

main

March 23, 2023

1 Plot RXE comparisons

```
[1]: library(ggpubr)
library(tidyverse)
```

Loading required package: ggplot2

```
Attaching packages: tidyverse
1.3.2
  tibble 3.1.8    dplyr  1.1.0
  tidyr  1.3.0    stringr 1.5.0
  readr  2.1.4    forcats 1.0.0
  purrr  1.0.1

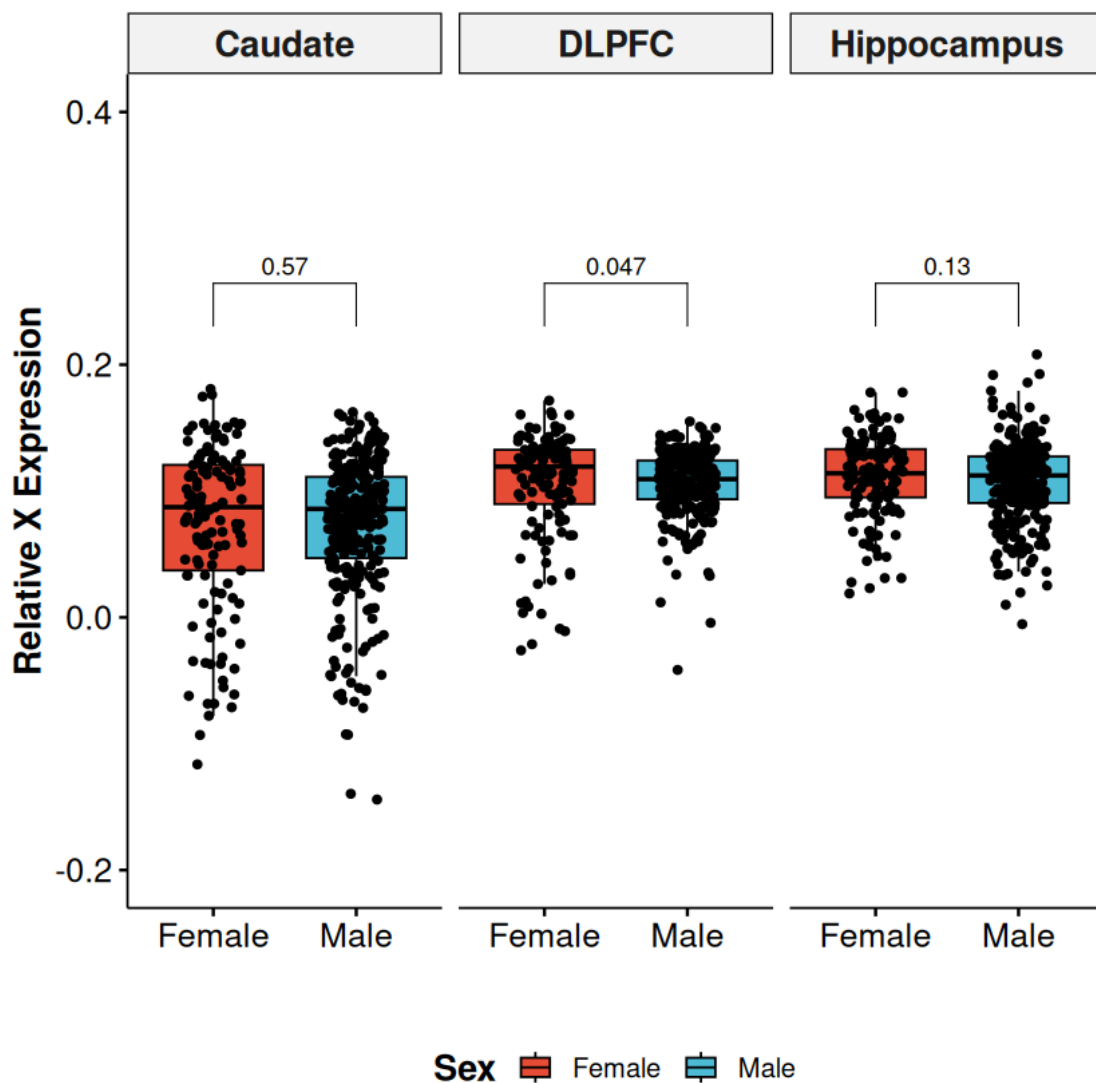
Conflicts:
tidyverse_conflicts()
dplyr::filter() masks stats::filter()
dplyr::lag()    masks stats::lag()
```

```
[2]: save_ggplots <- function(p, fn, w=7, h=7){
  for(ext in c('.svg', '.png', '.pdf')){
    ggsave(p, filename=paste0(fn, ext), width=w, height=h)
  }
}
```

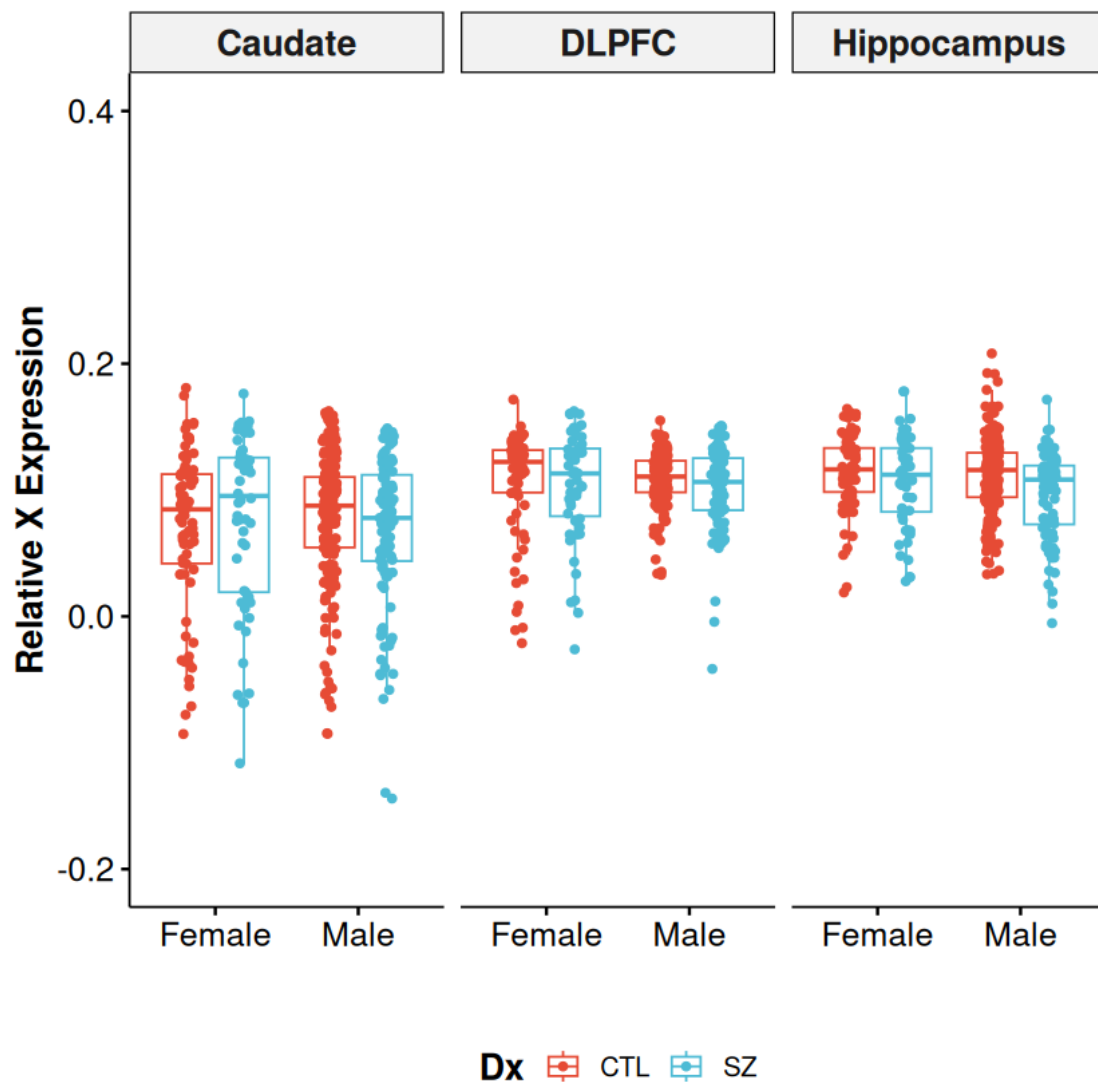
```
[3]: df = data.table::fread("../_m/RXE_public.csv") |>
  mutate_if(is.character, as.factor)
levels(df$Sex) <- c("Female", "Male")
levels(df$Dx) <- c("CTL", "SZ")
levels(df$Region) <- c("Caudate", "DLPFC", "Hippocampus")
df |> head(2)
```

	SAMPLE_ID	Autosome	X	sample	RXE	RNum	Sex	
	<fct>	<dbl>	<dbl>	<fct>	<dbl>	<fct>	<fct>	
