

Odoribacter

600

400

200

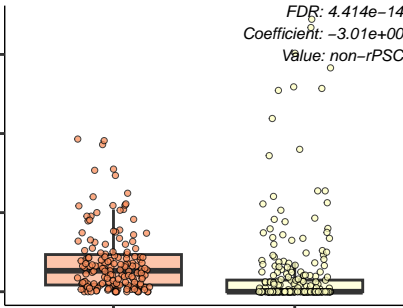
0

healthy (n=161)

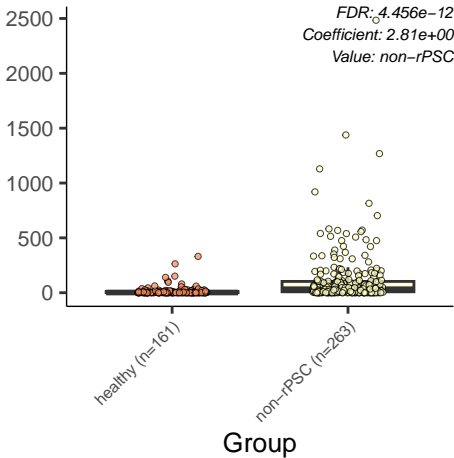
non-rPSC (n=263)

Group

*FDR: 4.414e-14*  
*Coefficient: -3.01e+00*  
*Value: non-rPSC*



Haemophilus



Veillonella

2000

1000

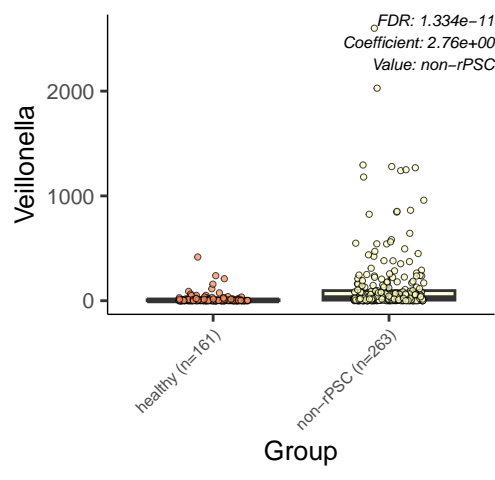
0

healthy (n=161)

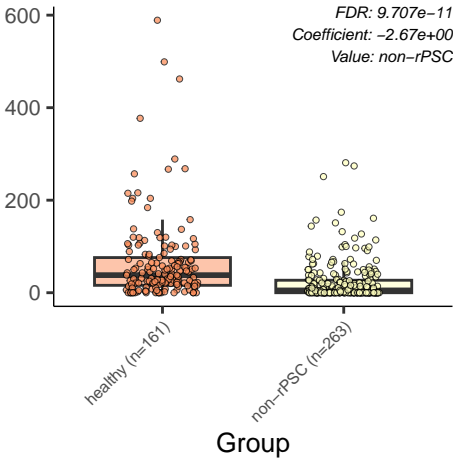
non-rPSC (n=263)

Group

FDR:  $1.334e-11$   
Coefficient:  $2.76e+00$   
Value: non-rPSC



Intestinimonas



Sphingobium

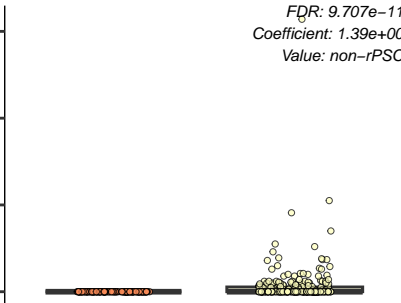
300  
200  
100  
0

healthy (n=161)

non-rPSC (n=263)

Group

*FDR: 9.707e-11*  
*Coefficient: 1.39e+00*  
*Value: non-rPSC*



Lachnoclostridium

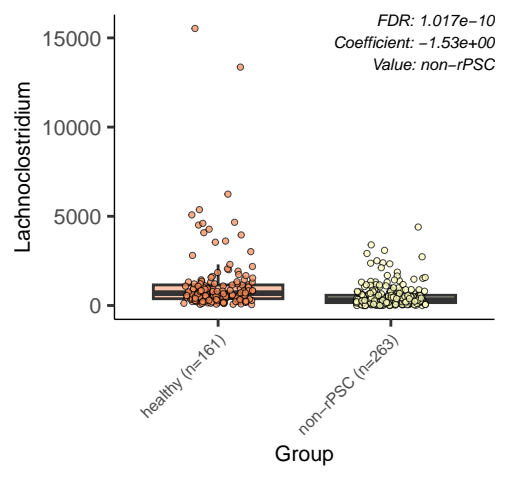
15000  
10000  
5000  
0

healthy (n=161)

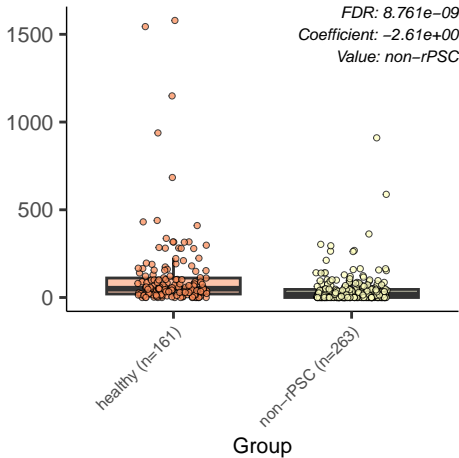
non-rPSC (n=263)

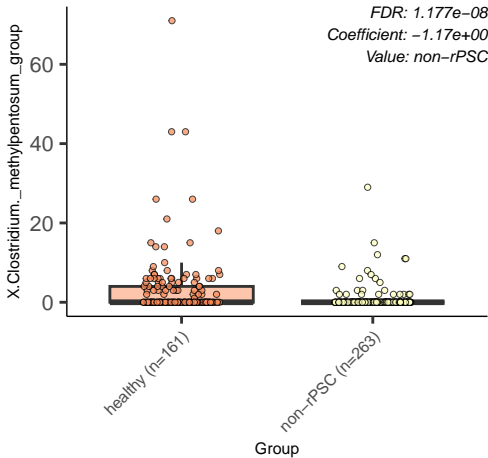
Group

*FDR: 1.017e-10*  
*Coefficient: -1.53e+00*  
*Value: non-rPSC*



Colidextribacter







Family\_XIII\_UCG.001

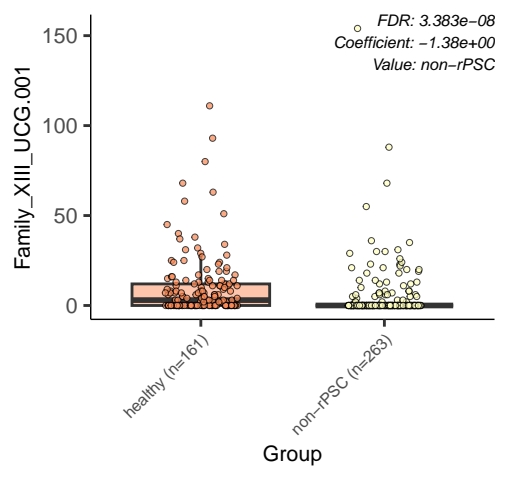
150  
100  
50  
0

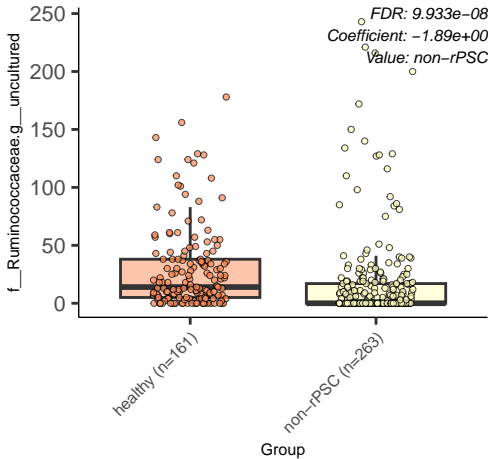
healthy (n=161)

