PRI-FLCPDX-miR correlation

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```r
library(dplyr)
library(ggpubr)
library(tibble)
```
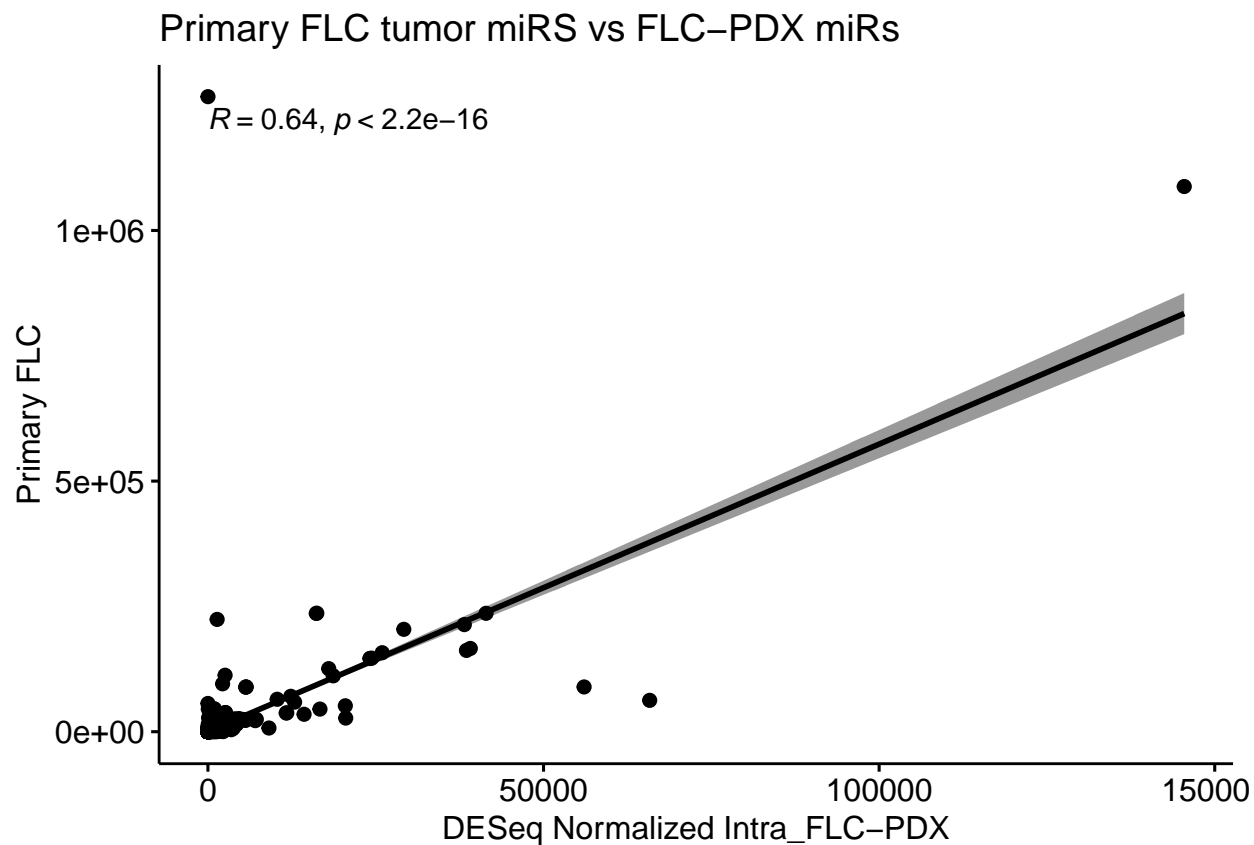
Load CSV

```r
flc.intra.deseq <- read.csv("FLC-PDX_DESeq_miRs.csv")
flc.pri <- read.csv("PRI-mIRs.csv")
flc.intra.rpmmm <- read.csv("FLC-PDX_RPMMM_miRs.csv")
```

Full join FLC primary tumor and FLC-PDX miRs (avg_DESeq). Changed is.na to 0

