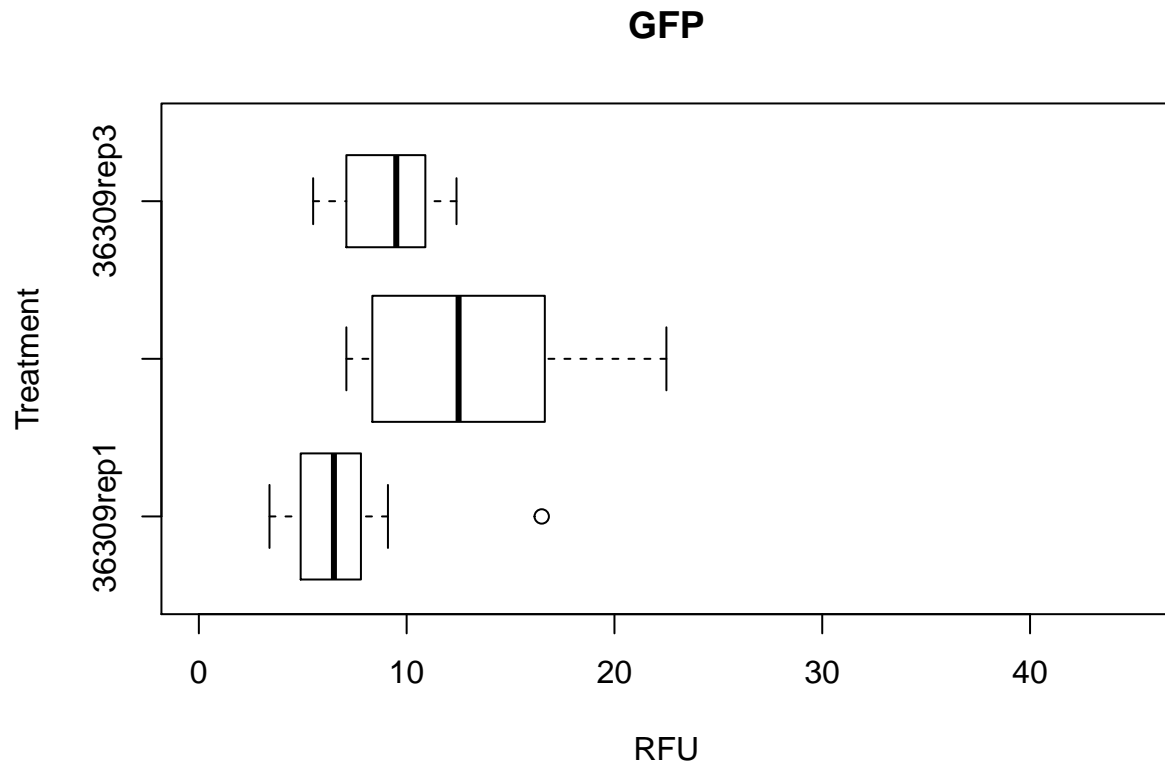
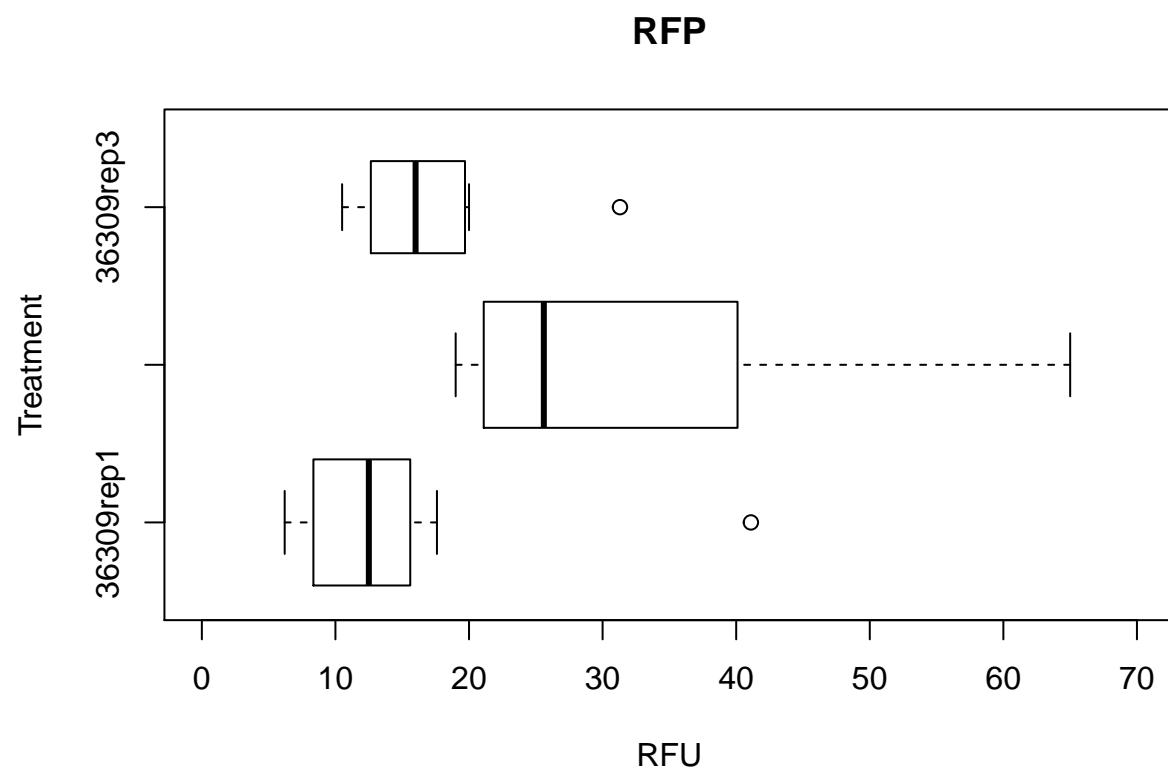


RdatAI190330

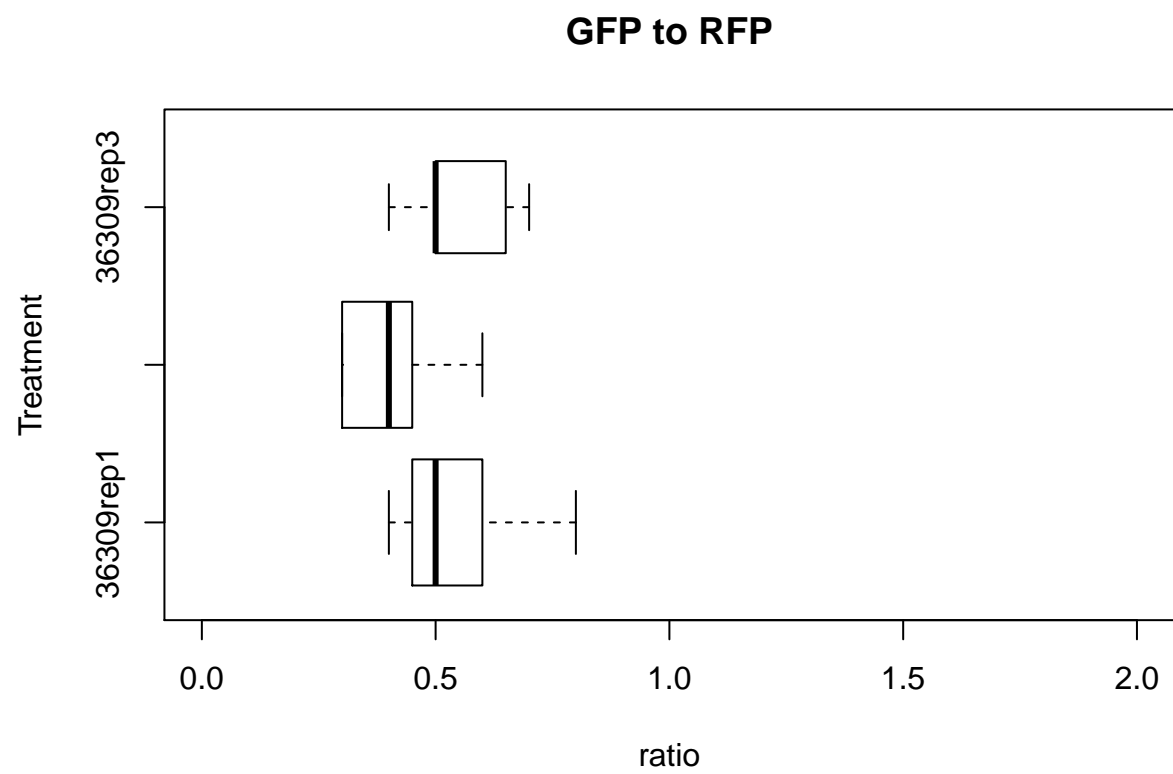
```
EC36309data1 <- read.table("Merge190320w190322w190330.csv", header=TRUE,  
                           sep=",") # merged fluorecence data of EC36309 treatments, three independent ex  
attach(EC36309data1)  
  
boxplot(GFP~ID, data=EC36309data1, main="GFP",horizontal=TRUE, varwidth=TRUE, xlab="RFU", ylab="Treatment