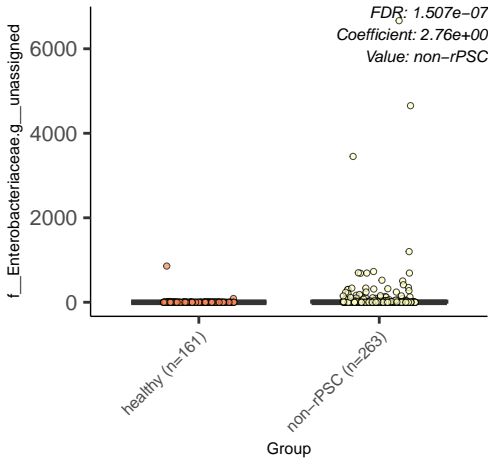
non-rPSC (n=263)

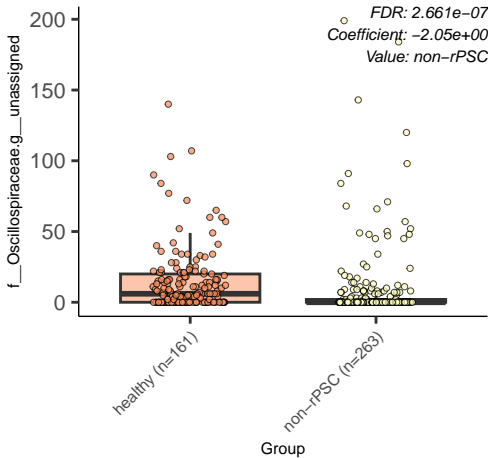
Group

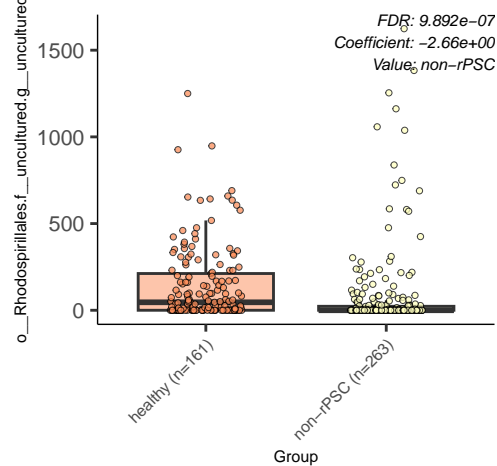
FDR:  $3.383e-08$   
Coefficient:  $-1.38e+00$   
Value: non-rPSC











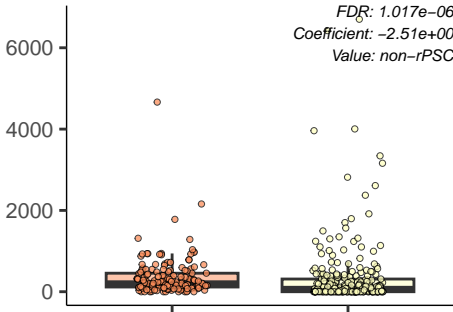
Parabacteroides

*FDR: 1.017e-06*  
*Coefficient: -2.51e+00*  
*Value: non-rPSC*

healthy (n=161)

non-rPSC (n=263)

Group



Christensenellaceae\_R.7\_group

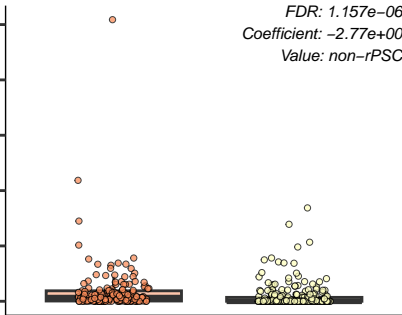
5000  
4000  
3000  
2000  
1000  
0

*FDR: 1.157e-06*  
*Coefficient: -2.77e+00*  
*Value: non-rPSC*

healthy (n=161)

non-rPSC (n=263)

Group



Clostridia\_UCG.014

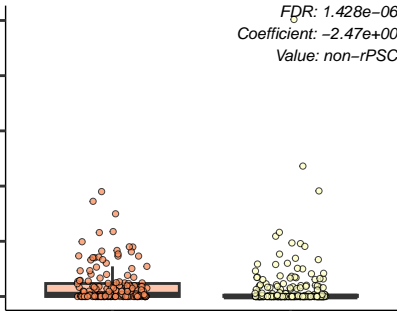
2500  
2000  
1500  
1000  
500  
0

healthy (n=161)

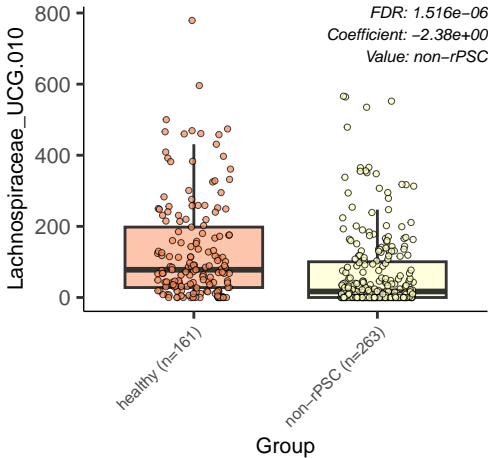
non-rPSC (n=263)

Group

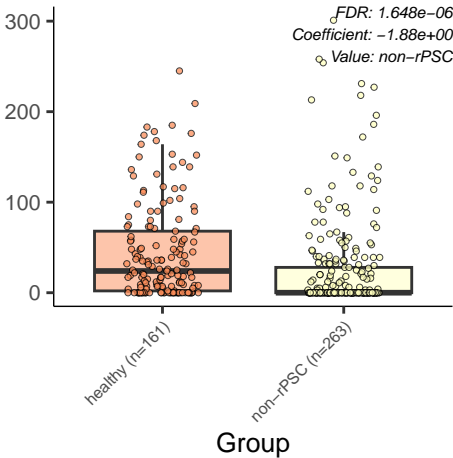
FDR:  $1.428 \times 10^{-6}$   
Coefficient:  $-2.47 \times 10^0$   
Value: non-rPSC







Butyricimonas



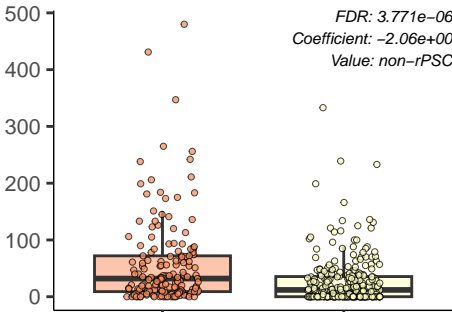
Oscillibacter

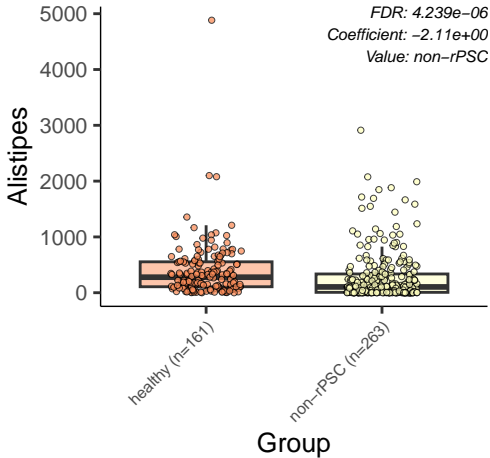
healthy (n=161)

non-rPSC (n=263)

Group

*FDR: 3.771e-06*  
*Coefficient: -2.06e+00*  
*Value: non-rPSC*





Escherichia.Shigella

30000

20000

10000

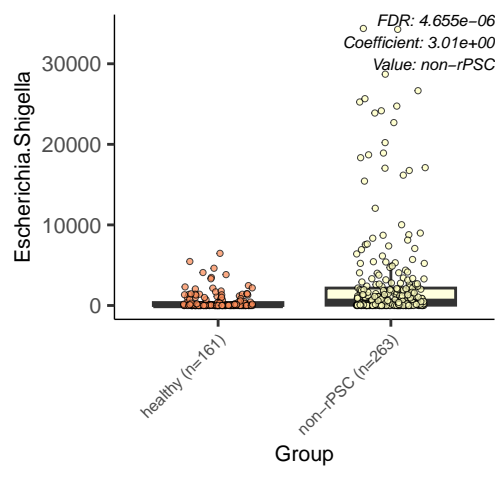
0

healthy (n=161)

non-rPSC (n=263)

