Data Science Using R

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What you will learn over the next 3 lectures

- Loading, Transforming, Visualizing Tabular Data (Tidyverse)
  - readr
  - dplyr
  - ggplot2
- Working with High-Throughput Genomic Data (Bioconductor)
  - GenomicRanges
  - Biostrings
  - GenomicAlignments

Example Datasets

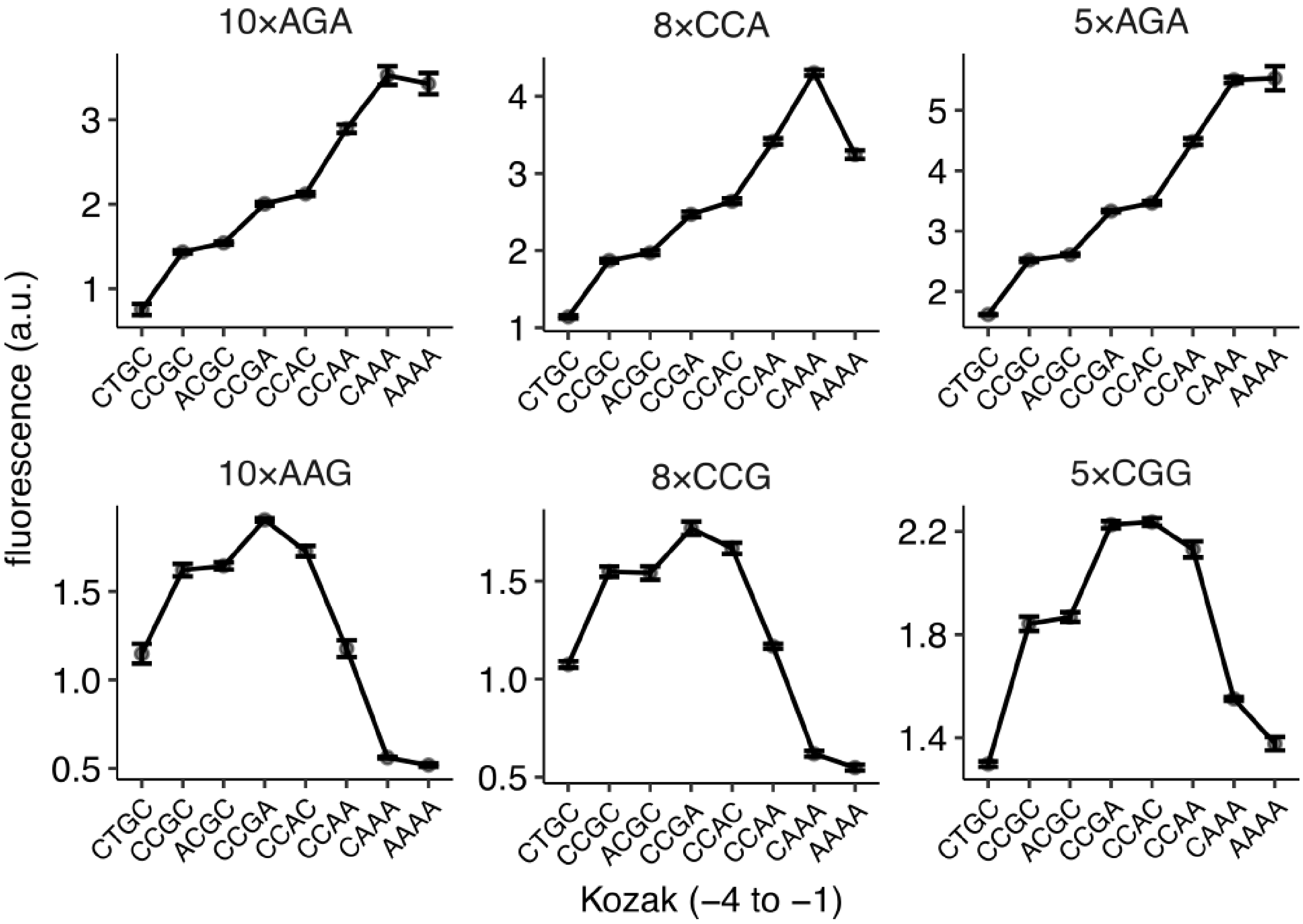
- Plate Reader Assay
- Flow Cytometry
- RNA-Seq

Raw Flow Cytometry Data

FSC.A	SSC.A	FITC.A	PE.Texas.Red.A	Time
79033	69338	9173	18690	3.02
101336	87574	13184	29886	3.04
51737	56161	3083	18324	3.06
79904	45085	9957	18099	3.08
124491	97305	15739	28730	3.09
54359	45015	6175	11918	3.11
64615	88989	11907	32413	3.13
109592	64132	12561	18824	3.15
58503	116384	11591	27629	3.19
38634	51511	7200	21930	3.21

```
5 cols × 2,720,000 rows
```

