REX: Gall Plots

Moriah Young

July 25, 2021

COLLABORATORS: Phoebe Zarnetske, Mark Hammond, Kara Dobson, Emily Parker, Kristin Wolford
DATA INPUT: Clean & plot gall csv from the shared Google drive
DATA OUTPUT: Code and Rmd are in the scripts folder in Github
PROJECT: REX

```
# Clear all existing data
rm(list=ls())

# Load packages
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.0 --
```

```
## v ggplot2 3.3.3      v purrr   0.3.4
## v tibble  3.0.6      v dplyr   1.0.4
## v tidyr   1.1.2      v stringr 1.4.0
## v readr   1.4.0      v forcats 0.5.1
```

```
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
# Set working directory from .Renviron
dir <- Sys.getenv("ANALYSIS_DIR")
list.files(dir)
```

```
##  [1] "animal"                 "GHG"
##  [3] "Irrigation"             "lookup_tables"
##  [5] "microbes"               "REX_Data_Management.gdoc"
##  [7] "REX_Data_Template.gsheet" "soil"
##  [9] "T7_ANPP"                "T7_plant_comp"
## [11] "T7_plant_phenology"     "T7_warmx_insect"
## [13] "T7_warmx_plant_traits"  "T7_warmx_VOC"
## [15] "weather"
```

```
# Read in data
galls <- read.csv(file.path(dir, "T7_warmx_plant_traits/L1/T7_warmx_galls_L1.csv"))

# making it so that plant_height, gall_diameter, and gall_height are on the same row for the same plant
# so each unique plant will have just one row ompared to two in the raw data.
```

```
#galls2 <- galls %>%
#        select(-date) %>%
#        group_by(rep, footprint, treatment, plant_num, gall_present) %>%
#        summarise(across(everything(), na.omit)) %>%
#        distinct()

galls3 <- galls %>% select(rep, footprint, treatment, plant_num, gall_present, plant_height) %>%
  na.omit()

galls4 <- galls %>% select(-plant_height) %>%
  na.omit() %>%
  full_join(galls3)


## Joining, by = c("rep", "footprint", "treatment", "plant_num", "gall_present")

galls5 <- galls4 %>% select(-date) # get rid of date - we don't need this and some have NAs for this

# create a dateframe that only contains galled plants
gall_only <- galls5[!(galls5$gall_present == "no_gall"),]

# Emily only wants to look at the effects of warming on goldenrod & galls so get rid of "drought" and "
# gall_warmed <- galls2[!(galls2$treatment == "drought" | galls2$treatment == "warmed_drought"),]
```

Looking at Plant Height - Galls vs No Galls

```
# Take subplot average of plant height
plant_height <- galls5 %>%
        group_by(rep, footprint, treatment, gall_present) %>%
        summarize(plant_height = mean(plant_height, na.rm = TRUE))
```

`summarise()` has grouped output by 'rep', 'footprint', 'treatment'. You can override using the `.gro

```
# Boxplot
ggplot(plant_height, aes(x = treatment, y = plant_height, fill = gall_present)) +
        geom_boxplot(color = "black", outlier.shape = NA) +
        labs(x = "Treatment", y = "Plant Height", fill = "Gall Presence") +
        scale_fill_manual(values = c("olivedrab", "darkgoldenrod1"), labels = c("Gall", "No Gall")) +
        scale_x_discrete(limits = c("irr_control", "ambient", "drought", "warmed", "warmed_drought"),
                        labels=c("ambient" = "Control",
                                "drought" = "Drought",
                                "irr_control" = "Irrigated Control",
                                "warmed" = "Warmed",
                                "warmed_drought" = "Warmed & Drought"),
                        guide = guide_axis(n.dodge=2)) +
        #geom_jitter(shape=16, position=position_jitterdodge(), alpha = 0.6, aes(colour = gall_present).