Group

FDR:  $4.655e-06$   
Coefficient:  $3.01e+00$   
Value: non-rPSC



Streptococcus

FDR:  $6.927 \times 10^{-6}$   
Coefficient:  $1.70 \times 10^0$   
Value: non-rPSC

healthy (n=161)

non-rPSC (n=263)

Group

9000  
6000  
3000  
0

Family\_XIII\_AD3011\_group

200

100

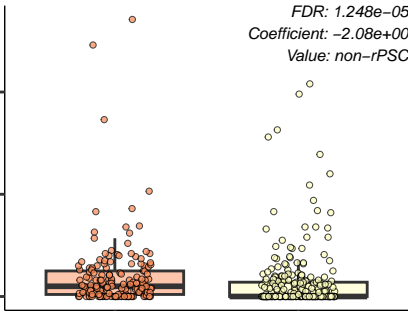
0

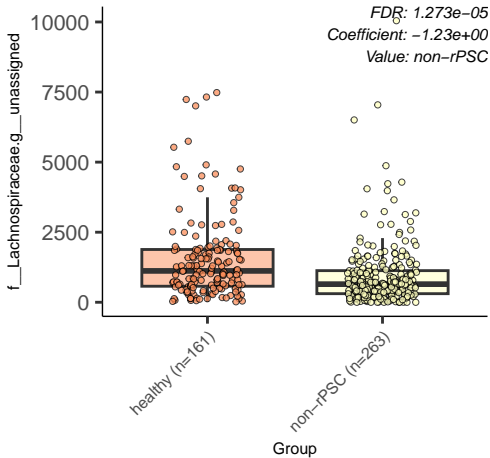
healthy (n=161)

non-rPSC (n=263)

Group

*FDR: 1.248e-05*  
*Coefficient: -2.08e+00*  
*Value: non-rPSC*







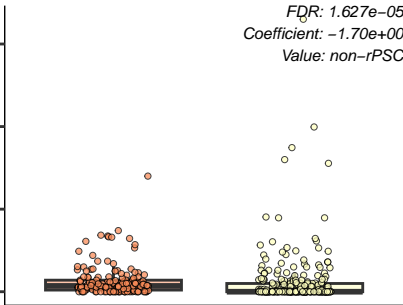
GCA.900066575

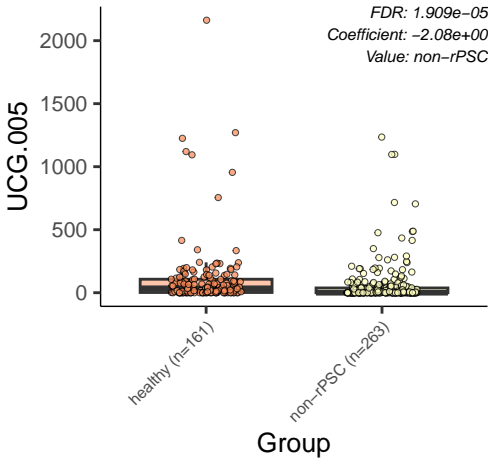
*FDR: 1.627e-05*  
*Coefficient: -1.70e+00*  
*Value: non-rPSC*

healthy (n=161)

non-rPSC (n=263)

Group





Enterococcus

30000

20000

10000

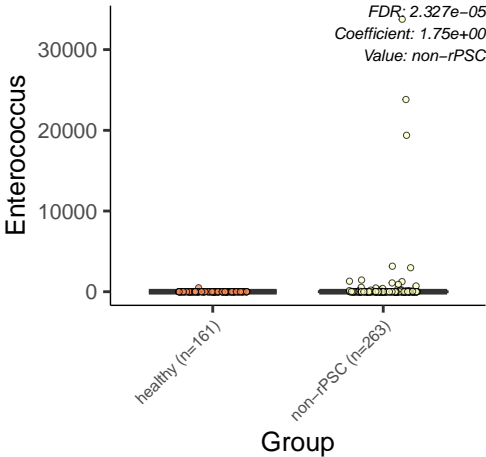
0

healthy (n=161)

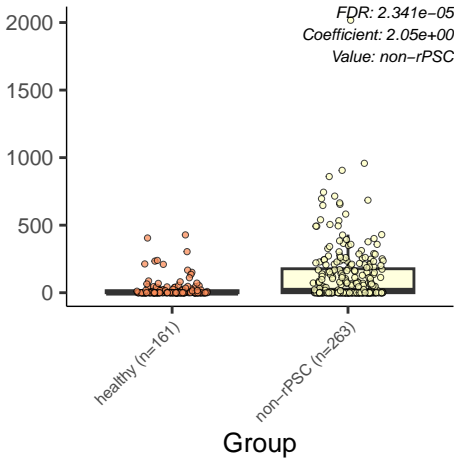
non-rPSC (n=263)

Group

*FDR: 2.327e-05*  
*Coefficient: 1.75e+00*  
*Value: non-rPSC*



Dialister



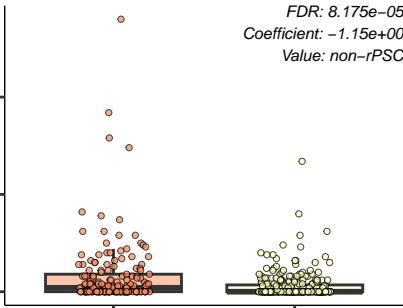
Holdemania

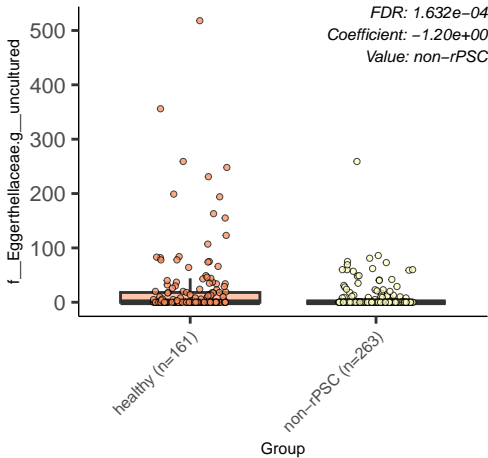
*FDR: 8.175e-05*  
*Coefficient: -1.15e+00*  
*Value: non-rPSC*

healthy (n=161)

non-rPSC (n=263)

Group





Marvinbryantia

400

200

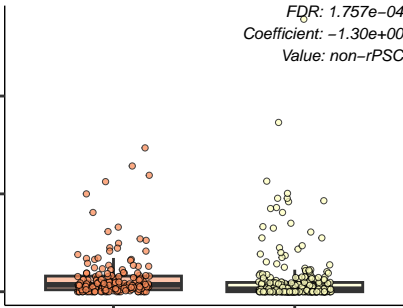
0

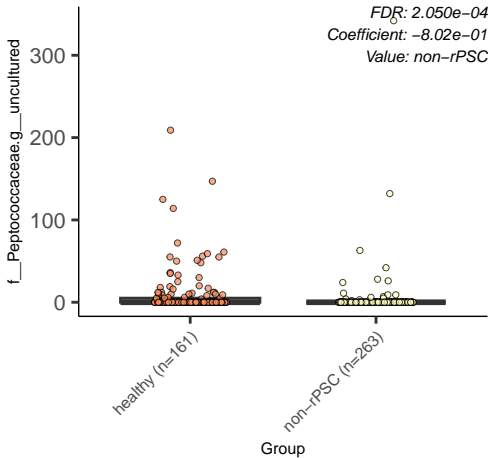
healthy (n=161)

non-rPSC (n=263)

Group

FDR:  $1.757e-04$   
Coefficient:  $-1.30e+00$   
Value: non-rPSC

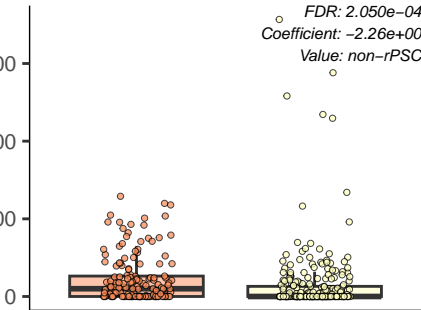






Phascolarctobacterium

*FDR: 2.050e-04*  
*Coefficient: -2.26e+00*  
*Value: non-rPSC*



healthy (n=161)

non-rPSC (n=263)

Group

Coprococcus

healthy (n=161)

non-rPSC (n=263)

