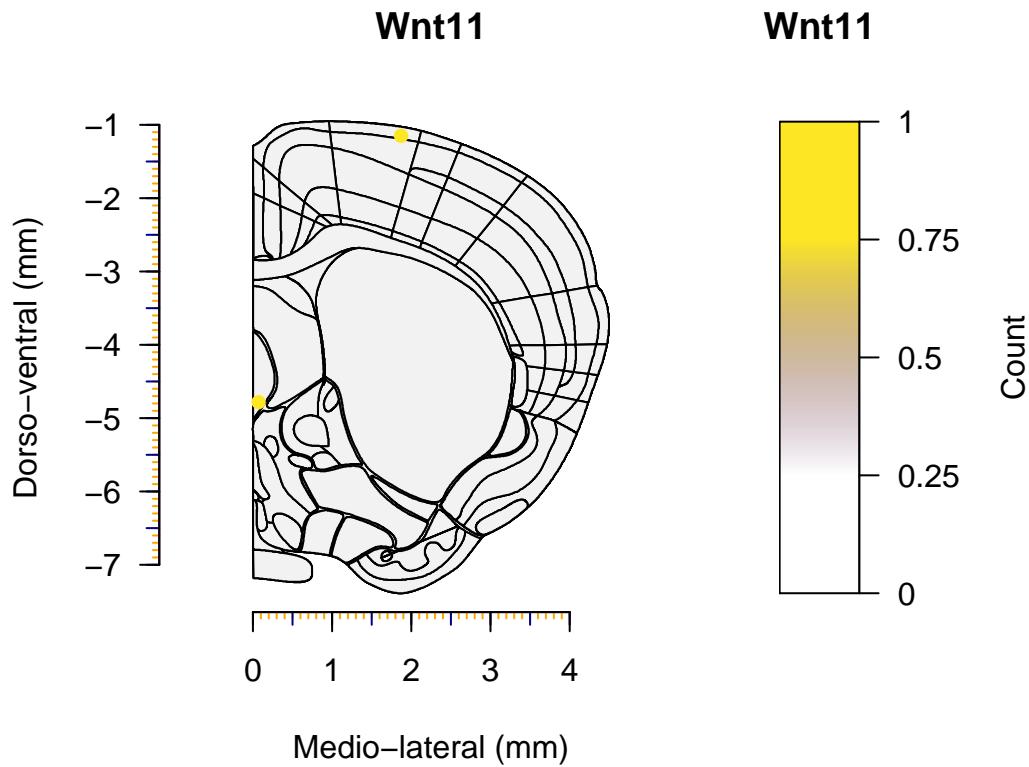
```
## Wnt9a          MARKER FOR SOMATOSENSORY!
## -----
## Average number of Wnt9a transcripts detected:
## CPu : M = 0.01 ( SD = 0.09 ) molecules
## SS  : M = 0.15 ( SD = 0.43 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = -3.7143, df = 134.08, p-value = 0.000298
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.22362692 -0.06822215
## sample estimates:
## mean of x  mean of y
## 0.008547009 0.154471545
```



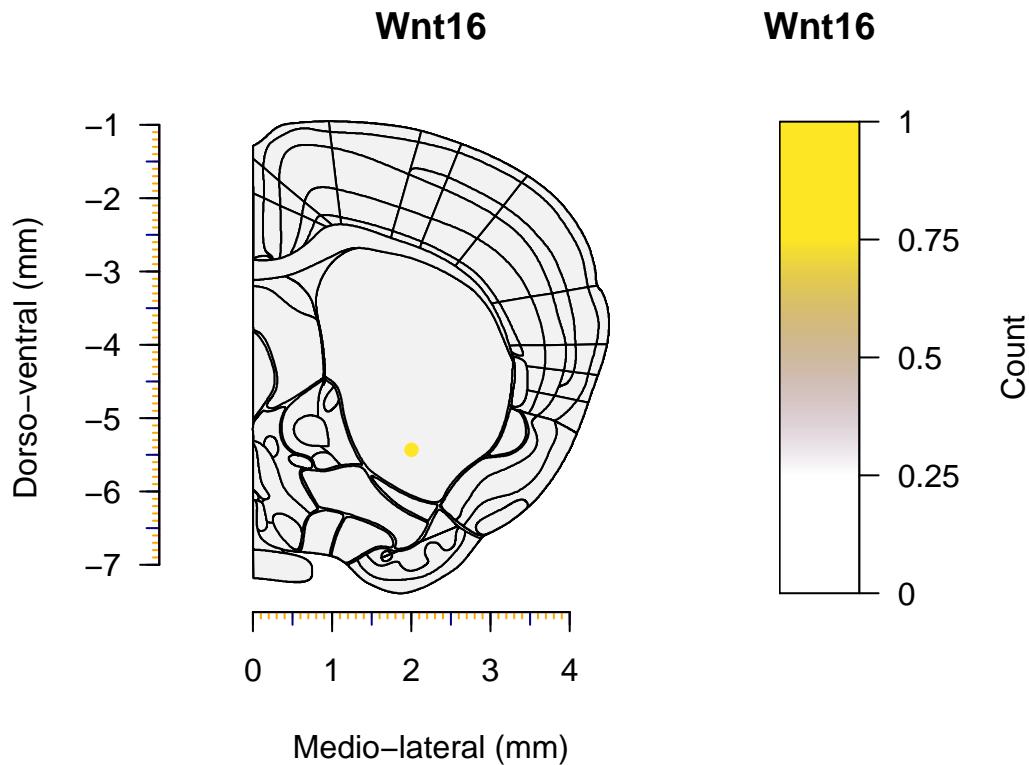
```
## Wnt10a
## -----
## Average number of Wnt10a transcripts detected:
## CPu : M = 0.04 ( SD = 0.2 ) molecules
## SS : M = 0.07 ( SD = 0.29 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = -0.94295, df = 218.6, p-value = 0.3467
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.09405000 0.03317862
## sample estimates:
## mean of x mean of y
## 0.04273504 0.07317073
```



