Supplementary figures legends

Fig S1: Changes in the spike IgG levels between (A) Healthy controls (HC) and people living with HIV (PLWH), (B) Individuals in different age groups, 18-39, 40-59 and >60 years, (C) Individuals with different BMI, 18-24.9, 25-29.9 and >30. (D) Males and female participants of the cohort, (E) PLWH with high and low actual $CD4^+$ count and (F) high and low CD4/CD8 ratio, (G) individuals with high and low total IgG levels at baseline.

Fig S2: β-diversity (NMDS) plots for investigating shifts in populations under high or responders for antibody levels in the (A) whole cohort, (B) HC group.

Fig S3: Linear regression analysis between microbial diversity and antibody levels within the HC group and within the PLWH group.

Fig S4: β-diversity (NMDS) plots for two groups based on their spike-specific $CD4^+$ T-cell responses.

Fig S5: Changes in microbial diversity between individuals categorized by spike-specific $CD4^+$ T-cell responses within HC and PLWH.

Fig S6: Spearman correlation for associating the $CD4^+$ T-cell responses-specific microbiome with antibody levels.

Fig S7:(A) Changes in the abundance of microbial genus in individuals with different total IgG levels at baseline. (B) LDA analysis showing different significant bacterial taxa within the HC and PLWH group, with high and low total IgG levels at baseline. (C) Spearman correlation for associating baseline total IgG-specific microbiome with antibody levels

Fig S8: Effect of age on gut microbiome. (A) Variation in the alpha diversity in the whole cohort among different age groups (18-39, 40-59 and >60 years). (B) Regression analysis showing the positive relationship between age and alpha diversity in the whole cohort among different age groups (18-39, 40-59 and >60 years). (C) Significantly abundant microbial markers for different age groups determined by LEfSe. (D) Microbial diversity and richness in three different age groups within the HC group. (E) Bacterial diversity in three different age groups within the PLWH group. (F) Relative abundance of Firmicutes and Bacteroidetes in the whole cohort, HC and PLWH group. The Firmicutes: Bacteroidetes ratio is essential for gut balance.

