

Odoribacter

600

400

200

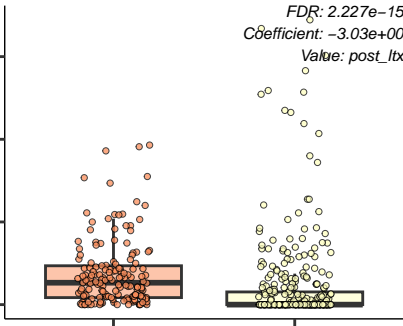
0

healthy (n=161)

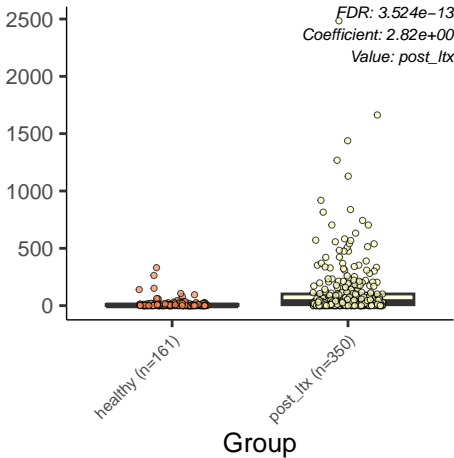
post_ltx (n=350)

Group

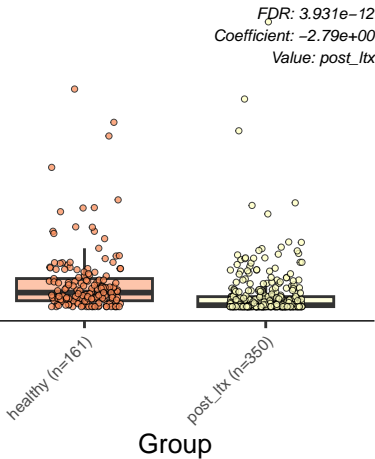
$FDR: 2.227e-15$
 $Coefficient: -3.03e+00$
 $Value: post_ltx$



Haemophilus



Intestinimonas



Veillonella

FDR: 3.931e-12
Coefficient: 2.80e+00
Value: post_ltx

2000

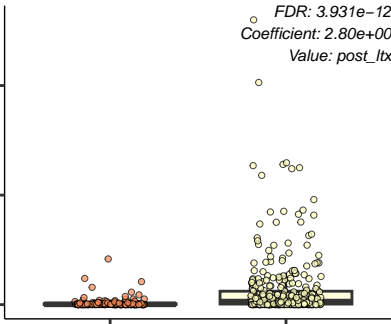
1000

0

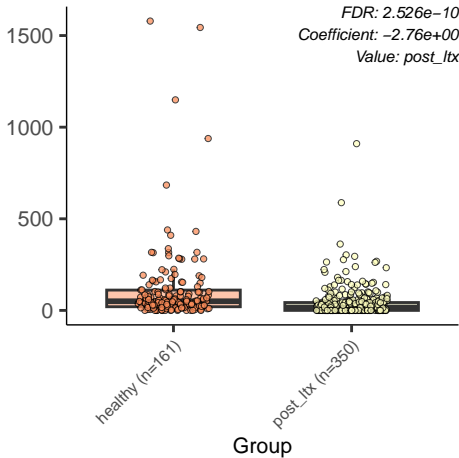
healthy (n=161)

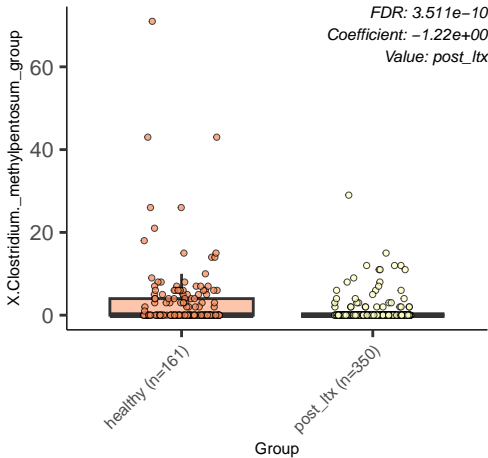
post_ltx (n=350)

Group

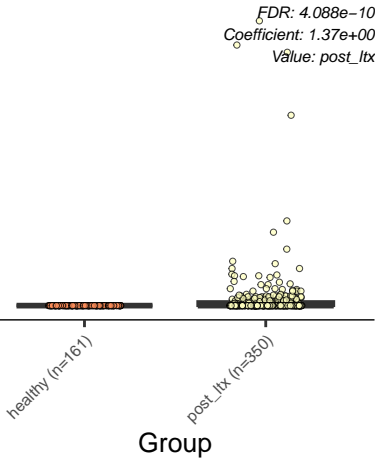


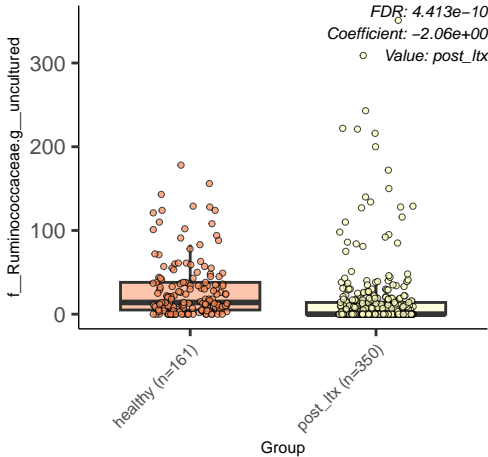
Colidextribacter

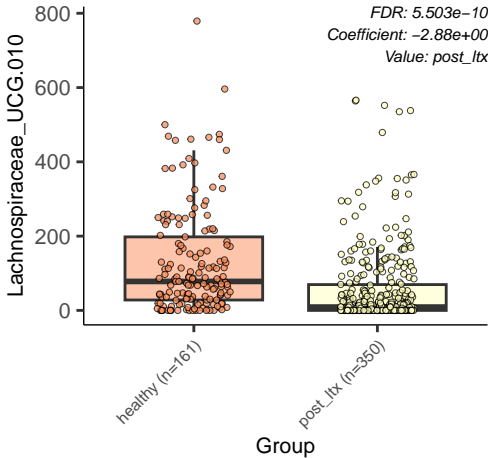




Spingobium







Family_XIII_UCG.001

FDR: 1.155e-09

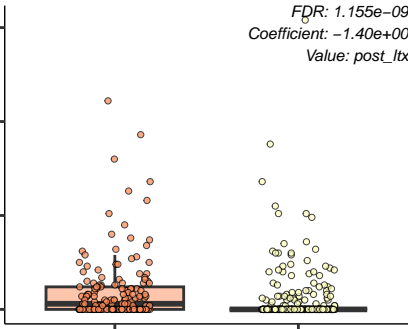
Coefficient: -1.40e+00

Value: post_ltx

healthy (n=161)

post_ltx (n=350)

Group



Lachnoclostridium

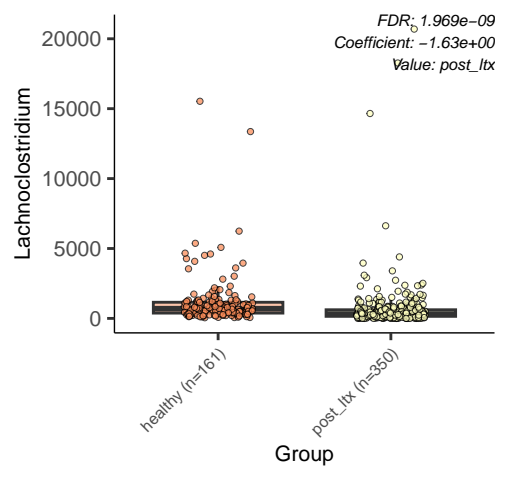
20000
15000
10000
5000
0

FDR: 1.969e-09
Coefficient: -1.63e+00
Value: post_ltx

healthy (n=161)

post_ltx (n=350)

Group



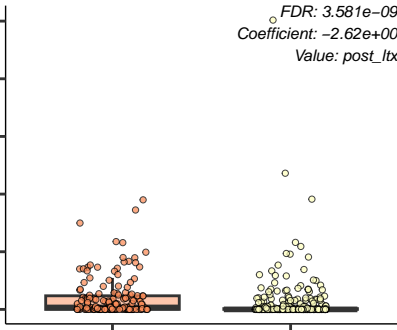
Clostridia_UCG.014

FDR: $3.581e-09$
Coefficient: $-2.62e+00$
Value: post_ltx

healthy (n=161)

post_ltx (n=350)

Group



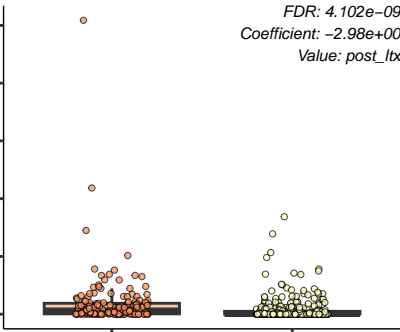
Christensenellaceae_R.7_group

FDR: 4.102e-09
Coefficient: -2.98e+00
Value: post_ltx

healthy (n=161)

post_ltx (n=350)

