

# Helminth Resist

```
library(readr)
#library(trelliscopejs)
library(tidyverse)
#library(plotly)
library(scales)
Fig1A_helminth_R <- read_csv("~/Desktop/recessive_figs/Fig1A_helminth-R.csv")
```

```
## Warning: Missing column names filled in: 'X1' [1]
```

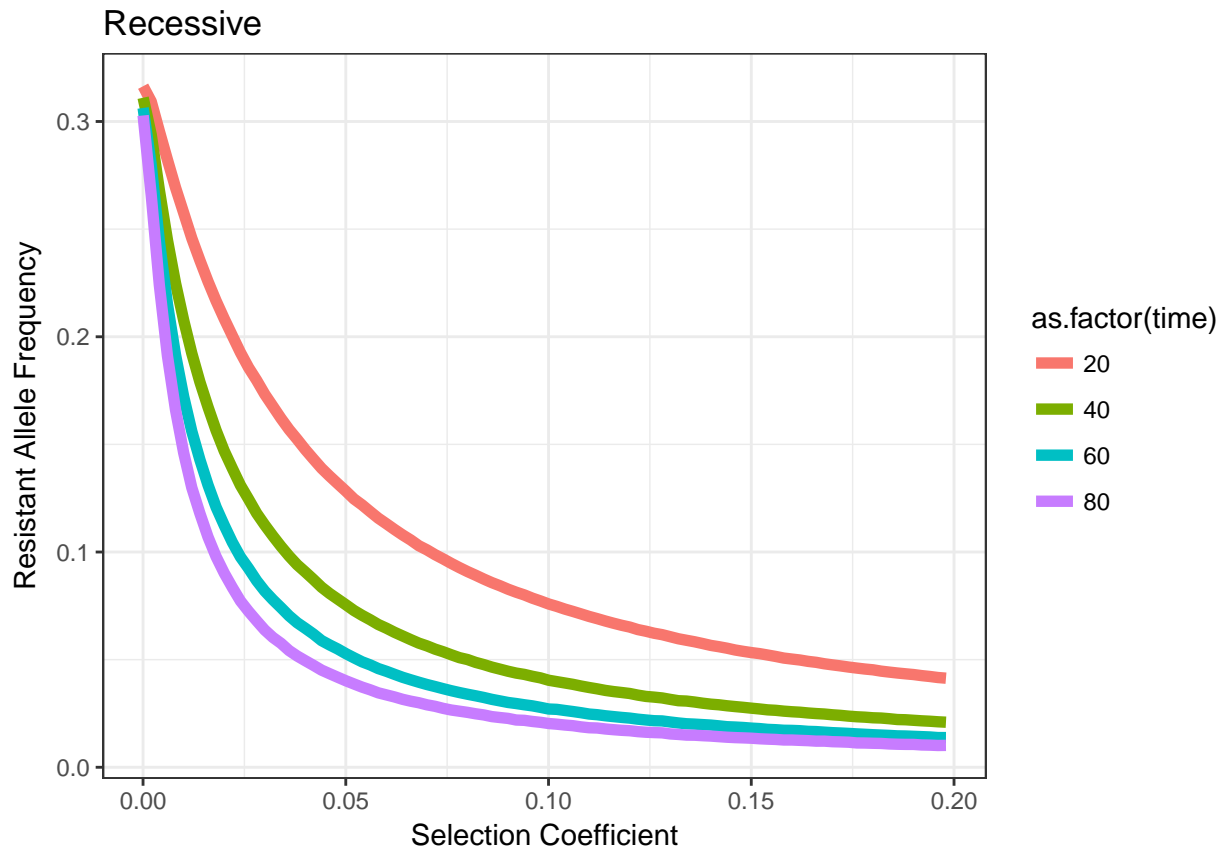
```
Fig1A_helminth_D <- read_csv("~/Desktop/recessive_figs/Fig1A_helminth-D.csv")
```

```