A data.table: 2 × 9	R12864_H5FM2BBXX	2.332196	2.461731	R12864	0.12953529	R12864	Female	\$
	R12865_H5FM2BBXX	2.740215	2.829693	R12865	0.08947798	R12865	Male	\$

```
[4]: bxp = df |>
      ggboxplot(x="Sex", y="RXE", fill='Sex', xlab='', palette="npg",
                add='jitter', outlier.shape=NA, facet.by='Region',
                ylab='Relative X Expression', ylim=c(-0.2, 0.4),
                panel.labs.font=list(face='bold', size=16),
                legend="bottom", ggtheme=theme_pubr(base_size=15)) +
      stat_compare_means(comparisons=list(c("Female", "Male")))+
      font("xy.title", size=16, face="bold") +
      font("legend.title", size=16, face="bold")
save_ggplots(bxp, "rxs_sex_byRegion", 7, 5)
bxp
```



```
[5]: bxp = df |>
      ggboxplot(x="Sex", y="RXE", color='Dx', xlab='', palette="npg",
                add='jitter', outlier.shape=NA, facet.by='Region',
                ylab='Relative X Expression', ylim=c(-0.2, 0.4),
                panel.labs.font=list(face='bold', size=16),
                legend="bottom", ggtheme=theme_pubr(base_size=15)) +
      font("xy.title", size=16, face="bold") +
      font("legend.title", size=16, face="bold")
save_ggplots(bxp, "rxs_sex_diagnosis_byRegion", 7, 5)
bxp
```

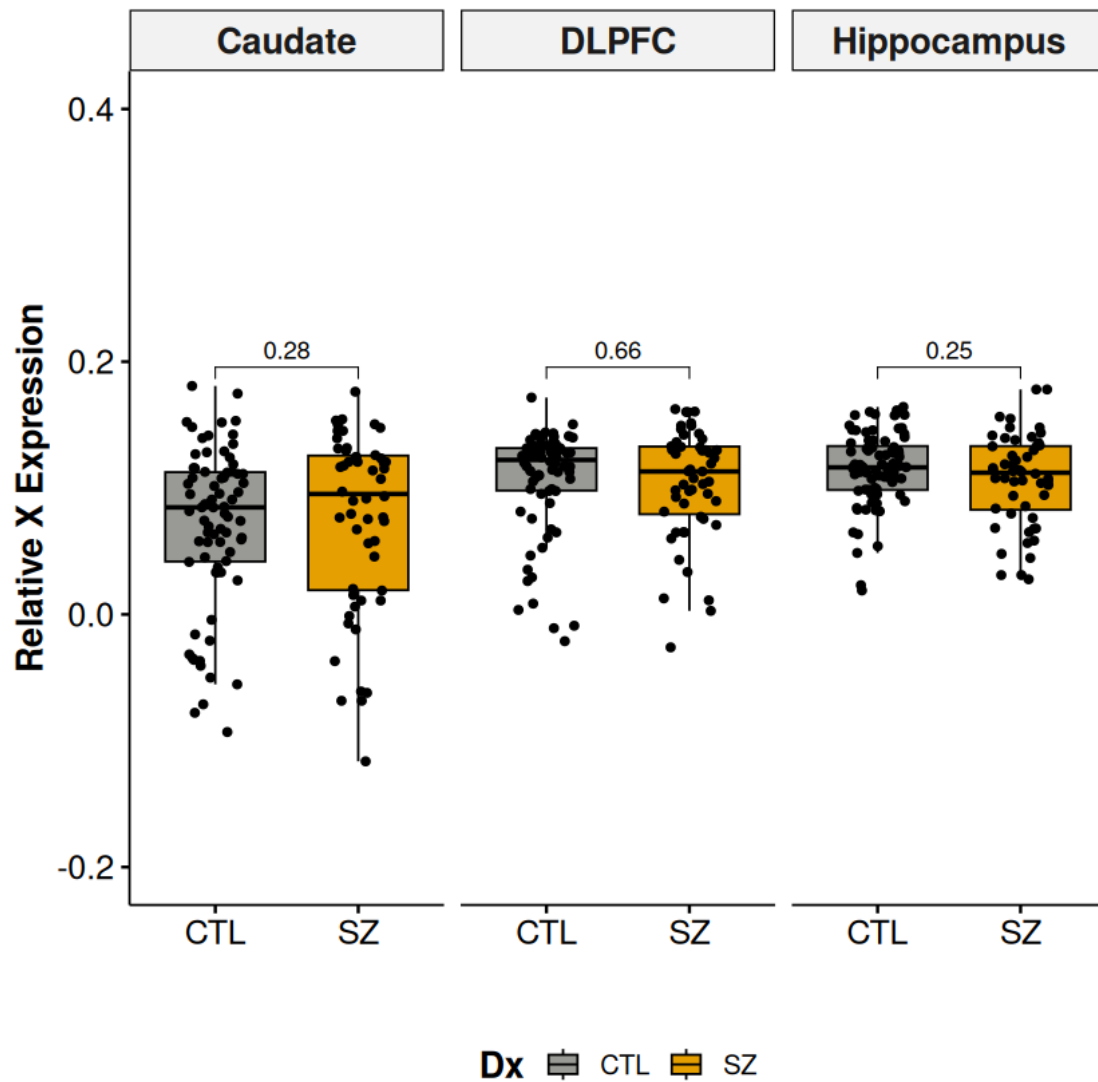


```
[6]: bxp_f = df |> filter(Sex=='Female') |>
      ggboxplot(x="Dx", y="RXE", fill='Dx', xlab='',
```

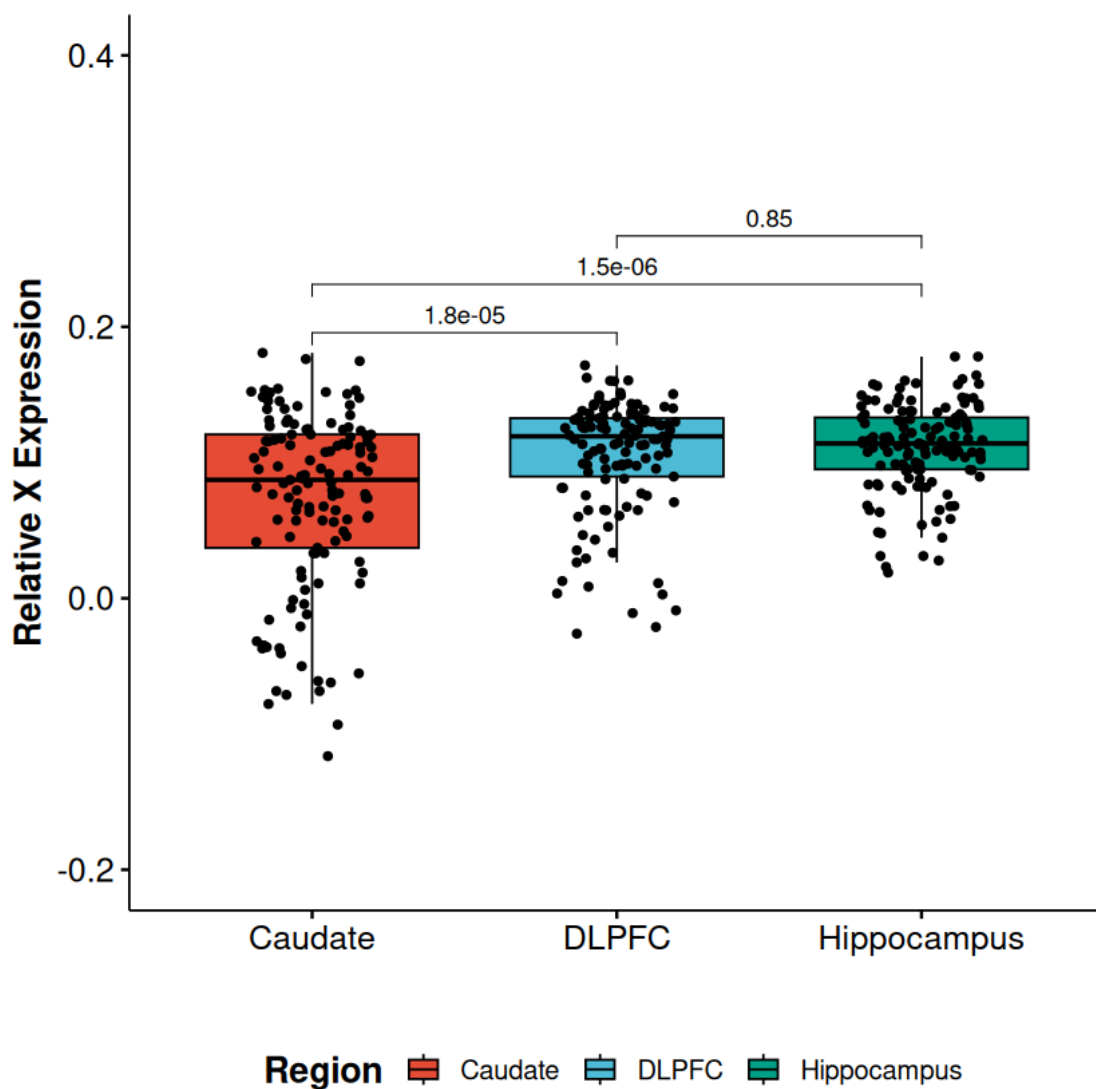
```

palette=c("#999995ff", "#e69f00ff"),
add='jitter', outlier.shape=NA, facet.by=c('Region'),
ylab='Relative X Expression', ylim=c(-0.2, 0.4),
panel.labs.font=list(face='bold', size=16),
legend="bottom", ggtheme=theme_pubr(base_size=15)) +
stat_compare_means(comparisons=list(c("CTL", "SZ")))+
font("xy.title", size=16, face="bold") +
font("legend.title", size=16, face="bold")
save_ggplots(bxp_f, "rxr_female_diagnosis_byRegion", 7, 5)
bxp_f

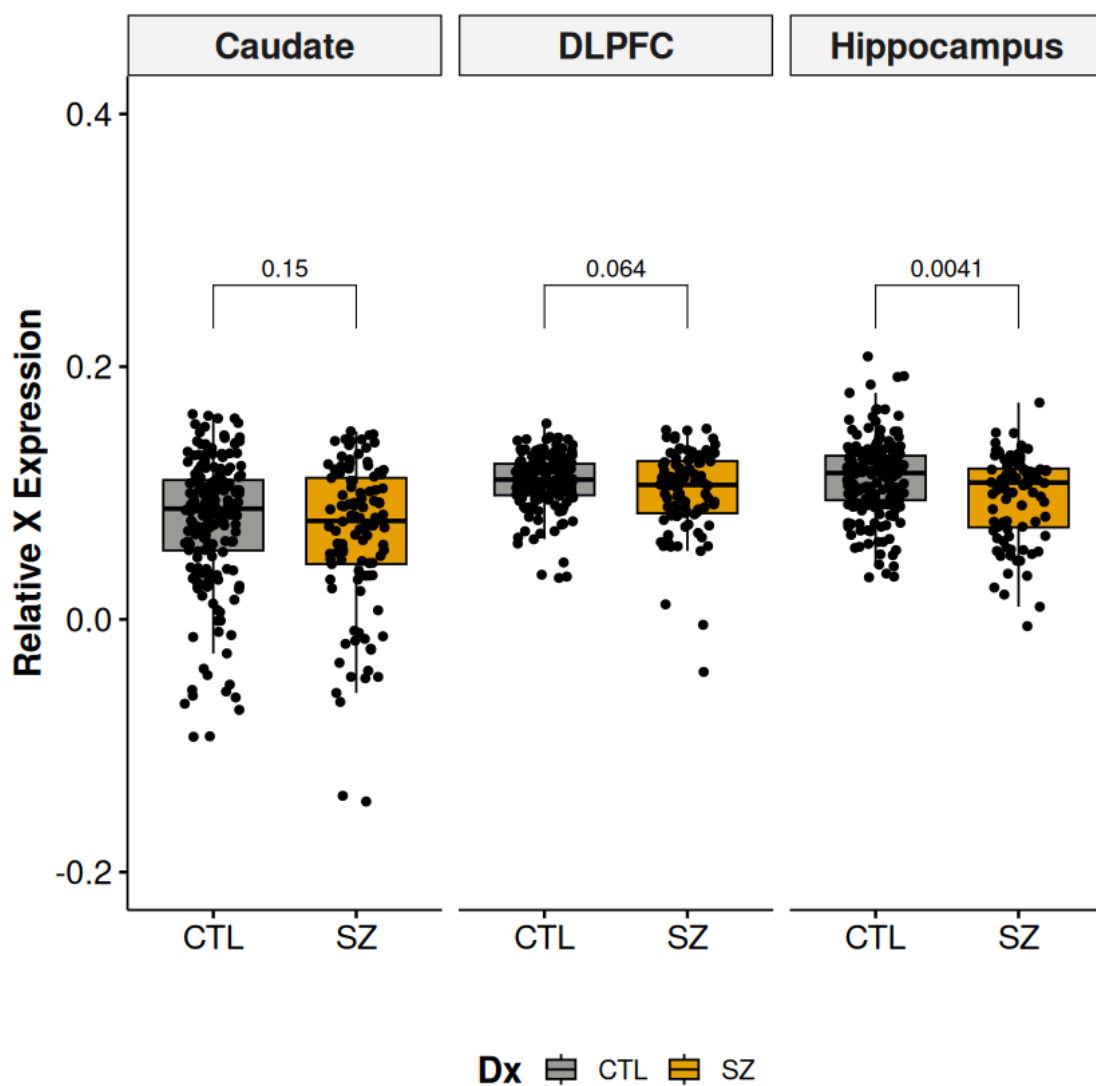
