

Patient FLC and FLC Spheroid miR correlation

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

Load CSV

```
flc.counts <- read.csv("../NML-PRI-MET_noDups_avg-normalized-counts-by-group.csv")
flc.sphereoids <- read.csv("FLC-PDX_DESeq_miRs.csv")
flc.pri <- flc.counts %>%
  select(miR, avg_PRI)
flc.mets <- flc.counts %>%
  select(miR, avg_MET)
```

Workflow with primary patient FLC primary tumors

```
#Join intracellular sphereoids miRs with primary tumor miRs
flc.combined.pri <- full_join(flc.sphereoids, flc.pri, by = "miR")
#change is.na rows to 0
flc.combined.pri[is.na(flc.combined.pri)] <- 0
#Move the column to rowname. this is necessary for the final clean up step of removing rows that contain
flc.combined.pri <- column_to_rownames(flc.combined.pri, var = "miR")
flc.clean.100 <- flc.combined.pri %>%
  filter_all(any_vars(. > 100))
write.csv(x = flc.clean.100, "PrimaryVsSpheroids100count.csv")
#this is done again with reads at least 50 reads in either column
flc.clean.50 <- flc.combined.pri %>%
  filter_all(any_vars(. > 50))
write.csv(x = flc.clean.50, "PrimaryVsSpheroids50count.csv")
```

```
most.dev.pri.genes <- flc.clean.100 %>%
  rownames_to_column(var = "miR") %>%
  filter(miR %in% c("hsa-mir-122-5p", "hsa-mir-21-5p", "hsa-mir-320a", "hsa-mir-192-5p", "hsa-mir-126-3p"))
```

