

# main

July 23, 2021

## 1 Quality control comparison between LIBD and public RNA-seq data

- CMC
- GTEx brain regions

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

```
Attaching packages: tidyverse
1.3.1
```

```
ggplot2 3.3.5    purrr  0.3.4
tibble  3.1.2    dplyr  1.0.7
tidyr   1.1.3    stringr 1.4.0
readr   1.4.0    forcats 0.5.1
```

### Conflicts

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

New synapser version detected:

You are using synapser version 0.9.77.

synapser version 0.11.7 is detected at <http://ran.synapse.org>.

To upgrade to the latest version of synapser, please run the following command:

```
install.packages("synapser", repos="http://ran.synapse.org")
```

### TERMS OF USE NOTICE:

When using Synapse, remember that the terms and conditions of use require that you:

1) Attribute data contributors when discussing these data or results from these data.

- 2) Not discriminate, identify, or recontact individuals or groups represented by the data.
- 3) Use and contribute only data de-identified to HIPAA standards.
- 4) Redistribute data only under these same terms of use.

## 1.1 Load metrics

### 1.1.1 Load Lieber RNA-seq metrics

```
[2]: libd = data.table::fread("/ceph/projects/v4_phase3_paper/inputs/phenotypes/_m/merged_phenotypes.csv") %>%
  select(-starts_with("snp"), -c("antipsychotics", "lifetime_antipsych")) %>%
  rename("Percent_Aligned"="overallMapRate", "rRNA_Rate"="rRNA_rate",
  ↪ "Brain_Region"="Region",
  ↪ "SampleID"="RNum")
libd %>% head(2)
```

	SampleID	Sex	Race	Dx	Age	mitoRate	rRNA_Rate	totalAssignedC
	<chr>	<chr>	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>
A data.table: 2 × 14	R11135	Male	EA	CTL	18.77	0.2572796	0.0001690954	0.5231321
	R11137	Male	EA	CTL	41.44	0.3840272	0.0000884558	0.5933431

### 1.1.2 Load CMC RNA-seq metrics

```
[3]: # Process functions
downloadFile_version <- function(id , version){
  data.table::fread(synGet(id, version = version)$path, data.table = F)
}
synLogin()

# Download clinical metadata
CLINICAL_ID = 'syn3354385'
clinical = downloadFile_version(CLINICAL_ID, version = 4)

# Download RNASeq metadata
METADATA_QC_DLPFC_ID = 'syn18358379'
metadata = downloadFile_version(METADATA_QC_DLPFC_ID, version = 3)

# Join clinical and RNASeq metadata
md = right_join(clinical, metadata, by = c("Individual ID" = "Individual_ID"))
↪ %>%
  mutate(Dx = fct_recode(Dx, AFF_BP = "BP", AFF_BP = "AFF", Other =
  ↪ "undetermined",
  ↪ Control = "Control", SCZ = "SCZ"))

# Compute read pair metrics and add Institution-Dx variable
```

```
md <- md %>%
  select(c("SampleID", "Dx", "Reported Gender", "Sex", "Ethnicity", "pH",
    ↪ "Age of Death",
    "Study", "Brain_Region", "Brodmann_Area", "RIN", "rRNA_Rate",
    ↪ "Percent_Aligned"))
colnames(md) <- gsub(' ', '_', colnames(md))
print(dim(md))
md %>% head(2)
```

Welcome, kj.benjamin!

NULL

[1] 991 13

A data.frame: 2 × 13		SampleID <chr>	Dx <fct>	Reported_Gender <chr>	Sex <chr>	Ethnicity <chr>
	1	MSSM_RNA_PFC_155	Control	Female	XX	African-American
	2	MSSM_RNA_PFC_280	Control	Female	XX	Caucasian

### 1.1.3 Load GTEx metrics and

```
[4]: gtex = data.table::fread(paste0("https://storage.googleapis.com/
  ↪ gtex_analysis_v8/annotations/",
  ↪
  ↪ "GTEx_Analysis_v8_Annotations_SampleAttributesDS.txt")) %>%
  select(c("SAMPID", "SMRIN", "SMTS", "SMTSD", "SMMAPRT", "SMRRNART")) %>%
  filter(SMTS == "Brain") %>%
  rename("RIN"="SMRIN", "Percent_Aligned"="SMMAPRT", "rRNA_Rate"="SMRRNART",
  ↪ "Brain_Region"="SMTSD",
  ↪ "SampleID"="SAMPID")
gtex %>% head()
```

A data.table: 6 × 6		SampleID <chr>	RIN <dbl>	SMTS <chr>	Brain_Region <chr>	P <
		GTEx-1117F-0011-R10a-SM-AHZ7F	NA	Brain	Brain - Frontal Cortex (BA9)	N
		GTEx-1117F-0011-R10b-SM-CYKQ8	7.2	Brain	Brain - Frontal Cortex (BA9)	N
		GTEx-1117F-3226-SM-5N9CT	6.2	Brain	Brain - Cortex	0.
		GTEx-111FC-0011-R10a-SM-AHZ7K	NA	Brain	Brain - Frontal Cortex (BA9)	N
		GTEx-111FC-0011-R10a-SM-CYKQ9	8.5	Brain	Brain - Frontal Cortex (BA9)	N
		GTEx-111FC-3126-SM-5GZZ2	6.1	Brain	Brain - Cortex	0.

