

Odoribacter

healthy (n=95)

post\_ltx (n=209)

Group

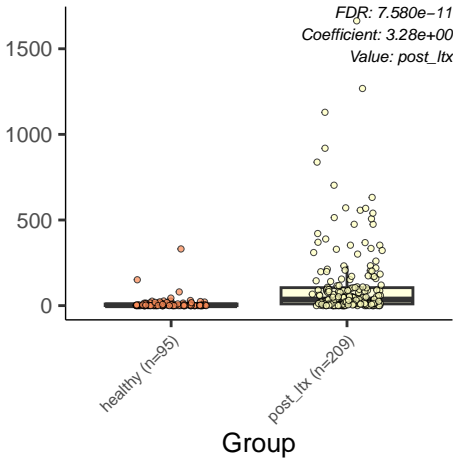
*FDR: 7.580e-11*  
*Coefficient: -3.15e+00*  
*Value: post\_ltx*

400

200

0

Haemophilus



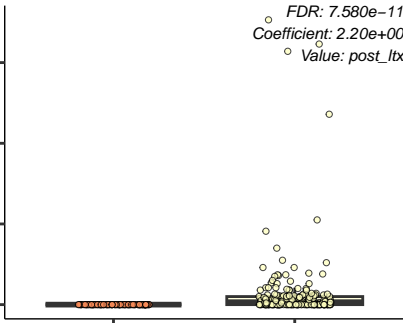
Sphingobium

FDR:  $7.580 \times 10^{-11}$   
Coefficient:  $2.20 \times 10^0$   
Value: post\_ltx

healthy (n=95)

post\_ltx (n=209)

Group



Veillonella

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

2000

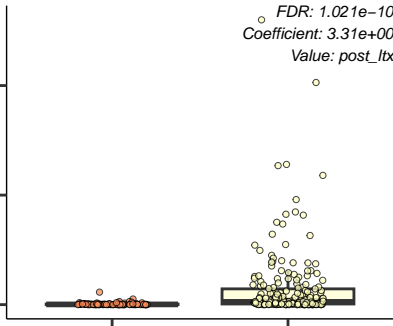
1000

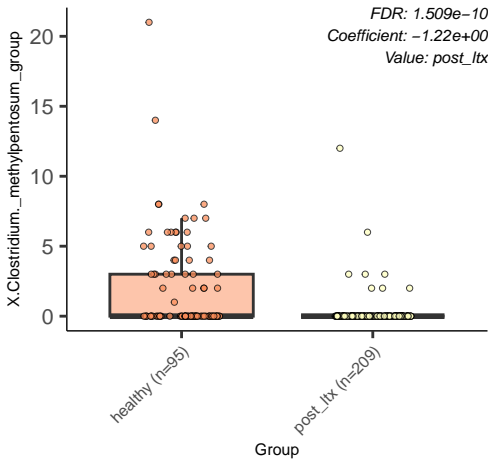
0

healthy (n=95)

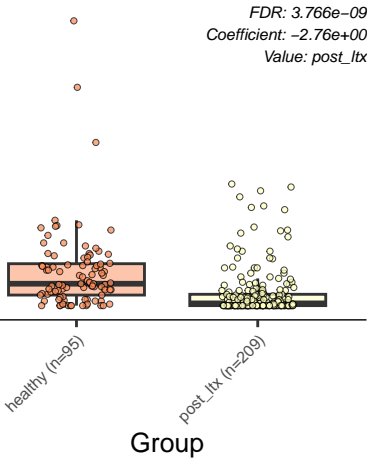
post\_ltx (n=209)

Group





Intestinimonas



Family\_XIII\_UCG.001

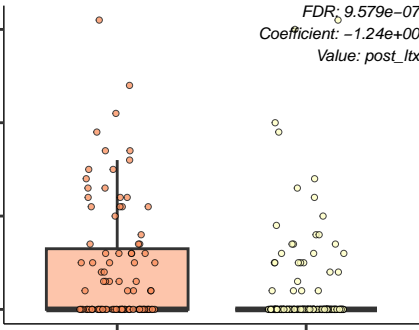
30  
20  
10  
0

healthy (n=95)

post\_ltx (n=209)

Group

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



Streptococcus

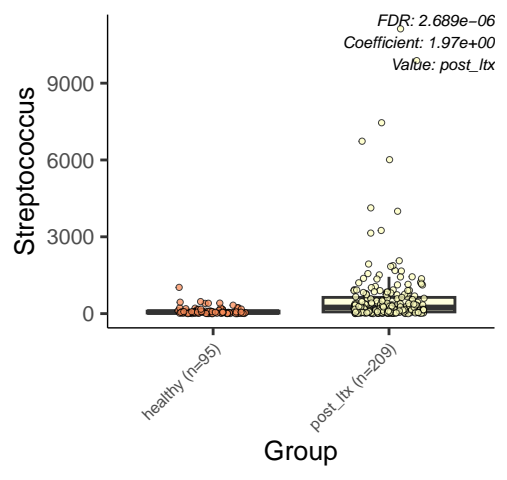
$FDR: 2.689e-06$   
 $Coefficient: 1.97e+00$   
 $Value: post\_ltx$

healthy (n=95)

post\_ltx (n=209)

Group

9000  
6000  
3000  
0





CAG.56

FDR:  $8.073e-06$

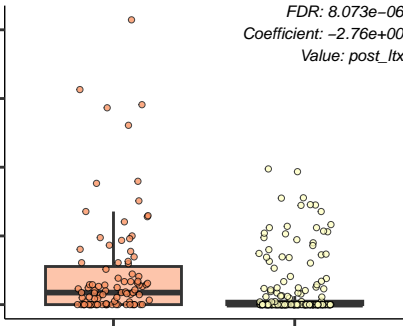
Coefficient:  $-2.76e+00$

Value: *post\_ltx*

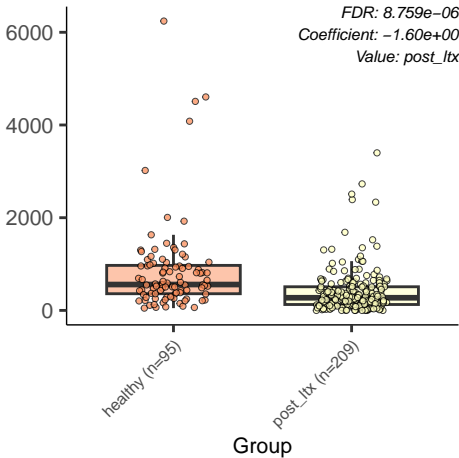
healthy (n=95)

post\_ltx (n=209)