Group



f_Oscillospiraceae.g__unassigned

FDR: 9.856×10^{-9}
Coefficient: -2.11×10^0
Value: post_ltx

200

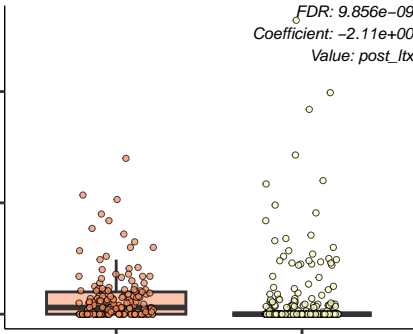
100

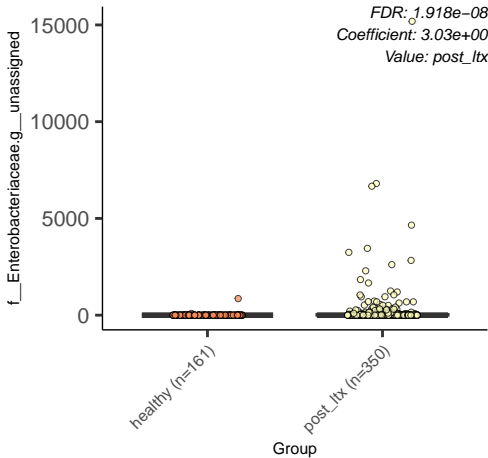
0

healthy (n=161)

post_ltx (n=350)

Group





Streptococcus

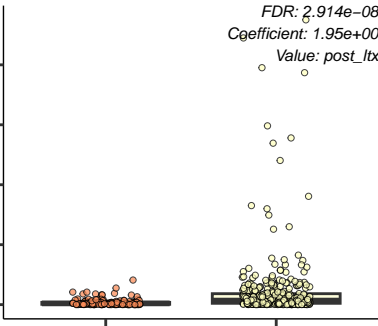
10000
7500
5000
2500
0

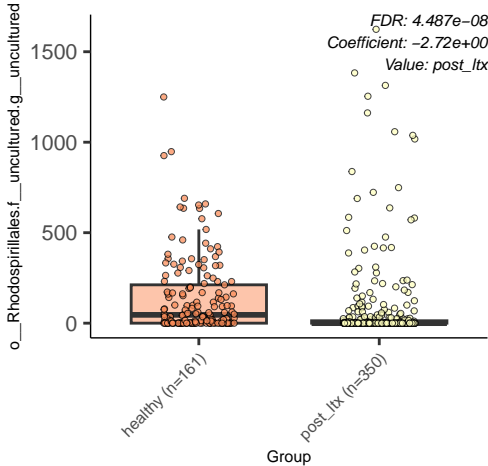
healthy (n=161)

post_ltx (n=350)

Group

FDR: 2.914e-08
Coefficient: 1.95e+00
Value: post_ltx





Family_XIII_AD3011_group

200

100

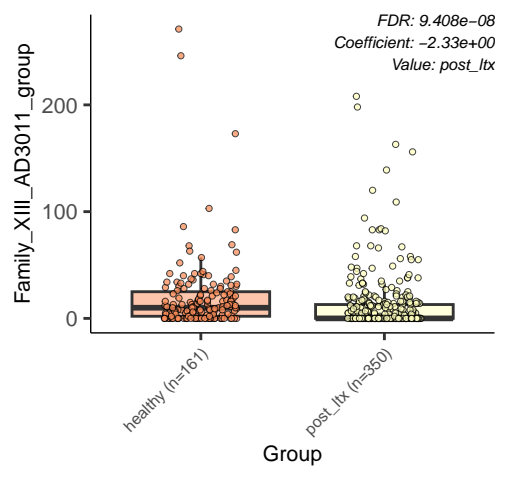
0

healthy (n=161)

post_ltx (n=350)

Group

FDR: 9.408e-08
Coefficient: -2.33e+00
Value: post_ltx



Enterococcus

30000

20000

10000

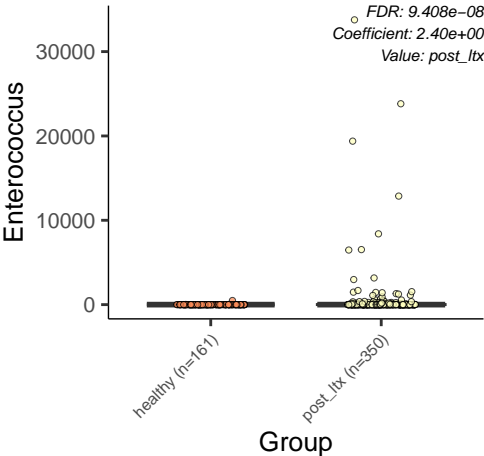
0

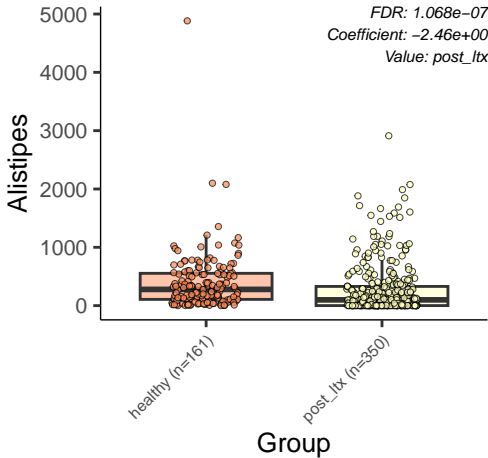
healthy (n=161)

post_ltx (n=350)

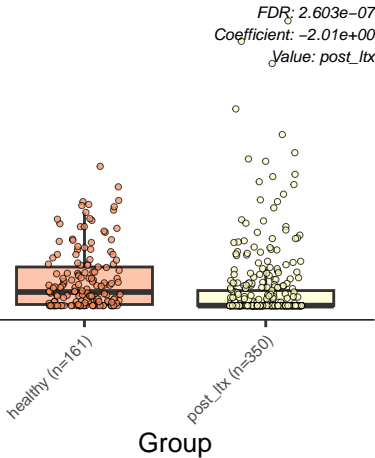
Group

FDR: 9.408×10^{-8}
Coefficient: 2.40×10^0
Value: post_ltx





Butyricimonas



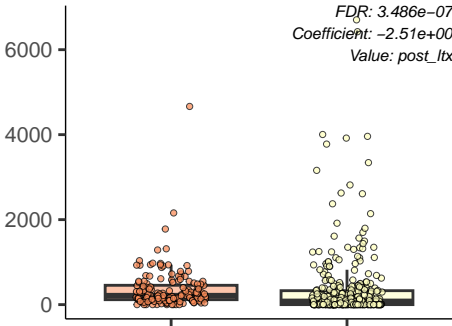
Parabacteroides

FDR: 3.486e-07
Coefficient: -2.51e+00
Value: post_ltx

healthy (n=161)

post_ltx (n=350)

Group



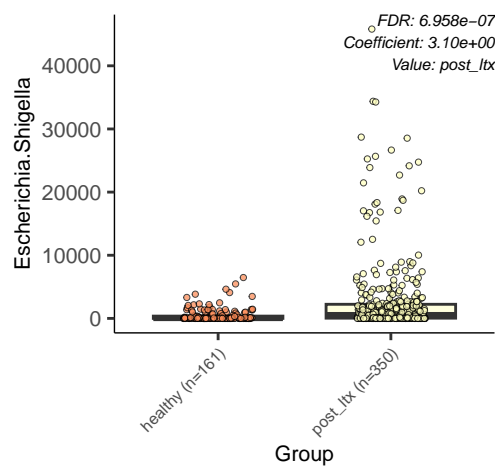
Escherichia.Shigella

FDR: $6.958e-07$
Coefficient: $3.10e+00$
Value: post_ltx

healthy (n=161)

post_ltx (n=350)

Group



UCG.005

FDR: 9.311e-07

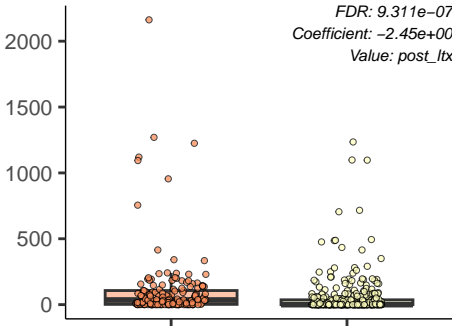
Coefficient: -2.45e+00

Value: post_ltx

healthy (n=161)

post_ltx (n=350)

Group



Holdemania

100

50

0

healthy (n=161)

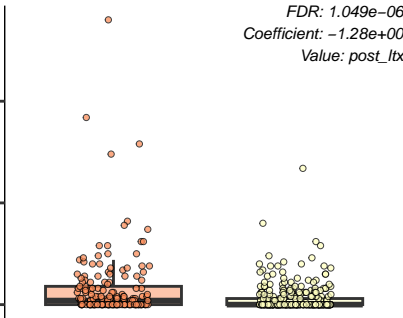
post_ltx (n=350)

