How Prevalent is Archaeological Garden Hunting?

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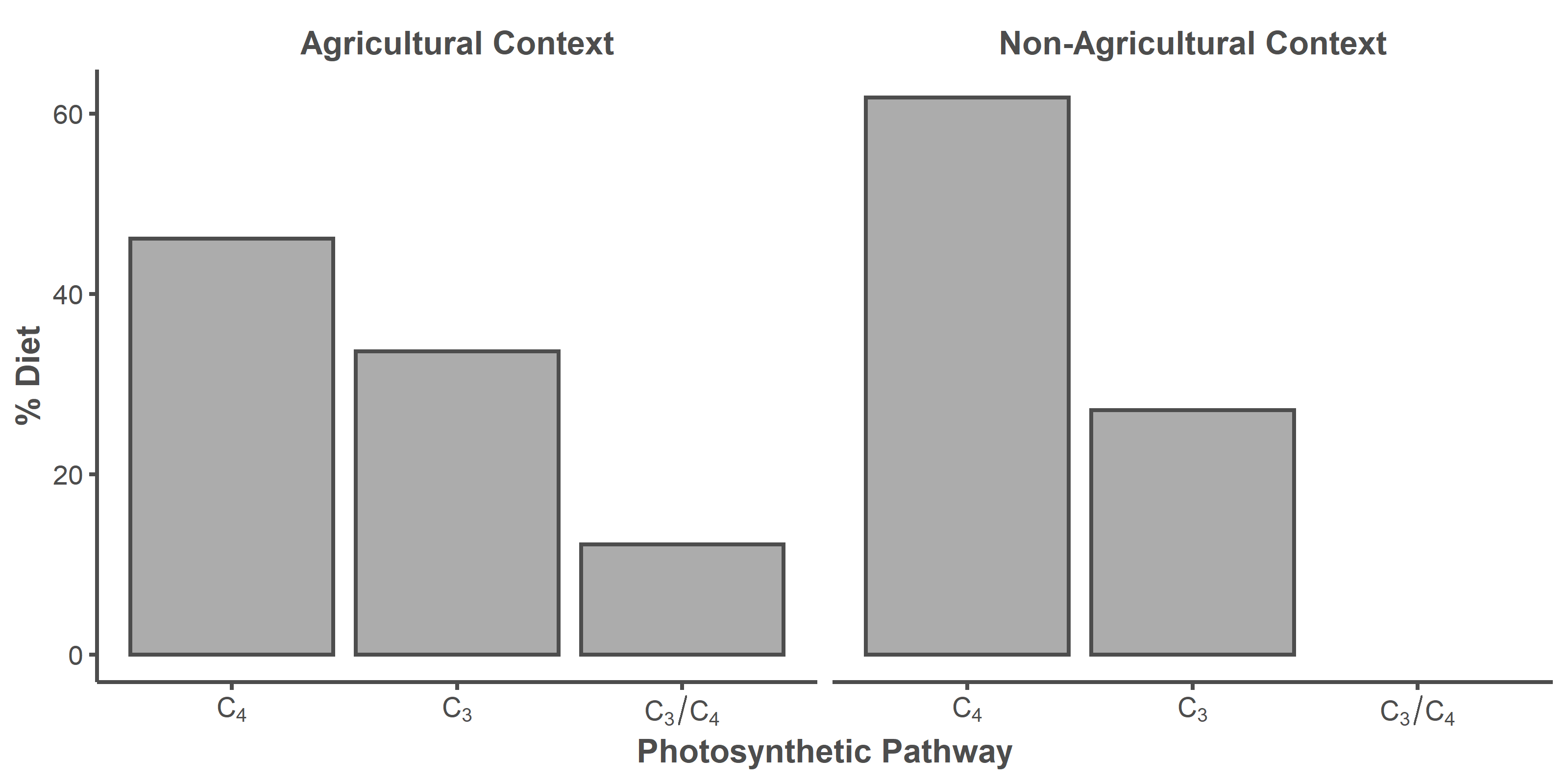
# Libraries

library(SIBER)  
library(tidyverse)  
library(cowplot)  
library(broom)  
library(car)

# Figure 1

Plant genera reported by Scribner and Krysel (1982) were assigned a photosynthetic pathway from the following sources: Basinger and Robertson (1997), Bruhl and Wilson (2007), Danneberger (1999), Giussani et al. (2001), Kocacinar and Sage (2003), Nelson (2012), Osborne et al. (2014), and Syvertsen et al. (1976).

Table\_2 <- read.csv("Scribner and Krysl\_Table 2/Table 2.csv", header = TRUE)  
  
Pathway <- Table\_2 %>%  
 select(Environmental.Context, Photosynthetic.pathway, DF....) %>%  
 group\_by(Environmental.Context, Photosynthetic.pathway) %>%  
 summarize(sum\_DF = sum(DF....), .groups = "keep")  
  
labels <- c("Agricultural Playa Basins" = "Agricultural Context",  
 "Playa Basins" = "Non-Agricultural Context")  
  
Pathway %>%  
ggplot(aes(x = reorder(Photosynthetic.pathway, -sum\_DF), y = sum\_DF)) +  
 geom\_bar(stat = "identity", size = 0.75, alpha = 0.5, color = "#4d4d4d") +  
 facet\_wrap(~ Environmental.Context, ncol = 2,   
 labeller = labeller(Environmental.Context = labels)) +  
 scale\_x\_discrete(labels = parse(text = c("C[4]", "C[3]", "C[3]/C[4]"))) +  
 theme\_classic() +  
 theme(legend.position="none",  
 strip.background = element\_blank(),  
 strip.text.x = element\_text(color = "#4d4d4d", size = 12,   
 face = "bold"),  
 axis.line = element\_line(color = "#4d4d4d", size = 0.75),  
 axis.text.x = element\_text(color = "#4d4d4d", size = 10),  
 axis.text.y = element\_text(color = "#4d4d4d", size = 10),  
 axis.title.x = element\_text(color = "#4d4d4d", size = 12,   
 face = "bold"),  
 axis.title.y = element\_text(color = "#4d4d4d", size = 12,   
 face = "bold"),  
 axis.ticks.x = element\_line(color = "#4d4d4d", size = 0.75),  
 axis.ticks.y = element\_line(color = "#4d4d4d", size = 0.75)) +  
 labs(x = "Photosynthetic Pathway", y = "% Diet")



# Isotope Data

Bone from the archaeo dataset was demineralized in 0.5 N hydrochloric acid, lipids were removed using 2:1 chloroform:methanol, and the resulting collagen pseudomorph was freeze-dried overnight. Between 0.5 and 0.6 mg of collagen was weighed out for the analysis of δ13C and δ15N. All seeds from the seeds dataset were purchased from Native seeds/SEARCH. Between 5.0 and 6.0 mg of ground corn and 2.0 and 2.5 mg of ground bean/squash was weighed out for the analysis of δ13C and δ15N. δ13C and δ15N were measured at the University of New Mexico Center for Stable Isotopes (UNM CSI, Albuquerque, NM) on a Thermo Scientific Delta V isotope ratio mass spectrometer (IRMS) with a dual inlet and Conflo IV interface coupled to a Costech 4010 elemental analyzer (EA). Stable isotope values are reported as parts per mil (‰).

