Supplementary figure legends

Fig S1: Significant changes in the microbial composition assessed using Linear discriminant effect size (LEfSe) analysis between patients with high and low $CD4^+$ T cell response in the (A) gut and (B) oral environment. High $CD4^+$ T-cell count, n=48; low $CD4^+$ T-cell count, n=21.

Fig S2: Linear discriminant effect size (LEfSe) analysis showing significant differences in bacterial taxa in the whole cohort in individuals with high and low BMI in the (A) gut and (B) oral environment. High BMI, n=81; low BMI, n=55.

Fig S3: Changes in the alpha diversity, beta diversity, and composition using Linear discriminant effect size (LEfSe) analysis in DTG-treated patients in different age groups (18-39, 40-59 and >60 years) in (A-C) the gut environment and (D-F) the oral environment. 18-39 years, n=8; 40-59 years, n=19; >60 years, n=14.

Fig S4: Changes in the alpha diversity and composition using Linear discriminant effect size (LEfSe) analysis in DTG-treated patients divided into groups based on the length of antiretroviral therapy (</≥5 years) in (A-B) the gut environment and (C-D) the oral environment. ≥5 years, n=26; <5years, n=15.

Fig S5: Changes in the alpha diversity and composition using Linear discriminant effect size (LEfSe) analysis in DTG-treated patients divided into groups based on $CD4^+$ T-cell count (</≥350) in (A-B) the gut environment and (C-D) the oral environment. ≥350 $CD4^+$ T-cell count, n=29; <350 $CD4^+$ T-cell count, n=12.

Fig S1

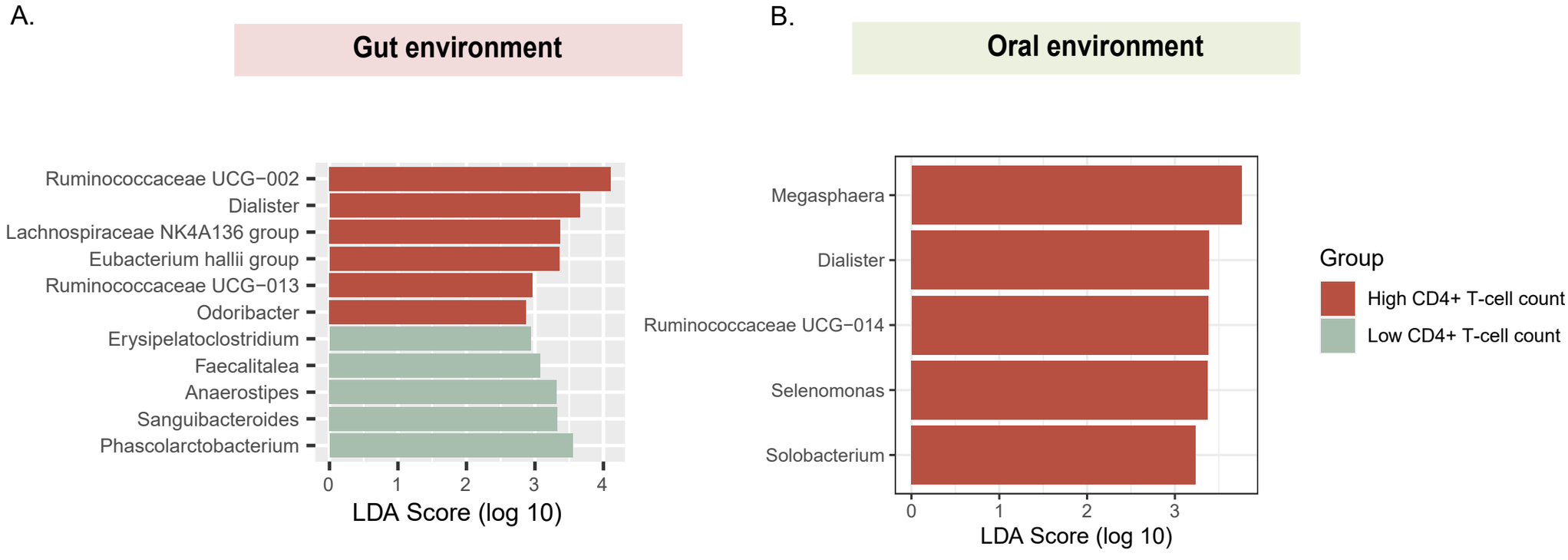
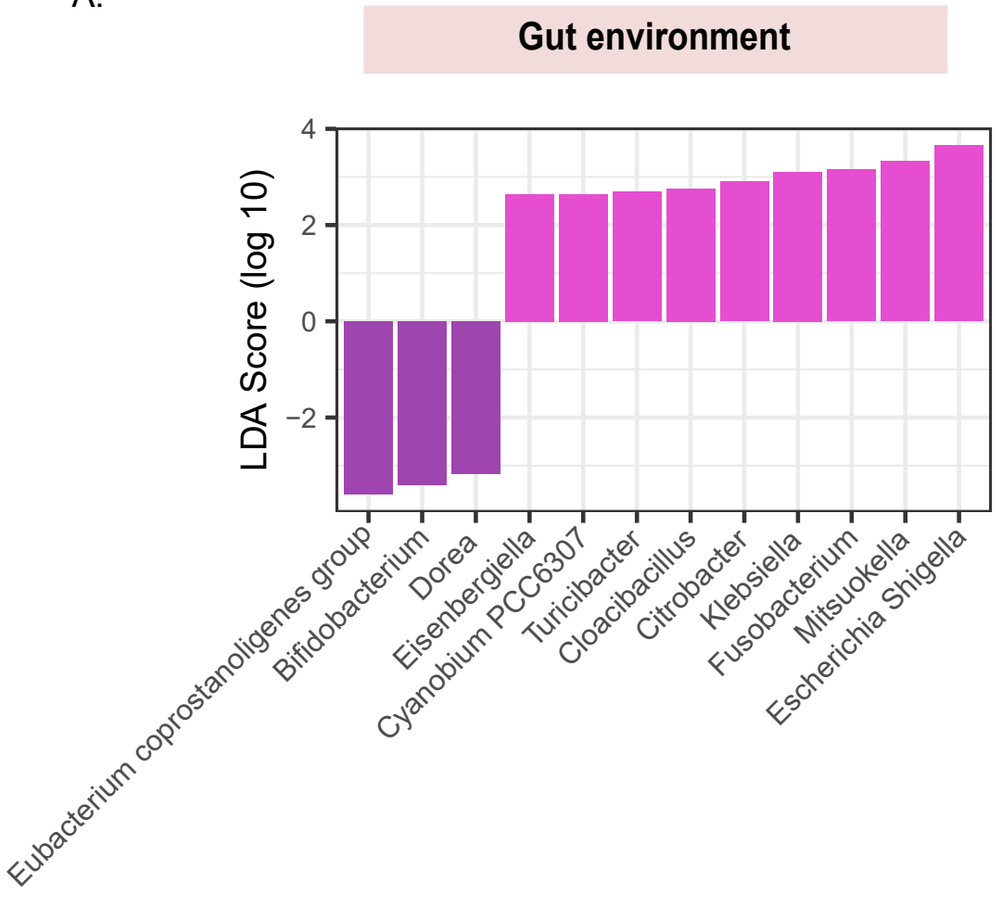