Group

FDR: 1.049e-06

Coefficient: -1.28e+00

Value: post_ltx



Oscillibacter

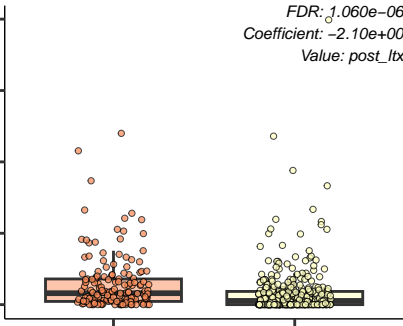
800
600
400
200
0

healthy (n=161)

post_ltx (n=350)

Group

FDR: 1.060e-06
Coefficient: -2.10e+00
Value: post_ltx



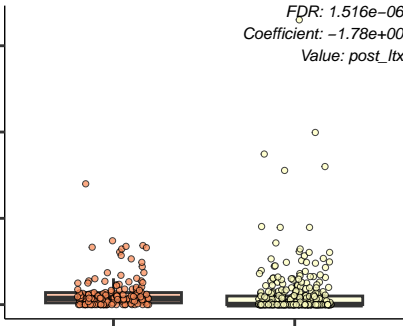
GCA.900066575

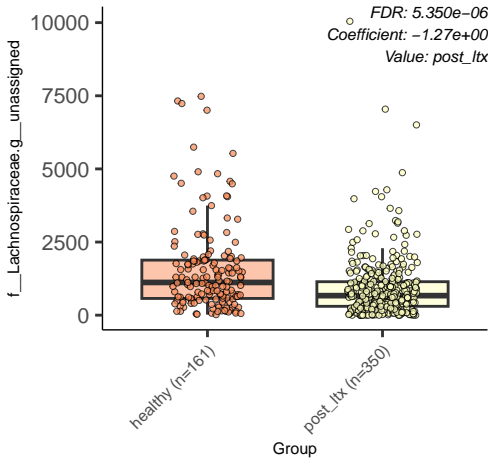
FDR: 1.516e-06
Coefficient: -1.78e+00
Value: post_ltx

healthy (n=161)

post_ltx (n=350)

Group





Coprococcus

FDR: 6.276e-06

Coefficient: -2.24e+00

Value: post_ltx

3000

2000

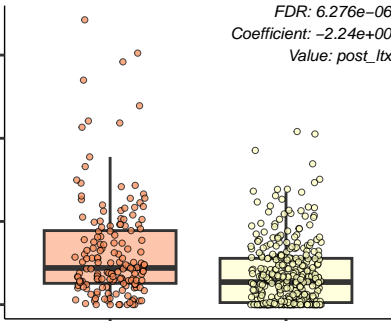
1000

0

healthy (n=161)

post_ltx (n=350)

Group



Marvinbryantia

400

200

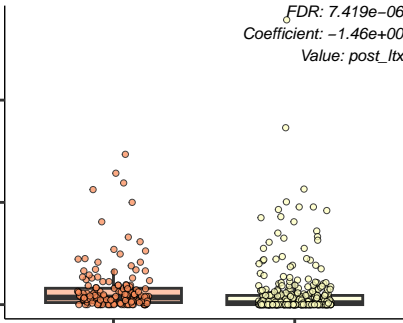
0

healthy (n=161)

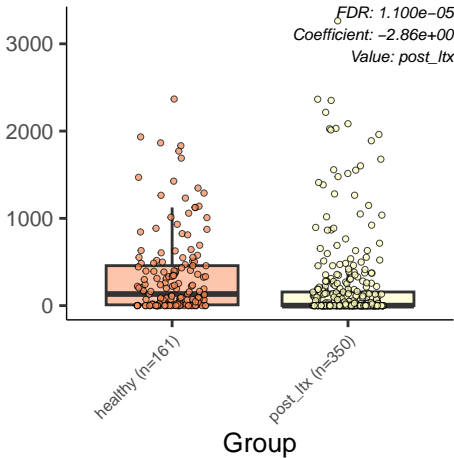
post_ltx (n=350)

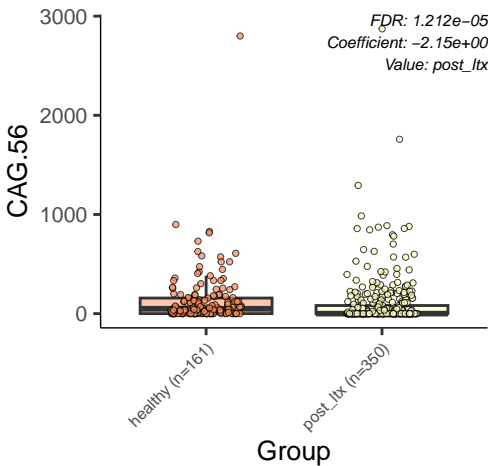
Group

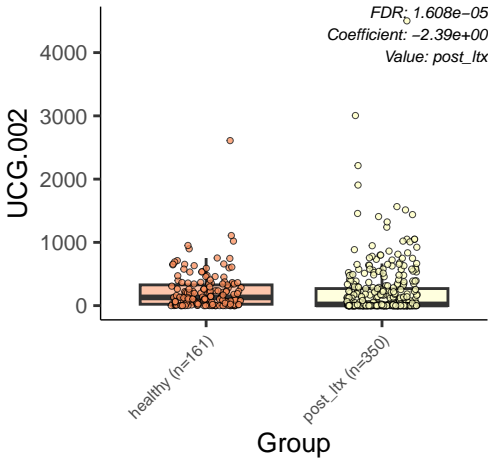
FDR: 7.419×10^{-6}
Coefficient: -1.46×10^0
Value: post_ltx



Barnesiella







Phascolarctobacterium

FDR: $1.608e-05$
Coefficient: $-2.44e+00$
Value: *post_ltx*

3000

2000

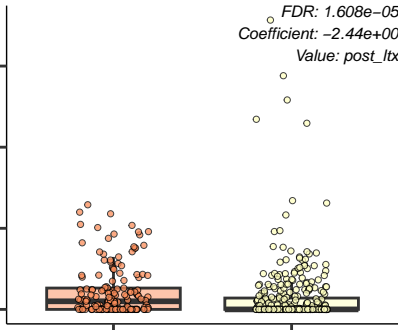
1000

0

healthy (n=161)

post_ltx (n=350)

Group



f__Peptococcaceae.g__uncultured

FDR: $1.686e-05$
Coefficient: $-8.65e-01$
Value: post_ltx

300

200

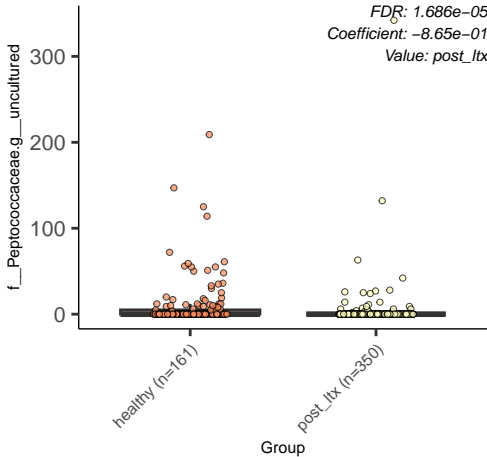
100

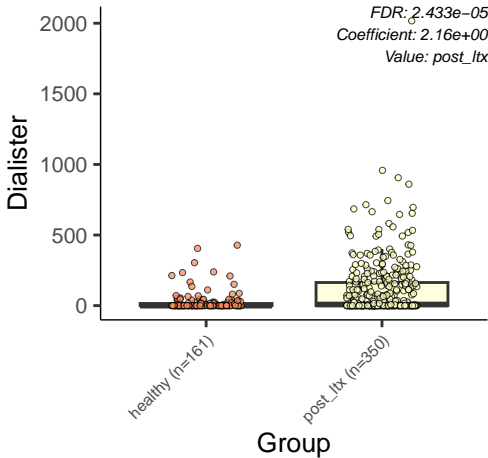
0

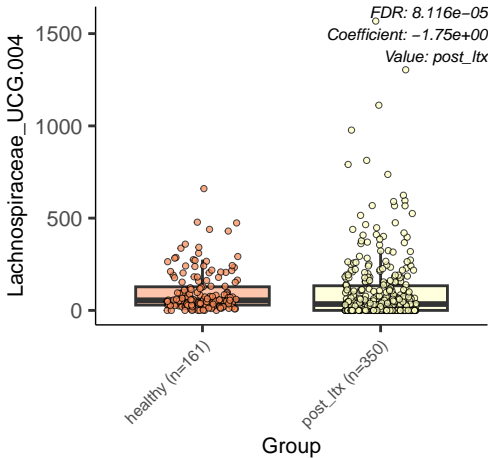
healthy (n=161)

post_ltx (n=350)

