

f__Barnesiellaceae

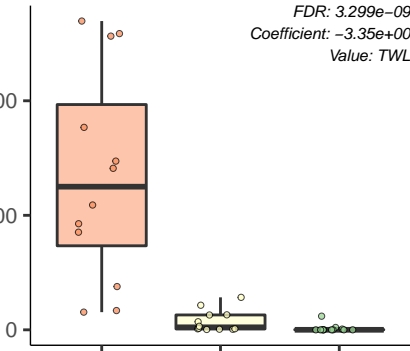
FDR: 3.299e-09
Coefficient: -3.35e+00
Value: TWL

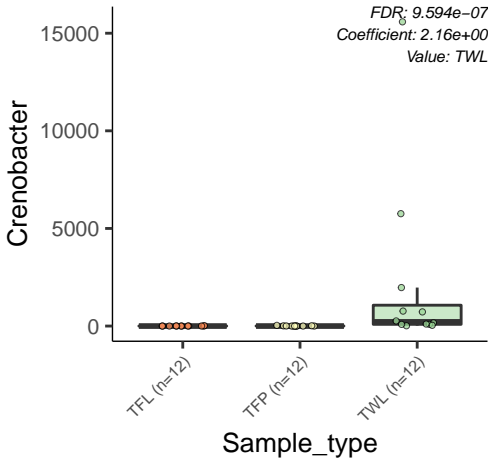
TFL (n=12)

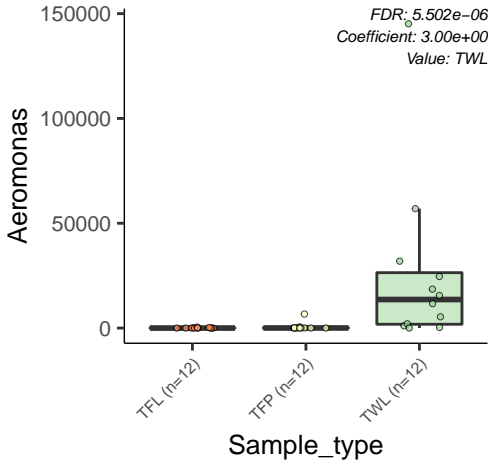
TFP (n=12)

TWL (n=12)

Sample_type







Macellibacteroides

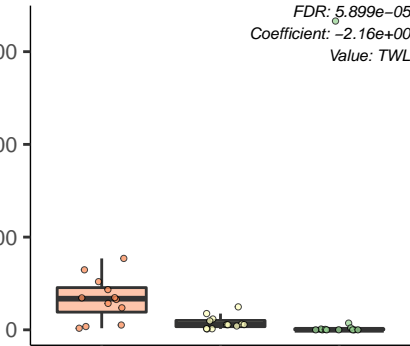
FDR: $5.899\text{e-}05$
Coefficient: $-2.16\text{e}+00$
Value: TWL

TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type



Ruminiclostridium.1

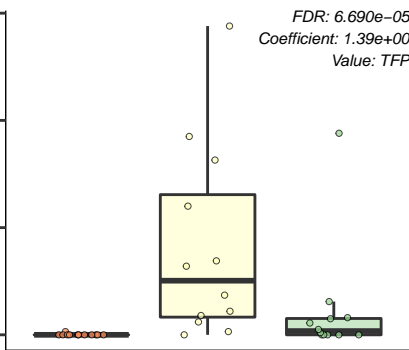
FDR: 6.690e-05
Coefficient: 1.39e+00
Value: TFP

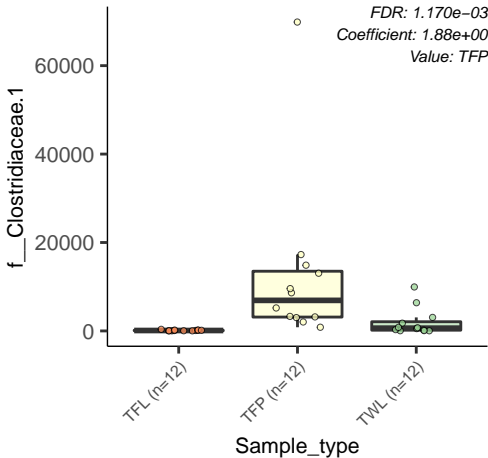
TFL (n=12)

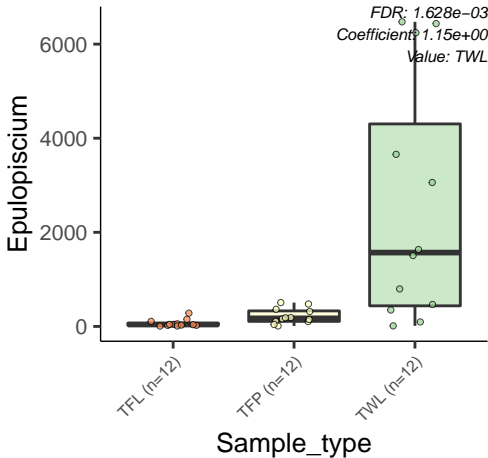
TFP (n=12)

TWL (n=12)

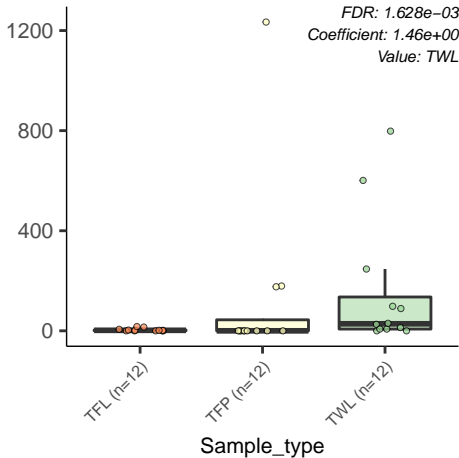
Sample_type

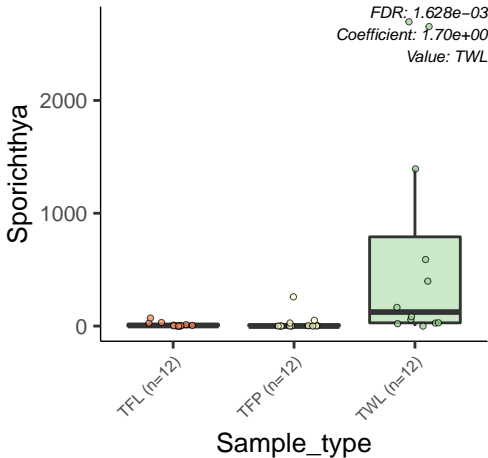


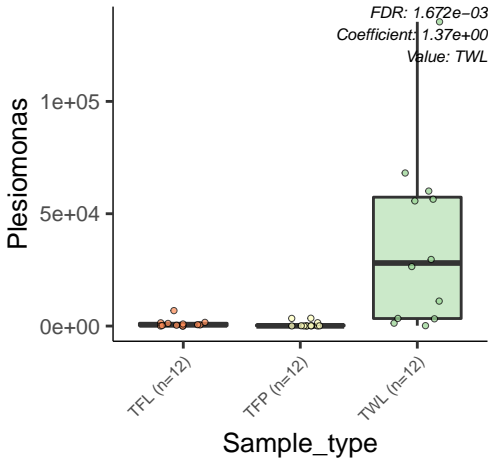


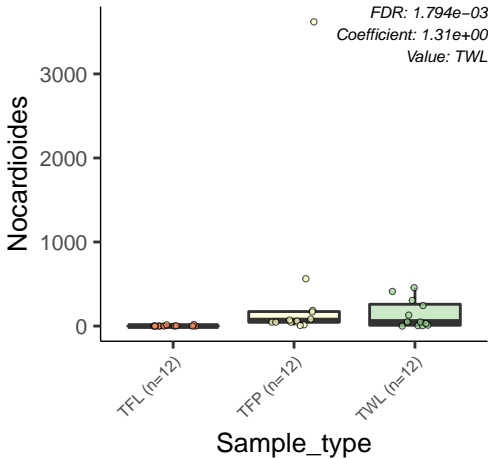


f__Sporichthyaceae









Pir4.lineage

600
400
200
0

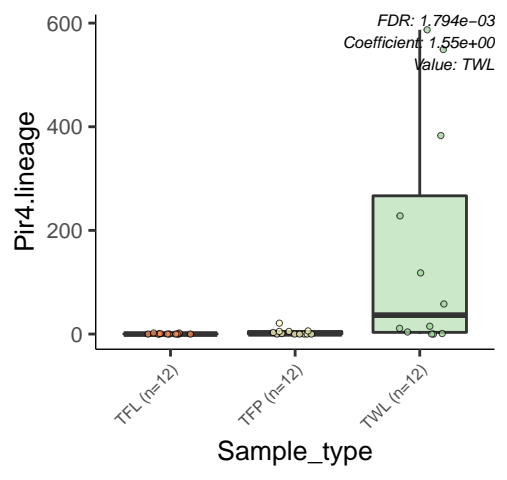
TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type