Plots for primary FLC primary tumors with and without log10 transformation

```
set.seed(1)
p.pri.noclean <- ggscatter(flc.combined.pri, x = "avg_Intra_FLC", y = "avg_PRI",
  add = "reg.line", conf.int = TRUE,
  cor.coef = TRUE, cor.method = "pearson",
  xlab = "FLC Spheroid", ylab = "Primary FLC Tumor", title = "Primary FLC tumor miRs vs FLC-PDX")

p.pri.100 <- ggscatter(flc.clean.100, x = "avg_Intra_FLC", y = "avg_PRI",
  add = "reg.line", conf.int = TRUE,
  cor.coef = TRUE, cor.method = "pearson",
  xlab = "FLC Spheroid", ylab = "Primary FLC Tumor", title = "Primary FLC tumor miRs vs FLC Sph")
geom_label_repel(data = most.dev.pri.genes,
  aes(label = miR),
  size = 3,
  force = 100,
  nudge_y = -30000)

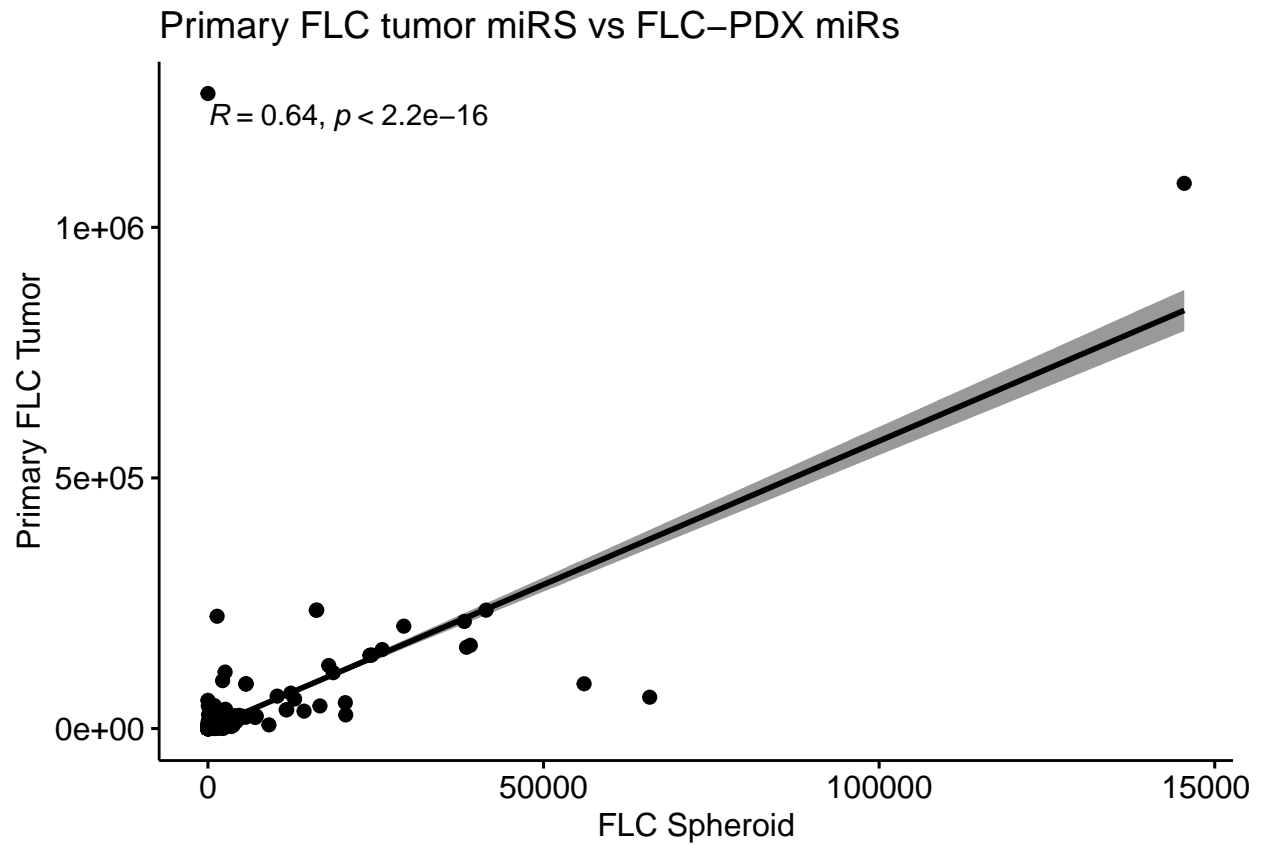
p.pri.100.log10 <- ggscatter(flc.clean.100, x = "avg_Intra_FLC", y = "avg_PRI",
  add = "reg.line", conf.int = TRUE,
  cor.coef = TRUE, cor.method = "pearson",
  xlab = "log10 FLC Spheroid", ylab = "log 10 Primary FLC", title = "log10(Primary FLC tumor miRs vs FLC Sph")
scale_x_log10() +
scale_y_log10() +
geom_label_repel(data = most.dev.pri.genes,
  aes(label = miR),
  size = 3) +
geom_label_repel(data = most.dev.pri.genes,
  aes(label = miR),
  size = 3,
  nudge_y = -1)

p.pri.50 <- ggscatter(flc.clean.50, x = "avg_Intra_FLC", y = "avg_PRI",
  add = "reg.line", conf.int = TRUE,
  cor.coef = TRUE, cor.method = "pearson",
  xlab = "FLC Spheroid", ylab = "Primary FLC Tumor", title = "Primary FLC tumor miRs vs FLC Sph")
geom_label_repel(data = most.dev.pri.genes,
  aes(label = miR),
  size = 3,
  force = 100,
  nudge_y = -30000)

p.pri.50.log10 <- ggscatter(flc.clean.50, x = "avg_Intra_FLC", y = "avg_PRI",
  add = "reg.line", conf.int = TRUE,
  cor.coef = TRUE, cor.method = "pearson",
  xlab = "log10 FLC Spheroid", ylab = "log 10 Primary FLC Tumor", title = "log10(Primary FLC tumor miRs vs FLC Sph")
scale_x_log10() +
scale_y_log10() +
geom_label_repel(data = most.dev.pri.genes,
  aes(label = miR),
  size = 3,
  nudge_y = -1)
```

```
p.pri.noclean
```