Group







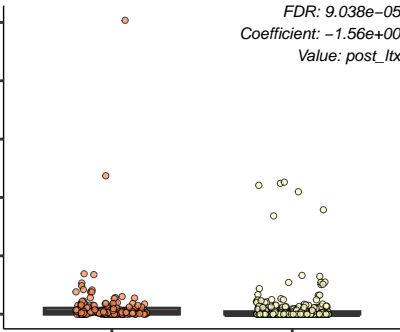
Lachnospiraceae_NK4A136_group

FDR: 9.038e-05
Coefficient: -1.56e+00
Value: post_ltx

healthy (n=161)

post_ltx (n=350)

Group



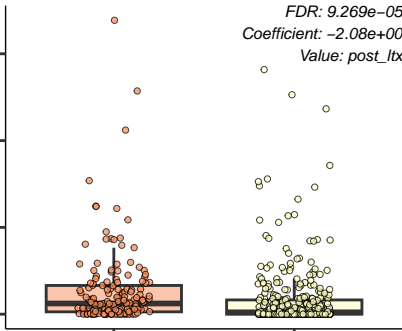
Erysipelotrichaceae_UCG.003

FDR: 9.269e-05
Coefficient: -2.08e+00
Value: post_ltx

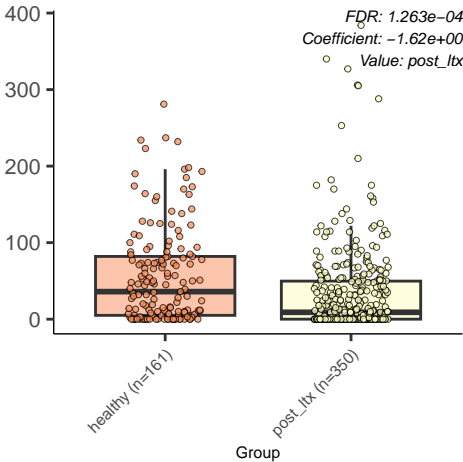
healthy (n=161)

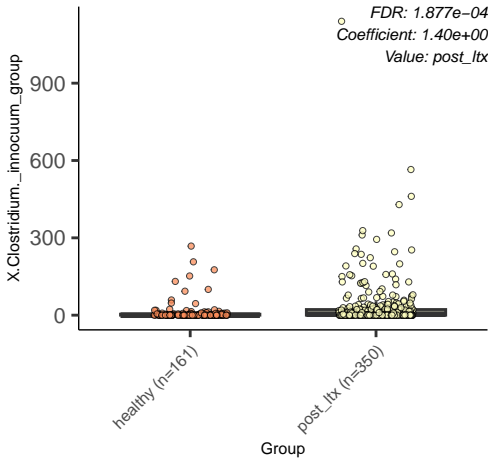
post_ltx (n=350)

Group

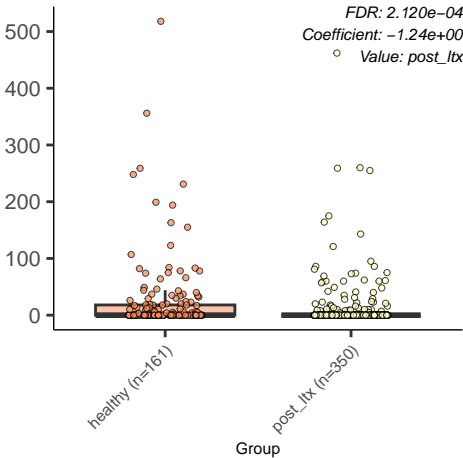


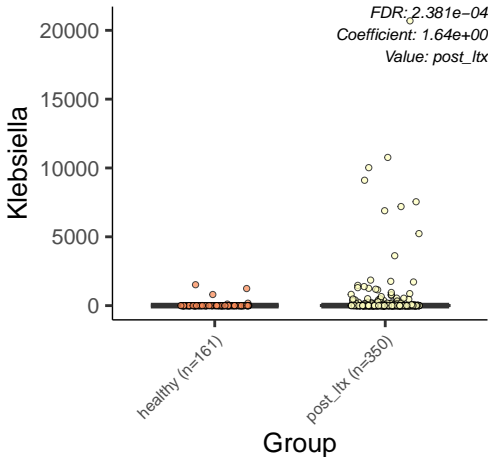
f_Oscillospiraceae.g__uncultured





f_Eggerthellaceae.g__uncultured





Adlercreutzia

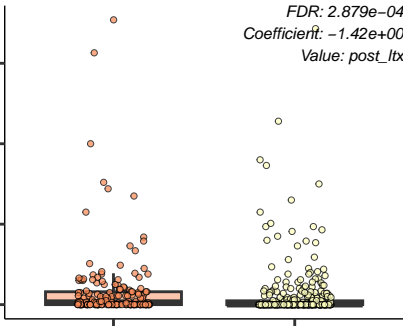
300
200
100
0

healthy (n=161)

post_ltx (n=350)

Group

FDR: 2.879×10^{-4}
Coefficient: -1.42×10^0
Value: post_ltx



f__Christensenellaceae.g__unassigned

1000

500

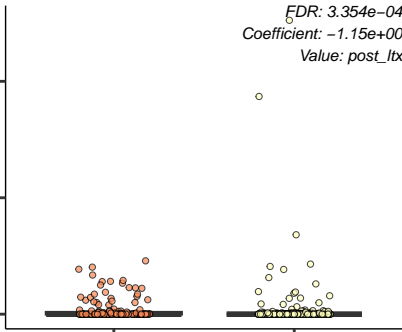
0

healthy (n=161)

post_ltx (n=350)

Group

FDR: $3.354e-04$
Coefficient: $-1.15e+00$
Value: post_ltx



UCG.009

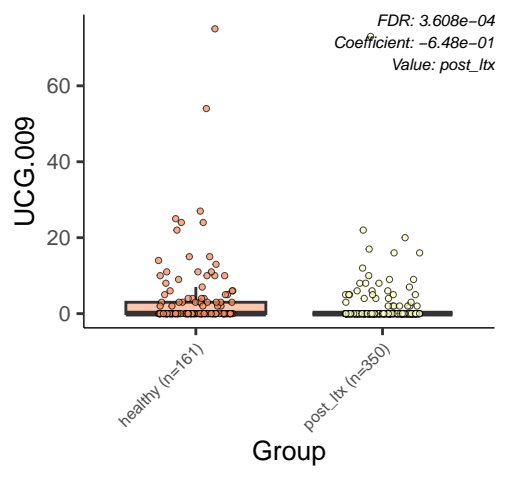
FDR: 3.608e-04
Coefficient: -6.48e-01
Value: post_ltx

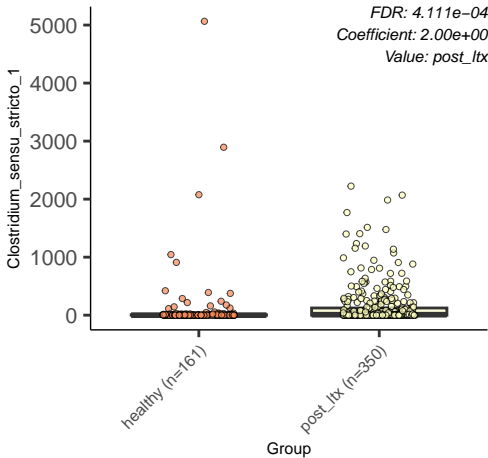
healthy (n=161)

post_ltx (n=350)

Group

60
40
20
0





Negativibacillus

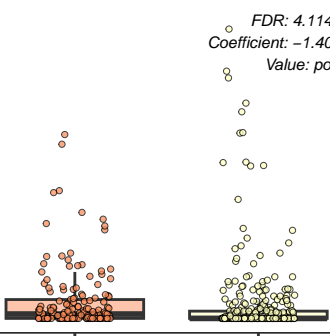
600
400
200
0

healthy (n=161)

post_ltx (n=350)

Group

FDR: $4.114e-04$
Coefficient: $-1.40e+00$
Value: post_ltx



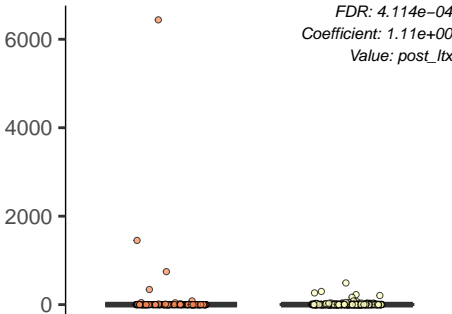
Pseudomonas

FDR: 4.114e-04
Coefficient: 1.11e+00
Value: post_ltx

healthy (n=161)

post_ltx (n=350)

