

Odoribacter

*FDR: 7.580e-11*  
*Coefficient: -3.15e+00*  
*Value: post\_ltx*

400

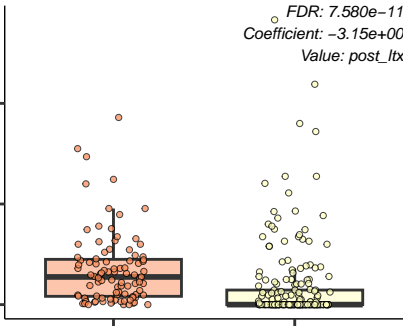
200

0

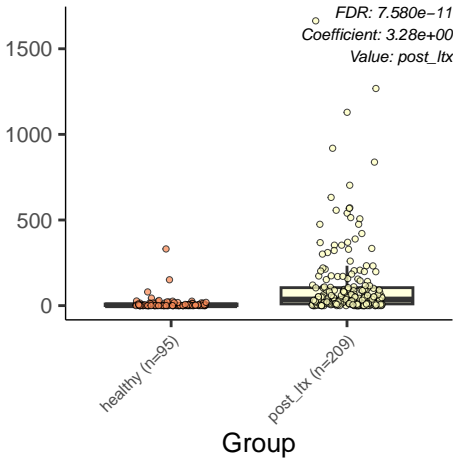
healthy (n=95)

post\_ltx (n=209)

Group



Haemophilus



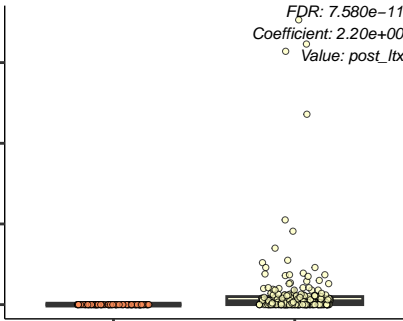
Spingobium

FDR:  $7.580e-11$   
Coefficient:  $2.20e+00$   
Value: post\_ltx

healthy (n=95)

post\_ltx (n=209)

Group



Veillonella

*FDR: 1.021e-10*  
*Coefficient: 3.31e+00*  
*Value: post\_ltx*

2000

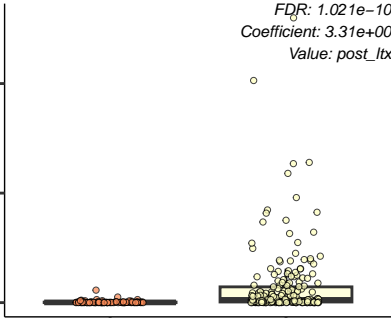
1000

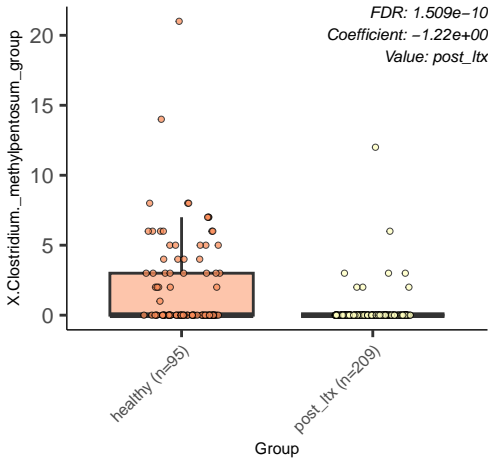
0

healthy (n=95)

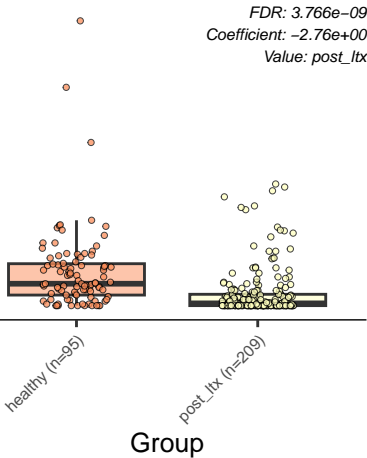
post\_ltx (n=209)

Group





Intestinimonas



Family\_XIII\_UCG.001

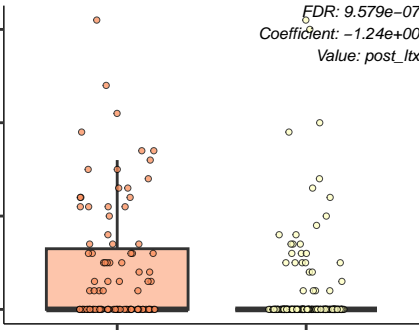
30  
20  
10  
0

healthy (n=95)

post\_ltx (n=209)

Group

FDR:  $9.579 \times 10^{-7}$   
Coefficient:  $-1.24 \times 10^0$   
Value: post\_ltx



Streptococcus

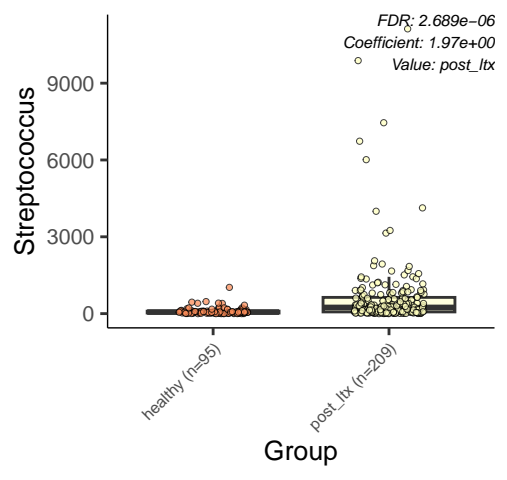
FDR: 2.689e-06  
Coefficient: 1.97e+00  
Value: post\_ltx

healthy (n=95)

post\_ltx (n=209)

Group

9000  
6000  
3000  
0





CAG.56

FDR:  $8.073e-06$

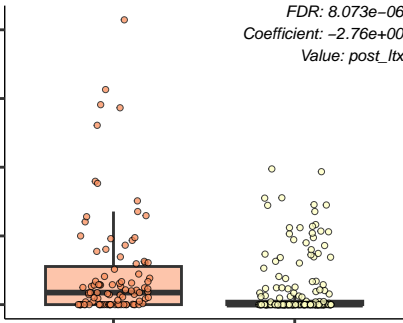
Coefficient:  $-2.76e+00$

Value: *post\_ltx*

healthy (n=95)

post\_ltx (n=209)

Group



Lachnoclostridium

6000

4000

2000

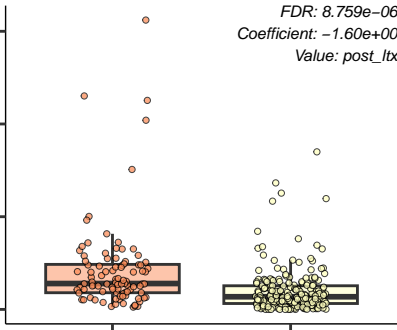
0

healthy (n=95)

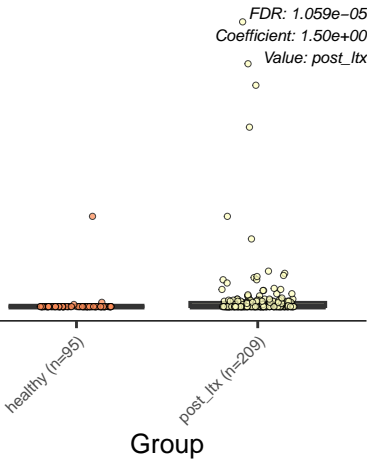
post\_ltx (n=209)

