

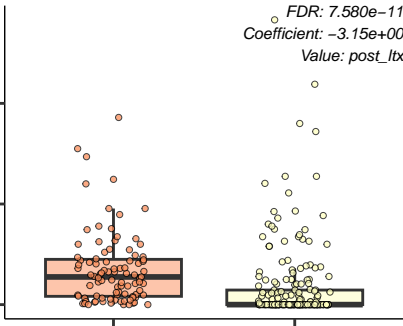
Odoribacter

FDR: 7.580e-11
Coefficient: -3.15e+00
Value: post_ltx

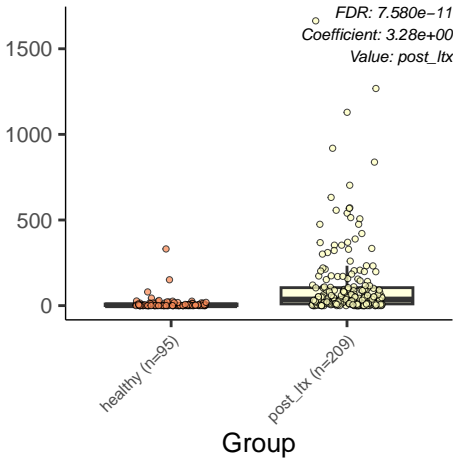
healthy (n=95)

post_ltx (n=209)

Group



Haemophilus



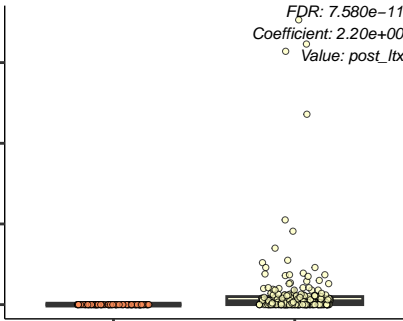
Spingobium

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

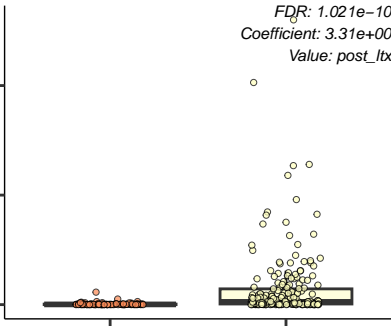
1000

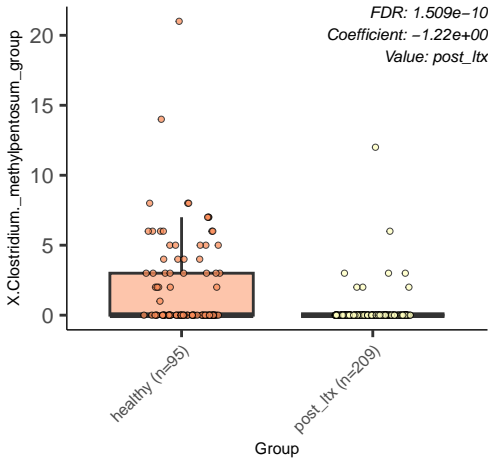
0

healthy (n=95)

post_ltx (n=209)

Group





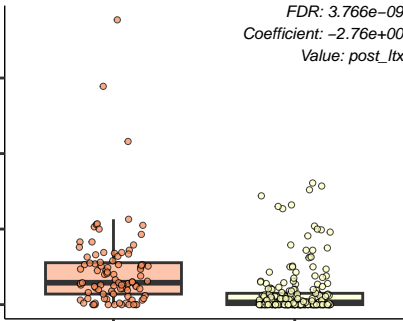
Intestinimonas

healthy (n=95)

post_ltx (n=209)

Group

FDR: 3.766e-09
Coefficient: -2.76e+00
Value: post_ltx



Family_XIII_UCG.001

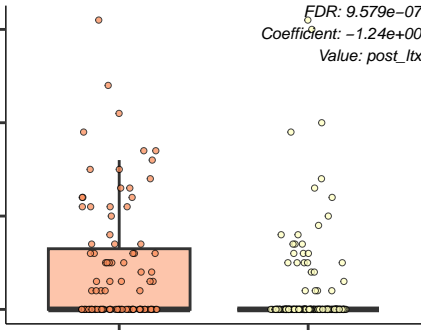
30
20
10
0

healthy (n=95)

post_ltx (n=209)

Group

FDR: 9.579×10^{-7}
Coefficient: -1.24×10^0
Value: post_ltx



Streptococcus

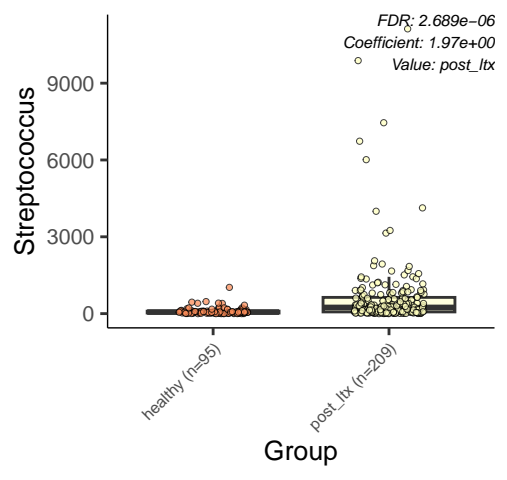
FDR: 2.689e-06
Coefficient: 1.97e+00
Value: post_ltx

healthy (n=95)

post_ltx (n=209)

Group

9000
6000
3000
0



CAG.56

FDR: $8.073e-06$

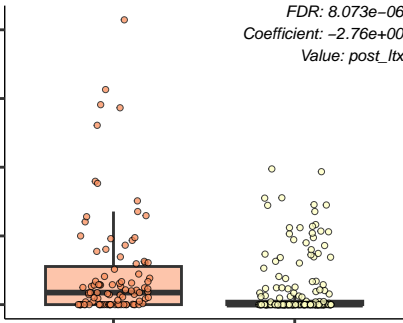
Coefficient: $-2.76e+00$

Value: *post_ltx*

healthy (n=95)

post_ltx (n=209)

Group



Lachnoclostridium

6000

4000

2000

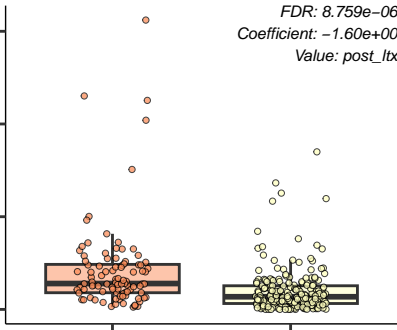
0

healthy (n=95)

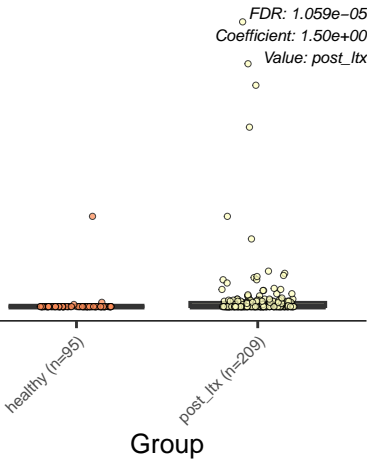
post_ltx (n=209)