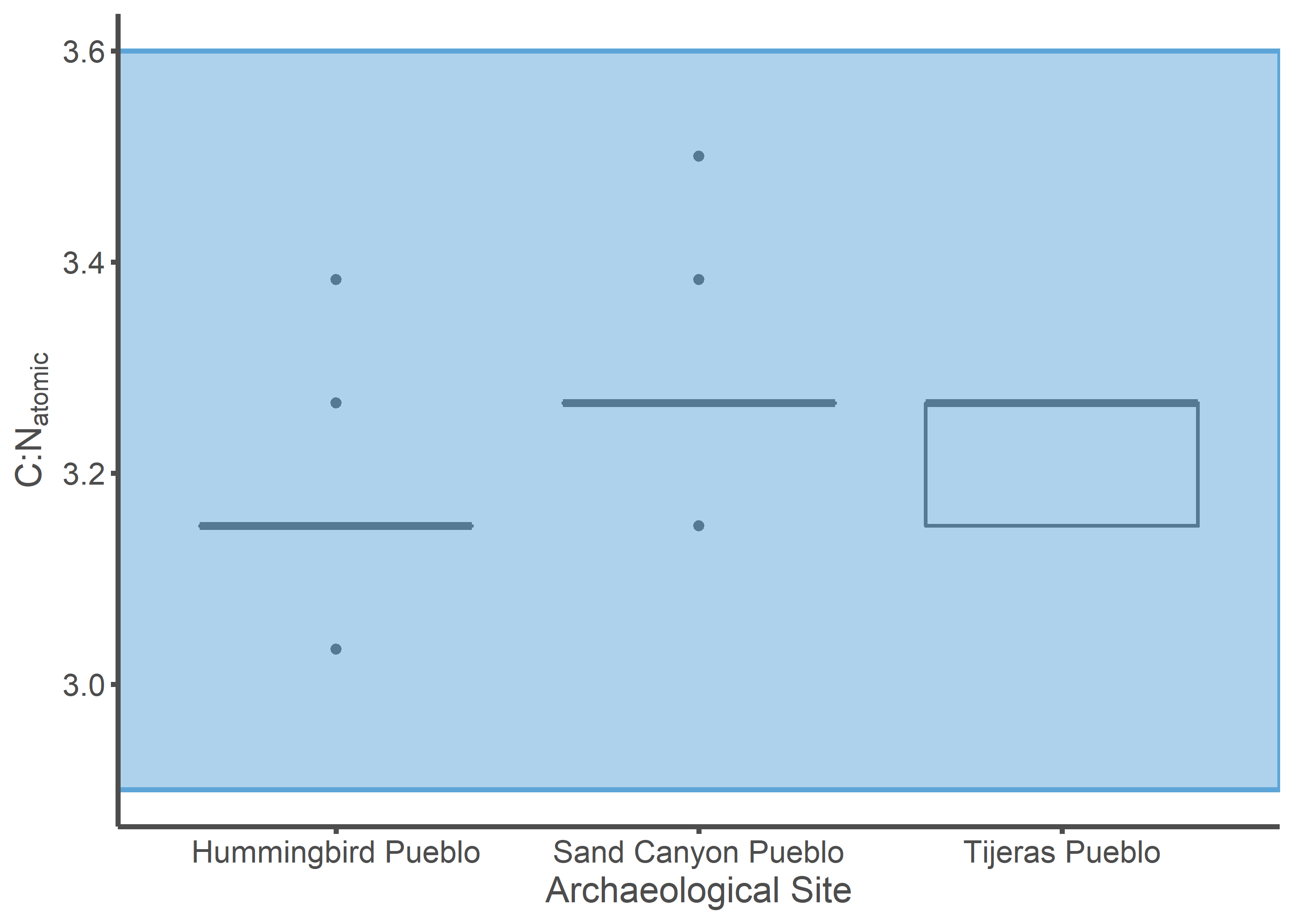
The humans and turkeys isotope values come from the following sources: Chisholm and Matson (1994), Coltrain et al. (2007), Conrad et al. (2016), Jones et al. (2016), Kellner et al. (2010), Kennett et al. (2017), Martin (1999), McCaffery et al. (2014), and Rawlings and Driver (2010).

archaeo <- read.csv("archaeological.csv", header = TRUE)  
seeds <- read.csv("modern seeds.csv", header = TRUE)  
turkeys <- read.csv("turkeys.csv", header = TRUE)   
humans <- read.csv("humans.csv", header = TRUE)

# Assessing Collagen Purity

Boxplots of C:Natomic values of archaeological leporid collagen per site. The blue box represents the acceptable range of collagen purity (2.9-3.6) reported by Ambrose (1990).

archaeo %>%  
 mutate(CNatomic = CN \* (14/12)) %>%  
 ggplot(mapping = aes(y = CNatomic, x = Site.Name, group = Site.Name)) +  
 geom\_boxplot(color = "#4d4d4d", size = 0.75) +  
 labs(y = expression("C:N"[atomic]), x = "Archaeological Site") +  
 theme\_classic() +  
 theme(legend.position="none",  
 axis.line = element\_line(color = "#4d4d4d", size = 1),  
 axis.text.x = element\_text(color = "#4d4d4d", size = 12),  
 axis.text.y = element\_text(color = "#4d4d4d", size = 12),  
 axis.title.x = element\_text(color = "#4d4d4d", size = 14),  
 axis.title.y = element\_text(color = "#4d4d4d", size = 14),  
 axis.ticks.x = element\_line(color = "#4d4d4d", size = 1),  
 axis.ticks.y = element\_line(color = "#4d4d4d", size = 1)) +  
 scale\_y\_continuous(limits=c(2.9, 3.6)) +  
 annotate(geom = "rect", xmin = -Inf, xmax = Inf, ymin = 2.9, ymax = 3.6,   
 color = "#5da5d8", fill = "#5da5d8", alpha = 0.5, size = 1)



# Data Wrangling

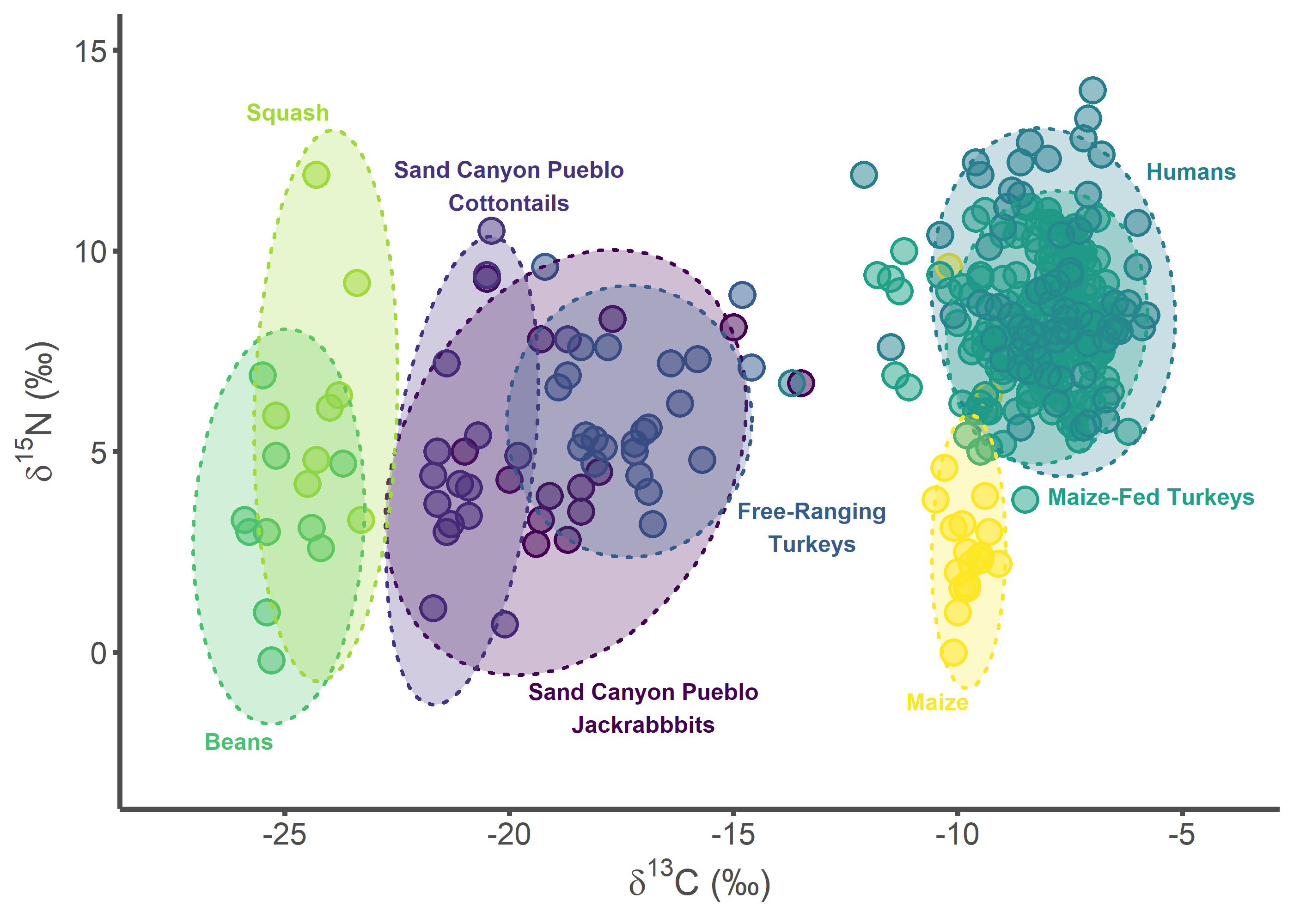
A 13C Suess correction of 2.0‰ was applied to the modern seed data (Dombrosky 2020).