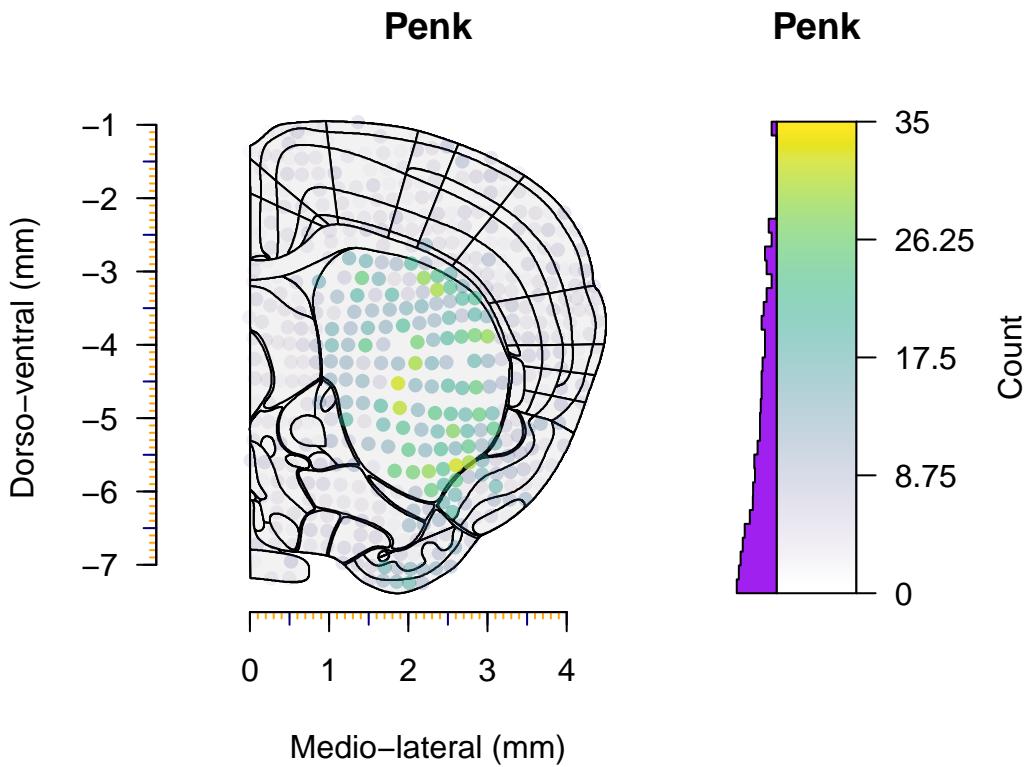
```
## Wnt10b
## -----
## Average number of Wnt10b transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0.01 ( SD = 0.09 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = -1, df = 122, p-value = 0.3193
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.024224389 0.007964227
## sample estimates:
## mean of x mean of y
## 0.000000000 0.008130081
```



```
## Wnt11
## -----
## Average number of Wnt11 transcripts detected:
## CPu : M = 0 ( SD = 0 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## Welch Two Sample t-test
##
## data: CP and SS
## t = NaN, df = NaN, p-value = NA
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##   NaN NaN
## sample estimates:
## mean of x mean of y
##           0          0
```



```
## Wnt16
## -----
## Average number of Wnt16 transcripts detected:
## CPu : M = 0.01 ( SD = 0.09 ) molecules
## SS : M = 0 ( SD = 0 ) molecules
## -----
## 
## Welch Two Sample t-test
##
## data: CP and SS
## t = 1, df = 116, p-value = 0.3194
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.008381419 0.025475436
## sample estimates:
## mean of x mean of y
## 0.008547009 0.000000000
```



```
## Penk
## -----
## Average number of Penk transcripts detected:
## CPu : M = 14 ( SD = 6.51 ) molecules
## SS : M = 2.52 ( SD = 1.83 ) molecules
## -----
## Welch Two Sample t-test
## 
## data: CP and SS
## t = 18.409, df = 133.32, p-value < 2.2e-16
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 10.24625 12.71310
## sample estimates:
## mean of x mean of y
## 14.000000 2.520325
## 
## 
## Nondetected genes:
## Gdf2, Bmp10, Gdf7, Bmp5, Bmp8b, Cntf, Csf3, Csf2, Epo, Fgf4, Fgf6, Fgf19, Fgf20, Fgf21, Fgf23, Pspn,
```