FDR: 1.794e-03
Coefficient: 1.55e+00
Value: TWL



f__Verrucomicrobiaceae

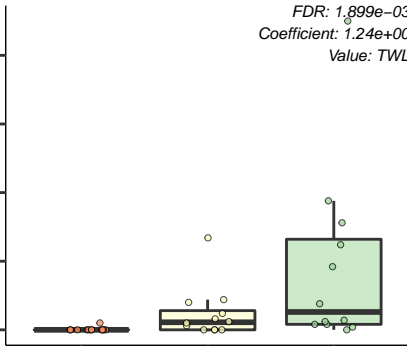
FDR: 1.899e-03
Coefficient: 1.24e+00
Value: TWL

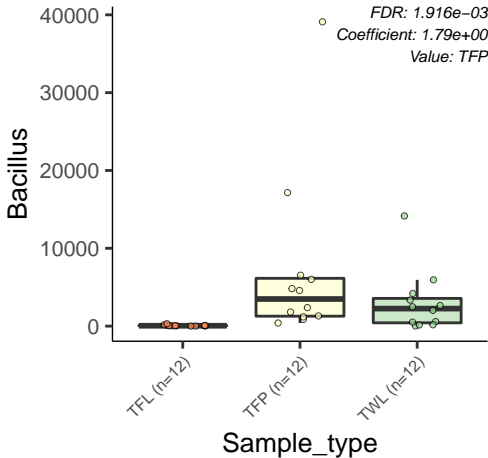
TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type





c_KIST.JJY010

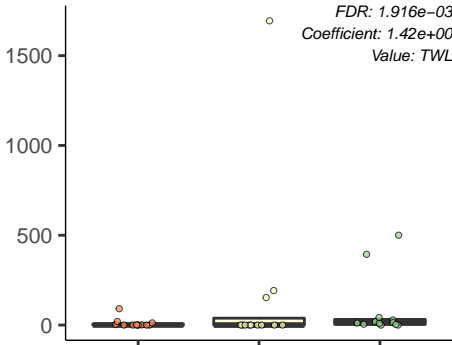
FDR: 1.916e-03
Coefficient: 1.42e+00
Value: TWL

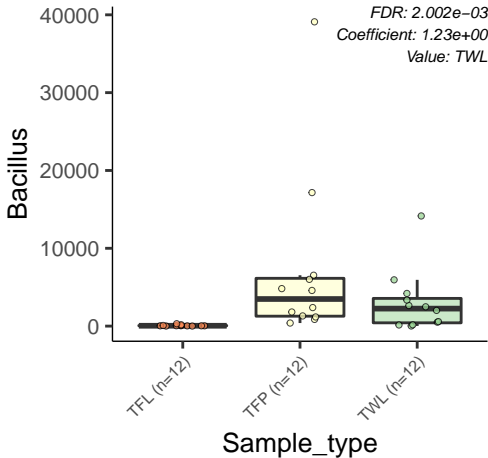
TFL (n=12)

TFP (n=12)

TWL (n=12)

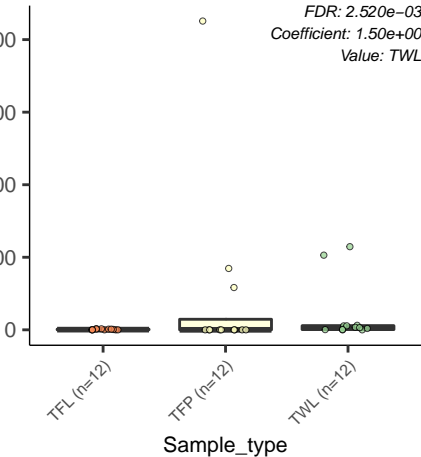
Sample_type

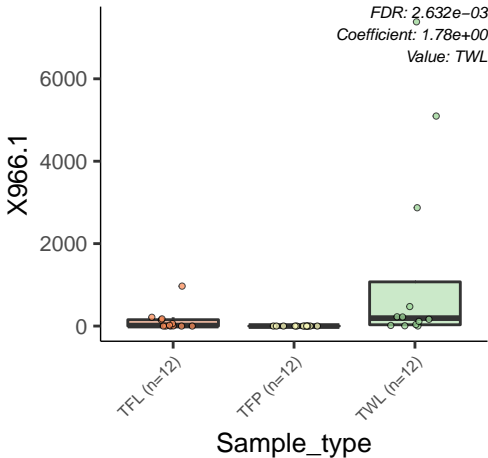




o_Obscurebacteriales

FDR: 2.520e-03
Coefficient: 1.50e+00
Value: TWL





Clostridium.sensu.stricto.5

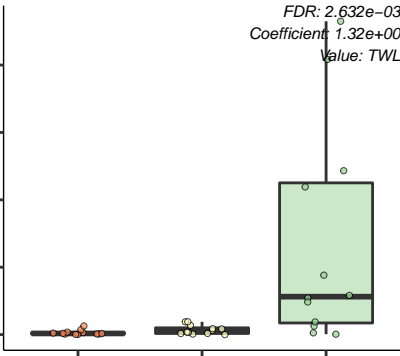
FDR: 2.632e-03
Coefficient: 1.32e+00
Value: TWL

TFL (n=12)

TFP (n=12)

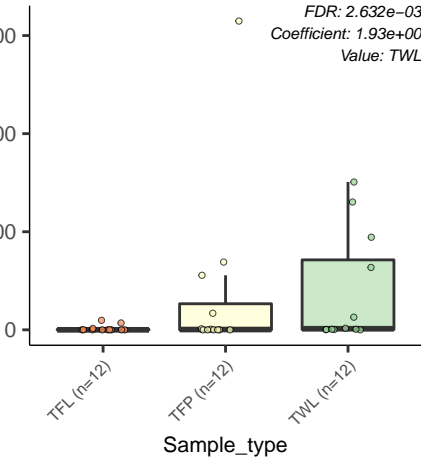
TWL (n=12)

Sample_type



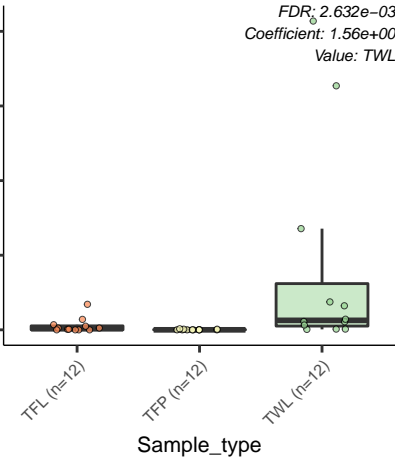
f__Acetobacteraceae

FDR: 2.632e-03
Coefficient: 1.93e+00
Value: TWL



f__Ilumatobacteraceae

FDR: 2.632e-03
Coefficient: 1.56e+00
Value: TWL



o_RBG.13.54.9

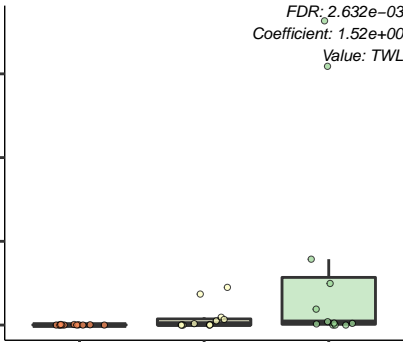
FDR: 2.632e-03
Coefficient: 1.52e+00
Value: TWL