Fig S1

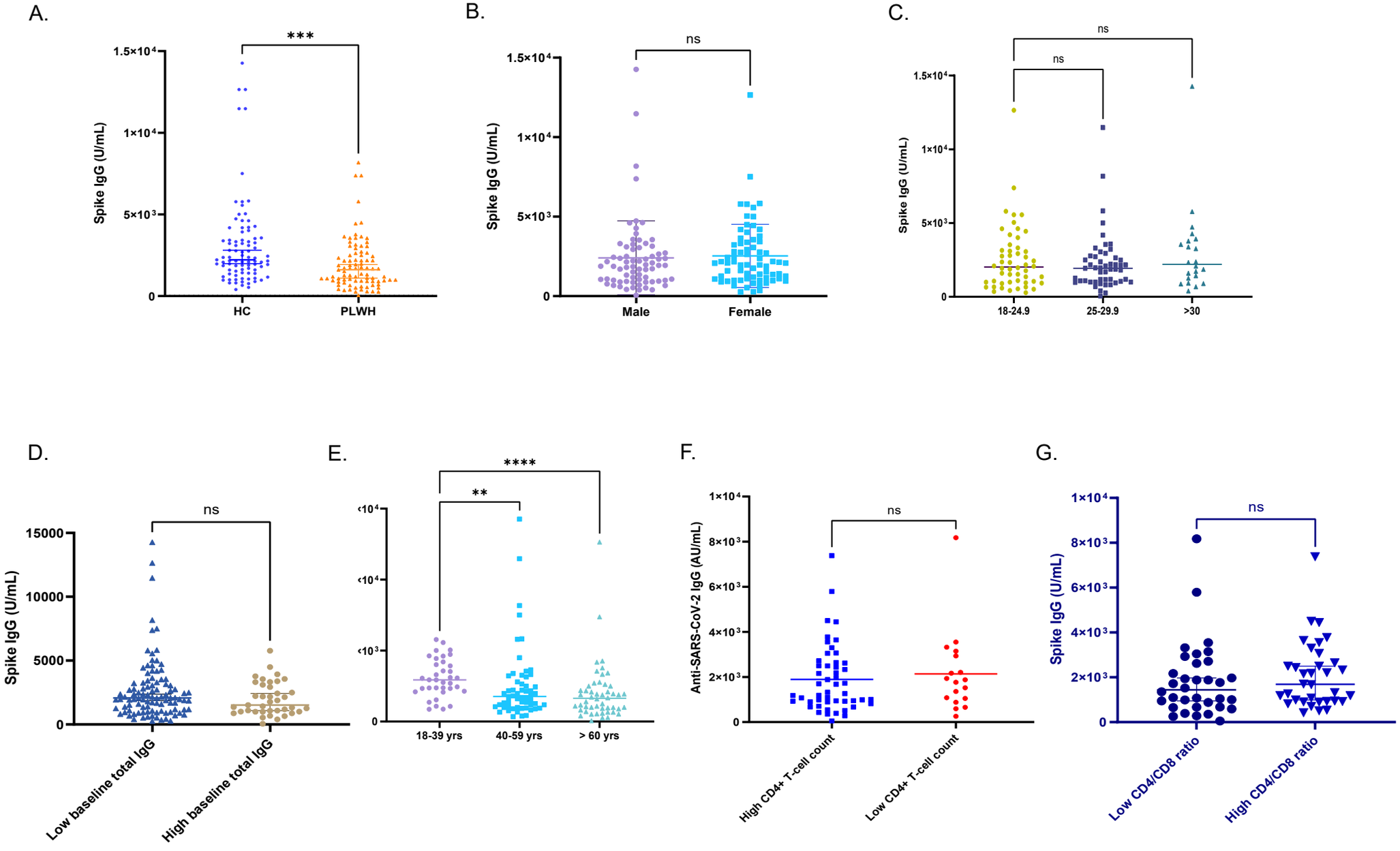
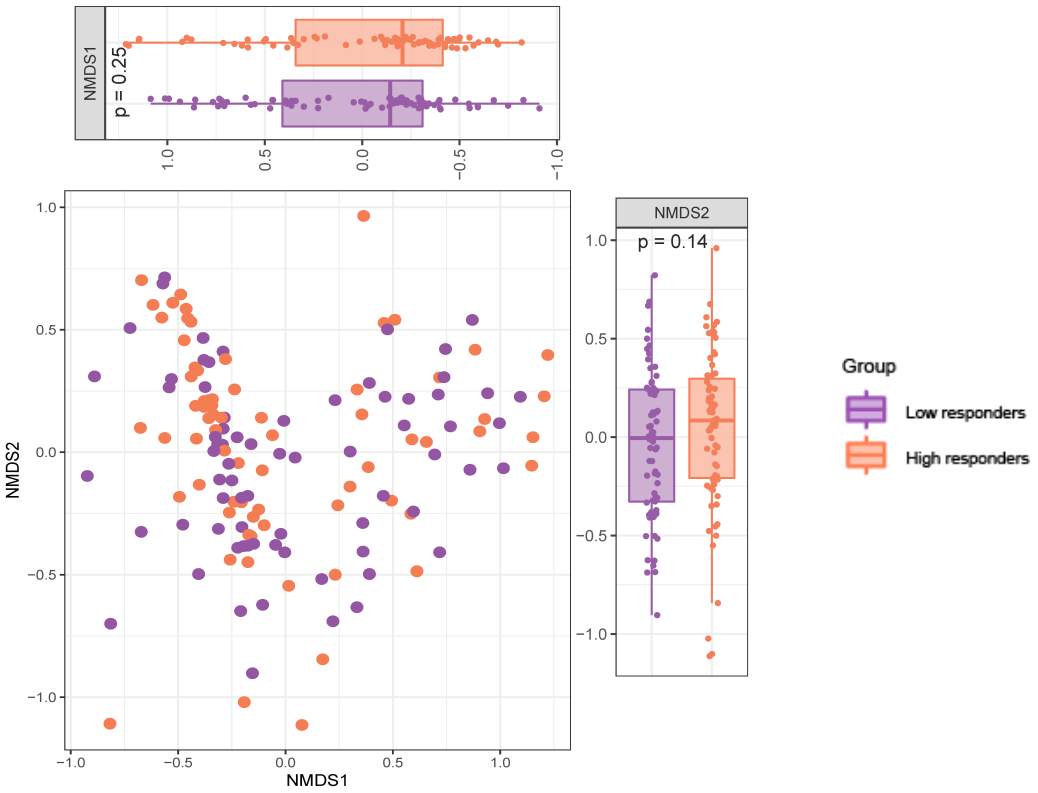

A.
***
1.5×10⁴
1×10⁴
5×10³
0
Spike IgG (U/mL)
HC
PLWH
B.
ns
1.5×10⁴
1×10⁴
5×10³
0
Spike IgG (U/mL)
Male
Female
C.
ns
ns
1.5×10⁴
1×10⁴
5×10³
0
Spike IgG (U/mL)
18-24.9
25-29.9
>30
D.
ns
15000
10000
5000
0
Spike IgG (U/mL)
Low baseline total IgG
High baseline total IgG
E.
****
**
18-39 yrs
40-59 yrs
> 60 yrs
F.
ns
1×10⁴
8×10³
6×10³
4×10³
2×10³
0
Anti-SARS-CoV-2 IgG (AU/mL)
High CD4+ T-cell count
Low CD4+ T-cell count
G.
ns
1×10⁴
8×10³
6×10³
4×10³
2×10³
0
Spike IgG (U/mL)
Low CD4/CD8 ratio
High CD4/CD8 ratio

Fig S2

A.


NMDS1
p = 0.25
NMDS2
p = 0.14
NMDS1
NMDS2
Group
Low responders
High responders

B.