Group

FDR:  $8.759e-06$   
Coefficient:  $-1.60e+00$   
Value: post\_ltx



Pseudomonas



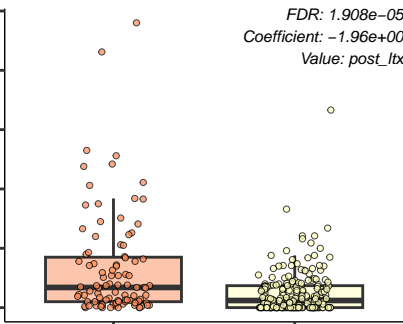
Oscillibacter

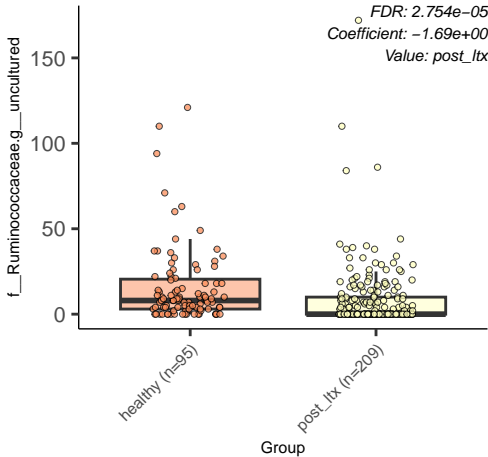
healthy (n=95)

post\_ltx (n=209)

Group

*FDR: 1.908e-05*  
*Coefficient: -1.96e+00*  
*Value: post\_ltx*





Clostridia\_UCG.014

FDR: 5.716e-05

Coefficient: -2.41e+00

Value: post\_ltx

750

500

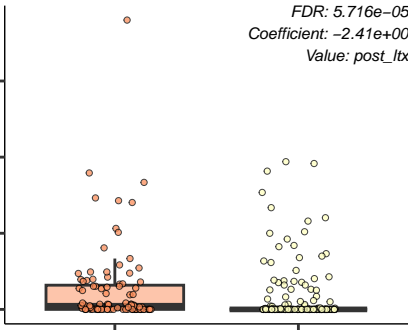
250

0

healthy (n=95)

post\_ltx (n=209)

Group



Colidextribacter

*FDR: 6.593e-05*

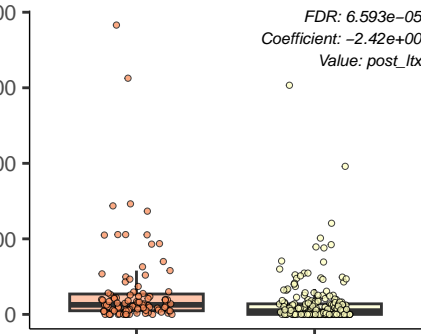
*Coefficient: -2.42e+00*

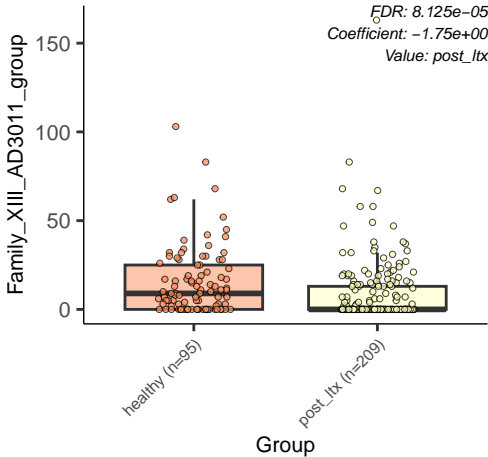
*Value: post\_ltx*

healthy (n=95)

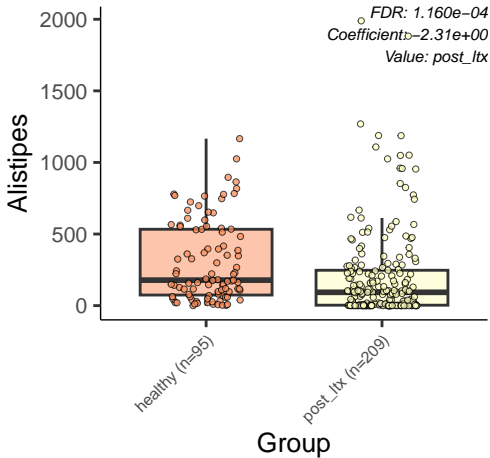
post\_ltx (n=209)

