ABT263 Effects on Gene Expression in CCDs Treated with TGFbeta.Rmd

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Read in data

Plot the Gene Expression data for powerpoint

```
## Saving 9 x 4 in image
```

Make a cool table

```
ccdgenedata %>%
  filter(Category == "TGFb") %>%
  mutate(max_col = mean(Col1A1))
```

```
## # A tibble: 16 x 6
##    Category Col1A1  MYLK   FN1 ACTA2 max_col
##    <ord>     <dbl> <dbl> <dbl> <dbl>   <dbl>
##  1 TGFb       5.18  3.56  5.20 3.40     2.48
##  2 TGFb       3.61  2.77  4.67 3.39     2.48
##  3 TGFb       2.02  2.14  3.87 2.99     2.48
##  4 TGFb       2.27  3.89  9.56 2.51     2.48
##  5 TGFb       2.51  2.49  5.90 1.99     2.48
##  6 TGFb       1.42  4.52  6.94 1.61     2.48
##  7 TGFb       2.11  2.12  3.90 1.66     2.48
##  8 TGFb       1.77  1.70  3.34 1.27     2.48
##  9 TGFb       1.89  2.91  5.39 1.85     2.48
## 10 TGFb       2.79  4.15  7.33 2.66     2.48
## 11 TGFb       2.23  2.82  4.46 1.62     2.48
## 12 TGFb       1.90  2.80  3.82 1.60     2.48
## 13 TGFb       2.03  2.35  4.85 1.44     2.48
## 14 TGFb       2.81  2.58  3.17 0.757    2.48
## 15 TGFb       3.30  2.90  4.47 1.43     2.48
## 16 TGFb       1.86  2.08  4.12 1.25     2.48
```

```
ccdgenedata %>%
  filter(Category == "Untreated") %>%
  mutate(min_col = mean(Col1A1)) %>%
  summarize(col_base = mean(min_col))
```

```
## # A tibble: 1 x 1
##   col_base
##      <dbl>
## 1     1.06
```

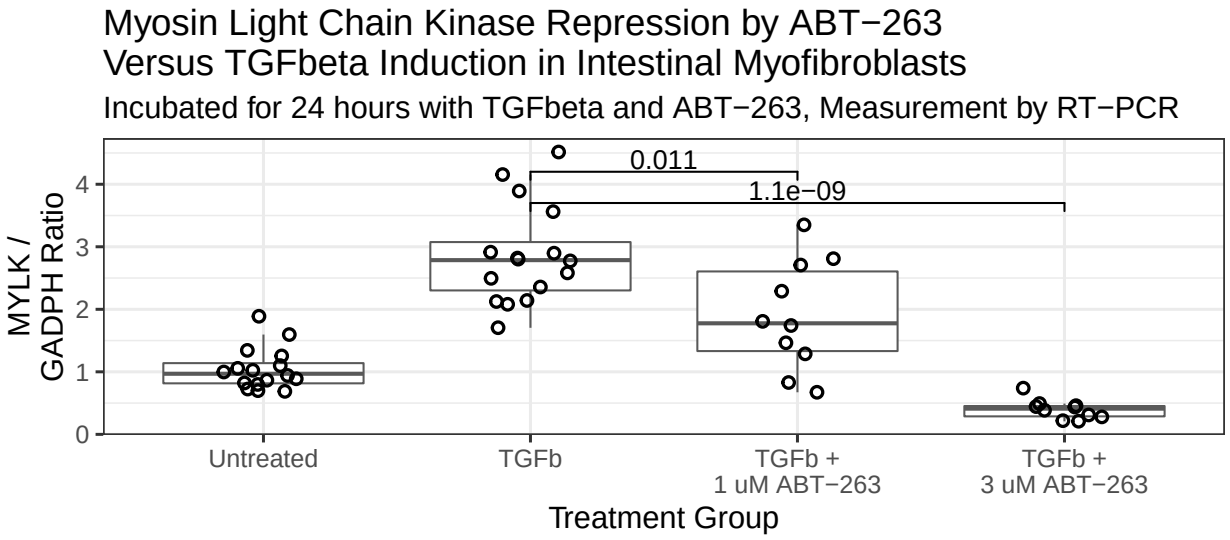

Figure 1: ABT-263 Gene Expr vs TGFb