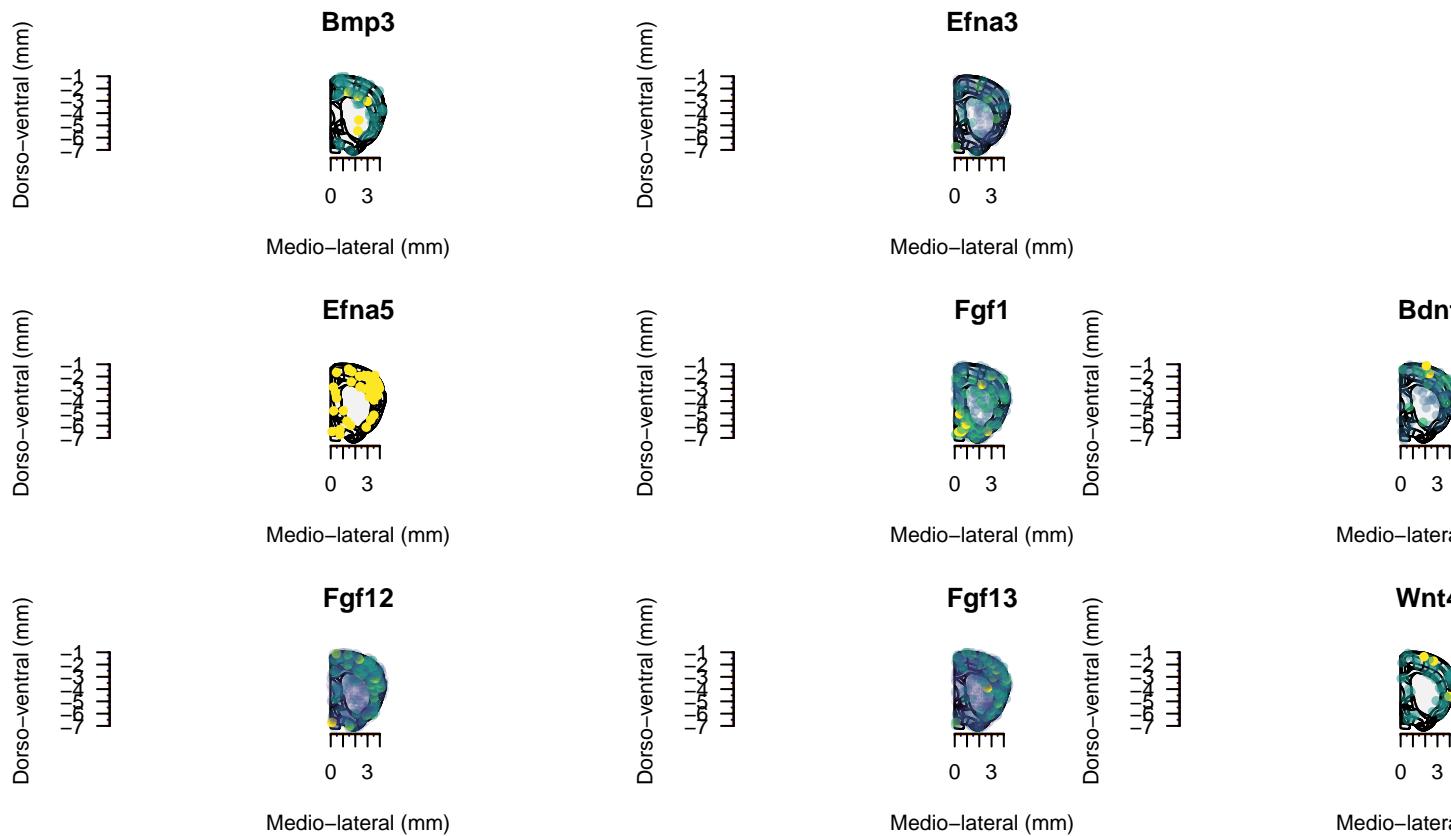
#### 10.4.1 Exploratory conclusion:

- Somatosensory:
- {r} cat(paste(expl.analysis\$somatosensory , collapse=' ,'))
- Striatal:
- {r} cat(paste(expl.analysis\$striatum , collapse=' ,'))
- Non detected:

- {r} cat(paste(expl.analysis\$non.detected , collapse=' '))

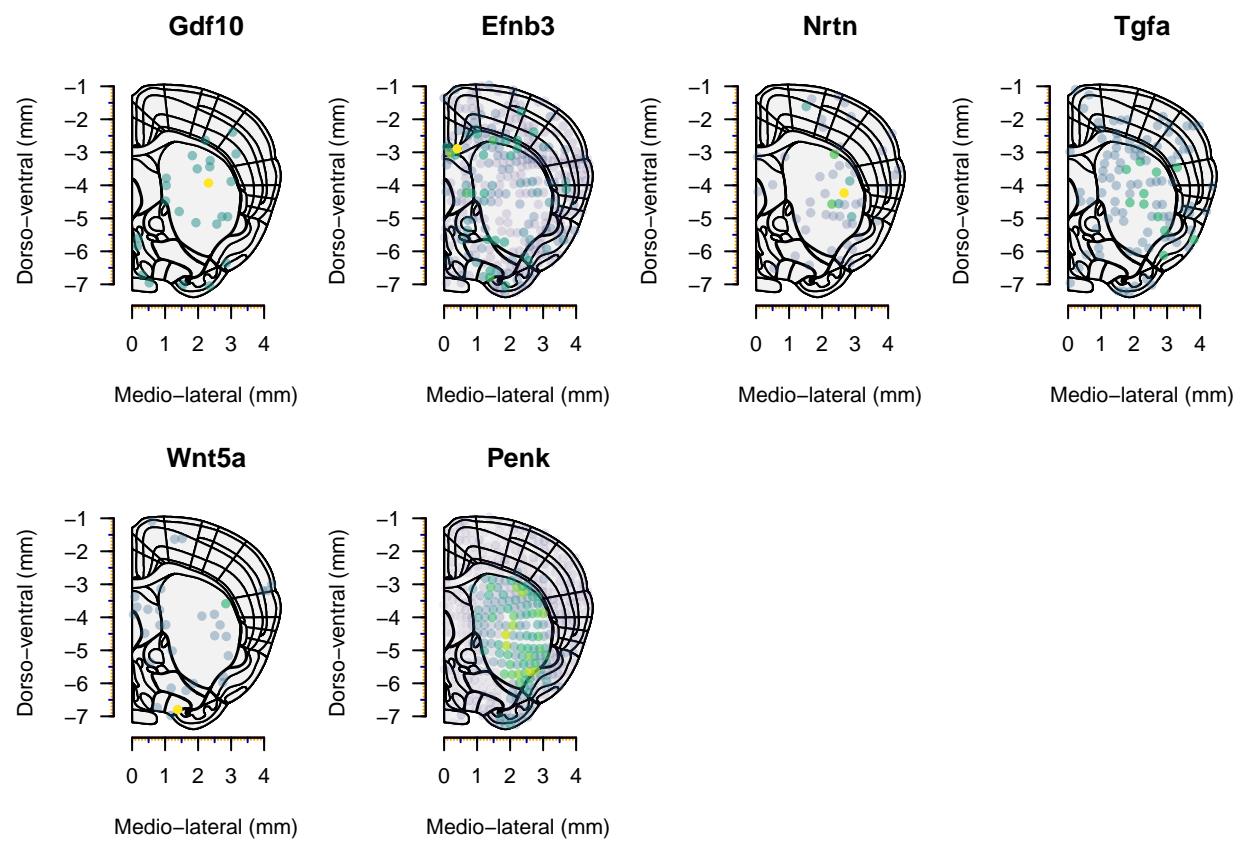
### 10.4.2 Somatosensory:

```
par(mfrow=c(length(expl.analysis$somatosensory)%%4+1,4%%4+1), mar=c(4,4,4,1))
invisible(sapply(expl.analysis$somatosensory, function(x)plot.gene(dataset, regi, gene=x, colorfunc=viridis)))
```



### 10.4.3 Striatal:

```
par(mfrow=c(length(expl.analysis$striatum)%%4+1,4), mar=c(4,4,4,1))
invisible(sapply(expl.analysis$striatum, function(x)plot.gene(dataset, regi, gene=x, colorfunc=viridis)))
```





# Chapter 11

## MAPseq

TBA.



# Bibliography