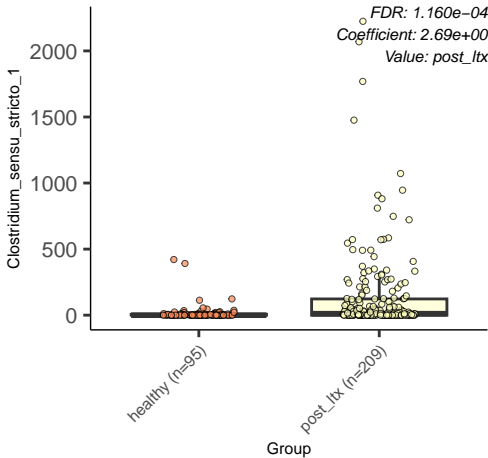
Group

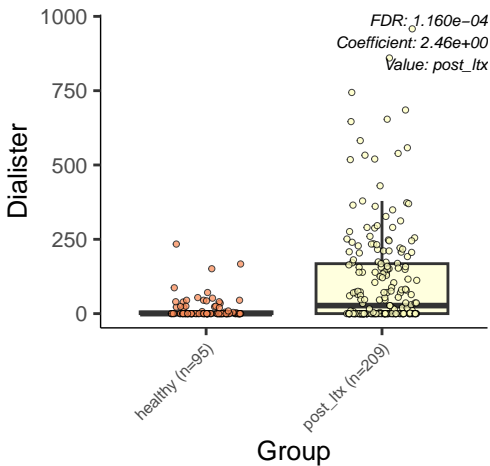


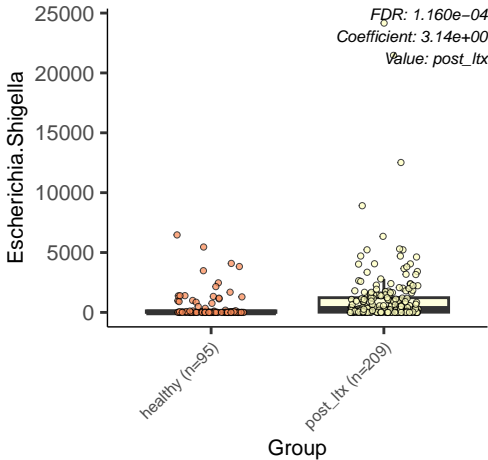


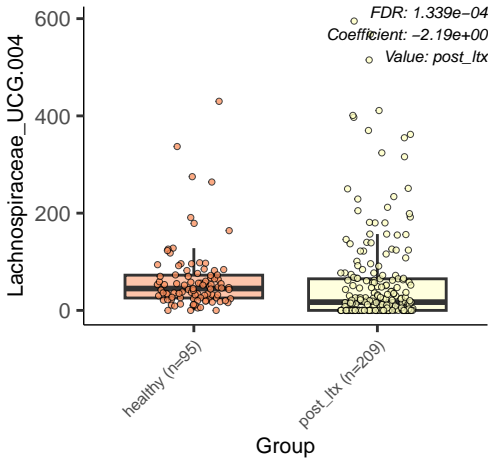


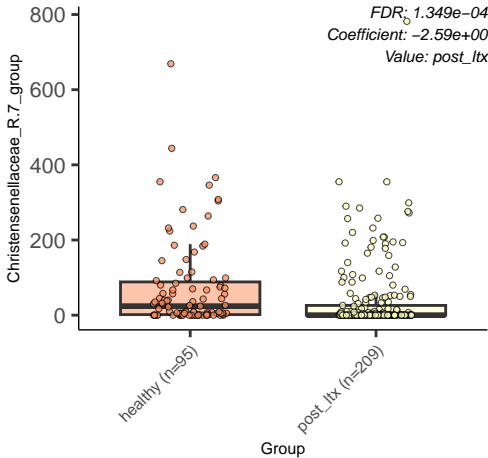












Holdemia

60

40

20

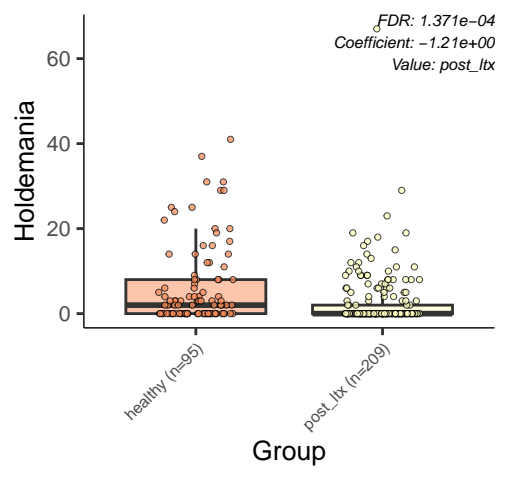
0

healthy (n=95)

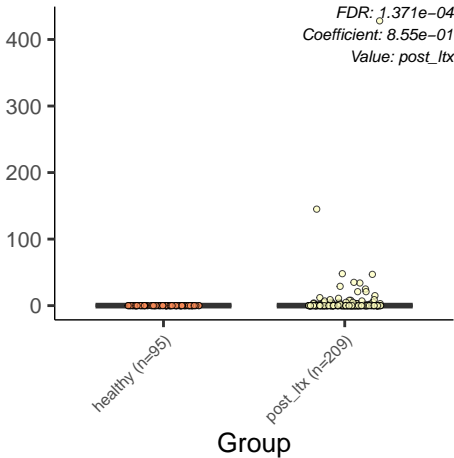
post\_ltx (n=209)

Group

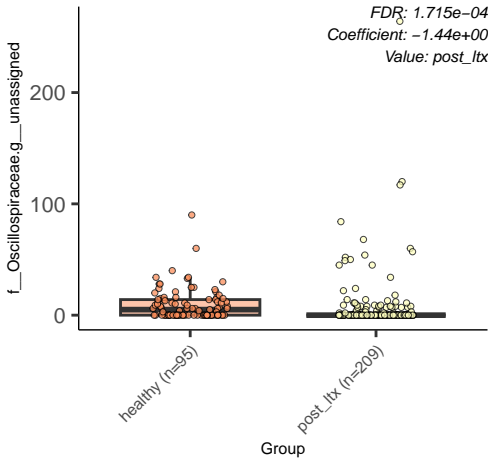
FDR:  $1.371\text{e-}04$   
Coefficient:  $-1.21\text{e}+00$   
Value: post\_ltx

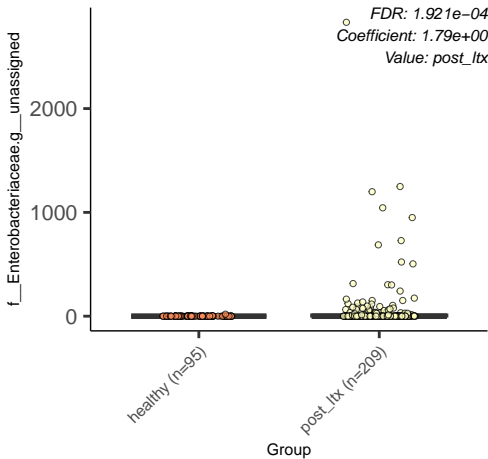


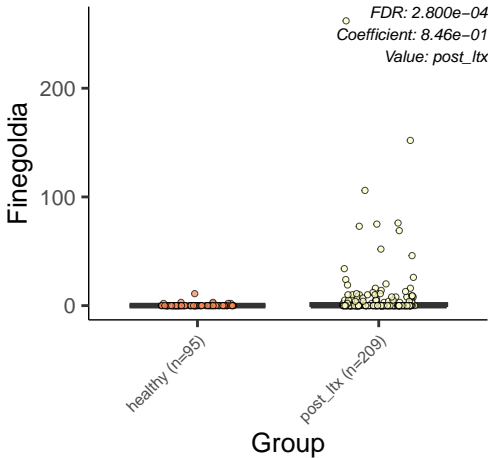
Peptoniphilus



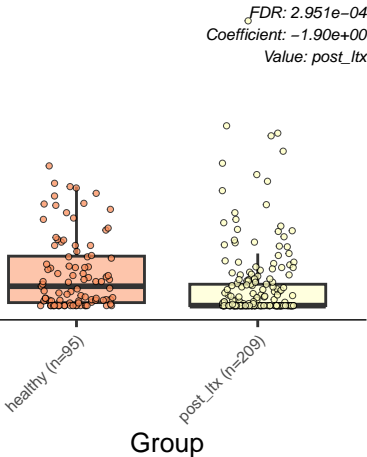




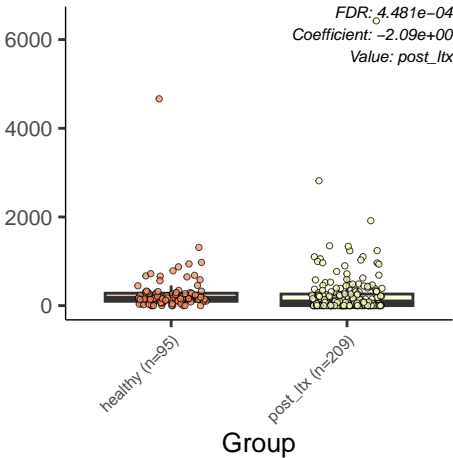


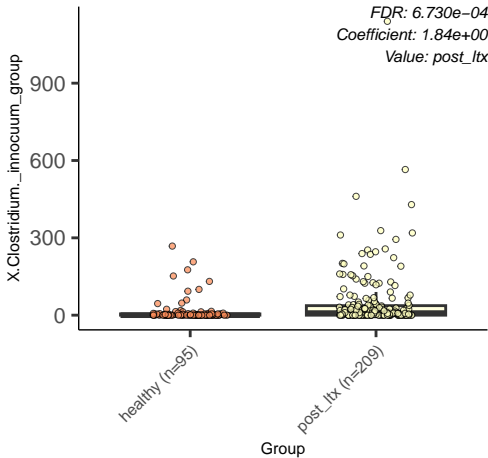


Butyricimonas



Parabacteroides





GCA.900066575

100

50

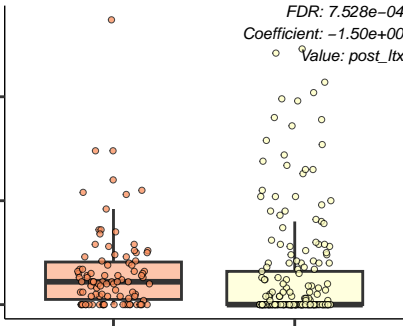
0

healthy (n=95)

post\_ltx (n=209)