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

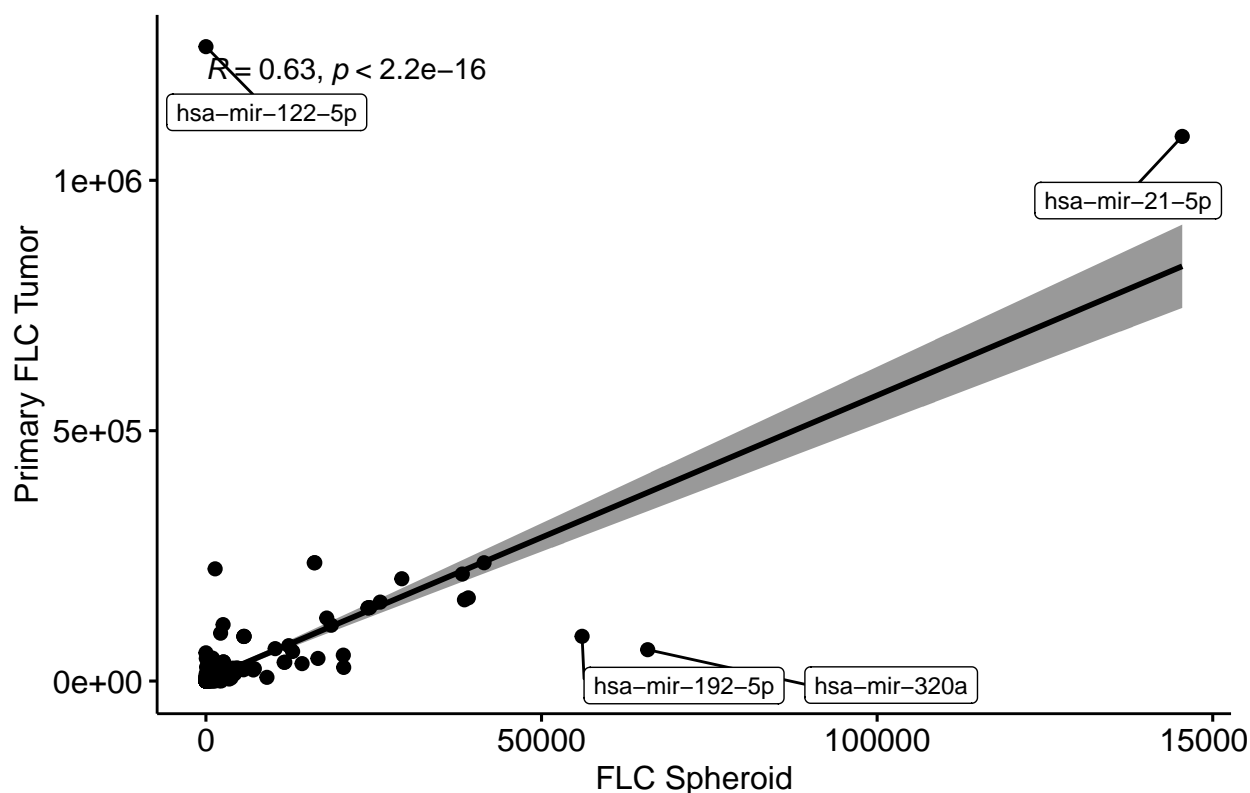


```
p.pri.100
```

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

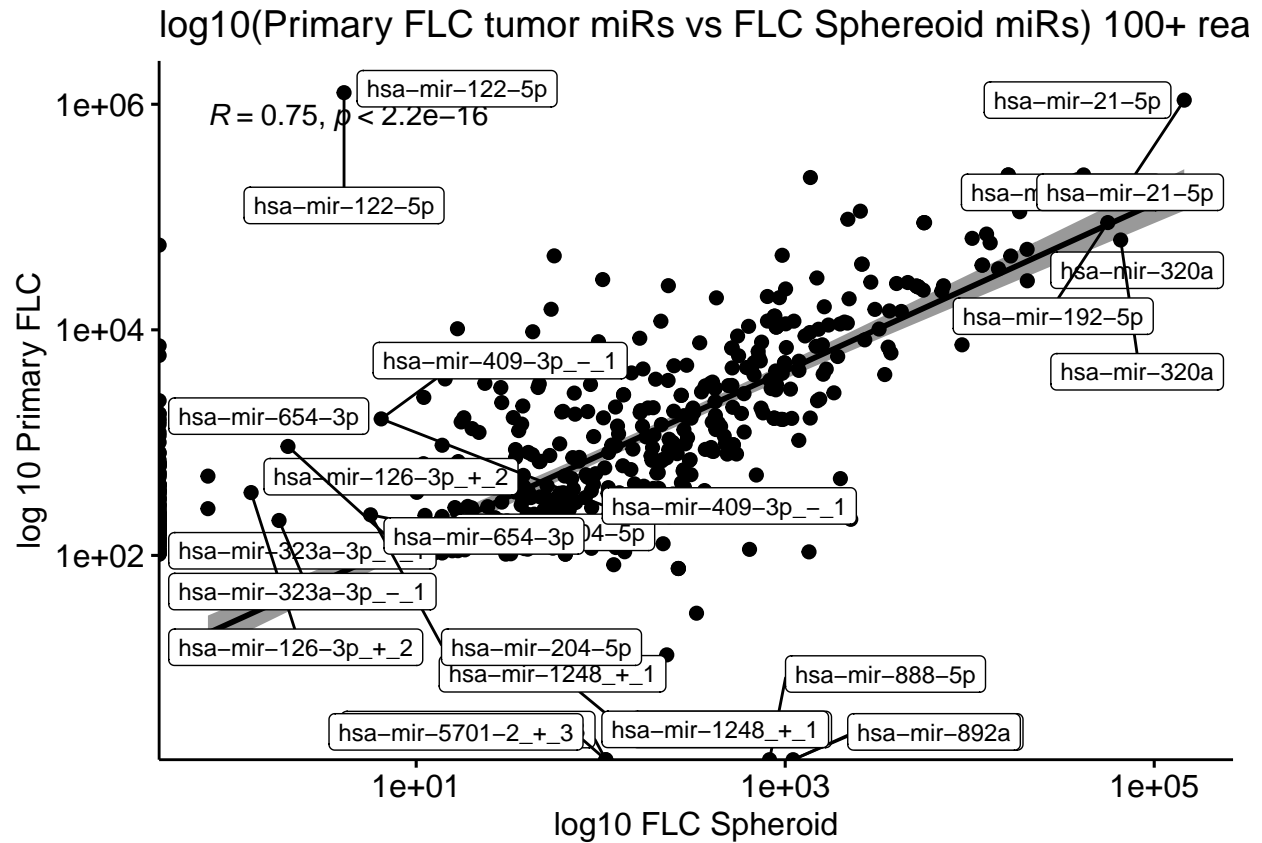
```
## Warning: ggrepel: 9 unlabeled data points (too many overlaps). Consider  
## increasing max.overlaps
```

