

main

July 12, 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 0.10.101 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	Dx	Reported_Gender	Sex	Ethnicity
		<chr>	<fct>	<chr>	<chr>	<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	RIN	SMTS	Brain_Region	P
	<chr>	<dbl>	<chr>	<chr>	<
	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 <dbl>
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_␣ <dbl>
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

GTEX

RIN

```
[10]: gtex %>% group_by(Brain_Region) %>% count(is.na(RIN)) %>%  
      pivot_wider(names_from=`is.na(RIN)`, values_from="n") %>%  
      mutate("TRUE"=replace_na(`TRUE`,0))
```

	Brain_Region <chr>	FALSE <int>	TRUE <dbl>
A grouped_df: 13 × 3	Amygdala	177	0
	Anterior cingulate cortex	213	0
	Caudate	291	0
	Cerebellar Hemisphere	263	0
	Cerebellum	297	1
	Cortex	325	0
	DLPFC	303	122
	Hippocampus	232	11
	Hypothalamus	236	0
	Nucleus accumbens	277	0
	Putamen	232	0
	Spinal cord	182	0
	Substantia nigra	164	0

rRNA Rate

```
[11]: gtex %>% group_by(Brain_Region) %>% count(is.na(rRNA_Rate)) %>%  
      pivot_wider(names_from=`is.na(rRNA_Rate)`, values_from="n") %>%  
      mutate("TRUE"=replace_na(`TRUE`,0))
```

	Brain_Region <chr>	FALSE <int>	TRUE <dbl>
A grouped_df: 13 × 3	Amygdala	161	16
	Anterior cingulate cortex	199	14
	Caudate	269	22
	Cerebellar Hemisphere	245	18
	Cerebellum	275	23
	Cortex	280	45
	DLPFC	221	204
	Hippocampus	214	29
	Hypothalamus	219	17
	Nucleus accumbens	258	19
	Putamen	219	13
	Spinal cord	171	11
	Substantia nigra	150	14

Percent Alignment

```
[12]: gtex %>% group_by(Brain_Region) %>% count(is.na(Percent_Aligned)) %>%  
      pivot_wider(names_from=`is.na(Percent_Aligned)`, values_from="n") %>%  
      mutate("TRUE"=replace_na(`TRUE`,0))
```

	Brain_Region	FALSE	TRUE
	<chr>	<int>	<dbl>
A grouped_df: 13 × 3	Amygdala	161	16
	Anterior cingulate cortex	199	14
	Caudate	269	22
	Cerebellar Hemisphere	245	18
	Cerebellum	275	23
	Cortex	280	45
	DLPFC	221	204
	Hippocampus	214	29
	Hypothalamus	219	17
	Nucleus accumbens	258	19
	Putamen	219	13
	Spinal cord	171	11
	Substantia nigra	150	14

CMC

RIN

```
[13]: cmc %>% group_by(Brain_Region) %>% count(is.na(RIN))
```

	Brain_Region	is.na(RIN)	n
	<chr>	<lgl>	<int>
A grouped_df: 1 × 3	DLPFC	FALSE	991

rRNA Rate

```
[14]: cmc %>% group_by(Brain_Region) %>% count(is.na(rRNA_Rate))
```

	Brain_Region	is.na(rRNA_Rate)	n
	<chr>	<lgl>	<int>
A grouped_df: 1 × 3	DLPFC	FALSE	991

Percent Alignment

```
[15]: cmc %>% group_by(Brain_Region) %>% count(is.na(Percent_Aligned))
```

	Brain_Region	is.na(Percent_Aligned)	n
	<chr>	<lgl>	<int>
A grouped_df: 1 × 3	DLPFC	FALSE	991

LIBD

RIN

```
[16]: libd %>% group_by(Brain_Region) %>% count(is.na(RIN))
```

	Brain_Region	is.na(RIN)	n
	<chr>	<lgl>	<int>
A grouped_df: 3 × 3	Caudate	FALSE	464
	DLPFC	FALSE	453
	Hippocampus	FALSE	447

rRNA Rate

```
[17]: libd %>% group_by(Brain_Region) %>% count(is.na(rRNA_Rate))
```

	Brain_Region <chr>	is.na(rRNA_Rate) <lgl>	n <int>
A grouped_df: 3 × 3	Caudate	FALSE	464
	DLPFC	FALSE	453
	Hippocampus	FALSE	447