Group

FDR: $8.759e-06$
Coefficient: $-1.60e+00$
Value: post_ltx



Pseudomonas



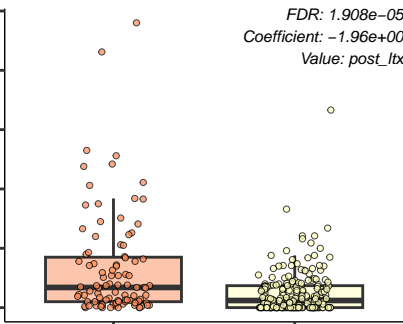
Oscillibacter

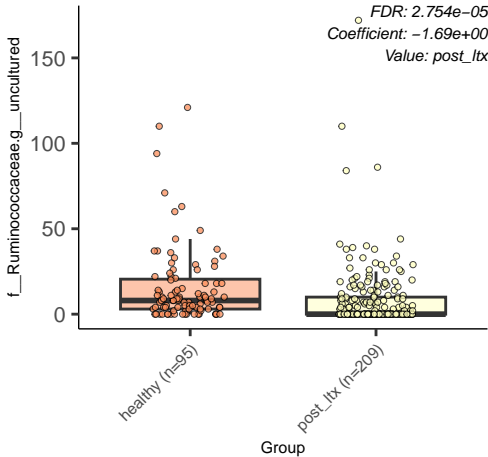
healthy (n=95)

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

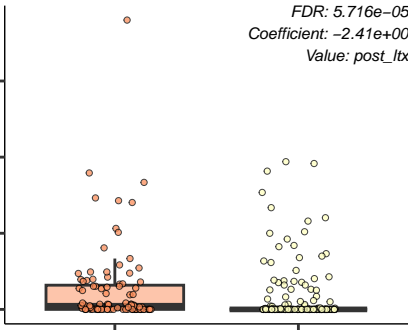
250

0

healthy (n=95)

post_ltx (n=209)

Group



Colidextribacter

FDR: 6.593e-05

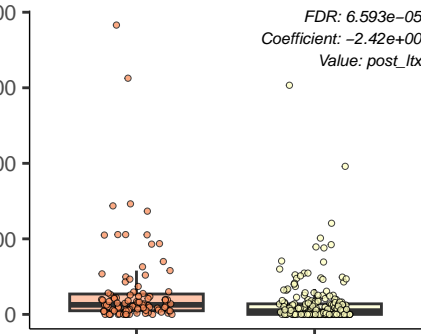
Coefficient: -2.42e+00

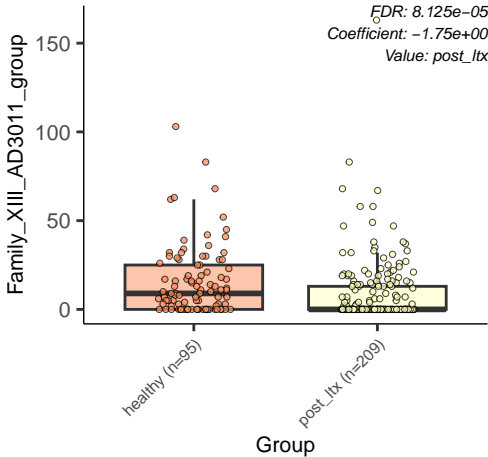
Value: post_ltx

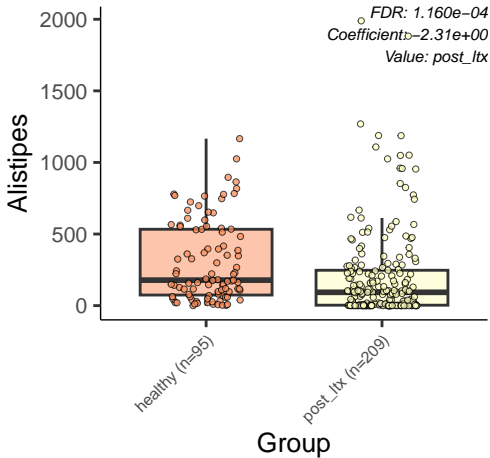
healthy (n=95)

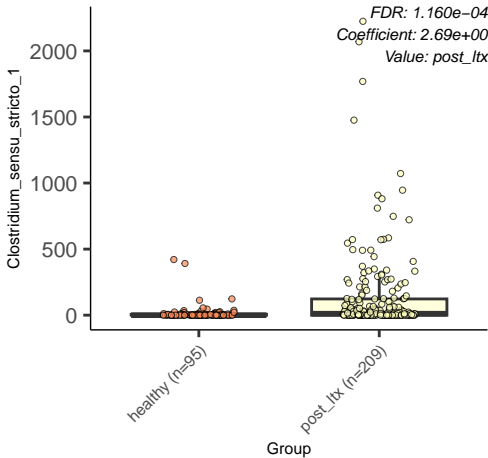
post_ltx (n=209)

