Sample 1

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Background

```
rawcount <- read_csv("../data/sample1.csv")
head(rawcount)
```

```
## # A tibble: 6 x 4
##   id      sgRNA                                                T0   T20
##   <chr>   <chr>                                             <dbl> <dbl>
## 1 sample1 mcf7_unique:TSS100024_-_17662045.23-CUFF.46609.1  1383     1
## 2 sample1 mcf7_unique:TSS100024_-_17662051.23-CUFF.46609.1  1229   304
## 3 sample1 mcf7_unique:TSS100024_-_17662250.23-CUFF.46609.1  1265   602
## 4 sample1 mcf7_unique:TSS100024_-_17662267.23-CUFF.46609.1  2897    10
## 5 sample1 mcf7_unique:TSS100024_+_17661984.23-CUFF.46609.1    67   264
## 6 sample1 mcf7_unique:TSS100024_+_17662123.23-CUFF.46609.1    90     0
```

we sent 10 samples to XYZ lab for expression profiles from NUMBER2 genes. the file is returned with the following column names `id, sgRNA, T0, T20`. We used the methods from (Breitling et al. 2004) in our analysis and maybe use the bioconductor package (Gentleman et al. 2004)

Summary

```
## Tidying
gene_dat <- rawcount %>%
  # separate the sgRNA column into multiple new columns based on the "_" character as a delimiter
    separate(col = sgRNA, into = c("something","TSS", "strand", "probe_gene"), sep = "_") %>%

  # separate the column that has the probe and gene info into two columns based on the "-" character
    separate(col = probe_gene, into = c("probe", "name"), sep = "-") %>%

  # remove wording from TSS
    mutate(TSS = str_remove(TSS, pattern = "unique:")) %>%

  ## mutate
  # Calculate fold change/ probe by using T20/T0
  mutate(fold_change = T20 / T0)

head(gene_dat)
```

```
## # A tibble: 6 x 9
##   id      something TSS      strand probe     name          T0   T20 fold_change
##   <chr>   <chr>     <chr>    <chr>  <chr>     <chr>      <dbl> <dbl>       <dbl>
## 1 sample1 mcf7      TSS1000~ -      17662045~ CUFF.4660~  1383     1    0.000723
## 2 sample1 mcf7      TSS1000~ -      17662051~ CUFF.4660~  1229   304    0.247
## 3 sample1 mcf7      TSS1000~ -      17662250~ CUFF.4660~  1265   602    0.476
## 4 sample1 mcf7      TSS1000~ -      17662267~ CUFF.4660~  2897    10    0.00345
## 5 sample1 mcf7      TSS1000~ +      17661984~ CUFF.4660~    67   264    3.94
## 6 sample1 mcf7      TSS1000~ +      17662123~ CUFF.4660~    90     0    0
```

```
# join our probe data to the output
probe <- read_delim("../data/probes.csv", delim = "\t")

#head(probe)

gene_dat <- gene_dat %>%
  left_join(.,probe) %>%
  select(-something)

head(gene_dat)
```

```
## # A tibble: 6 x 12
##   id    TSS   strand probe name     T0   T20 fold_change   chr  start    end
##   <chr> <chr> <chr>  <chr> <chr> <dbl> <dbl>       <dbl> <dbl>  <dbl>  <dbl>
## 1 samp~ TSS1~ -      1766~ CUFF~  1383     1    0.000723     4 8.81e7 8.82e7
## 2 samp~ TSS1~ -      1766~ CUFF~  1229   304    0.247        4 8.81e7 8.82e7
## 3 samp~ TSS1~ -      1766~ CUFF~  1265   602    0.476        4 8.81e7 8.82e7
## 4 samp~ TSS1~ -      1766~ CUFF~  2897    10    0.00345      4 8.81e7 8.82e7
## 5 samp~ TSS1~ +      1766~ CUFF~    67   264    3.94         4 8.81e7 8.82e7
## 6 samp~ TSS1~ +      1766~ CUFF~    90     0    0            4 8.81e7 8.82e7
## # ... with 1 more variable: gene <chr>
```