```



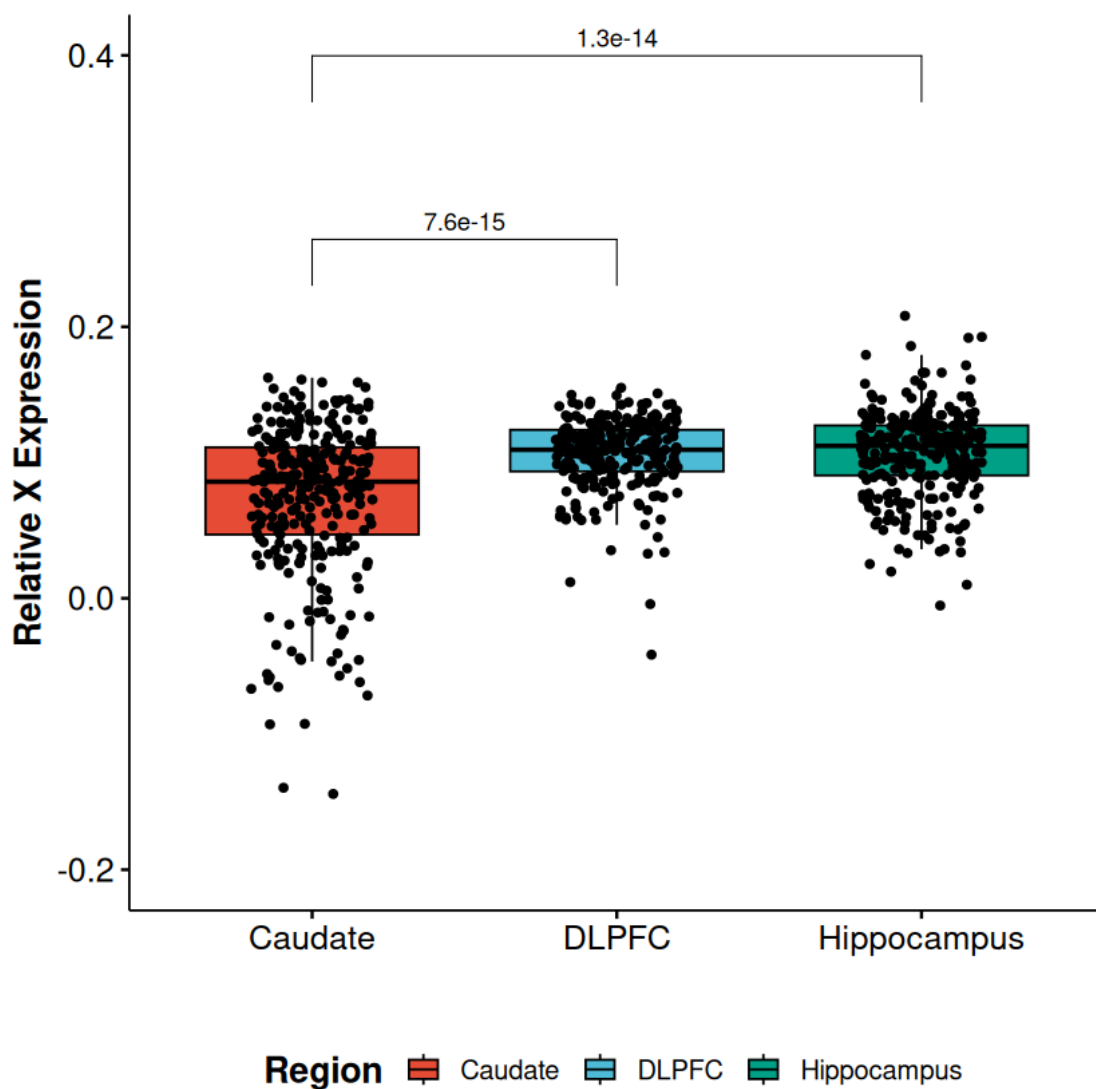
```
[7]: bxp_f2 = df |> filter(Sex=='Female') |>
      ggboxplot(x="Region", y="RXE", fill='Region', xlab='', palette="npg",
                add='jitter', outlier.shape=NA,
                ylab='Relative X Expression', ylim=c(-0.2, 0.4),
                panel.labs.font=list(face='bold', size=16),
                legend="bottom", ggtheme=theme_pubr(base_size=15)) +
      stat_compare_means(comparisons=list(c("Caudate", "DLPFC"),
                                           c("Caudate", "Hippocampus"),
                                           c("DLPFC", "Hippocampus")))+
      font("xy.title", size=16, face="bold") +
      font("legend.title", size=16, face="bold")
      save_ggplots(bxp_f2, "rx_e_female_region", 6, 6)
      bxp_f2
```



```
[8]: bxp_m = df |> filter(Sex=='Male') |>
      ggboxplot(x="Dx", y="RXE", fill='Dx', xlab='',
                palette=c("#999999ff", "#e69f00ff"),