## 1.2 Clean and organize data

```
[5]: gtex = gtex %>% mutate("Dataset"="GTEx", "Dx"="Control",
  ↪ "Brain_Region"=gsub("Brain - ", "",
  ↪
  ↪ str_replace(gtex$Brain_Region, "\\(.*", ""))) %>%
  select("SampleID", "Dx", "Brain_Region", "RIN", "rRNA_Rate",
  ↪ "Percent_Aligned", "Dataset")
```

```
gtex$Brain_Region = gsub(" $", "", str_replace(gtex$Brain_Region, "Frontal_
↪Cortex", "DLPFC"))
gtex %>% head(2)
```

	SampleID <chr>	Dx <chr>	Brain_Region <chr>	RIN <dbl>	rRNA_Rate <dbl>	P
A data.table: 2 × 7	GTEX-1117F-0011-R10a-SM-AHZ7F	Control	DLPFC	NA	NA	N
	GTEX-1117F-0011-R10b-SM-CYKQ8	Control	DLPFC	7.2	NA	N

```
[6]: cmc = md %>% select("SampleID", "Dx", "Brain_Region", "RIN", "rRNA_Rate",
↪ "Percent_Aligned") %>%
mutate("Dataset"="CMC")
cmc %>% head(2)
```

	SampleID <chr>	Dx <fct>	Brain_Region <chr>	RIN <dbl>	rRNA_Rate <dbl>	Percent_
A data.frame: 2 × 7	1 MSSM_RNA_PFC_155	Control	DLPFC	8.4	0.000250992	0.9798915
	2 MSSM_RNA_PFC_280	Control	DLPFC	8.4	0.000373524	0.9688145

```
[7]: libd = libd %>% select("SampleID", "Dx", "Brain_Region", "RIN", "rRNA_Rate",
↪ "Percent_Aligned") %>%
mutate("Dataset"="LIBD", "Dx"=gsub("CTL", "Control", libd$Dx),
"Brain_Region"=gsub("HIPPO", "Hippocampus", libd$Brain_Region))
libd %>% head(2)
```

	SampleID <chr>	Dx <chr>	Brain_Region <chr>	RIN <dbl>	rRNA_Rate <dbl>	Percent_Aligned <dbl>	Dataset <chr>
A data.table: 2 × 7	R11135	Control	Hippocampus	5.9	0.0001690954	0.8746	LIBD
	R11137	Control	Hippocampus	9.2	0.0000884558	0.9149	LIBD

```
[8]: df = bind_rows(libd, gtex, cmc) #>% mutate_if(is.character, as.factor)
df %>% head(2)
```

	SampleID <chr>	Dx <chr>	Brain_Region <chr>	RIN <dbl>	rRNA_Rate <dbl>	Percent_Aligned <dbl>	Dataset <chr>
A data.table: 2 × 7	R11135	Control	Hippocampus	5.9	0.0001690954	0.8746	LIBD
	R11137	Control	Hippocampus	9.2	0.0000884558	0.9149	LIBD

```
[9]: df$Brain_Region %>% unique
```

1. 'Hippocampus' 2. 'DLPFC' 3. 'Caudate' 4. 'Cortex' 5. 'Cerebellum' 6. 'Cerebellar Hemisphere'  
7. 'Nucleus accumbens' 8. 'Putamen' 9. 'Hypothalamus' 10. 'Spinal cord' 11. 'Anterior cingulate  
cortex' 12. 'Substantia nigra' 13. 'Amygdala'

## 1.3 Descriptive analysis

### 1.3.1 Check if NA present

RIN

```
[10]: rin = df %>% group_by(Dataset, Brain_Region) %>% count(is.na(RIN)) %>%
      pivot_wider(names_from=`is.na(RIN)`, values_from="n") %>%
      mutate("TRUE"=replace_na(`TRUE`,0), `RIN (%na)`=`TRUE`/(`FALSE`+`TRUE`))
      rin %>% head(2)
```

	Dataset	Brain_Region	FALSE	TRUE	RIN (%na)
	<chr>	<chr>	<int>	<dbl>	<dbl>
A grouped_df: 2 × 5	CMC	DLPFC	991	0	0
	GTEEx	Amygdala	177	0	0