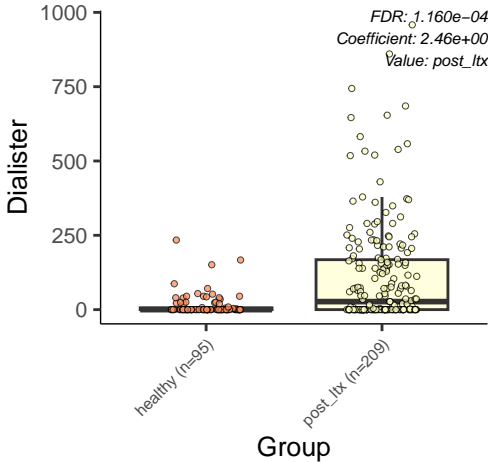
Group

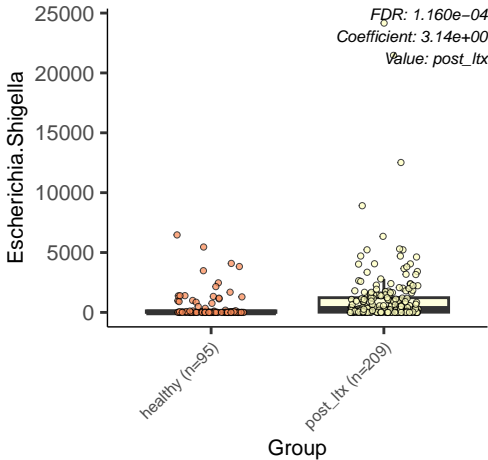


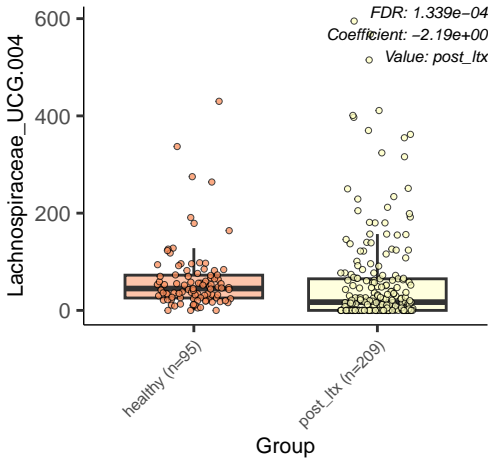


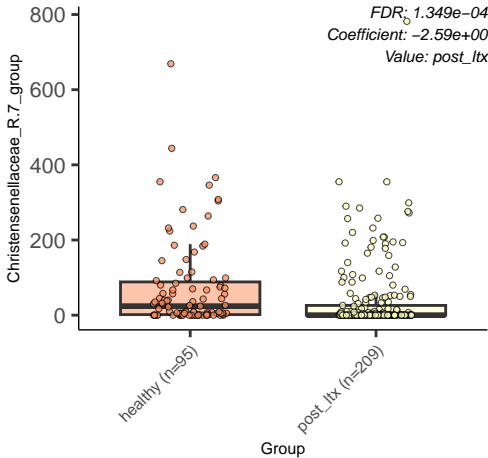












Holdemania

60

40

20

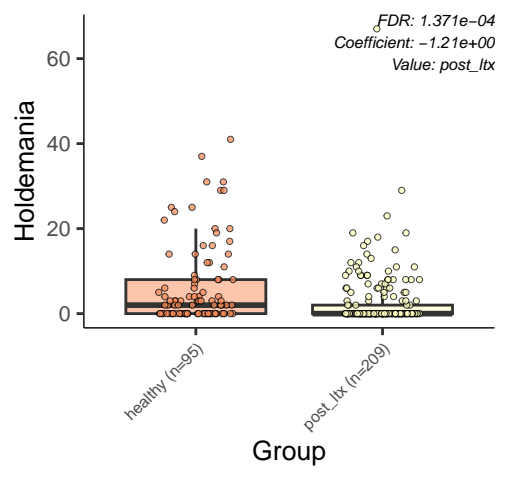
0

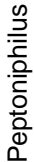
healthy (n=95)

post_ltx (n=209)

Group

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





FDR: 1.371e-04

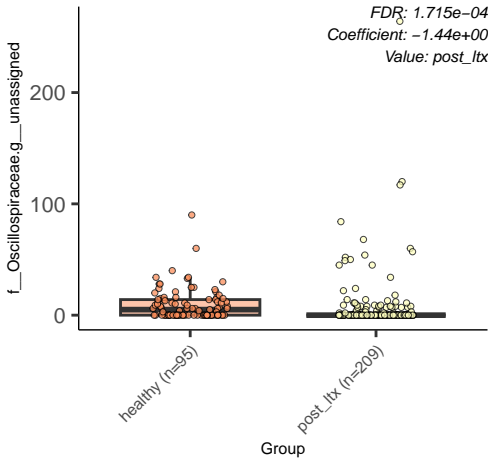
Coefficient: $8.55e-01$

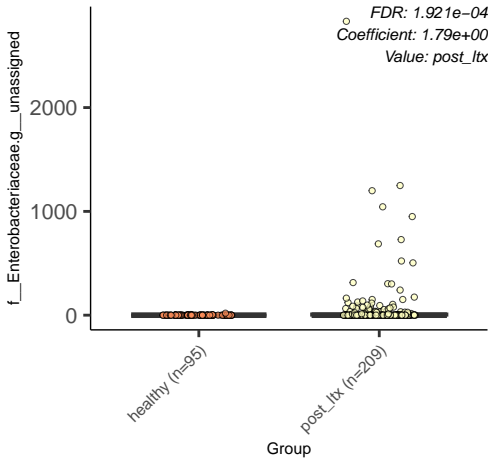
Value: *post_ltx*

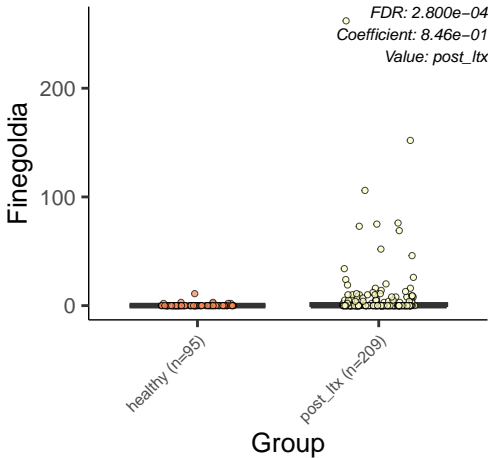
healthy (n=95)

post_ltx (n=209)

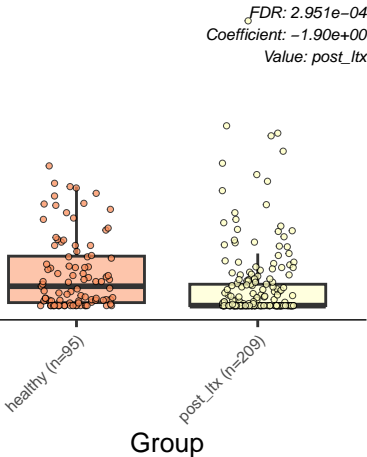
Group



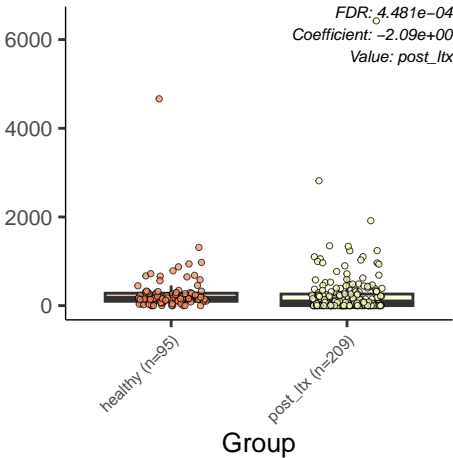




Butyricimonas



Parabacteroides



X.Clostridium._innocuum_group

FDR: 6.730e-04
Coefficient: 1.84e+00
Value: post_ltx

900

600

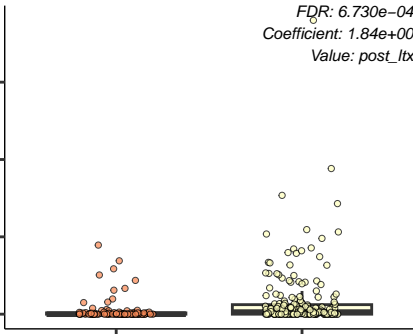
300

0

healthy (n=95)

post_ltx (n=209)

Group



GCA.900066575

100

50

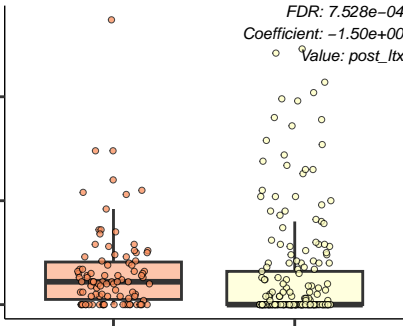
0

healthy (n=95)

post_ltx (n=209)

