

# PRI-FLCH-miRs

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```
library(dplyr)
library(ggpubr)
library(tibble)
```

## Load CSV

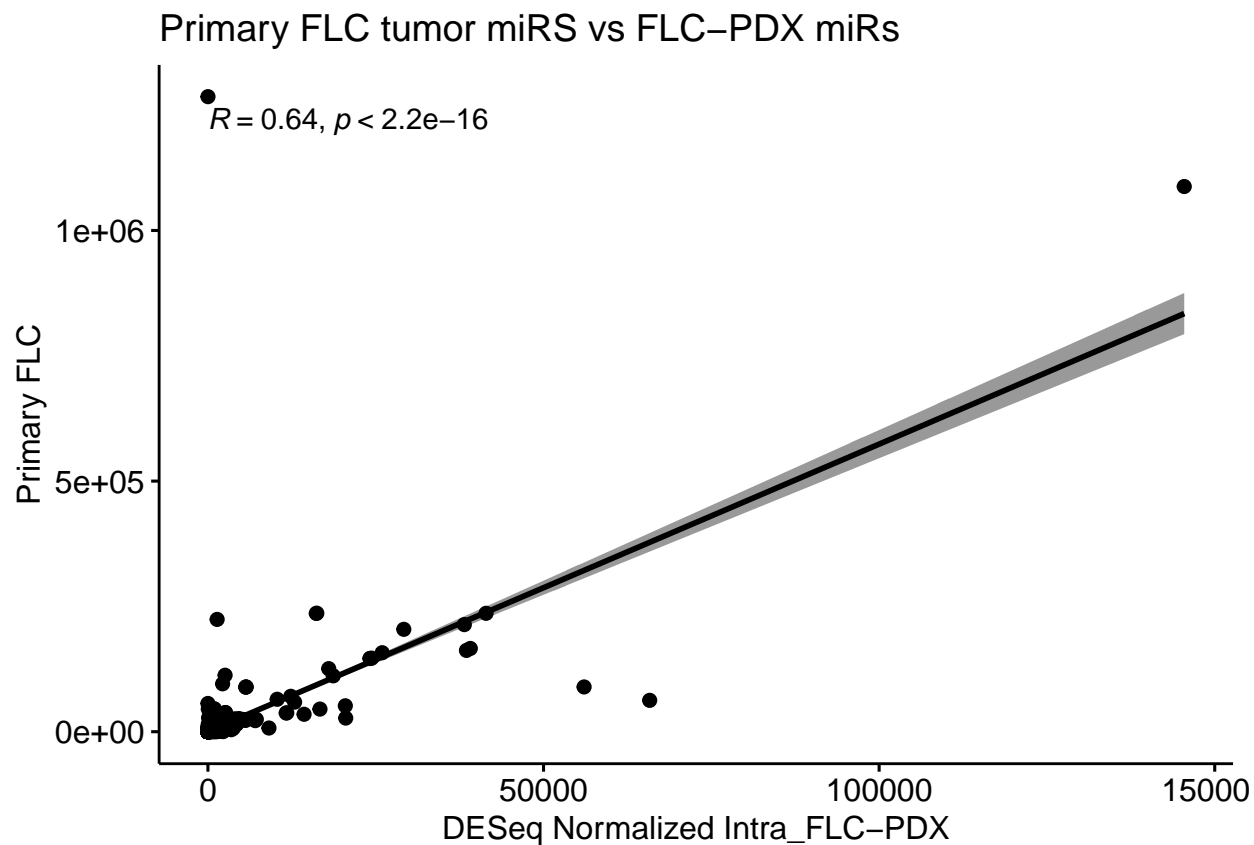
```
flc.intra.deseq <- read.csv("FLC-PDX_DESeq_miRs.csv")
flc.pri <- read.csv("PRI-miRs.csv")
flc.intra.rpmmm <- read.csv("FLC-PDX_RPMMM_miRs.csv")
```

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

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