                add='jitter', outlier.shape=NA, facet.by=c('Region'),
                ylab='Relative X Expression', ylim=c(-0.2, 0.4),
                panel.labs.font=list(face='bold', size=16),
                legend="bottom", ggtheme=theme_pubr(base_size=15)) +
      stat_compare_means(comparisons=list(c("CTL", "SZ")))+
      font("xy.title", size=16, face="bold") +
      font("legend.title", size=16, face="bold")
      save_ggplots(bxp_m, "rx_male_diagnosis_byRegion", 7, 5)
      bxp_m
```



```
[9]: bxp_m2 = df |> filter(Sex=='Male') |>
      ggboxplot(x="Region", y="RXE", fill='Region', xlab='', palette="npg",
                add='jitter', outlier.shape=NA,
                ylab='Relative X Expression', ylim=c(-0.2, 0.4),
                panel.labs.font=list(face='bold', size=16),
                legend="bottom", ggtheme=theme_pubr(base_size=15)) +
      stat_compare_means(comparisons=list(c("Caudate", "DLPFC"),
                                           c("Caudate", "Hippocampus"),
                                           c("DLPFC", "Hippocampus")))+
      font("xy.title", size=16, face="bold") +
      font("legend.title", size=16, face="bold")
      save_ggplots(bxp_m2, "rx_e_male_region", 6, 6)
      bxp_m2
```



1.1 Reproducibility Information

```
[10]: Sys.time()  
      proc.time()  
      options(width = 120)  
      sessioninfo::session_info()
```

```
[1] "2023-03-23 10:08:09 EDT"
```

```
      user  system elapsed  
8.200    0.089   11.096
```

```
$platform $version 'R version 4.2.3 (2023-03-15)'
```

```
$os 'Arch Linux'
```

```
$system 'x86_64, linux-gnu'
```

```
$ui 'X11'
```

```
$language '(EN)'
```

```
$collate 'en_US.UTF-8'
```

```
$ctype 'en_US.UTF-8'
```

```
$tz 'America/New_York'
```

```
$date '2023-03-23'
```

```
$pandoc '3.0.1 @ /usr/bin/pandoc'
```


	package <chr>	ondiskversion <chr>	loadedversion <chr>	path <chr>
abind	abind	1.4.5	1.4-5	/home/kynor