#### rRNA Rate

```
[11]: rrna = df %>% group_by(Dataset, Brain_Region) %>% count(is.na(rRNA_Rate)) %>%
      pivot_wider(names_from=`is.na(rRNA_Rate)`, values_from="n") %>%
      mutate("TRUE"=replace_na(`TRUE`,0), `rRNA Rate (%na)`=`TRUE`/
      ↪(`FALSE`+`TRUE`))
      rrna %>% head(2)
```

	Dataset	Brain_Region	FALSE	TRUE	rRNA Rate (%na)
	<chr>	<chr>	<int>	<dbl>	<dbl>
A grouped_df: 2 × 5	CMC	DLPFC	991	0	0.00000000
	GTEEx	Amygdala	161	16	0.09039548

#### Percent Alignment

```
[12]: palign = df %>% group_by(Dataset, Brain_Region) %>% count(is.
      ↪na(Percent_Aligned)) %>%
      pivot_wider(names_from=`is.na(Percent_Aligned)`, values_from="n") %>%
      mutate("TRUE"=replace_na(`TRUE`,0), `Percent Aligned (%na)`=`TRUE`/
      ↪(`FALSE`+`TRUE`))
      palign %>% head(2)
```

	Dataset	Brain_Region	FALSE	TRUE	Percent Aligned (%na)
	<chr>	<chr>	<int>	<dbl>	<dbl>
A grouped_df: 2 × 5	CMC	DLPFC	991	0	0.00000000
	GTEEx	Amygdala	161	16	0.09039548

#### Combined summary

```
[13]: tbl = rin %>% select(-c(`FALSE`, `TRUE`)) %>%
      inner_join(select(rrna, -c(`FALSE`, `TRUE`)), by=c("Dataset",
      ↪"Brain_Region")) %>%
      inner_join(select(palign, -c(`FALSE`, `TRUE`)), by=c("Dataset",
      ↪"Brain_Region"))
      tbl %>% as.data.frame %>% data.table::fwrite("qc_metric_NAs_libd_gtex_cmc.csv")
      tbl
```

	Dataset <chr>	Brain_Region <chr>	RIN (%na) <dbl>	rRNA Rate (%na) <dbl>	Percent Aligned <dbl>
A grouped_df: 17 × 5	CMC	DLPFC	0.000000000	0.00000000	0.00000000
	GTEX	Amygdala	0.000000000	0.09039548	0.09039548
	GTEX	Anterior cingulate cortex	0.000000000	0.06572770	0.06572770
	GTEX	Caudate	0.000000000	0.07560137	0.07560137
	GTEX	Cerebellar Hemisphere	0.000000000	0.06844106	0.06844106
	GTEX	Cerebellum	0.003355705	0.07718121	0.07718121
	GTEX	Cortex	0.000000000	0.13846154	0.13846154
	GTEX	DLPFC	0.287058824	0.48000000	0.48000000
	GTEX	Hippocampus	0.045267490	0.11934156	0.11934156
	GTEX	Hypothalamus	0.000000000	0.07203390	0.07203390
	GTEX	Nucleus accumbens	0.000000000	0.06859206	0.06859206
	GTEX	Putamen	0.000000000	0.05603448	0.05603448
	GTEX	Spinal cord	0.000000000	0.06043956	0.06043956
	GTEX	Substantia nigra	0.000000000	0.08536585	0.08536585
	LIBD	Caudate	0.000000000	0.00000000	0.00000000
	LIBD	DLPFC	0.000000000	0.00000000	0.00000000
	LIBD	Hippocampus	0.000000000	0.00000000	0.00000000

### 1.3.2 Summarize data

```
[14]: tbl = df %>% group_by(Dataset, Brain_Region) %>%
  summarise(RIN_mean=mean(RIN, na.rm=TRUE), RIN_sd=sd(RIN, na.rm=TRUE),
    rRNA_mean=mean(rRNA_Rate, na.rm=TRUE), rRNA_sd=sd(rRNA_Rate, na.
    ↪rm=TRUE),
    PercentAligned_mean=mean(Percent_Aligned, na.rm=TRUE),
    PercentAligned_sd=sd(Percent_Aligned, na.rm=TRUE))
tbl %>% as.data.frame %>% data.table::fwrite("qc_metric_summary_libd_gtex_cmc.
    ↪csv")
tbl
```

`summarise()` has grouped output by 'Dataset'. You can override using the `.groups` argument.