Flow Cytometry Analysis Using Tidyverse

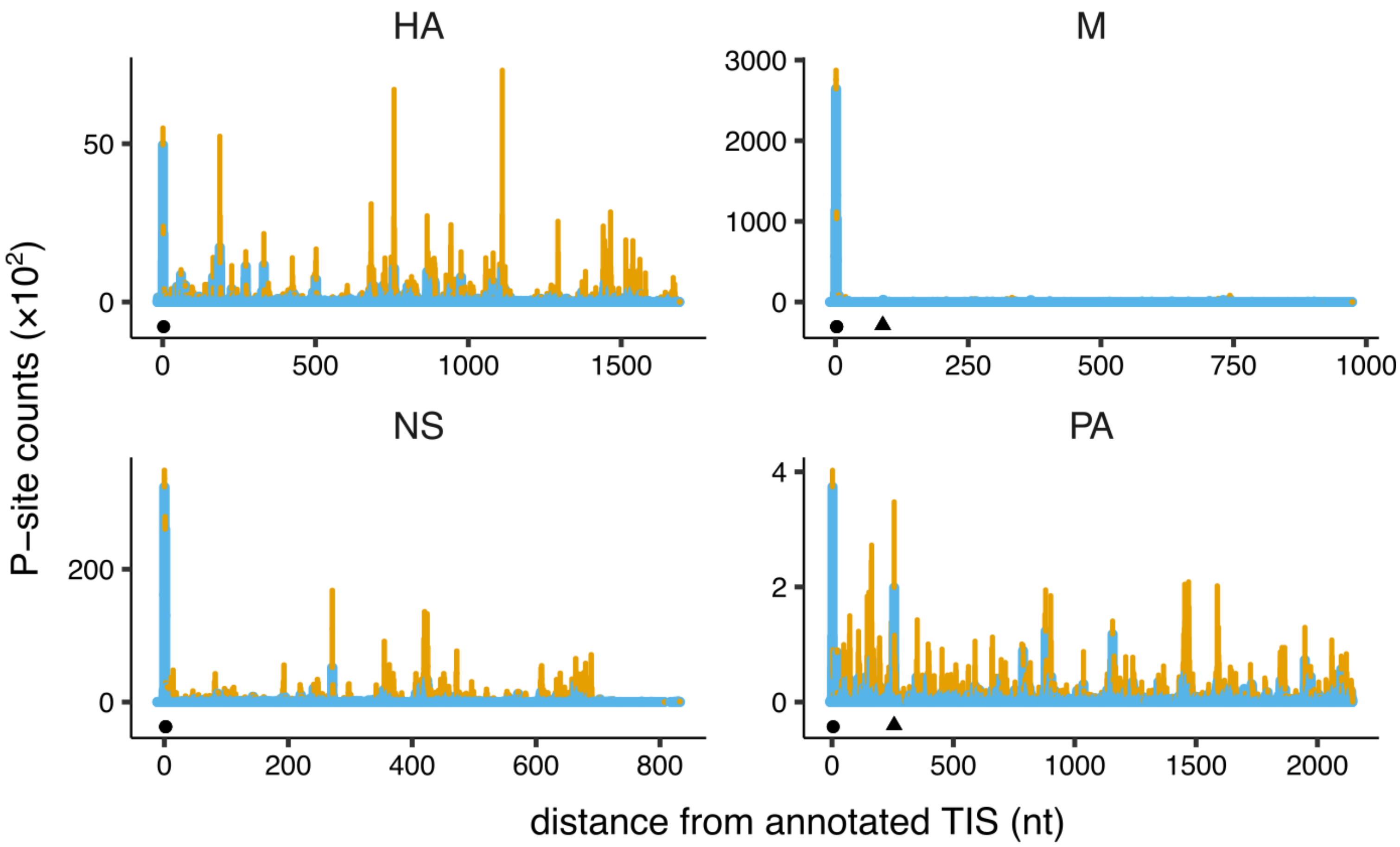


Raw Deep Sequencing Data

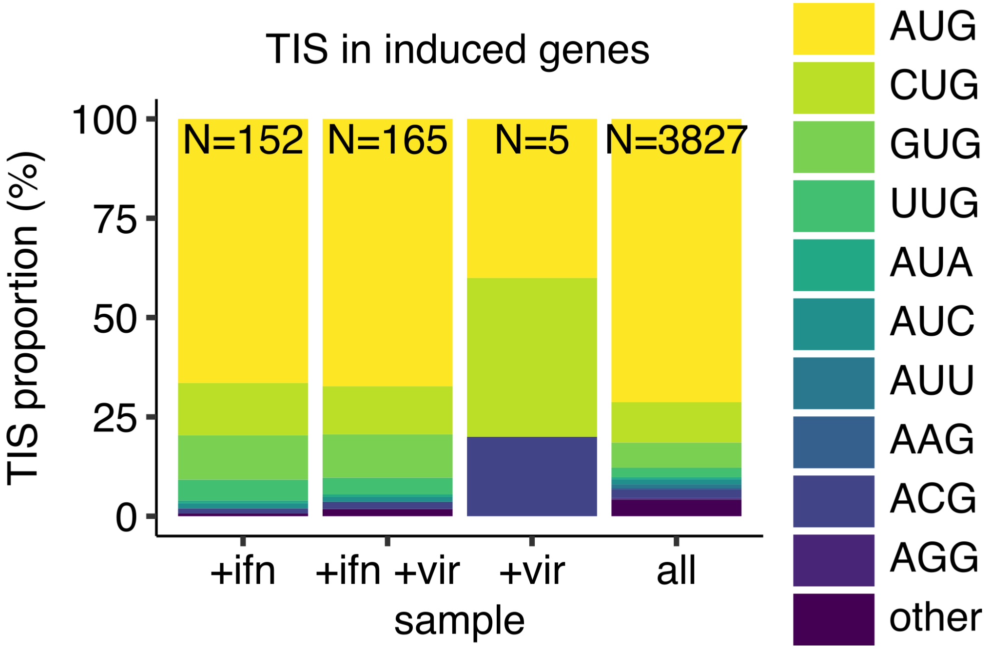
```
TACCTGGTTGATCCTGCCAGTAGCATATGCTTGTCTAAAAANAAAAAAAA
TCGGGGCCCGAAGCGTTTACTTTGAAATAAAAAAAAAAAAAAAAAAAGAT
ATTGATCATCGACACTTCGAACGCACTTGCGGCCCCGGGTAAAAAAAAAA
TCATTGATCATCGACACTTCGAACGCACTTGCGGCCCCGGGTAAAAAAAA
ATATTAAATGGATTTTTGGAGCAGGGAGATGGAAAAAAAAAAAAAAAAAA
TCCCTGGTGGTCTAGTGGTTAGGATTCAAAAAAAAAAAAAAAAAAAGATC
TCGTCGCGCGCGTCCGCTGGGGGCGGGGAGCGGTAAAAAAAAAAAAAAAA
TCGCGCCGTCGGCCAAAAAAAAAAAAAAAAAAAAGATCGGAAGAGCACAC
ATAAAGGTGCCCGGCGCCGGCTTCAAAAAAAAAAAAAAAAAAAAGATCGG
TGGTGGCGGCGGCGGCGGCGGCGGGAAAAAAAAAAAAAAAAAAAAAAGAT
TTGACTGCATAATTTGTGGTAGTGAGGGAAAAAAAAAAAAAAAAAAAAAT
TAGAGTGAGACTCCGTCTGCAAAAAAAAAAAAAAAAAAAAAGATCGGAAG
CCGAGGGAGCGAGACCCAAAAAAAAAAAAAAAAAAAAAAATCGGAAAAGC
ATTTTCAAGAAGATCATCTTTTAGACCAGCACTGGAGAAAAAAAAAAAAA
ATTGATCATCGACACTTCGAACGCACTTGCGGCCCCGGGAAAAAAAAAAA
```