```
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'
```



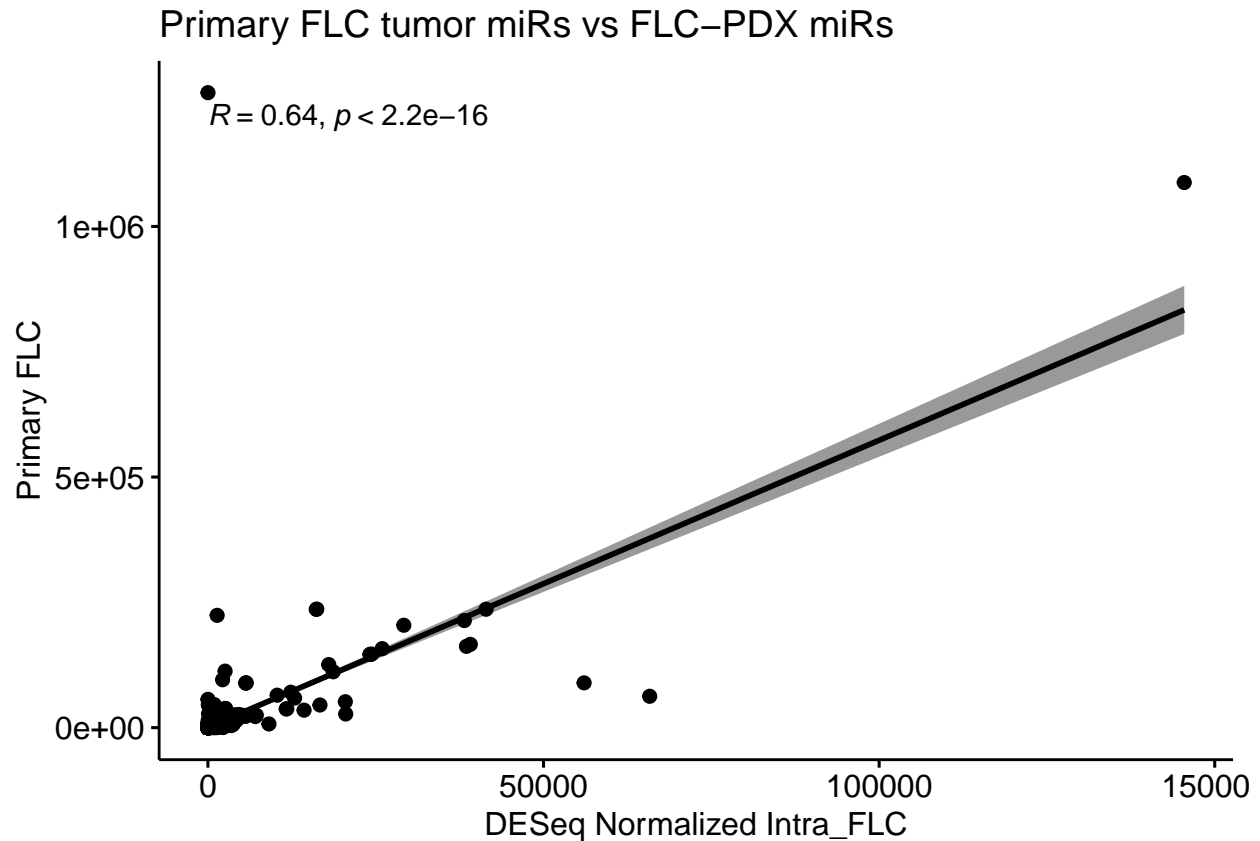
Removed rows that equal 0