A.
Gut environment
Ruminococcaceae UCG−002
Dialister
Lachnospiraceae NK4A136 group
Eubacterium hallii group
Ruminococcaceae UCG−013
Odoribacter
Erysipelatoclostridium
Faecalitalea
Anaerostipes
Sanguibacteroides
Phascolarctobacterium
0
1
2
3
4
LDA Score (log 10)
B.
Oral environment
Megasphaera
Dialister
Ruminococcaceae UCG−014
Selenomonas
Solobacterium
0
1
2
3
LDA Score (log 10)
Group
High CD4+ T-cell count
Low CD4+ T-cell count

Fig S2

A.


Gut environment
LDA Score (log 10)
4
2
0
−2
Eubacterium coprostanoligenes group
Bifidobacterium
Dorea
Eisenbergiella
Cyanobium PCC6307
Turicibacter
Cloacibacillus
Citrobacter
Klebsiella
Fusobacterium
Mitsuokella
Escherichia Shigella

B.

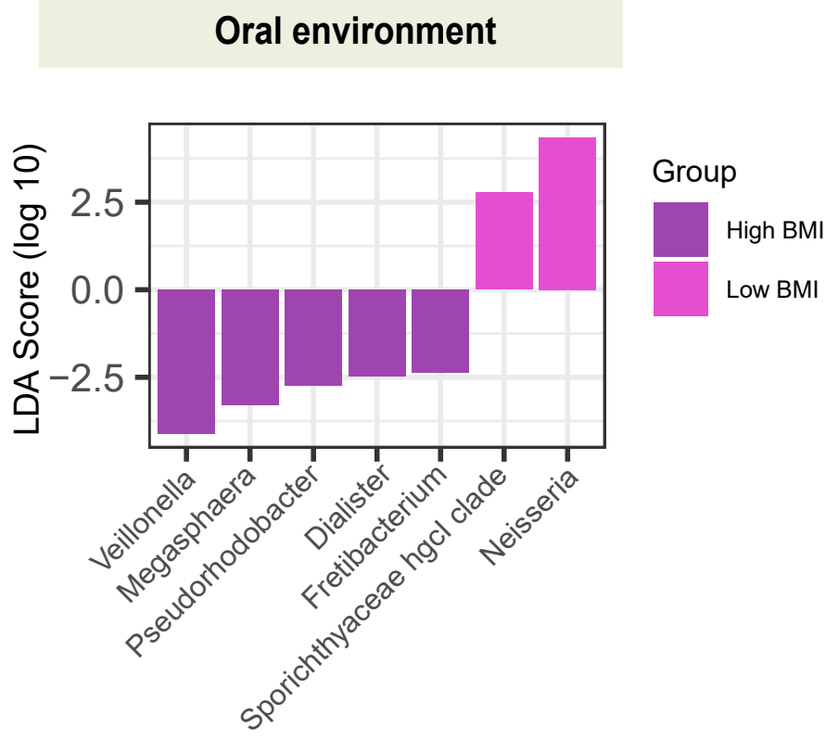
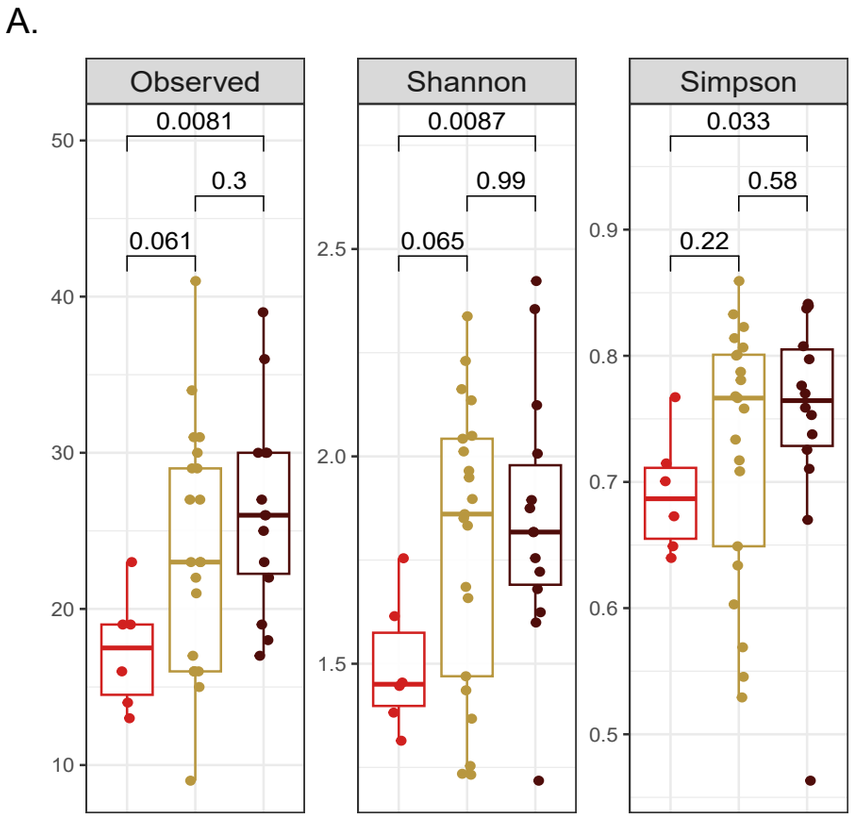
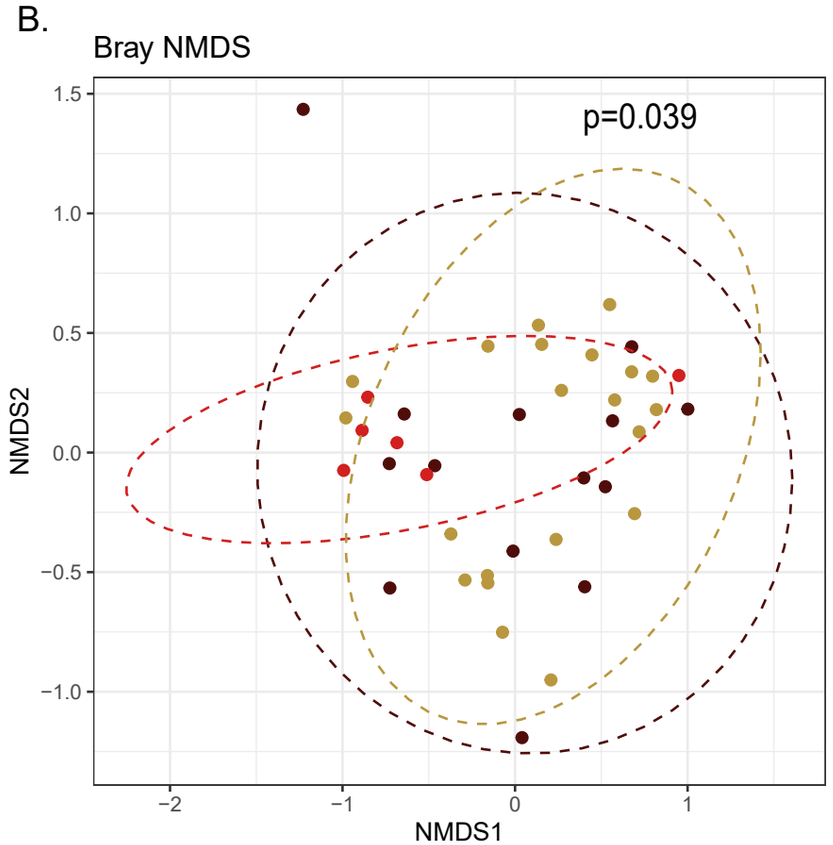
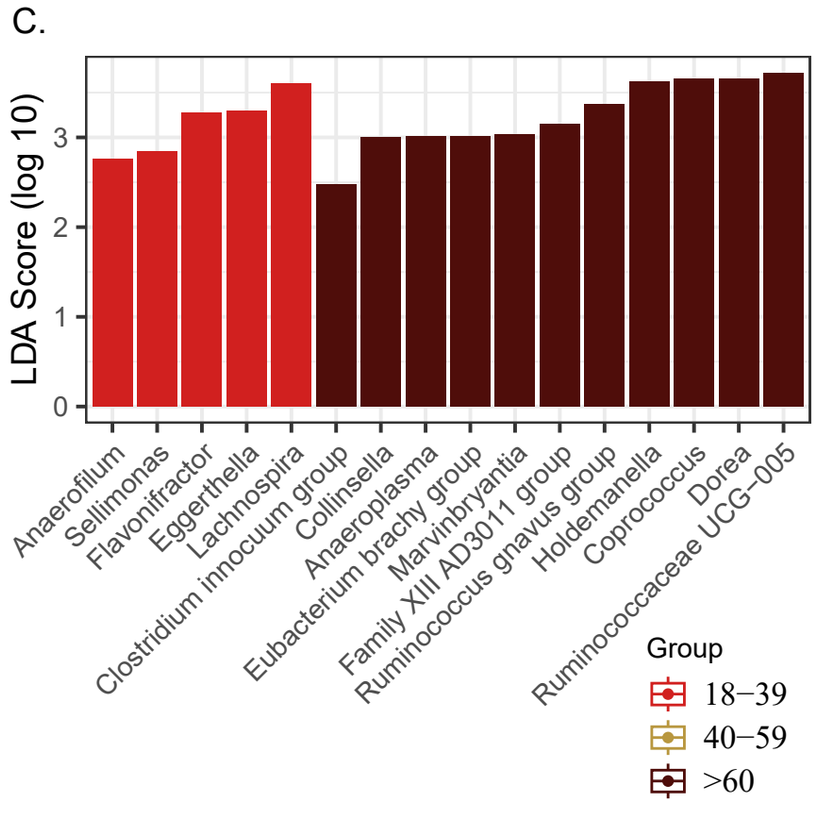