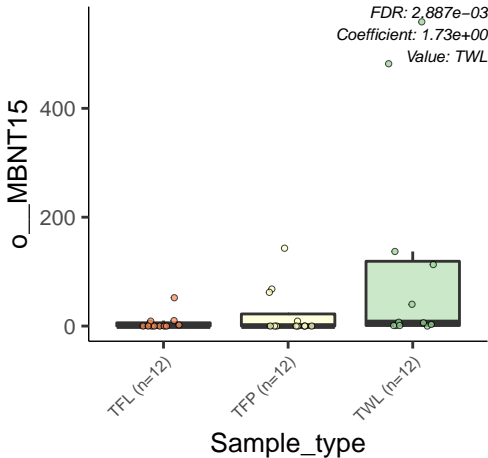
TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type





f_Methyloligellaceae

FDR: 3.195e-03
Coefficient: 1.20e+00
Value: TWL

400

200

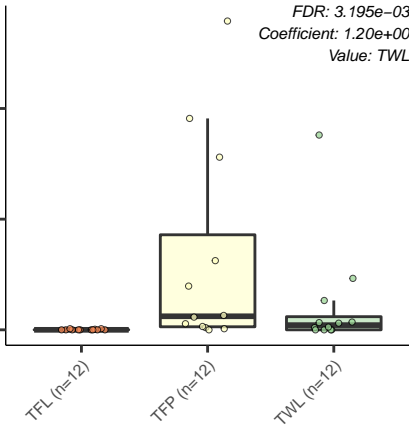
0

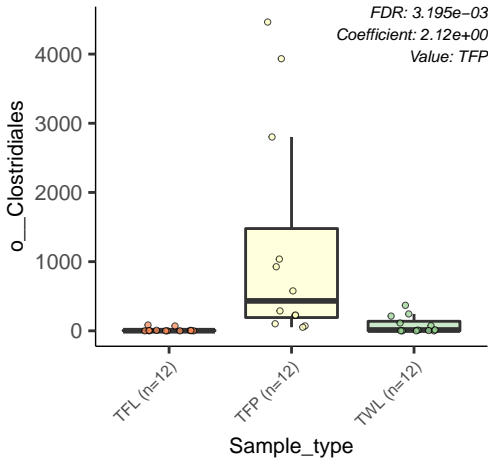
TFL (n=12)

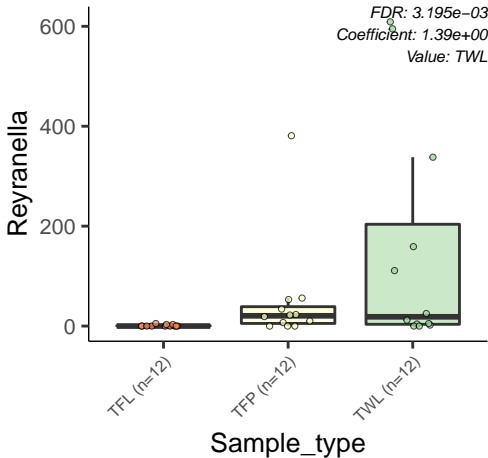
TFP (n=12)

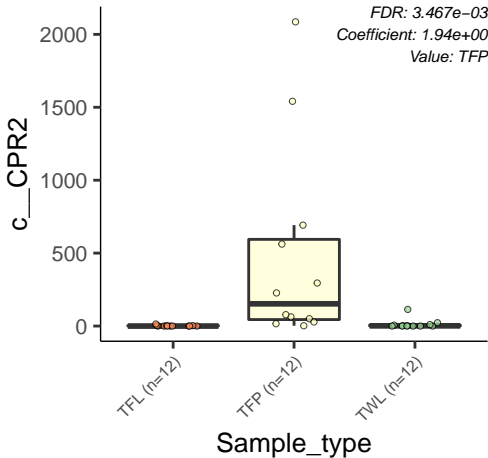
TWL (n=12)

Sample_type









f_Xanthobacteraceae

FDR: 3.467e-03
Coefficient: 1.69e+00
Value: TWL

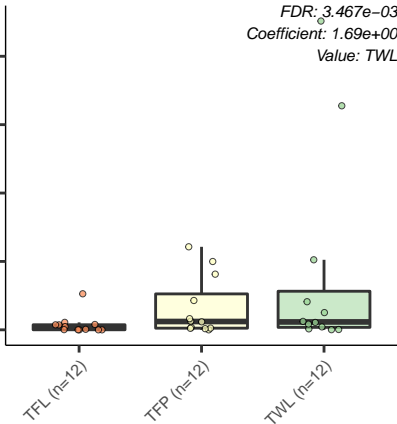
4000
3000
2000
1000
0

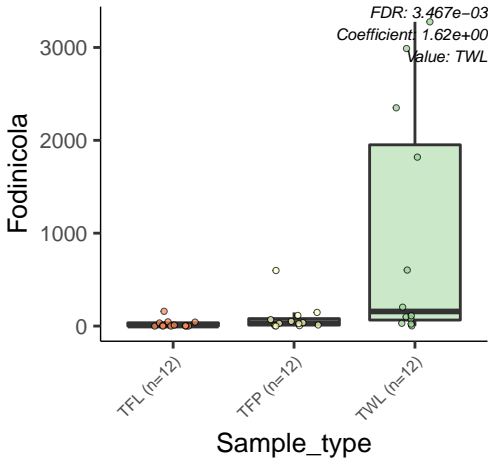
TFL (n=12)

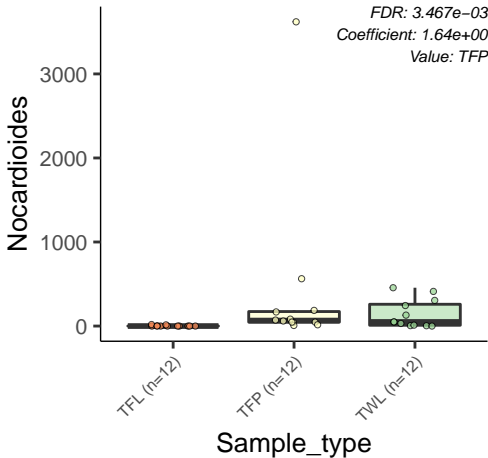
TFP (n=12)

TWL (n=12)

Sample_type







Dechloromonas

20000

15000

10000

5000

0

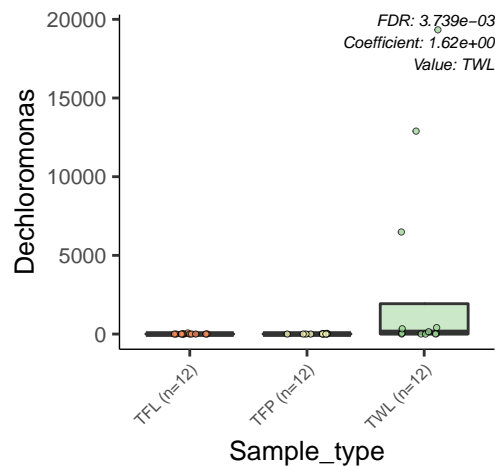
TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type

FDR: 3.739e-03
Coefficient: 1.62e+00
Value: TWL

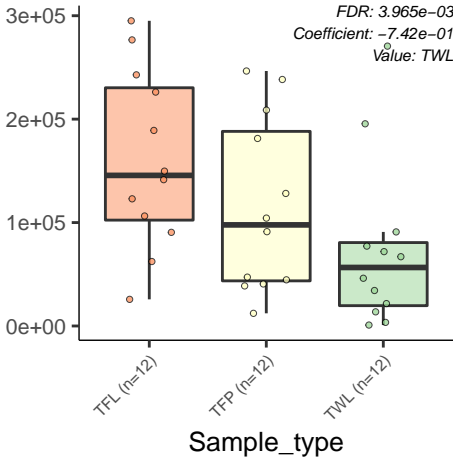


Cetobacterium

FDR: 3.965e-03

Coefficient: -7.42e-01

Value: TWL



Clostridium.sensu.stricto.3

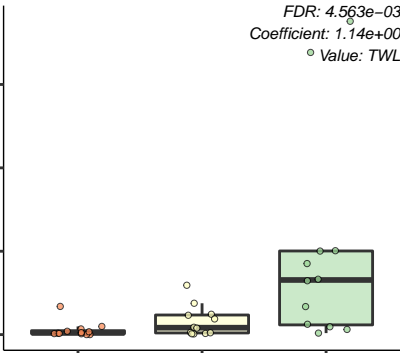
FDR: 4.563e-03
Coefficient: 1.14e+00
● Value: TWL

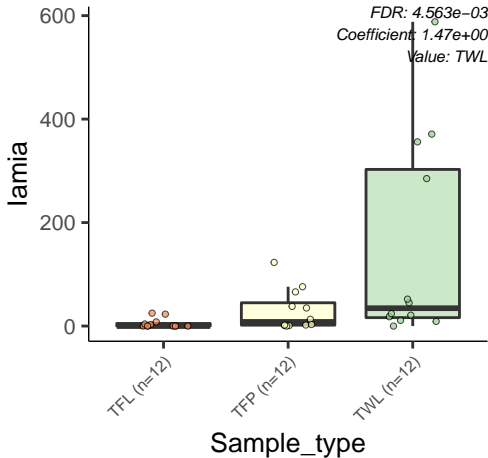
TFL (n=12)

TFP (n=12)

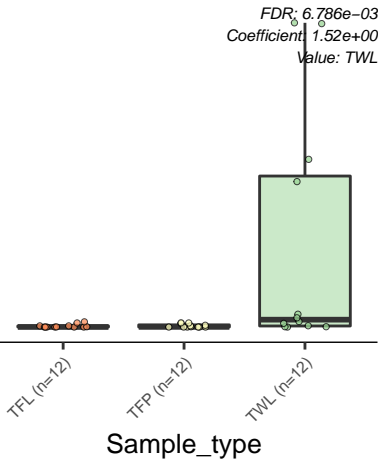
TWL (n=12)