## Warning: Missing column names filled in: 'X1' [1]
```

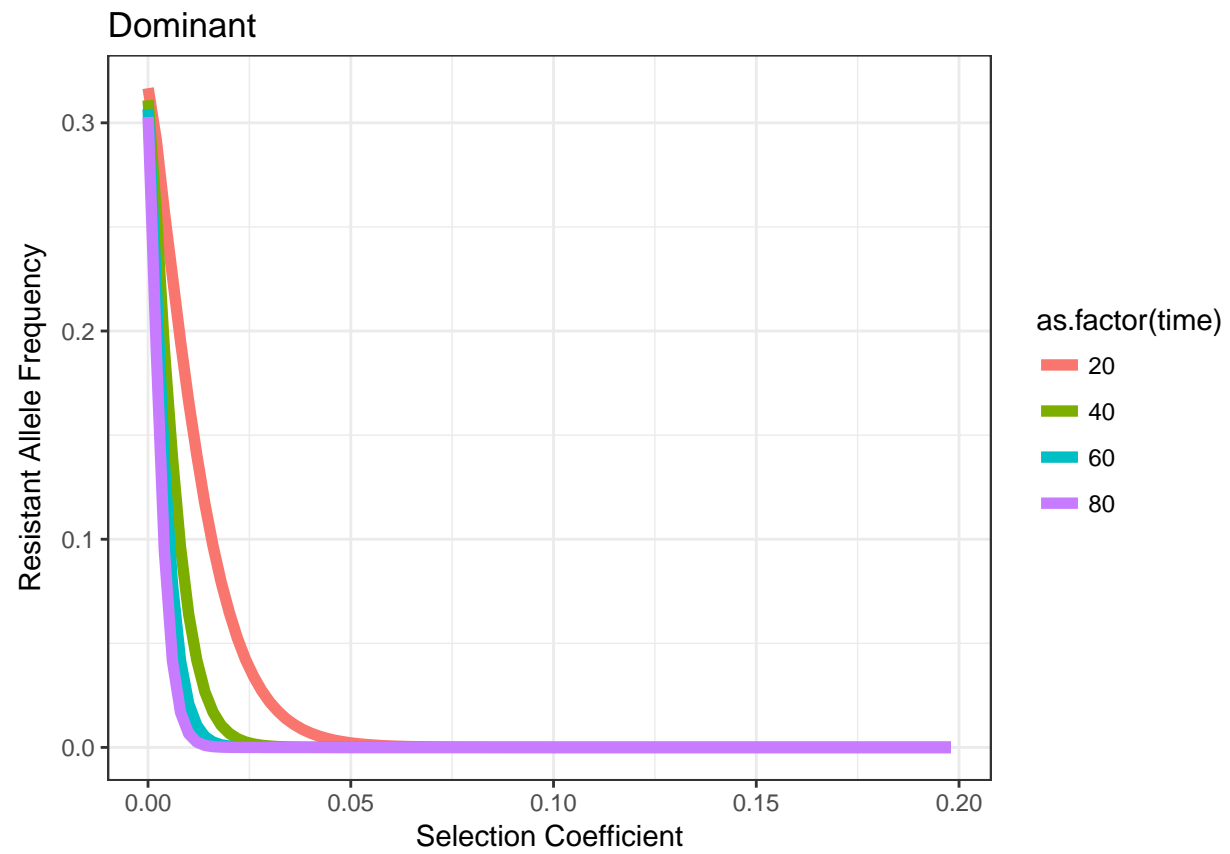
```
Fig1A_helminth_A <- read_csv("~/Desktop/recessive_figs/Fig1A_helminth-A.csv")
```

```
## Warning: Missing column names filled in: 'X1' [1]
```

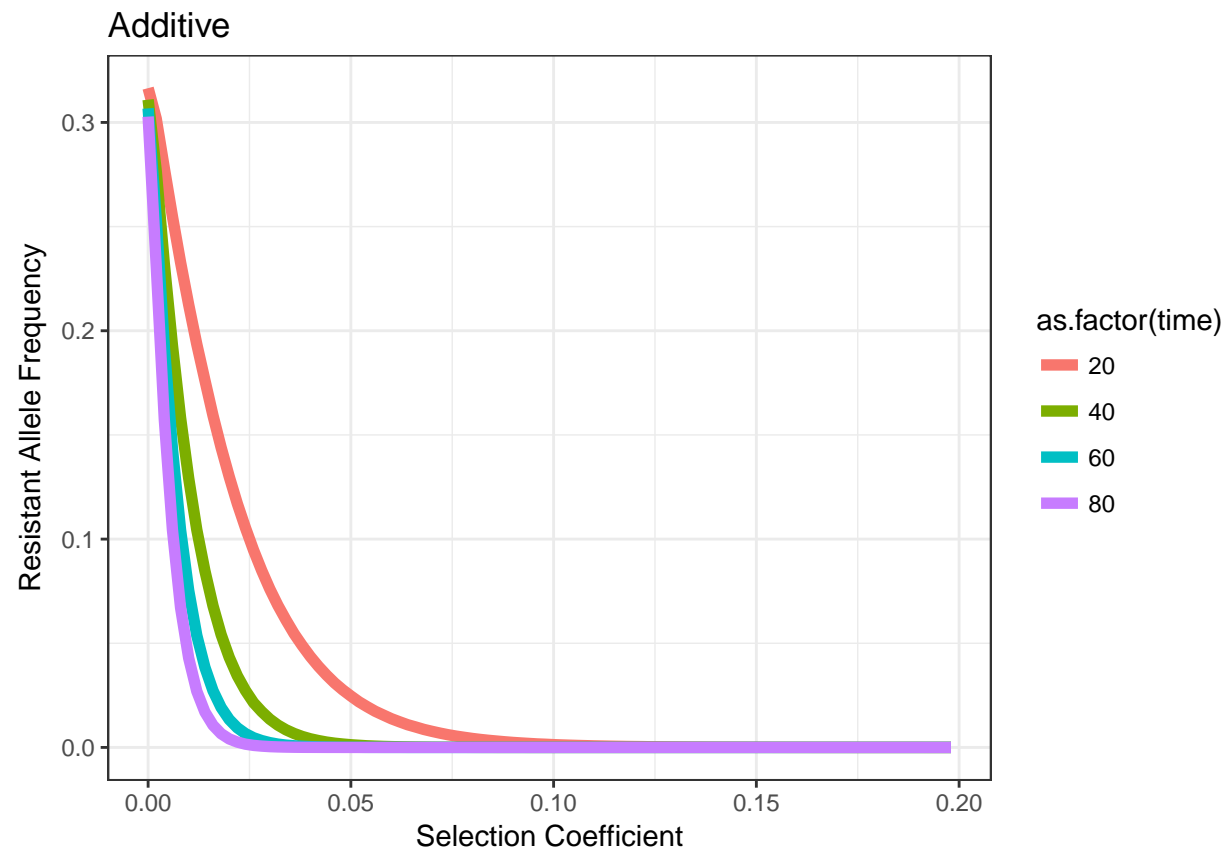
```
ggplot(data=Fig1A_helminth_R,aes(x=SAA,y=freq), color = as.factor(time))) + geom_line(size=2) + ylab("Resistant Allele Frequency")
```



