eRNA and mRNA

Andrew Holding

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Effect of GRHL2 overexpression on eRNA transcription

```
library("ggpubr")
```

```
eRNA<-read.csv("txt/eRNA_values.csv")

oe<-eRNA[eRNA$Experiment=="overexpression",]

oe_comparisons <- list( c("Control","GRHL2") )
oe_p <- ggboxplot(oe, x = "Treatment", y = "eRNA",
               add = "jitter", color="Treatment",
               facet.by="Gene", ylab="Relative eRNA levels")
oe_p <- oe_p + stat_compare_means(comparisons = oe_comparisons,
                        method = "wilcox.test" ,
                        paired=TRUE)
oe_p
```

Effect of GRHL2 knockdown on eRNA transcription

```
si<-eRNA[eRNA$Experiment=="knockdown",]

si_comparisons <- list( c("siCtrl","siGRHL2") )
p <- ggboxplot(si, x = "Treatment", y = "eRNA",
               add = "jitter", color="Treatment",
               facet.by="Gene", ylab="Relative eRNA levels")
p + stat_compare_means(comparisons = si_comparisons,
                        method = "wilcox.test" ,
                        paired = TRUE)
```

siRNA combined test

```
wilcox.test(si$eRNA[si$Treatment=='siCtrl'],
            si$eRNA[si$Treatment=='siGRHL2'],
            paired=TRUE, alternative="less")
```

```
##
##  Wilcoxon signed rank test
##
## data:  si$eRNA[si$Treatment == "siCtrl"] and si$eRNA[si$Treatment == "siGRHL2"]
## V = 45, p-value = 0.04071
## alternative hypothesis: true location shift is less than 0
```