```
f1c.combined.deseq <- column_to_rownames(f1c.combined.deseq, var = "miR")
f1c.clean <- f1c.combined.deseq[rowSums(f1c.combined.deseq[])>0,]
```

Plotted cleaned DEseq\_dataframe with and without log10 transformation

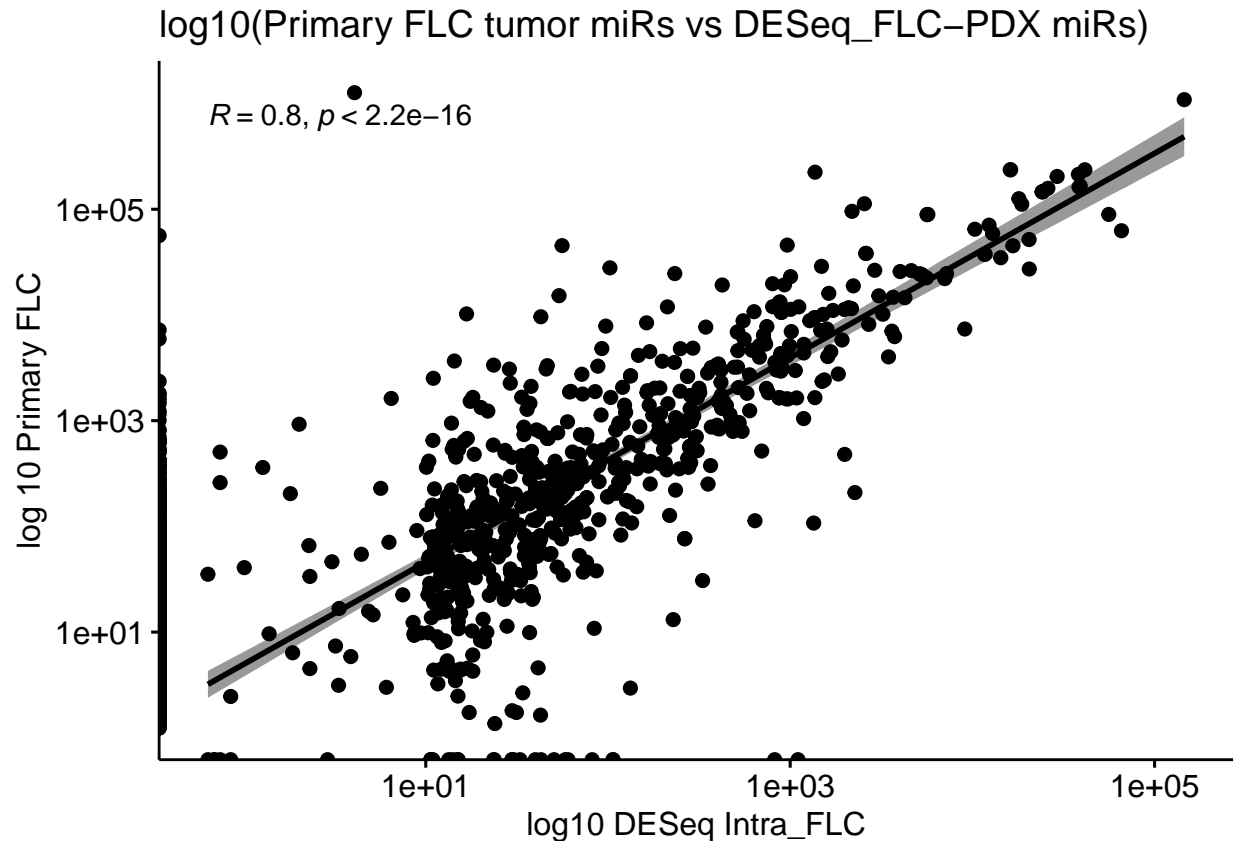
```
p2 <- ggscatter(f1c.clean, x = "avg_Intra_FLC", y = "avg_PRI",
  add = "reg.line", conf.int = TRUE,
  cor.coef = TRUE, cor.method = "pearson",
  xlab = "DESeq Normalized Intra_FLC", ylab = "Primary FLC", title = "Primary FLC tumor miRs vs
p3 <- ggscatter(f1c.clean, x = "avg_Intra_FLC", y = "avg_PRI",
  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'
```



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).
```