Group

FDR: $7.528e-04$
Coefficient: $-1.50e+00$
Value: post_ltx





FDR: 8.154e-04

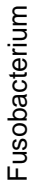
Coefficient: 9.63e-01

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

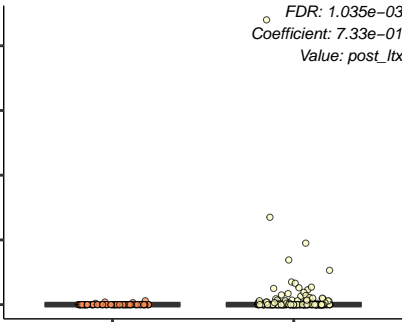
400
300
200
100
0

healthy (n=95)

post_ltx (n=209)

Group

FDR: 1.035e-03
Coefficient: 7.33e-01
Value: post_ltx



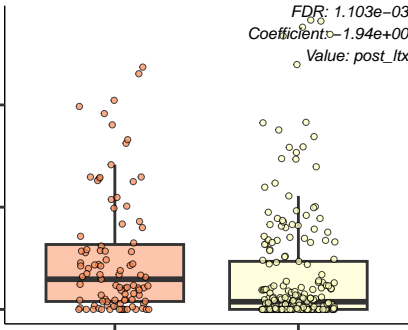
Lachnospiraceae_UCG.010

FDR: $1.103e-03$
Coefficient: $-1.94e+00$
Value: post_ltx

healthy (n=95)

post_ltx (n=209)

Group



UCG.005

1000

500

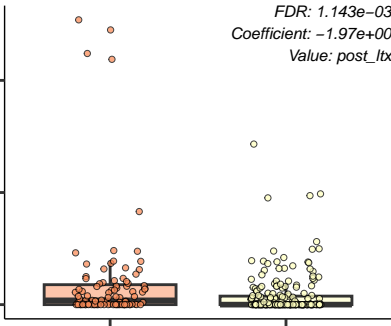
0

healthy (n=95)

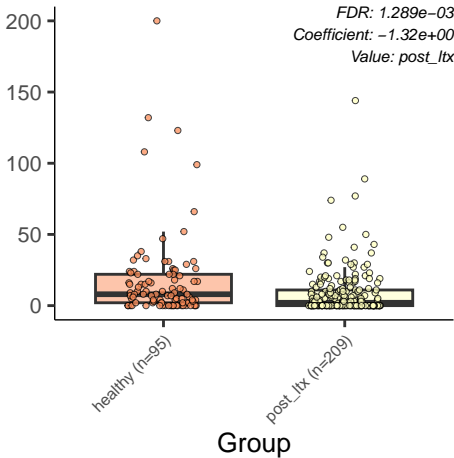
post_ltx (n=209)

Group

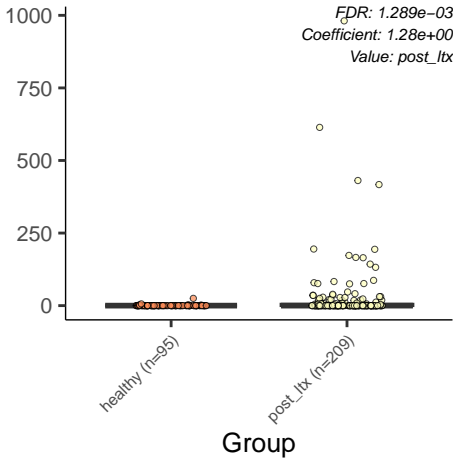
FDR: 1.143e-03
Coefficient: -1.97e+00
Value: post_ltx



Marvinbryantia



Lactobacillus



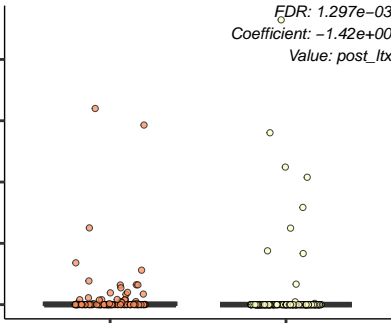
CAG.352

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

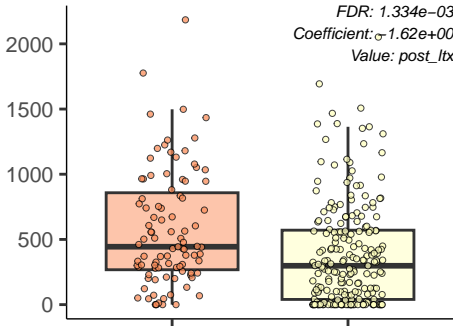
Coefficient: $-1.62e+00$

Value: post_ltx

healthy (n=95)

post_ltx (n=209)

Group



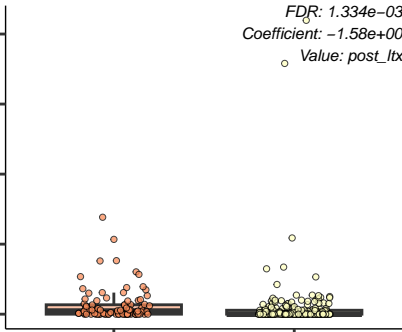
Lachnospiraceae_NK4A136_group

FDR: 1.334e-03
Coefficient: -1.58e+00
Value: post_ltx

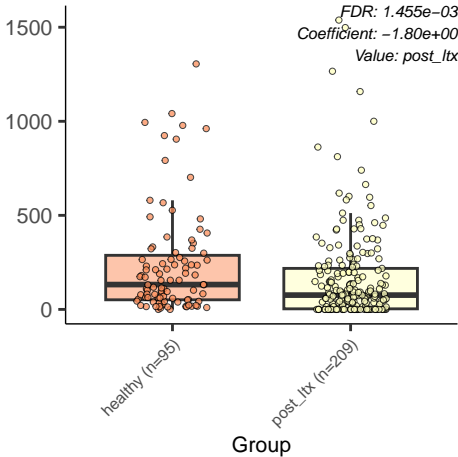
healthy (n=95)

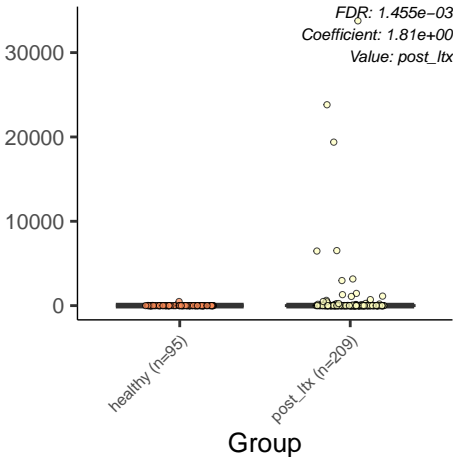
post_ltx (n=209)