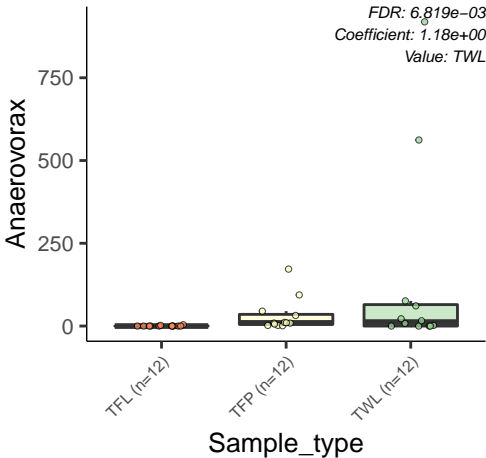
Sample_type





Gaiella





c_Alphaproteobacteria

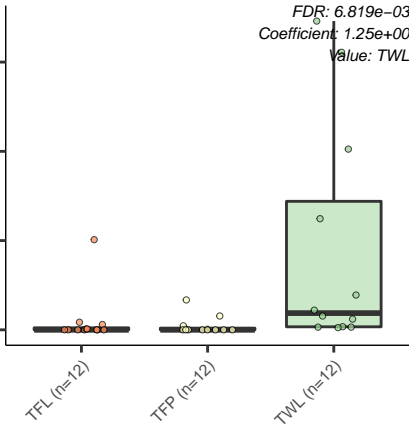
FDR: 6.819e-03
Coefficient: 1.25e+00
Value: TWL

TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type



Anaeromyxobacter

FDR: 6.979e-03
Coefficient: 2.06e+00
Value: TFP

2000

1000

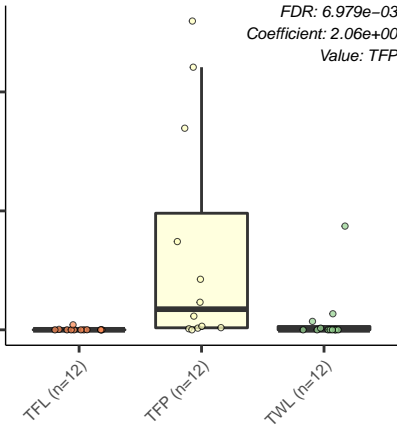
0

TFL (n=12)

TFP (n=12)

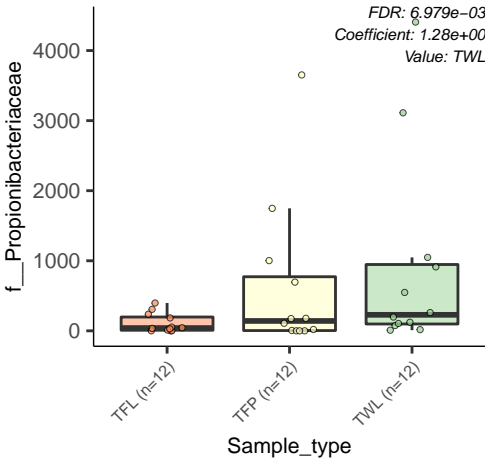
TWL (n=12)

Sample_type



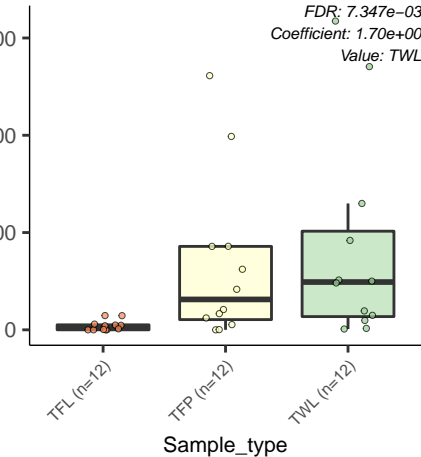
f__Propionibacteriaceae

FDR: $6.979e-03$
Coefficient: $1.28e+00$
Value: TWL



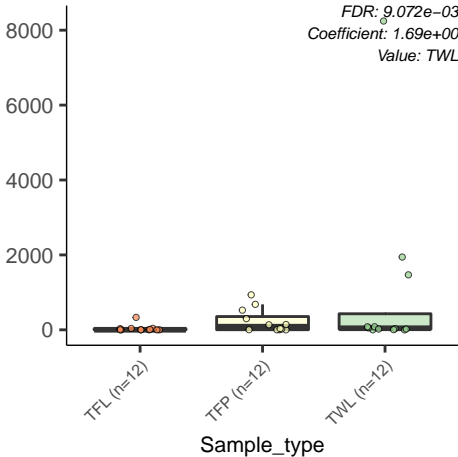
f__Burkholderiaceae

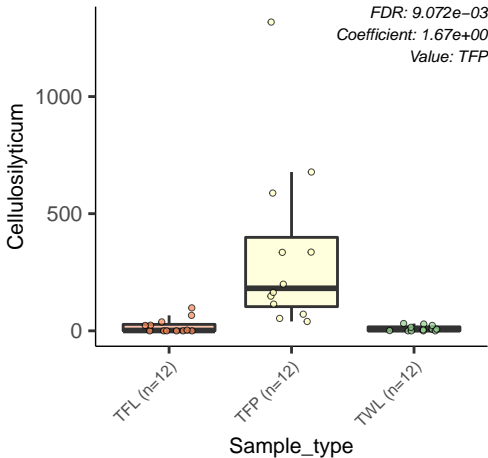
FDR: 7.347e-03
Coefficient: 1.70e+00
Value: TWL



Candidatus.Competibacter

FDR: 9.072e-03
Coefficient: 1.69e+00
Value: TWL





f_Rhodobacteraceae

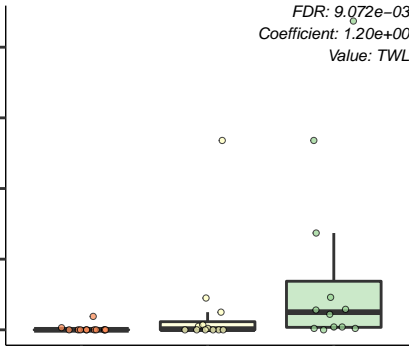
FDR: 9.072e-03
Coefficient: 1.20e+00
Value: TWL

TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type



f__Lachnospiraceae

FDR: 1.002e-02
Coefficient: 1.31e+00
Value: TFP

1000

500

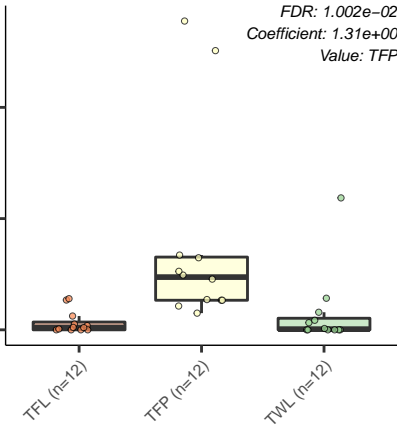
0

TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type



Clostridium_sensu_stricto.11

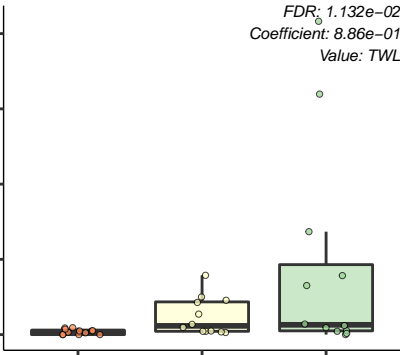
FDR: 1.132e-02
Coefficient: 8.86e-01
Value: TWL

TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type



Fimbriiglobus

600
400
200
0

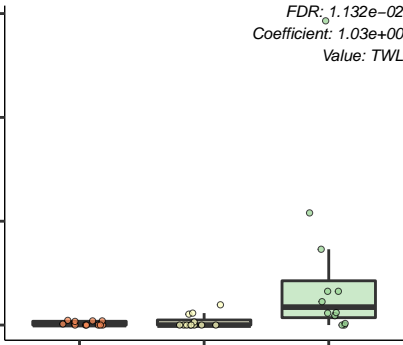
FDR: 1.132e-02
Coefficient: 1.03e+00
Value: TWL

TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type



f_JG30.KF.CM45

FDR: 1.180e-02
Coefficient: 1.22e+00
Value: TWL

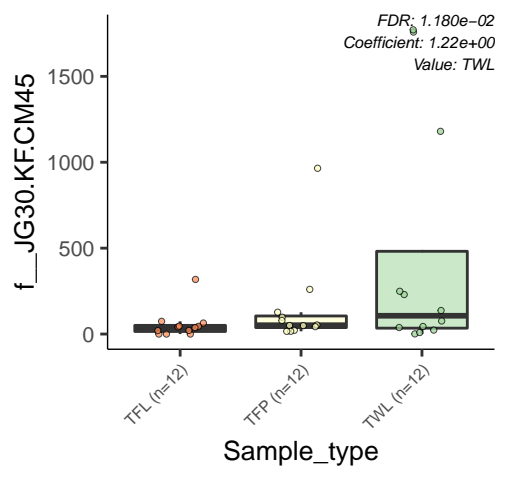
TFL (n=12)

TFP (n=12)

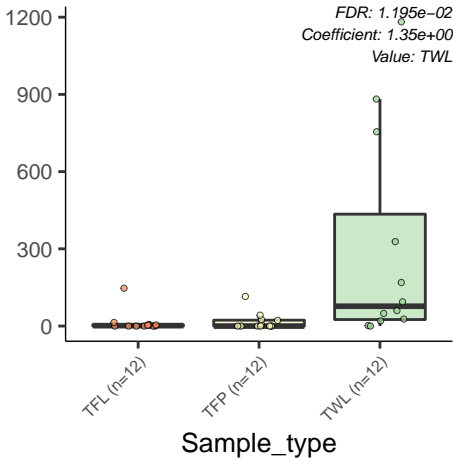
TWL (n=12)

Sample_type

1500
1000
500
0



Blastopirellula



Clostridium.sensu.stricto.1

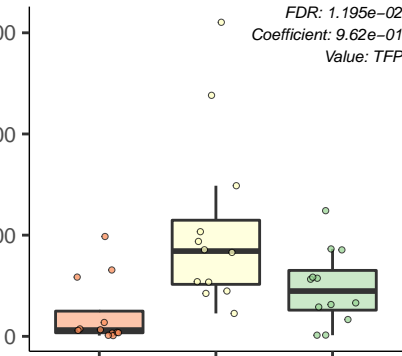
FDR: 1.195e-02
Coefficient: 9.62e-01
Value: TFP

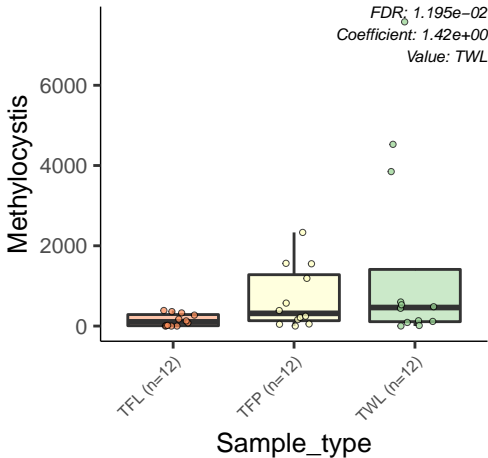
TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type





Methyloparacoccus

FDR: 1.195e-02
Coefficient: 1.95e+00
Value: TFP

6000

4000

2000

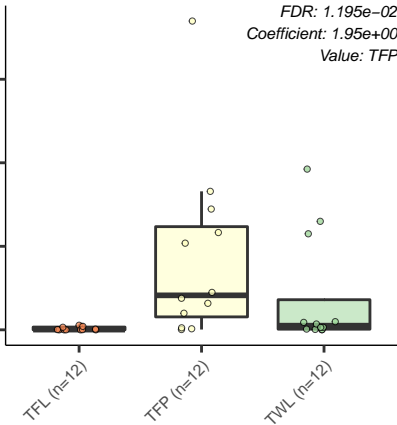
0

TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type



Tyzerella.3

FDR: 1.216e-02
Coefficient: 1.21e+00
Value: TWL

TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type

2000

1500

1000

500

0

f__Barnesiellaceae

FDR: 1.237e-02

Coefficient: -1.56e+00

Value: TFP

40000

20000

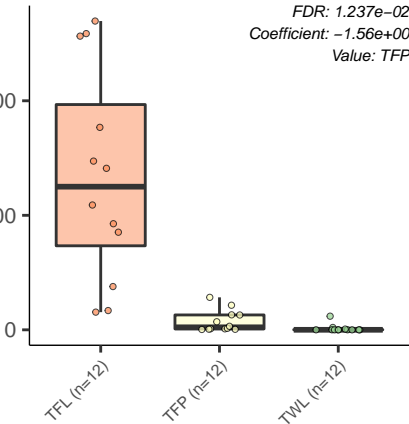
0

TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type



o_Rhizobiales

FDR: 1.237e-02
Coefficient: 1.36e+00
Value: TWL

TFL (n=12)

TFP (n=12)

TWL (n=12)

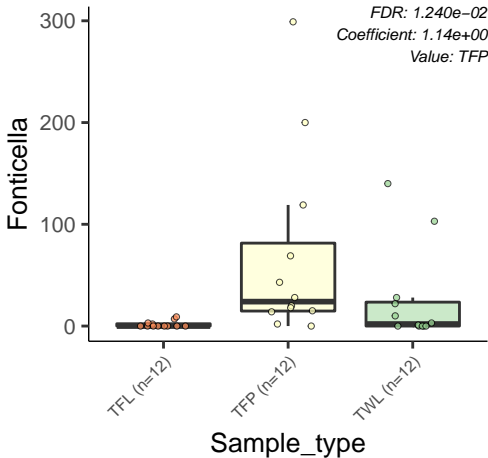
Sample_type

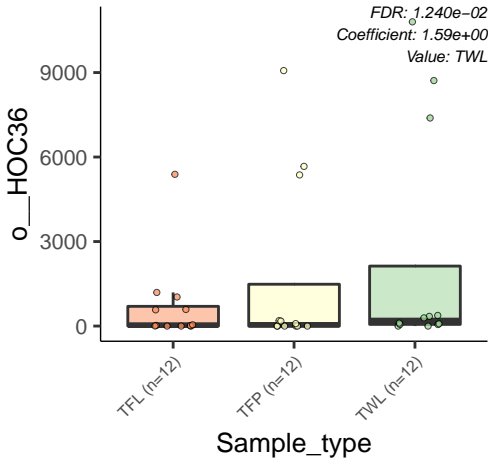
1500

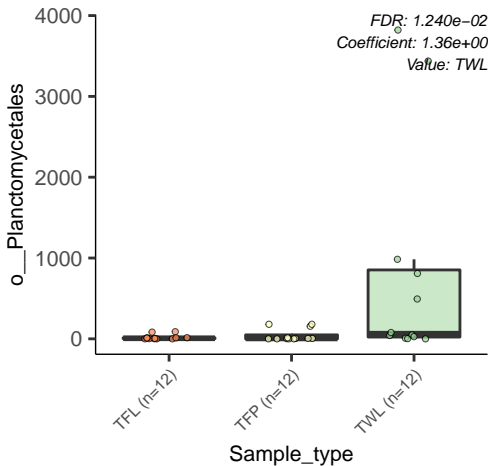
1000

500

0

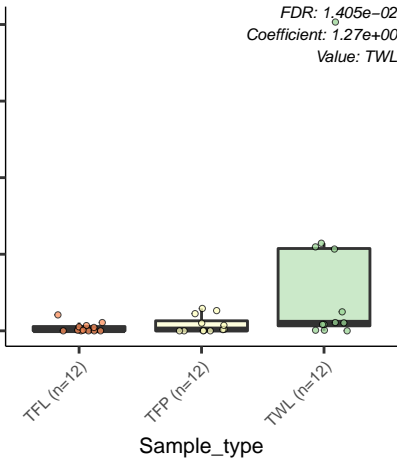






f_Microtrichaceae

FDR: 1.405e-02
Coefficient: 1.27e+00
Value: TWL



f__Desulfarculaceae

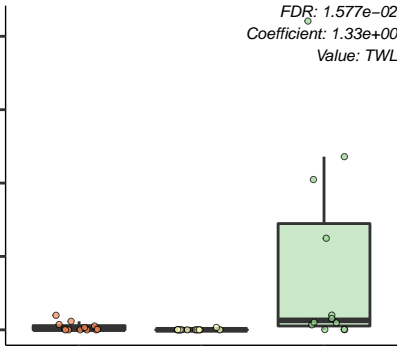
FDR: 1.577e-02
Coefficient: 1.33e+00
Value: TWL

TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type



Hyphomicrobium

FDR: 1.632e-02
Coefficient: 1.34e+00
Value: TWL

1000

500

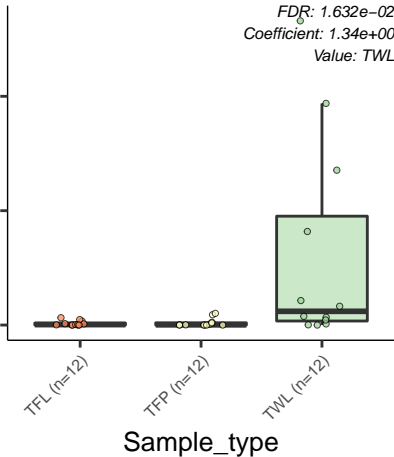
0

TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type



Methylcaldum

FDR: 1.632e-02
Coefficient: 1.46e+00
Value: TWL

TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type

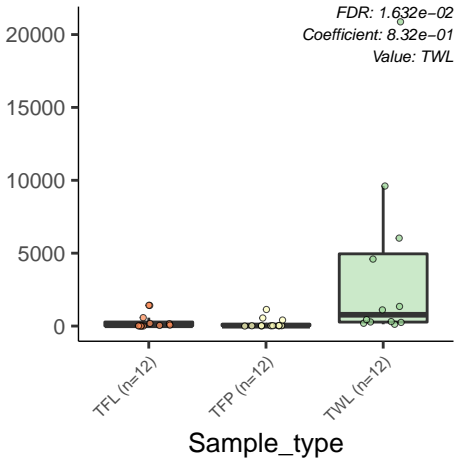
7500

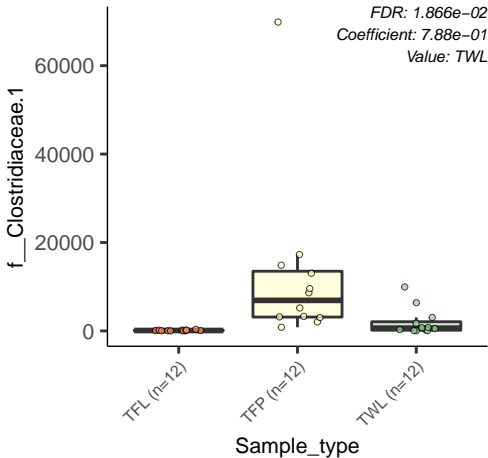
5000

2500

0

Paraclostridium





f__Gemmataceae

FDR: 1.974e-02
Coefficient: 1.22e+00
Value: TWL

4000

2000

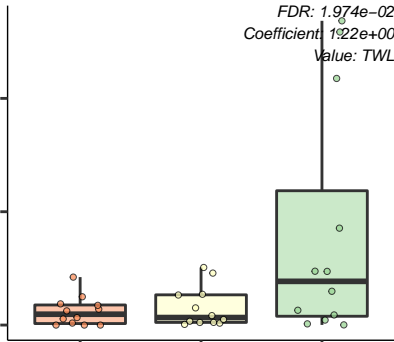
0

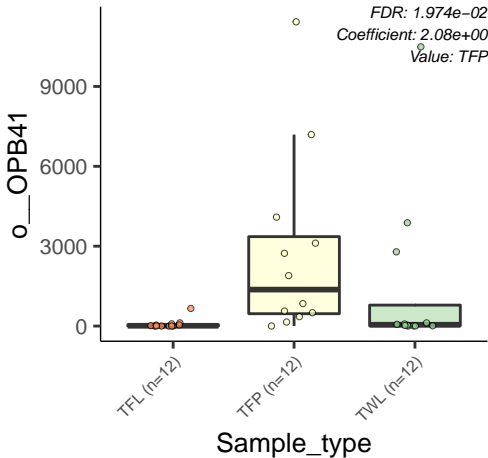
TFL (n=12)

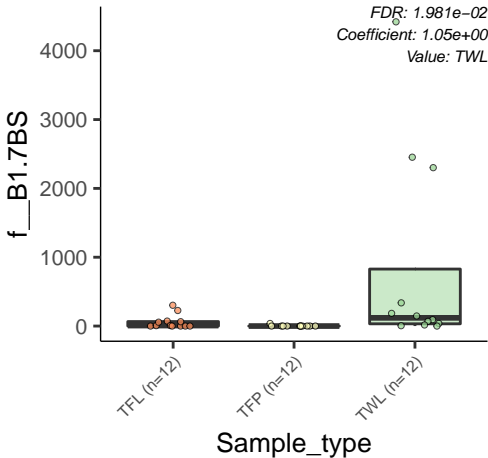
TFP (n=12)

TWL (n=12)

Sample_type







f__Peptostreptococcaceae

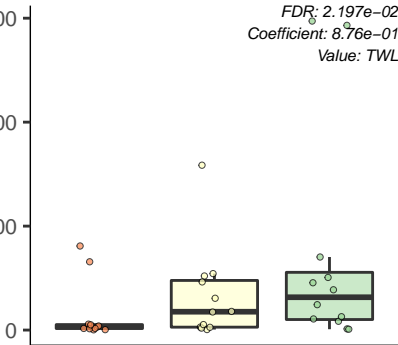
FDR: 2.197e-02
Coefficient: 8.76e-01
Value: TWL

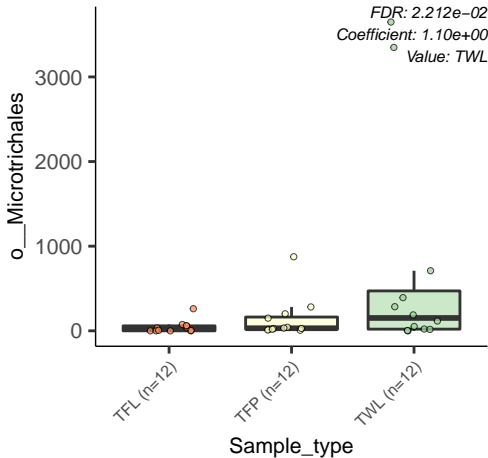
TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type





f_Ruminococcaceae

FDR: 2.284e-02
Coefficient: 1.26e+00
Value: TFP

400

200

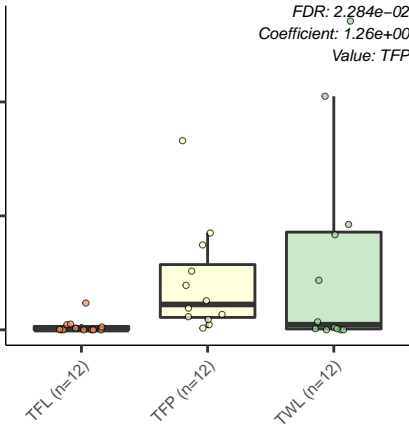
0

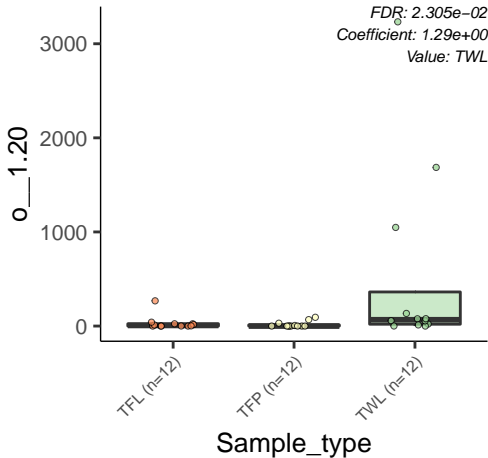
TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type





Methyloparacoccus

FDR: 2.350e-02
Coefficient: 1.26e+00
Value: TWL

6000

4000

2000

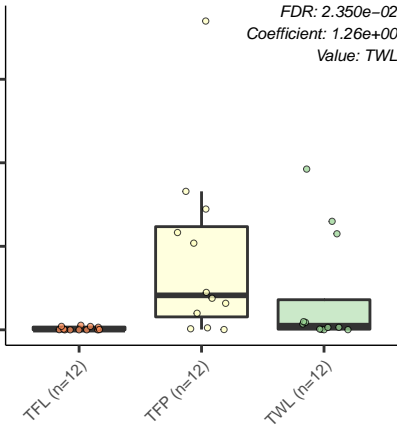
0

TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type



Aquisphaera

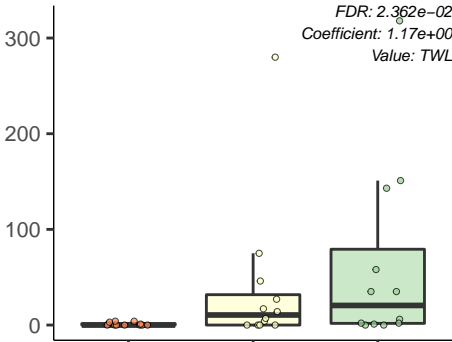
FDR: $2.362e-02$
Coefficient: $1.17e+00$
Value: TWL