Group

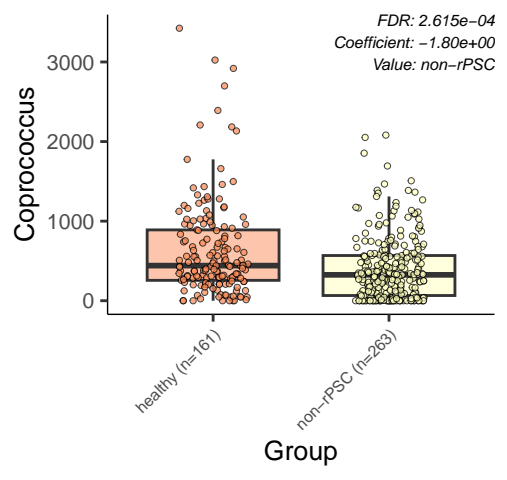
*FDR: 2.615e-04*  
*Coefficient: -1.80e+00*  
*Value: non-rPSC*

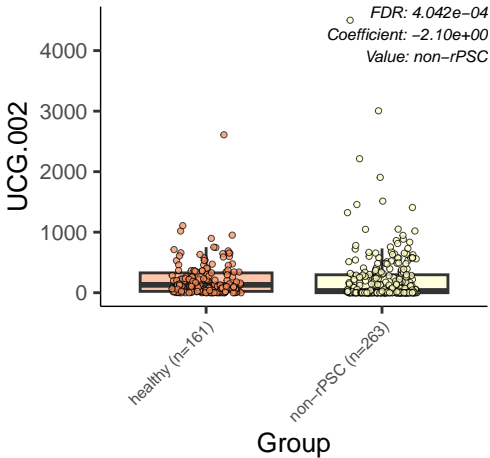
3000

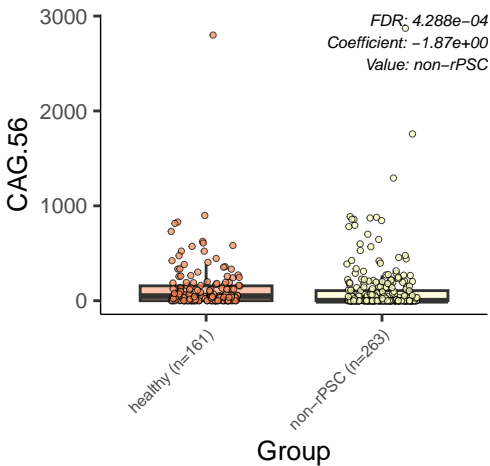
2000

1000

0







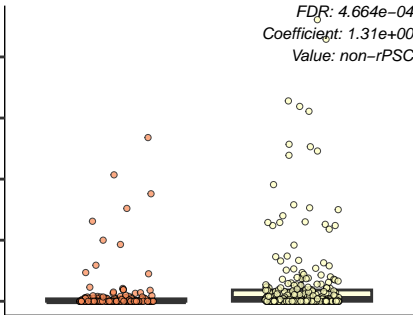
X.Clostridium.\_innocuum\_group

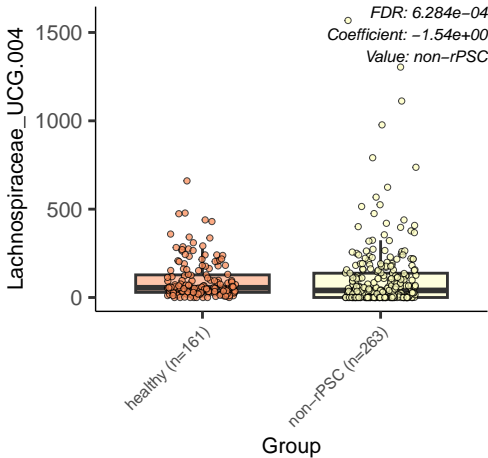
*FDR: 4.664e-04*  
*Coefficient: 1.31e+00*  
*Value: non-rPSC*

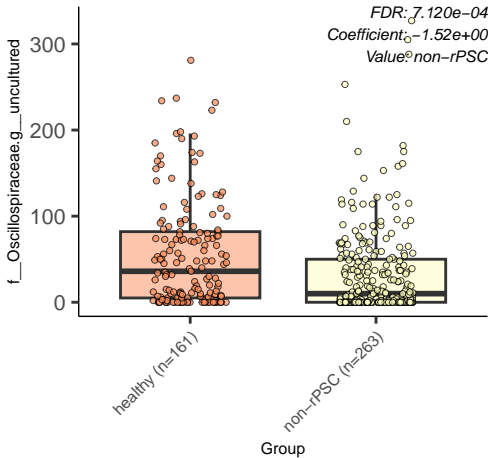
healthy (n=161)

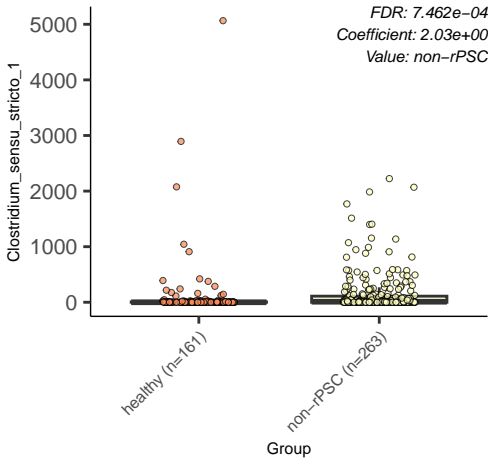
non-rPSC (n=263)

Group



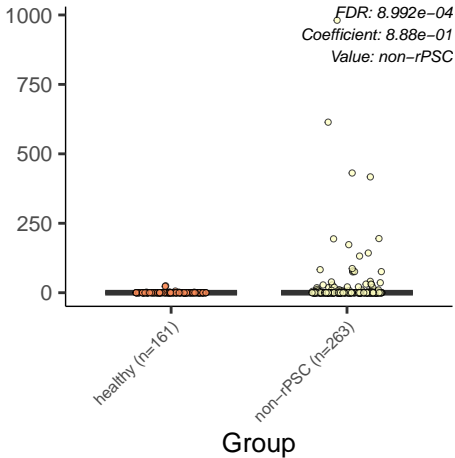


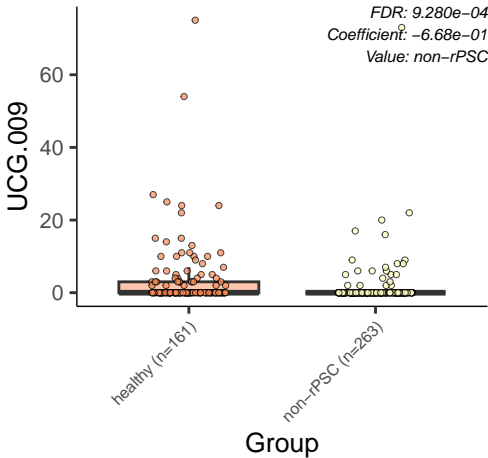


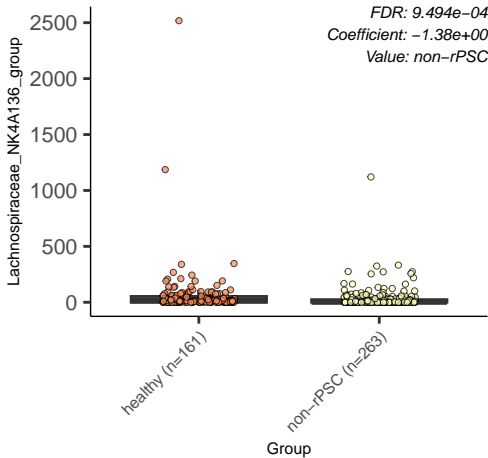




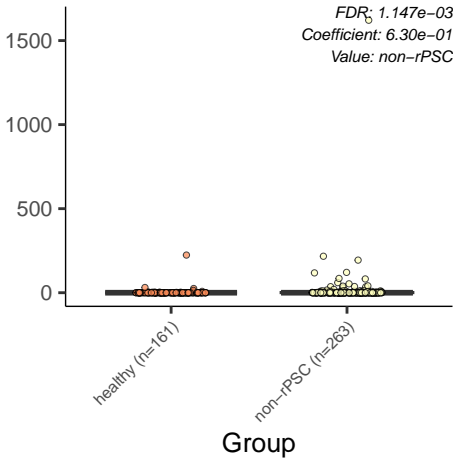
Lactobacillus







Corynebacterium



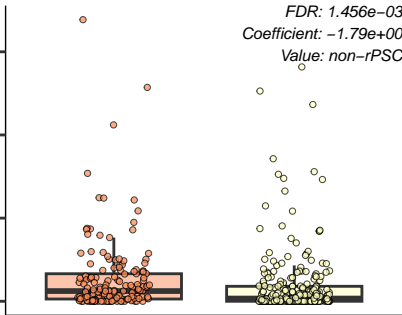
Erysipelotrichaceae\_UCG.003

*FDR: 1.456e-03*  
*Coefficient: -1.79e+00*  
*Value: non-rPSC*

healthy (n=161)

non-rPSC (n=263)