Oral environment
LDA Score (log 10)
2.5
0.0
−2.5
Veillonella
Megasphaera
Pseudorhodobacter
Dialister
Fretibacterium
Sporichthyaceae hgcI clade
Neisseria
Group
High BMI
Low BMI

Fig S3

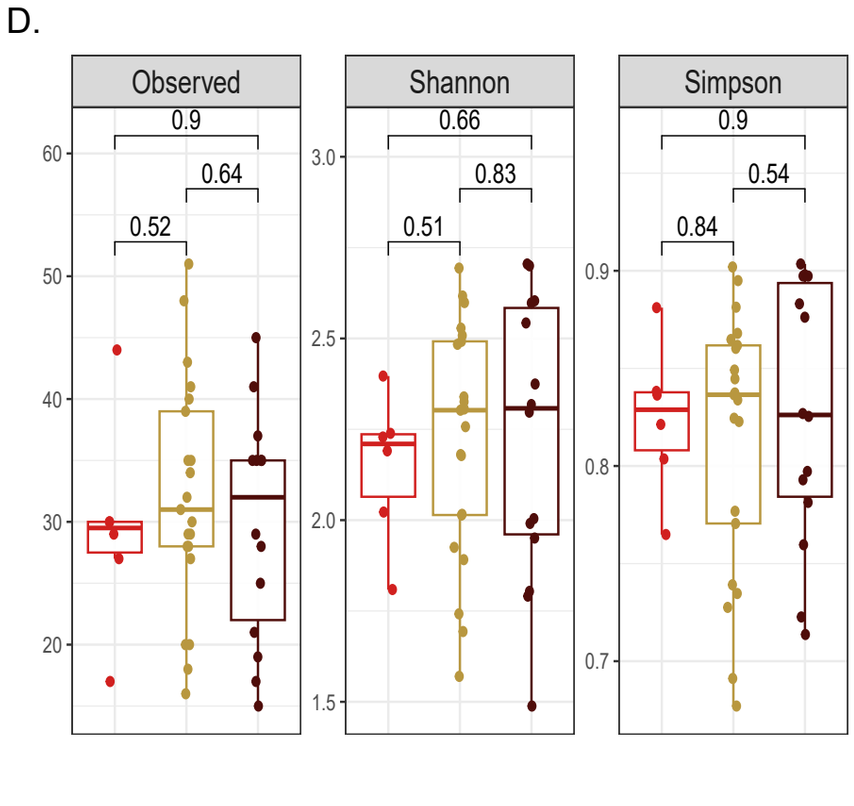
Gut environment

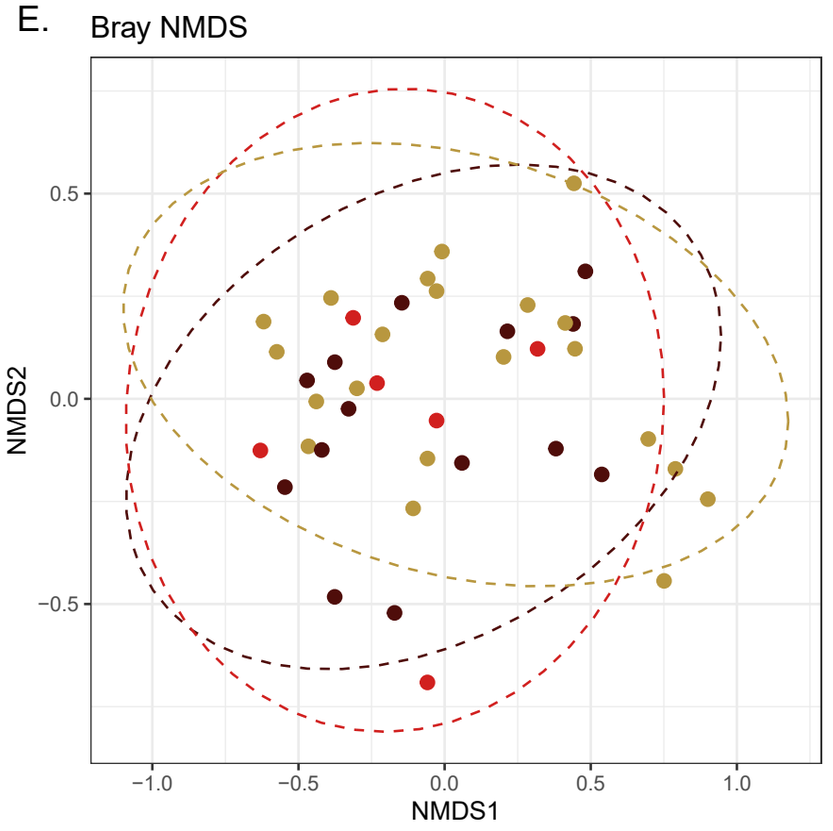






Oral environment





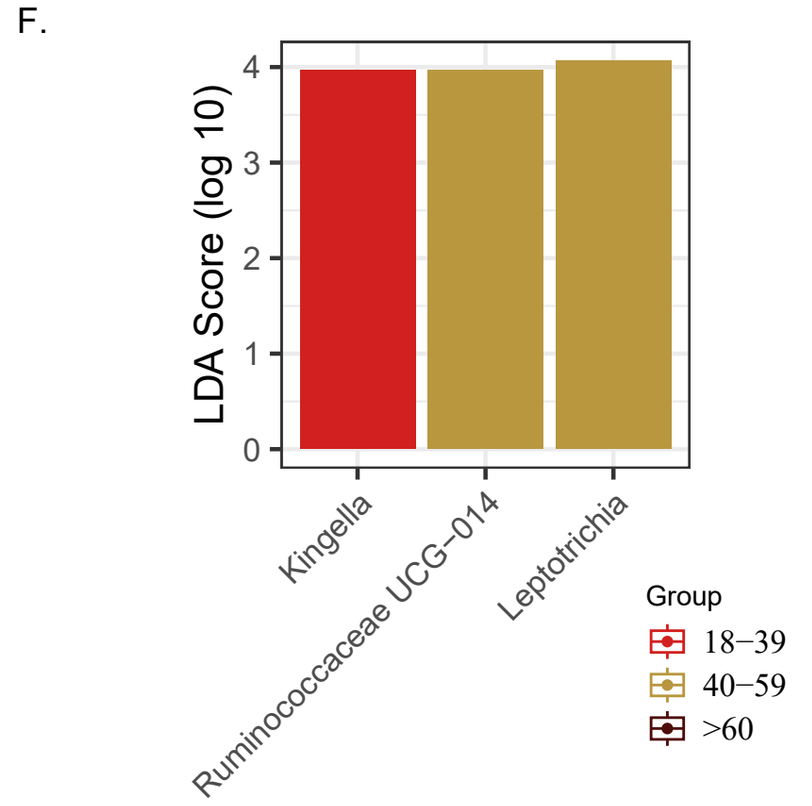
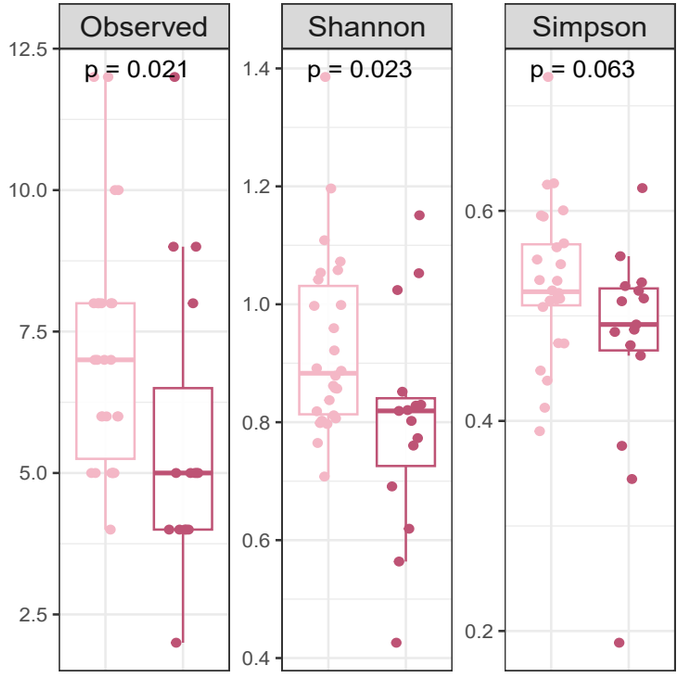