#Work flow with RPM

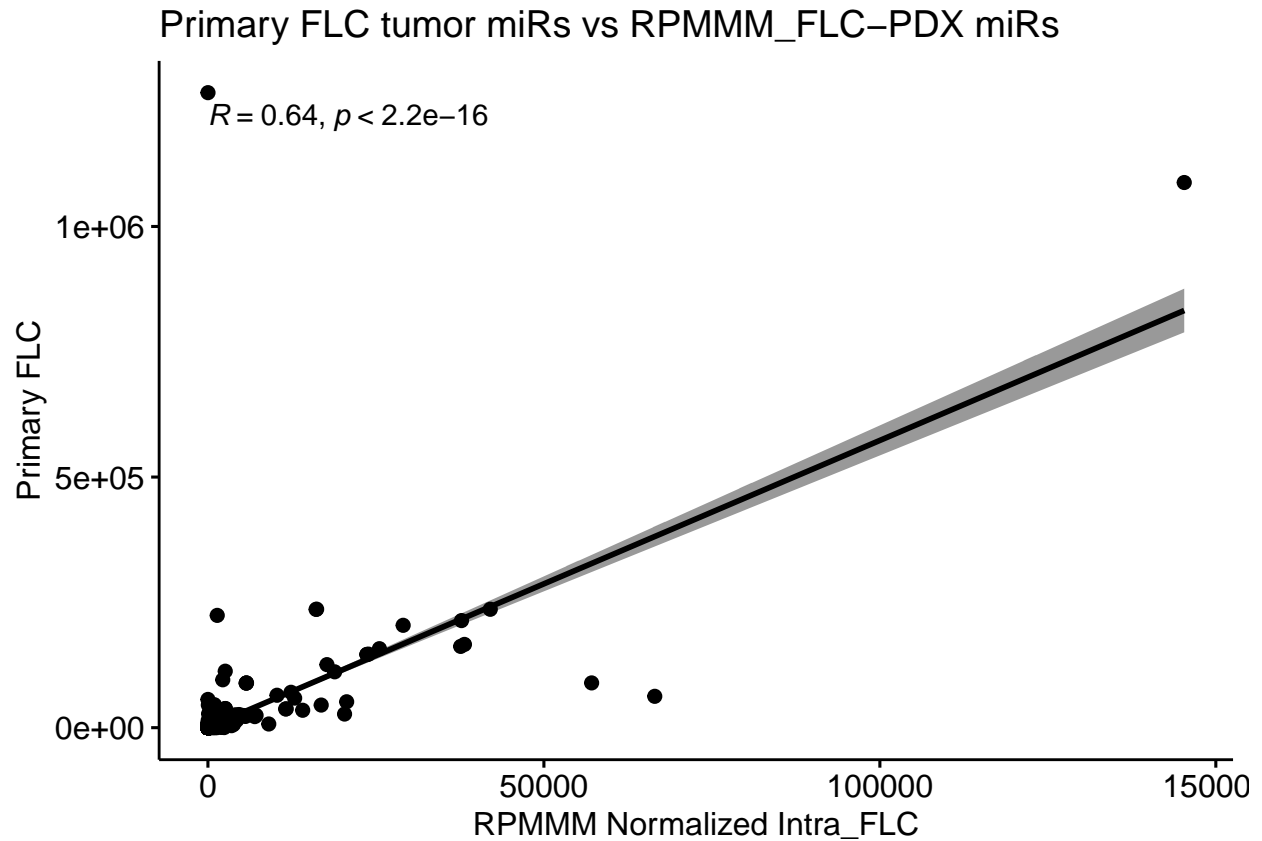
```
f1c.combined.rpmm <- full_join(f1c.intra.rpmm, f1c.pri, by = "miR")
f1c.combined.rpmm[is.na(f1c.combined.rpmm)] <- 0
f1c.combined.rpmm <- column_to_rownames(f1c.combined.rpmm, var = "miR")
f1c.clean.rpmm <- f1c.combined.rpmm[rowSums(f1c.combined.rpmm[])>0,]
```

```
p4 <- ggscatter(f1c.clean.rpmm, x = "AVG_Intra_FLC", y = "avg_PRI",
  add = "reg.line", conf.int = TRUE,
  cor.coef = TRUE, cor.method = "pearson",
  xlab = "RPM Normalized Intra_FLC", ylab = "Primary FLC", title = "Primary FLC tumor miRs vs")

p5 <- ggscatter(f1c.clean.rpmm, x = "AVG_Intra_FLC", y = "avg_PRI",
  add = "reg.line", conf.int = TRUE,
  cor.coef = TRUE, cor.method = "pearson",
  xlab = "log10 RPM Normalized Intra_FLC", ylab = "log10 Primary FLC", title = "log10(Primary
  scale_x_log10() +
  scale_y_log10())
```

p4

## 'geom\_smooth()' using formula 'y ~ x'



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).
```