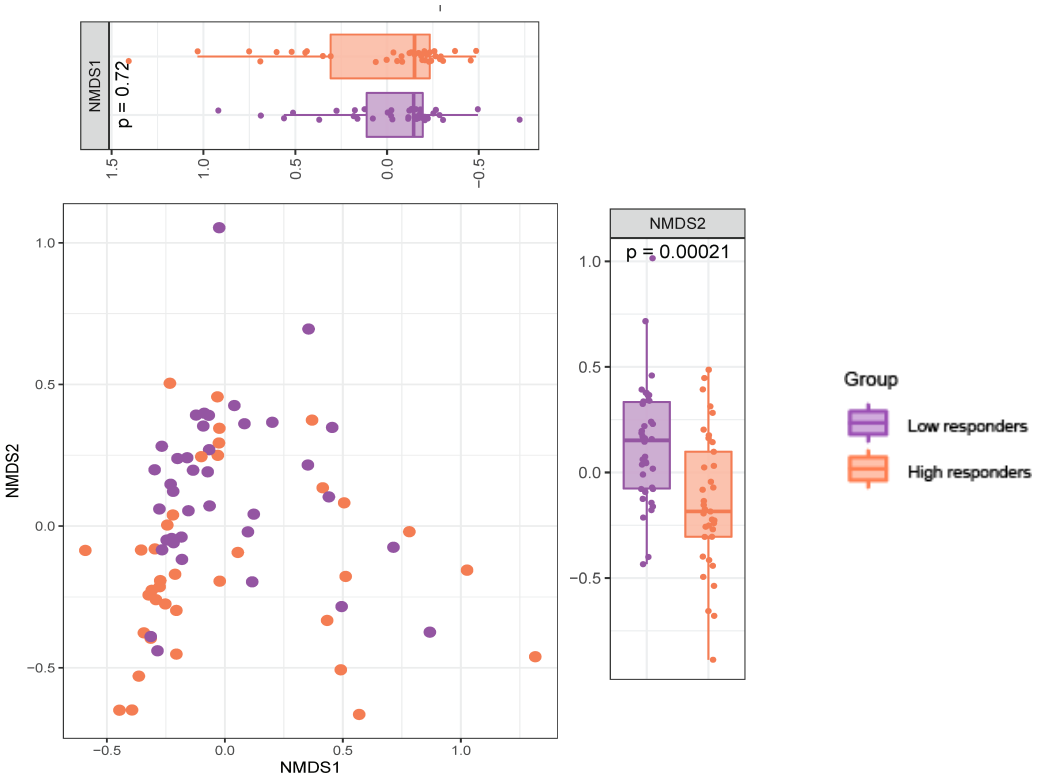
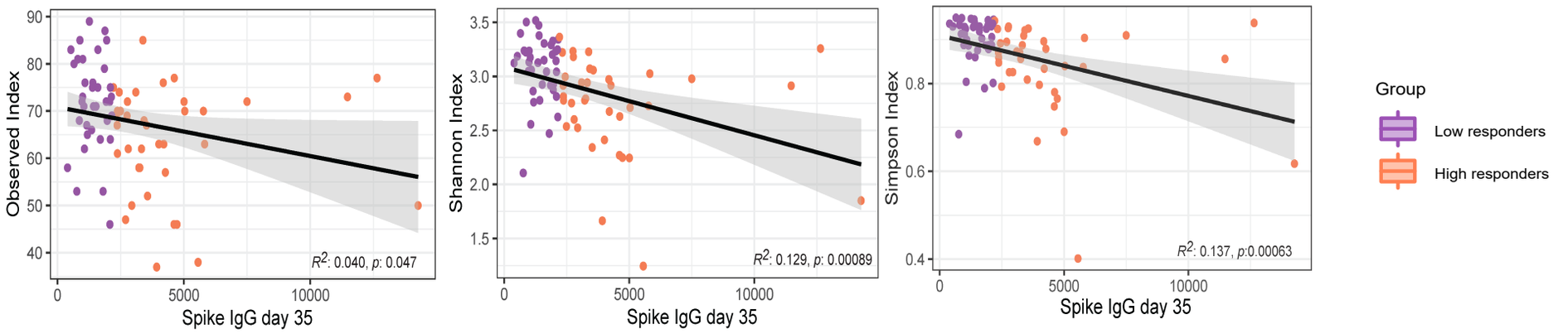

NMDS1
p = 0.72
NMDS2
p = 0.00021
NMDS1
NMDS2
Group
Low responders
High responders

Fig S3

A.


Observed Index
Spike IgG day 35
R^2: 0.040, p: 0.047
Shannon Index
Spike IgG day 35
R^2: 0.129, p: 0.00089
Simpson Index
Spike IgG day 35
R^2: 0.137, p:0.00063
Group
Low responders
High responders

B.

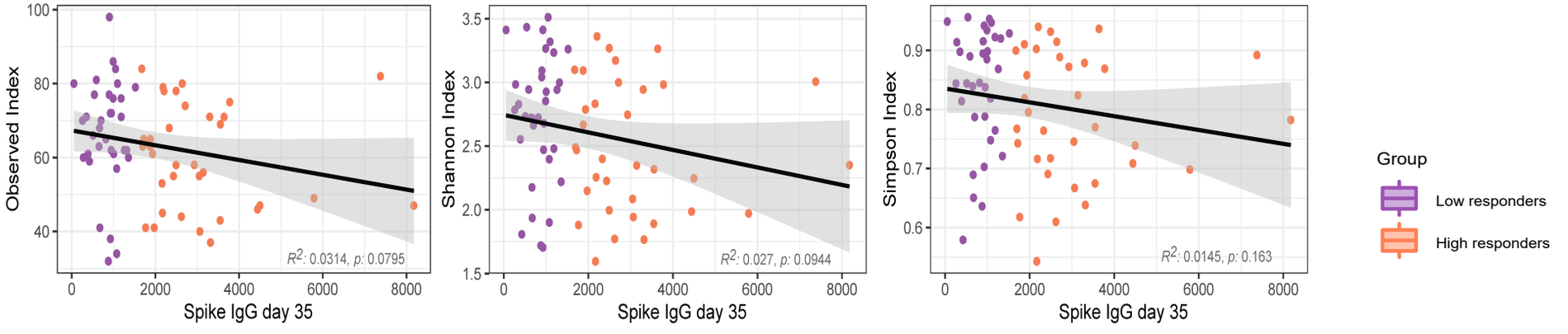

Observed Index
Spike IgG day 35
R^2: 0.0314, p: 0.0795
Shannon Index
Spike IgG day 35
R^2: 0.027, p: 0.0944
Simpson Index
Spike IgG day 35
R^2: 0.0145, p: 0.163
Group
Low responders
High responders