Table of Gene Summary Data

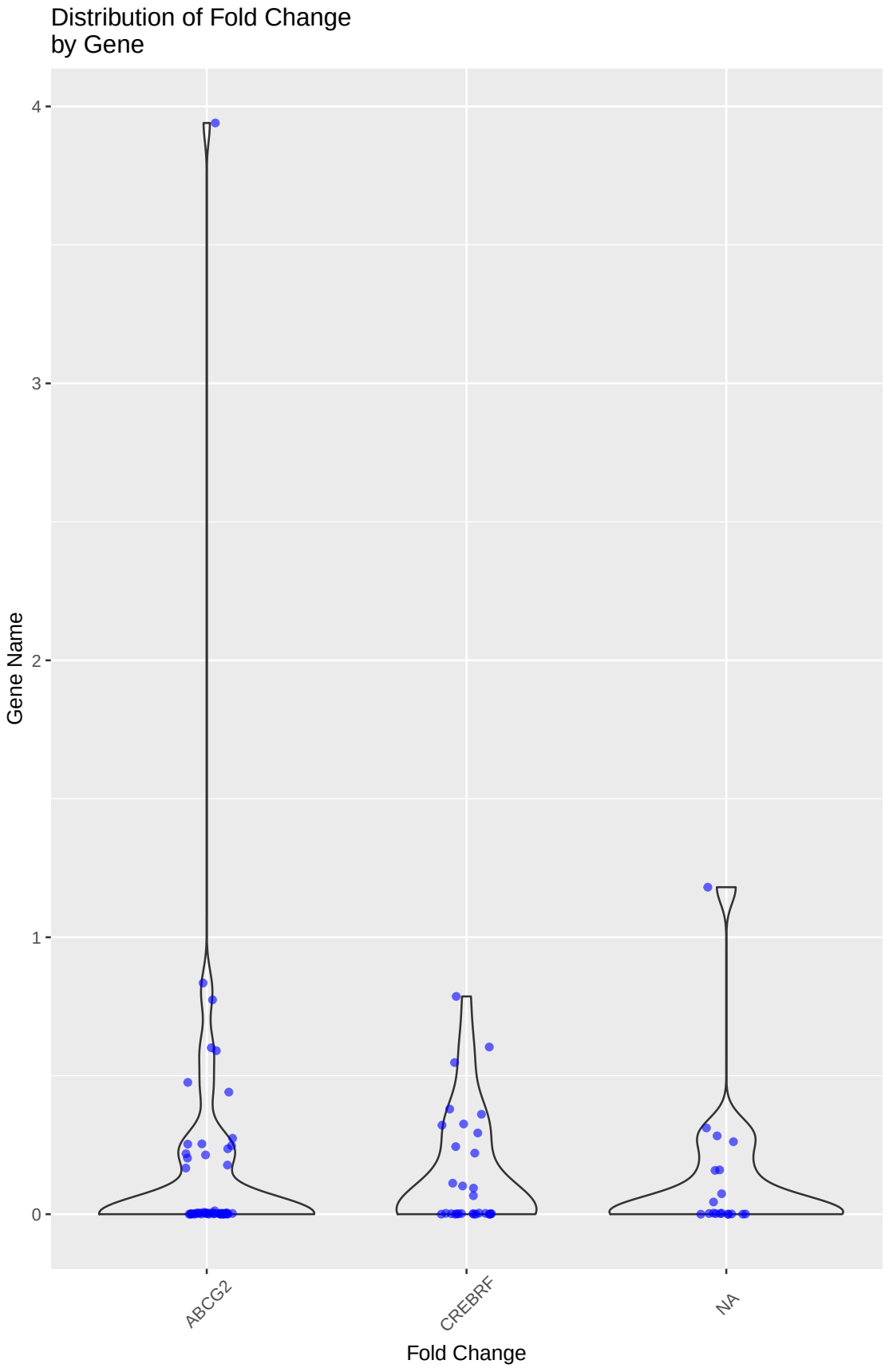
```
## gene summary
gene_summary <- gene_dat %>%
    group_by(name) %>%
    summarise(mean = mean(fold_change, na.rm = T),
              sd = sd(fold_change, na.rm = T),
              n_probes = n())

knitr::kable(gene_summary,
             digits = 3, # number of digits
             align = "lccc", # column alignment
             caption = "Summary fold change"
             )
```