seeds <- seeds %>%  
 mutate(d13Csuess = d13C + 2)  
  
archaeo\_SIBER <- archaeo %>%  
 unite(group, Site.Name, Genus, sep = " ") %>%  
 select(group, d13C, d15N)  
  
seeds\_SIBER <- seeds %>%  
 select(Comparative.Group, d13Csuess, d15N) %>%  
 rename(group = Comparative.Group,  
 d13C = d13Csuess)  
  
turkeys\_SIBER <- turkeys %>%  
 mutate(animal = "Turkey") %>%  
 unite(group, Diet.Type, animal, sep = " ") %>%  
 select(group, d13C, d15N)  
   
  
humans\_SIBER <- humans %>%  
 mutate(group = "Humans") %>%  
 select(group, d13C, d15N)  
  
SIBER\_data <- rbind(archaeo\_SIBER, seeds\_SIBER, turkeys\_SIBER, humans\_SIBER)

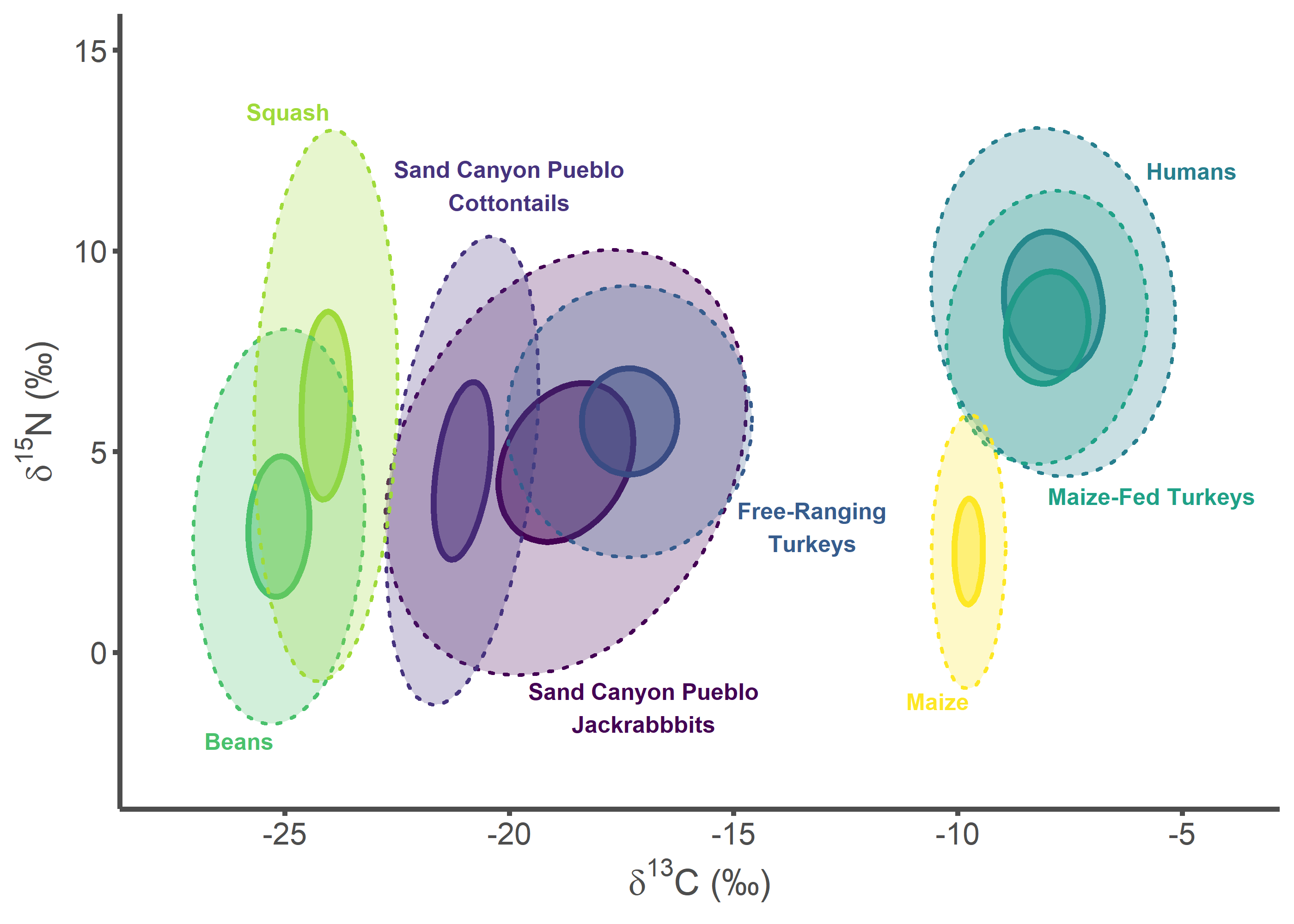
# Figure 2

## Sand Canyon Pueblo Figures

sand\_label\_df <- data.frame(  
 group = c("Sand Canyon Pueblo Lepus", "Sand Canyon Pueblo Sylvilagus",  
 "Free-ranging Turkey", "Humans", "Maize-fed Turkey", "Bean",  
 "Squash", "Corn"),  
 label = c("Sand Canyon Pueblo\nJackrabbbits",  
 "Sand Canyon Pueblo\nCottontails",  
 "Free-Ranging\nTurkeys", "Humans", "Maize-Fed Turkeys", "Beans",  
 "Squash", "Maize"),  
 d13C = c(-17, -20, -13.25, -5.8, -8, -25.25, -24, -9.75),  
 d15N = c(-0.75, 11, 2.5, 12.2, 4.1, -2, 13.25, -1),  
 hjust = c(0.5, 0.5, 0.5, 0, 0, 1, 1, 1),  
 vjust = c(1, 0, 0, 1, 1, 1, 0, 1))  
  
sand\_label\_df$group <- factor(sand\_label\_df$group,   
 levels = c("Sand Canyon Pueblo Lepus",  
 "Sand Canyon Pueblo Sylvilagus",  
 "Free-ranging Turkey", "Humans",   
 "Maize-fed Turkey", "Bean", "Squash",  
 "Corn"))  
  
sand\_plot <- SIBER\_data %>%  
 filter(group %in% c("Sand Canyon Pueblo Lepus",   
 "Sand Canyon Pueblo Sylvilagus",  
 "Bean", "Corn", "Squash", "Free-ranging Turkey",  
 "Maize-fed Turkey", "Humans"))  
   
sand\_plot$group <- factor(sand\_plot$group,   
 levels = c("Sand Canyon Pueblo Lepus",  
 "Sand Canyon Pueblo Sylvilagus",  
 "Free-ranging Turkey", "Humans",   
 "Maize-fed Turkey", "Bean", "Squash",  
 "Corn"))   
   
sand\_p1 <- ggplot(sand\_plot, aes(x = d13C, y = d15N)) +  
 geom\_point(aes(fill = group, color = group), stroke = 1, size = 4,   
 alpha = 0.5, shape = 21) +  
 geom\_point(aes(color = group), fill = NA, stroke = 1, size = 4,   
 shape = 21) +  
 ylab(expression(paste(delta^{15}, "N (\u2030)"))) +  
 xlab(expression(paste(delta^{13}, "C (\u2030)"))) +   
 theme\_classic() +  
 theme(legend.position = "none",  
 axis.line = element\_line(color = "#4d4d4d", size = 1),  
 axis.text.x = element\_text(color = "#4d4d4d", size = 12),  
 axis.text.y = element\_text(color = "#4d4d4d", size = 12),  
 axis.title.x = element\_text(color = "#4d4d4d", size = 14,   
 face = "bold"),  
 axis.title.y = element\_text(color = "#4d4d4d", size = 14,   
 face = "bold"),  
 axis.ticks.x = element\_line(color = "#4d4d4d", size = 1),  
 axis.ticks.y = element\_line(color = "#4d4d4d", size = 1)) +   
 scale\_color\_viridis\_d() +  
 stat\_ellipse(aes(group = interaction(group), color = group, fill = group),   
 alpha = 0.25, size = 0.75, linetype = 3, level = 0.95,   
 type = "t", geom = "polygon") +   
 geom\_text(data = sand\_label\_df,aes(x = d13C, y = d15N,   
 label = label, color = group, hjust = hjust,  
 vjust = vjust),  
 size = 9/.pt, fontface = "bold") +  
 scale\_fill\_viridis\_d() +  
 scale\_x\_continuous(limits=c(-27.5, -4),   
 breaks = c(-25, -20, -15, -10, -5)) +  
 scale\_y\_continuous(limits=c(-3, 15))  
  