Fig S4

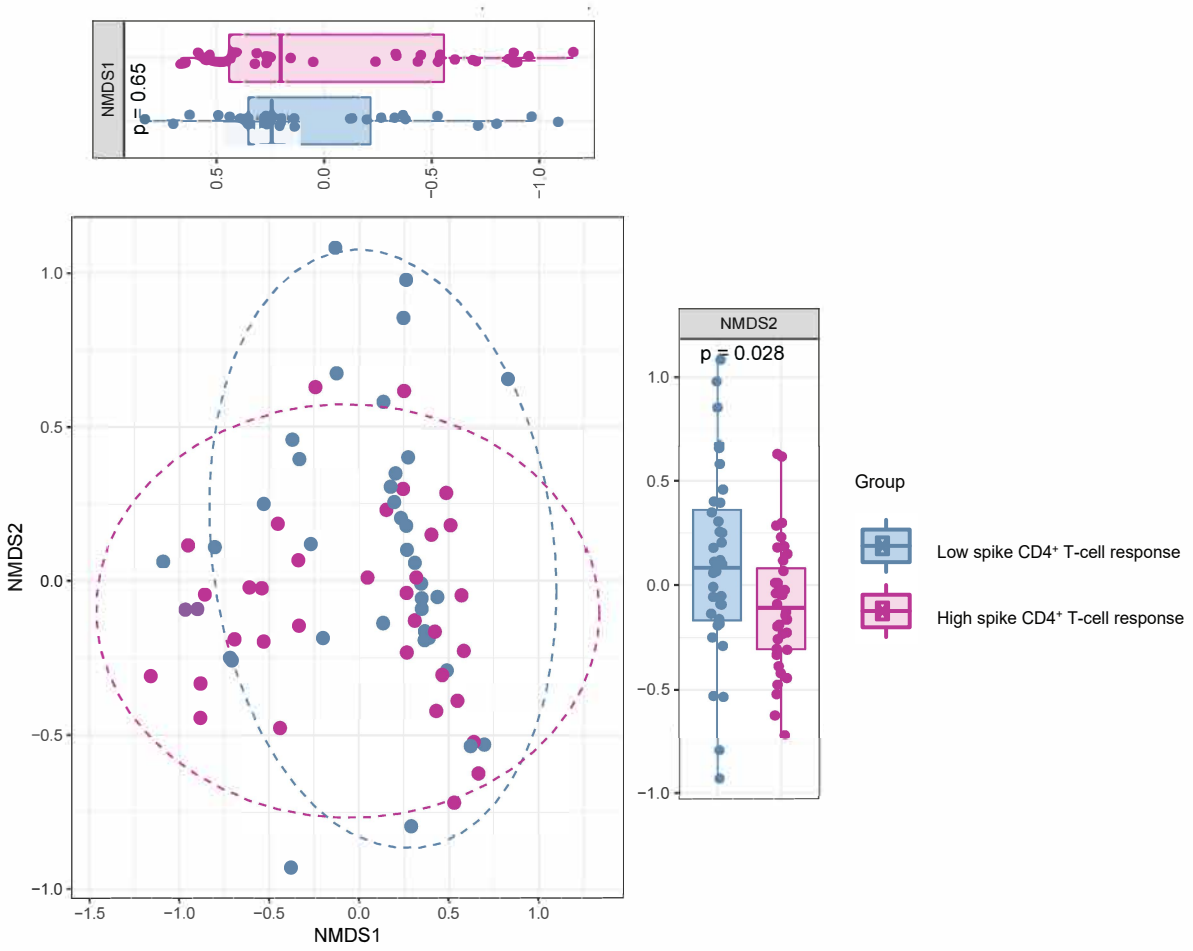
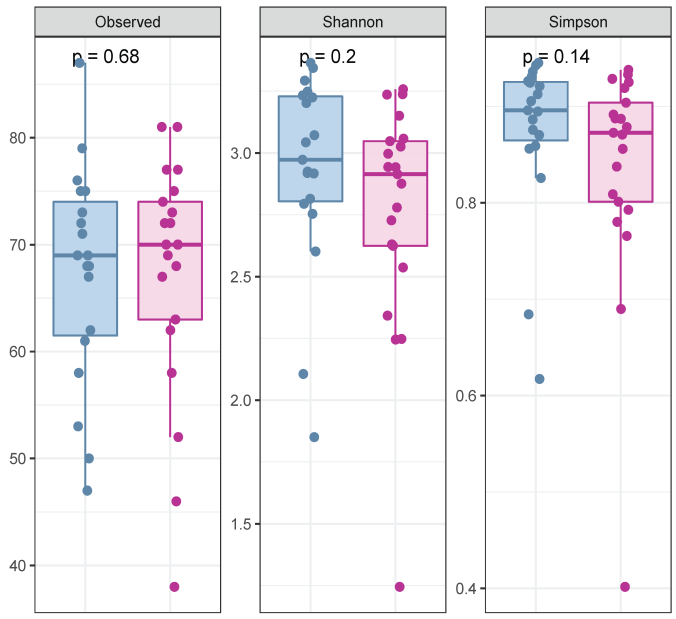
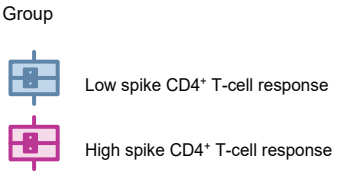