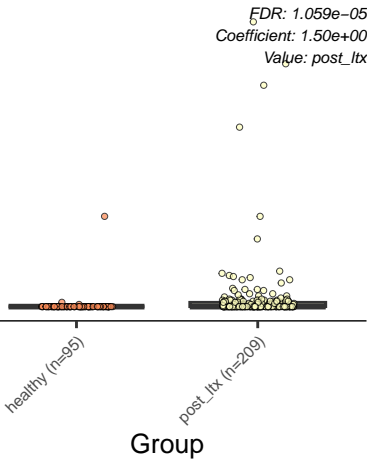
Group



Lachnoclostridium



Pseudomonas



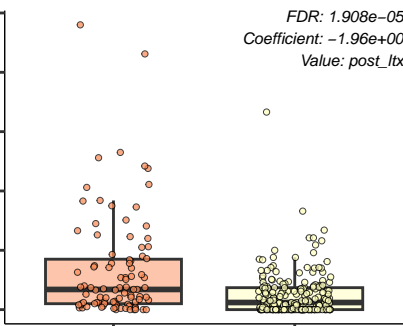
Oscillibacter

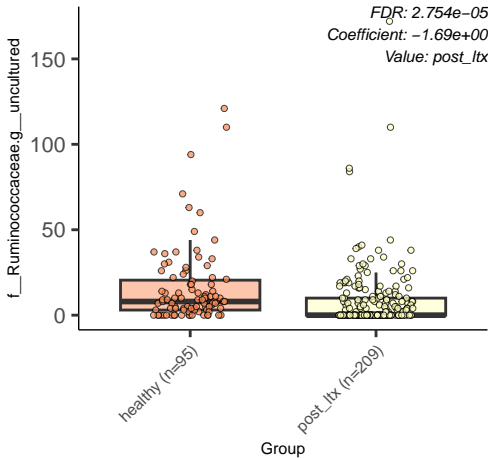
healthy (n=95)

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

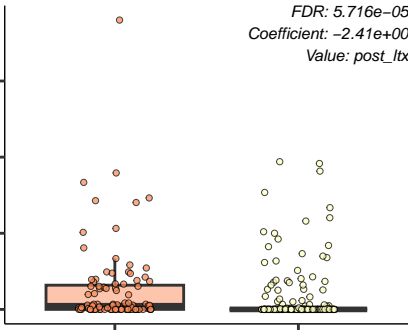
250

0

healthy (n=95)

post\_ltx (n=209)

Group



Colidextribacter

*FDR: 6.593e-05*

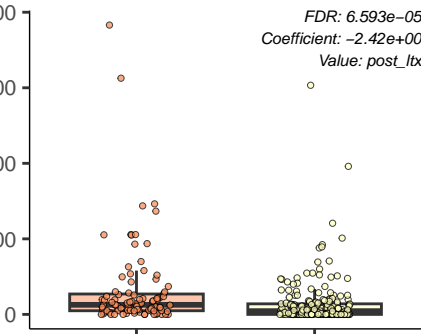
*Coefficient: -2.42e+00*

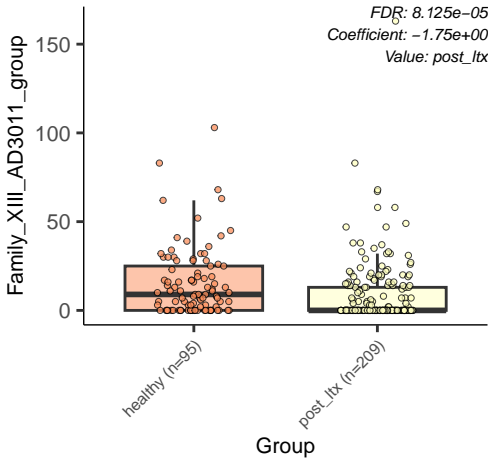
*Value: post\_ltx*

healthy (n=95)

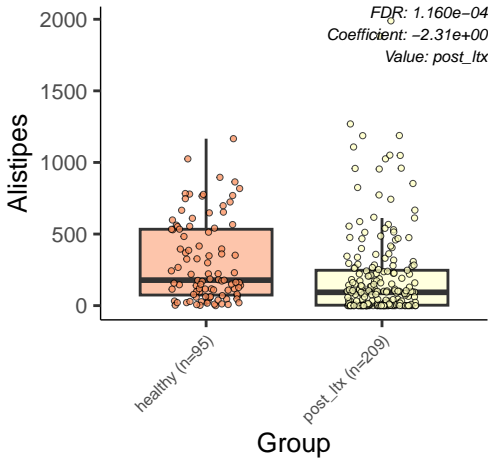
post\_ltx (n=209)

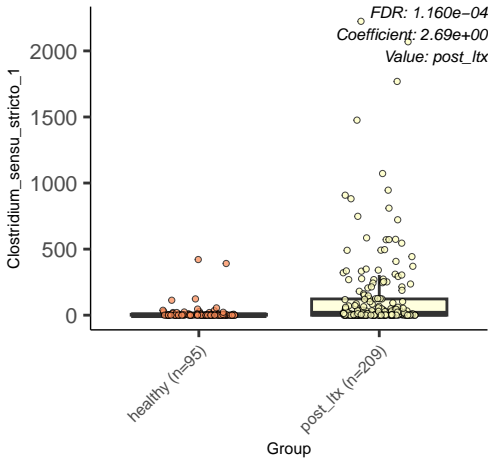
Group

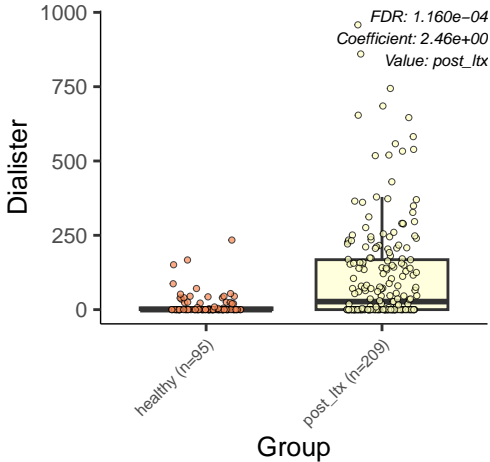












Escherichia.Shigella

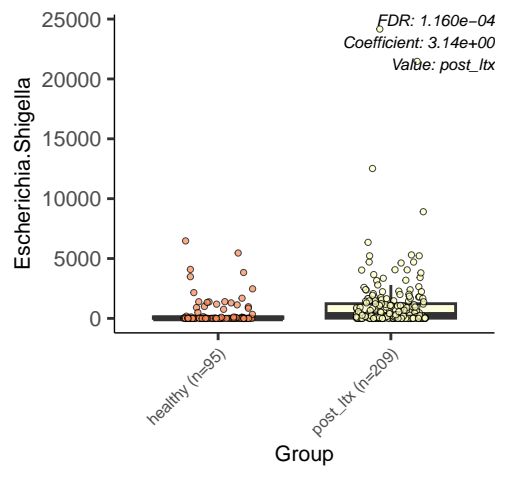
25000  
20000  
15000  
10000  
5000  
0

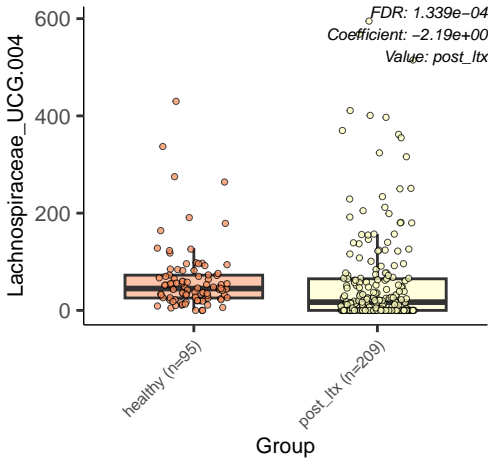
FDR: 1.160e-04  
Coefficient: 3.14e+00  
Value: post\_ltx