sand\_p1

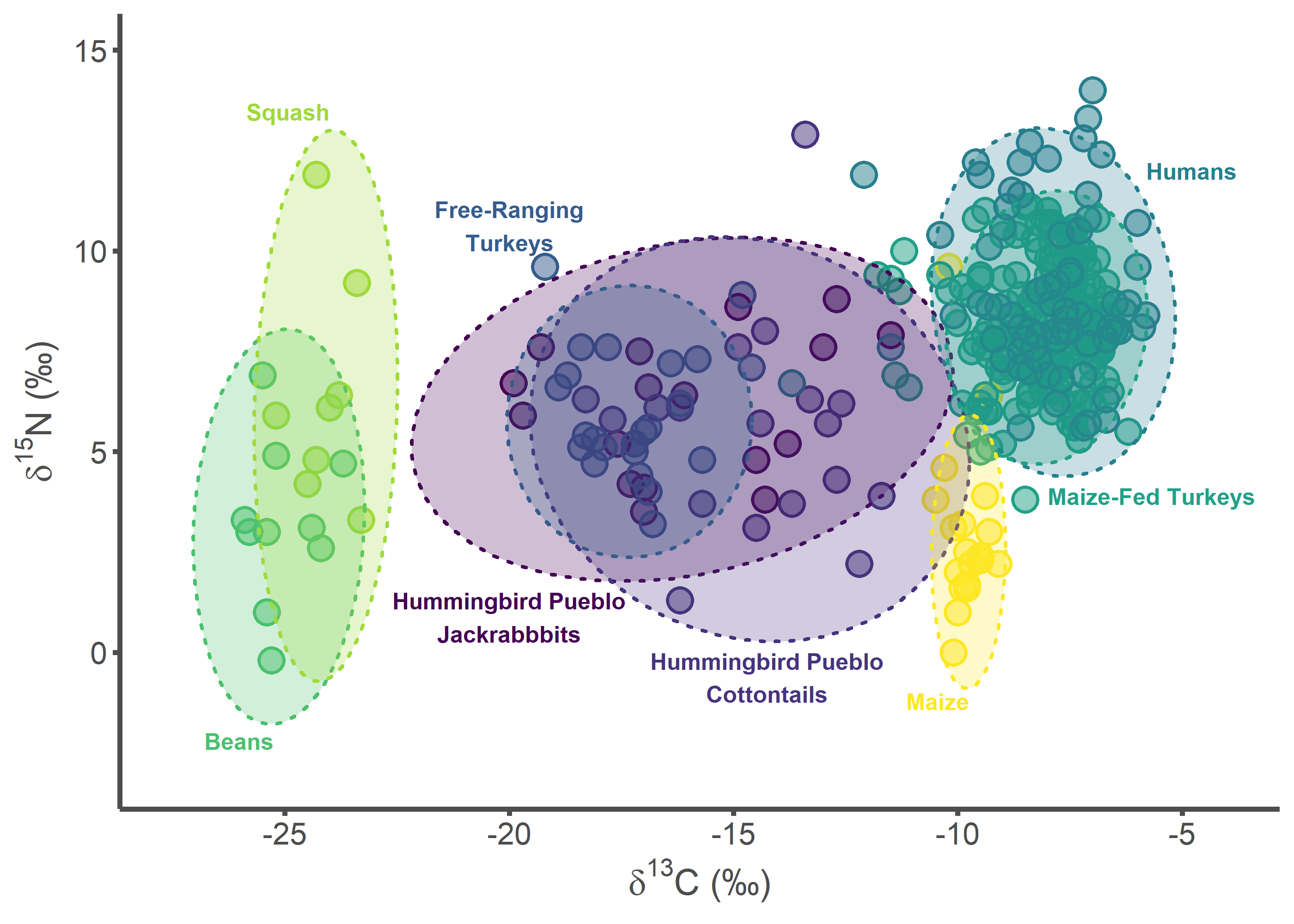


sand\_p2 <- ggplot(sand\_plot, aes(x = d13C, y = d15N)) +  
 ylab(expression(paste(delta^{15}, "N (\u2030)"))) +  
 xlab(expression(paste(delta^{13}, "C (\u2030)"))) +   
 theme\_classic() +  
 theme(legend.position = "none",  
 axis.line = element\_line(color = "#4d4d4d", size = 1),  
 axis.text.x = element\_text(color = "#4d4d4d", size = 12),  
 axis.text.y = element\_text(color = "#4d4d4d", size = 12),  
 axis.title.x = element\_text(color = "#4d4d4d", size = 14,   
 face = "bold"),  
 axis.title.y = element\_text(color = "#4d4d4d", size = 14,   
 face = "bold"),  
 axis.ticks.x = element\_line(color = "#4d4d4d", size = 1),  
 axis.ticks.y = element\_line(color = "#4d4d4d", size = 1)) +   
 scale\_color\_viridis\_d() +  
 stat\_ellipse(aes(group = interaction(group), color = group, fill = group),   
 alpha = 0.5, size = 1.1, linetype = 1, level = 0.40,   
 type = "t", geom = "polygon") +  
 stat\_ellipse(aes(group = interaction(group), color = group, fill = group),   
 alpha = 0.25, size = 0.75, linetype = 3, level = 0.95,   
 type = "t", geom = "polygon") +   
 geom\_text(data = sand\_label\_df,aes(x = d13C, y = d15N,   
 label = label, color = group, hjust = hjust,  
 vjust = vjust),  
 size = 9/.pt, fontface = "bold") +  
 scale\_fill\_viridis\_d() +  
 scale\_x\_continuous(limits=c(-27.5, -4),   
 breaks = c(-25, -20, -15, -10, -5)) +  
 scale\_y\_continuous(limits=c(-3, 15))  
  