	Dataset <chr>	Brain_Region <chr>	RIN_mean <dbl>	RIN_sd <dbl>	rRNA_mean <dbl>	rRNA_sd <dbl>
A grouped_df: 17 × 8	CMC	DLPFC	7.595863	0.9002318	2.825332e-04	1.016402e-
	GTEEx	Amygdala	6.594915	0.6356163	8.679170e-02	3.724921e-
	GTEEx	Anterior cingulate cortex	6.683568	0.7626681	7.020330e-02	3.407544e-
	GTEEx	Caudate	7.390034	0.8786767	6.669918e-02	2.858002e-
	GTEEx	Cerebellar Hemisphere	7.457034	1.0033617	2.524327e-02	2.178709e-
	GTEEx	Cerebellum	6.851852	0.7893323	2.060865e-02	1.212267e-
	GTEEx	Cortex	6.588308	0.6811292	4.852958e-02	2.031282e-
	GTEEx	DLPFC	7.168647	0.8580205	5.299829e-02	2.901991e-
	GTEEx	Hippocampus	6.765517	0.7559981	7.530126e-02	3.385451e-
	GTEEx	Hypothalamus	6.855085	0.7763085	6.479683e-02	3.499553e-
	GTEEx	Nucleus accumbens	7.140433	0.8426733	7.279581e-02	3.489604e-
	GTEEx	Putamen	7.085776	0.9074560	7.632170e-02	2.873567e-
	GTEEx	Spinal cord	7.063187	0.7335050	4.625480e-02	2.817331e-
	GTEEx	Substantia nigra	6.578659	0.7163100	7.752818e-02	3.039102e-
	LIBD	Caudate	7.834483	0.8673440	5.759414e-05	3.599073e-
	LIBD	DLPFC	7.779691	0.9663740	5.022716e-05	3.060435e-
	LIBD	Hippocampus	7.723490	1.1208014	2.929714e-05	2.628273e-

## 1.4 Plot metrics

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

[16]: set.seed(20210723)
bxp = df %>% ggboxplot(x="Brain_Region", y="RIN", color="Dataset", add='jitter',
  panel.labs.font=list(face='bold', size = 14),
  ↪palette="npg",
  outlier.shape=NA, ylab='RIN', add.params=list(alpha=0.5),
  legend="bottom", xlab="Brain Region",
  ggtheme=theme_pubr(base_size=20)) +
  font("xy.title", face="bold") + font("legend.title", face="bold") +
  rotate_x_text(45)
save_ggplots("boxplot_brain_region_comparison_rin", bxp, 12, 8)
bxp
```

Warning message:

"Removed 134 rows containing non-finite values (stat\_boxplot)."

Warning message:

"Removed 134 rows containing missing values (geom\_point)."

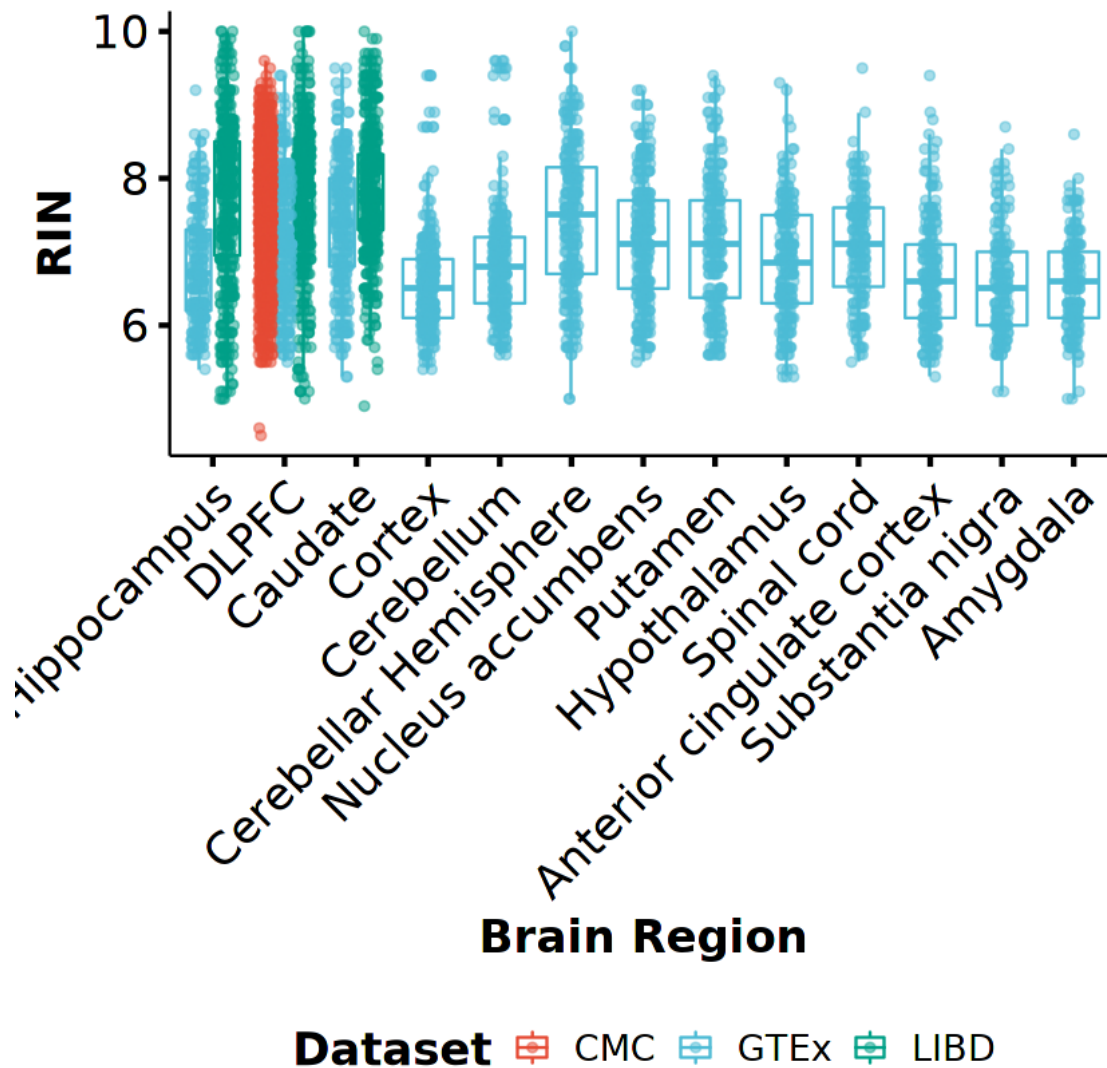
Warning message:

"Removed 134 rows containing non-finite values (stat\_boxplot)."

Warning message:

"Removed 134 rows containing missing values (geom\_point)."

Warning message:  
 "Removed 134 rows containing non-finite values (stat\_boxplot)."  
 Warning message:  
 "Removed 134 rows containing missing values (geom\_point)."  
 Warning message:  
 "Removed 134 rows containing non-finite values (stat\_boxplot)."  
 Warning message:  
 "Removed 134 rows containing missing values (geom\_point)."