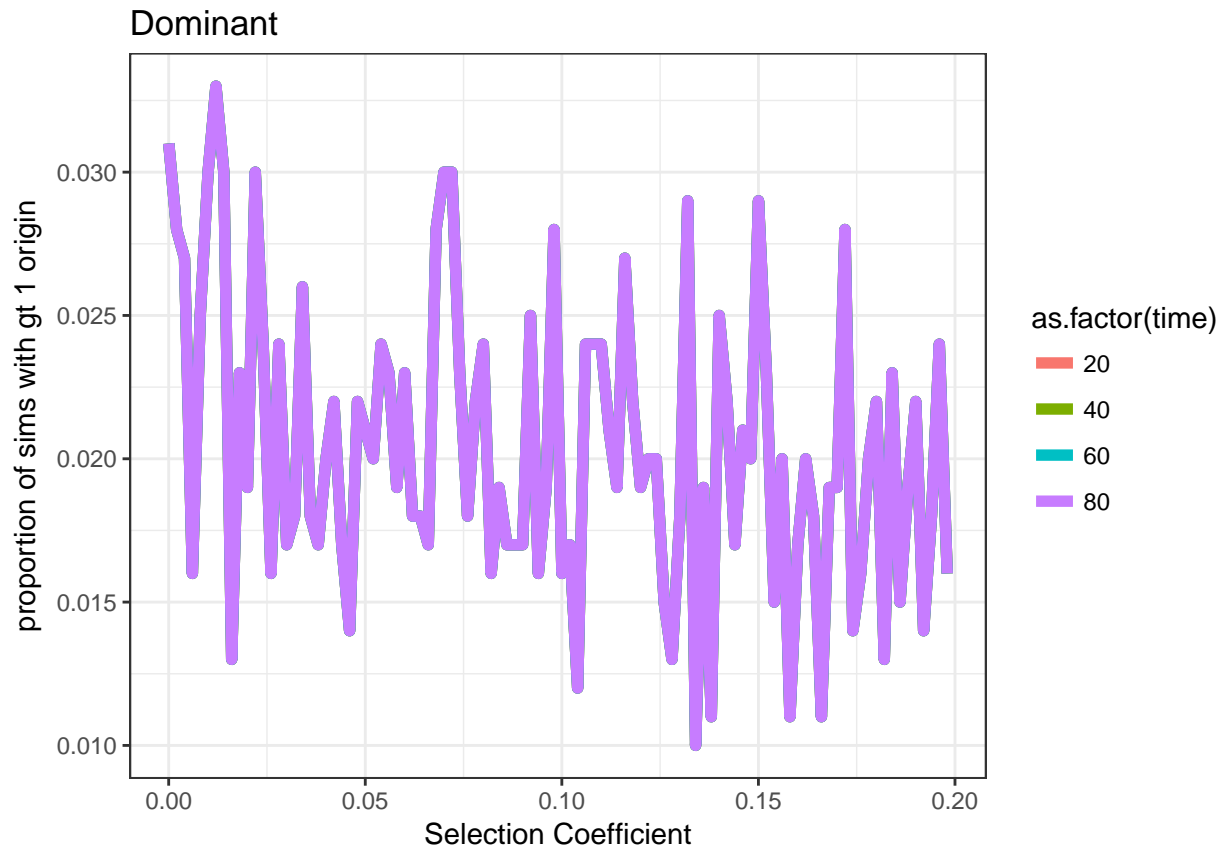
```
ggplot(data=Fig1A_helminth_D,aes(x=SAA,y=freq), color = as.factor(time))) + geom_line(size=2) + ylab("Resistant Allele Frequency")
```



```
ggplot(data=Fig1A_helminth_A,aes(x=SAA,y=freq), color = as.factor(time))) + geom_line(size=2) + ylab("Resistant Allele Frequency")
```

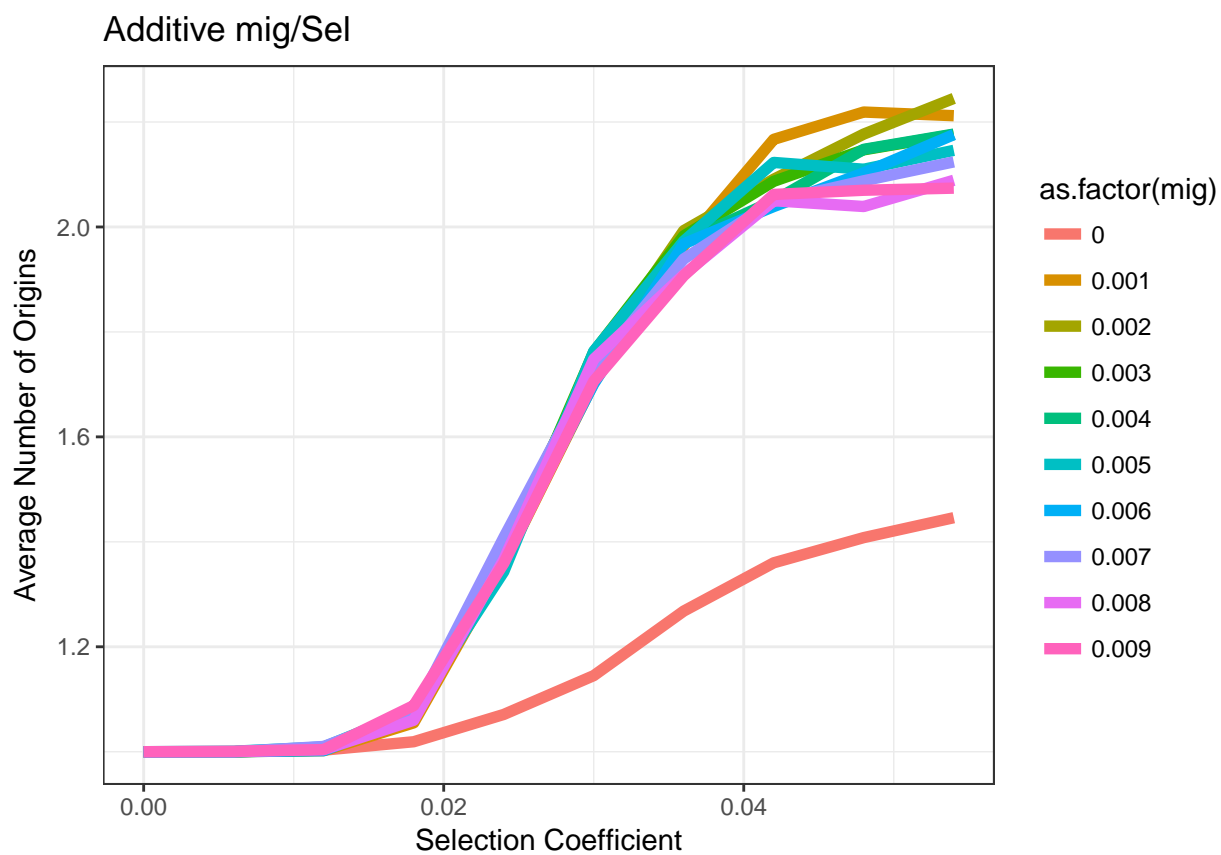


```
ggplot(data=Fig1A_helminth_D,aes(x=SAA,y=(orig), color = as.factor(time))) + geom_line(size=2) + ylab("Resistant Allele Frequency")