```r
flc.combined.deseq <- full_join(flc.intra.deseq, flc.pri, by = "miR")
flc.combined.deseq[is.na(flc.combined.deseq)] <- 0
```

```r
p <- ggscatter(flc.combined.deseq, x = "avg_Intra_FLC", y = "avg_PRI",
        add = "reg.line", conf.int = TRUE,
        cor.coef = TRUE, cor.method = "pearson",
        xlab = "DESeq Normalized Intra_FLC-PDX", ylab = "Primary FLC", title = "Primary FLC tumor miR

p
```

```
## `geom_smooth()` using formula 'y ~ x'
```
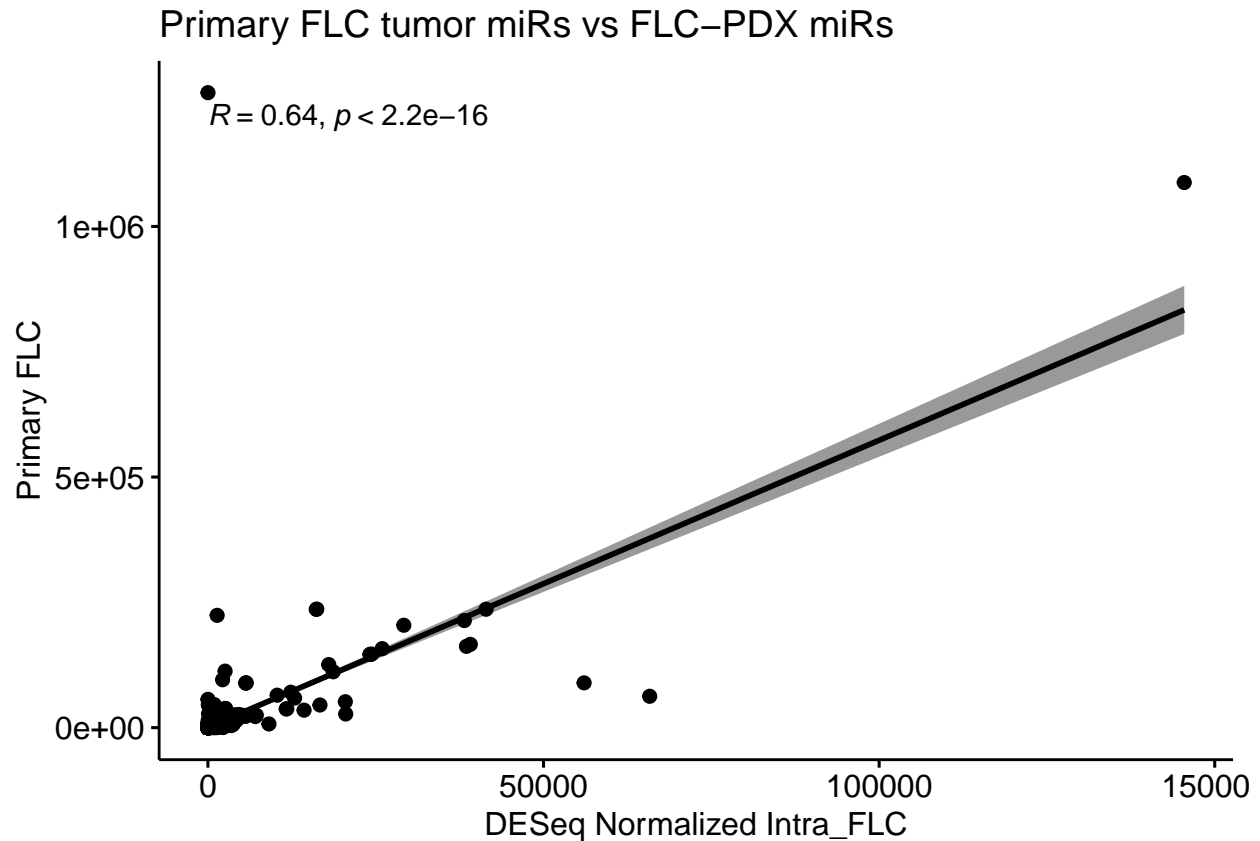
Primary FLC tumor miRS vs FLC-PDX miRs

$R = 0.64, p < 2.2e{-}16$

(y-axis: Primary FLC — 1e+06, 5e+05, 0e+00)

(x-axis: DESeq Normalized Intra_FLC-PDX — 0, 50000, 100000, 15000)

Removed rows that equal 0