Primary FLC tumor miRs vs FLC Spheroid miRs – 100+ reads in



```
p.pri.100.log10
```

```
## 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
## Warning: Transformation introduced infinite values in continuous y-axis
## Warning: Transformation introduced infinite values in continuous y-axis
## 'geom_smooth()' using formula 'y ~ x'
## Warning: Removed 119 rows containing non-finite values (stat_smooth).
## Warning: Removed 119 rows containing non-finite values (stat_cor).
```

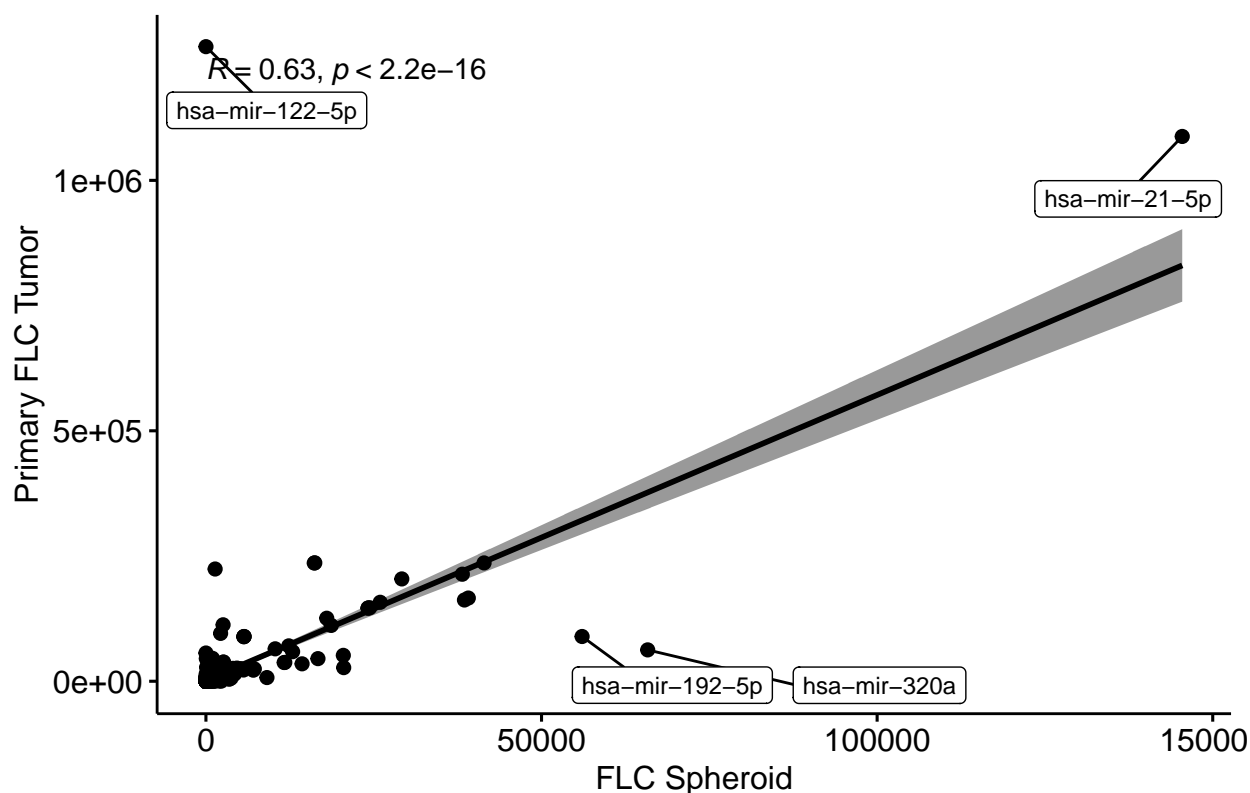


p.pri.50

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

```
## Warning: ggrepel: 9 unlabeled data points (too many overlaps). Consider
## increasing max.overlaps
```