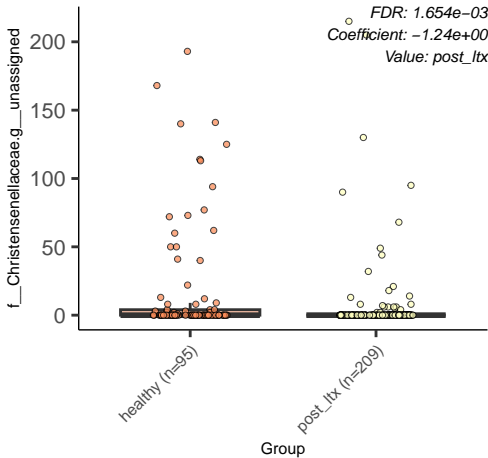
Group



Fusicatenibacter







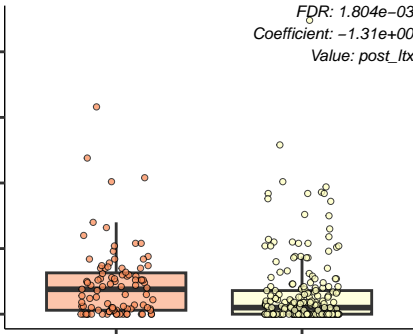
Lachnospiraceae_FCS020_group

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

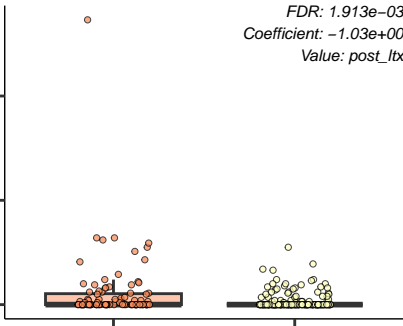
100

0

healthy (n=95)

post_ltx (n=209)

Group



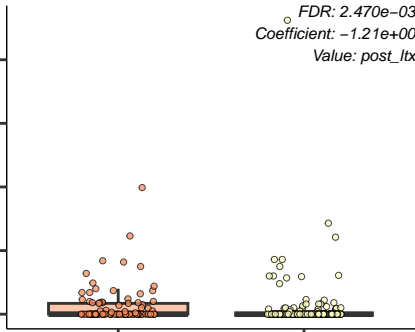
f__Eggerthellaceae.g__uncultured

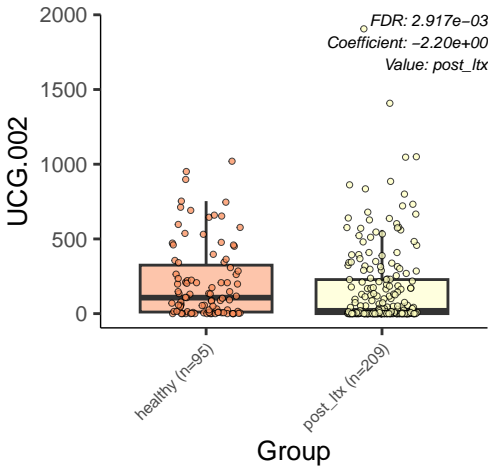
FDR: 2.470e-03
Coefficient: -1.21e+00
Value: post_ltx

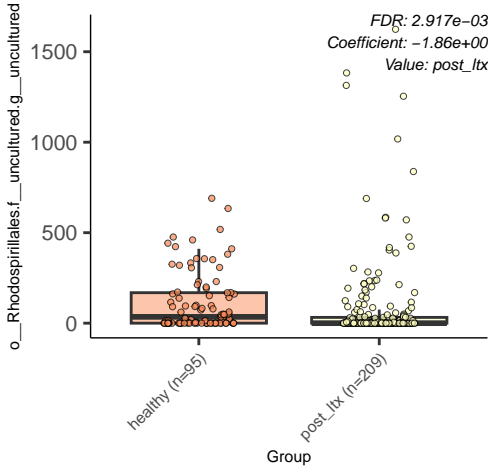
healthy (n=95)

post_ltx (n=209)

Group







Enterorhabdus

FDR: 3.371e-03

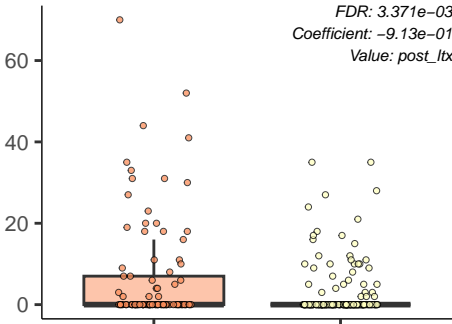
Coefficient: -9.13e-01

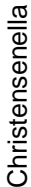
Value: post_ltx

healthy (n=95)

post_ltx (n=209)

Group





FDR: 3.396e-03

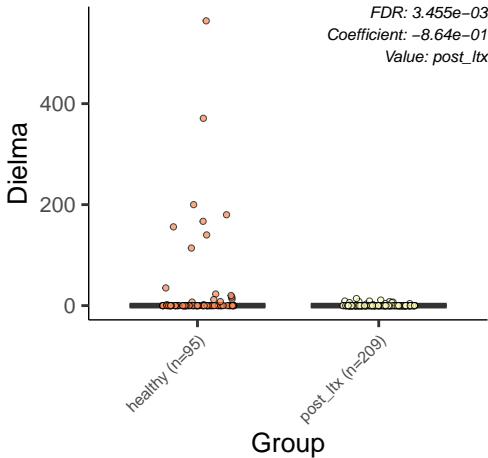
Coefficient: $-1.06e-01$

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

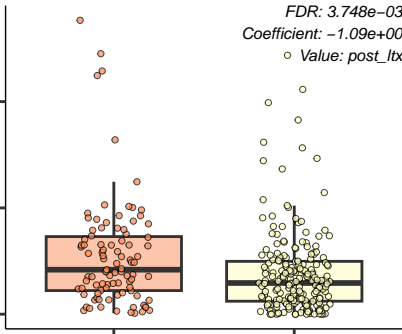
2000

0

healthy (n=95)

post_ltx (n=209)

Group



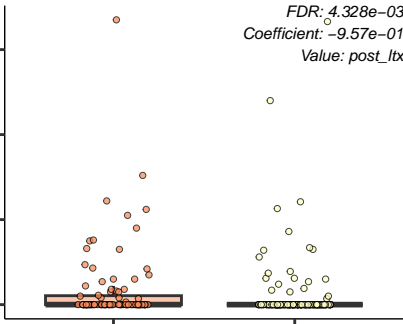
Howardella

healthy (n=95)

post_ltx (n=209)

Group

FDR: $4.328e-03$
Coefficient: $-9.57e-01$
Value: post_ltx



Barnesiella

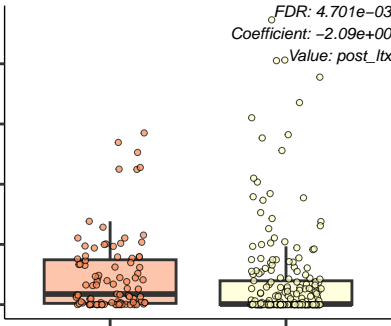
2000
1500
1000
500
0

healthy (n=95)

post_ltx (n=209)