Fig S4

Gut environment

A.



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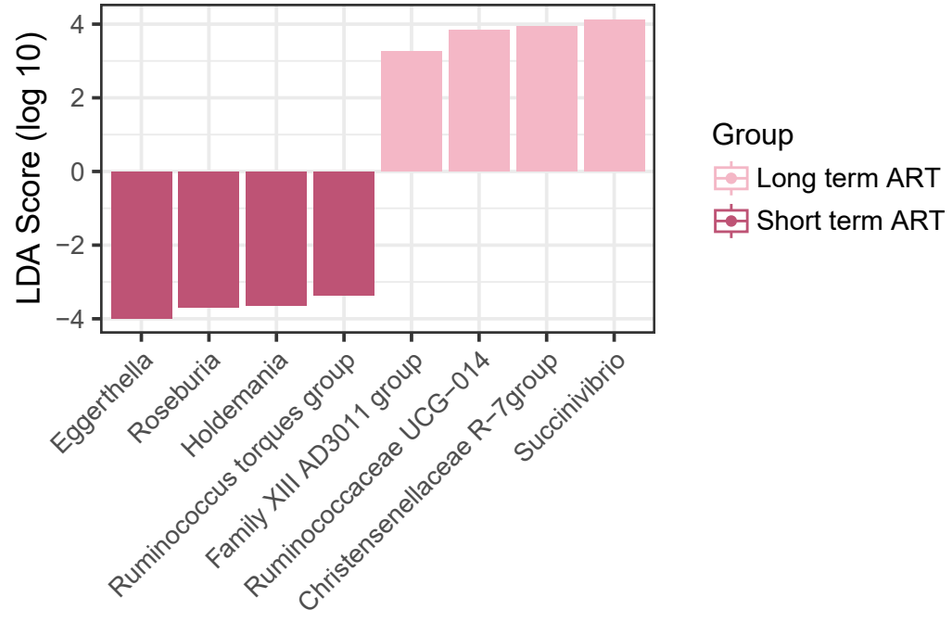
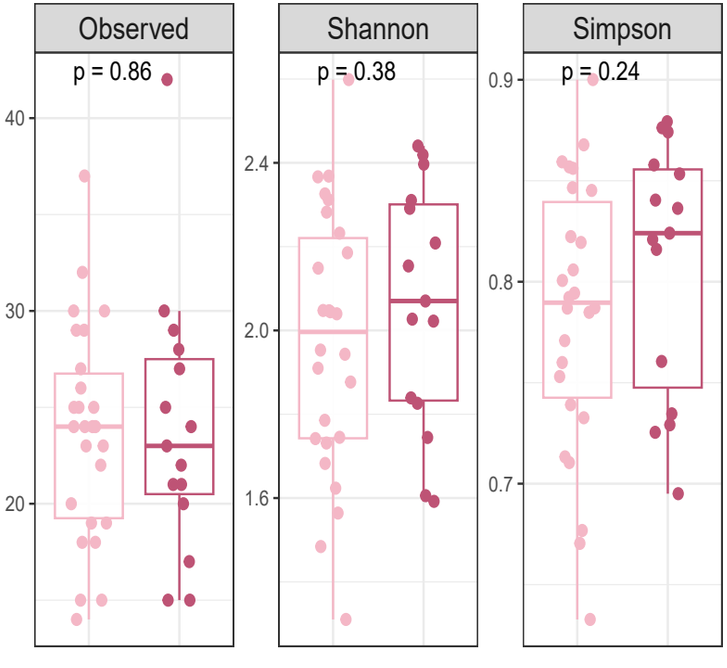


Oral environment

C.



D.