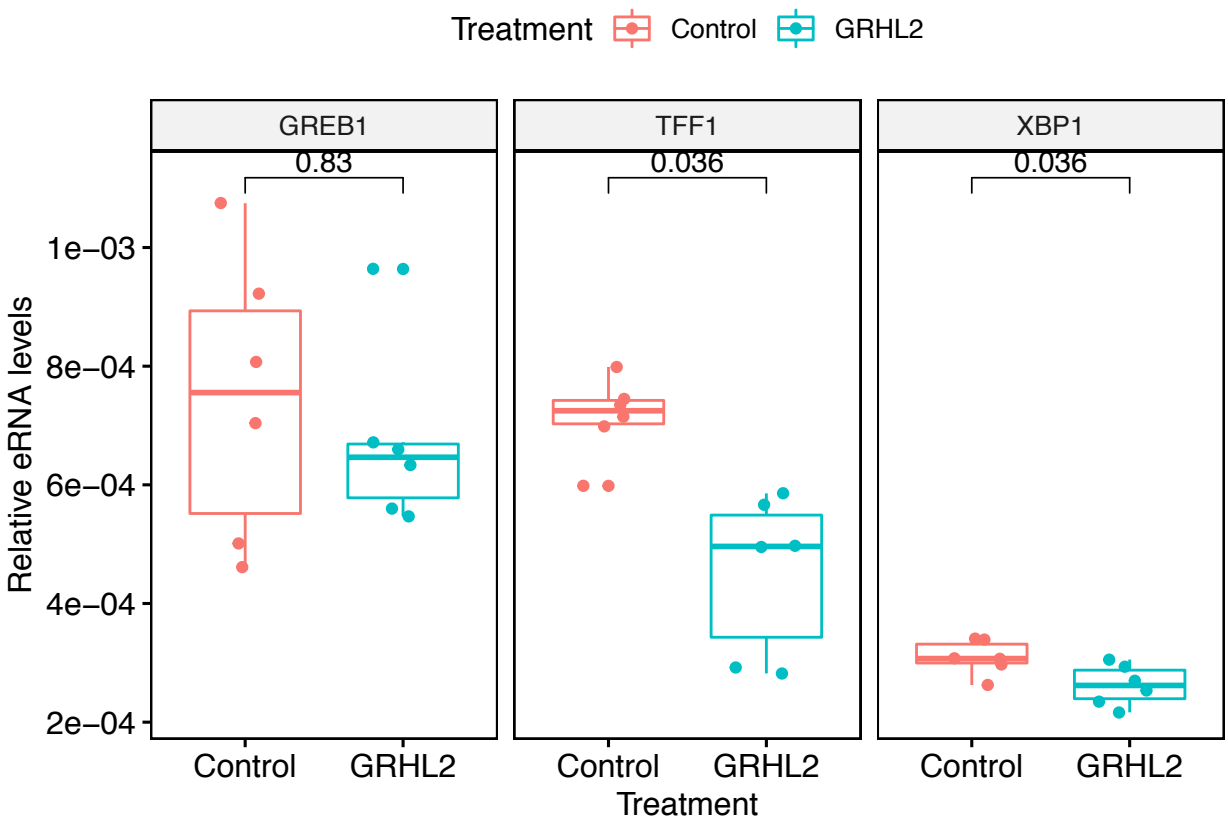

Figure 1: Effect of Overexpression of GRHL2 on eRNA at E2 responsive binding sites.

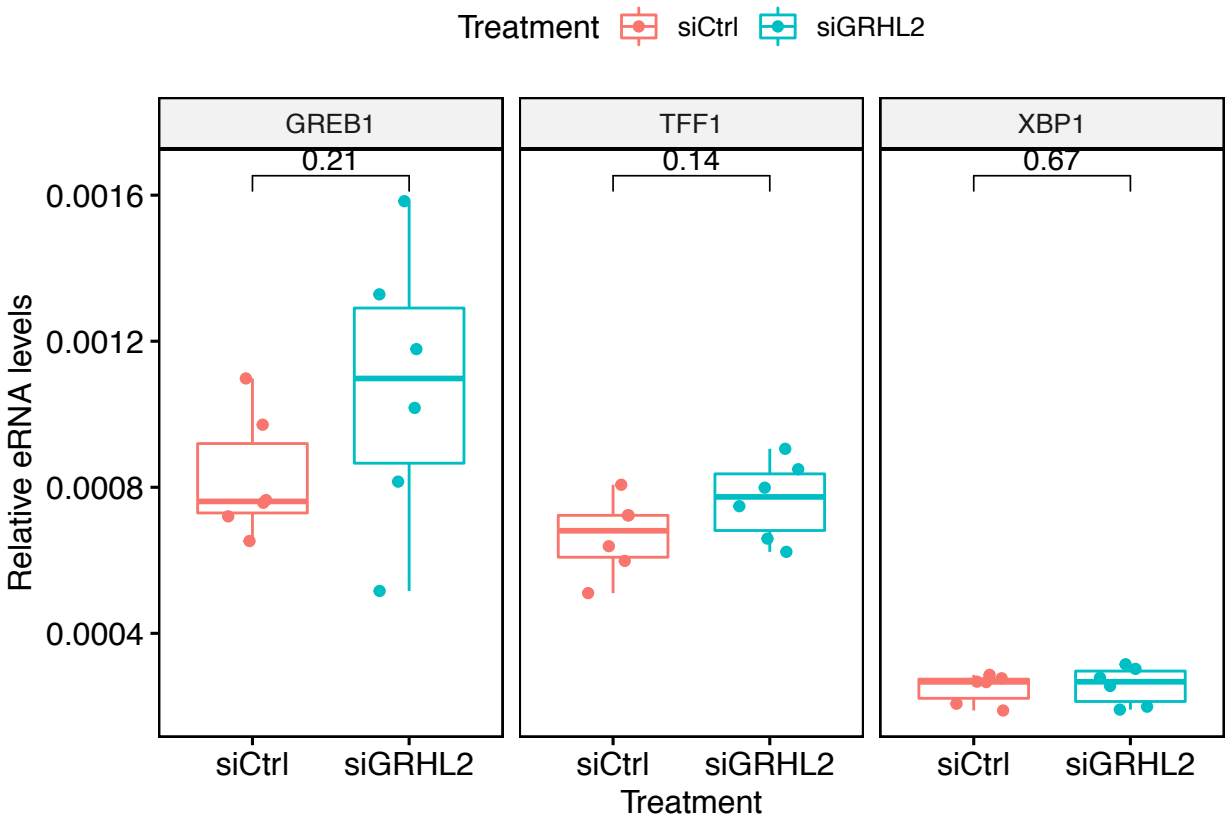

Figure 2: Effect of knockdown of GRHL2 on eRNA at E2 responsive binding sites.