Group



Fusicatenibacter

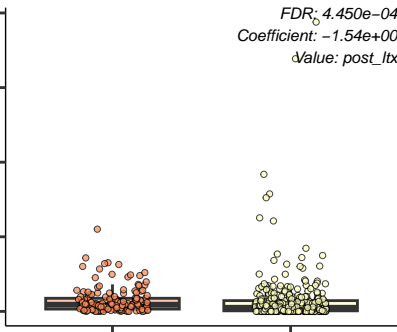
8000
6000
4000
2000
0

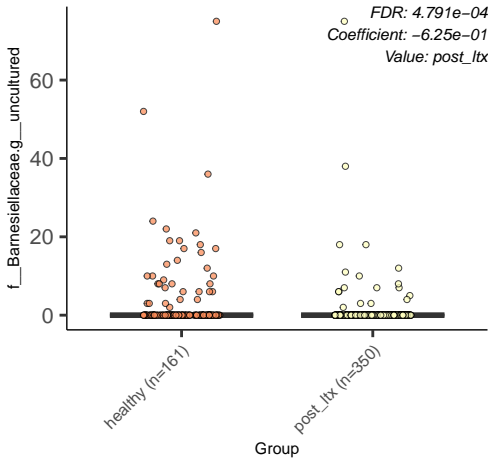
healthy (n=161)

post_ltx (n=350)

Group

FDR: 4.450e-04
Coefficient: -1.54e+00
Value: post_ltx





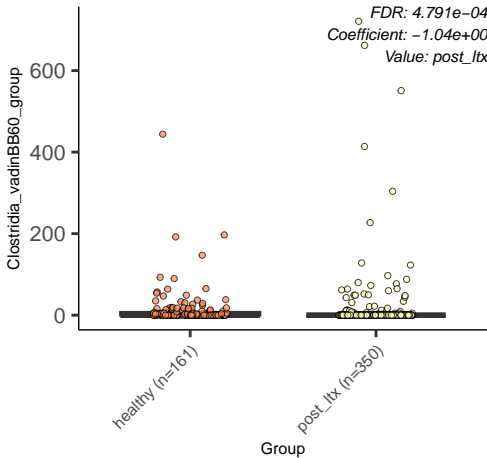
Clostridia_vadinBB60_group

FDR: 4.791e-04
Coefficient: -1.04e+00
Value: post_ltx

healthy (n=161)

post_ltx (n=350)

Group



Bilophila

900

600

300

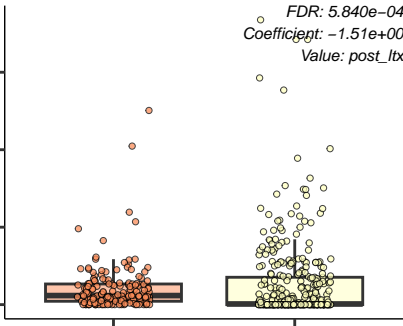
0

healthy (n=161)

post_ltx (n=350)

Group

FDR: 5.840e-04
Coefficient: -1.51e+00
Value: post_ltx



Paraprevotella

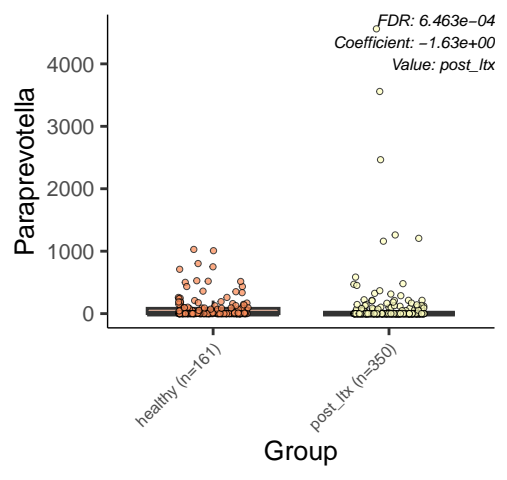
FDR: 6.463×10^{-4}
Coefficient: -1.63×10^0
Value: post_ltx

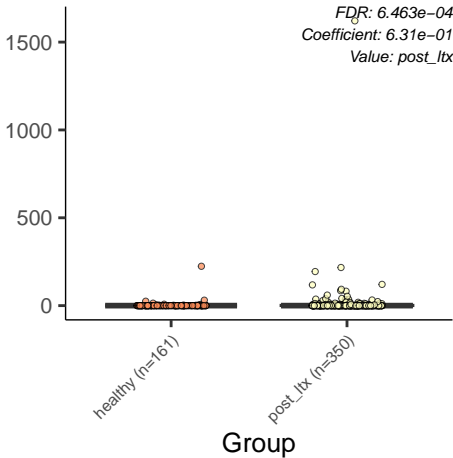
healthy (n=161)

post_ltx (n=350)

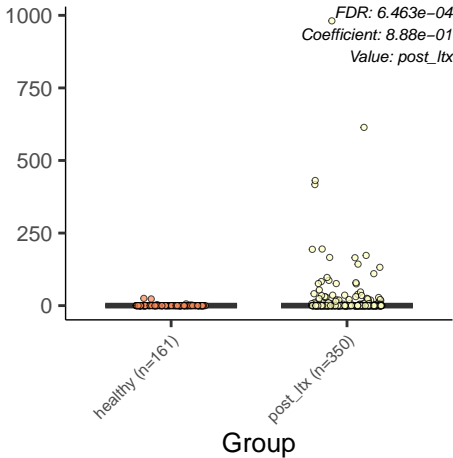
Group

4000
3000
2000
1000
0

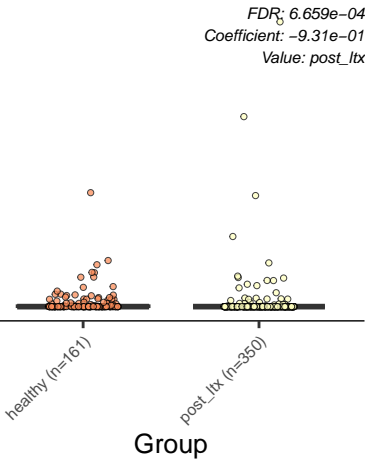


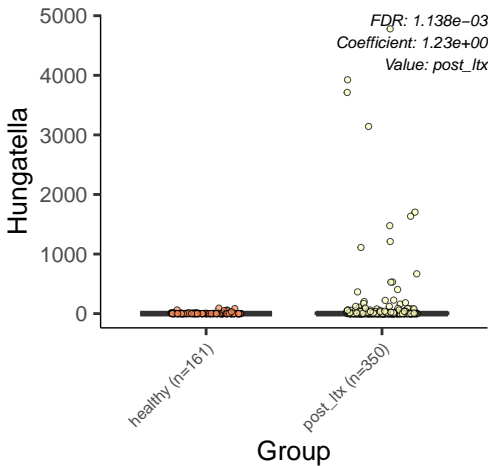


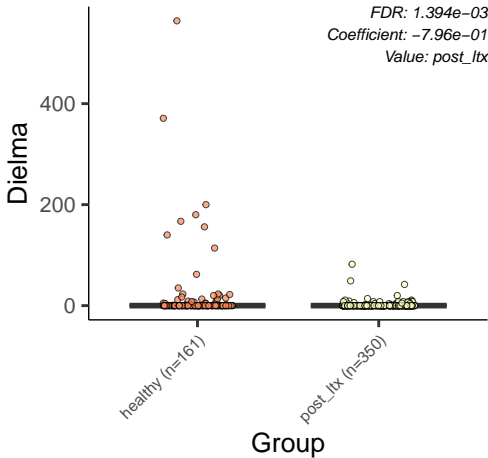
Lactobacillus



Muribaculaceae







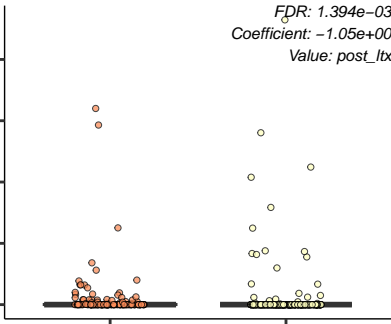
CAG.352

FDR: 1.394e-03
Coefficient: -1.05e+00
Value: post_ltx

healthy (n=161)

post_ltx (n=350)

Group



Faecalibacterium

healthy (n=161)

post_ltx (n=350)

Group

FDR: $1.424e-03$
Coefficient: $-1.42e+00$
Value: post_ltx

20000

15000

10000

5000

0

Candidatus_Soleaferrea

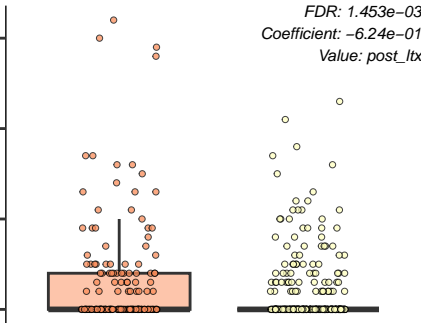
30
20
10
0

healthy (n=161)

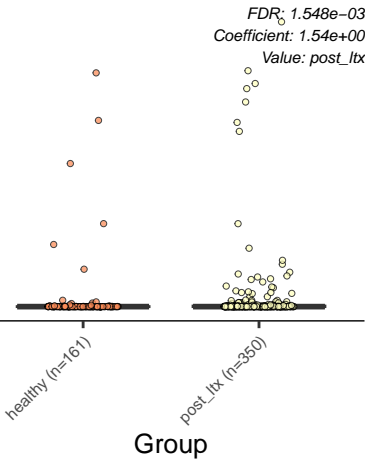
post_ltx (n=350)