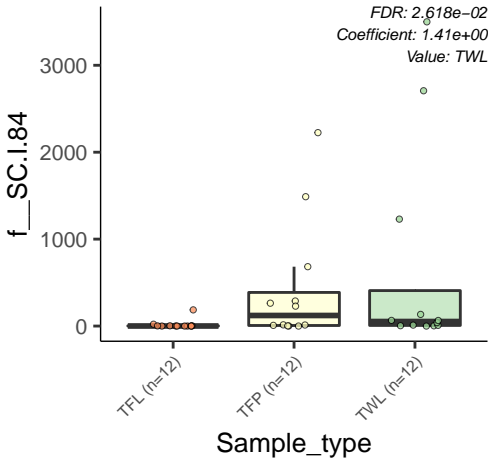
TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type





f_Methyloligellaceae

FDR: 2.669e-02
Coefficient: 1.54e+00
Value: TFP

400

200

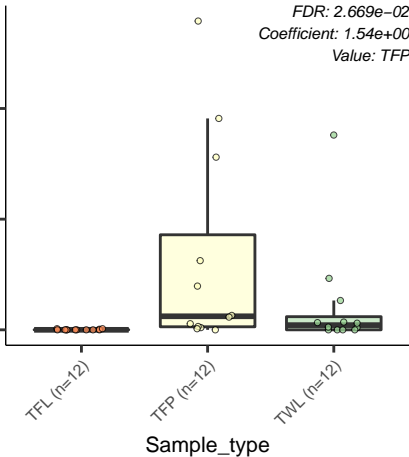
0

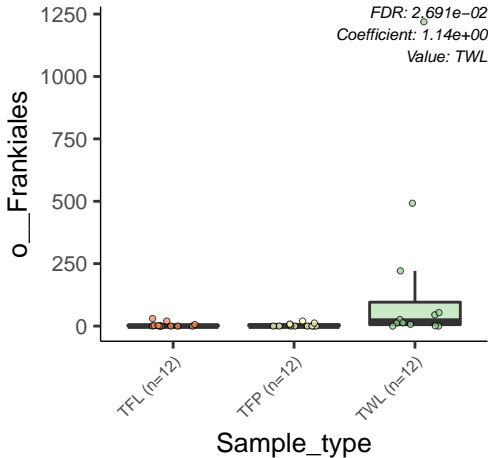
TFL (n=12)

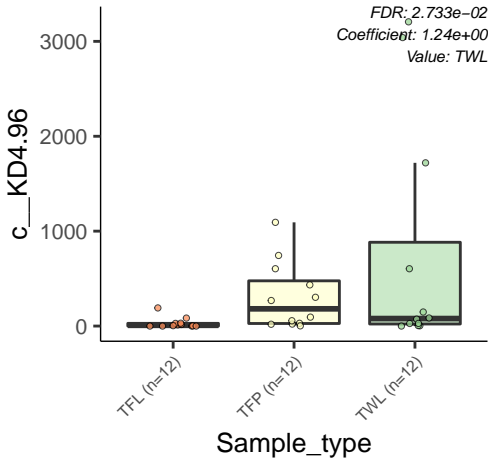
TFP (n=12)

TWL (n=12)

Sample_type







Clostridium.sensu.stricto.13

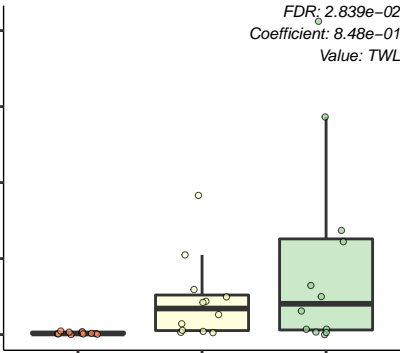
FDR: 2.839e-02
Coefficient: 8.48e-01
Value: TWL

TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type



Hydrogenispora

FDR: 2.839e-02
Coefficient: 1.42e+00
Value: TFP

750

500

250

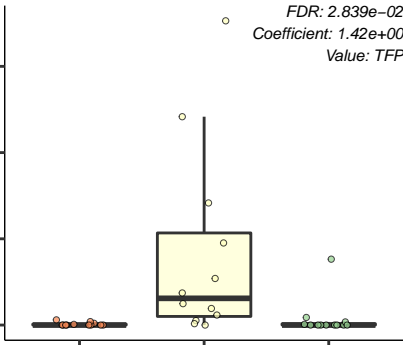
0

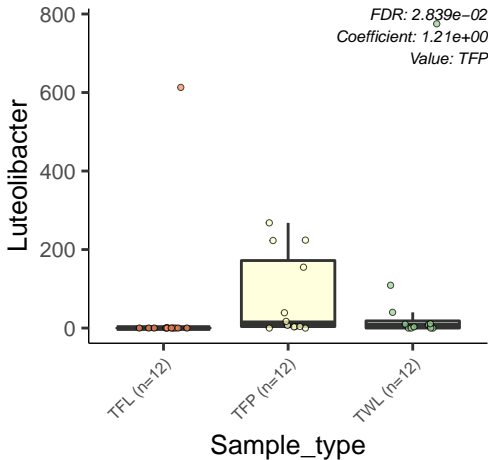
TFL (n=12)

TFP (n=12)

TWL (n=12)

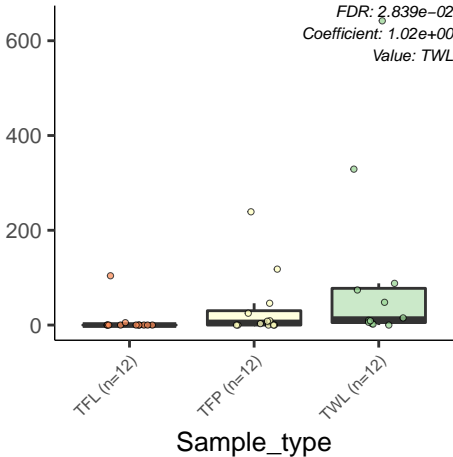
Sample_type





Rhodobacter

FDR: 2.839e-02
Coefficient: 1.02e+00
Value: TWL



Phreatobacter

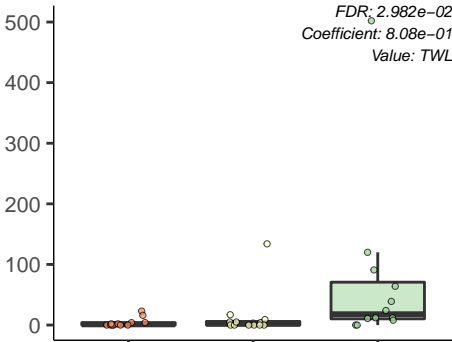
FDR: 2.982e-02
Coefficient: 8.08e-01
Value: TWL

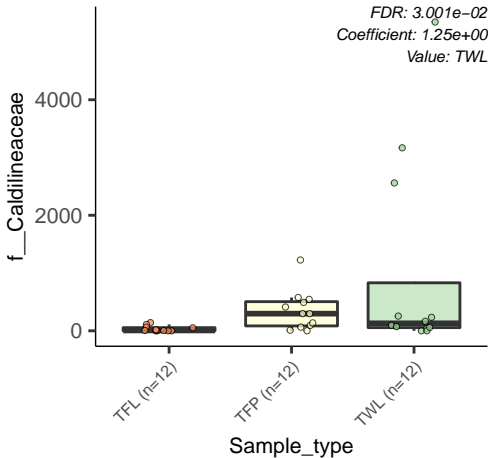
TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type





Conexibacter

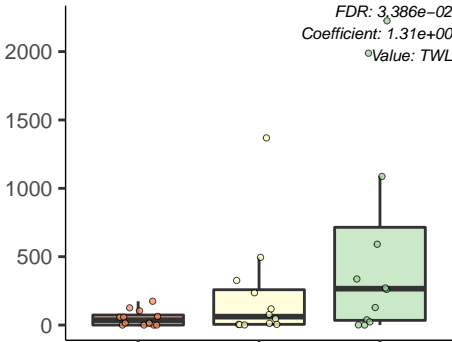
FDR: 3.386e-02
Coefficient: 1.31e+00
● *Value: TWL*

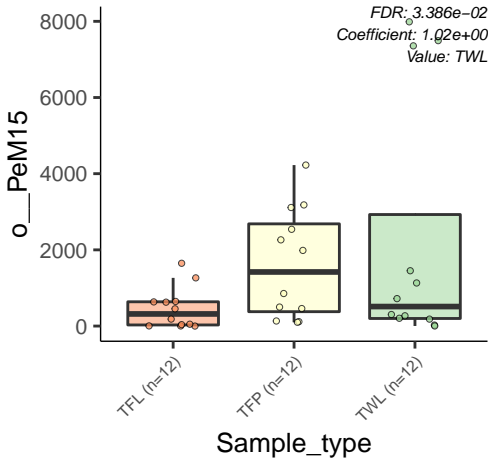
TFL (n=12)