NMDS1
p = 0.65
0.5
0.0
−0.5
−1.0
NMDS2
1.0
0.5
0.0
−0.5
−1.0
−1.5
−1.0
−0.5
0.0
0.5
1.0
NMDS1
NMDS2
p = 0.028
Group
Low spike CD4⁺ T-cell response
High spike CD4⁺ T-cell response

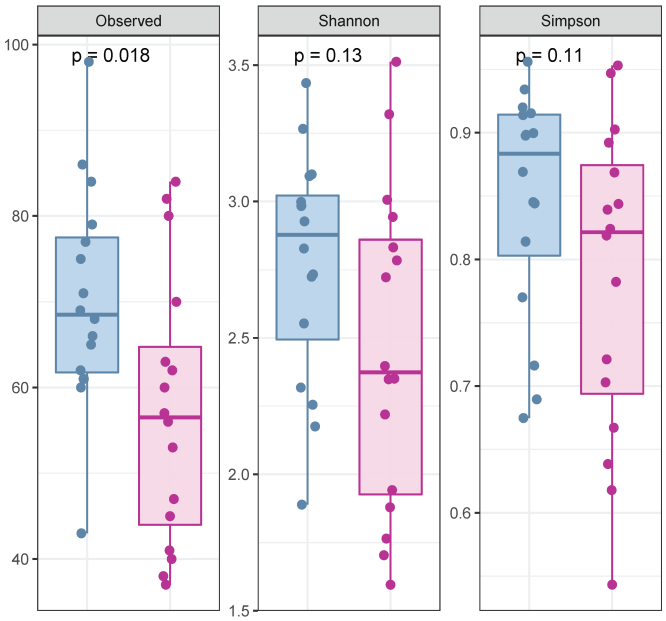
Fig S5

A.


Observed
p = 0.68
Shannon
p = 0.2
Simpson
p = 0.14
80
70
60
50
40
3.0
2.5
2.0
1.5
0.8
0.6
0.4


Group
Low spike CD4⁺ T-cell response
High spike CD4⁺ T-cell response

B.


Observed
p = 0.018
Shannon
p = 0.13
Simpson
p = 0.11
100
80
60
40
3.5
3.0
2.5
2.0
1.5
0.9
0.8
0.7
0.6