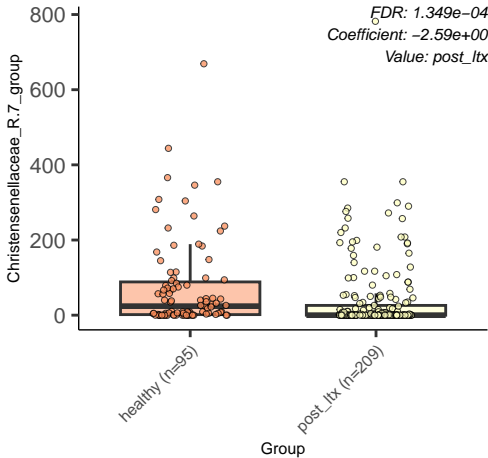
healthy (n=95)

post\_ltx (n=209)

Group







Holdmania

60

40

20

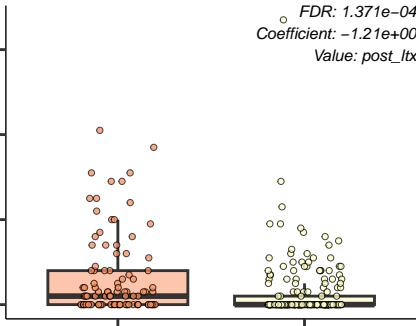
0

healthy (n=95)

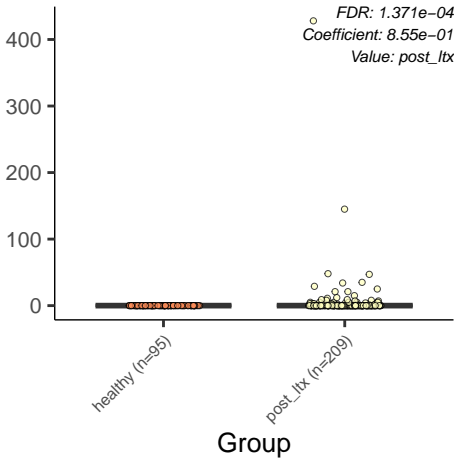
post\_ltx (n=209)

Group

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



Peptoniphilus





f\_Oscillospiraceae.g\_\_unassigned

FDR:  $1.715 \times 10^{-4}$   
Coefficient:  $-1.44 \times 10^0$   
Value: post\_ltx

200

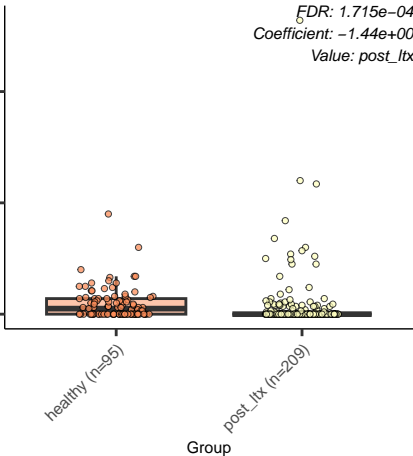
100

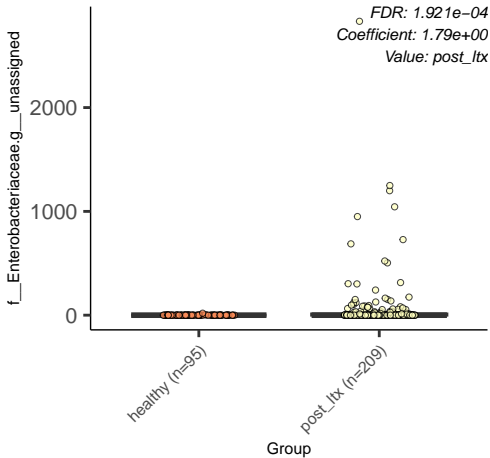
0

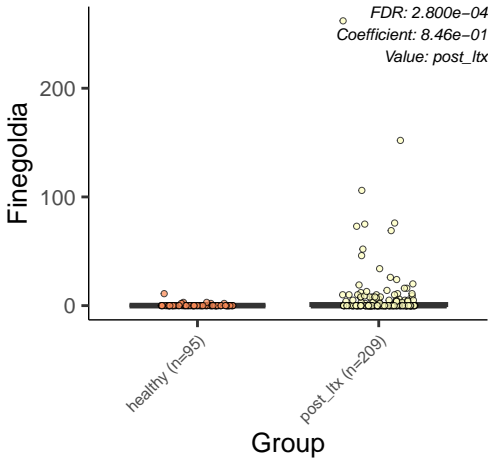
healthy (n=95)

post\_ltx (n=209)

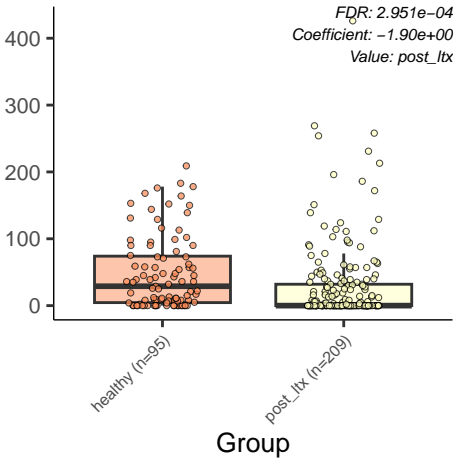
Group



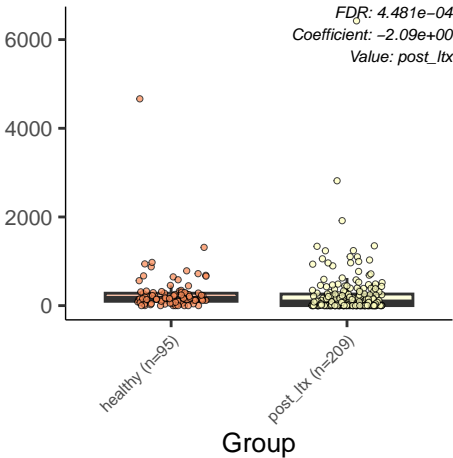


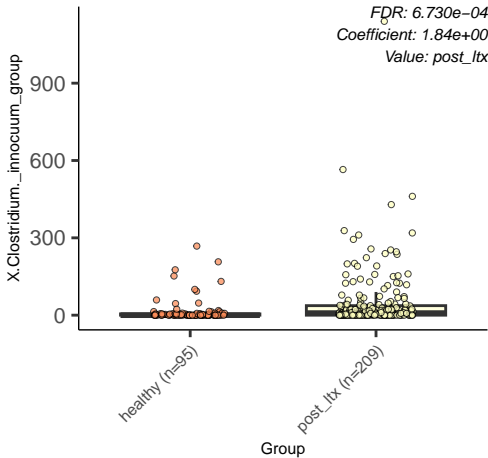


Butyricimonas



Parabacteroides





GCA.900066575

100

50

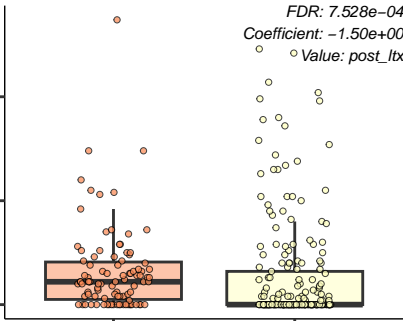
0

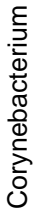
healthy (n=95)