sand\_p2

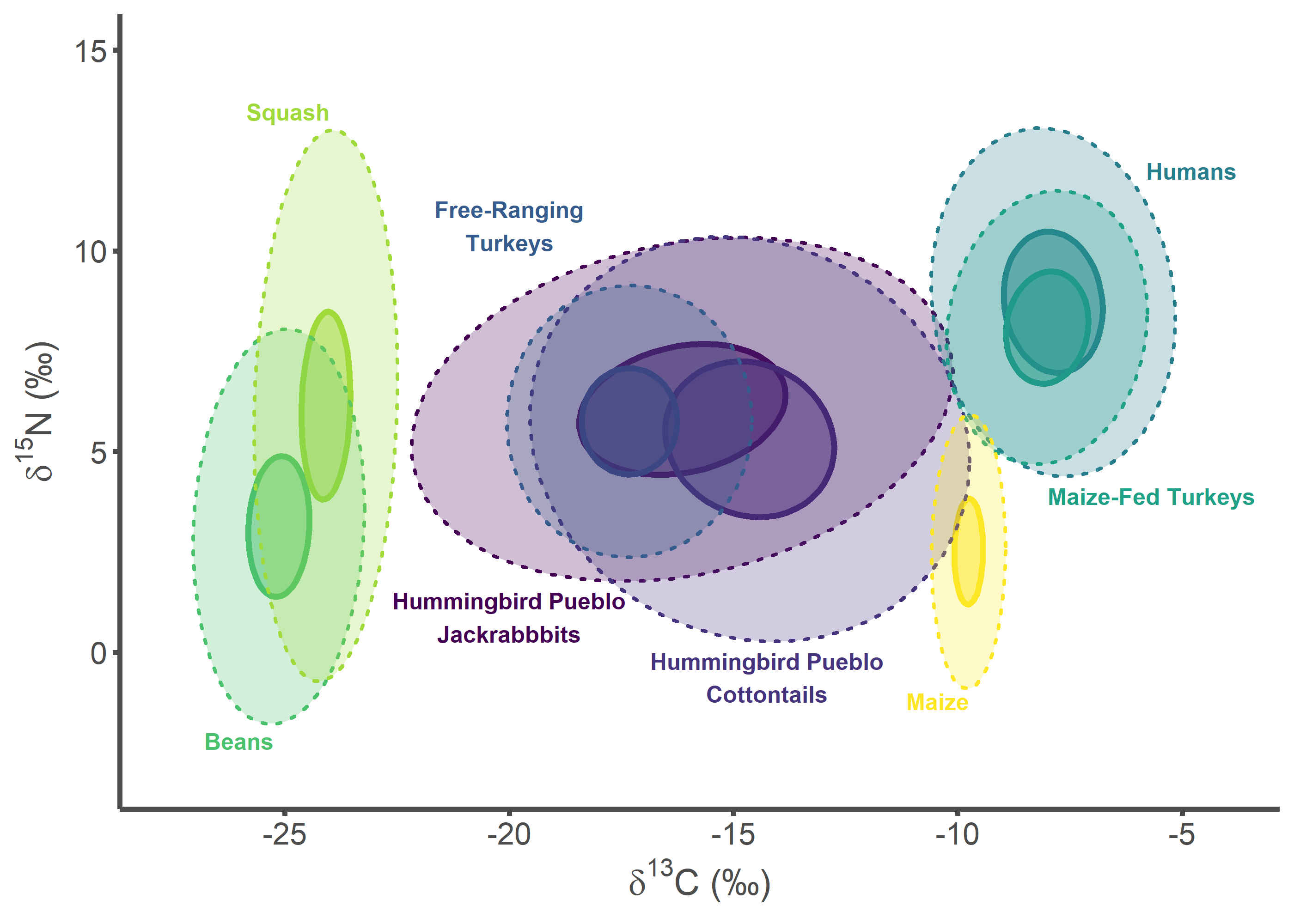


## Hummingbird Pueblo Figures

hum\_label\_df <- data.frame(  
 group = c("Hummingbird Pueblo Lepus", "Hummingbird Pueblo Sylvilagus",  
 "Free-ranging Turkey", "Humans", "Maize-fed Turkey", "Bean",  
 "Squash", "Corn"),  
 label = c("Hummingbird Pueblo\nJackrabbbits",  
 "Hummingbird Pueblo\nCottontails",  
 "Free-Ranging\nTurkeys", "Humans", "Maize-Fed Turkeys", "Beans",  
 "Squash", "Maize"),  
 d13C = c(-20, -14.25, -20, -5.8, -8, -25.25, -24, -9.75),  
 d15N = c(1.5, -1.25, 10, 12.2, 4.1, -2, 13.25, -1),  
 hjust = c(0.5, 0.5, 0.5, 0, 0, 1, 1, 1),  
 vjust = c(1, 0, 0, 1, 1, 1, 0, 1))  
  
hum\_label\_df$group <- factor(hum\_label\_df$group,   
 levels = c("Hummingbird Pueblo Lepus",  
 "Hummingbird Pueblo Sylvilagus",  
 "Free-ranging Turkey", "Humans",   
 "Maize-fed Turkey", "Bean", "Squash",  
 "Corn"))  
  
hum\_plot <- SIBER\_data %>%  
 filter(group %in% c("Hummingbird Pueblo Lepus",   
 "Hummingbird Pueblo Sylvilagus",  
 "Bean", "Corn", "Squash", "Free-ranging Turkey",  
 "Maize-fed Turkey", "Humans"))  
   
hum\_plot$group <- factor(hum\_plot$group,   
 levels = c("Hummingbird Pueblo Lepus",  
 "Hummingbird Pueblo Sylvilagus",  
 "Free-ranging Turkey", "Humans",   
 "Maize-fed Turkey", "Bean", "Squash",  
 "Corn"))   
   
hum\_p1 <- ggplot(hum\_plot, aes(x = d13C, y = d15N)) +  
 geom\_point(aes(fill = group, color = group), stroke = 1, size = 4,   
 alpha = 0.5, shape = 21) +  
 geom\_point(aes(color = group), fill = NA, stroke = 1, size = 4,   
 shape = 21) +  
 ylab(expression(paste(delta^{15}, "N (\u2030)"))) +  
 xlab(expression(paste(delta^{13}, "C (\u2030)"))) +   
 theme\_classic() +  
 theme(legend.position = "none",  
 axis.line = element\_line(color = "#4d4d4d", size = 1),  
 axis.text.x = element\_text(color = "#4d4d4d", size = 12),  
 axis.text.y = element\_text(color = "#4d4d4d", size = 12),  
 axis.title.x = element\_text(color = "#4d4d4d", size = 14,   
 face = "bold"),  
 axis.title.y = element\_text(color = "#4d4d4d", size = 14,   
 face = "bold"),  
 axis.ticks.x = element\_line(color = "#4d4d4d", size = 1),  
 axis.ticks.y = element\_line(color = "#4d4d4d", size = 1)) +   
 scale\_color\_viridis\_d() +  
 stat\_ellipse(aes(group = interaction(group), color = group, fill = group),   
 alpha = 0.25, size = 0.75, linetype = 3, level = 0.95,   
 type = "t", geom = "polygon") +   
 geom\_text(data = hum\_label\_df,aes(x = d13C, y = d15N,   
 label = label, color = group, hjust = hjust,  
 vjust = vjust),  
 size = 9/.pt, fontface = "bold") +  
 scale\_fill\_viridis\_d() +  
 scale\_x\_continuous(limits=c(-27.5, -4),   
 breaks = c(-25, -20, -15, -10, -5)) +  
 scale\_y\_continuous(limits=c(-3, 15))  
  