assertthat	assertthat	0.2.1	0.2.1	/home/kynor
backports	backports	1.4.1	1.4.1	/home/kynor
base64enc	base64enc	0.1.3	0.1-3	/home/kynor
broom	broom	1.0.3	1.0.3	/home/kynor
car	car	3.1.1	3.1-1	/home/kynor
carData	carData	3.0.5	3.0-5	/home/kynor
cellranger	cellranger	1.1.0	1.1.0	/home/kynor
cli	cli	3.6.0	3.6.0	/home/kynor
colorspace	colorspace	2.1.0	2.1-0	/home/kynor
crayon	crayon	1.5.2	1.5.2	/home/kynor
data.table	data.table	1.14.8	1.14.8	/home/kynor
DBI	DBI	1.1.3	1.1.3	/home/kynor
dbplyr	dbplyr	2.3.0	2.3.0	/home/kynor
digest	digest	0.6.31	0.6.31	/home/kynor
dplyr	dplyr	1.1.0	1.1.0	/home/kynor
ellipsis	ellipsis	0.3.2	0.3.2	/home/kynor
evaluate	evaluate	0.20	0.20	/home/kynor
fansi	fansi	1.0.4	1.0.4	/home/kynor
farver	farver	2.1.1	2.1.1	/home/kynor
fastmap	fastmap	1.1.0	1.1.0	/home/kynor
forcats	forcats	1.0.0	1.0.0	/home/kynor
fs	fs	1.6.1	1.6.1	/home/kynor
gargle	gargle	1.3.0	1.3.0	/home/kynor
generics	generics	0.1.3	0.1.3	/home/kynor