Percent Alignment

```
[18]: libd %>% group_by(Brain_Region) %>% count(is.na(Percent_Aligned))
```

	Brain_Region <chr>	is.na(Percent_Aligned) <lgl>	n <int>
A grouped_df: 3 × 3	Caudate	FALSE	464
	DLPFC	FALSE	453
	Hippocampus	FALSE	447

1.3.2 Summarize data

```
[19]: 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))
```

`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

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

[21]: 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") +
  font("xy.text", size=14) + font("xy.title", size=16, face="bold") +
  font("legend.title", size=18, face="bold") + font("legend.text", size=18) +
  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:

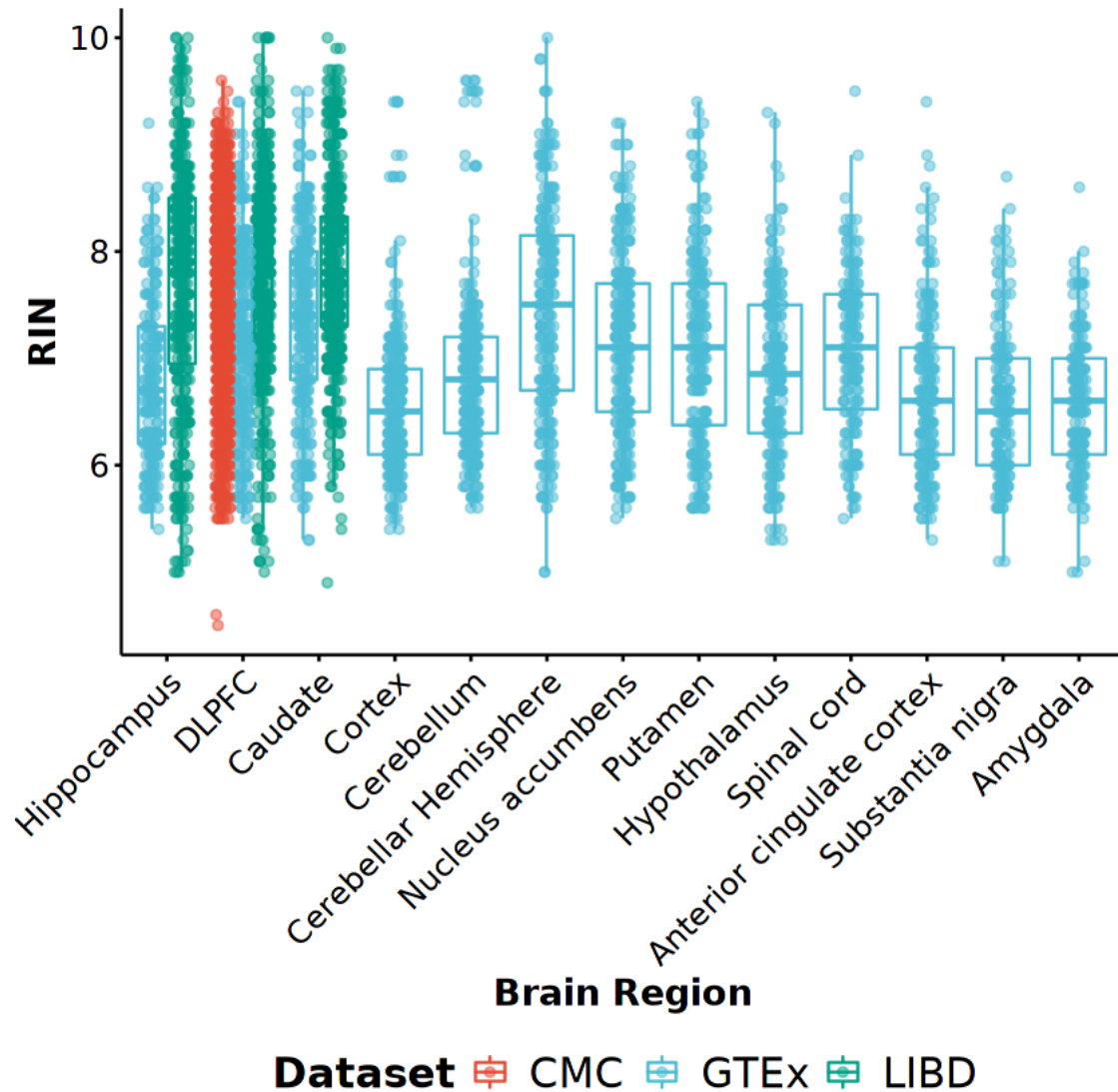
"Removed 134 rows containing non-finite values (stat_boxplot)."