```
[17]: set.seed(20210723)
      bxp = df %>% ggboxplot(x="Brain_Region", y="rRNA_Rate", color="Dataset",
      ↪add='jitter',
```



```

        panel.labs.font=list(face='bold', size = 14),
    ↪palette="npg",
        outlier.shape=NA, ylab='rRNA Rate', add.
    ↪params=list(alpha=0.5),
        legend="bottom", xlab="Brain Region",
    ↪ggtheme=theme_pubr(base_size=20)) +
        font("xy.title", face="bold") + font("legend.title", face="bold") +
    ↪rotate_x_text(45)
save_ggplots("boxplot_brain_region_comparison_rRNA_rate", bxp, 12, 8)
bxp

```

Warning message:

"Removed 445 rows containing non-finite values (stat\_boxplot)."

Warning message:

"Removed 445 rows containing missing values (geom\_point)."

Warning message:

"Removed 445 rows containing non-finite values (stat\_boxplot)."

Warning message:

"Removed 445 rows containing missing values (geom\_point)."

Warning message:

"Removed 445 rows containing non-finite values (stat\_boxplot)."

Warning message:

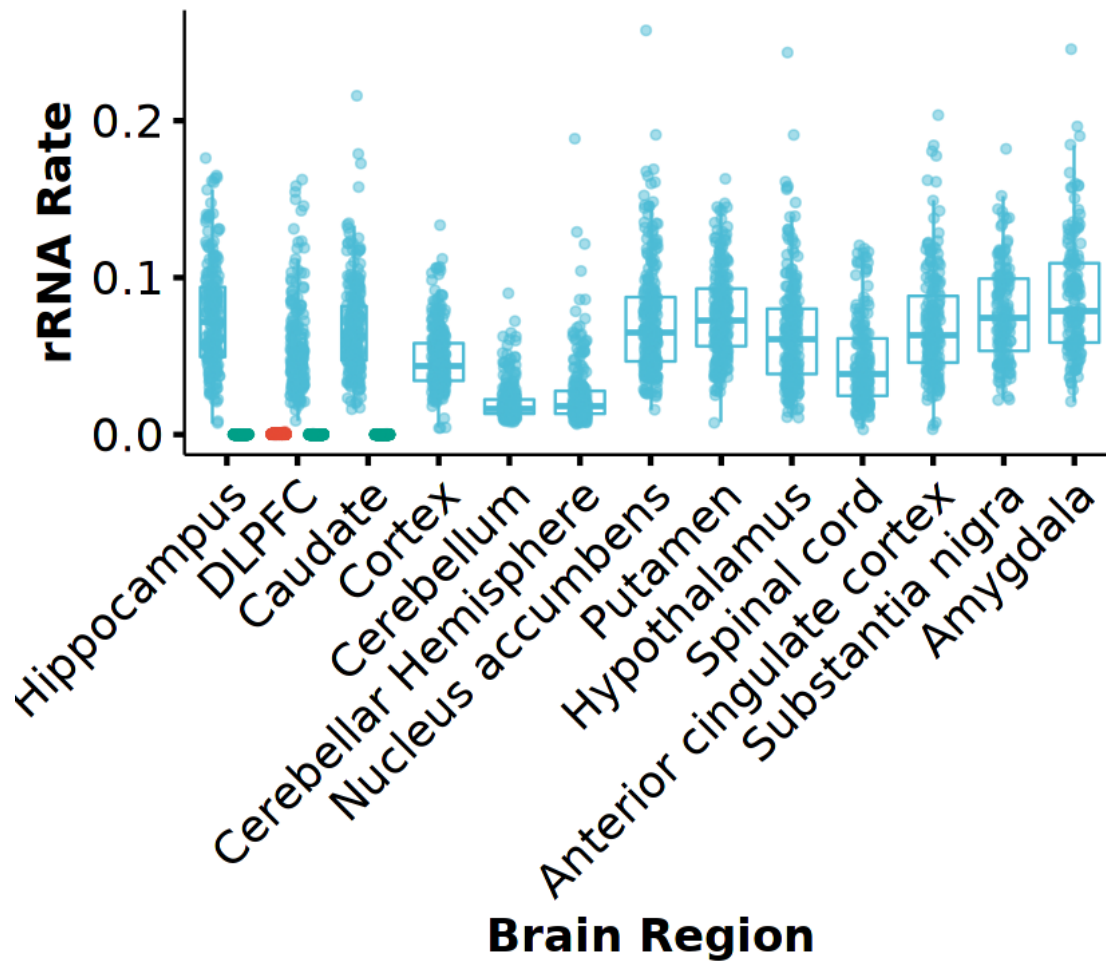
"Removed 445 rows containing missing values (geom\_point)."

Warning message:

"Removed 445 rows containing non-finite values (stat\_boxplot)."

Warning message:

"Removed 445 rows containing missing values (geom\_point)."



**Dataset** CMC GTEx LIBD