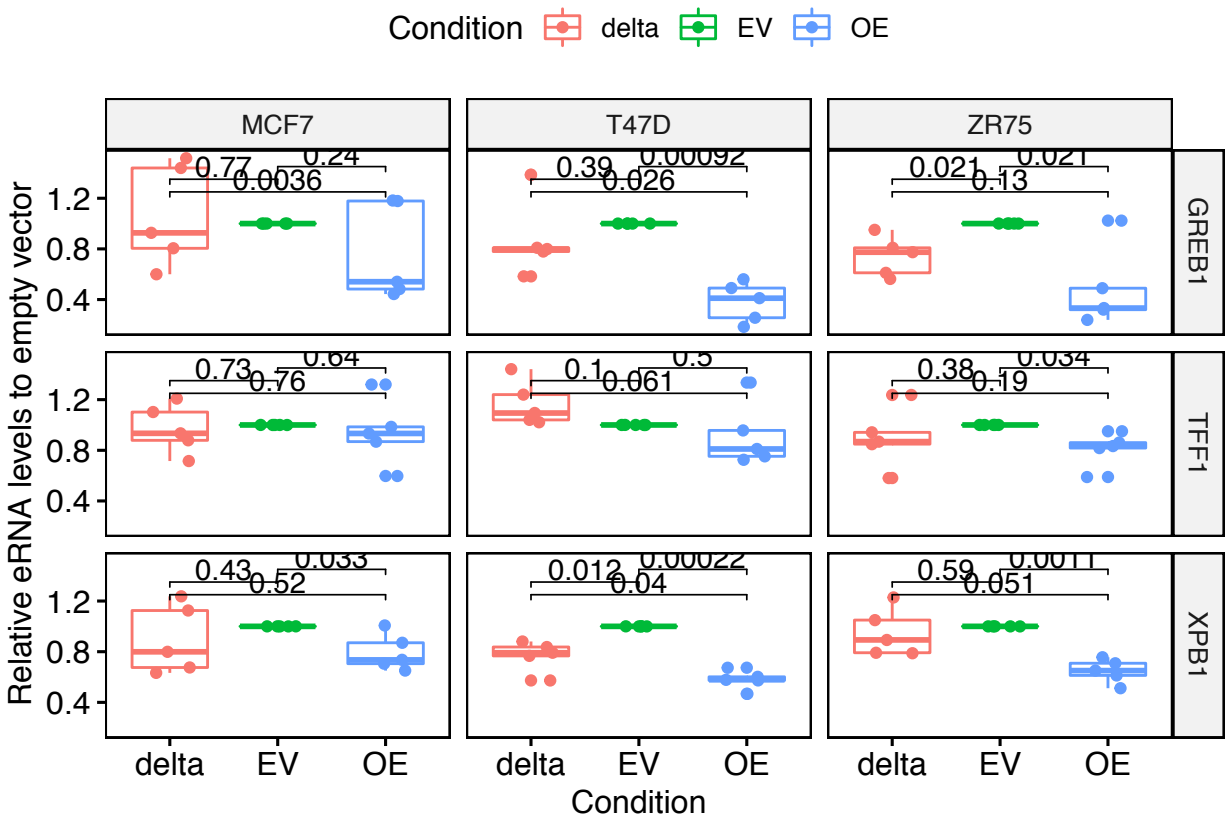

Figure 3: Overexpression of GRHL2 delta 425-437.

Effect of GRHL2 and GRLH2 delta 425-437 overexpression on eRNA transcription

```
eRNA<-read.csv("txt/oe.csv")

eRNA<-eRNA[1:135,]

p <- ggboxplot(eRNA, x = "Condition", y = "Fold",
                   add = "jitter", color="Condition",
                   facet.by=c("Gene","CellTye"),ylab="Relative eRNA levels to empty vector")
comp.ev<-list(c("delta","OE"),c("delta","EV"),c("EV","OE"))
p2<-p + stat_compare_means(comparisons=comp.ev,
                           method = "t.test",paired=TRUE,alternative="greater",label.y=c(1.25,1.35,1.45)
p2
```