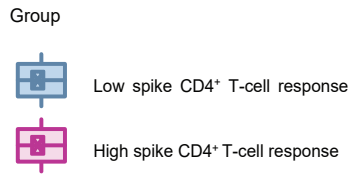

Group
Low spike CD4⁺ T-cell response
High spike CD4⁺ T-cell response

Fig S6

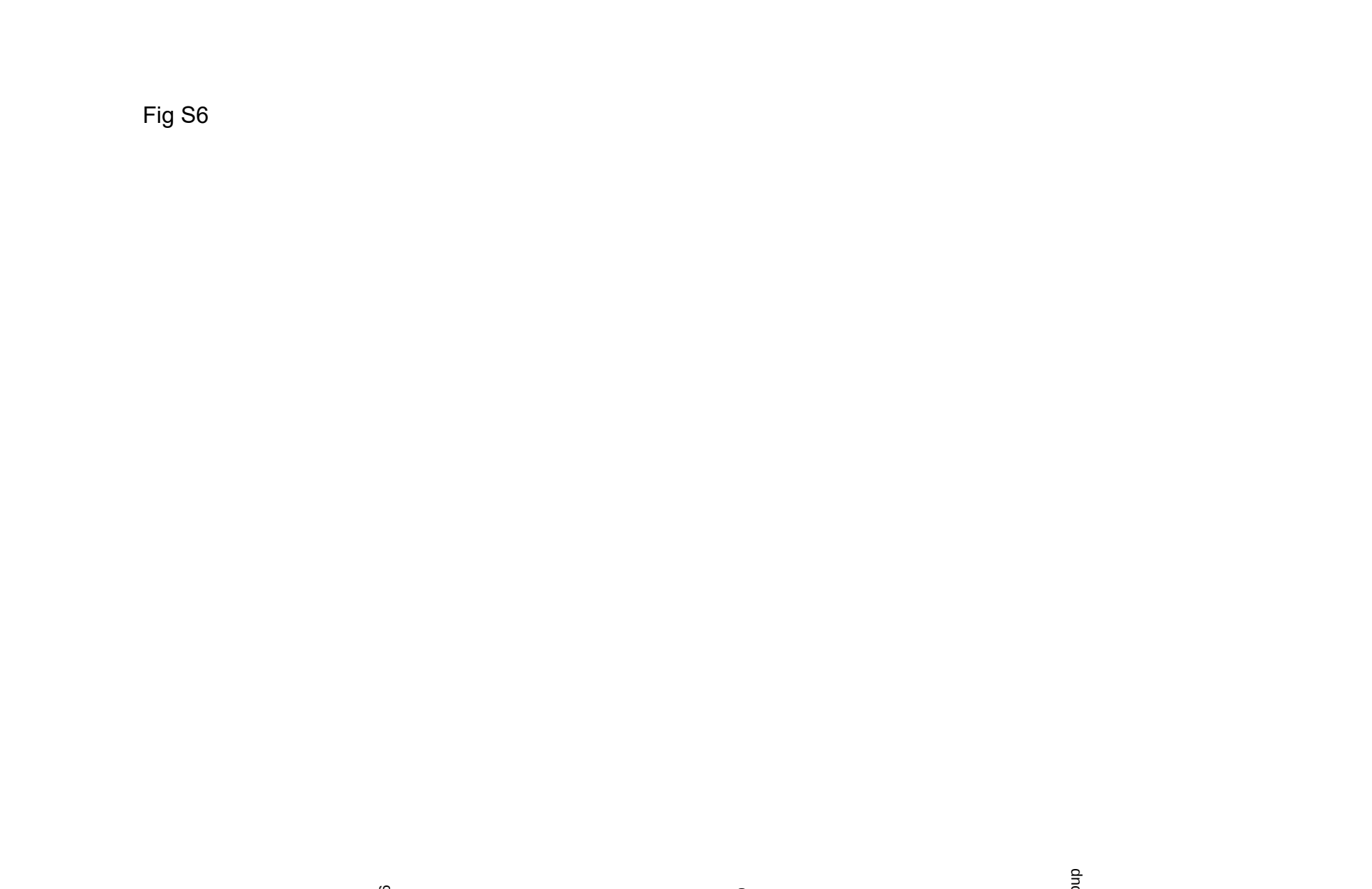
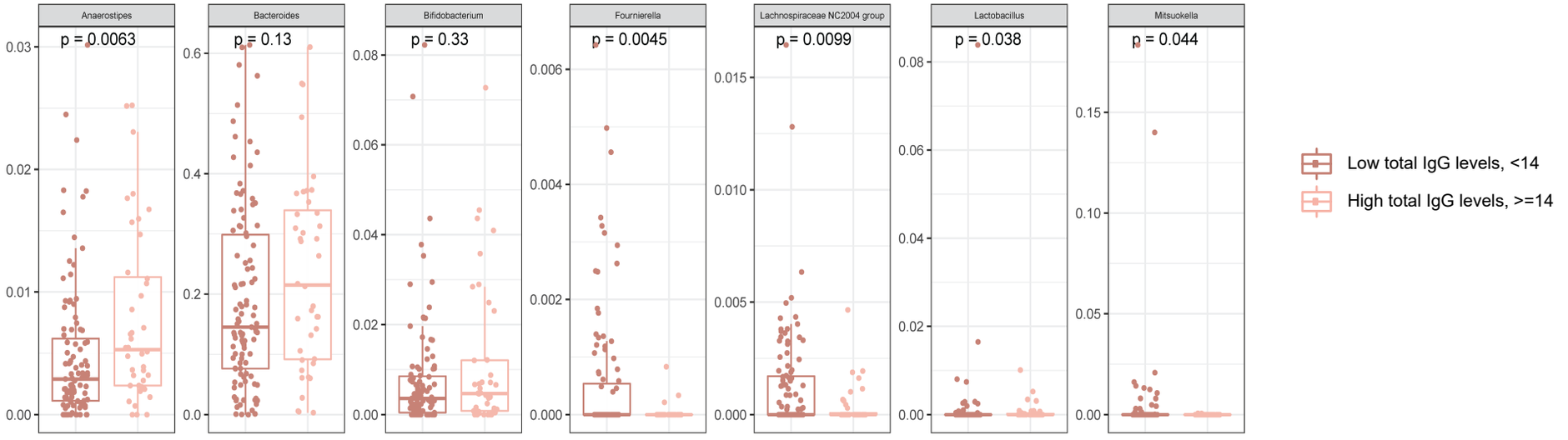
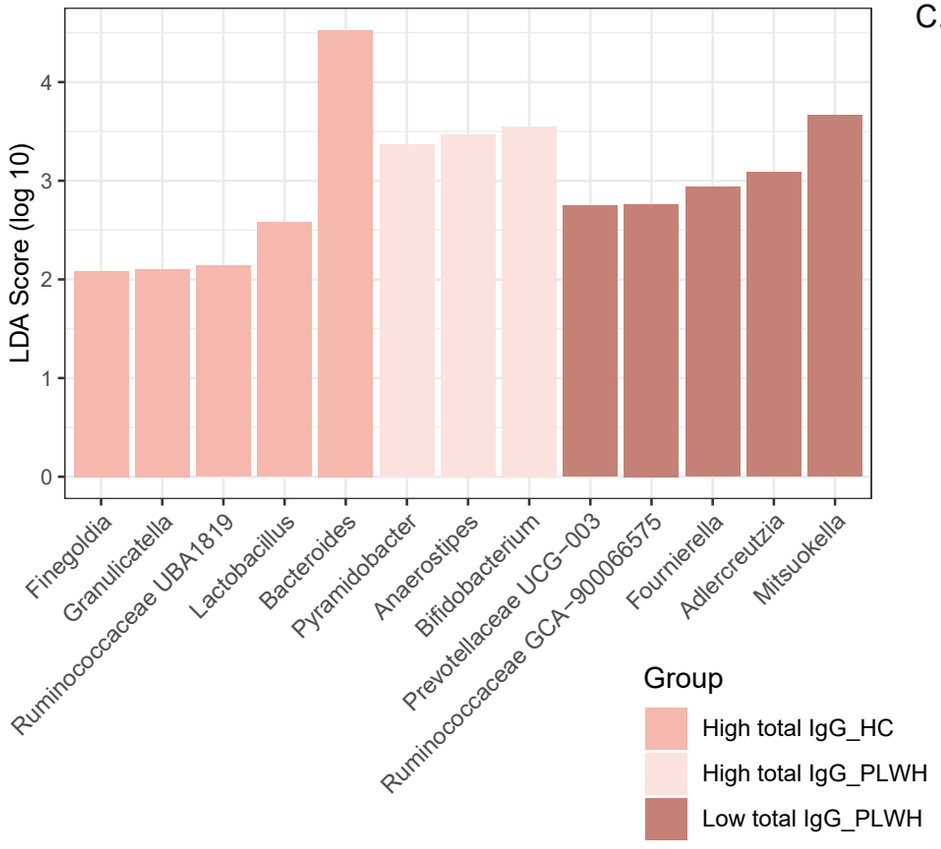

