

```
1 library(ggplot2)~
2 setwd("~/Dropbox/Luciferase")~
3 prolif <- read.table("figure2.csv", header=T, sep=",")~
4 ~
5 gene <- rep(names(prolif)[4:7], each=dim(prolif)[1])~
6 value <- unlist(c(prolif[4:7]))~
7 cdata <- rbind(rbind(rbind(prolif[1:3], prolif[1:3]), prolif[1:3]),
. prolif[1:3])~
8 clean_data <- data.frame(cbind(cdata, gene, value))~
9 jit <- position_jitter(height = 0.2)~
10 ~
11 reduced_data <- clean_data[clean_data$gene!='pre.31.GAPDH',]~
12 levels(reduced_data$gene) <- c('LOC554202', 'miR31', 'GAPDH', 'pre-miR31')~
13 p1 <- ggplot(reduced_data, aes(Treatment, value)) + geom_boxplot() +
. facet_grid(gene ~ ., scales="free")~
14 p1 <- ggplot(reduced_data, aes(Treatment, value)) + geom_histogram() +
. facet_grid(gene ~ ., scales="free")~
15 p1 + ylab("expression") + xlab("") + theme_set(theme_bw()) +
. geom_abline(intercept=1, linetype="dashed", slope=0, color="grey") +
. opts(panel.grid.major=theme_blank(), panel.grid.minor=theme_blank())~
16 ~
17 ~
18
```