Group



Clostridia\_vadinBB60\_group

FDR:  $1.604e-03$   
Coefficient:  $-1.03e+00$   
Value: non-rPSC

600

400

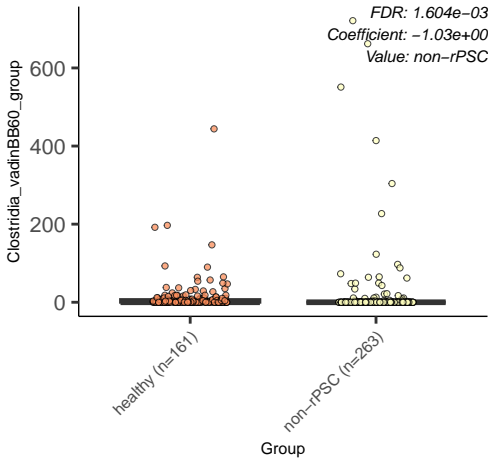
200

0

healthy (n=161)

non-rPSC (n=263)

Group



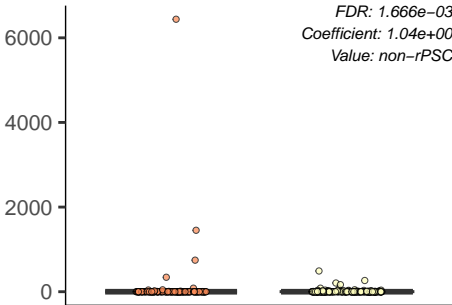
Pseudomonas

*FDR: 1.666e-03*  
*Coefficient: 1.04e+00*  
*Value: non-rPSC*

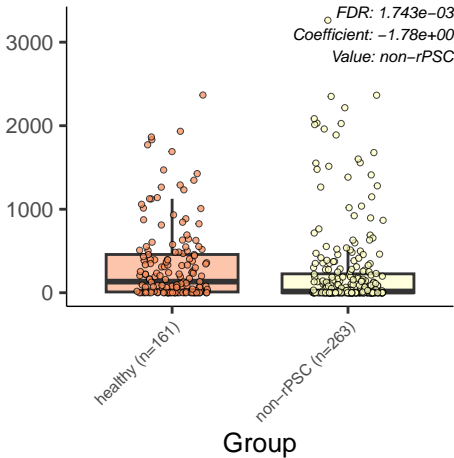
healthy (n=161)

non-rPSC (n=263)

Group



Barnesiella





Enterorhabdus

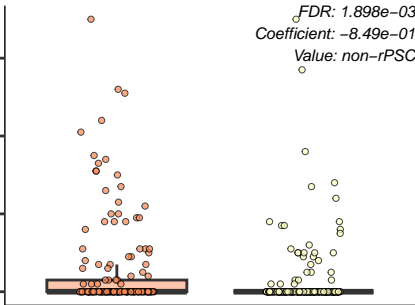
60  
40  
20  
0

healthy (n=161)

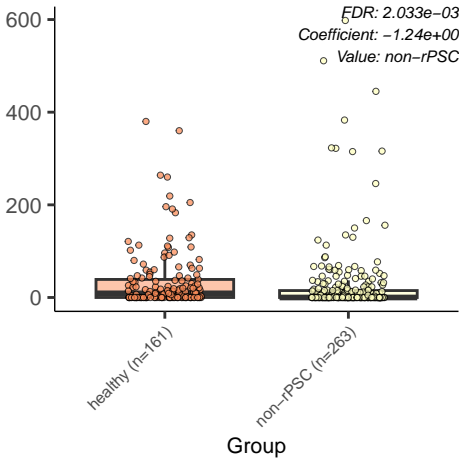
non-rPSC (n=263)

Group

$FDR: 1.898e-03$   
 $Coefficient: -8.49e-01$   
 $Value: non-rPSC$



Negativibacillus



Klebsiella

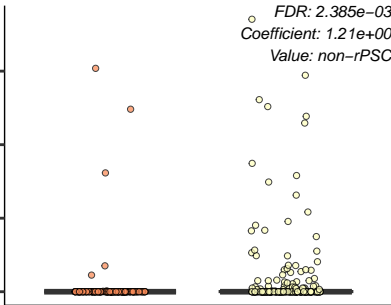
1500  
1000  
500  
0

healthy (n=161)

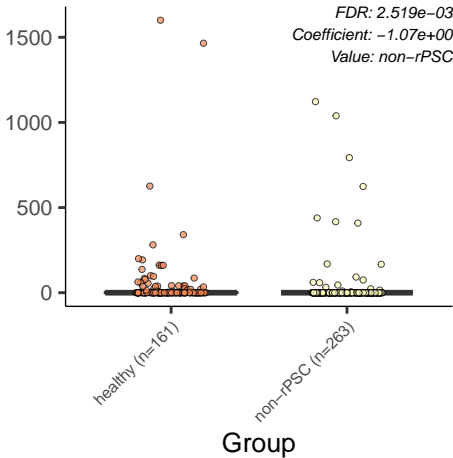
non-rPSC (n=263)

Group

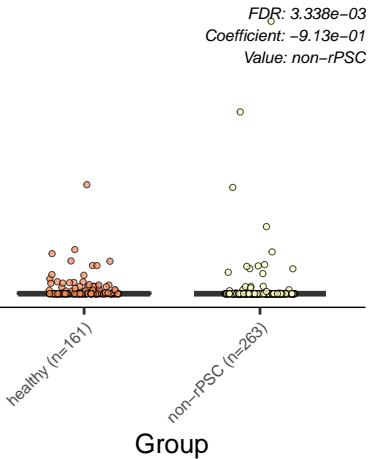
FDR: 2.385e-03  
Coefficient: 1.21e+00  
Value: non-rPSC



CAG.352



# Muribaculaceae



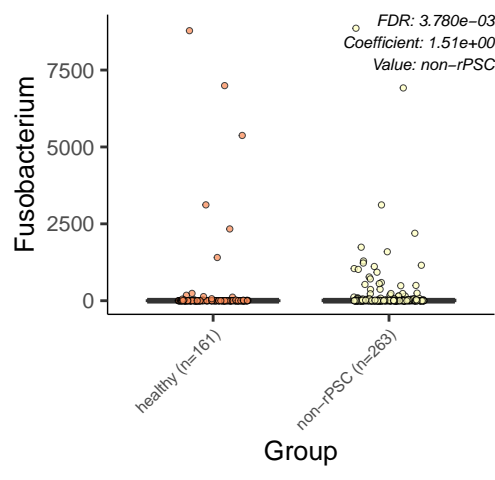
Fusobacterium

FDR: 3.780e-03  
Coefficient: 1.51e+00  
Value: non-rPSC

healthy (n=161)

non-rPSC (n=263)

Group



Paraprevotella

1000

500

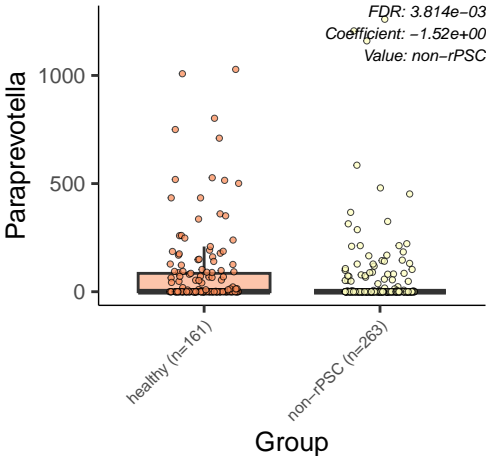
0

healthy (n=161)

non-rPSC (n=263)