Acidaminococcus
Adlercreutzia
Akkermansia
Alistipes
Anaerofilum
Anaerotruncus
Bacteroides
Bifidobacterium
Butyrivibrio
Candidatus Soleaferrea
Christensenellaceae R−7 group
Cloacibacillus
Clostridium sp. K4410.MGS−306
Coprobacter
Coprococcus
Desulfovibrio
Dorea
Enterococcus
Escherichia−Shigella
Eubacterium eligens group
Faecalibacterium
Family XIII AD3011 group
Haemophilus
Helicobacter
Holdemania
Intestinimonas
Lachnospira
Lachnospiraceae CAG−56
Lachnospiraceae NC2004 group
Lachnospiraceae UCG−004
Lactobacillus
Marvinbryantia
Megamonas
Methanobrevibacter
Moryella
Oscillospira
Parabacteroides
Parasutterella
Phocea
Prevotella
Prevotellaceae UCG−004
Ruminiclostridium
Ruminococcaceae DTU089
Ruminococcaceae NK4A214 group
Shuttleworthia
Staphylococcus
Streptococcus
Succinivibrio
Sutterella
Entire Cohort
HC
PLWH
0.4
0.31
0.21
0.11
0.02
−0.08
−0.17
−0.27
−0.37
−0.46
−0.56

Fig S7

A.


Anaerostipes
p = 0.0063
Bacteroides
p = 0.13
Bifidobacterium
p = 0.33
Fournierella
p = 0.0045
Lachnospiraceae NC2004 group
p = 0.0099
Lactobacillus
p = 0.038
Mitsuokella
p = 0.044
Low total IgG levels, <14
High total IgG levels, >=14

B.


LDA Score (log 10)
Finegoldia
Granulicatella
Ruminococcaceae UBA1819
Lactobacillus
Bacteroides
Pyramidobacter
Anaerostipes
Bifidobacterium
Prevotellaceae UCG-003
Ruminococcaceae GCA-900066575
Fournierella
Adlercreutzia
Mitsuokella
Group
High total IgG_HC
High total IgG_PLWH
Low total IgG_PLWH

C.