Group

FDR: $4.701e-03$
Coefficient: $-2.09e+00$
Value: post_ltx



Negativibacillus

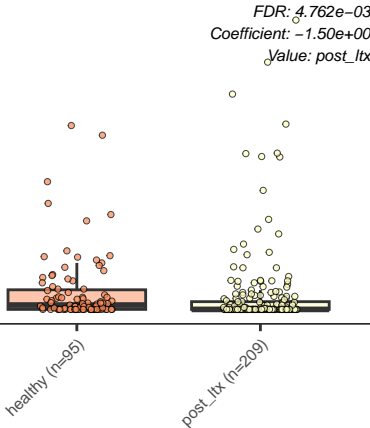
600
400
200
0

healthy (n=95)

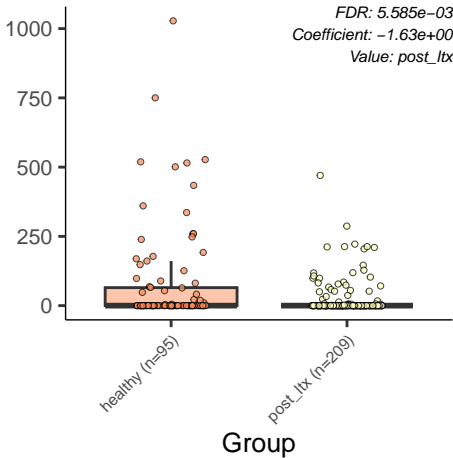
post_ltx (n=209)

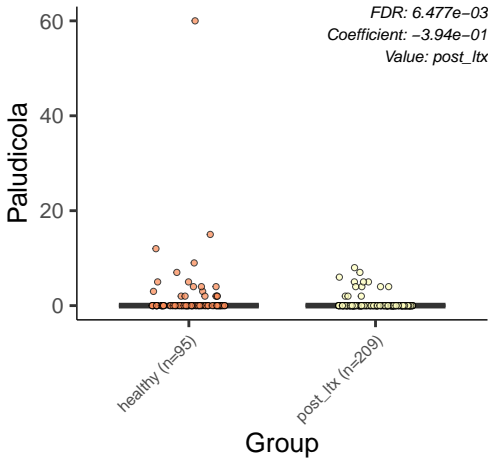
Group

FDR: 4.762e-03
Coefficient: -1.50e+00
Value: post_ltx



Paraprevotella





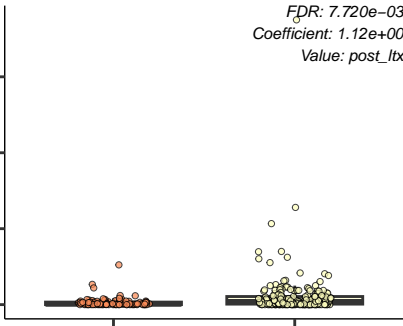
Actinomyces

FDR: 7.720e-03
Coefficient: 1.12e+00
Value: post_ltx

healthy (n=95)

post_ltx (n=209)

Group



Faecalibacterium

7500

5000

2500

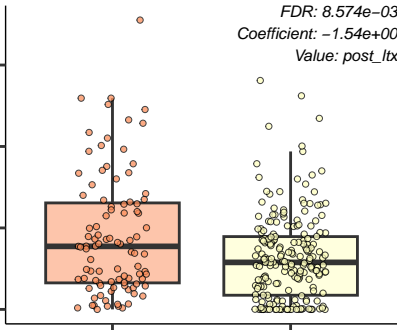
0

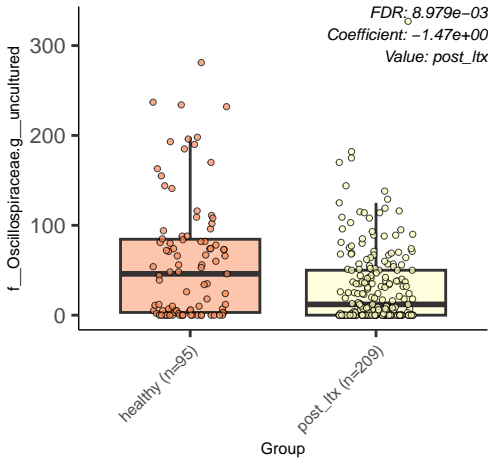
healthy (n=95)

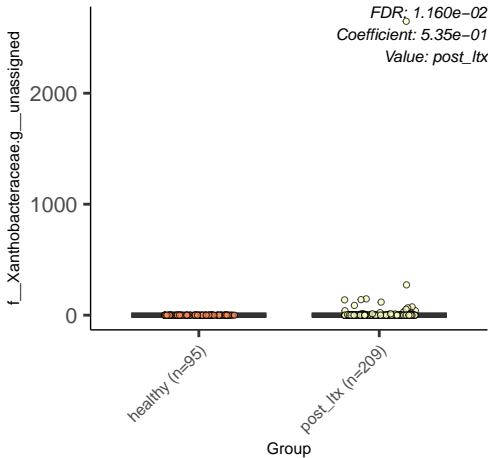
post_ltx (n=209)

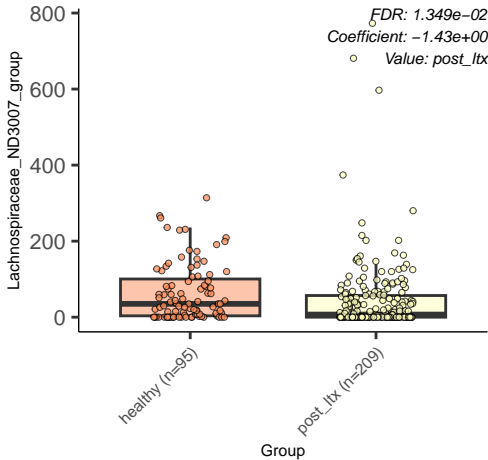
Group

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

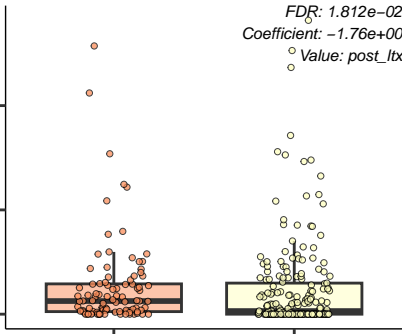
1000

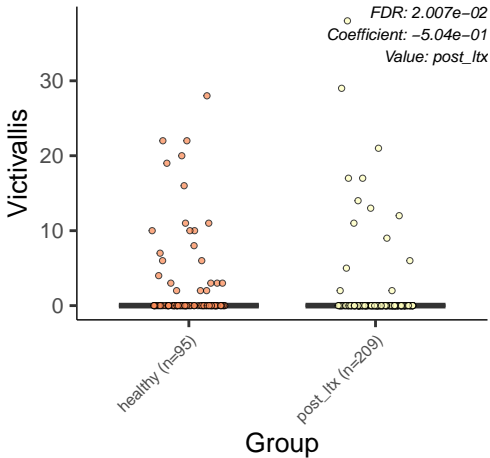
0

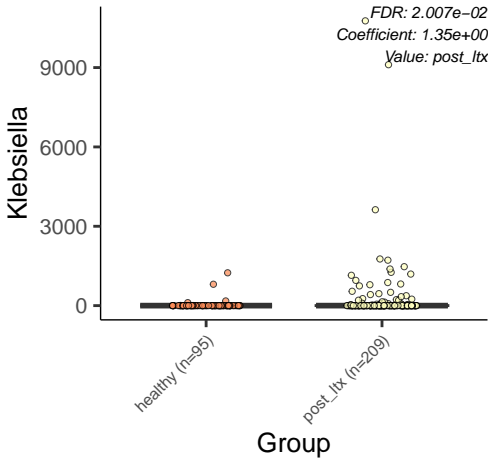
healthy (n=95)