```



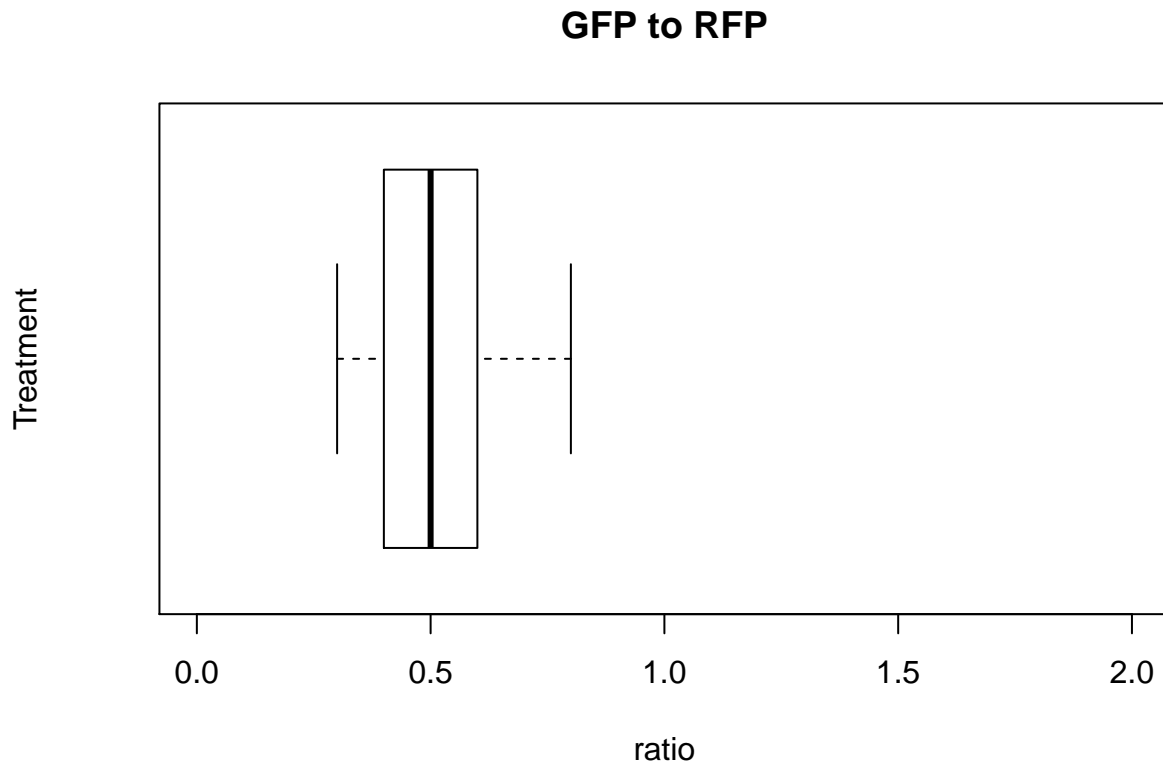
```
boxplot(RFP~ID, data=EC36309data1, main="RFP", horizontal=TRUE, varwidth=TRUE, xlab="RFU", ylab="Treatment
```



```
boxplot(GFP.RFP~ID, data=EC36309data1, main="GFP to RFP", horizontal=TRUE, varwidth=TRUE, xlab="ratio",
```



```
boxplot(GFP.RFP, data=EC36309data1, main="GFP to RFP", horizontal=TRUE, varwidth=TRUE, xlab="ratio", ylab="Treatment")