Primary FLC tumor miRs vs FLC Spheroid miRs – 50+ reads in a



```
p.pri.50.log10
```

```
## 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
## Warning: Transformation introduced infinite values in continuous y-axis
## 'geom_smooth()' using formula 'y ~ x'
## Warning: Removed 213 rows containing non-finite values (stat_smooth).
## Warning: Removed 213 rows containing non-finite values (stat_cor).
```



```

p.met.100 <- ggscatter(flc.clean.mets.100, x = "avg_Intra_FLC", y = "avg_MET",
  add = "reg.line", conf.int = TRUE,
  cor.coef = TRUE, cor.method = "pearson",
  xlab = "FLC Spheroid", ylab = "Metastatic FLC Tumor", title = "Metastatic FLC tumor miRs vs FLC",
  geom_label_repel(data = most.dev.met.genes,
    aes(label = miR),
    size = 3,
    force = 100,
    nudge_x = 30000,
    nudge_y = 300000)

p.met.100.log10 <- ggscatter(flc.clean.mets.100, x = "avg_Intra_FLC", y = "avg_MET",
  add = "reg.line", conf.int = TRUE,
  cor.coef = TRUE, cor.method = "pearson",
  xlab = "log10 FLC SpheroidC", ylab = "log10 Metastatic FLC Tumor", title = "log10(Metastatic FLC tumor miRs vs FLC)",
  scale_x_log10() +