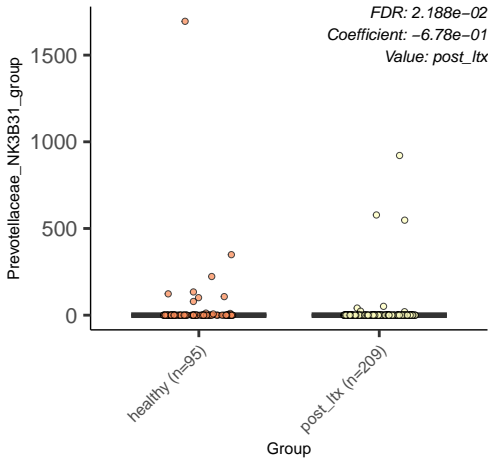
post_ltx (n=209)

Group









UCG.009

60

40

20

0

healthy (n=95)

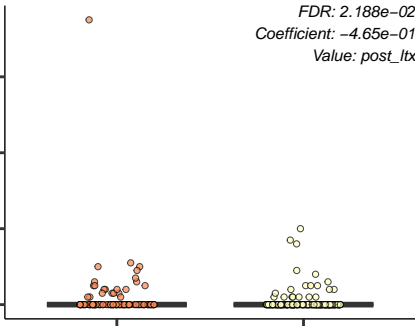
post_ltx (n=209)

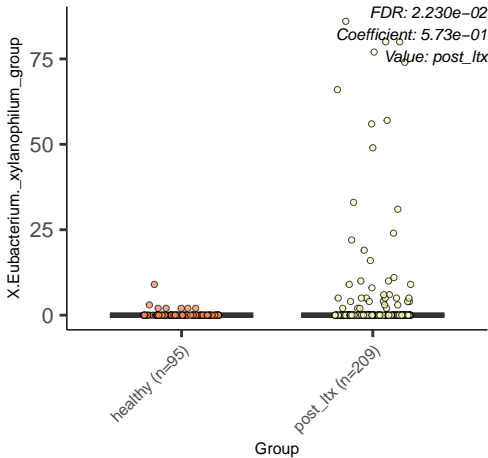
Group

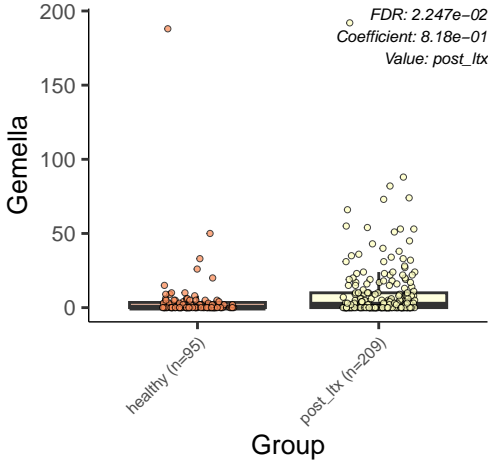
FDR: $2.188e-02$

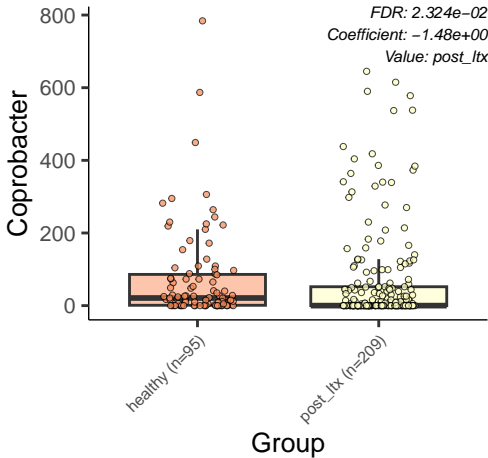
Coefficient: $-4.65e-01$

Value: post_ltx









Phascolarctobacterium

FDR: 2.324e-02

Coefficient: -1.66e+00

Value: post_ltx

1000

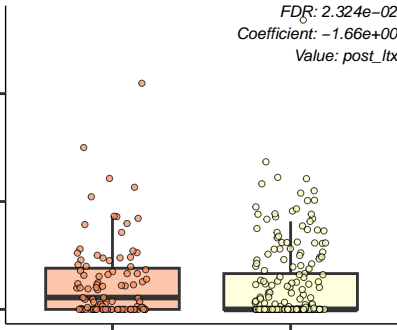
500

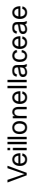
0

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

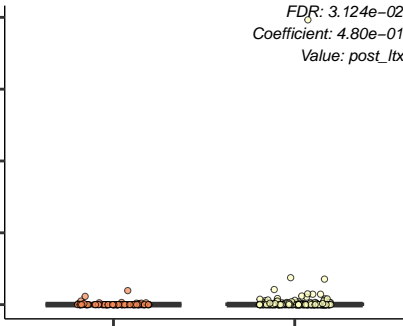
800
600
400
200
0

FDR: 3.124e-02
Coefficient: 4.80e-01
Value: post_ltx

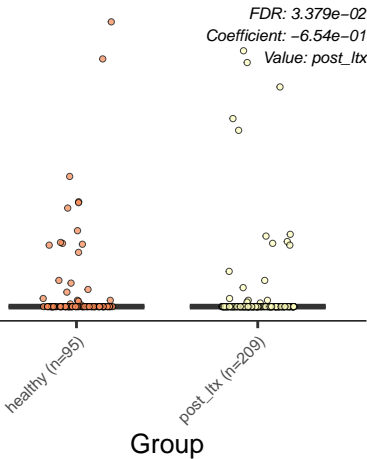
healthy (n=95)

post_ltx (n=209)

Group



Muribaculaceae



Bacteroides

10000

5000

0

healthy (n=95)

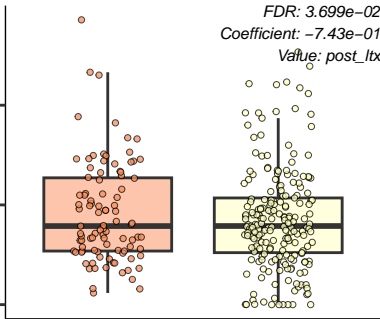
post_ltx (n=209)