hum\_p1

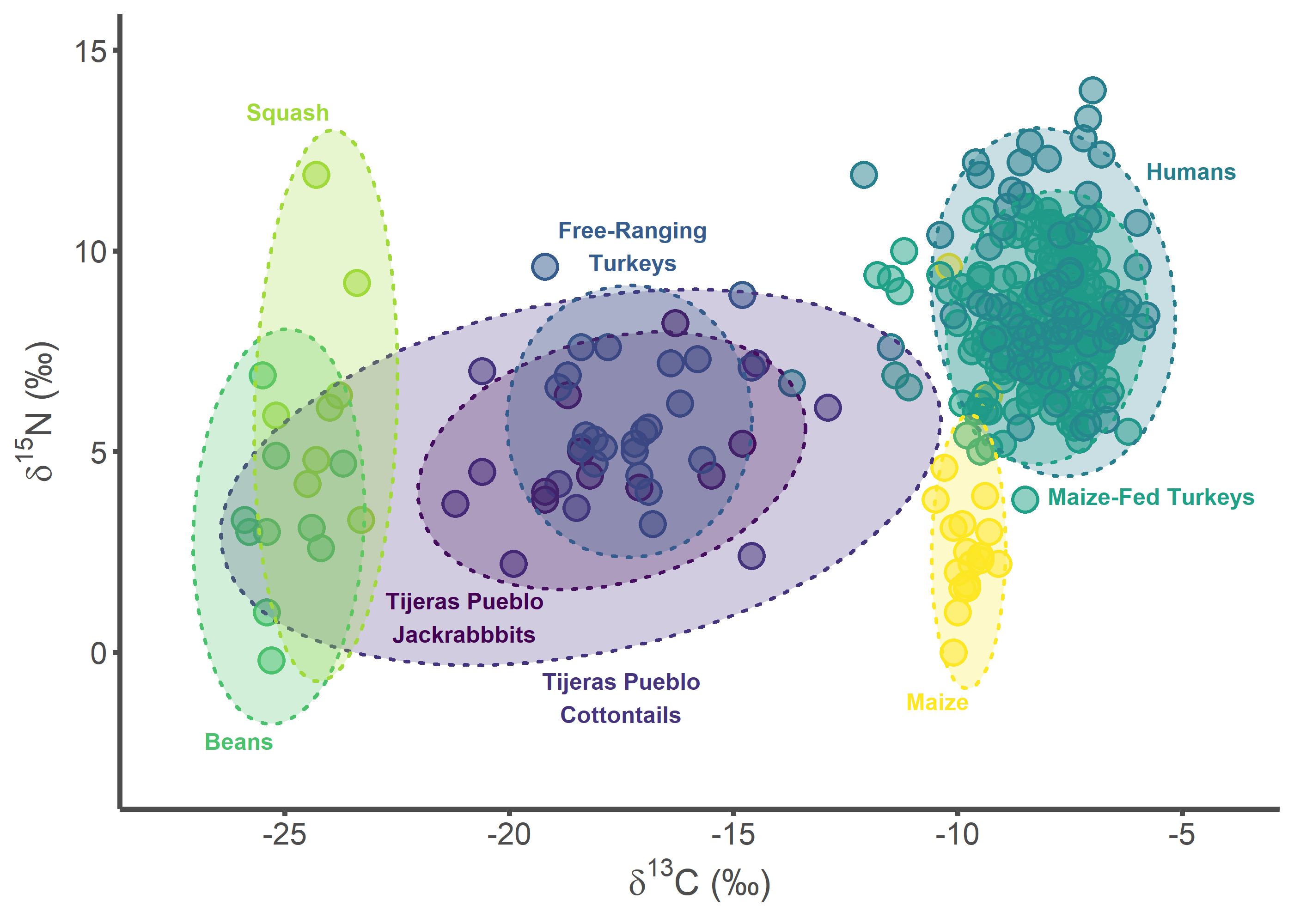


hum\_p2 <- ggplot(hum\_plot, aes(x = d13C, y = d15N)) +  
 ylab(expression(paste(delta^{15}, "N (\u2030)"))) +  
 xlab(expression(paste(delta^{13}, "C (\u2030)"))) +   
 theme\_classic() +  
 theme(legend.position = "none",  
 axis.line = element\_line(color = "#4d4d4d", size = 1),  
 axis.text.x = element\_text(color = "#4d4d4d", size = 12),  
 axis.text.y = element\_text(color = "#4d4d4d", size = 12),  
 axis.title.x = element\_text(color = "#4d4d4d", size = 14,   
 face = "bold"),  
 axis.title.y = element\_text(color = "#4d4d4d", size = 14,   
 face = "bold"),  
 axis.ticks.x = element\_line(color = "#4d4d4d", size = 1),  
 axis.ticks.y = element\_line(color = "#4d4d4d", size = 1)) +   
 scale\_color\_viridis\_d() +  
 stat\_ellipse(aes(group = interaction(group), color = group, fill = group),   
 alpha = 0.5, size = 1.1, linetype = 1, level = 0.40, type = "t",   
 geom = "polygon") +  
 stat\_ellipse(aes(group = interaction(group), color = group, fill = group),   
 alpha = 0.25, size = 0.75, linetype = 3, level = 0.95,   
 type = "t", geom = "polygon") +   
 geom\_text(data = hum\_label\_df,aes(x = d13C, y = d15N,   
 label = label, color = group, hjust = hjust,  
 vjust = vjust),  
 size = 9/.pt, fontface = "bold") +  
 scale\_fill\_viridis\_d() +  
 scale\_x\_continuous(limits=c(-27.5, -4),   
 breaks = c(-25, -20, -15, -10, -5)) +  
 scale\_y\_continuous(limits=c(-3, 15))  
  
hum\_p2

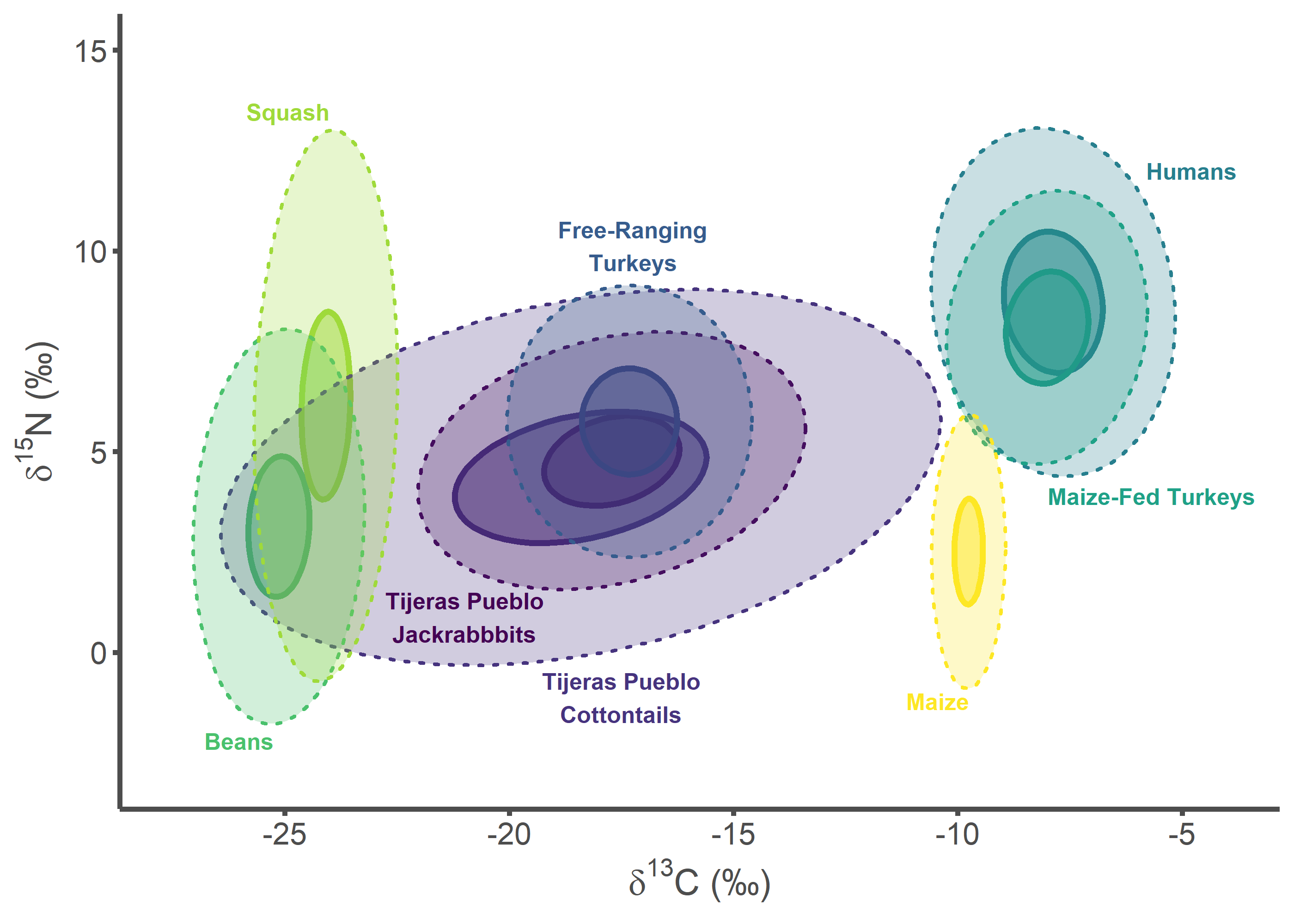


## Tijeras Pueblo Figures

tij\_label\_df <- data.frame(  
 group = c("Tijeras Pueblo Lepus", "Tijeras Pueblo Sylvilagus",  
 "Free-ranging Turkey", "Humans", "Maize-fed Turkey", "Bean",  
 "Squash", "Corn"),  
 label = c("Tijeras Pueblo\nJackrabbbits",  
 "Tijeras Pueblo\nCottontails",  
 "Free-Ranging\nTurkeys", "Humans", "Maize-Fed Turkeys", "Beans",  
 "Squash", "Maize"),  
 d13C = c(-21, -17.5, -17.25, -5.8, -8, -25.25, -24, -9.75),  
 d15N = c(1.5, -1.75, 9.5, 12.2, 4.1, -2, 13.25, -1),  
 hjust = c(0.5, 0.5, 0.5, 0, 0, 1, 1, 1),  
 vjust = c(1, 0, 0, 1, 1, 1, 0, 1))  
  
tij\_label\_df$group <- factor(tij\_label\_df$group,   
 levels = c("Tijeras Pueblo Lepus",  
 "Tijeras Pueblo Sylvilagus",  
 "Free-ranging Turkey", "Humans",   
 "Maize-fed Turkey", "Bean", "Squash",  
 "Corn"))  
  