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*

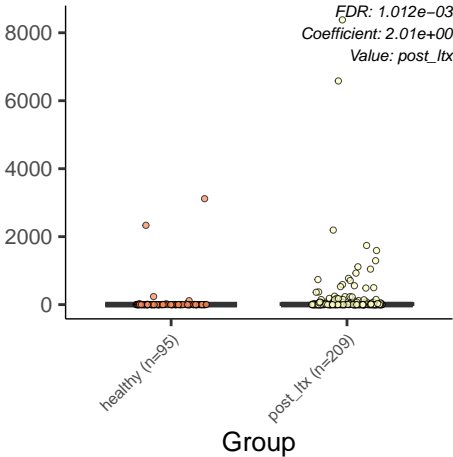
healthy (n=95)

post\_ltx (n=209)

Group



Fusobacterium



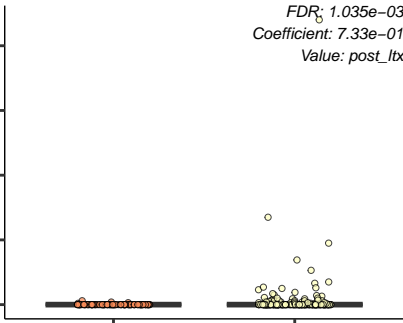
Anaerococcus

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

healthy (n=95)

post\_ltx (n=209)

Group



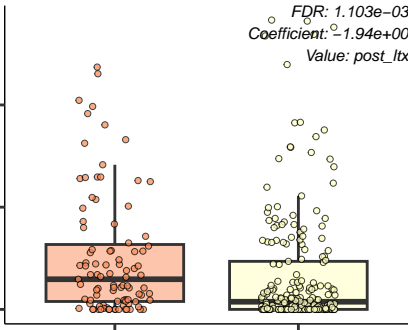
Lachnospiraceae\_UCG.010

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

healthy (n=95)

post\_ltx (n=209)

Group



UCG.005

1000

500

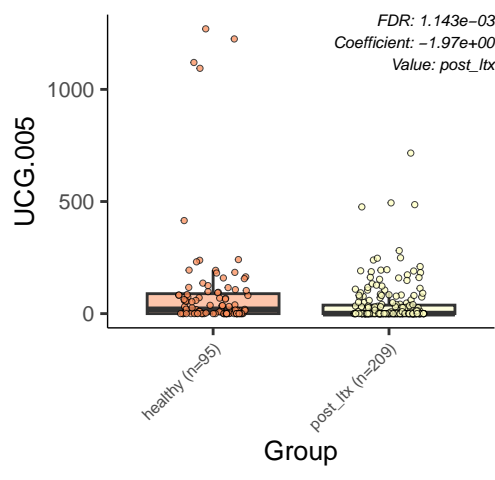
0

healthy (n=95)

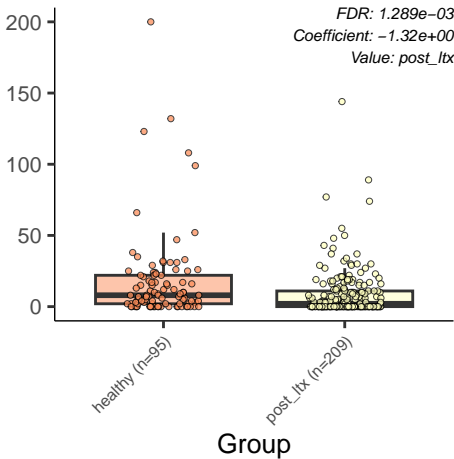
post\_ltx (n=209)

Group

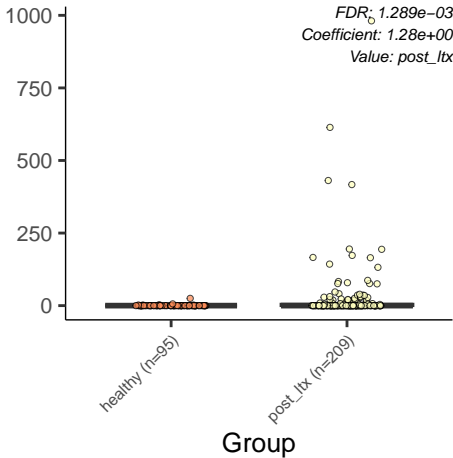
*FDR: 1.143e-03*  
*Coefficient: -1.97e+00*  
*Value: post\_ltx*



Marvinbryantia



Lactobacillus



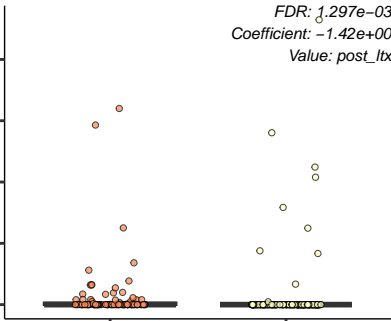
CAG.352

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

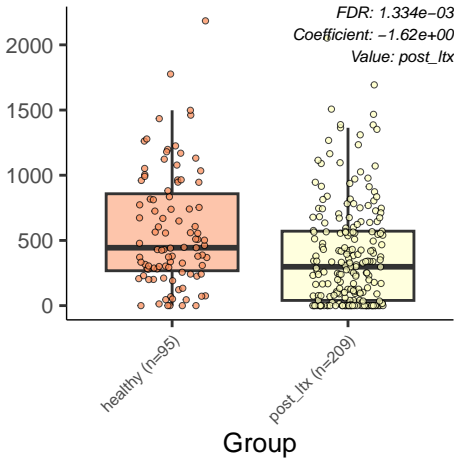
healthy (n=95)

post\_ltx (n=209)

Group



Coprococcus





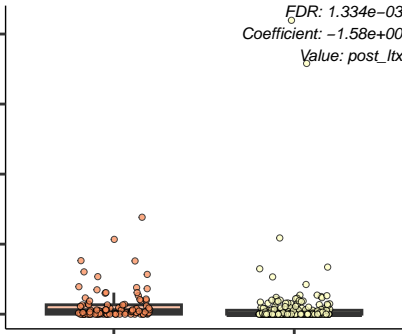
Lachnospiraceae\_NK4A136\_group

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

healthy (n=95)

post\_ltx (n=209)

Group



Fusicatenibacter

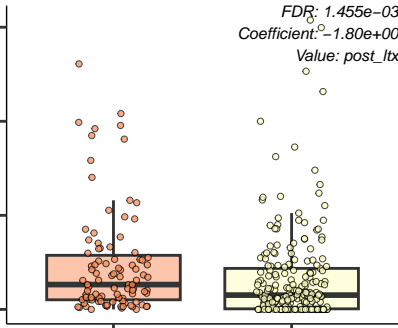
1500  
1000  
500  
0

healthy (n=95)

post\_ltx (n=209)