Group

FDR:  $7.528e-04$   
Coefficient:  $-1.50e+00$   
Value: post\_ltx





FDR: 8.154e-04

Coefficient: 9.63e-01

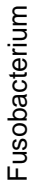
Value: *post\_ltx*

healthy (n=95)

post\_ltx (n=209)

Group





FDR: 1.012e-03

Coefficient: 2.01e+00

Value: *post\_ltx*

healthy (n=95)

post\_ltx (n=209)

Group

Anaerococcus

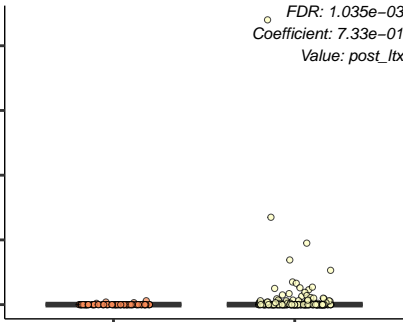
400  
300  
200  
100  
0

*FDR: 1.035e-03*  
*Coefficient: 7.33e-01*  
*Value: post\_ltx*

healthy (n=95)

post\_ltx (n=209)

Group



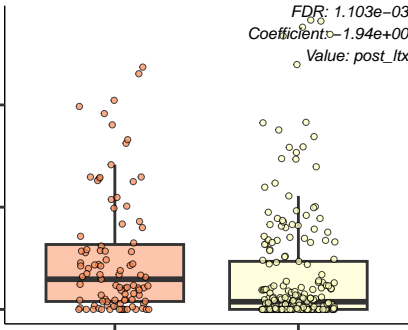
Lachnospiraceae\_UCG.010

FDR:  $1.103e-03$   
Coefficient:  $-1.94e+00$   
Value: post\_ltx

healthy (n=95)

post\_ltx (n=209)

Group



UCG.005

1000

500

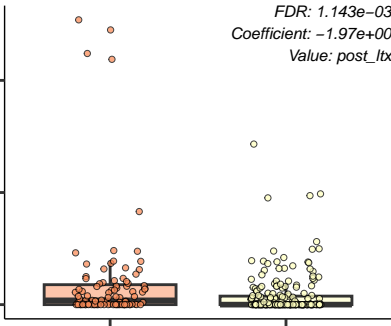
0

healthy (n=95)

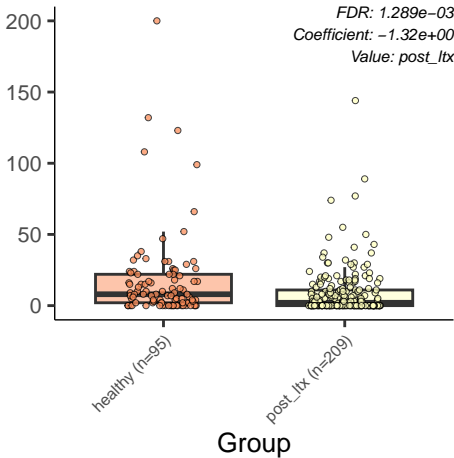
post\_ltx (n=209)

Group

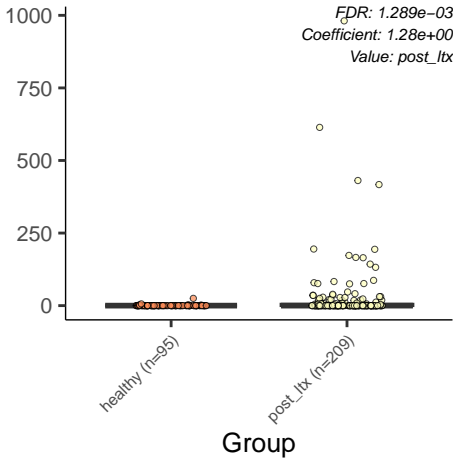
*FDR: 1.143e-03*  
*Coefficient: -1.97e+00*  
*Value: post\_ltx*



Marvinbryantia



Lactobacillus



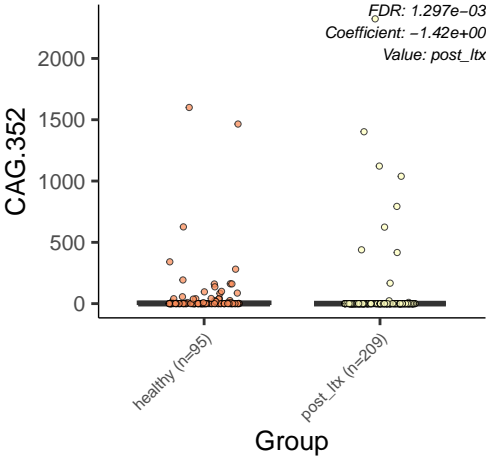
CAG.352

FDR:  $1.297\text{e-}03$   
Coefficient:  $-1.42\text{e}+00$   
Value: post\_ltx

healthy (n=95)

post\_ltx (n=209)

Group



Coprococcus

FDR:  $1.334e-03$

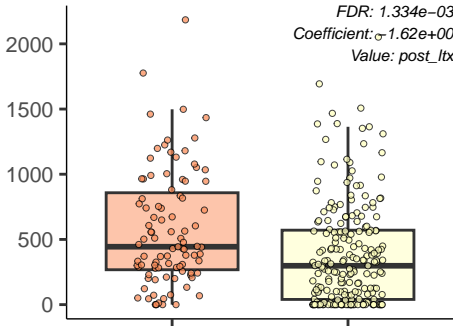
Coefficient:  $-1.62e+00$

Value: post\_ltx

healthy (n=95)

post\_ltx (n=209)

Group





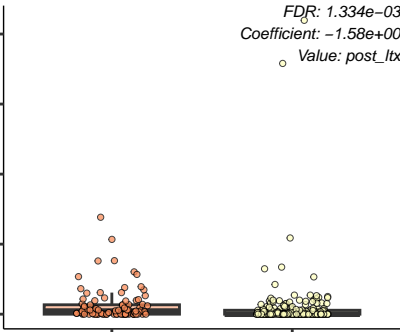
Lachnospiraceae\_NK4A136\_group

*FDR: 1.334e-03*  
*Coefficient: -1.58e+00*  
*Value: post\_ltx*

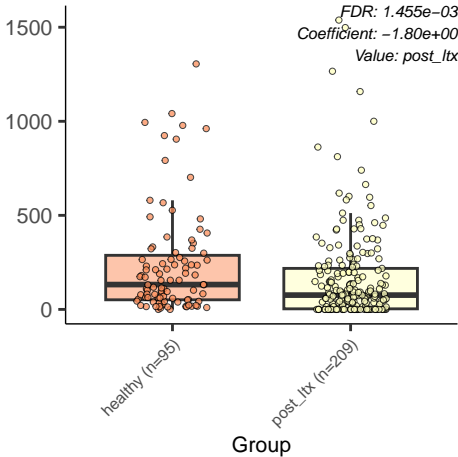
healthy (n=95)