Group

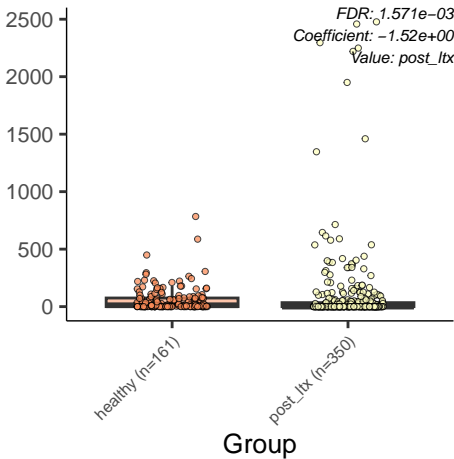
FDR: 1.453×10^{-3}
Coefficient: -6.24×10^{-1}
Value: post_ltx

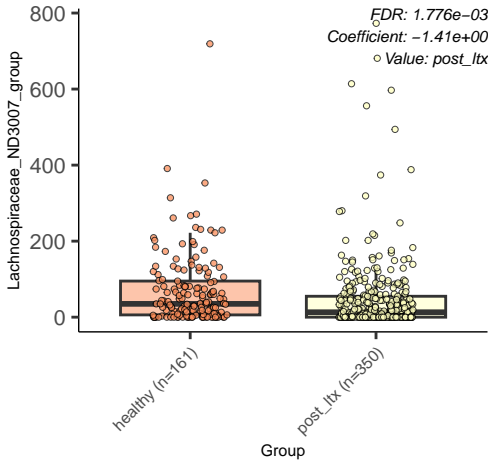


Fusobacterium



Coprobacter





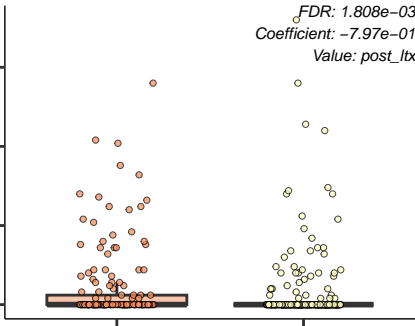
Enterorhabdus

FDR: $1.808e-03$
Coefficient: $-7.97e-01$
Value: *post_ltx*

healthy (n=161)

post_ltx (n=350)

Group



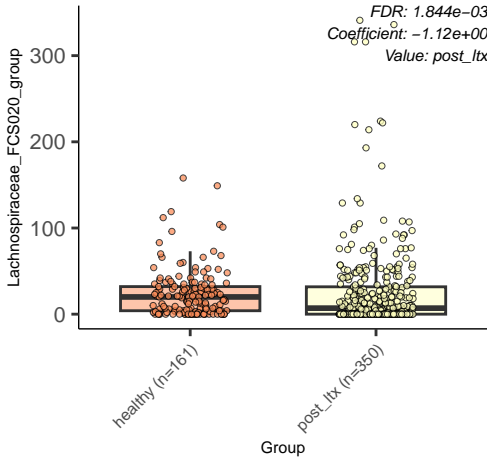
Lachnospiraceae_FCS020_group

FDR: $1.844\text{e-}03$
Coefficient: $-1.12\text{e}+00$
Value: *post_ltx*

healthy (n=161)

post_ltx (n=350)

Group



Pseudoflavonifractor

FDR: 2.722e-03

Coefficient: -5.70e-01

Value: post_ltx

100

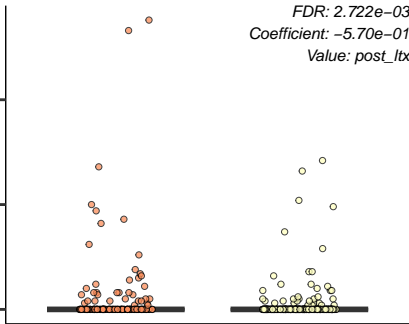
50

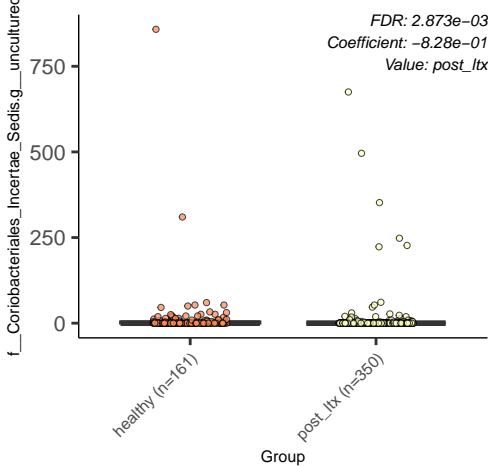
0

healthy (n=161)

post_ltx (n=350)

Group





Gordonibacter

FDR: 3.303e-03

Coefficient: -7.46e-01

Value: post_ltx

200

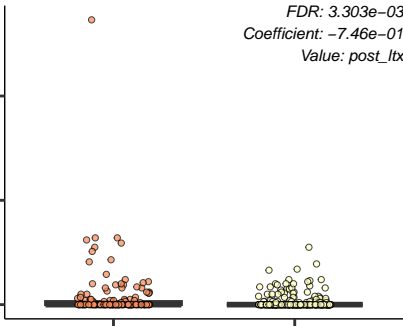
100

0

healthy (n=161)

post_ltx (n=350)

Group



Actinomyces

FDR: 3.571e-03
Coefficient: 1.01e+00
Value: post_ltx

900

600

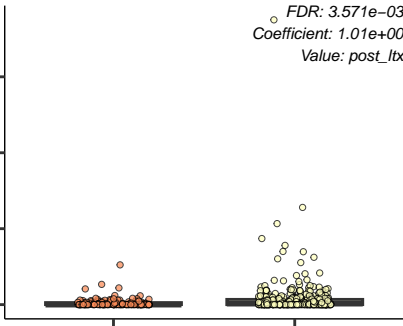
300

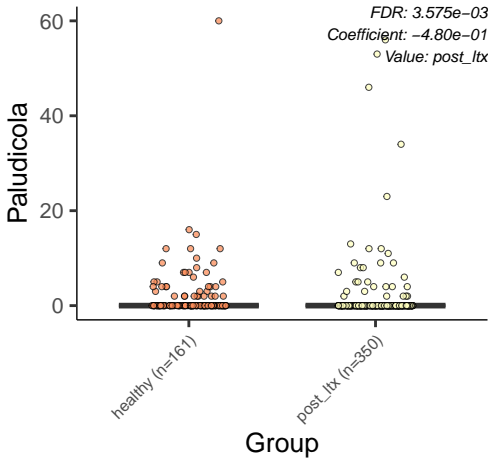
0

healthy (n=161)

post_ltx (n=350)

Group





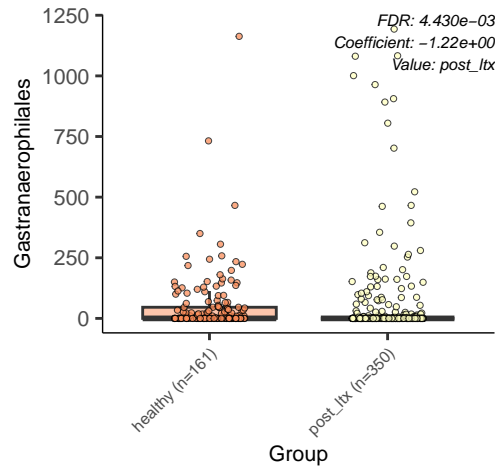
Gastranaerophilales

healthy (n=161)

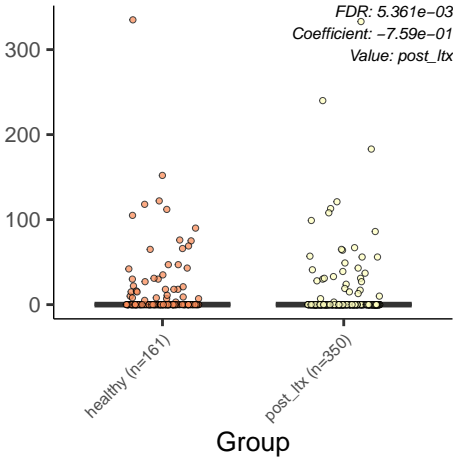
post_ltx (n=350)