Group

*FDR: 1.455e-03*  
*Coefficient: -1.80e+00*  
*Value: post\_ltx*



Enterococcus

30000

20000

10000

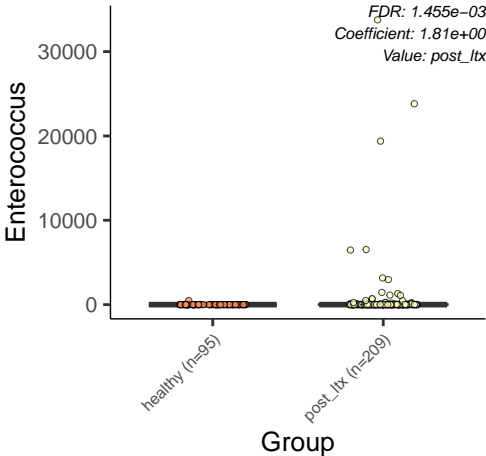
0

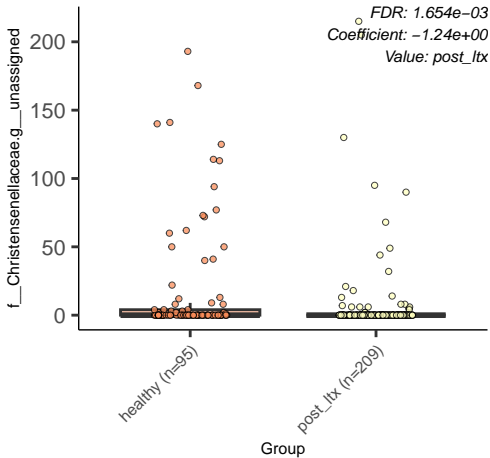
healthy (n=95)

post\_ltx (n=209)

Group

FDR:  $1.455e-03$   
Coefficient:  $1.81e+00$   
Value: post\_ltx





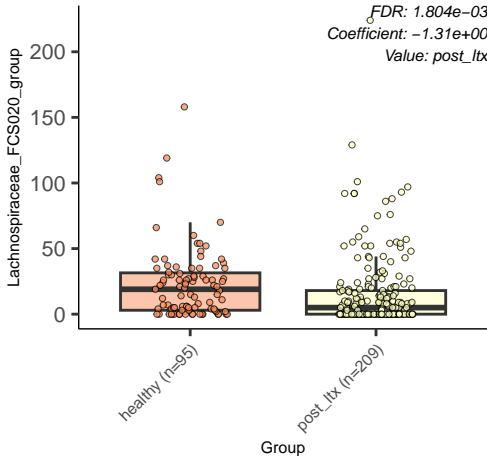
Lachnospiraceae\_FCS020\_group

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

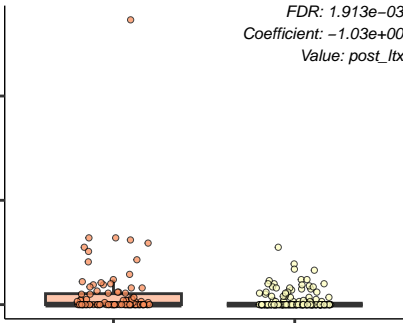
100

0

healthy (n=95)

post\_ltx (n=209)

Group



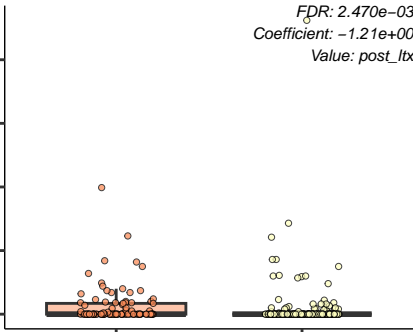
f\_\_Eggerthellaceae.g\_\_uncultured

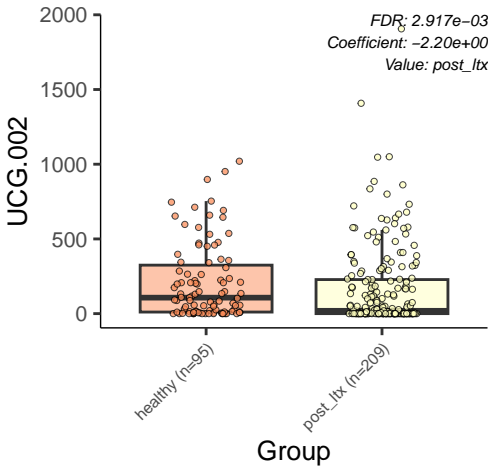
FDR: 2.470e-03  
Coefficient: -1.21e+00  
Value: post\_ltx

healthy (n=95)

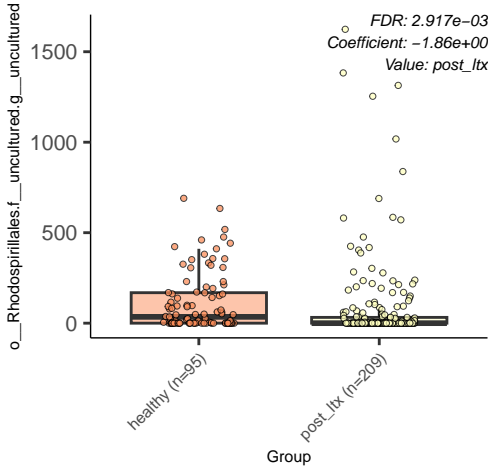
post\_ltx (n=209)

Group









Enterorhabdus

FDR: 3.371e-03

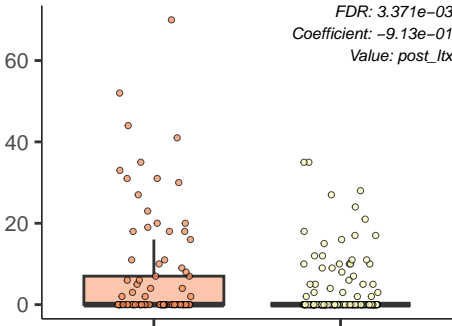
Coefficient: -9.13e-01

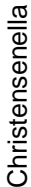
Value: post\_ltx

healthy (n=95)

post\_ltx (n=209)

Group





*FDR: 3.396e-03*

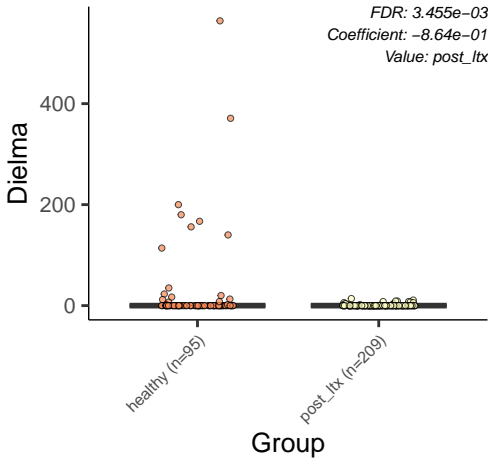
Coefficient:  $-1.06e-01$

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

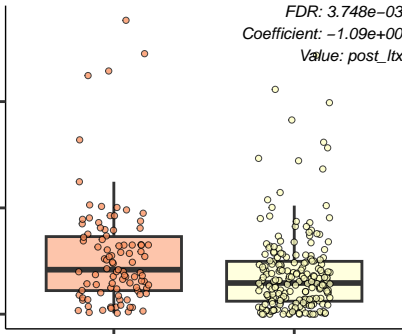
2000

0

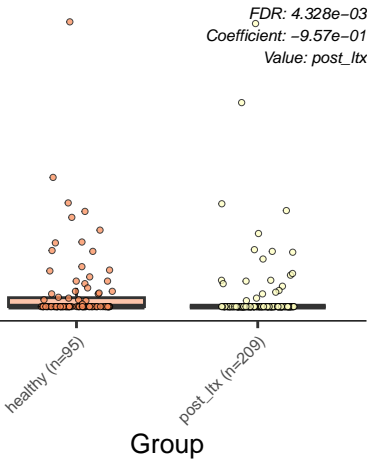
healthy (n=95)

post\_ltx (n=209)