165,000,000 reads

Deep Sequencing Analysis Using Bioconductor



Deep Sequencing Analysis Using Bioconductor



Tidyverse Functions for Tabular Data

Import	Visualize	Transform
read_tsv	geom_point	select
	geom_line	filter
	facet_grid	arrange

☞ Use `tsv` and `csv` file formats for tabular data

Tab **S**eparated **V**alues

```
strain mean_yfp mean_rfp mean_ratio se_ratio
schp674 1270 20316 0.561 0.004 10×AAG CAAA
schp675 3687 20438 1.621 0.036 10×AAG CCGC
schp676 2657 20223 1.177 0.048 10×AAG CCAA
schp677 3967 20604 1.728 0.03 10×AAG CCAC
```

Comma **S**eparated **V**alues

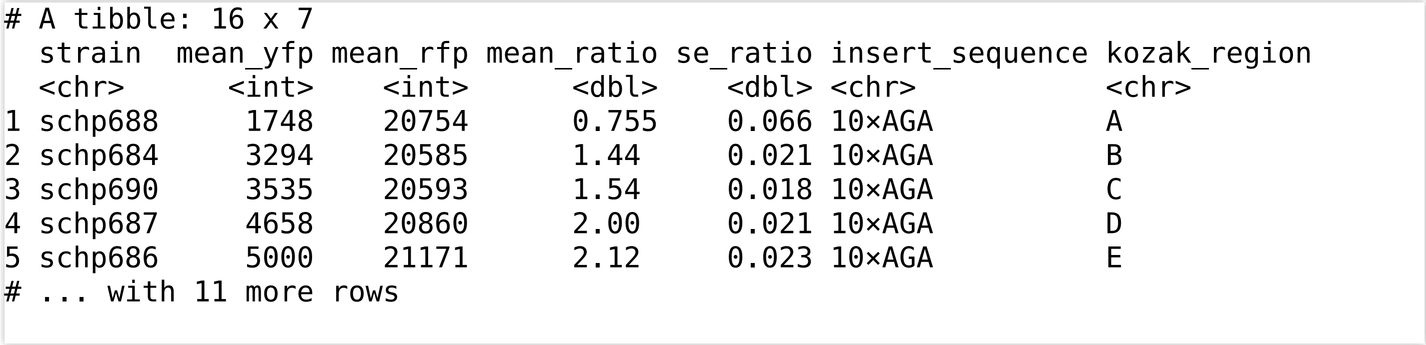
```
strain,mean_yfp,mean_rfp,mean_ratio,se_ratio,insert_sequence,kozak_r
schp674,1270,20316,0.561,0.004,10×AAG,CAAA
schp675,3687,20438,1.621,0.036,10×AAG,CCGC
schp676,2657,20223,1.177,0.048,10×AAG,CCAA
schp677,3967,20604,1.728,0.03,10×AAG,CCAC
```

Reading tabular data into R

```r
library(tidyverse)

data <- read_tsv("tables/example_dataset_1.tsv")
```

Read tabular data into a DataFrame (tibble)

```r
library(tidyverse)

data <- read_tsv("tables/example_dataset_1.tsv")

print(data, n = 5)
```



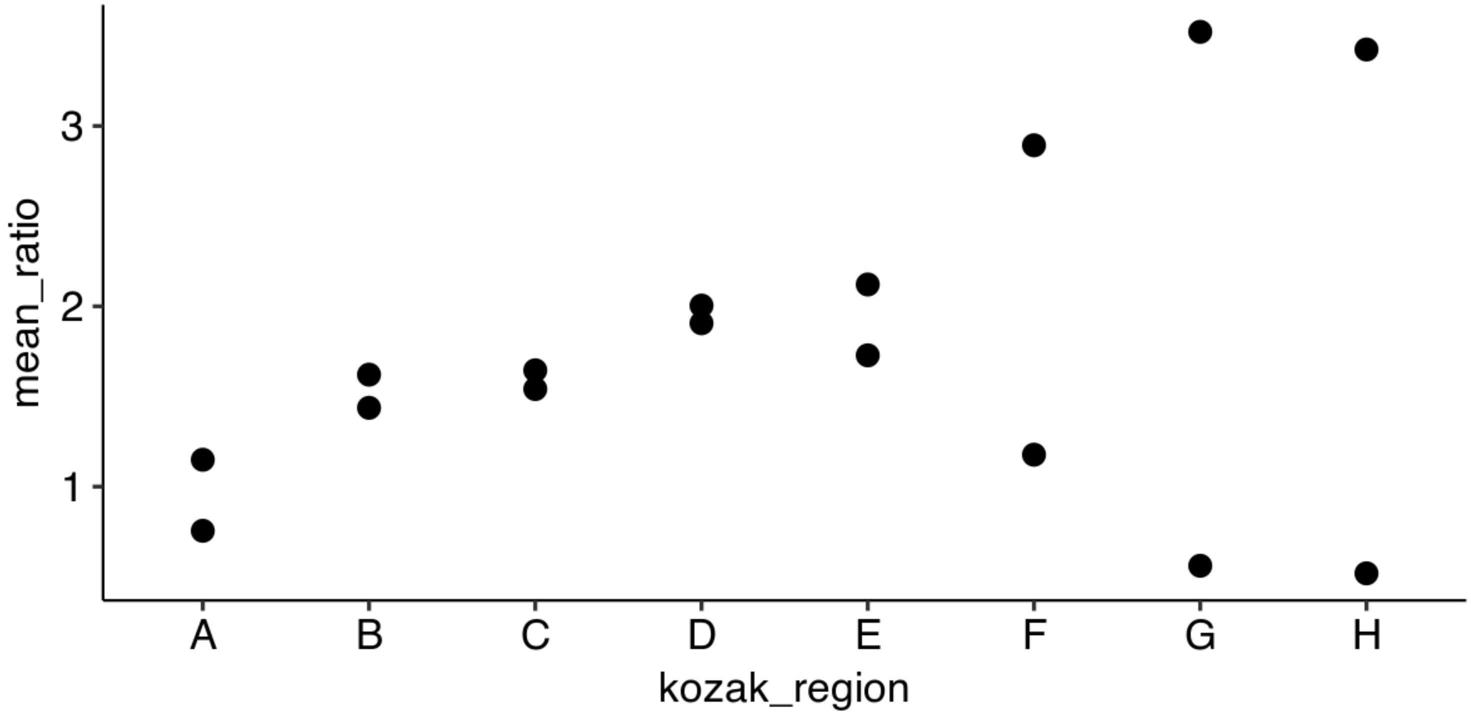
```
# A tibble: 16 x 7
  strain  mean_yfp mean_rfp mean_ratio se_ratio insert_sequence kozak_region
  <chr>      <int>    <int>      <dbl>    <dbl> <chr>           <chr>
1 schp688     1748    20754      0.755    0.066 10×AGA          A
2 schp684     3294    20585      1.44     0.021 10×AGA          B
3 schp690     3535    20593      1.54     0.018 10×AGA          C
4 schp687     4658    20860      2.00     0.021 10×AGA          D
5 schp686     5000    21171      2.12     0.023 10×AGA          E
# ... with 11 more rows
```