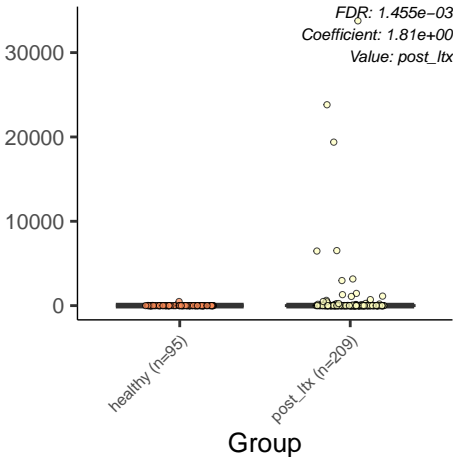
post\_ltx (n=209)

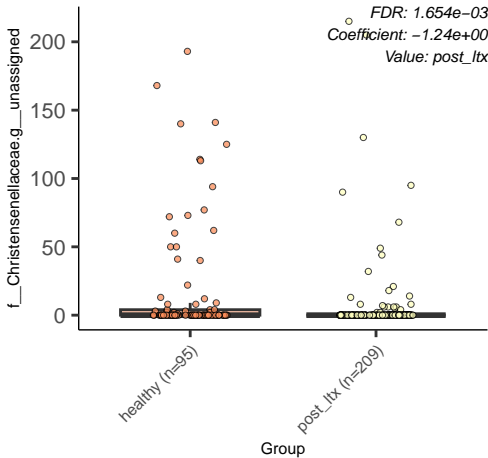
Group



Fusicatenibacter







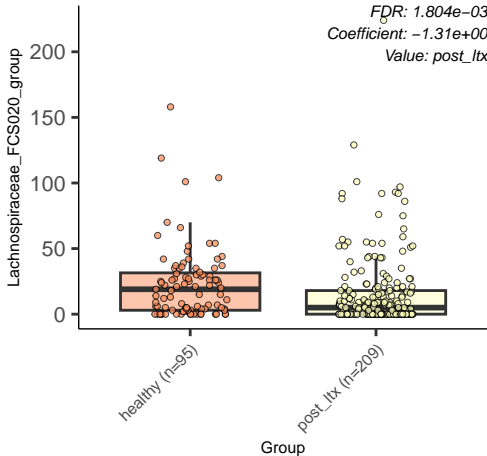
Lachnospiraceae\_FCS020\_group

FDR:  $1.804e-03$   
Coefficient:  $-1.31e+00$   
Value: *post\_ltx*

healthy (n=95)

post\_ltx (n=209)

Group



Gordonibacter

FDR: 1.913e-03

Coefficient: -1.03e+00

Value: post\_ltx

200

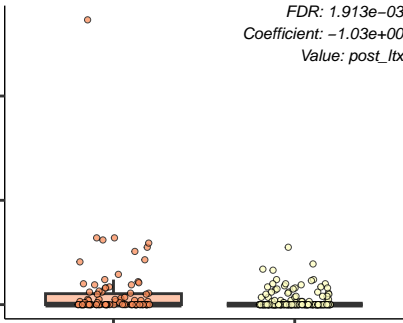
100

0

healthy (n=95)

post\_ltx (n=209)

Group



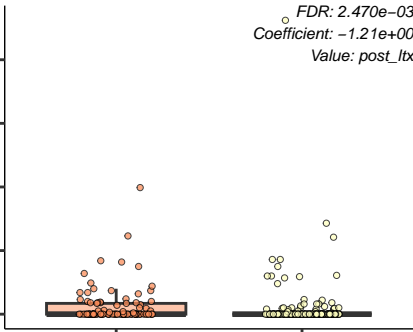
f\_\_Eggerthellaceae.g\_\_uncultured

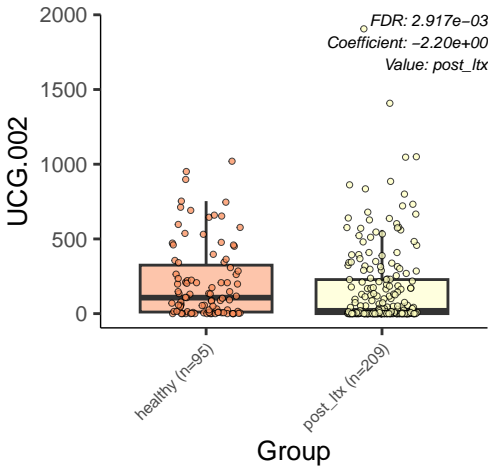
FDR: 2.470e-03  
Coefficient: -1.21e+00  
Value: post\_ltx

healthy (n=95)

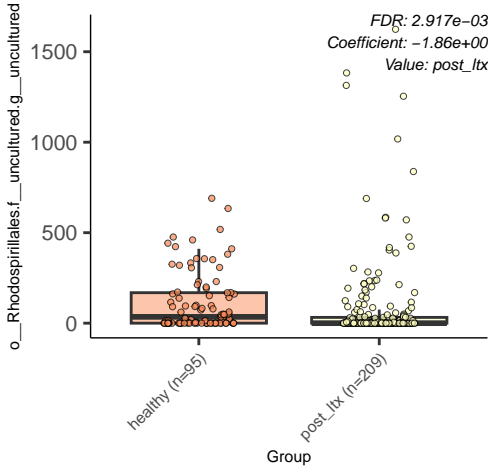
post\_ltx (n=209)

Group









Enterorhabdus

FDR: 3.371e-03

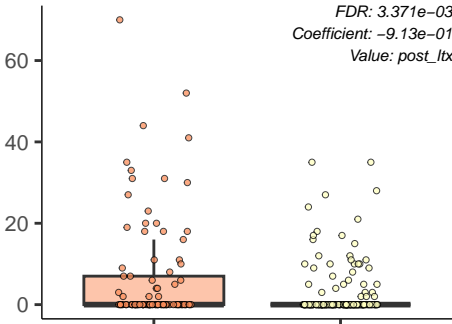
Coefficient: -9.13e-01

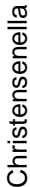
Value: post\_ltx

healthy (n=95)

post\_ltx (n=209)

Group





*FDR: 3.396e-03*

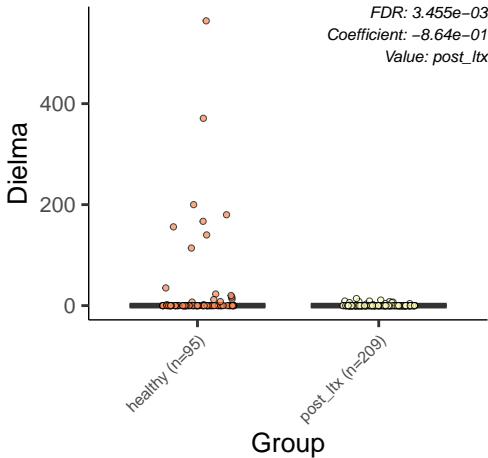
Coefficient:  $-1.06e-01$

Value: *post\_ltx*

healthy (n=95)

post\_ltx (n=209)

Group



f\_\_Lachnospiraceae.g\_\_unassigned

FDR: 3.748e-03  
Coefficient: -1.09e+00  
○ Value: post\_ltx

4000

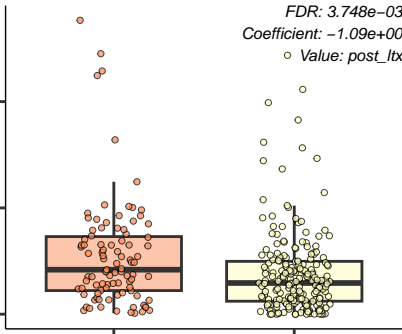
2000

0

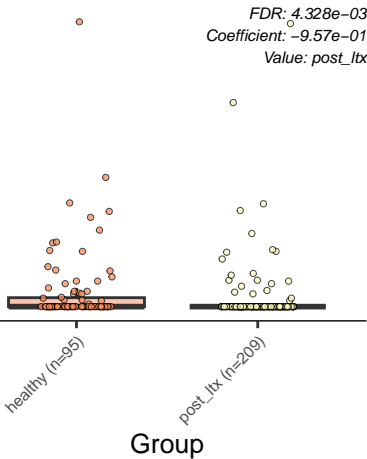
healthy (n=95)

post\_ltx (n=209)