        theme_classic()
```
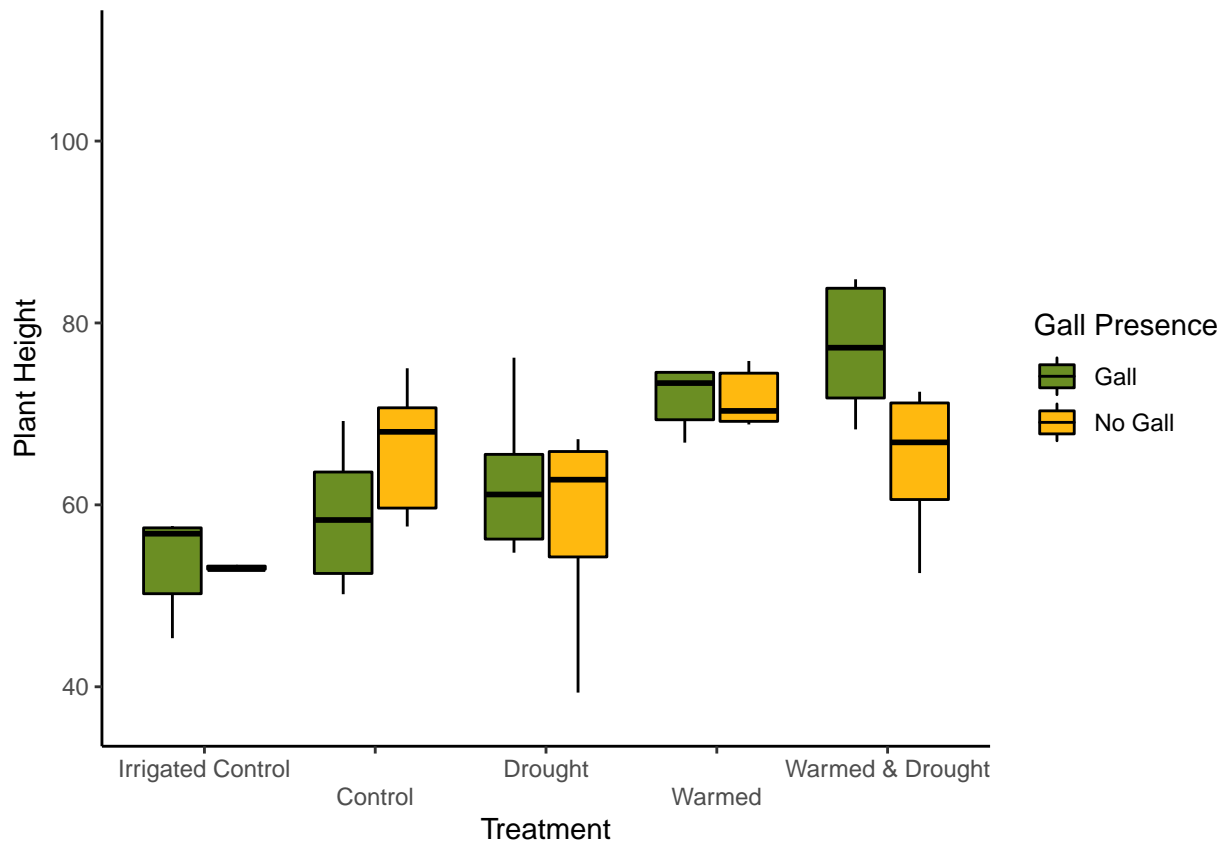
```
# Gall average plot
ggplot(plant_height, aes(x = gall_present, y = plant_height, fill = gall_present)) +
      geom_jitter(shape=16, position=position_jitterdodge(), alpha = 0.6, aes(colour = gall_present))
      scale_color_manual(values = c("gall" = "olivedrab", "no_gall" = "darkgoldenrod1")) +
      geom_boxplot(color = "black", outlier.shape = NA) +
      labs(x = "Gall Presence", y = "Plant Height") +
      scale_fill_manual(values = c("olivedrab", "darkgoldenrod1")) +
      scale_x_discrete(labels=c("gall" = "Gall",
                                "no_gall" = "No Gall")) +
      theme_classic() +
      theme(legend.position = "none")
```
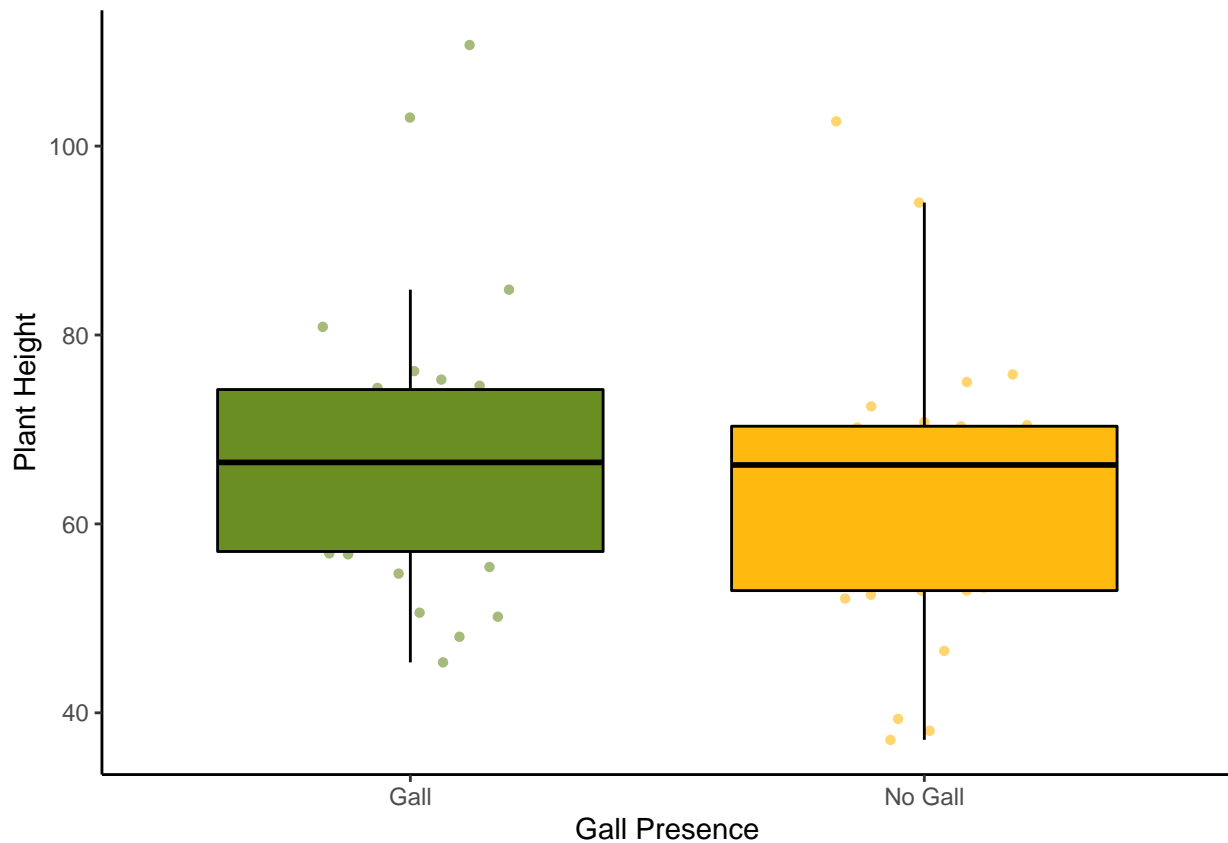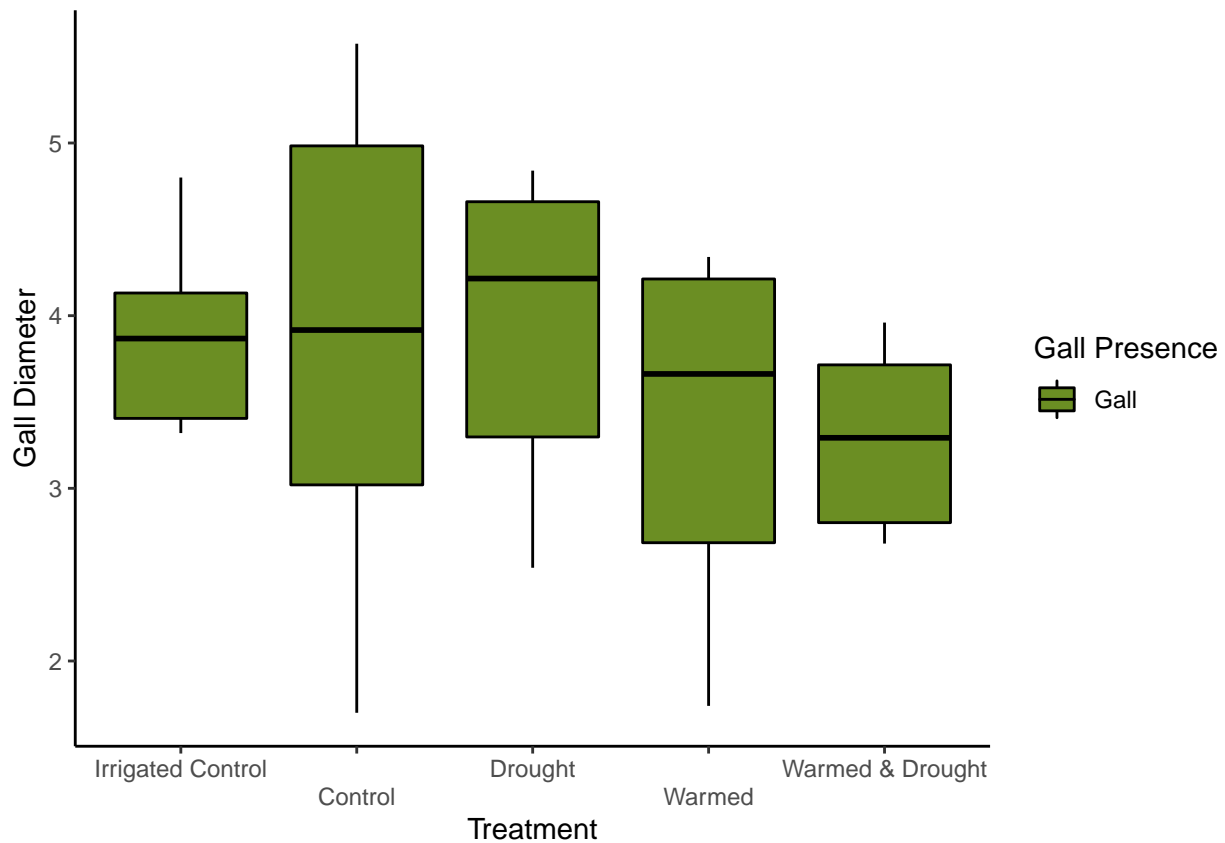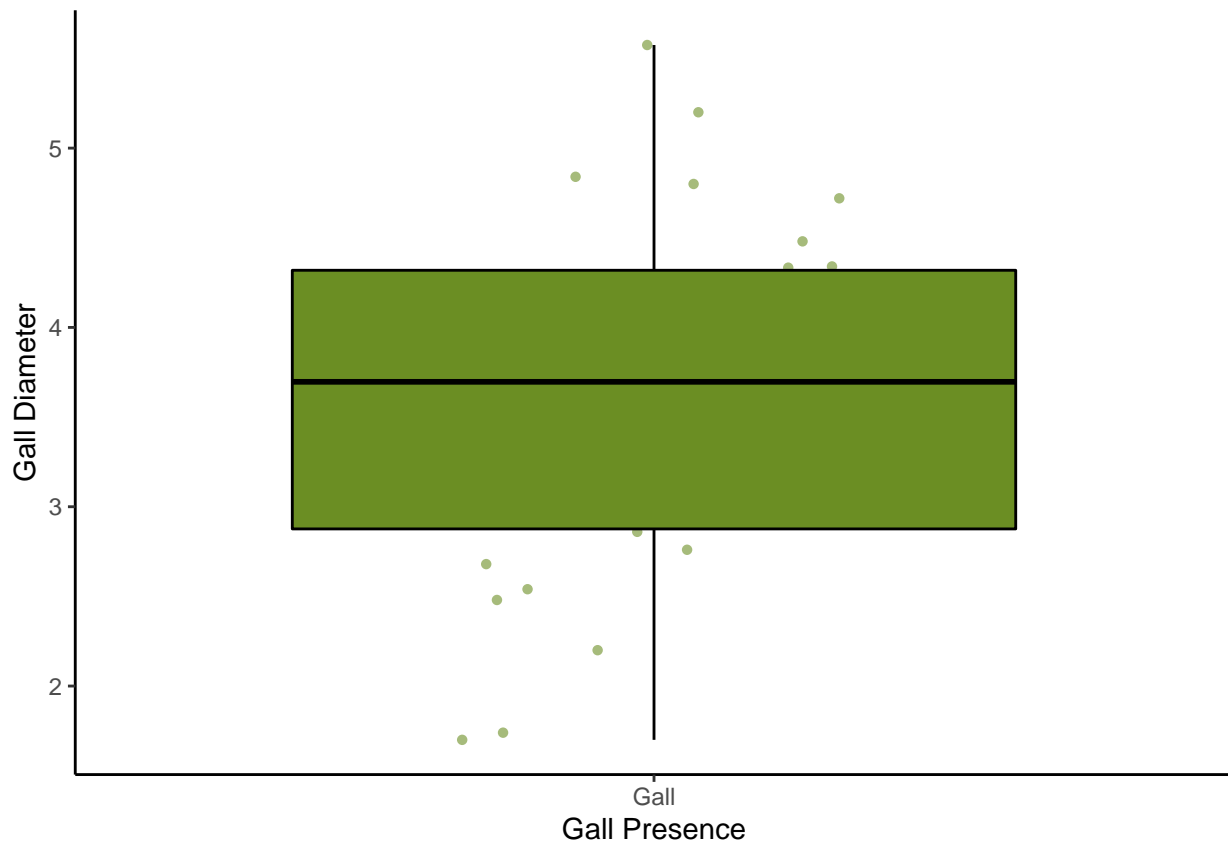
Looking at Gall Diameter

```r
# Take subplot average of gall diameter
gall_diameter <- gall_only %>%