tij\_plot <- SIBER\_data %>%  
 filter(group %in% c("Tijeras Pueblo Lepus",   
 "Tijeras Pueblo Sylvilagus",  
 "Bean", "Corn", "Squash", "Free-ranging Turkey",  
 "Maize-fed Turkey", "Humans"))  
   
tij\_plot$group <- factor(tij\_plot$group,   
 levels = c("Tijeras Pueblo Lepus",  
 "Tijeras Pueblo Sylvilagus",  
 "Free-ranging Turkey", "Humans",   
 "Maize-fed Turkey", "Bean", "Squash",  
 "Corn"))   
   
tij\_p1 <- ggplot(tij\_plot, aes(x = d13C, y = d15N)) +  
 geom\_point(aes(fill = group, color = group), stroke = 1, size = 4,   
 alpha = 0.5, shape = 21) +  
 geom\_point(aes(color = group), fill = NA, stroke = 1, size = 4,   
 shape = 21) +  
 ylab(expression(paste(delta^{15}, "N (\u2030)"))) +  
 xlab(expression(paste(delta^{13}, "C (\u2030)"))) +   
 theme\_classic() +  
 theme(legend.position = "none",  
 axis.line = element\_line(color = "#4d4d4d", size = 1),  
 axis.text.x = element\_text(color = "#4d4d4d", size = 12),  
 axis.text.y = element\_text(color = "#4d4d4d", size = 12),  
 axis.title.x = element\_text(color = "#4d4d4d", size = 14,   
 face = "bold"),  
 axis.title.y = element\_text(color = "#4d4d4d", size = 14,   
 face = "bold"),  
 axis.ticks.x = element\_line(color = "#4d4d4d", size = 1),  
 axis.ticks.y = element\_line(color = "#4d4d4d", size = 1)) +   
 scale\_color\_viridis\_d() +  
 stat\_ellipse(aes(group = interaction(group), color = group, fill = group),   
 alpha = 0.25, size = 0.75, linetype = 3, level = 0.95,   
 type = "t", geom = "polygon") +   
 geom\_text(data = tij\_label\_df,aes(x = d13C, y = d15N,   
 label = label, color = group, hjust = hjust,  
 vjust = vjust),  
 size = 9/.pt, fontface = "bold") +  
 scale\_fill\_viridis\_d() +  
 scale\_x\_continuous(limits=c(-27.5, -4),   
 breaks = c(-25, -20, -15, -10, -5)) +  
 scale\_y\_continuous(limits=c(-3, 15))  
  
tij\_p1

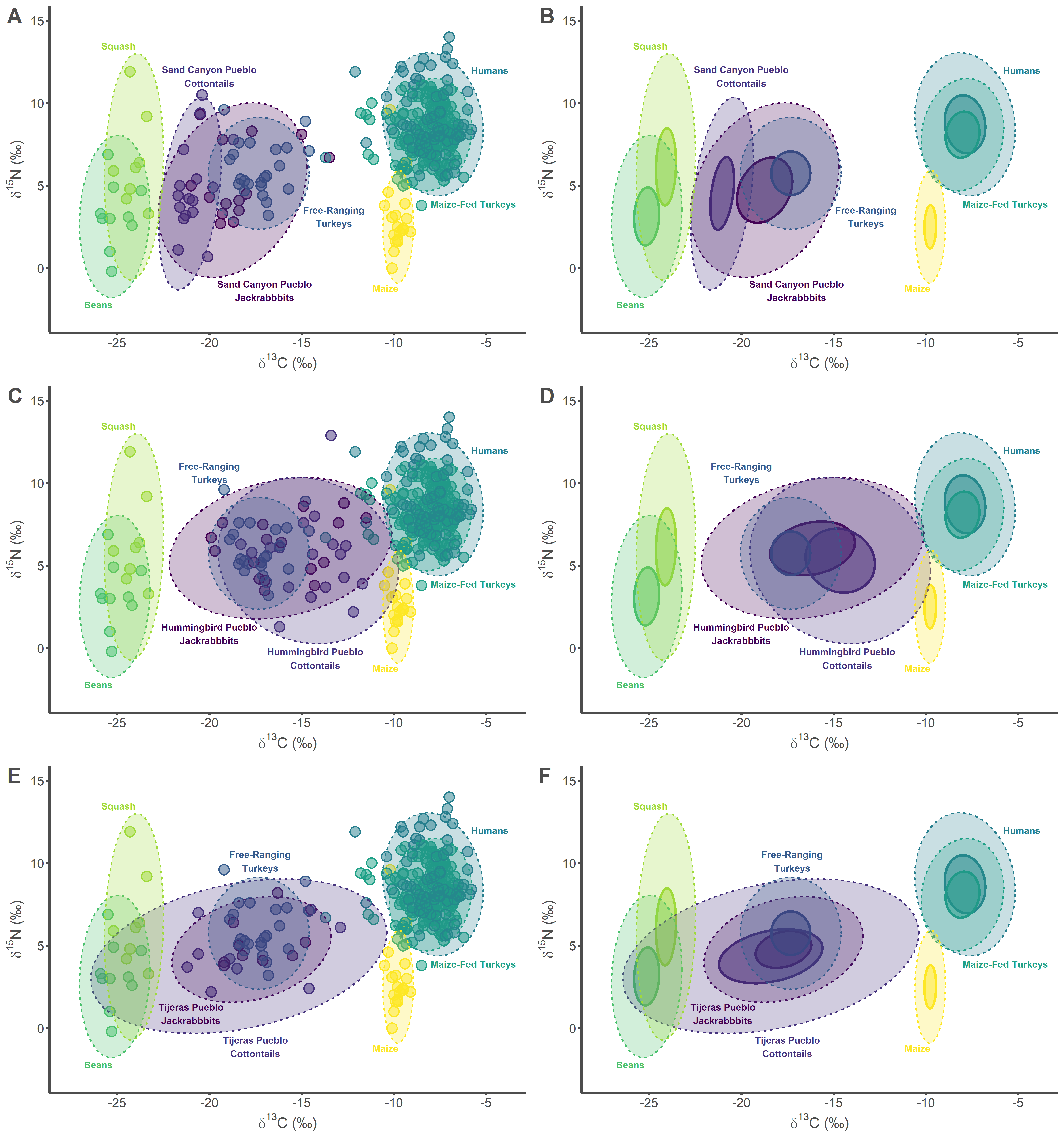


tij\_p2 <- ggplot(tij\_plot, aes(x = d13C, y = d15N)) +  
 ylab(expression(paste(delta^{15}, "N (\u2030)"))) +  
 xlab(expression(paste(delta^{13}, "C (\u2030)"))) +   
 theme\_classic() +  
 theme(legend.position = "none",  
 axis.line = element\_line(color = "#4d4d4d", size = 1),  
 axis.text.x = element\_text(color = "#4d4d4d", size = 12),  
 axis.text.y = element\_text(color = "#4d4d4d", size = 12),  
 axis.title.x = element\_text(color = "#4d4d4d", size = 14,   
 face = "bold"),  
 axis.title.y = element\_text(color = "#4d4d4d", size = 14,   
 face = "bold"),  
 axis.ticks.x = element\_line(color = "#4d4d4d", size = 1),  
 axis.ticks.y = element\_line(color = "#4d4d4d", size = 1)) +   
 scale\_color\_viridis\_d() +  
 stat\_ellipse(aes(group = interaction(group), color = group, fill = group),   
 alpha = 0.5, size = 1.1, linetype = 1, level = 0.40,   
 type = "t", geom = "polygon") +  
 stat\_ellipse(aes(group = interaction(group), color = group, fill = group),   
 alpha = 0.25, size = 0.75, linetype = 3, level = 0.95,   
 type = "t", geom = "polygon") +   
 geom\_text(data = tij\_label\_df,aes(x = d13C, y = d15N,   
 label = label, color = group, hjust = hjust,  
 vjust = vjust),  
 size = 9/.pt, fontface = "bold") +  
 scale\_fill\_viridis\_d() +  
 scale\_x\_continuous(limits=c(-27.5, -4),   
 breaks = c(-25, -20, -15, -10, -5)) +  
 scale\_y\_continuous(limits=c(-3, 15))  
  
tij\_p2



## Combine Figures

all\_plots <- plot\_grid(sand\_p1, sand\_p2, hum\_p1, hum\_p2, tij\_p1, tij\_p2,  
 labels = "AUTO", label\_colour = "#4d4d4d",   
 label\_size = 20, ncol = 2, nrow = 3)  
  
all\_plots



ggsave("Figure 2.jpg", dpi = 300)

## Saving 14 x 15 in image

## Test for Normality

Some isotope values per group are non-normal. Thus, ellipses in Figure 2 are visualized based on the t-distribution, which is also good for small sample sizes.