Group



Howardella



Barnesiella

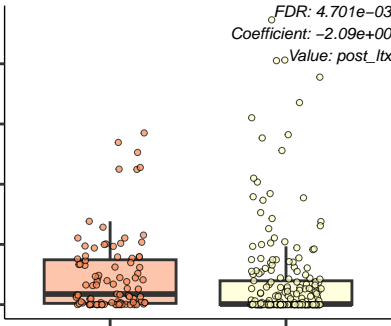
2000  
1500  
1000  
500  
0

healthy (n=95)

post\_ltx (n=209)

Group

FDR: 4.701e-03  
Coefficient: -2.09e+00  
Value: post\_ltx



Negativibacillus

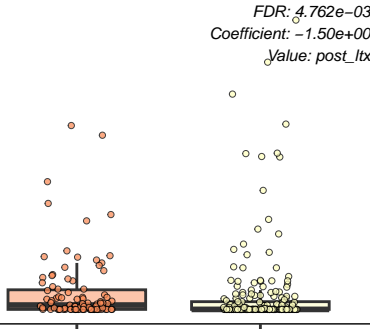
600  
400  
200  
0

healthy (n=95)

post\_ltx (n=209)

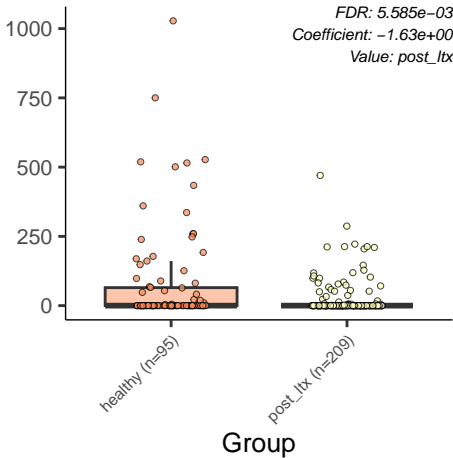
Group

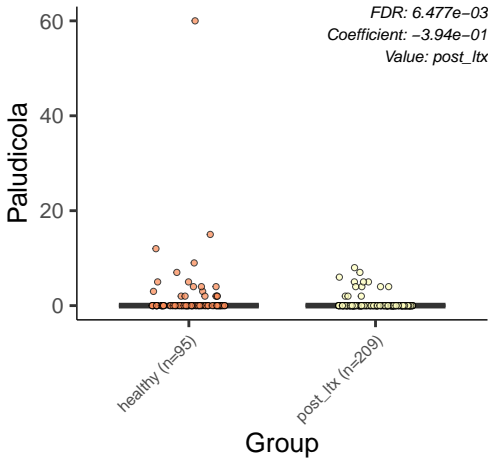
*FDR: 4.762e-03*  
*Coefficient: -1.50e+00*  
*Value: post\_ltx*





Paraprevotella





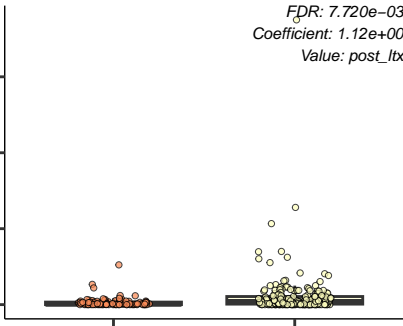
Actinomyces

FDR:  $7.720 \times 10^{-3}$   
Coefficient:  $1.12 \times 10^0$   
Value: post\_ltx

healthy (n=95)

post\_ltx (n=209)

Group



Faecalibacterium

7500

5000

2500

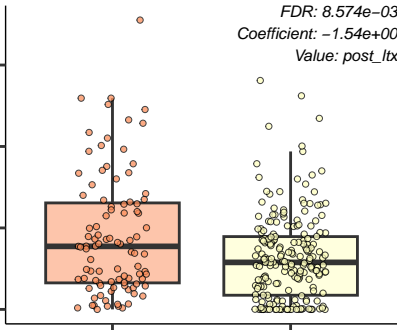
0

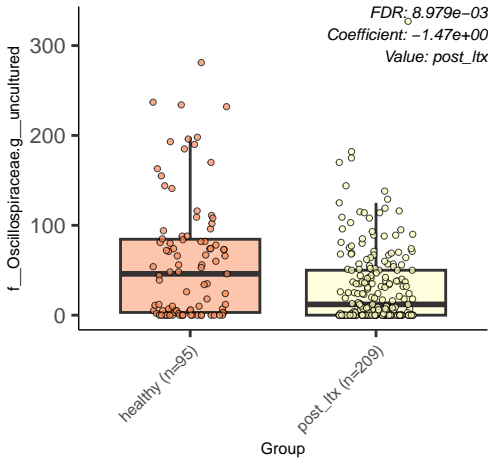
healthy (n=95)

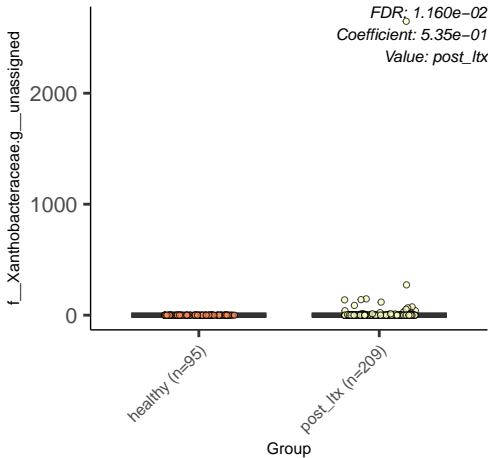
post\_ltx (n=209)

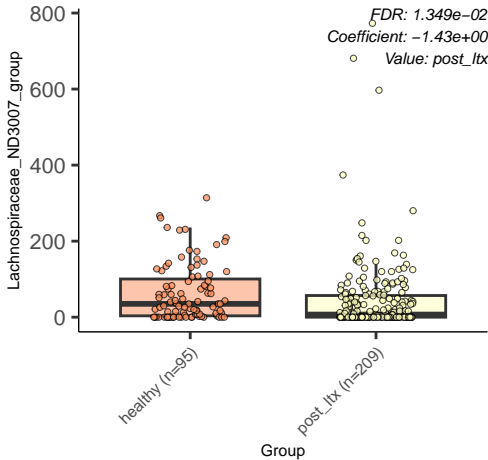
Group

FDR:  $8.574e-03$   
Coefficient:  $-1.54e+00$   
Value: post\_ltx









Erysipelotrichaceae\_UCG.003

FDR:  $1.812 \times 10^{-2}$   
Coefficient:  $-1.76 \times 10^0$   
Value: post\_ltx