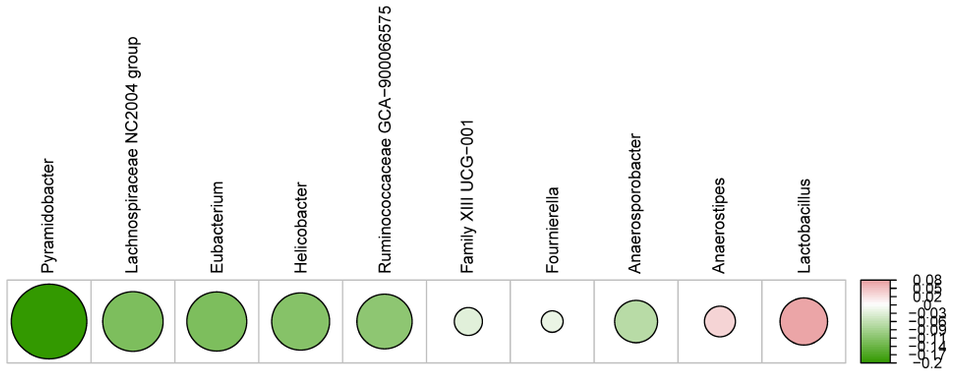
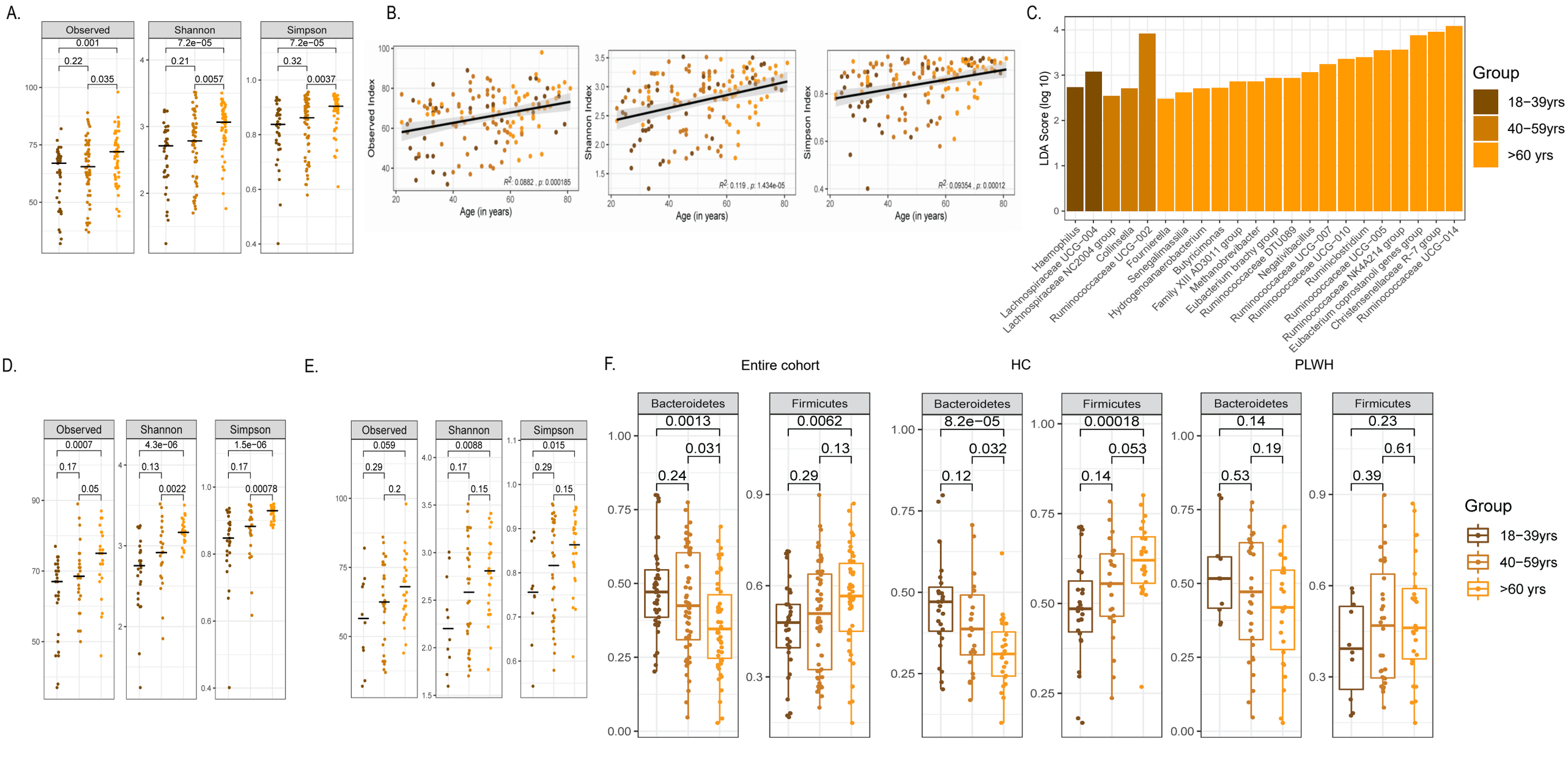

Pyramidobacter
Lachnospiraceae NC2004 group
Eubacterium
Helicobacter
Ruminococcaceae GCA-900066575
Family XIII UCG-001
Fournierella
Anaerosporobacter
Anaerostipes
Lactobacillus

Fig S8


A.
Observed
Shannon
Simpson
0.001
0.22
0.035
7.2e−05
0.21
0.0057
7.2e−05
0.32
0.0037
B.
Observed Index
Shannon Index
Simpson Index
Age (in years)
R2: 0.0882 , p: 0.000185
R2: 0.119 , p: 1.434e−05
R2: 0.09354 , p: 0.00012
C.
LDA Score (log 10)
Haemophilus
Lachnospiraceae UCG−004
Lachnospiraceae NC2004 group
Ruminococcaceae UCG−002
Collinsella
Fournierella
Senegalimassilia
Hydrogenoanaerobacterium
Butyricimonas
Family XIII AD3011 group
Methanobrevibacter
Eubacterium brachy group
Ruminococcaceae DTU089
Negativibacillus
Ruminococcaceae UCG−007
Ruminococcaceae UCG−010
Ruminiclostridium
Ruminococcaceae UCG−005
Ruminococcaceae NK4A214 group
Eubacterium coprostanoli genes group
Christensenellaceae R−7 group
Ruminococcaceae UCG−014
Group
18−39yrs
40−59yrs
>60 yrs
D.
Observed
Shannon
Simpson
0.0007
0.17
0.05
4.3e−06
0.13
0.0022
1.5e−06
0.17
0.00078
E.
Observed
Shannon
Simpson
0.059
0.29
0.2
0.0088
0.17
0.15
0.015
0.29
0.15
F.
Entire cohort
HC
PLWH
Bacteroidetes
Firmicutes
0.0013
0.031
0.24
0.0062
0.13
0.29
8.2e−05
0.032
0.12
0.00018
0.053
0.14
0.14
0.19
0.53
0.23
0.61
0.39
Group
18−39yrs
40−59yrs
>60 yrs