☞ Comment your code

```r
# library to work with tabular data
library(tidyverse)

# read the tsv file into a tibble and
# assign it to the 'data' variable
data <- read_tsv("tables/example_dataset_1.tsv")

# display the contents of 'data'
print(data, n = 5)
```

Plotting a point graph

```
ggplot(data, aes(x = kozak_region,
                 y = mean_ratio)) +
  geom_point()
```

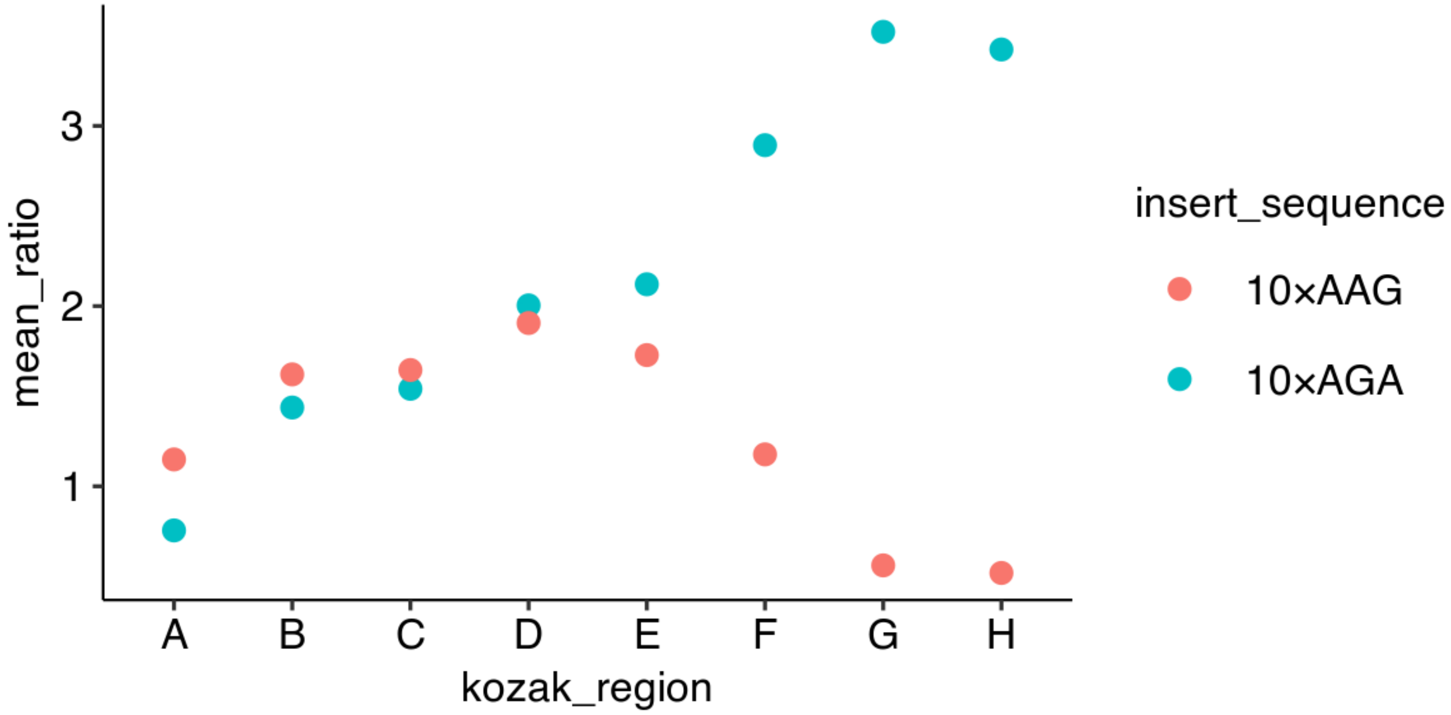


How do we show multiple experimental parameters?

strain	mean_ratio	insert_sequence	kozak_region
schp688	0.755	10×AGA	A
schp684	1.437	10×AGA	B
schp690	1.541	10×AGA	C
schp687	2.004	10×AGA	D
schp686	2.121	10×AGA	E
schp685	2.893	10×AGA	F
schp683	3.522	10×AGA	G
schp689	3.424	10×AGA	H
schp679	1.149	10×AAG	A
schp675	1.621	10×AAG	B
schp681	1.645	10×AAG	C
schp678	1.906	10×AAG	D
schp677	1.728	10×AAG	E
schp676	1.177	10×AAG	F
schp674	0.561	10×AAG	G
schp680	0.519	10×AAG	H