Group

FDR:  $3.814e-03$   
Coefficient:  $-1.52e+00$   
Value: non-rPSC



Fusicatenibacter

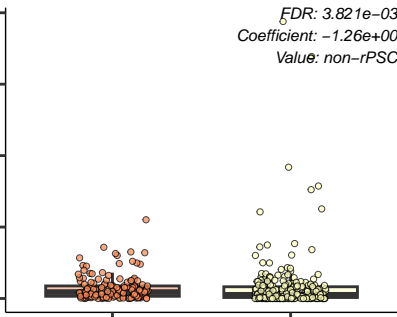
8000  
6000  
4000  
2000  
0

FDR:  $3.821e-03$   
Coefficient:  $-1.26e+00$   
Value: non-rPSC

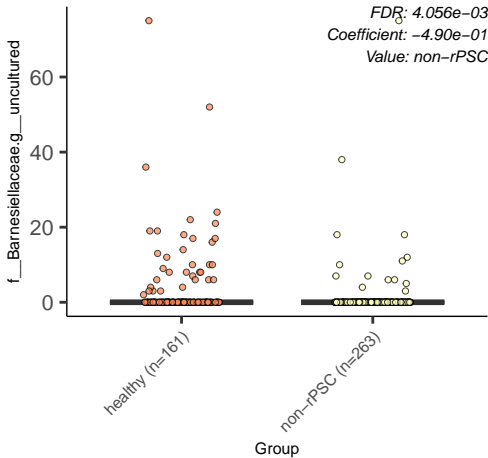
healthy (n=161)

non-rPSC (n=263)

Group







Candidatus\_Soleaferrea

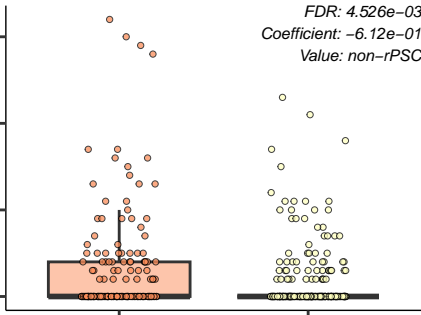
30  
20  
10  
0

healthy (n=161)

non-rPSC (n=263)

Group

FDR:  $4.526e-03$   
Coefficient:  $-6.12e-01$   
Value: non-rPSC



Actinomycetes

*FDR: 4.594e-03*  
*Coefficient: 1.03e+00*  
*Value: non-rPSC*

900

600

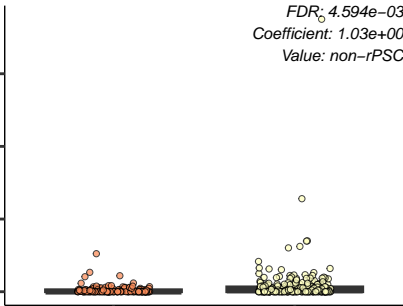
300

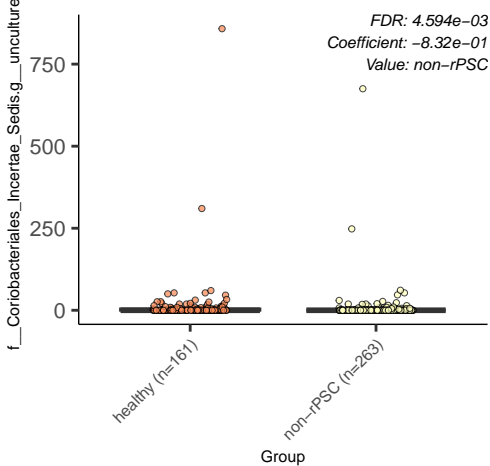
0

healthy (n=161)

non-rPSC (n=263)

Group





Adlercreutzia

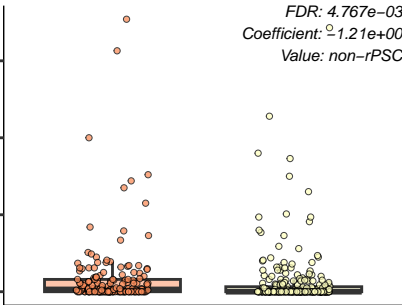
healthy (n=161)

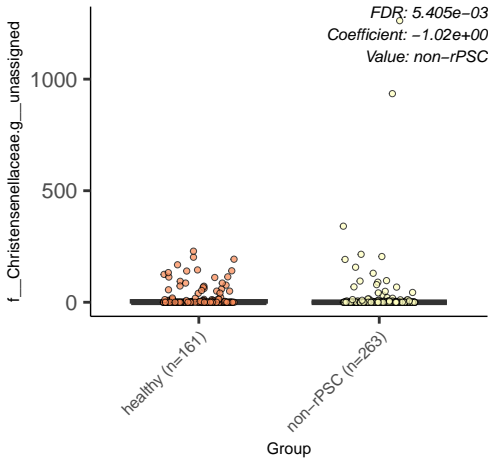
non-rPSC (n=263)

Group

FDR:  $4.767 \times 10^{-3}$   
Coefficient:  $-1.21 \times 10^0$   
Value: non-rPSC

300  
200  
100  
0





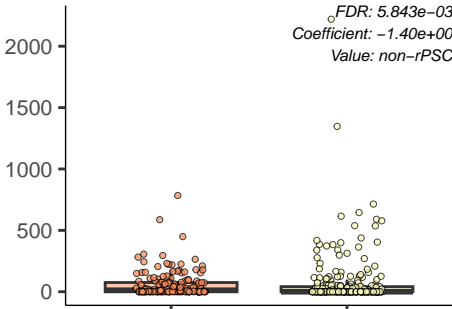
Coprobacter

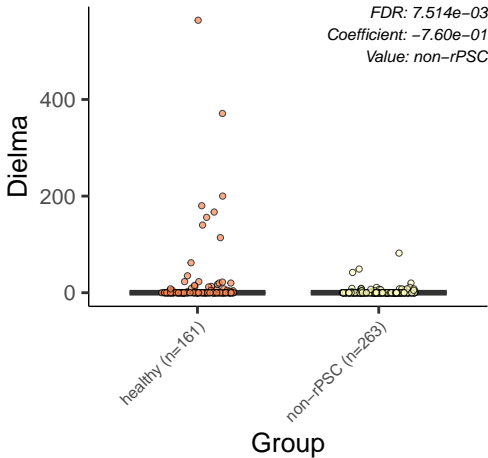
FDR:  $5.843e-03$   
Coefficient:  $-1.40e+00$   
Value: non-rPSC

healthy (n=161)

non-rPSC (n=263)

Group







Gordonibacter

*FDR: 8.957e-03*

*Coefficient: -6.29e-01*

*Value: non-rPSC*

200

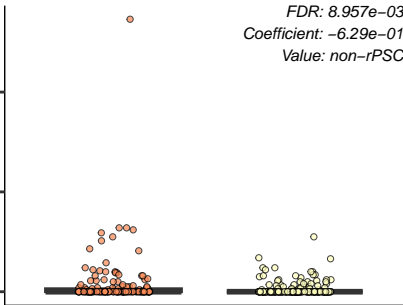
100

0

healthy (n=161)

non-rPSC (n=263)

Group



Paludicola

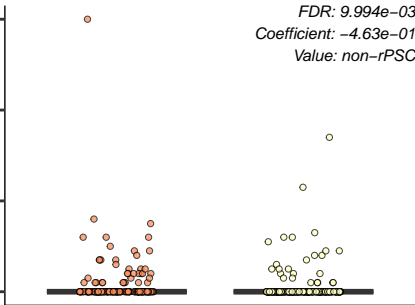
60  
40  
20  
0

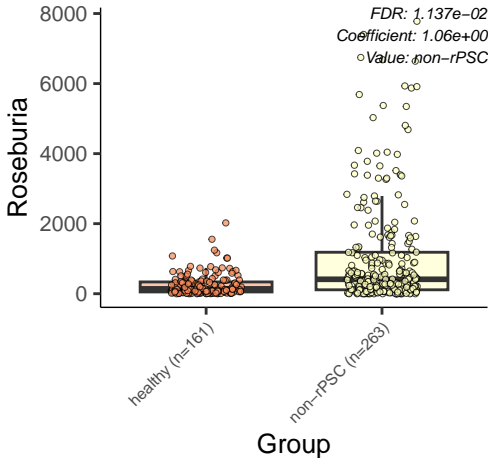
healthy (n=161)

non-rPSC (n=263)