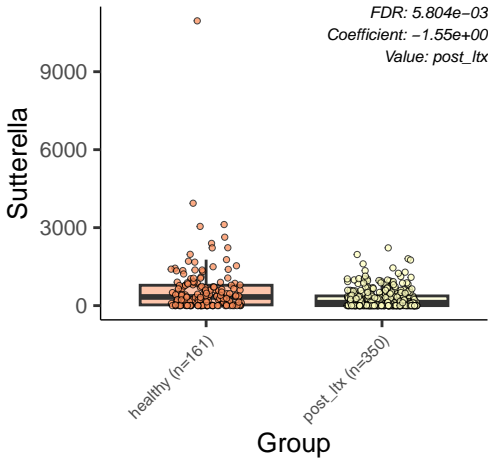
Group

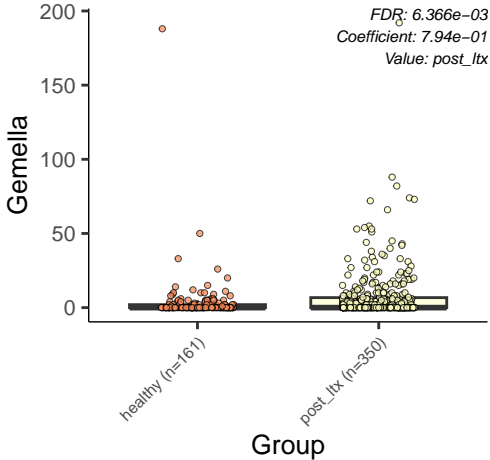
FDR: 4.430e-03
Coefficient: -1.22e+00
Value: post_ltx

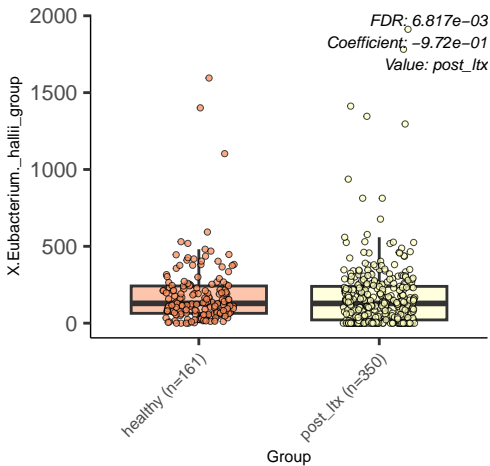


Howardella









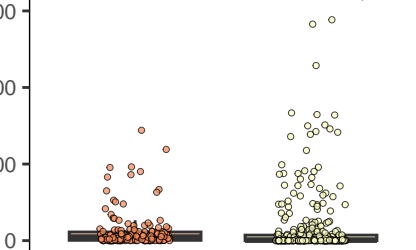
Ruminococcus

healthy (n=161)

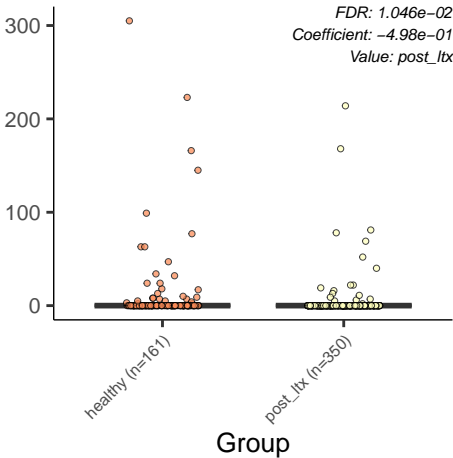
post_ltx (n=350)

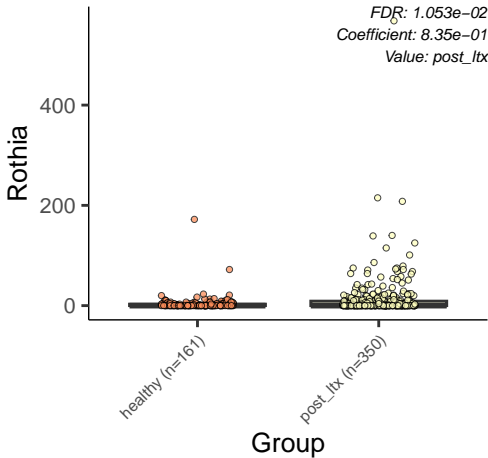
Group

FDR: $8.243e-03$
Coefficient: $-1.34e+00$
Value: *post_ltx*



Tannerellaceae





Senegalimassilia

400

200

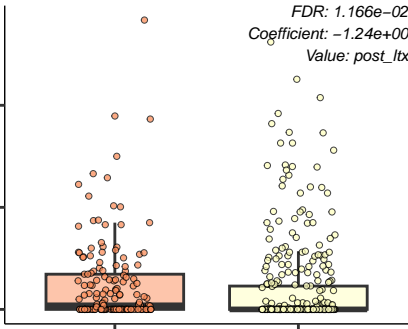
0

healthy (n=161)

post_ltx (n=350)

Group

FDR: 1.166e-02
Coefficient: -1.24e+00
Value: post_ltx



UCG.003

FDR: $1.193e-02$
Coefficient: $-9.65e-01$
Value: *post_ltx*

1000

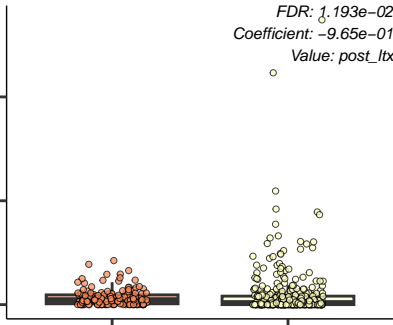
500

0

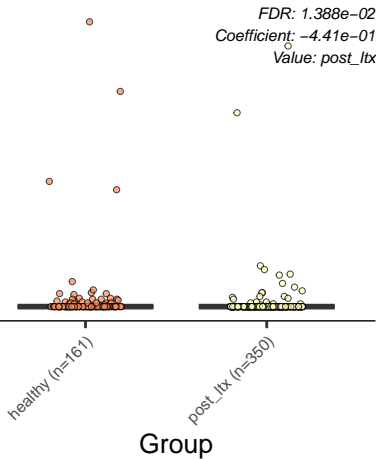
healthy (n=161)

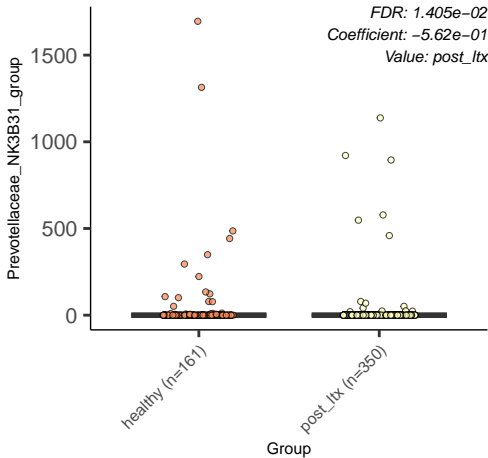
post_ltx (n=350)

Group



Anaerofilum





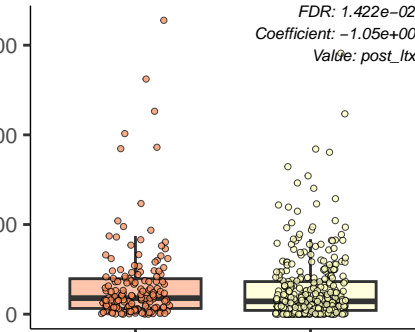
X.Ruminococcus_torques_group

FDR: $1.422e-02$
Coefficient: $-1.05e+00$
Value: post_ltx

healthy (n=161)

post_ltx (n=350)

Group



Parasutterella

2000

1000

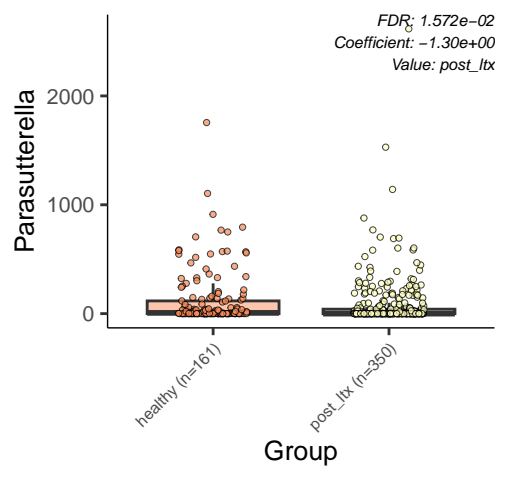
0

healthy (n=161)

post_ltx (n=350)

Group

FDR: $1.572e-02$
Coefficient: $-1.30e+00$
Value: post_ltx



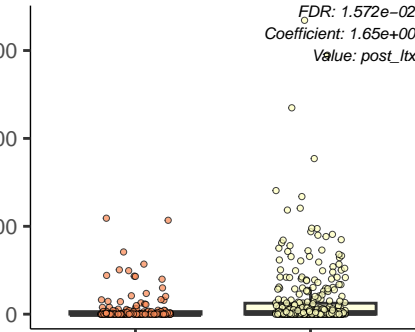
X.Ruminococcus_gnavus_group

FDR: 1.572e-02
Coefficient: 1.65e+00
Value: post_ltx

healthy (n=161)

post_ltx (n=350)

Group



Bacteroides

30000

20000

10000

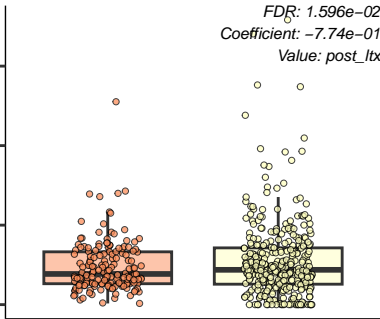
0

healthy (n=161)