Group

FDR: 3.699e-02

Coefficient: -7.43e-01

Value: post_ltx



Clostridia_vadinBB60_group

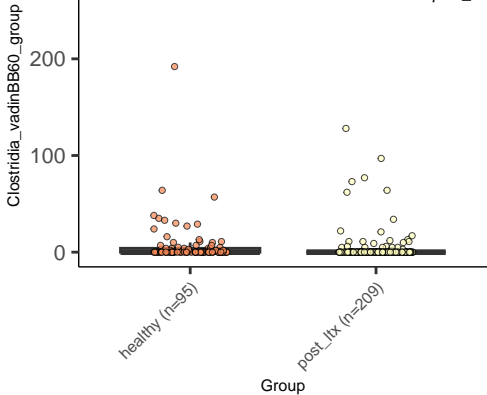
300
200
100
0

healthy (n=95)

post_ltx (n=209)

Group

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



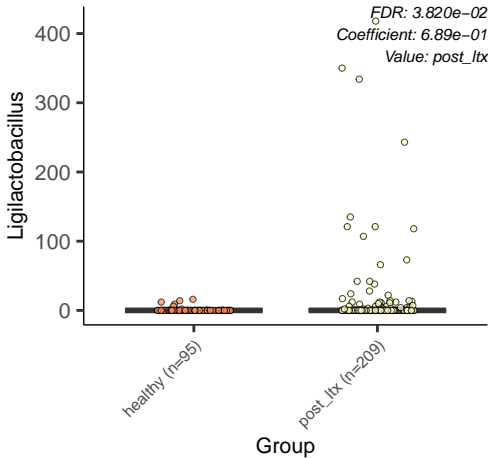


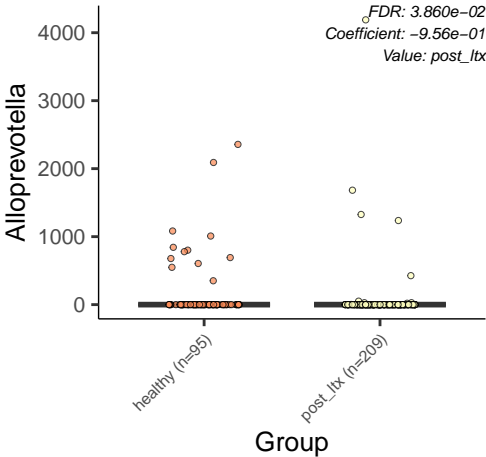
FDR: 3.699e-02
Coefficient: 5.65e-01
Value: post_ltx

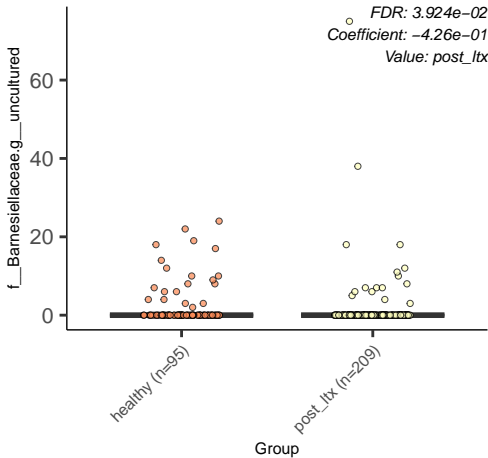
healthy (n=95)

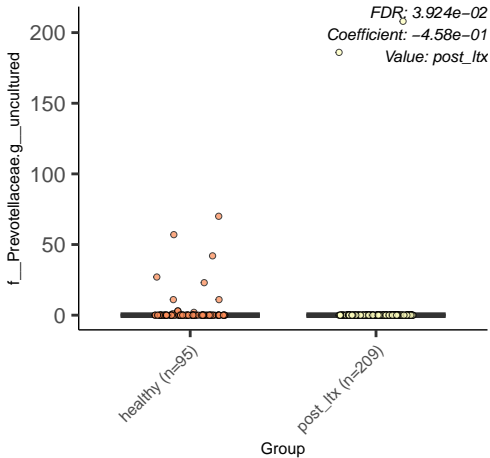
post_ltx (n=209)

Group

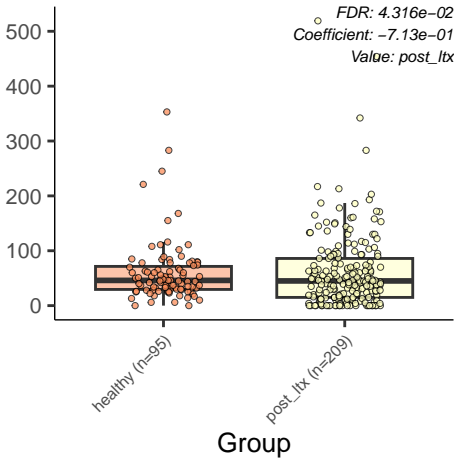


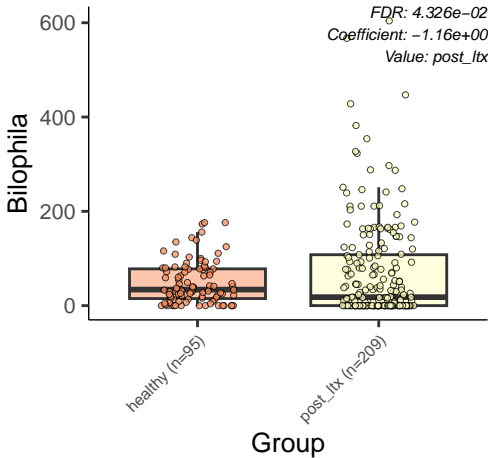


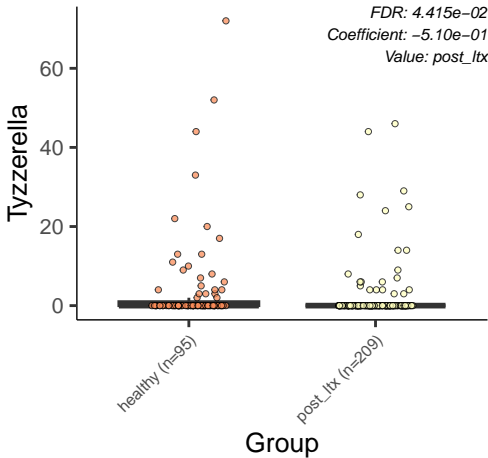




Butyricoccus







UCG.003

300

200

100

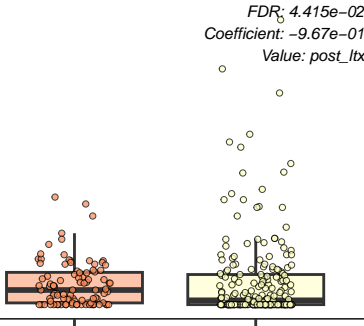
0

healthy (n=95)

post_ltx (n=209)

Group

FDR: $4.415e-02$
Coefficient: $-9.67e-01$
Value: post_ltx



Intestinibacter