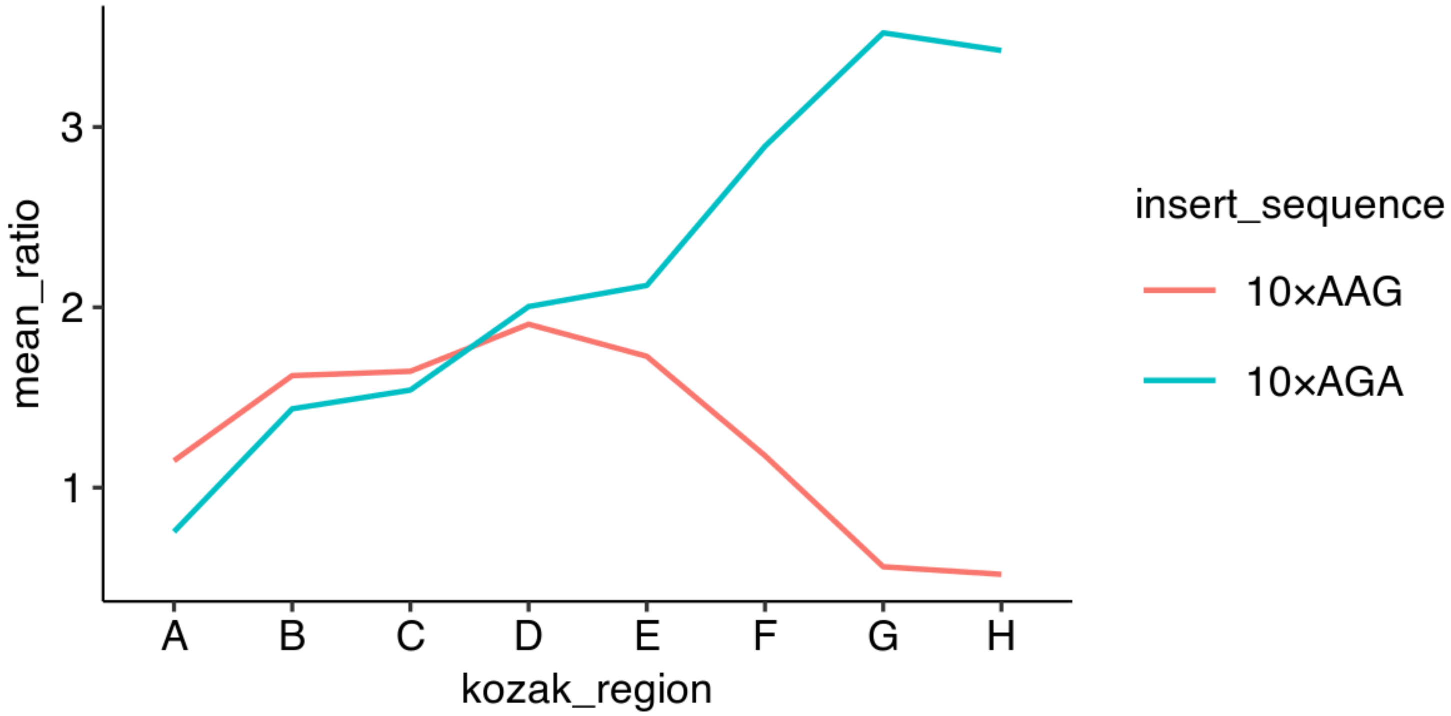
Plotting a point graph with color

```
ggplot(data, aes(x = kozak_region,
                 y = mean_ratio,
                 color = insert_sequence)) +
  geom_point()
```



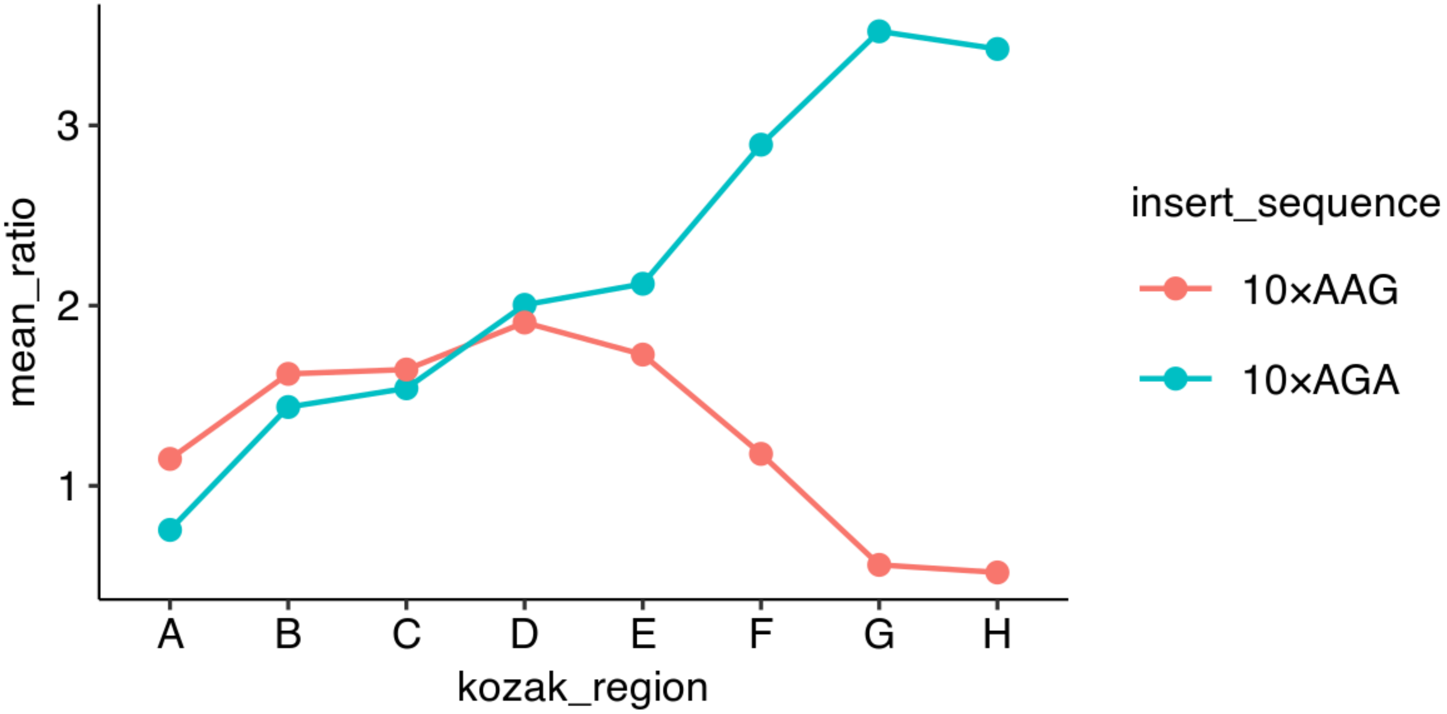
Plotting a line graph

```
ggplot(data, aes(x = kozak_region,
                 y = mean_ratio,
                 color = insert_sequence,
                 group = insert_sequence)) +
  geom_line()
```