```
[18]: set.seed(20210723)
bxp = df %>% ggboxplot(x="Brain_Region", y="Percent_Aligned", color="Dataset",
  ↪add='jitter',
                                panel.labs.font=list(face='bold', size = 14),
  ↪palette="npg",
                                outlier.shape=NA, ylab='Percent Aligned', add.
  ↪params=list(alpha=0.5),
                                legend="bottom", xlab="Brain Region",
  ↪ggtheme=theme_pubr(base_size=20)) +
  font("xy.title", face="bold") + font("legend.title", face="bold") +
  ↪rotate_x_text(45)
save_ggplots("boxplot_brain_region_comparison_Percent_Aligned", bxp, 12, 8)
```

```
bxp
```

Warning message:

"Removed 445 rows containing non-finite values (stat\_boxplot)."

Warning message:

"Removed 445 rows containing missing values (geom\_point)."

Warning message:

"Removed 445 rows containing non-finite values (stat\_boxplot)."

Warning message:

"Removed 445 rows containing missing values (geom\_point)."

Warning message:

"Removed 445 rows containing non-finite values (stat\_boxplot)."

Warning message:

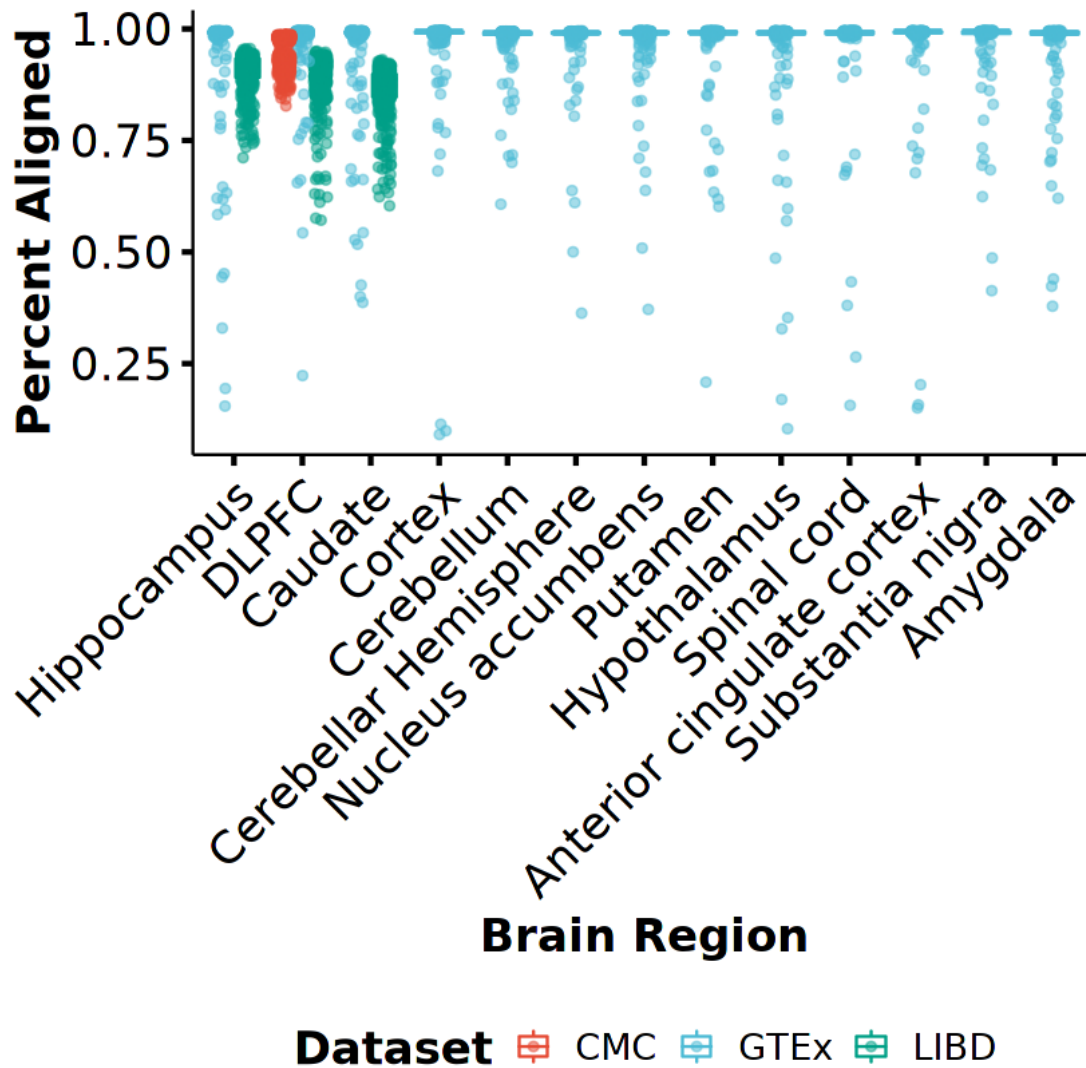
"Removed 445 rows containing missing values (geom\_point)."

Warning message:

"Removed 445 rows containing non-finite values (stat\_boxplot)."

Warning message:

"Removed 445 rows containing missing values (geom\_point)."



## 1.5 Session Info

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