  scale_y_log10() +
  geom_text_repel(data = most.dev.met.genes,
    aes(label = miR),
    size = 3,
    force = 100,
    nudge_y = .5)

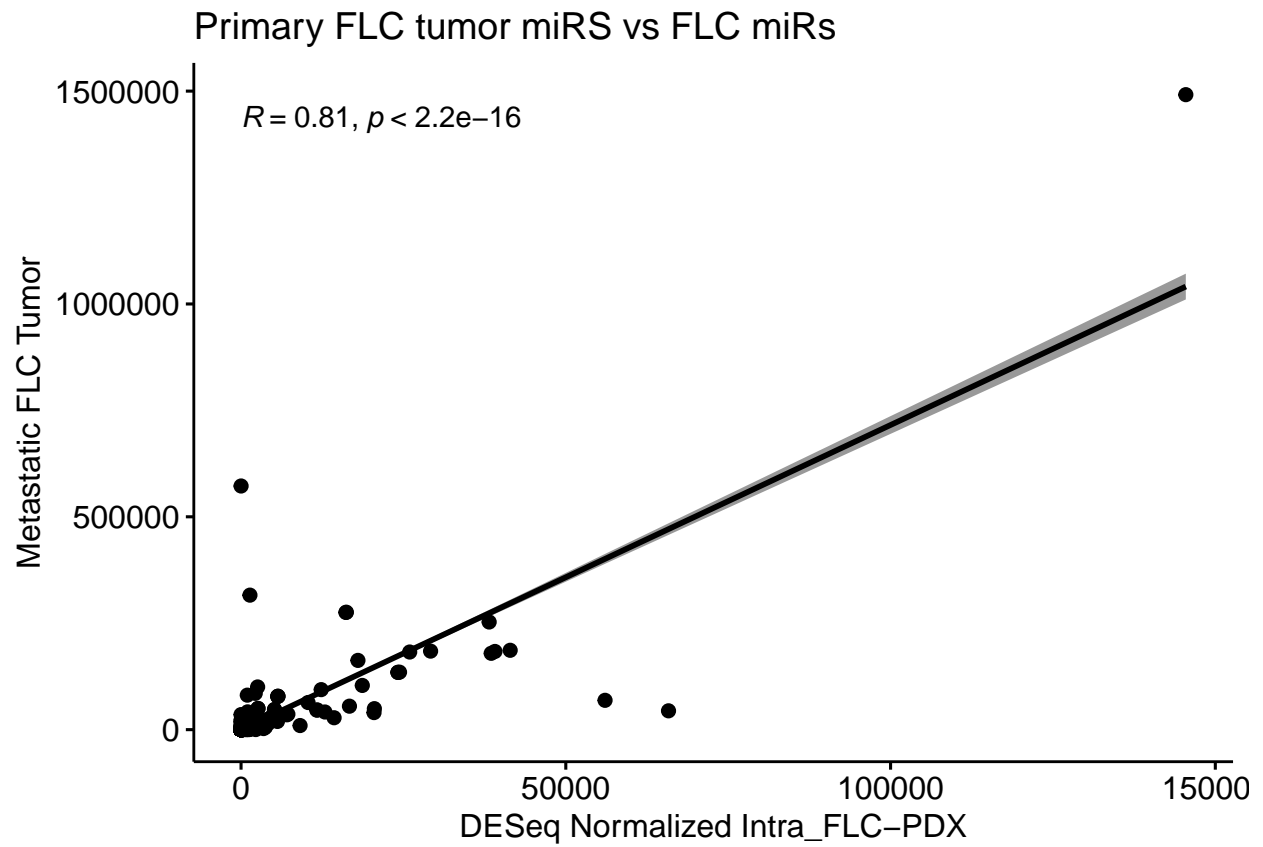
p.met.50 <- ggscatter(flc.clean.mets.50, x = "avg_Intra_FLC", y = "avg_MET",
  add = "reg.line", conf.int = TRUE,
  cor.coef = TRUE, cor.method = "pearson",
  xlab = "FLC Spheroid", ylab = "Metastatic FLC Tumor", title = "Metastatic FLC tumor miRs vs FLC",
  geom_label_repel(data = most.dev.met.genes,
    aes(label = miR),
    size = 3,
    force = 100,
    nudge_x = 30000,
    nudge_y = 300000)

p.met.50.log10 <- ggscatter(flc.clean.mets.50, x = "avg_Intra_FLC", y = "avg_MET",
  add = "reg.line", conf.int = TRUE,
  cor.coef = TRUE, cor.method = "pearson",
  xlab = "log10 FLC Spheroid", ylab = "log10 Metastatic FLC Tumor", title = "log10(Metastatic FLC tumor miRs vs FLC)",
  scale_x_log10() +
  scale_y_log10() +
  geom_text_repel(data = most.dev.met.genes,
    aes(label = miR),
    size = 3,
    force = 100,
    nudge_y = .5)

p.met.noclean

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

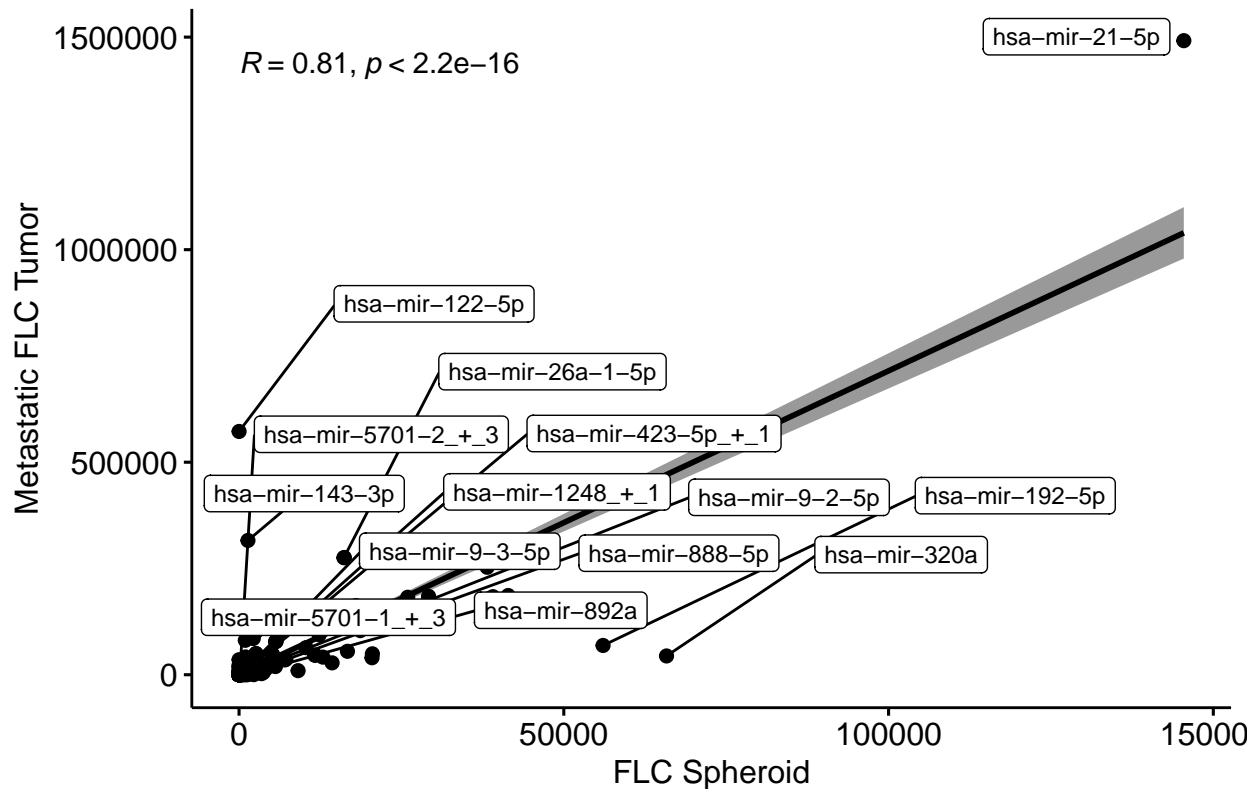
```