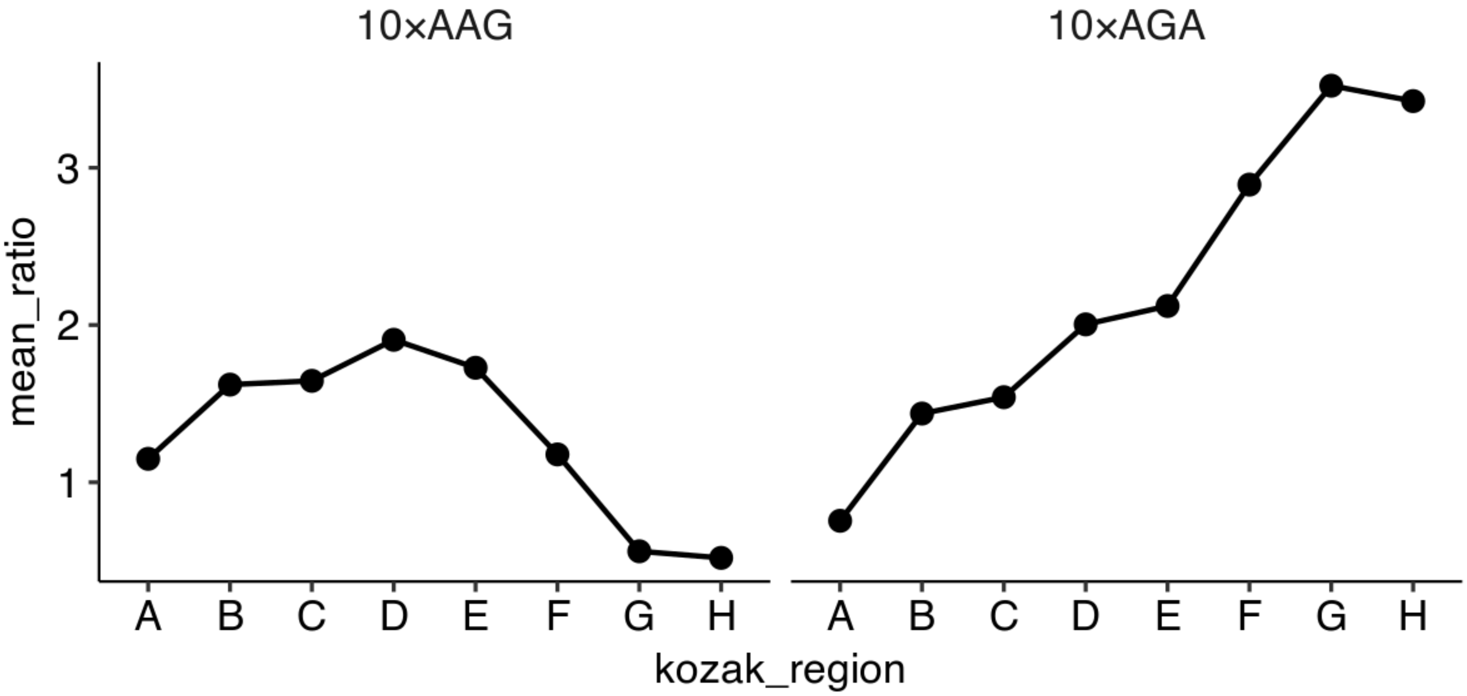
Plotting point and line graphs

```
ggplot(data, aes(x = kozak_region,
                 y = mean_ratio,
                 color = insert_sequence,
                 group = insert_sequence)) +
  geom_line() +
  geom_point()
```



‘Faceting’ – Plotting in multiple panels

```
ggplot(data, aes(x = kozak_region,
                 y = mean_ratio,
                 group = insert_sequence)) +
  geom_line() +
  geom_point() +
  facet_grid(~ insert_sequence)
```