SIBER\_data %>%  
 group\_by(group) %>%  
 do(tidy(shapiro.test(.$d13C)))

## # A tibble: 12 x 4  
## # Groups: group [12]  
## group statistic p.value method   
## <chr> <dbl> <dbl> <chr>   
## 1 Bean 0.882 0.139 Shapiro-Wilk normality t~  
## 2 Corn 0.980 0.928 Shapiro-Wilk normality t~  
## 3 Free-ranging Turkey 0.960 0.462 Shapiro-Wilk normality t~  
## 4 Humans 0.914 0.000106 Shapiro-Wilk normality t~  
## 5 Hummingbird Pueblo Lepus 0.956 0.565 Shapiro-Wilk normality t~  
## 6 Hummingbird Pueblo Sylvilagus 0.956 0.502 Shapiro-Wilk normality t~  
## 7 Maize-fed Turkey 0.938 0.000000566 Shapiro-Wilk normality t~  
## 8 Sand Canyon Pueblo Lepus 0.862 0.0328 Shapiro-Wilk normality t~  
## 9 Sand Canyon Pueblo Sylvilagus 0.882 0.0415 Shapiro-Wilk normality t~  
## 10 Squash 0.958 0.788 Shapiro-Wilk normality t~  
## 11 Tijeras Pueblo Lepus 0.900 0.251 Shapiro-Wilk normality t~  
## 12 Tijeras Pueblo Sylvilagus 0.857 0.0878 Shapiro-Wilk normality t~

SIBER\_data %>%  
 group\_by(group) %>%  
 do(tidy(shapiro.test(.$d15N)))

## # A tibble: 12 x 4  
## # Groups: group [12]  
## group statistic p.value method   
## <chr> <dbl> <dbl> <chr>   
## 1 Bean 0.958 0.766 Shapiro-Wilk normality test  
## 2 Corn 0.825 0.00206 Shapiro-Wilk normality test  
## 3 Free-ranging Turkey 0.960 0.462 Shapiro-Wilk normality test  
## 4 Humans 0.943 0.00241 Shapiro-Wilk normality test  
## 5 Hummingbird Pueblo Lepus 0.946 0.390 Shapiro-Wilk normality test  
## 6 Hummingbird Pueblo Sylvilagus 0.900 0.0496 Shapiro-Wilk normality test  
## 7 Maize-fed Turkey 0.986 0.0793 Shapiro-Wilk normality test  
## 8 Sand Canyon Pueblo Lepus 0.884 0.0664 Shapiro-Wilk normality test  
## 9 Sand Canyon Pueblo Sylvilagus 0.942 0.376 Shapiro-Wilk normality test  
## 10 Squash 0.904 0.314 Shapiro-Wilk normality test  
## 11 Tijeras Pueblo Lepus 0.820 0.0348 Shapiro-Wilk normality test  
## 12 Tijeras Pueblo Sylvilagus 0.917 0.371 Shapiro-Wilk normality test

# SIBER Area Calculations

TA = Total Area, SEA = Standard Ellipse Area, and SEAc = Small Sample Size Corrected Standard Ellipse Area (see Jackson et al. 2011)

siber.example <- SIBER\_data %>%  
 select(d13C, d15N, group) %>%  
 mutate(community = 1) %>%  
 rename(iso1 = d13C,  
 iso2 = d15N)  
   
siber.example <- createSiberObject(siber.example)  
  
group.ML1 <- data.frame(groupMetricsML(siber.example)) %>%  
 rename("Hummingbird Jackrabbits" = X1.Hummingbird.Pueblo.Lepus,  
 "Hummingbird Cottontails" = X1.Hummingbird.Pueblo.Sylvilagus,  
 "Sand Canyon Jackrabbit" = X1.Sand.Canyon.Pueblo.Lepus,  
 "Sand Canyon Cottontails" = X1.Sand.Canyon.Pueblo.Sylvilagus,  
 "Tijeras Pueblo Jackrabbits" = X1.Tijeras.Pueblo.Lepus,  
 "Tijeras Pueblo Cottontails" = X1.Tijeras.Pueblo.Sylvilagus,  
 "Beans" = X1.Bean,  
 "Maize" = X1.Corn,  
 "Squash" = X1.Squash,  
 "Free-ranging Turkey" = X1.Free.ranging.Turkey,  
 "Maize-fed Turkey" = X1.Maize.fed.Turkey,  
 "Humans" = X1.Humans) %>%  
 t() %>%  
 round(digits = 2)  
   
group.ML1

## TA SEA SEAc  
## Hummingbird Jackrabbits 28.91 13.02 13.88  
## Hummingbird Cottontails 44.81 15.47 16.38  
## Sand Canyon Jackrabbit 29.74 13.82 14.97  
## Sand Canyon Cottontails 18.75 6.43 6.89  
## Tijeras Pueblo Cottontails 33.91 17.58 20.09  
## Tijeras Pueblo Jackrabbits 11.71 7.01 8.01  
## Beans 8.41 4.53 5.10  
## Maize 8.21 2.40 2.53  
## Squash 10.09 5.47 6.38  
## Free-ranging Turkey 19.40 6.16 6.46  
## Maize-fed Turkey 28.55 5.19 5.22  
## Humans 46.75 8.81 8.93

# SIBER Maximum Likelihood Overlap with Humans Calculations

results <- data.frame()  
taxa <- c("1.Hummingbird Pueblo Lepus", "1.Hummingbird Pueblo Sylvilagus",   
 "1.Sand Canyon Pueblo Lepus",   
 "1.Sand Canyon Pueblo Sylvilagus",  
 "1.Tijeras Pueblo Lepus",   
 "1.Tijeras Pueblo Sylvilagus",  
 "1.Maize-fed Turkey")  
  
for (i in seq\_along(taxa)) {  
   
 sea.overlap <- maxLikOverlap(taxa[[i]], "1.Humans", siber.example,   
 p.interval = 0.95, n = 100)  
   
 results[i, 1] <- taxa[[i]]  
 results[i, 2] <- round(sea.overlap[[3]], digits = 2)  
 results[i, 3] <- round(sea.overlap[[3]]/sea.overlap[[2]]\*100, digits = 2)  
 results[i, 4] <- round(sea.overlap[[3]]/sea.overlap[[1]]\*100, digits = 2)  
 results[i, 5] <- round(sea.overlap[[3]]/(sea.overlap[[2]] +   
 sea.overlap[[1]] -   
 sea.overlap[[3]])\*100, digits = 2)  
}  
  
colnames(results) <- c("group", "overlap ‰", "% human niche", "% group niche",   
 "% overlap")  
  
results$group <- gsub("1.","", as.character(results$group))  
results$group <- gsub("Lepus","Jackrabbits", as.character(results$group))  
results$group <- gsub("Sylvilagus","Cottontails", as.character(results$group))  
  
results

## group overlap ‰ % human niche % group niche  
## 1 Hummingbird Pueblo Jackrabbits 4.55 8.50 5.47  
## 2 Hummingbird Pueblo Cottontails 4.61 8.62 4.70  
## 3 Sand Canyon Pueblo Jackrabbits 0.00 0.00 0.00  
## 4 Sand Canyon Pueblo Cottontails 0.00 0.00 0.00  
## 5 Tijeras Pueblo Jackrabbits 0.00 0.00 0.00  
## 6 Tijeras Pueblo Cottontails 2.38 4.45 1.98  
## 7 Maize-fed Turkey 31.23 58.39 100.00  
## % overlap  
## 1 3.44  
## 2 3.14  
## 3 0.00  
## 4 0.00  
## 5 0.00  
## 6 1.39  
## 7 58.39

round(mean(results$`% human niche`[1:6]), digits = 2)

## [1] 3.59

round(mean(results$`% group niche`[1:6]), digits = 2)

## [1] 2.02

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