2000

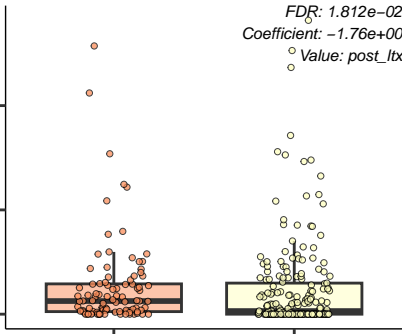
1000

0

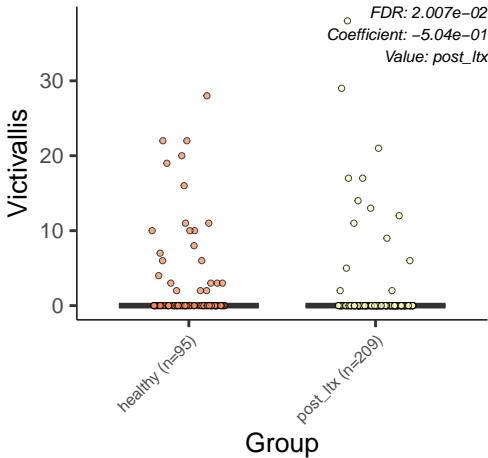
healthy (n=95)

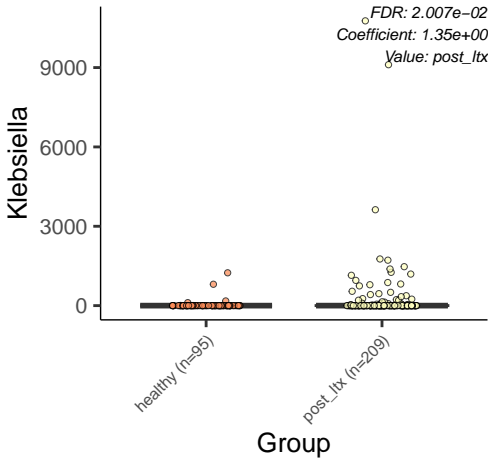
post\_ltx (n=209)

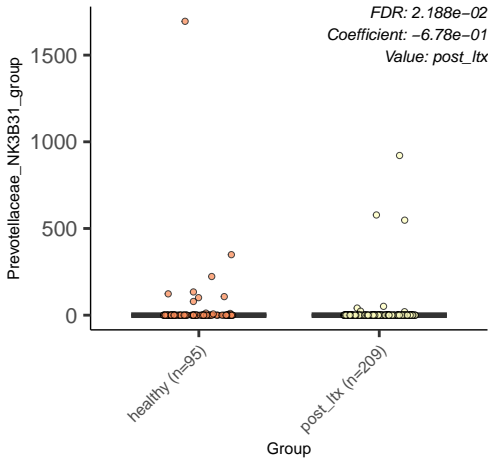
Group











UCG.009

60

40

20

0

healthy (n=95)

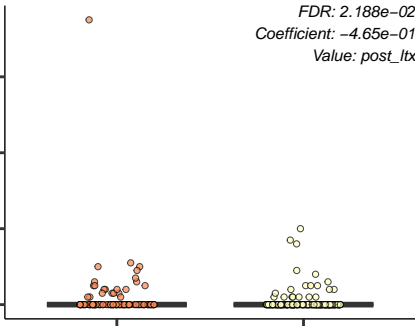
post\_ltx (n=209)

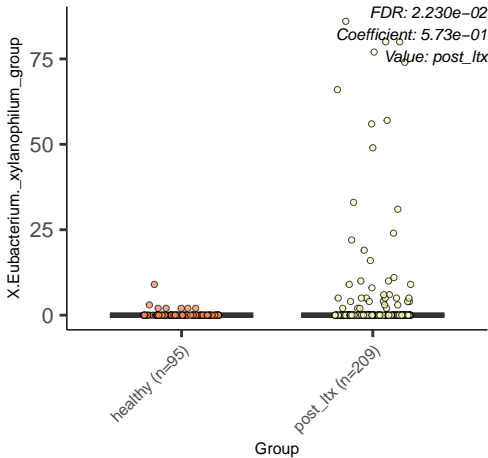
Group

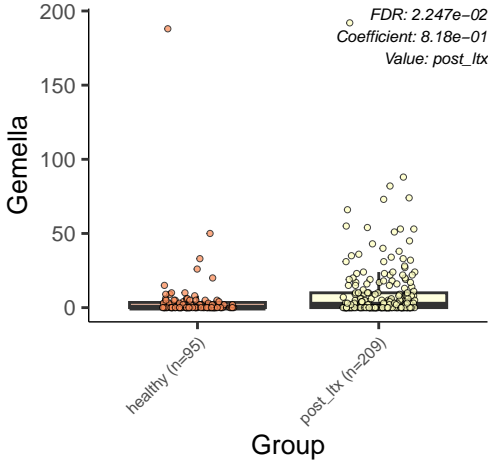
FDR:  $2.188e-02$

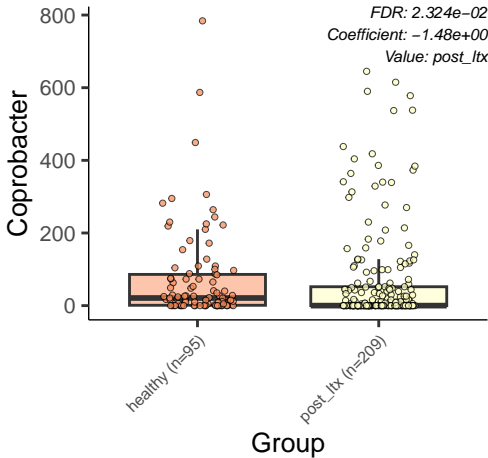
Coefficient:  $-4.65e-01$

Value: post\_ltx









Phascolarctobacterium

FDR:  $2.324e-02$

Coefficient:  $-1.66e+00$

Value: post\_ltx

1000

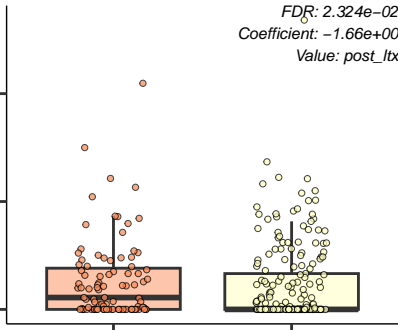
500

0

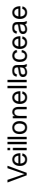
healthy (n=95)

post\_ltx (n=209)

Group







FDR: 2.324e-02  
Coefficient: 8.26e-01  
Value: post\_ltx

healthy (n=95)

post\_ltx (n=209)

Group

Staphylococcus

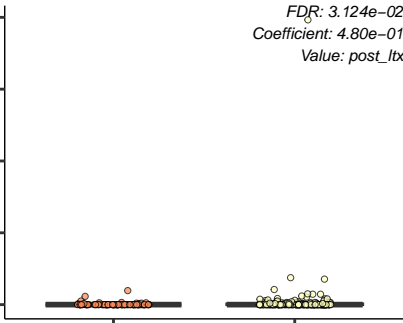
800  
600  
400  
200  
0

*FDR: 3.124e-02*  
*Coefficient: 4.80e-01*  
*Value: post\_ltx*

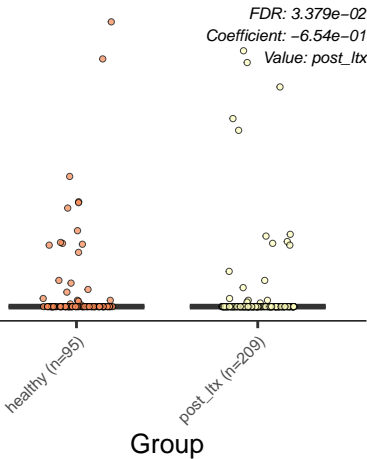
healthy (n=95)

post\_ltx (n=209)