```
[1] "2021-07-23 14:07:33 EDT"
```

```
   user  system elapsed
19.432   1.062  18.182
```

```
Session info
setting  value
```

```

version R version 4.0.3 (2020-10-10)
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    2021-07-23

```

#### Packages

package	* version	date	lib	source
abind	1.4-5	2016-07-21	[1]	CRAN (R 4.0.2)
assertthat	0.2.1	2019-03-21	[1]	CRAN (R 4.0.2)
backports	1.2.1	2020-12-09	[1]	CRAN (R 4.0.2)
base64enc	0.1-3	2015-07-28	[1]	CRAN (R 4.0.2)
broom	0.7.8	2021-06-24	[1]	CRAN (R 4.0.3)
Cairo	1.5-12.2	2020-07-07	[1]	CRAN (R 4.0.2)
car	3.0-11	2021-06-27	[1]	CRAN (R 4.0.3)
carData	3.0-4	2020-05-22	[1]	CRAN (R 4.0.2)
cellranger	1.1.0	2016-07-27	[1]	CRAN (R 4.0.2)
cli	3.0.0	2021-06-30	[1]	CRAN (R 4.0.3)
codetools	0.2-16	2018-12-24	[2]	CRAN (R 4.0.3)
colorspace	2.0-2	2021-06-24	[1]	CRAN (R 4.0.3)
crayon	1.4.1	2021-02-08	[1]	CRAN (R 4.0.3)
curl	4.3.2	2021-06-23	[1]	CRAN (R 4.0.3)
data.table	1.14.0	2021-02-21	[1]	CRAN (R 4.0.3)
DBI	1.1.1	2021-01-15	[1]	CRAN (R 4.0.2)
dbplyr	2.1.1	2021-04-06	[1]	CRAN (R 4.0.3)
digest	0.6.27	2020-10-24	[1]	CRAN (R 4.0.2)
dplyr	* 1.0.7	2021-06-18	[1]	CRAN (R 4.0.3)
ellipsis	0.3.2	2021-04-29	[1]	CRAN (R 4.0.3)
evaluate	0.14	2019-05-28	[1]	CRAN (R 4.0.2)
fansi	0.5.0	2021-05-25	[1]	CRAN (R 4.0.3)
farver	2.1.0	2021-02-28	[1]	CRAN (R 4.0.3)
forcats	* 0.5.1	2021-01-27	[1]	CRAN (R 4.0.2)
foreign	0.8-80	2020-05-24	[2]	CRAN (R 4.0.3)
fs	1.5.0	2020-07-31	[1]	CRAN (R 4.0.2)
generics	0.1.0	2020-10-31	[1]	CRAN (R 4.0.2)
ggplot2	* 3.3.5	2021-06-25	[1]	CRAN (R 4.0.3)
ggpubr	* 0.4.0	2020-06-27	[1]	CRAN (R 4.0.2)
ggsci	2.9	2018-05-14	[1]	CRAN (R 4.0.2)
ggsignif	0.6.2	2021-06-14	[1]	CRAN (R 4.0.3)
glue	1.4.2	2020-08-27	[1]	CRAN (R 4.0.2)
gtable	0.3.0	2019-03-25	[1]	CRAN (R 4.0.2)
haven	2.4.1	2021-04-23	[1]	CRAN (R 4.0.3)
hms	1.1.0	2021-05-17	[1]	CRAN (R 4.0.3)
htmltools	0.5.1.1	2021-01-22	[1]	CRAN (R 4.0.2)

httr	1.4.2	2020-07-20	[1]	CRAN	(R 4.0.2)
IRdisplay	1.0	2021-01-20	[1]	CRAN	(R 4.0.2)