Group



Howardella



Barnesiella

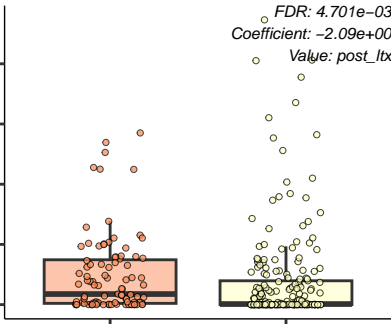
2000  
1500  
1000  
500  
0

healthy (n=95)

post\_ltx (n=209)

Group

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



Negativibacillus

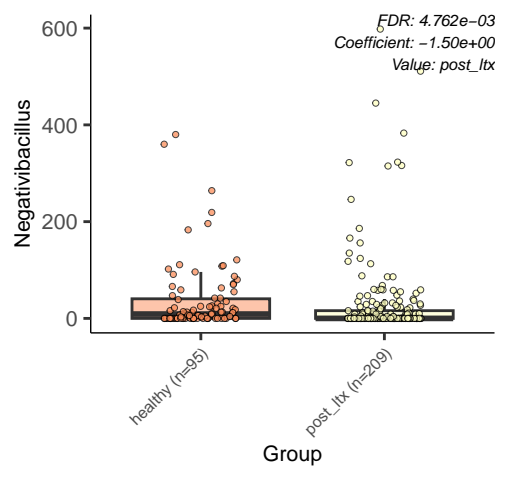
600  
400  
200  
0

healthy (n=95)

post\_ltx (n=209)

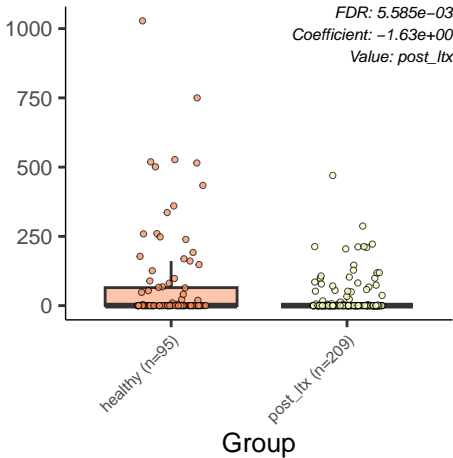
Group

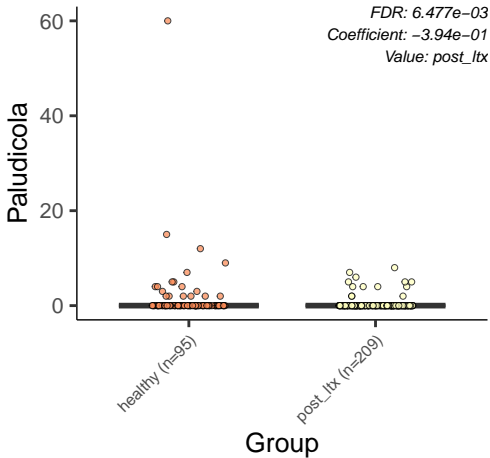
FDR:  $4.762e-03$   
Coefficient:  $-1.50e+00$   
Value: *post\_ltx*





Paraprevotella





Actinomyces

*FDR: 7.720e-03*  
*Coefficient: 1.12e+00*  
*Value: post\_ltx*

900

600

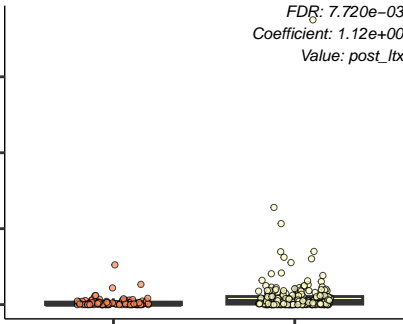
300

0

healthy (n=95)

post\_ltx (n=209)

Group



Faecalibacterium

7500

5000

2500

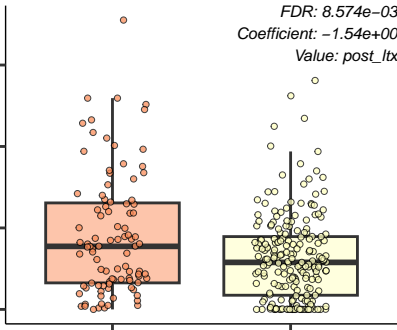
0

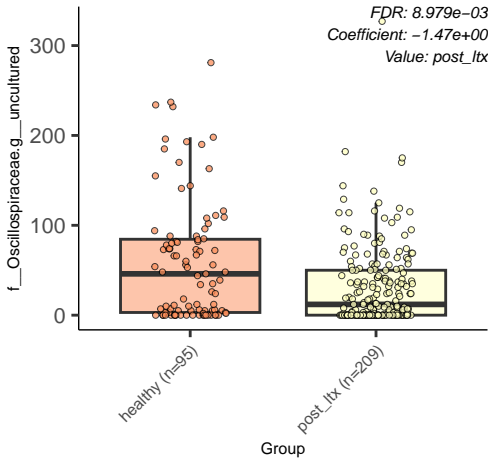
healthy (n=95)

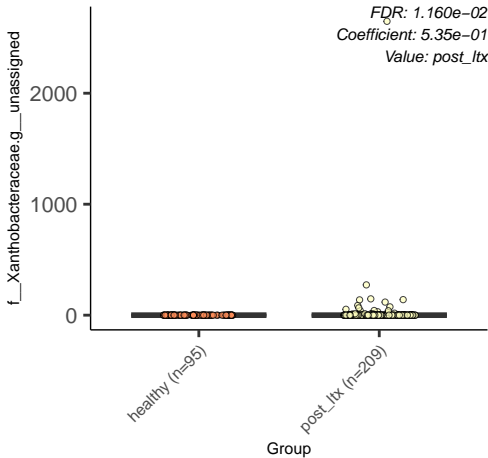
post\_ltx (n=209)