☞ Use the pipe %>% operator to chain commands

```
print(data, n = 3)
```

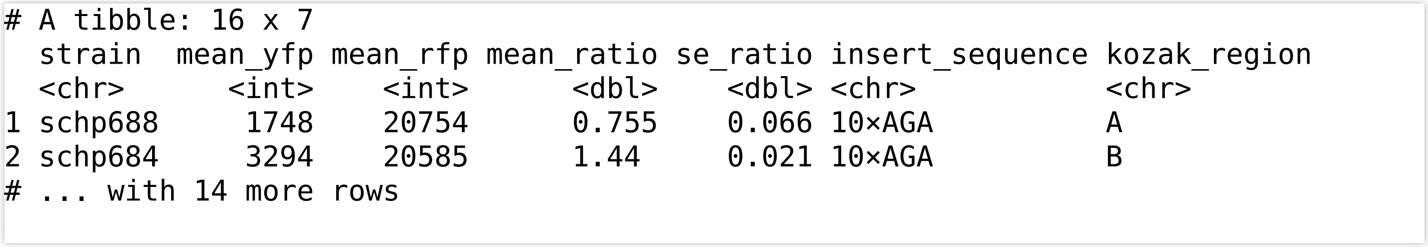
```
# A tibble: 16 x 7
  strain  mean_yfp mean_rfp mean_ratio se_ratio insert_sequence kozak_region
  <chr>      <int>    <int>      <dbl>    <dbl> <chr>           <chr>
1 schp688     1748    20754      0.755    0.066 10×AGA          A
2 schp684     3294    20585      1.44     0.021 10×AGA          B
3 schp690     3535    20593      1.54     0.018 10×AGA          C
# ... with 13 more rows
```

```
data %>%
  print(n = 3)
```

```
# A tibble: 16 x 7
  strain  mean_yfp mean_rfp mean_ratio se_ratio insert_sequence kozak_region
  <chr>      <int>    <int>      <dbl>    <dbl> <chr>           <chr>
1 schp688     1748    20754      0.755    0.066 10×AGA          A
2 schp684     3294    20585      1.44     0.021 10×AGA          B
3 schp690     3535    20593      1.54     0.018 10×AGA          C
# ... with 13 more rows
```

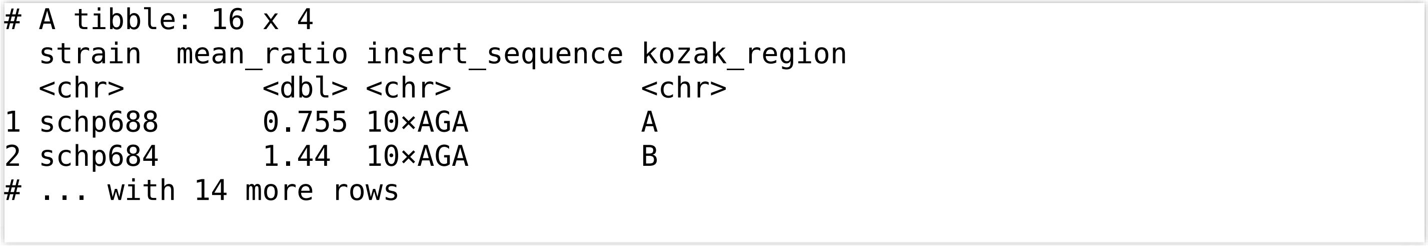
Simple Data Manipulations – `select` columns

```
data %>%
  print(n = 2)
```



```
# A tibble: 16 x 7
  strain  mean_yfp mean_rfp mean_ratio se_ratio insert_sequence kozak_region
  <chr>      <int>    <int>      <dbl>    <dbl> <chr>           <chr>
1 schp688     1748    20754      0.755    0.066 10×AGA          A
2 schp684     3294    20585      1.44     0.021 10×AGA          B
# ... with 14 more rows
```

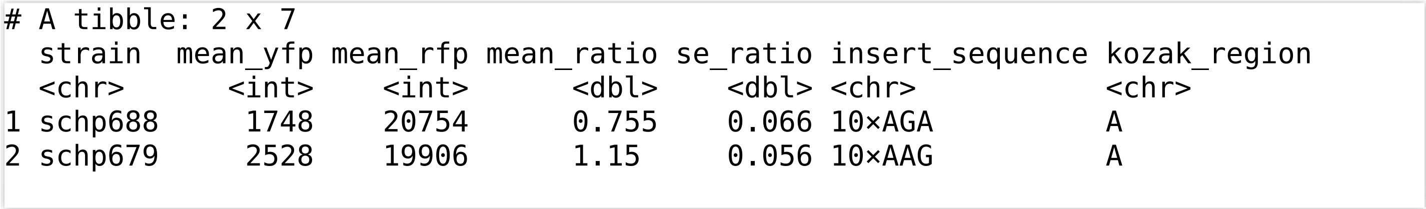
```
data %>%
  select(strain, mean_ratio, insert_sequence, kozak_region) %>%
  print(n = 2)
```



```
# A tibble: 16 x 4
  strain  mean_ratio insert_sequence kozak_region
  <chr>        <dbl> <chr>           <chr>
1 schp688      0.755 10×AGA          A
2 schp684      1.44  10×AGA          B
# ... with 14 more rows
```

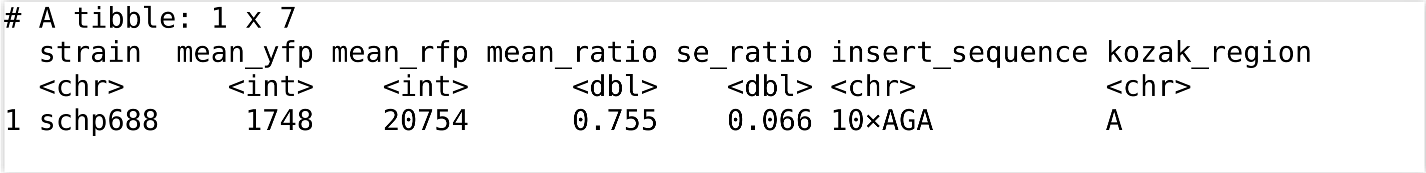
Simple Data Manipulations – `filter` rows

```
data %>%
  filter(kozak_region == "A")
```