IRkernel	1.2	2021-05-11	[1]	CRAN	(R 4.0.3)
jsonlite	1.7.2	2020-12-09	[1]	CRAN	(R 4.0.2)
labeling	0.4.2	2020-10-20	[1]	CRAN	(R 4.0.2)
lifecycle	1.0.0	2021-02-15	[1]	CRAN	(R 4.0.3)
lubridate	1.7.10	2021-02-26	[1]	CRAN	(R 4.0.3)
magrittr	2.0.1	2020-11-17	[1]	CRAN	(R 4.0.2)
modelr	0.1.8	2020-05-19	[1]	CRAN	(R 4.0.2)
munsell	0.5.0	2018-06-12	[1]	CRAN	(R 4.0.2)
openxlsx	4.2.4	2021-06-16	[1]	CRAN	(R 4.0.3)
pack	0.1-1	2021-02-23	[1]	local	
pbdZMQ	0.3-5	2021-02-10	[1]	CRAN	(R 4.0.3)
pillar	1.6.1	2021-05-16	[1]	CRAN	(R 4.0.3)
pkgconfig	2.0.3	2019-09-22	[1]	CRAN	(R 4.0.2)
purrr	* 0.3.4	2020-04-17	[1]	CRAN	(R 4.0.2)
PythonEmbedInR	0.6.76	2021-02-23	[1]	local	
R6	2.5.0	2020-10-28	[1]	CRAN	(R 4.0.2)
Rcpp	1.0.7	2021-07-07	[1]	CRAN	(R 4.0.3)
readr	* 1.4.0	2020-10-05	[1]	CRAN	(R 4.0.2)
readxl	1.3.1	2019-03-13	[1]	CRAN	(R 4.0.2)
repr	1.1.3	2021-01-21	[1]	CRAN	(R 4.0.2)
reprex	2.0.0	2021-04-02	[1]	CRAN	(R 4.0.3)
rio	0.5.27	2021-06-21	[1]	CRAN	(R 4.0.3)
rlang	0.4.11	2021-04-30	[1]	CRAN	(R 4.0.3)
rstatix	0.7.0	2021-02-13	[1]	CRAN	(R 4.0.3)
rstudioapi	0.13	2020-11-12	[1]	CRAN	(R 4.0.2)
rvest	1.0.0	2021-03-09	[1]	CRAN	(R 4.0.3)
scales	1.1.1	2020-05-11	[1]	CRAN	(R 4.0.2)
sessioninfo	1.1.1	2018-11-05	[1]	CRAN	(R 4.0.2)
stringi	1.7.3	2021-07-16	[1]	CRAN	(R 4.0.3)
stringr	* 1.4.0	2019-02-10	[1]	CRAN	(R 4.0.2)
svglite	2.0.0	2021-02-20	[1]	CRAN	(R 4.0.3)
synapser	* 0.9.77	2021-02-23	[1]	local	
systemfonts	1.0.2	2021-05-11	[1]	CRAN	(R 4.0.3)
tibble	* 3.1.2	2021-05-16	[1]	CRAN	(R 4.0.3)
tidyr	* 1.1.3	2021-03-03	[1]	CRAN	(R 4.0.3)
tidyselect	1.1.1	2021-04-30	[1]	CRAN	(R 4.0.3)
tidyverse	* 1.3.1	2021-04-15	[1]	CRAN	(R 4.0.3)
utf8	1.2.1	2021-03-12	[1]	CRAN	(R 4.0.3)
uuid	0.1-4	2020-02-26	[1]	CRAN	(R 4.0.2)
vctrs	0.3.8	2021-04-29	[1]	CRAN	(R 4.0.3)
withr	2.4.2	2021-04-18	[1]	CRAN	(R 4.0.3)
xml2	1.3.2	2020-04-23	[1]	CRAN	(R 4.0.2)
zip	2.2.0	2021-05-31	[1]	CRAN	(R 4.0.3)

[1] /home/jbenja13/R/x86\_64-pc-linux-gnu-library/4.0

[2] /usr/lib/R/library