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)."



```
[22]: 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") +
    font("xy.text", size=14) + font("xy.title", size=16, face="bold") +
    font("legend.title", size=18, face="bold") + font("legend.text", size=18) +
    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:

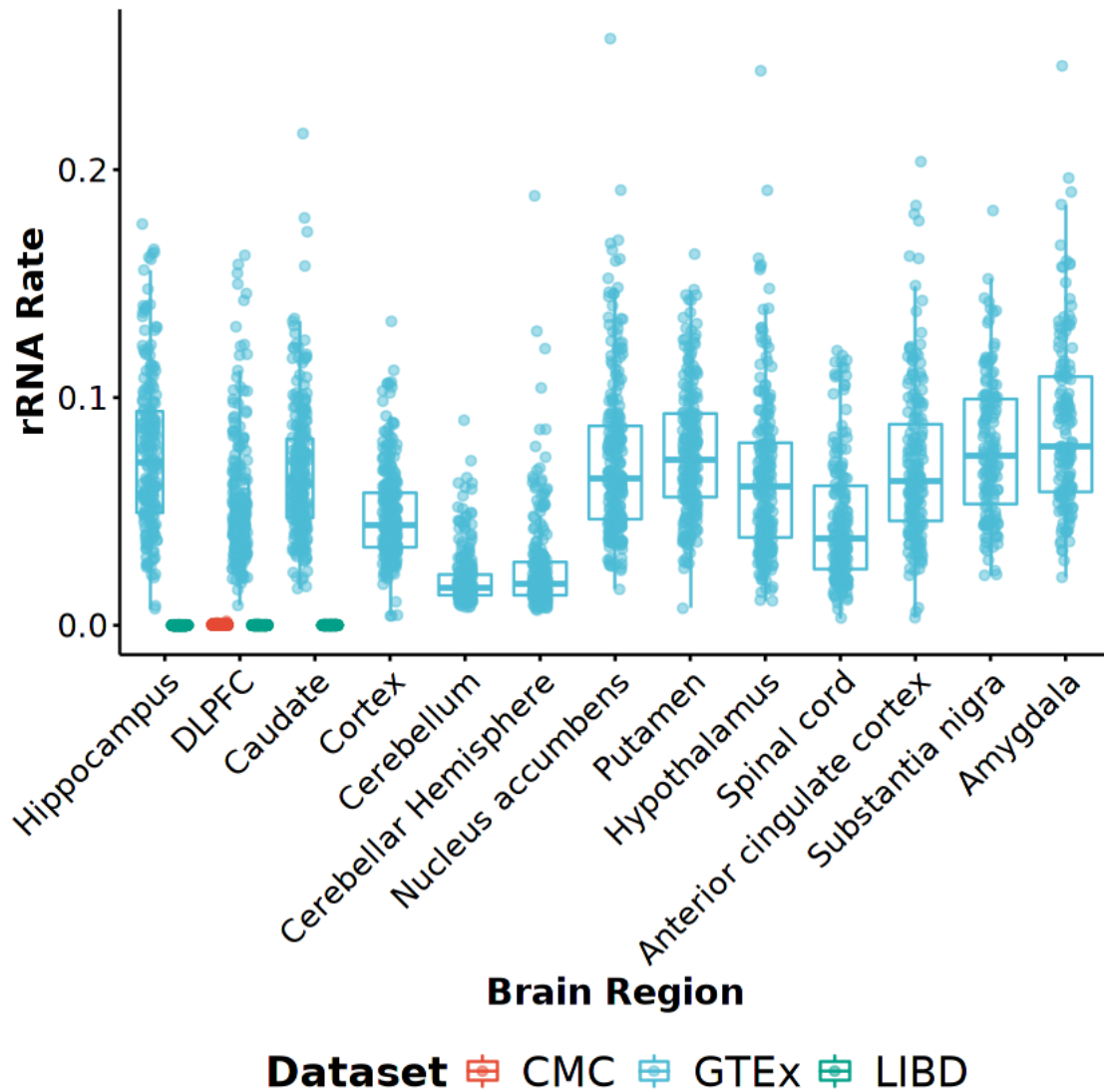
"Removed 445 rows containing missing values (geom_point)."

Warning message:

"Removed 445 rows containing non-finite values (stat_boxplot)."

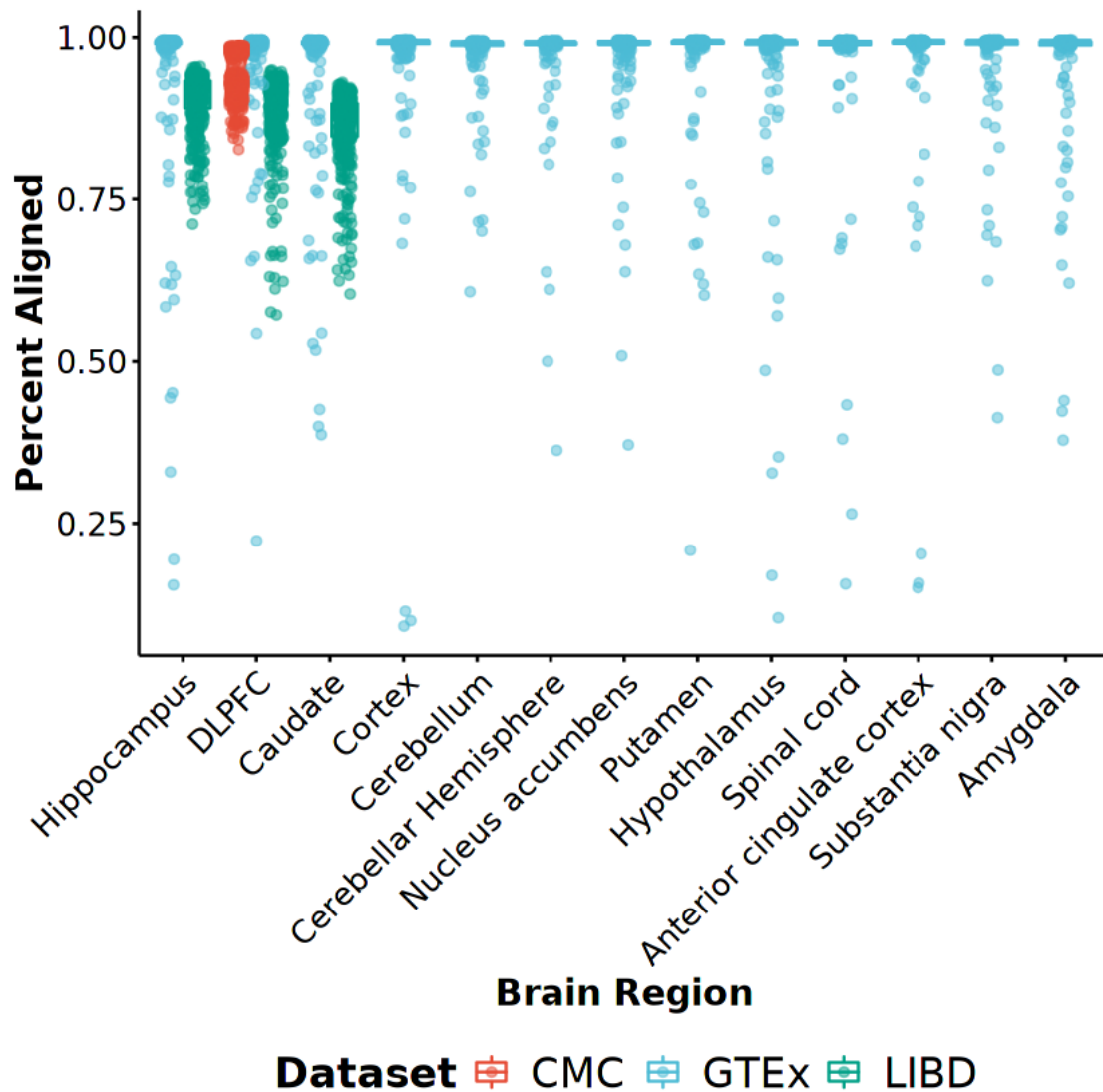
Warning message:

"Removed 445 rows containing missing values (geom_point)."



```
[23]: 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") +
  font("xy.text", size=14) + font("xy.title", size=16, face="bold") +
  font("legend.title", size=18, face="bold") + font("legend.text", size=18) +
  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

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

```
[1] "2021-07-12 15:50:21 EDT"
```

```
   user  system elapsed
17.106   0.769   15.800
```

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     2021-07-12
```

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	1.6.2	2021-05-17	[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