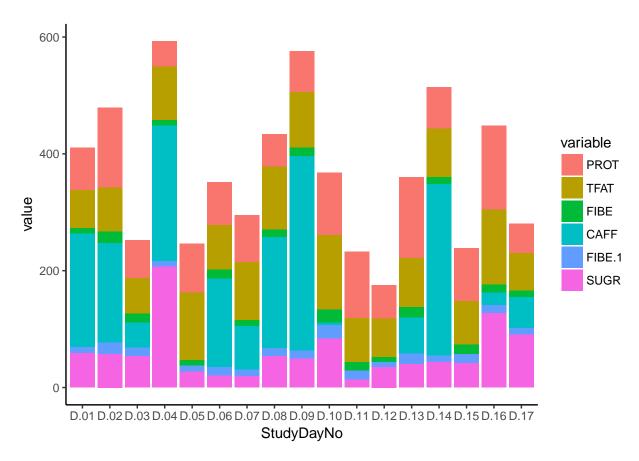
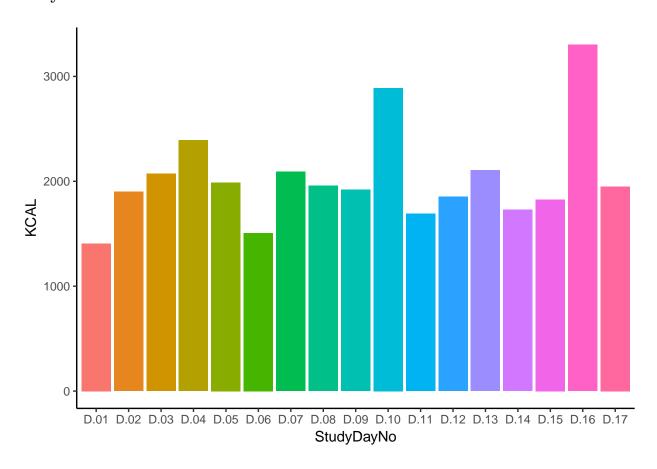
${\bf Subject_42}$

Type	Your Average	Total Average
CALORIES	2034.06	2080.11
PROTEIN	85.22	88.57
TOTAL FAT	87.66	89.97
CARBS	195.69	225.55
FIBER	13.72	21.96

MicroNutrients



Daily Calorie Intake



Microbiome Daily Relative Abundance

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

```
# 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.

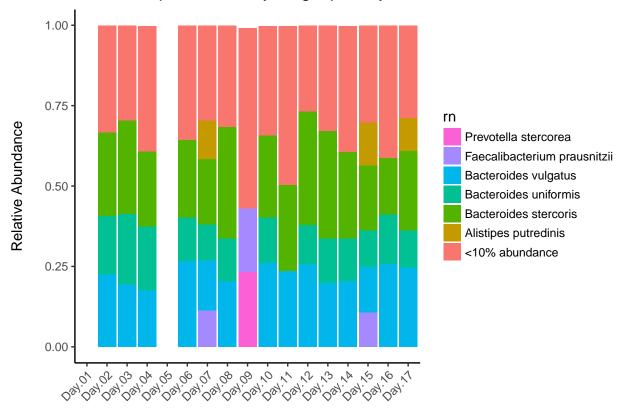
#merge to get access to Day var
mergedf<- merge(x=meltdf, y=map, by.x = "variable", by.y= "X.SampleID", all.x=TRUE)

#convert our dataframe species (rn) column to a character
mergedf$rn <- as.character(mergedf$rn)</pre>
```

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

```
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'