Group



# Muribaculaceae



Bacteroides

10000

5000

0

healthy (n=95)

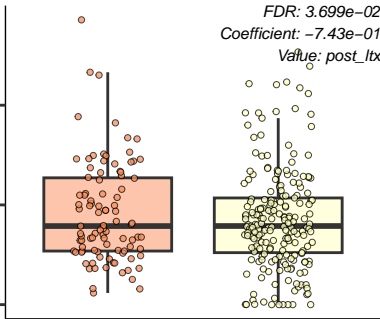
post\_ltx (n=209)

Group

*FDR: 3.699e-02*

*Coefficient: -7.43e-01*

*Value: post\_ltx*



Clostridia\_vadinBB60\_group

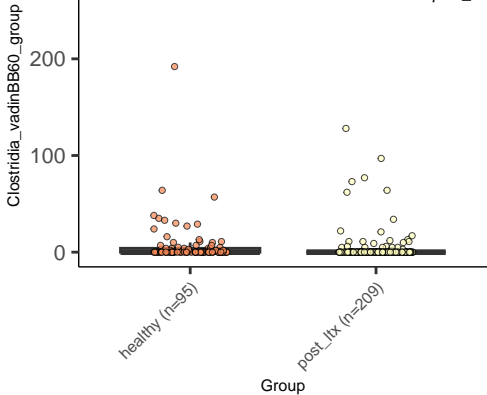
300  
200  
100  
0

healthy (n=95)

post\_ltx (n=209)

Group

FDR:  $3.699\text{e-}02$   
Coefficient:  $-6.82\text{e-}01$   
Value: post\_ltx



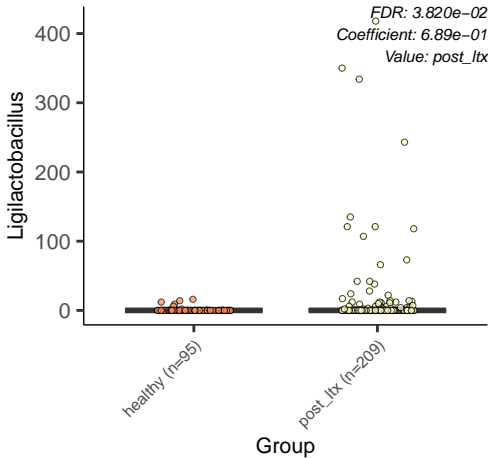


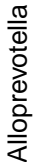
FDR: 3.699e-02  
Coefficient: 5.65e-01  
Value: post\_ltx

healthy (n=95)

post\_ltx (n=209)

Group





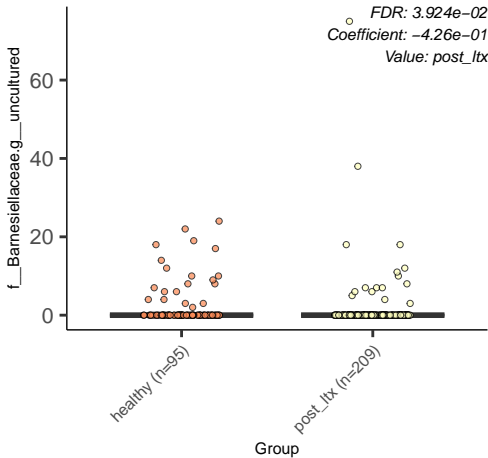
FDR: 3.860e-02  
Coefficient: -9.56e-01  
Value: post\_ltx

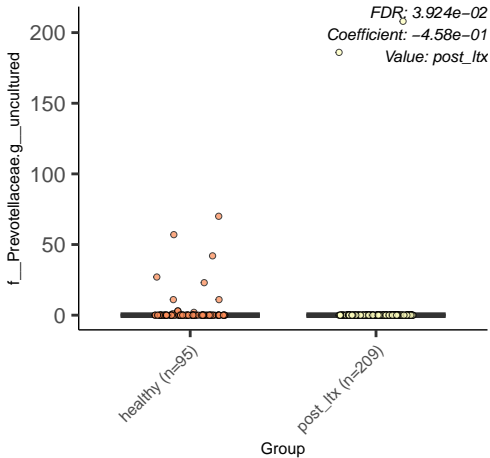
healthy (n=95)

post\_ltx (n=209)

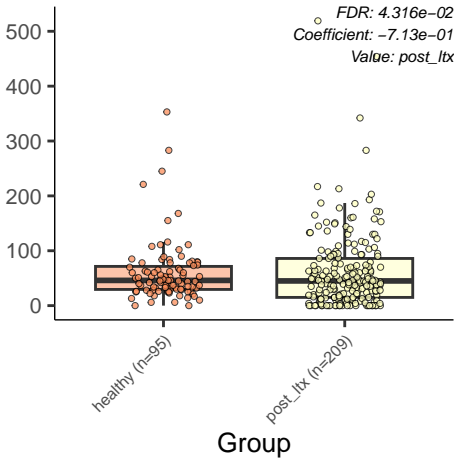
Group

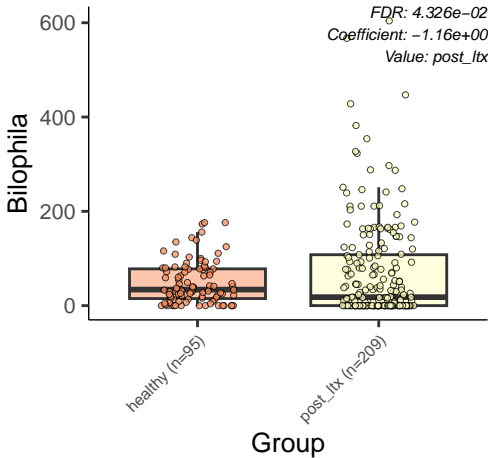


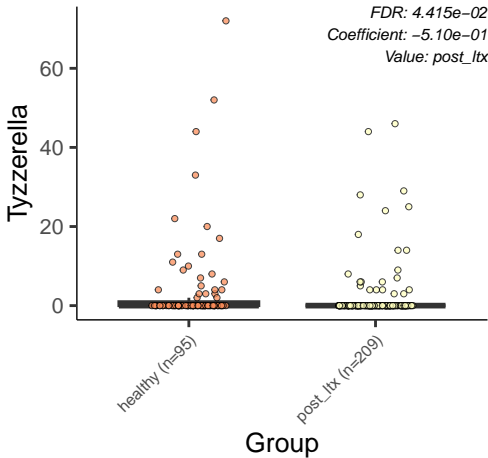


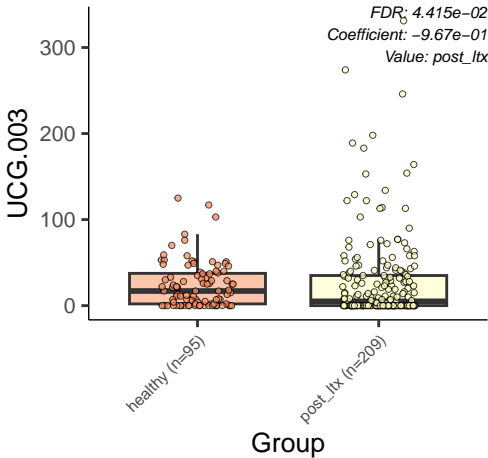


Butyricoccus









Intestinibacter