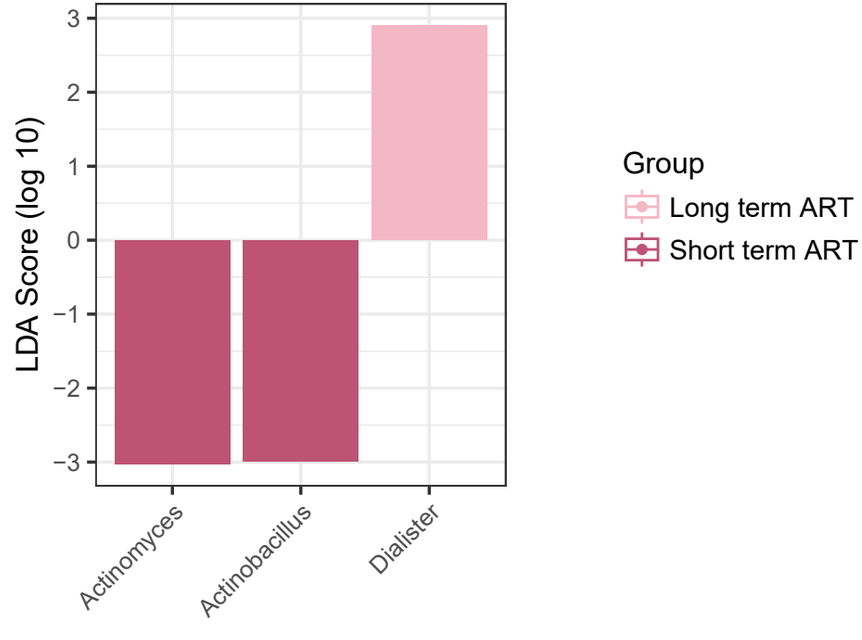
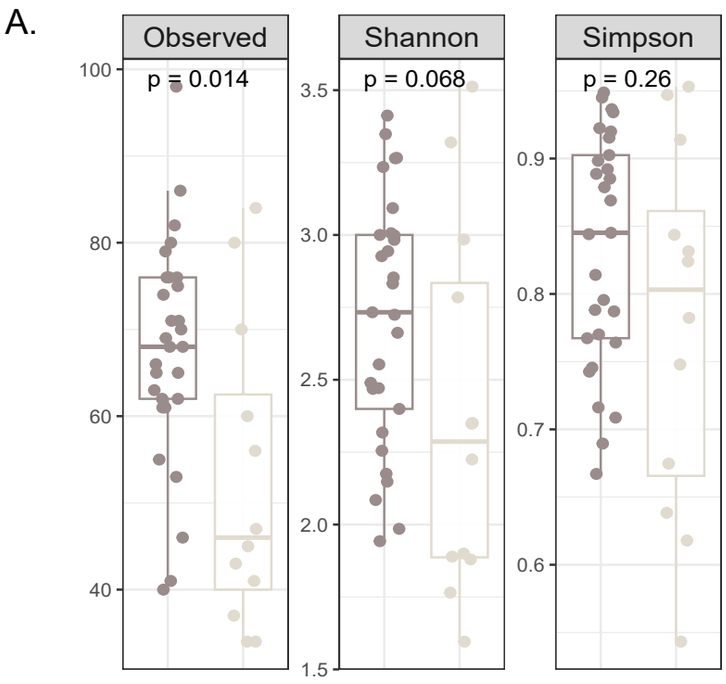
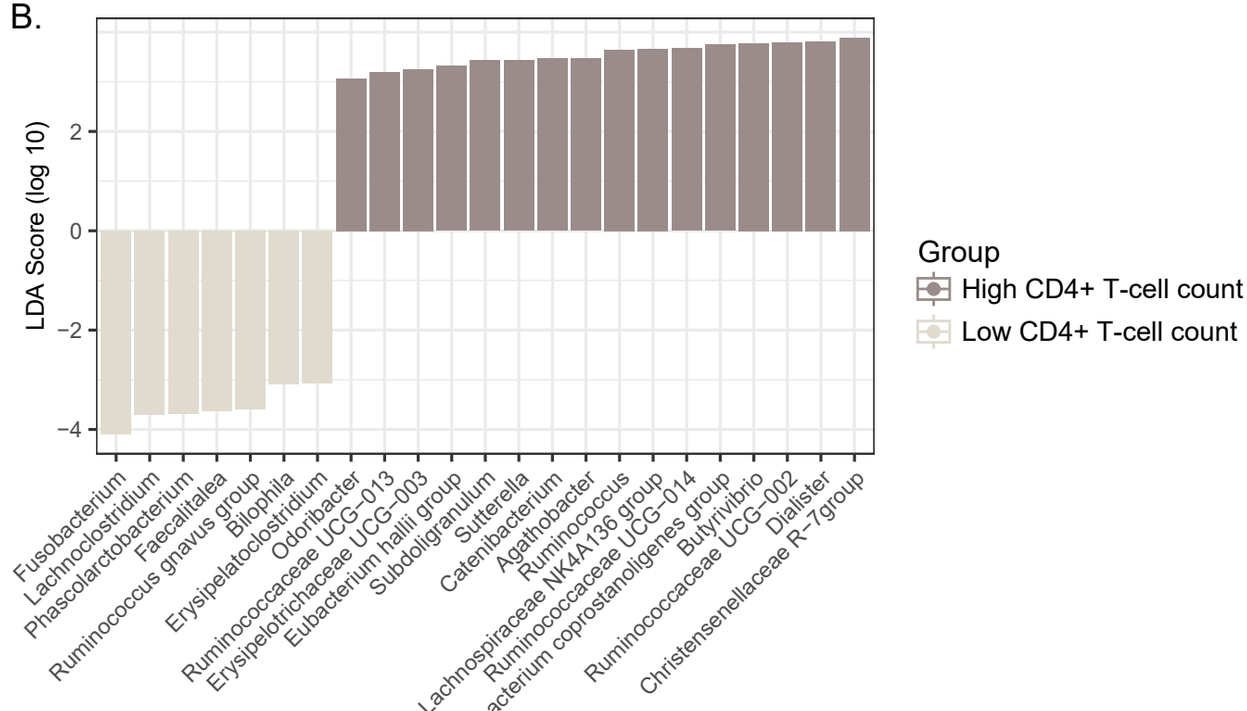