Group

*FDR: 9.994e-03*  
*Coefficient: -4.63e-01*  
*Value: non-rPSC*





Faecalibacterium

20000

15000

10000

5000

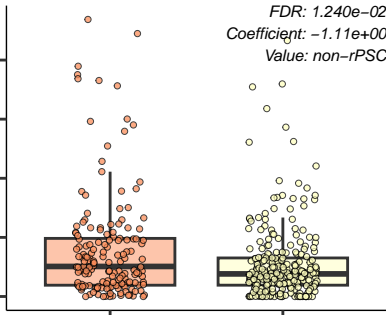
0

healthy (n=161)

non-rPSC (n=263)

Group

*FDR: 1.240e-02*  
*Coefficient: -1.11e+00*  
*Value: non-rPSC*



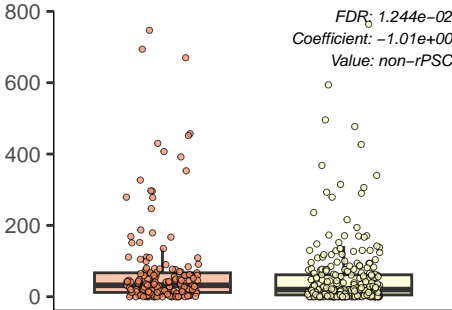
Flavonifractor

healthy (n=161)

non-rPSC (n=263)

Group

FDR:  $1.244\text{e-}02$   
Coefficient:  $-1.01\text{e}+00$   
Value: non-rPSC



Parasutterella

1500

1000

500

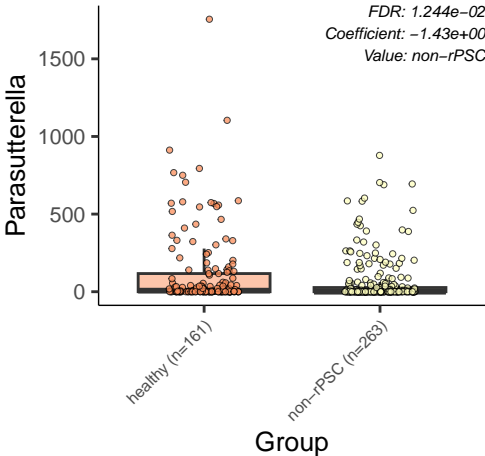
0

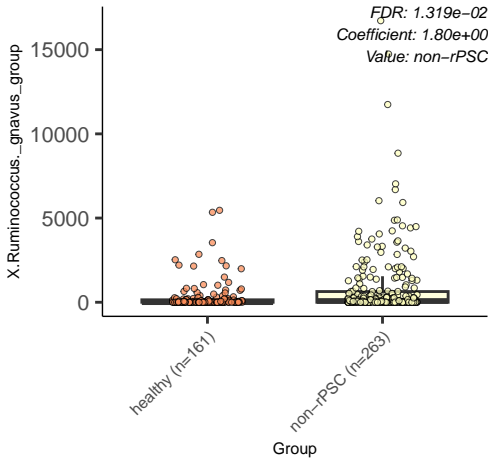
healthy (n=161)

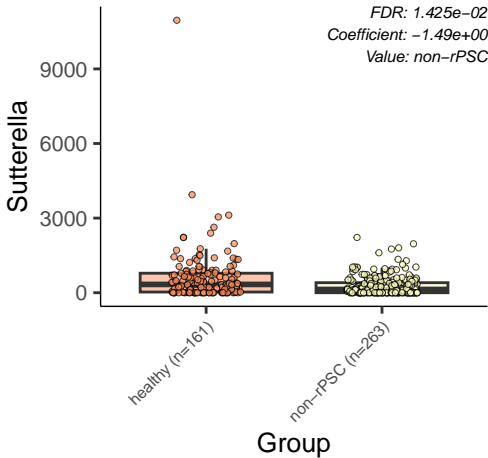
non-rPSC (n=263)

Group

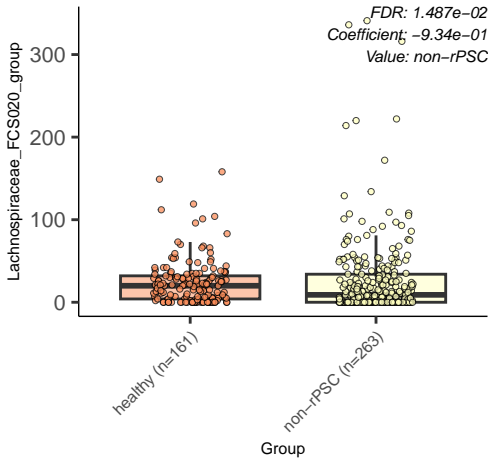
FDR:  $1.244e-02$   
Coefficient:  $-1.43e+00$   
Value: non-rPSC











Pseudoflavonifractor

*FDR: 1.650e-02*

*Coefficient: -5.10e-01*

*Value: non-rPSC*

100

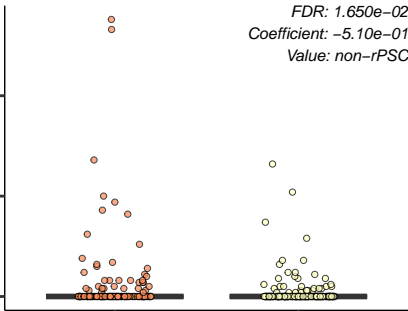
50

0

healthy (n=161)

non-rPSC (n=263)

Group



Allisonella

100

50

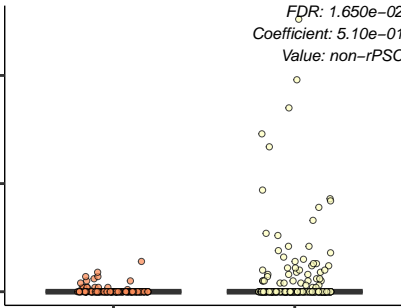
0

healthy (n=161)

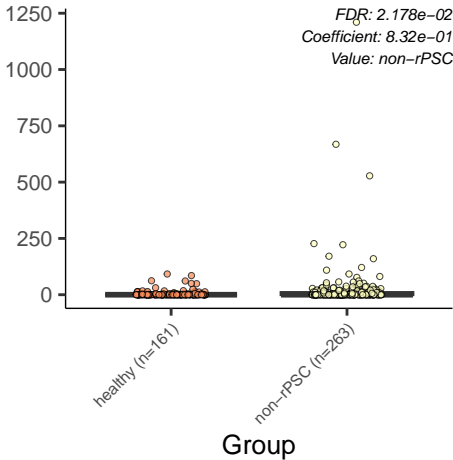
non-rPSC (n=263)

Group

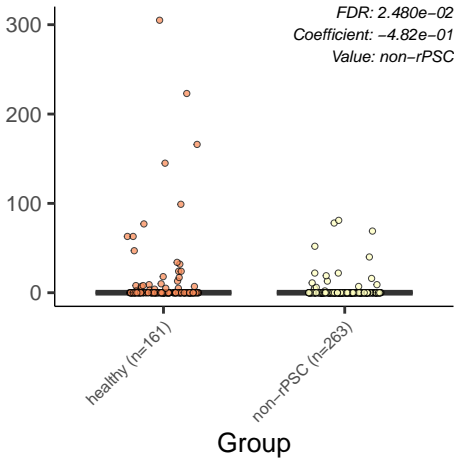
FDR:  $1.650 \times 10^{-2}$   
Coefficient:  $5.10 \times 10^{-1}$   
Value: non-rPSC