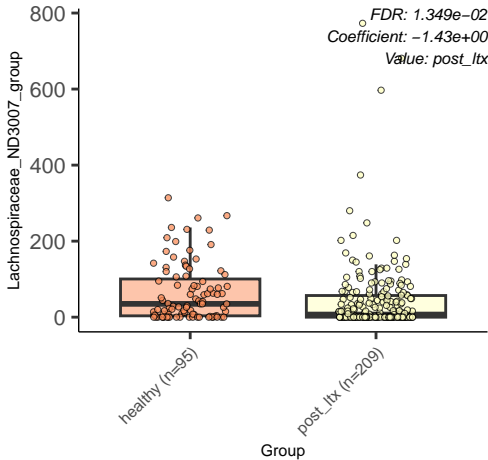
Group

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









Erysipelotrichaceae\_UCG.003

FDR: 1.812e-02  
Coefficient: -1.76e+00  
Value: post\_ltx

2000

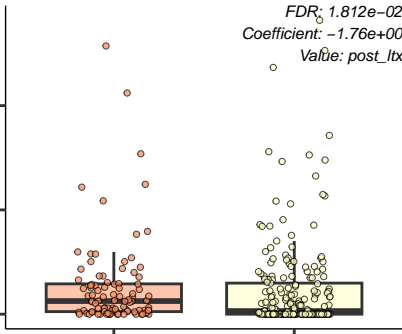
1000

0

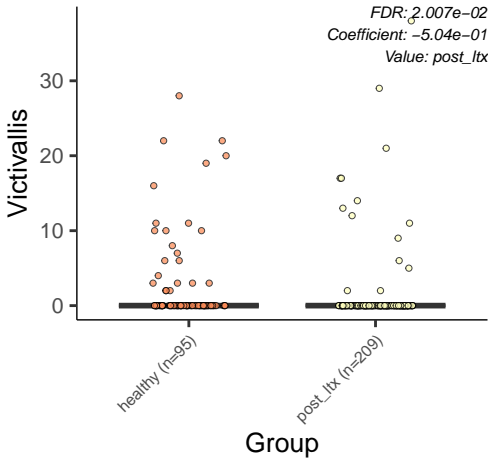
healthy (n=95)

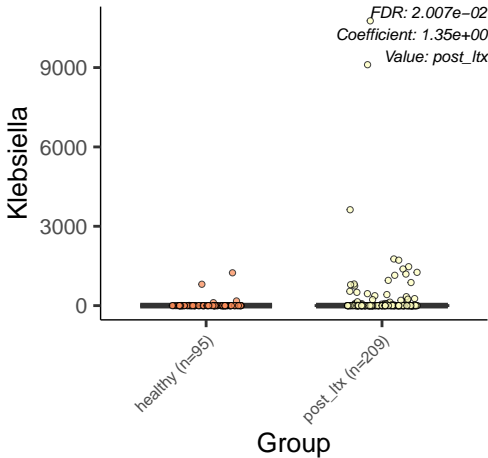
post\_ltx (n=209)

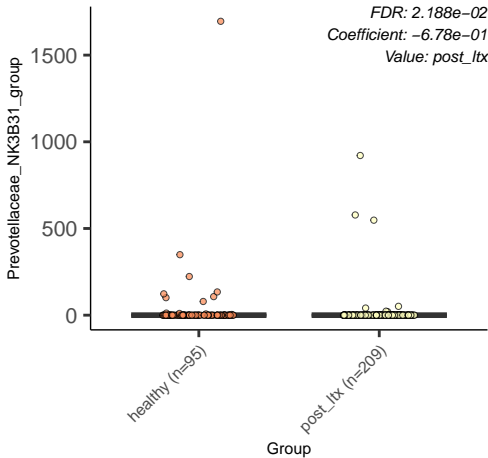
Group

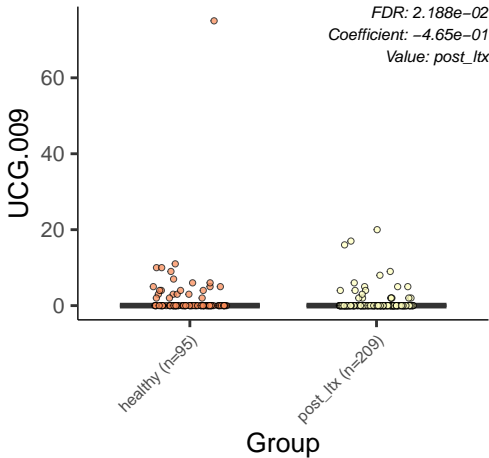


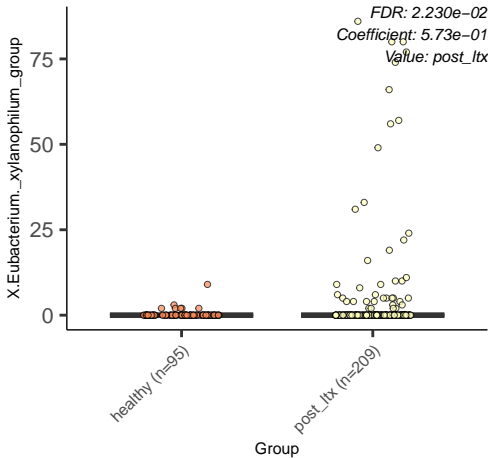


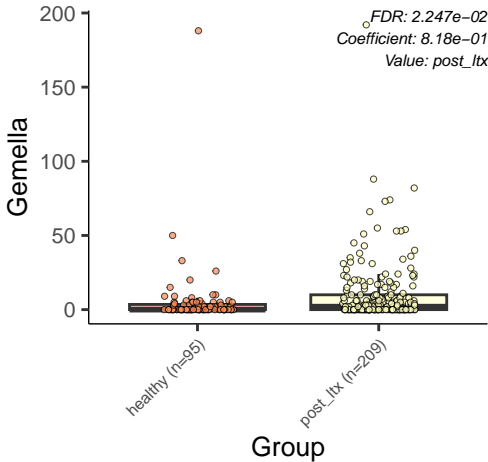












Coprobacter

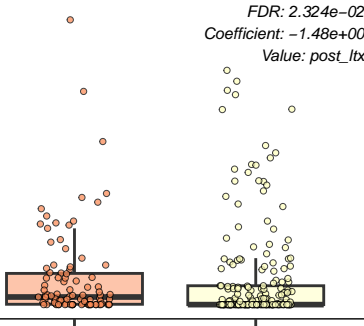
800  
600  
400  
200  
0

healthy (n=95)

post\_ltx (n=209)

Group

FDR:  $2.324 \times 10^{-2}$   
Coefficient:  $-1.48 \times 10^0$   
Value: post\_ltx



Phascolarctobacterium

FDR: 2.324e-02

Coefficient: -1.66e+00

Value: post\_ltx

1000

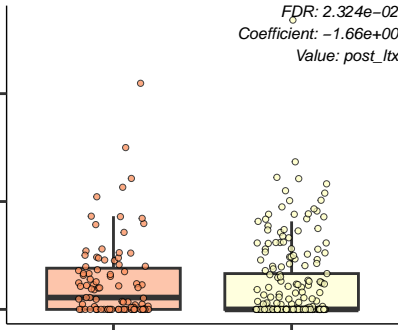
500

0

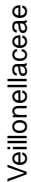
healthy (n=95)

post\_ltx (n=209)