```

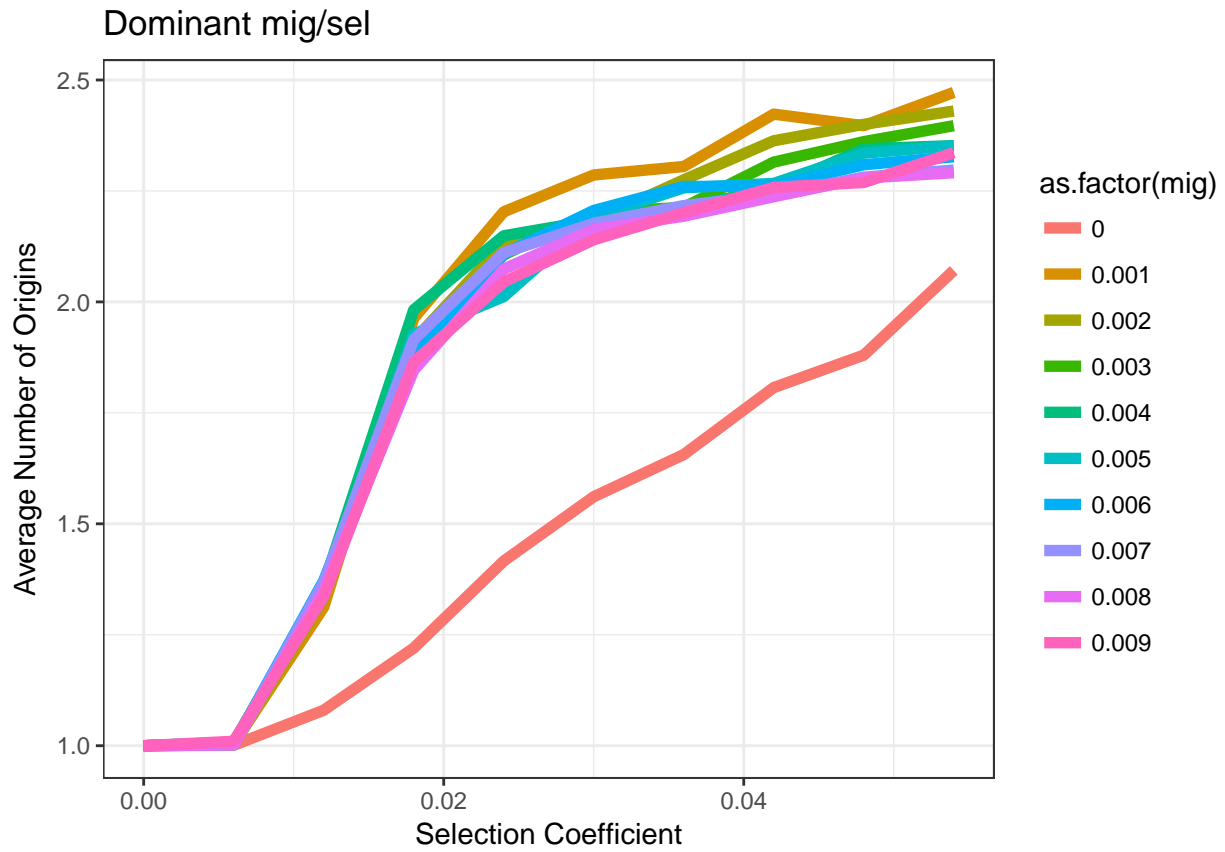


```
Fig1B_helminth_A <- read_csv("~/Desktop/recessive_figs/Fig1B_helminth-A.csv.rename")
Fig1B_helminth_D <- read_csv("~/Desktop/recessive_figs/Fig1B_helminth-D.csv.rename")
```

```
ggplot(data=Fig1B_helminth_A,aes(x=sel,y=(orig), color = as.factor(mig))) + geom_line(size=2) + ylab("A")
```



```
