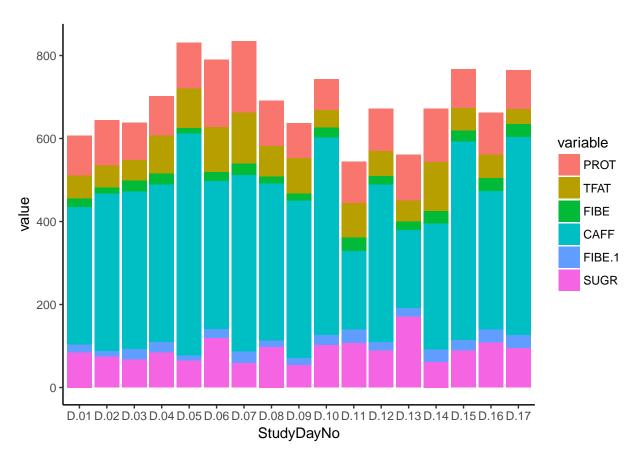
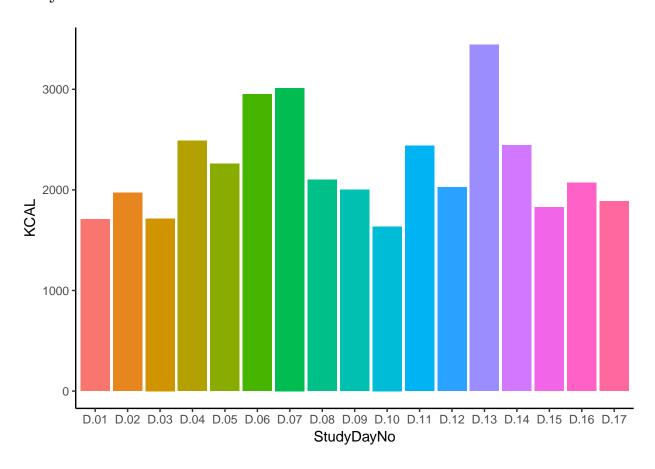
Subject_11

Type	Your Average	Total Average
CALORIES	2233.97	2080.11
PROTEIN	107.54	88.57
TOTAL FAT	72.79	89.97
CARBS	246.32	225.55
FIBER	23.53	21.96

MicroNutrients



Daily Calorie Intake



Microbiome Daily Relative Abundance

mergedf\$rn <- as.character(mergedf\$rn)</pre>

mergedf\$rn <- gsub(".*s__", "", mergedf\$rn)
mergedf\$rn <- gsub("\\[", "",mergedf\$rn)</pre>

#convert our dataframe species (rn) column to a character

#series of gsub commands meant to neaten and clarify legend content

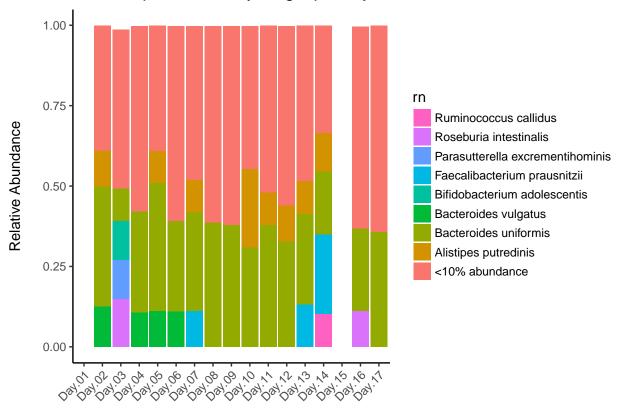
```
# make ggplot bar chart of top 10 most abundant species per day
#melt subtaxasp to get our dataframe in the long format for future usage
  meltdf<- melt(subtaxasp)

## Warning in melt.data.table(subtaxasp): To be consistent with reshape2's
## melt, id.vars and measure.vars are internally guessed when both are 'NULL'.
## All non-numeric/integer/logical type columns are conisdered id.vars, which
## in this case are columns [rn]. Consider providing at least one of 'id' or
## 'measure' vars in future.

#merge to get access to Day var
mergedf<- merge(x=meltdf, y=map, by.x = "variable", by.y= "X.SampleID", all.x=TRUE)</pre>
```

```
mergedf$rn <- gsub("\\]", "",mergedf$rn)</pre>
  mergedf$rn <- gsub("_", " ",mergedf$rn)</pre>
  #create <10% abundance category
  mergedf$rn[mergedf$value < 0.1] <- "<10% abundance"</pre>
ggplot(mergedf, aes(x = StudyDayNo, y = value, fill = rn)) +
  geom_bar(stat = "identity") +
  scale_x_discrete(drop = FALSE) +
  theme_classic() +
  theme(strip.text.y = element_text(angle = 0, size = 8, face = "italic"),
        axis.text.x = element_text(angle = 45, hjust = 1),
        axis.title.x = element_blank(),
        plot.title = element_text(hjust = 0.5),
        strip.background = element_rect(color = "grey")) +
  guides(fill = guide_legend(reverse = TRUE,
                              keywidth = 1,
                              keyheight = 1,
                              ncol = 1)) +
  ylab("Relative Abundance\n") +
  ggtitle("Main species within your gut per day")
```

Main species within your gut per day



`geom_smooth()` using method = 'loess'