        group_by(rep, footprint, treatment, gall_present) %>%
        summarize(gall_diameter = mean(gall_diameter, na.rm = TRUE))
```

```
## `summarise()` has grouped output by 'rep', 'footprint', 'treatment'. You can override using the `.gr
```

```r
# Boxplot
ggplot(gall_diameter, aes(x = treatment, y = gall_diameter, fill = gall_present)) +
        geom_boxplot(color = "black", outlier.shape = NA) +
        labs(x = "Treatment", y = "Gall Diameter", fill = "Gall Presence") +
        scale_fill_manual(values = c("olivedrab"), labels = c("Gall")) +
        scale_x_discrete(limits = c("irr_control", "ambient", "drought", "warmed", "warmed_drought"),
                        labels=c("ambient" = "Control",
                                "drought" = "Drought",
                                "irr_control" = "Irrigated Control",
                                "warmed" = "Warmed",
                                "warmed_drought" = "Warmed & Drought"),
                        guide = guide_axis(n.dodge=2)) +
        #geom_jitter(shape=16, position=position_jitterdodge(), alpha = 0.6, aes(colour = gall_present)
        theme_classic()
```

```r
# Gall average plot
ggplot(gall_diameter, aes(x = gall_present, y = gall_diameter, fill = gall_present)) +
        geom_jitter(shape=16, position=position_jitterdodge(), alpha = 0.6, aes(colour = gall_present))
        scale_color_manual(values = c("gall" = "olivedrab", "no_gall" = "darkgoldenrod1")) +
        geom_boxplot(color = "black", outlier.shape = NA) +
        labs(x = "Gall Presence", y = "Gall Diameter") +
        scale_fill_manual(values = c("olivedrab", "darkgoldenrod1")) +
        scale_x_discrete(labels=c("gall" = "Gall")) +
        theme_classic() +
        theme(legend.position = "none")
```
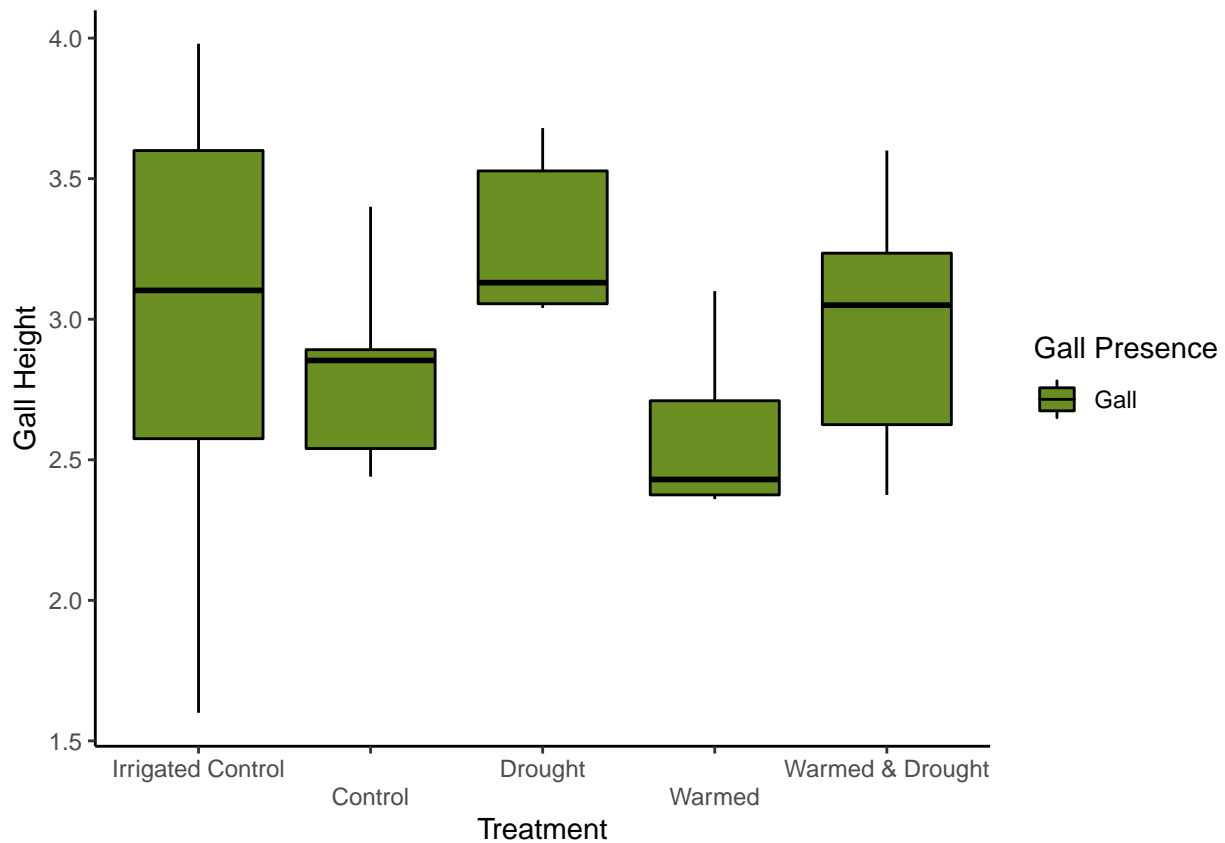