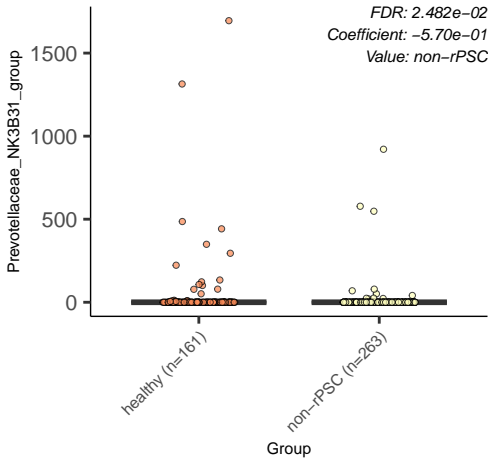


Hungatella

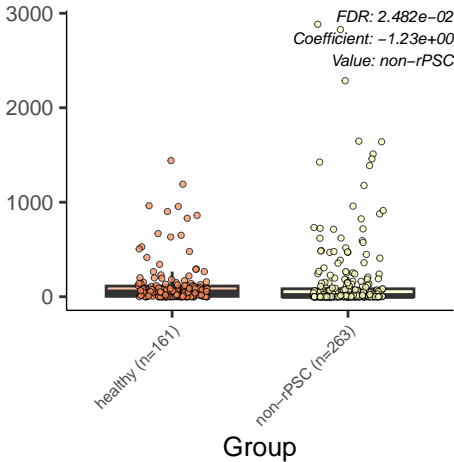


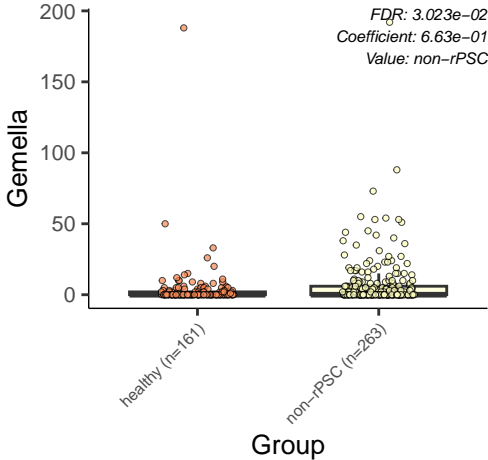
Tannerellaceae



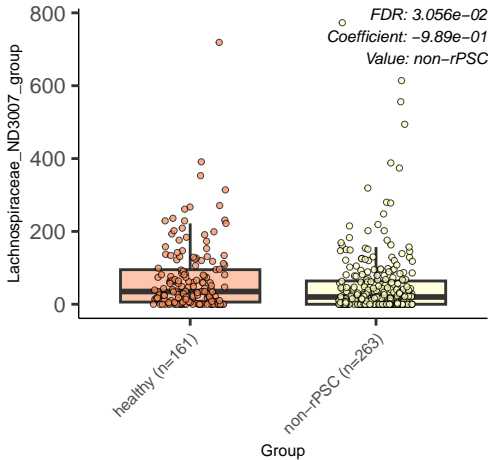


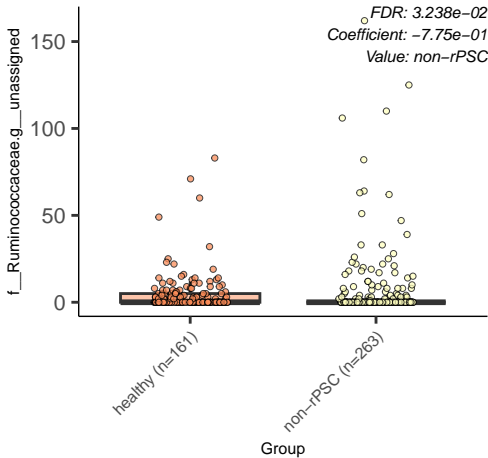
Ruminococcus











UCG.003

1000

500

0

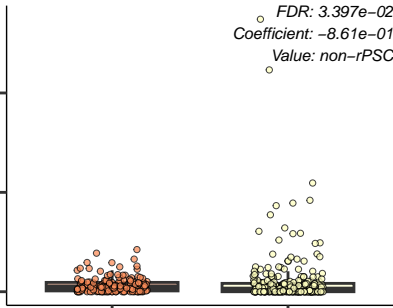
healthy (n=161)

non-rPSC (n=263)

Group

FDR:  $3.397e-02$   
Coefficient:  $-8.61e-01$

Value: non-rPSC



Bacteroides

30000

20000

10000

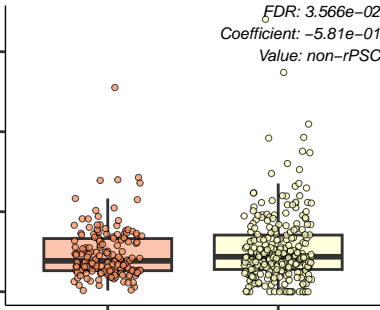
0

healthy (n=161)

non-rPSC (n=263)

Group

FDR:  $3.566e-02$   
Coefficient:  $-5.81e-01$   
Value: non-rPSC



Staphylococcus

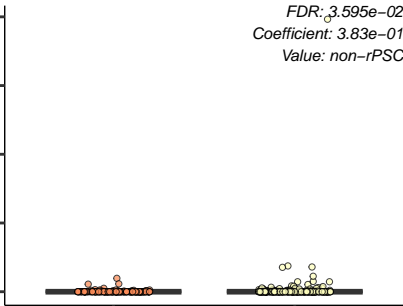
800  
600  
400  
200  
0

*FDR: 3.595e-02*  
*Coefficient: 3.83e-01*  
*Value: non-rPSC*

healthy (n=161)

non-rPSC (n=263)

Group



Ligilactobacillus

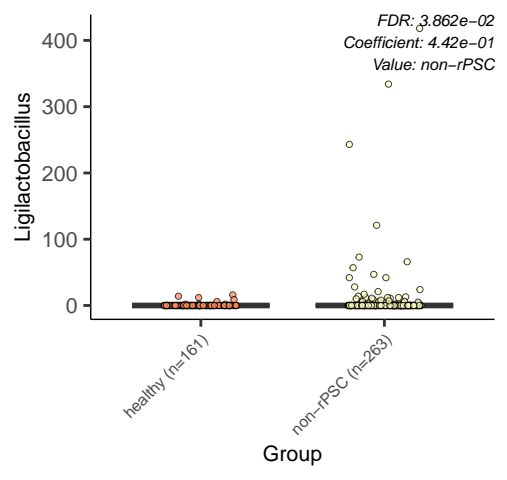
400  
300  
200  
100  
0

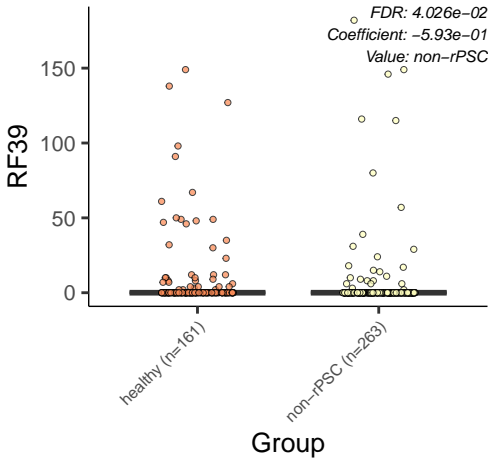
healthy (n=161)

non-rPSC (n=263)

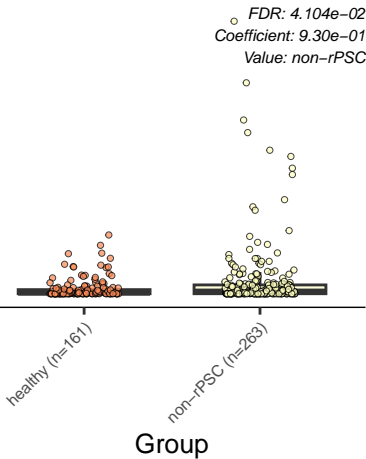
Group

*FDR: 3.862e-02*  
*Coefficient: 4.42e-01*  
*Value: non-rPSC*





Lachnospira





Bilophila

900

600

300

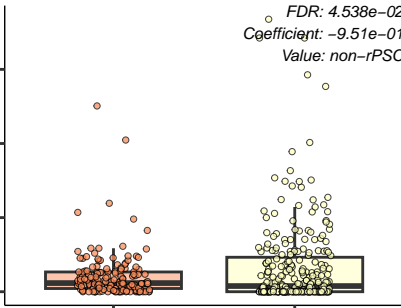
0

healthy (n=161)

non-rPSC (n=263)

Group

FDR:  $4.538e-02$   
Coefficient:  $-9.51e-01$   
Value: non-rPSC



Akkermansia

10000

5000

0

healthy (n=161)

non-rPSC (n=263)

Group

FDR:  $4.552e-02$   
Coefficient:  $-1.30e+00$   
Value: non-rPSC