p.met.100

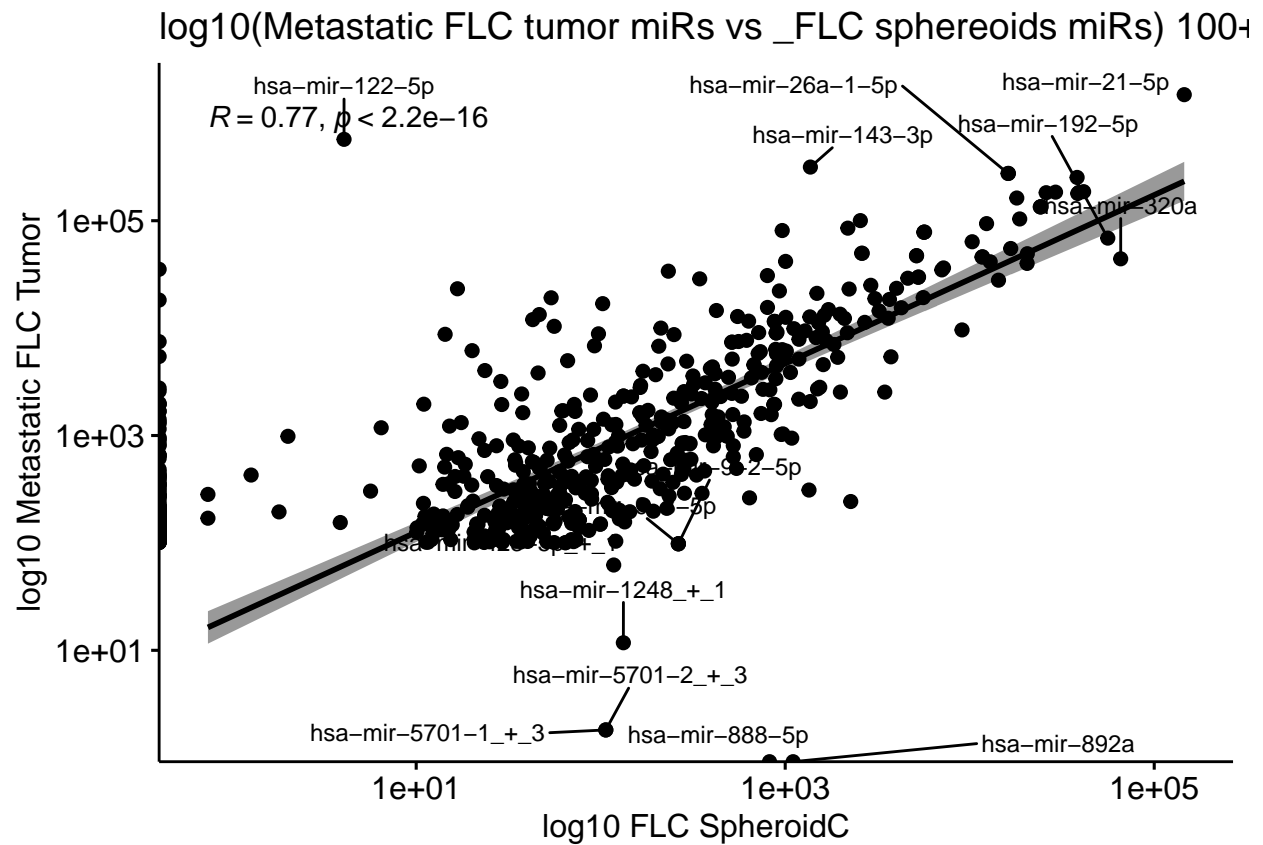
```
## 'geom_smooth()' using formula 'y ~ x'
```