```
flc.combined.deseq <- column_to_rownames(flc.combined.deseq, var = "miR")
flc.clean <- flc.combined.deseq[rowSums(flc.combined.deseq[])>0,]
```

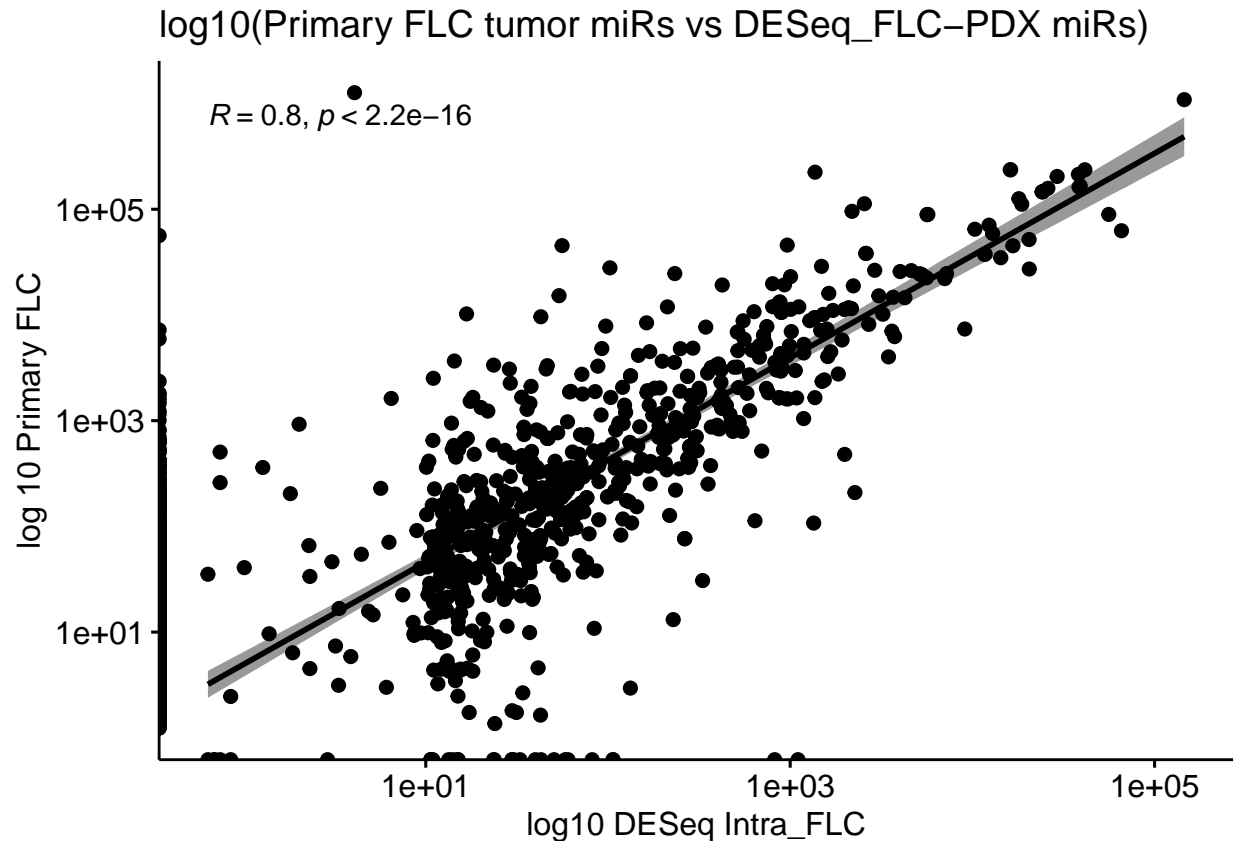Plotted cleaned DEseq_dataframe with and without log10 transformation