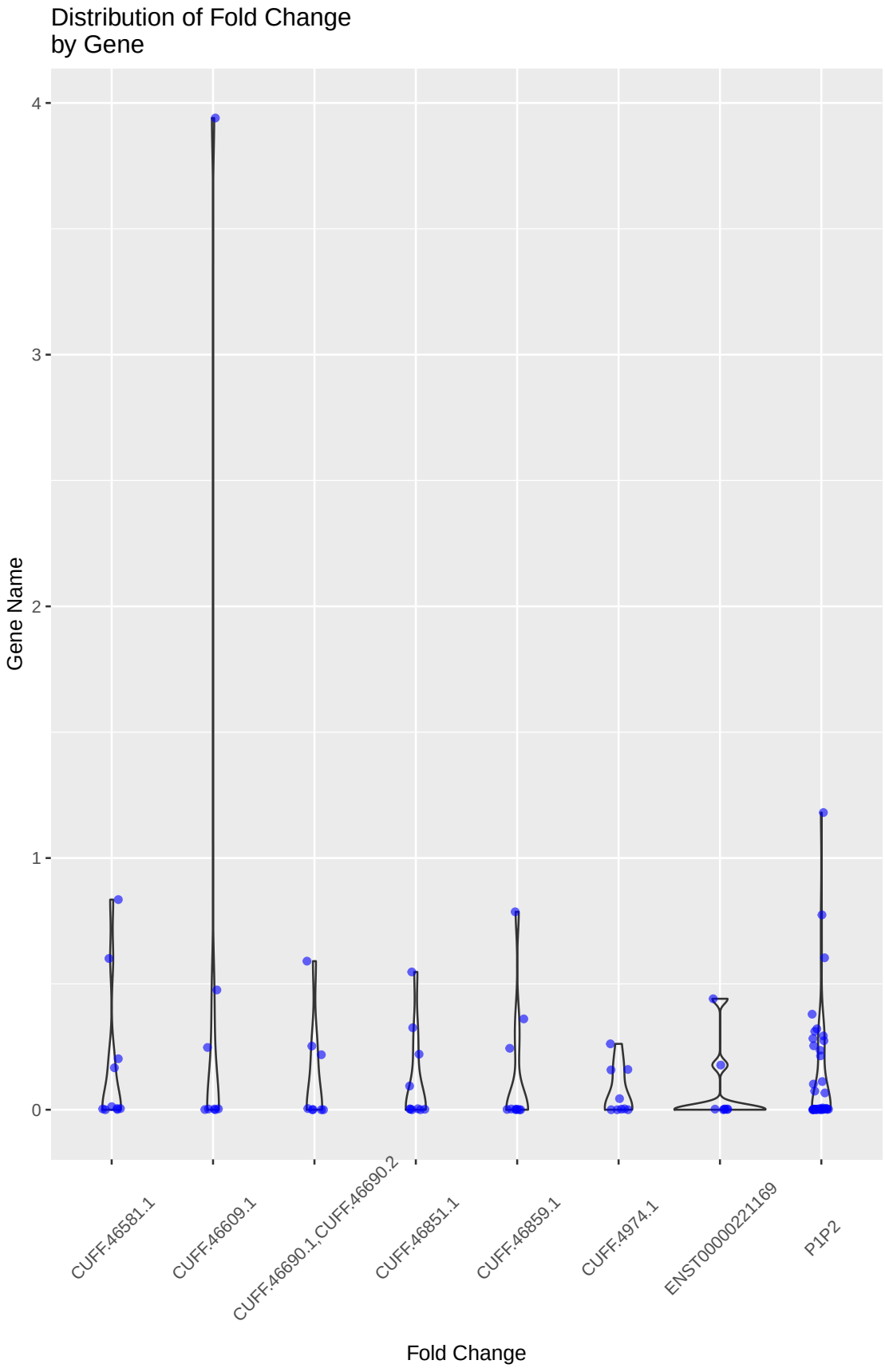
Table 1: Summary fold change

name	mean	sd	n_probes
CUFF.46581.1	0.183	0.297	10
CUFF.46609.1	0.584	1.367	8

name	mean	sd	n_probes
CUFF.46690.1,CUFF.46690.2	0.133	0.213	8
CUFF.46851.1	0.120	0.188	10
CUFF.46859.1	0.140	0.261	10
CUFF.4974.1	0.070	0.098	9
ENST00000221169	0.079	0.159	8
P1P2	0.149	0.254	37

Plot Fold Change by Gene


Distribution of Fold Change
by Gene
Gene Name
4
3
2
1
0
ABCG2
CREBRF
NA
Fold Change


Distribution of Fold Change
by Gene
Gene Name
Fold Change
4
3
2
1
0
CUFF.46581.1
CUFF.46609.1
CUFF.46690.1,CUFF.46690.2
CUFF.46851.1
CUFF.46859.1
CUFF.4974.1
ENST00000221169
P1P2

Discussion

```
best <- gene_summary %>%
  filter(n_probes == max(n_probes)) # filter to the gene with most probes
```

For no better reason than it's a tidy looking name and has the most probes (n = 37), we are interested in the gene ******

References

Breitling, Rainer, Patrick Armengaud, Anna Amtmann, and Pawel Herzyk. 2004. "Rank products: A simple, yet powerful, new method to detect differentially regulated genes in replicated microarray experiments." *FEBS Lett.* 573 (1-3): 83–92. https://doi.org/10.1016/j.febslet.2004.07.055.

Gentleman, Robert C., Vincent J. Carey, Douglas M. Bates, Ben Bolstad, Marcel Dettling, Sandrine Dudoit, Byron Ellis, et al. 2004. "Bioconductor: open software development for computational biology and bioinformatics." *Genome Biol.* 5 (10). https://doi.org/10.1186/gb-2004-5-10-r80.