Group







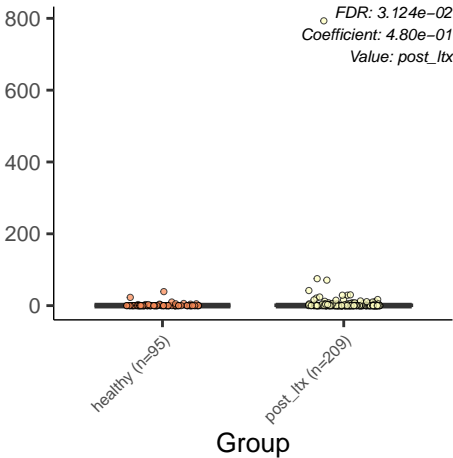
FDR: 2.324e-02  
Coefficient: 8.26e-01  
Value: post\_ltx

healthy (n=95)

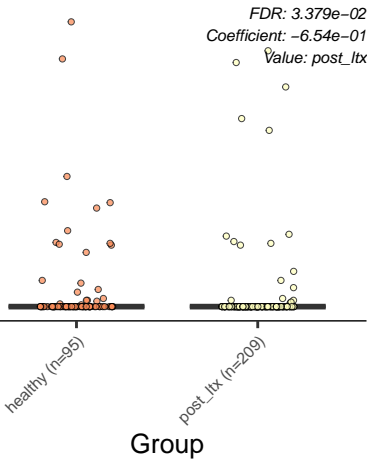
post\_ltx (n=209)

Group

Staphylococcus



Muribaculaceae



Bacteroides

10000

5000

0

healthy (n=95)

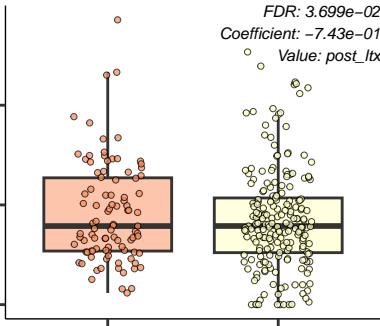
post\_ltx (n=209)

Group

*FDR: 3.699e-02*

*Coefficient: -7.43e-01*

*Value: post\_ltx*



Clostridia\_vadinBB60\_group

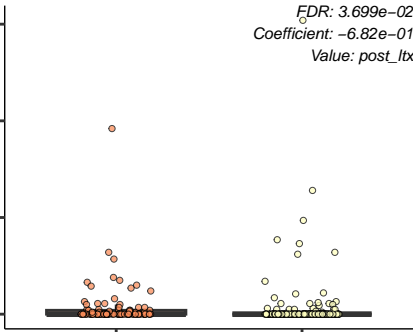
300  
200  
100  
0

healthy (n=95)

post\_ltx (n=209)

Group

FDR: 3.699e-02  
Coefficient: -6.82e-01  
Value: post\_ltx





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

healthy (n=95)

post\_ltx (n=209)

Group

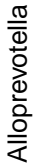


FDR: 3.820e-02  
Coefficient: 6.89e-01  
Value: post\_ltx

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



f\_\_Barnesiellaceae.g\_\_uncultured

FDR:  $3.924e-02$   
Coefficient:  $-4.26e-01$   
Value: post\_ltx

60

40

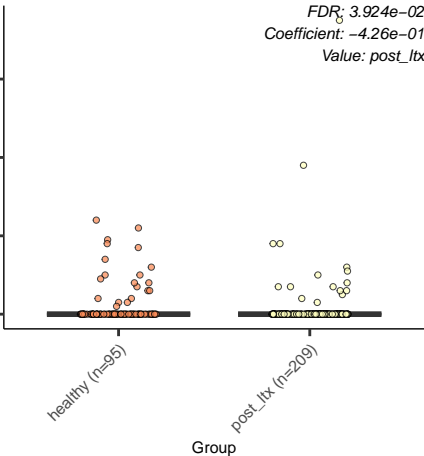
20

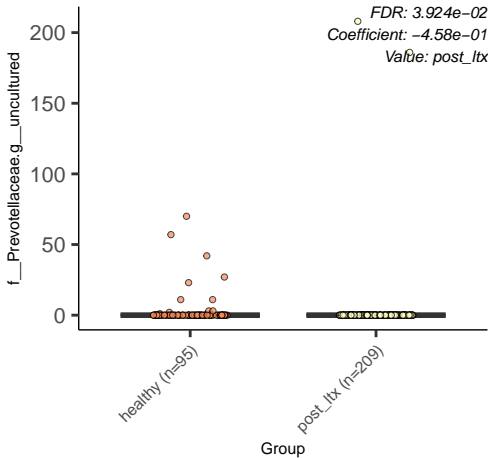
0

healthy (n=95)

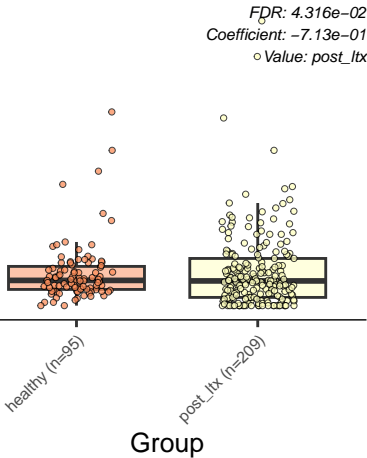
post\_ltx (n=209)

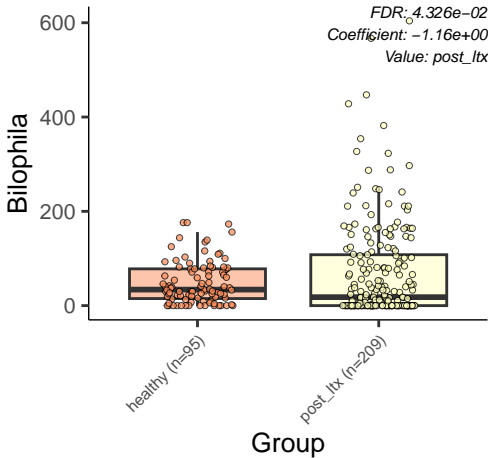
Group

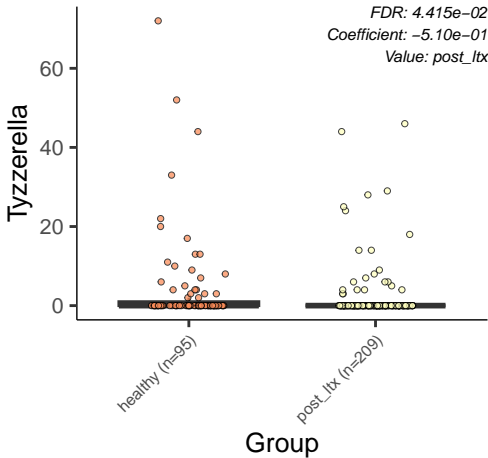




Butyricoccus







UCG.003

300

200

100

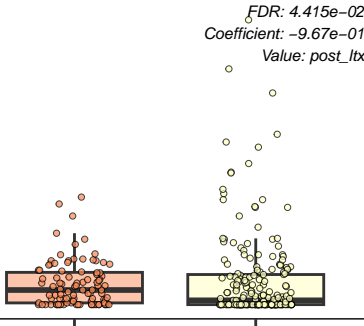
0

healthy (n=95)

post\_ltx (n=209)

Group

FDR:  $4.415e-02$   
Coefficient:  $-9.67e-01$   
Value: post\_ltx



Intestinibacter