```
p2 <- ggscatter(flc.clean, x = "avg_Intra_FLC", y = "avg_PRI",
        add = "reg.line", conf.int = TRUE,
        cor.coef = TRUE, cor.method = "pearson",
        xlab = "DESeq Normalized Intra_FLC", ylab = "Primary FLC", title = "Primary FLC tumor miRs vs

p3 <- ggscatter(flc.clean, x = "avg_Intra_FLC", y = "avg_PRI",
        add = "reg.line", conf.int = TRUE,
        cor.coef = TRUE, cor.method = "pearson",
        xlab = "log10 DESeq Intra_FLC", ylab = "log 10 Primary FLC", title = "log10(Primary FLC tumor
  scale_x_log10() +
  scale_y_log10()

p2
```

```
## `geom_smooth()` using formula 'y ~ x'
```

Primary FLC tumor miRs vs FLC–PDX miRs

$R = 0.64$, $p < 2.2e{-}16$

Primary FLC

1e+06

5e+05

0e+00

0   50000   100000   15000

DESeq Normalized Intra_FLC

p3

```
## Warning: Transformation introduced infinite values in continuous x-axis

## Warning: Transformation introduced infinite values in continuous y-axis

## Warning: Transformation introduced infinite values in continuous x-axis

## Warning: Transformation introduced infinite values in continuous y-axis

## Warning: Transformation introduced infinite values in continuous x-axis

## Warning: Transformation introduced infinite values in continuous y-axis

## 'geom_smooth()' using formula 'y ~ x'

## Warning: Removed 1020 rows containing non-finite values (stat_smooth).

## Warning: Removed 1020 rows containing non-finite values (stat_cor).
```
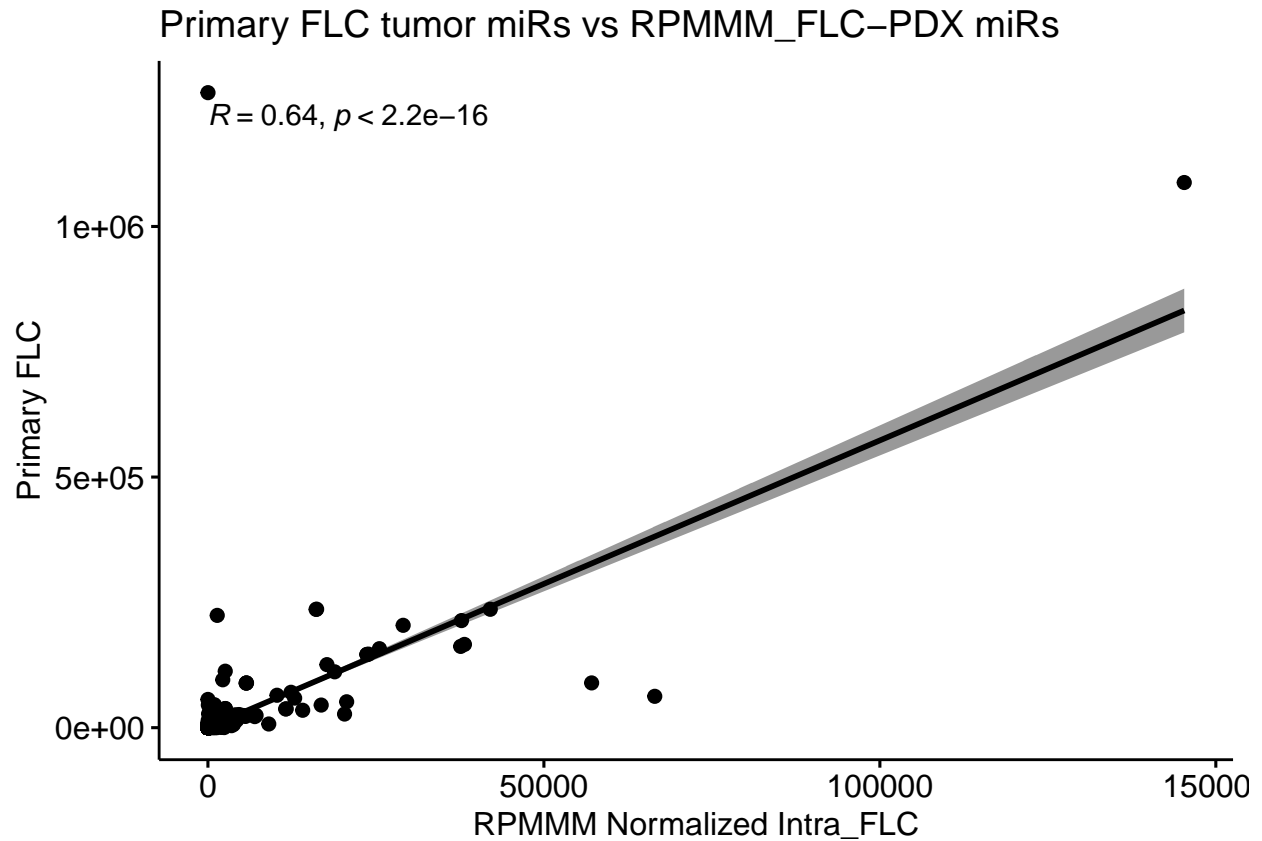
log10(Primary FLC tumor miRs vs DESeq_FLC–PDX miRs)

$R = 0.8, p < 2.2e-16$

#Work flow with RPMMM