ggplot2	ggplot2	3.4.1	3.4.1	/home/kynor
ggpubr	ggpubr	0.6.0	0.6.0	/home/kynor
ggsci	ggsci	2.9	2.9	/home/kynor
ggsignif	ggsignif	0.6.4	0.6.4	/home/kynor
glue	glue	1.6.2	1.6.2	/home/kynor
munsell	munsell	0.5.0	0.5.0	/home/kynor
pbdZMQ	pbdZMQ	0.3.9	0.3-9	/home/kynor
pillar	pillar	1.8.1	1.8.1	/home/kynor
pkgconfig	pkgconfig	2.0.3	2.0.3	/home/kynor
purrr	purrr	1.0.1	1.0.1	/home/kynor
R6	R6	2.5.1	2.5.1	/home/kynor
readr	readr	2.1.4	2.1.4	/home/kynor
readxl	readxl	1.4.2	1.4.2	/home/kynor
repr	repr	1.1.6	1.1.6	/home/kynor
reprex	reprex	2.0.2	2.0.2	/home/kynor
rlang	rlang	1.0.6	1.0.6	/home/kynor
rstatix	rstatix	0.7.2	0.7.2	/home/kynor
rvest	rvest	1.0.3	1.0.3	/home/kynor
scales	scales	1.2.1	1.2.1	/home/kynor
sessioninfo	sessioninfo	1.2.2	1.2.2	/home/kynor
stringi	stringi	1.7.12	1.7.12	/home/kynor
stringr	stringr	1.5.0	1.5.0	/home/kynor
svglite	svglite	2.1.1	2.1.1	/home/kynor
systemfonts	systemfonts	1.0.4	1.0.4	/home/kynor
tibble	tibble	3.1.8	3.1.8	/home/kynor