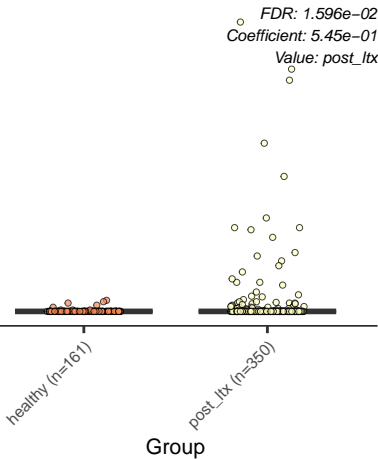
post_ltx (n=350)

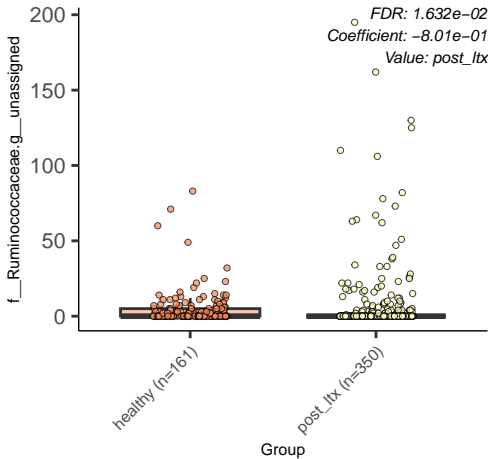
Group

FDR: 1.596e-02
Coefficient: -7.74e-01
Value: post_ltx



Ligilactobacillus





Butyricoccus

1000

500

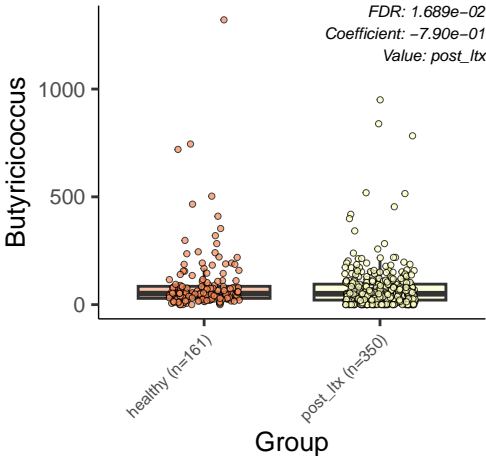
0

healthy (n=161)

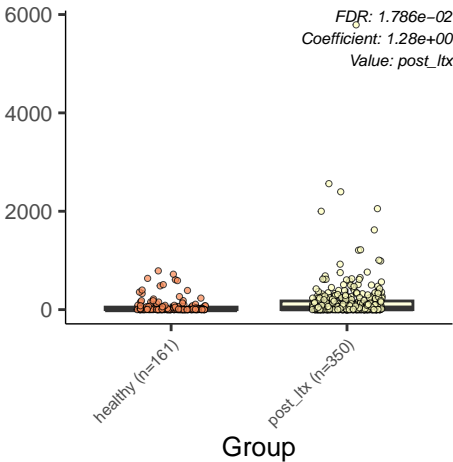
post_ltx (n=350)

Group

FDR: 1.689e-02
Coefficient: -7.90e-01
Value: post_ltx



Intestinibacter



Collinsella

4000

2000

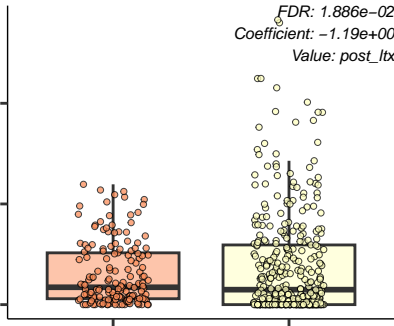
0

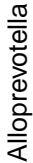
healthy (n=161)

post_ltx (n=350)

Group

FDR: 1.886e-02
Coefficient: -1.19e+00
Value: post_ltx





FDR: 2.255e-02

Coefficient: -8.98e-01

Value: post_ltx

healthy (n=161)

post_ltx (n=350)

Group

Staphylococcus

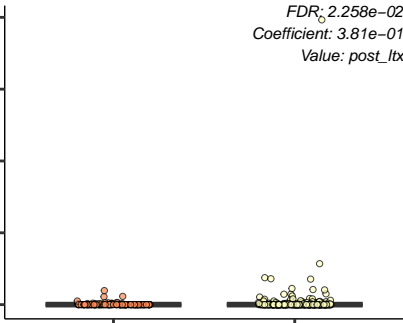
800
600
400
200
0

FDR: 2.258e-02
Coefficient: 3.81e-01
Value: post_ltx

healthy (n=161)

post_ltx (n=350)

Group



RF39

healthy (n=161)

post_ltx (n=350)

Group

FDR: 2.450e-02
Coefficient: -6.00e-01
Value: post_ltx

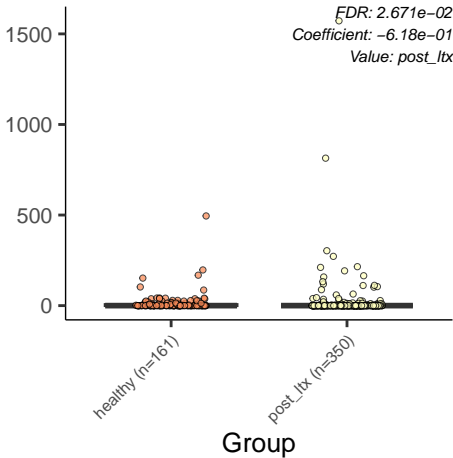
150

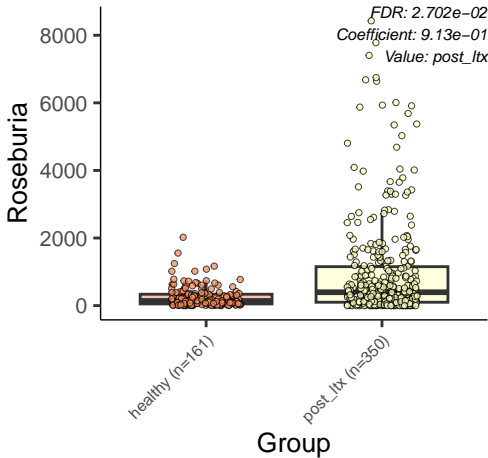
100

50

0

UCG.010





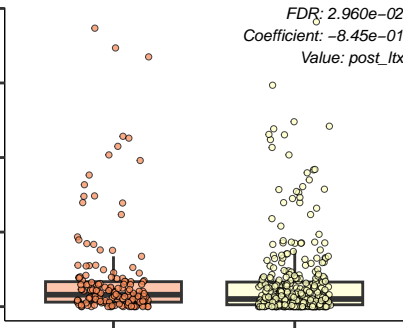
Flavonifractor

FDR: 2.960e-02
Coefficient: -8.45e-01
Value: post_ltx

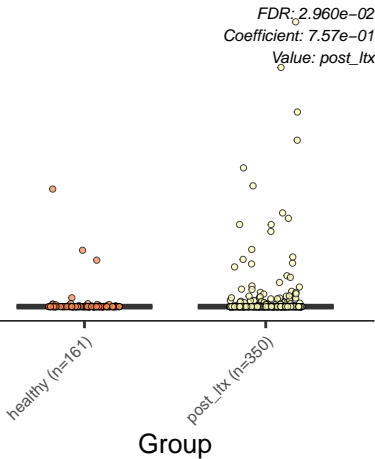
healthy (n=161)

post_ltx (n=350)

Group



Faecalitalea



Akkermansia

10000

5000

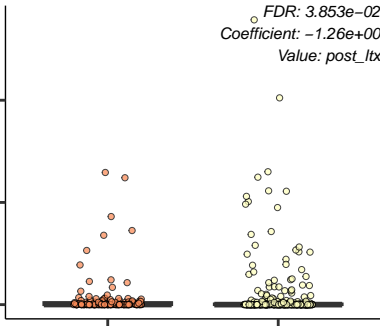
0

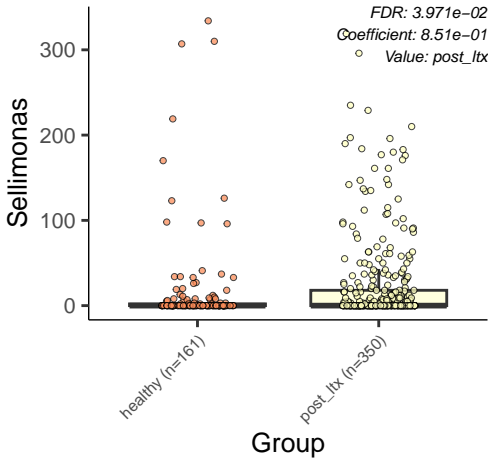
healthy (n=161)

post_ltx (n=350)

Group

FDR: $3.853e-02$
Coefficient: $-1.26e+00$
Value: post_ltx





Tuzzerella