ggplot(data=Fig1B_helminth_D,aes(x=sel,y=(orig), color = as.factor(mig))) + geom_line(size=2) + ylab("A
```

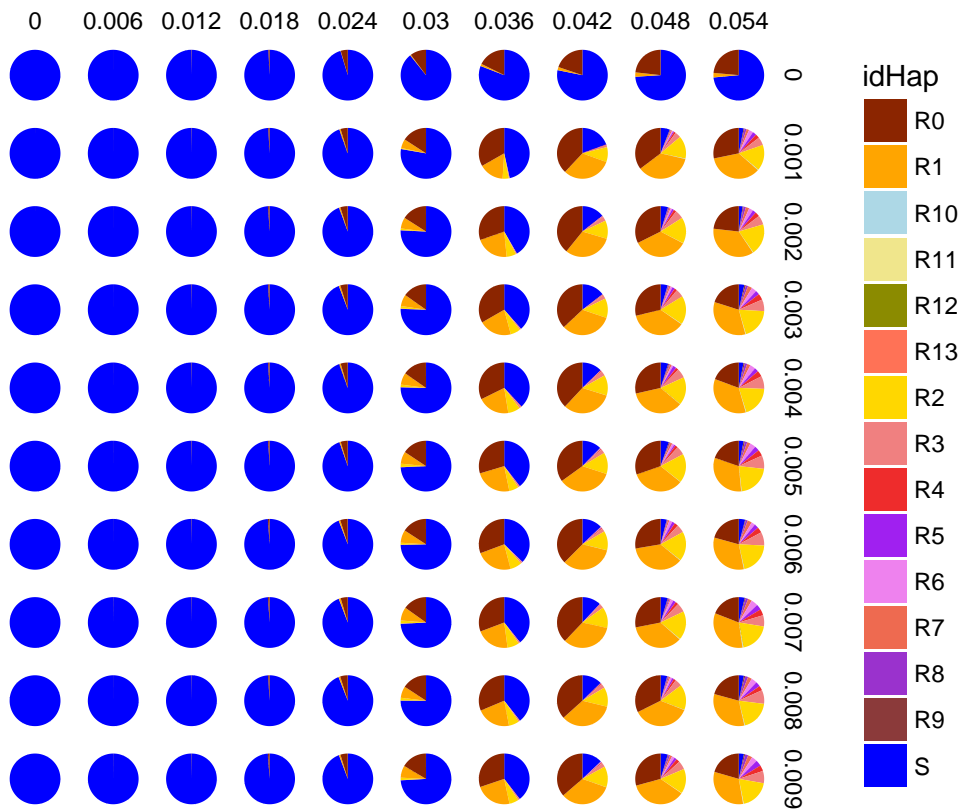


```
#dominant <- ggplot(subset(Fig1B_helminth_D, piHap/20000 > 0.05)) + aes(x = reorder(mig,sel), y = piHap/20000)
#dominant + facet_trelliscope(sel ~ mig, nrow = 10, ncol = 10, path="helminthFigs", name="Dominant Selection")

#additive <- ggplot(subset(Fig1B_helminth_A, piHap/20000 > 0.05)) + aes(x = reorder(mig,sel), y = piHap/20000)
#additive + facet_trelliscope(sel ~ mig, nrow = 10, ncol = 10, name="Additive Selection", self_contained = TRUE)

ggplot(data=Fig1B_helminth_A, aes(x = reorder(mig,sel), y = piHap/20000, fill = idHap)) + geom_bar(width=0.5)
```

additive



```
ggplot(data=Fig1B_helminth_D, aes(x = reorder(mig,sel), y = piHap/20000, fill = idHap)) + geom_bar(width=1)
```

dominant