Metastatic FLC tumor miRs vs FLC sphereoids miRs – 100+ rea



p.met.100.log10

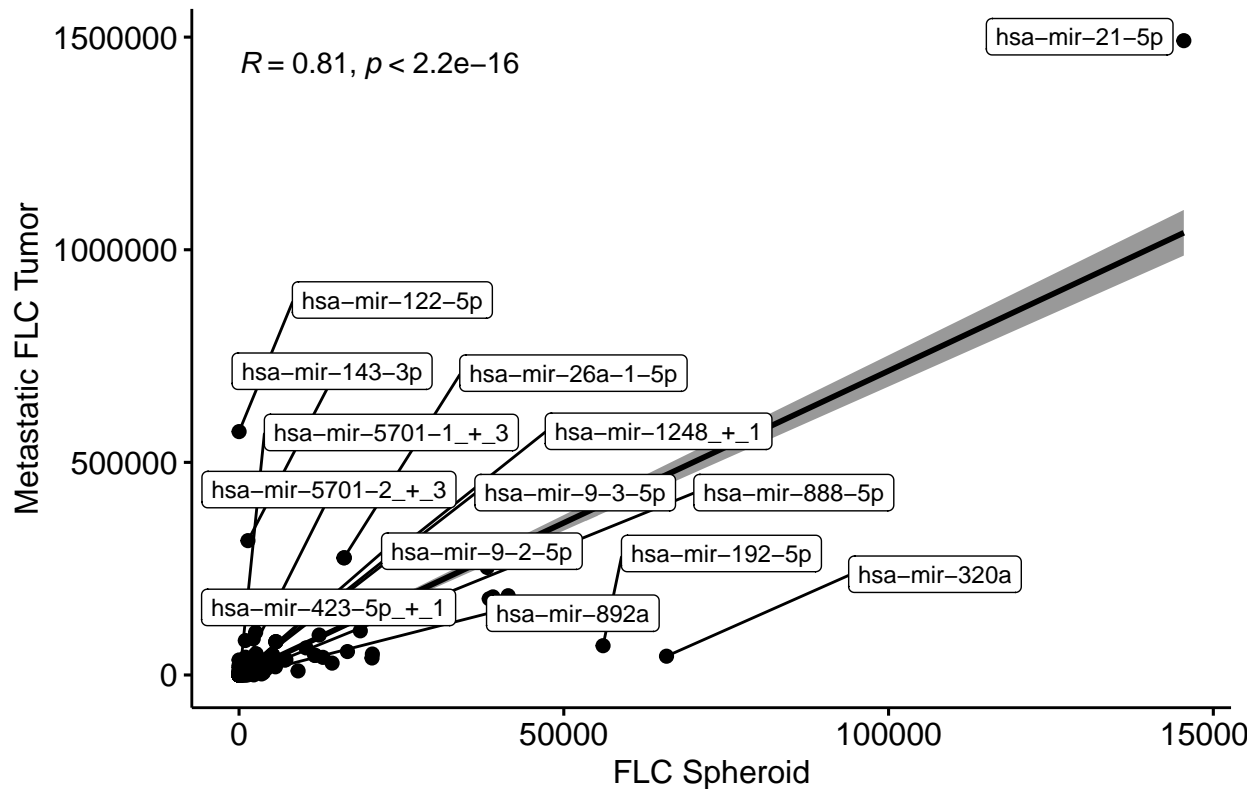
```
## Warning: Transformation introduced infinite values in continuous x-axis
## Warning: Transformation introduced infinite values in continuous y-axis
## Warning: Transformation introduced infinite values in continuous x-axis
## Warning: Transformation introduced infinite values in continuous y-axis
## Warning: Transformation introduced infinite values in continuous x-axis
## Warning: Transformation introduced infinite values in continuous y-axis
## Warning: Transformation introduced infinite values in continuous y-axis
## 'geom_smooth()' using formula 'y ~ x'
## Warning: Removed 120 rows containing non-finite values (stat_smooth).
## Warning: Removed 120 rows containing non-finite values (stat_cor).
```



p.met.50

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

Metastatic FLC tumor miRs vs FLC sphereoids miRs – 50+ read



p.met.50.log10

```
## 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
## Warning: Transformation introduced infinite values in continuous y-axis
## 'geom_smooth()' using formula 'y ~ x'
## Warning: Removed 203 rows containing non-finite values (stat_smooth).
## Warning: Removed 203 rows containing non-finite values (stat_cor).
```