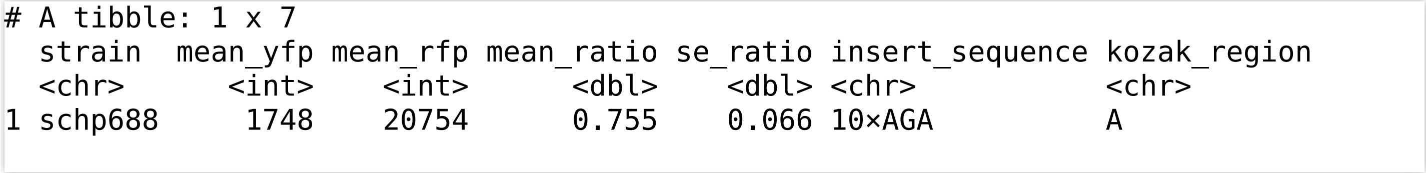
```
# A tibble: 2 x 7
  strain  mean_yfp mean_rfp mean_ratio se_ratio insert_sequence kozak_region
  <chr>      <int>    <int>      <dbl>    <dbl> <chr>           <chr>
1 schp688     1748    20754      0.755    0.066 10×AGA          A
2 schp679     2528    19906      1.15     0.056 10×AAG          A
```

```
data %>%
  filter(kozak_region == "A", insert_sequence == "10×AGA")
```



```
# A tibble: 1 x 7
  strain  mean_yfp mean_rfp mean_ratio se_ratio insert_sequence kozak_region
  <chr>      <int>    <int>      <dbl>    <dbl> <chr>           <chr>
1 schp688     1748    20754      0.755    0.066 10×AGA          A
```

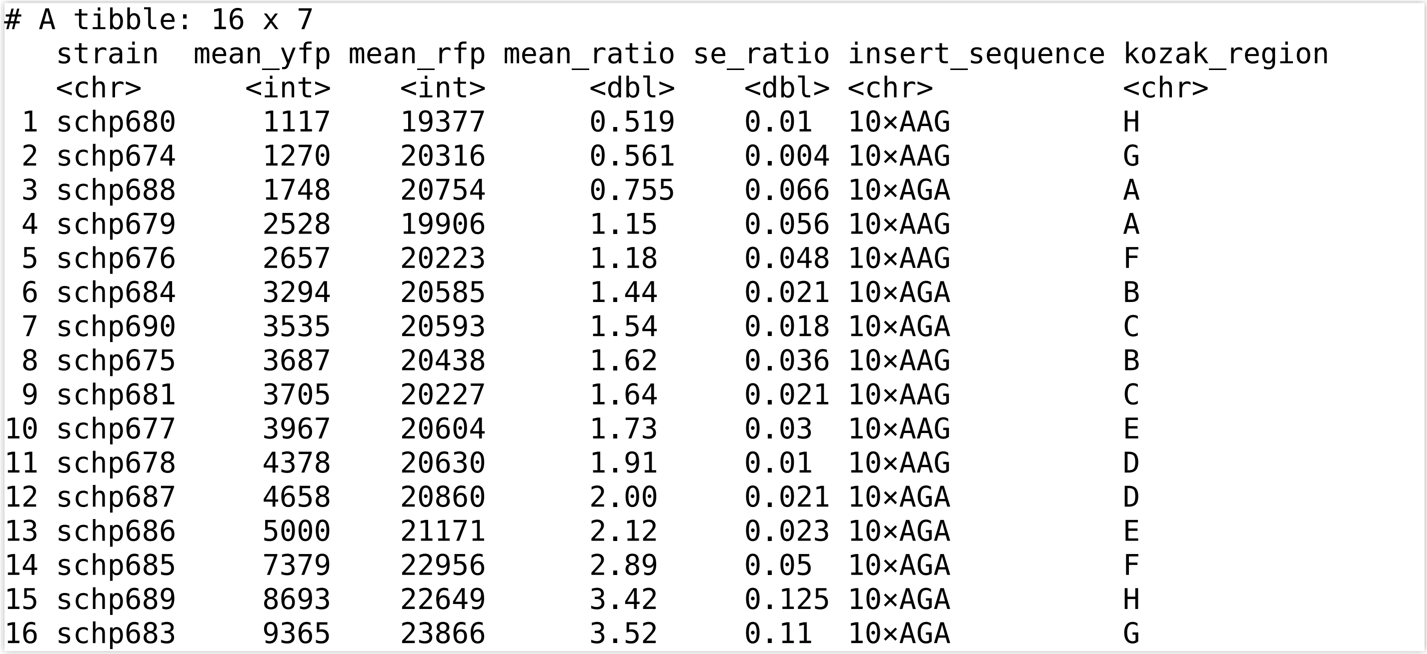
```
data %>%
  filter(kozak_region == "A") %>%
  filter(insert_sequence == "10×AGA")
```



```
# A tibble: 1 x 7
  strain  mean_yfp mean_rfp mean_ratio se_ratio insert_sequence kozak_region
  <chr>      <int>    <int>      <dbl>    <dbl> <chr>           <chr>
1 schp688     1748    20754      0.755    0.066 10×AGA          A
```

Simple Data Manipulations – `arrange` rows

```
data %>%
  arrange(mean_ratio)
```



```
# A tibble: 16 x 7
   strain  mean_yfp mean_rfp mean_ratio se_ratio insert_sequence kozak_region
   <chr>      <int>    <int>      <dbl>    <dbl> <chr>           <chr>
 1 schp680     1117    19377      0.519    0.01  10×AAG          H
 2 schp674     1270    20316      0.561    0.004 10×AAG          G
 3 schp688     1748    20754      0.755    0.066 10×AGA          A
 4 schp679     2528    19906      1.15     0.056 10×AAG          A
 5 schp676     2657    20223      1.18     0.048 10×AAG          F
 6 schp684     3294    20585      1.44     0.021 10×AGA          B
 7 schp690     3535    20593      1.54     0.018 10×AGA          C
 8 schp675     3687    20438      1.62     0.036 10×AAG          B
 9 schp681     3705    20227      1.64     0.021 10×AAG          C
10 schp677     3967    20604      1.73     0.03  10×AAG          E
11 schp678     4378    20630      1.91     0.01  10×AAG          D
12 schp687     4658    20860      2.00     0.021 10×AGA          D
13 schp686     5000    21171      2.12     0.023 10×AGA          E
14 schp685     7379    22956      2.89     0.05  10×AGA          F
15 schp689     8693    22649      3.42     0.125 10×AGA          H
16 schp683     9365    23866      3.52     0.11  10×AGA          G
```

What you learned today

Import	Visualize	Transform
`read_tsv`	`geom_point`	`select`
	`geom_line`	`filter`
	`facet_grid`	`arrange`