Looking at Gall Height

```r
# Take subplot average of gall height
gall_height <- gall_only %>%
        group_by(rep, footprint, treatment, gall_present) %>%
        summarize(gall_height= mean(gall_height, na.rm = TRUE))
```

```
## `summarise()` has grouped output by 'rep', 'footprint', 'treatment'. You can override using the `.gr
```

```r
# Boxplot of gall height by treatment
ggplot(gall_height, aes(x = treatment, y = gall_height, fill = gall_present)) +
        geom_boxplot(color = "black", outlier.shape = NA) +
        labs(x = "Treatment", y = "Gall Height", fill = "Gall Presence") +
        scale_fill_manual(values = c("olivedrab"), labels = c("Gall")) +
        scale_x_discrete(limits = c("irr_control", "ambient", "drought", "warmed", "warmed_drought"),
                        labels=c("ambient" = "Control",
                                "drought" = "Drought",
                                "irr_control" = "Irrigated Control",
                                "warmed" = "Warmed",
                                "warmed_drought" = "Warmed & Drought"),
                        guide = guide_axis(n.dodge=2)) +
        #geom_jitter(shape=16, position=position_jitterdodge(), alpha = 0.6, aes(colour = gall_present)
        theme_classic()
```

```r
# Gall average plot
ggplot(gall_height, aes(x = gall_present, y = gall_height, fill = gall_present)) +
    geom_jitter(shape=16, position=position_jitterdodge(), alpha = 0.6, aes(colour = gall_present))
    scale_color_manual(values = c("gall" = "olivedrab")) +
    geom_boxplot(color = "black", outlier.shape = NA) +
    labs(x = "Gall Presence", y = "Gall Height") +
    scale_fill_manual(values = c("olivedrab", "darkgoldenrod1")) +
    scale_x_discrete(labels=c("gall" = "Gall")) +
    theme_classic() +
    theme(legend.position = "none")
```