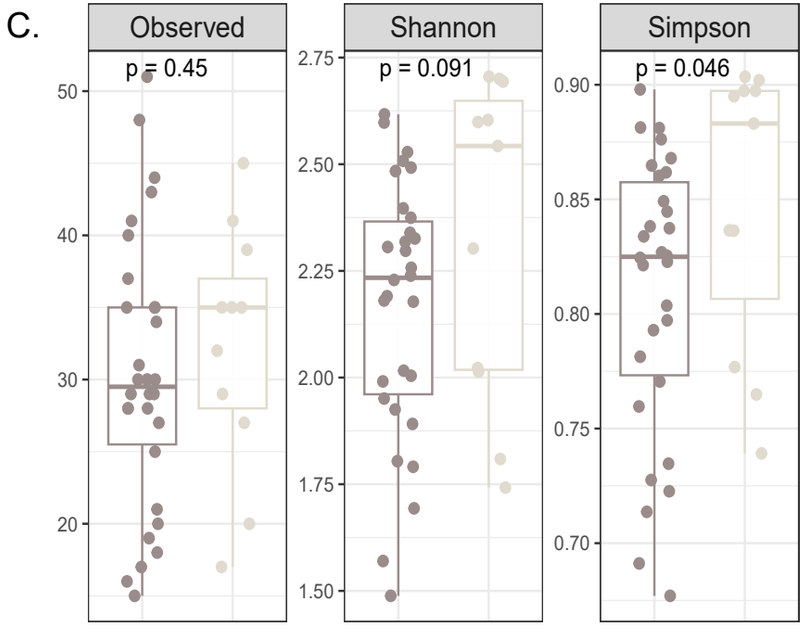
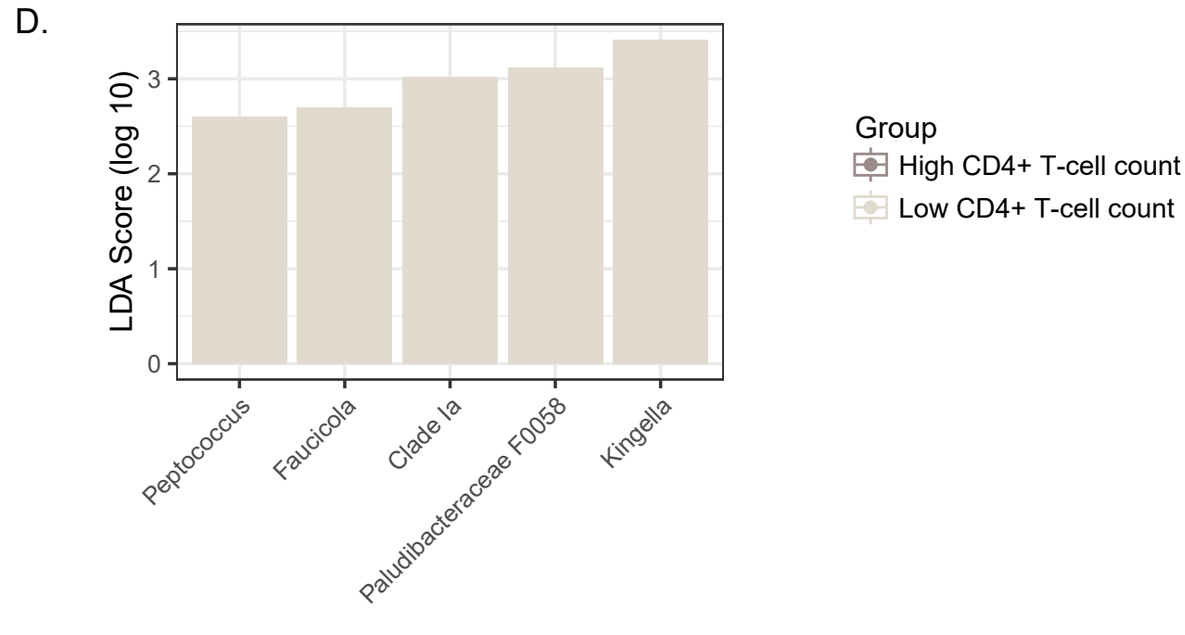


Fig S5

Gut environment





Oral environment