```
flc.combined.rpmmm <- full_join(flc.intra.rpmmm, flc.pri, by = "miR")
flc.combined.rpmmm[is.na(flc.combined.rpmmm)] <- 0
flc.combined.rpmmm <- column_to_rownames(flc.combined.rpmmm, var = "miR")
flc.clean.rpmmm <- flc.combined.rpmmm[rowSums(flc.combined.rpmmm[])>0,]
```

```
p4 <- ggscatter(flc.clean.rpmmm, x = "AVG_Intra_FLC", y = "avg_PRI",
        add = "reg.line", conf.int = TRUE,
        cor.coef = TRUE, cor.method = "pearson",
        xlab = "RPMMM Normalized Intra_FLC", ylab = "Primary FLC", title = "Primary FLC tumor miRs vs

p5 <- ggscatter(flc.clean.rpmmm, x = "AVG_Intra_FLC", y = "avg_PRI",
        add = "reg.line", conf.int = TRUE,
        cor.coef = TRUE, cor.method = "pearson",
        xlab = "log10 RPMMM Normalized Intra_FLC", ylab = "log10 Primary FLC", title = "log10(Primary
  scale_x_log10() +
  scale_y_log10()

p4
```

```
## `geom_smooth()` using formula 'y ~ x'
```

Primary FLC tumor miRs vs RPMMM_FLC–PDX miRs

$R = 0.64, p < 2.2e{-}16$

Primary FLC

RPMMM Normalized Intra_FLC

p5

```
## Warning: Transformation introduced infinite values in continuous x-axis

## Warning: Transformation introduced infinite values in continuous y-axis

## Warning: Transformation introduced infinite values in continuous x-axis

## Warning: Transformation introduced infinite values in continuous y-axis

## Warning: Transformation introduced infinite values in continuous x-axis

## Warning: Transformation introduced infinite values in continuous y-axis

## 'geom_smooth()' using formula 'y ~ x'

## Warning: Removed 1098 rows containing non-finite values (stat_smooth).

## Warning: Removed 1098 rows containing non-finite values (stat_cor).
```

log10(Primary FLC tumor miRs vs RPMMM_FLC−PDX miRs)

$R = 0.78$, $p < 2.2e{-}16$

log10 Primary FLC

log10 RPMMM Normalized Intra_FLC