```



```
summary(EC36309data1)
```

```
##          ID          GFP          RFP          GFP.RFP
## 36309rep1:15  Min.   : 3.400  Min.   : 6.20  Min.   :0.3000
## 36309rep2:15  1st Qu.: 6.825  1st Qu.:12.62  1st Qu.:0.4000
## 36309rep3: 8  Median : 8.350  Median :18.30  Median :0.5000
##              Mean    : 9.787  Mean    :21.99  Mean    :0.4868
##              3rd Qu.:12.175  3rd Qu.:25.50  3rd Qu.:0.6000
##              Max.    :22.500  Max.    :65.00  Max.    :0.8000
```

```
sd(EC36309data1$GFP.RFP, na.rm = FALSE) # combined mean 36309 GFP/RFP, n=38, mean=0.49, sd=0.13
```

```
## [1] 0.1298045
```

Including data on EC36309 from third independent experiment, $n = 8$, mean GFP/RFP ratio converges more towards 0.5.

CRISPR treatments 9-18, 9-19 and 9-20 again unusable due to HR.

CRISPR validation:

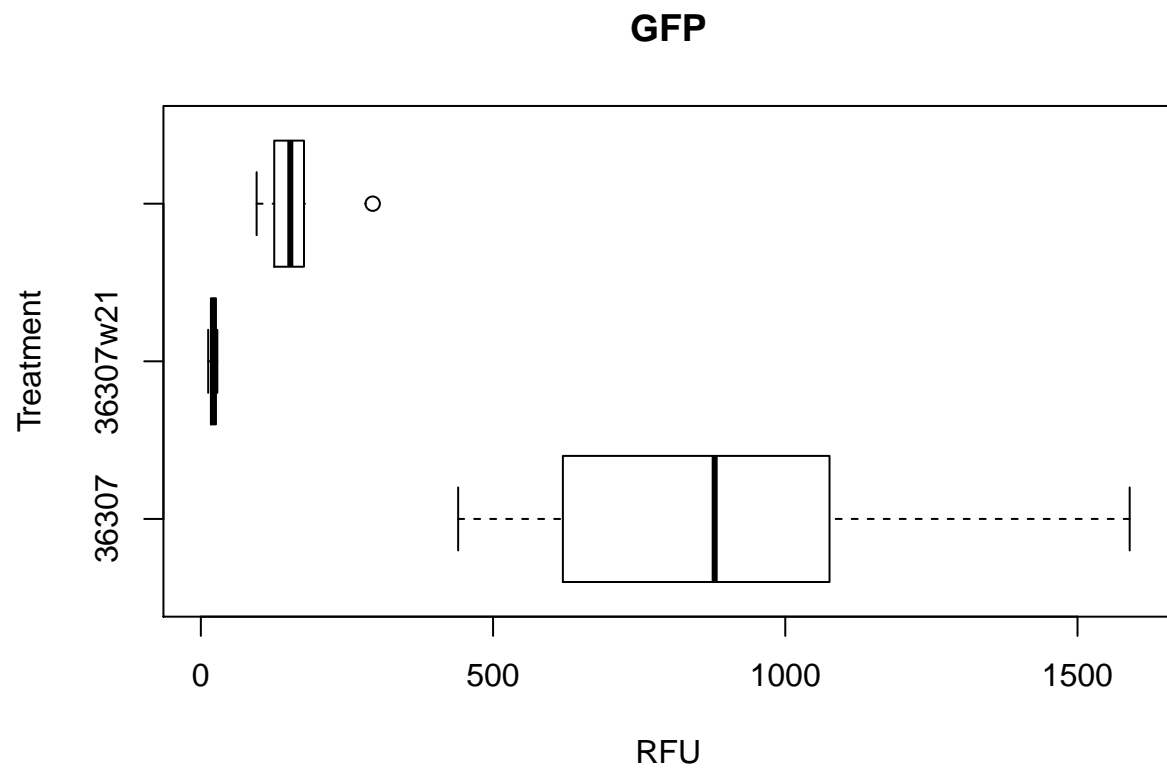
```
EC36307data1 <- read.table("36307dat.csv", header=TRUE,
                           sep=",") # fluorescence data of 36307 CRISPR treatments
attach(EC36307data1)
```

```
## The following objects are masked from EC36309data1:
```

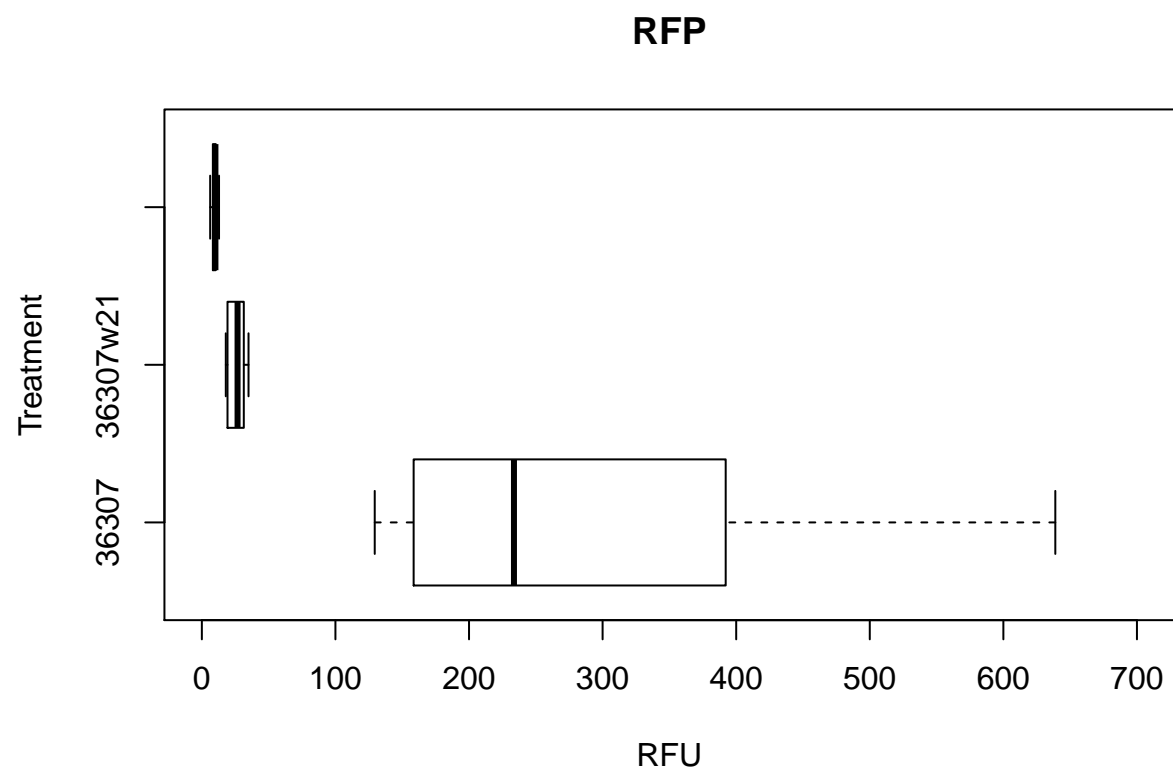
```
##
```

```
## GFP, GFP.RFP, ID, RFP
```

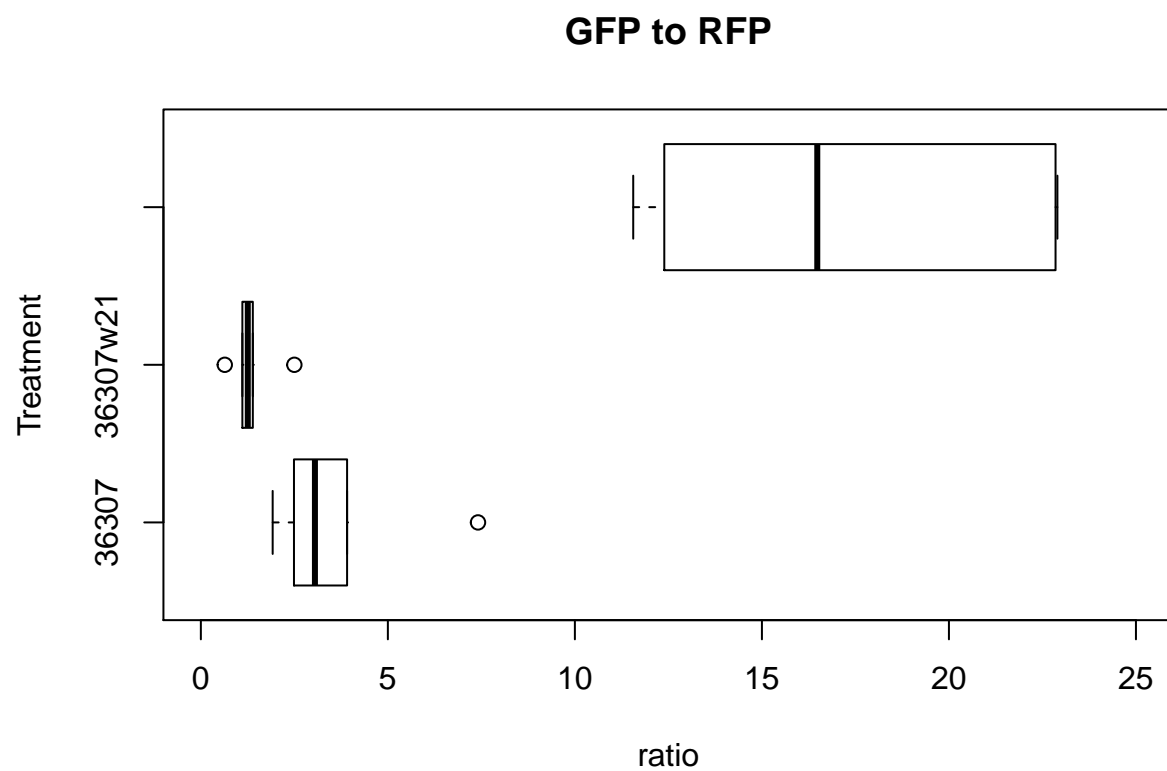
```
boxplot(GFP~ID, data=EC36307data1, main="GFP",horizontal=TRUE, varwidth=TRUE, xlab="RFU", ylab="Treatment")
```



```
boxplot(RFP~ID, data=EC36307data1, main="RFP", horizontal=TRUE, varwidth=TRUE, xlab="RFU", ylab="Treatment")
```



```
boxplot(GFP.RFP~ID, data=EC36307data1, main="GFP to RFP", horizontal=TRUE, varwidth=TRUE, xlab="ratio",
```



```
boxplot(GFP.RFP, data=EC36307data1, main="GFP to RFP", horizontal=TRUE, varwidth=TRUE, xlab="ratio", ylab="Treatment")
```

GFP to RFP