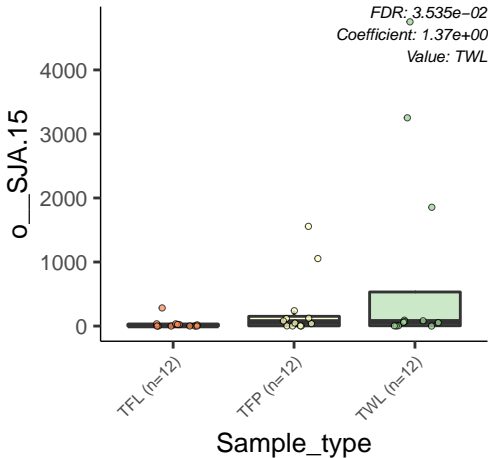
TFP (n=12)

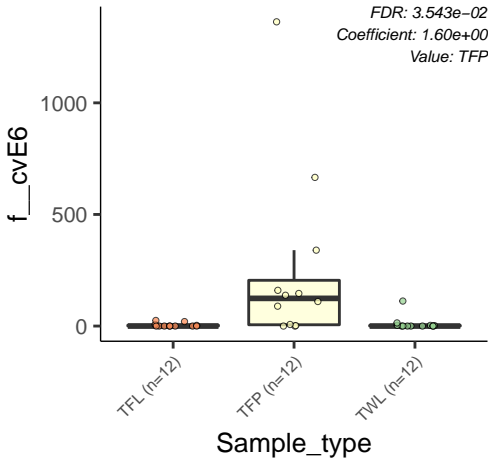
TWL (n=12)

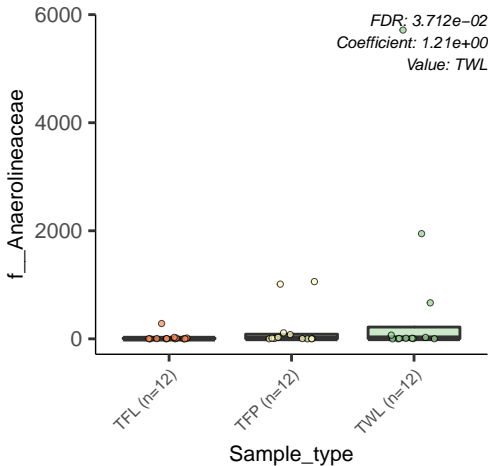
Sample_type

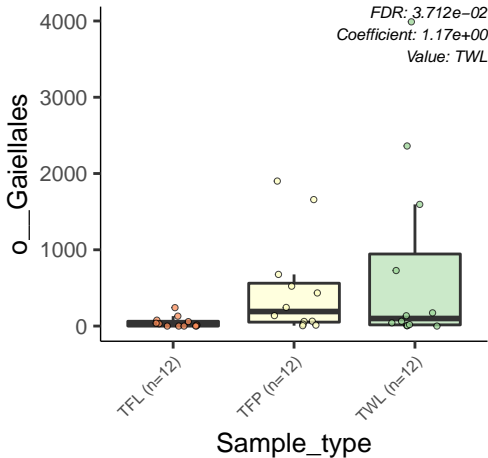


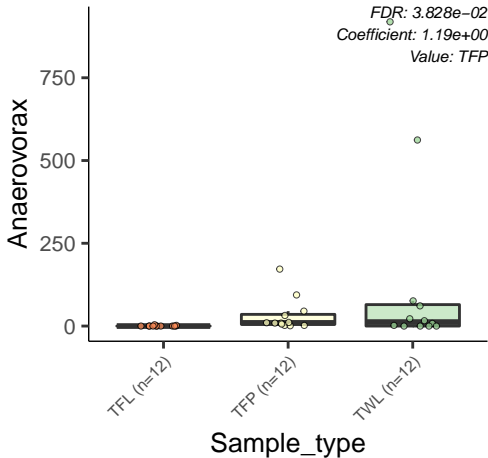


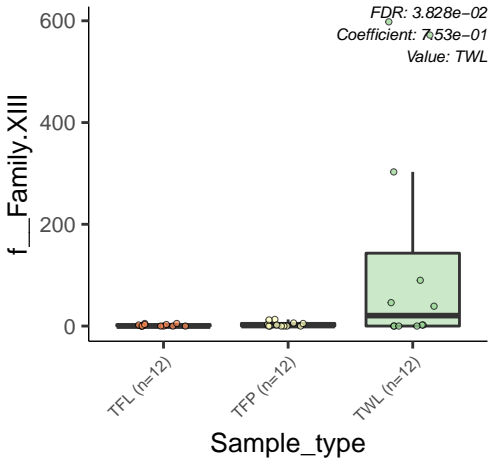


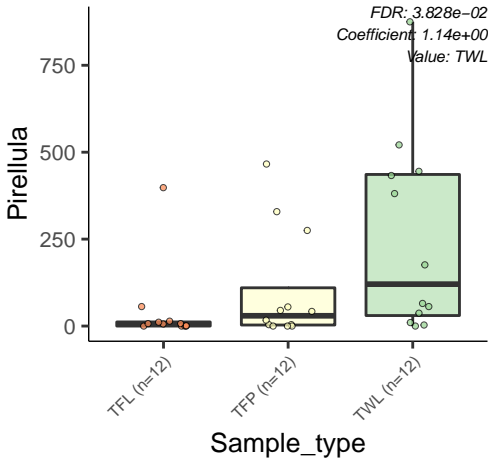


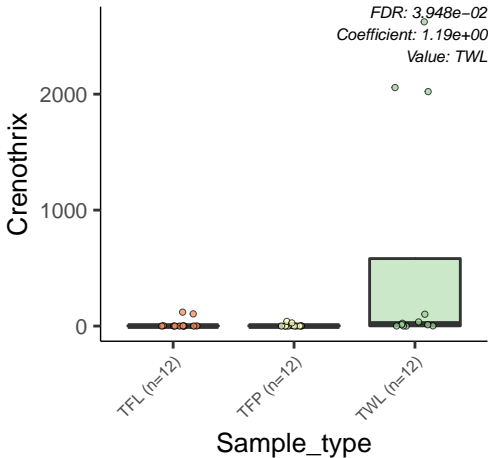












f__Verrucomicrobiaceae

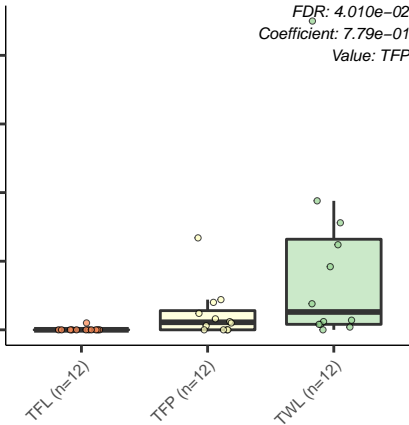
FDR: 4.010e-02
Coefficient: 7.79e-01
Value: TFP

TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type



Clostridium.sensu.stricto.6

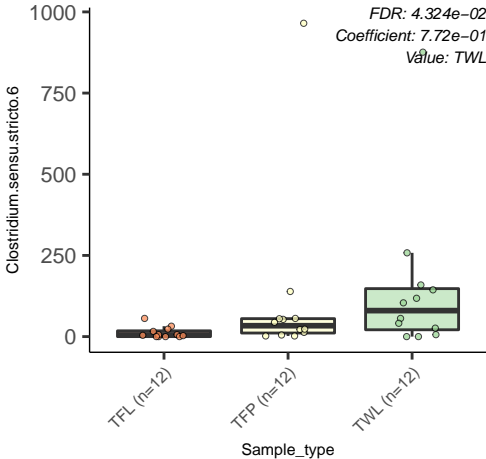
FDR: 4.324e-02
Coefficient: 7.72e-01
Value: TWL

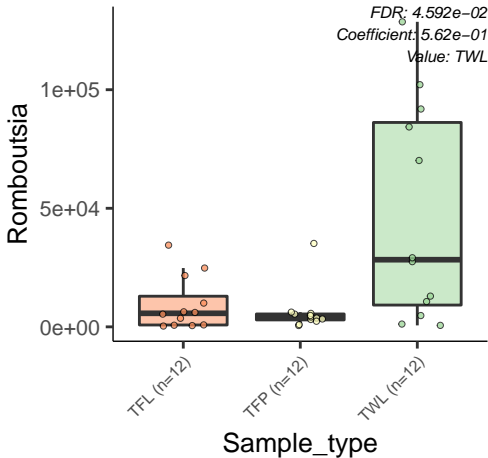
TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type





o_IMCC26256

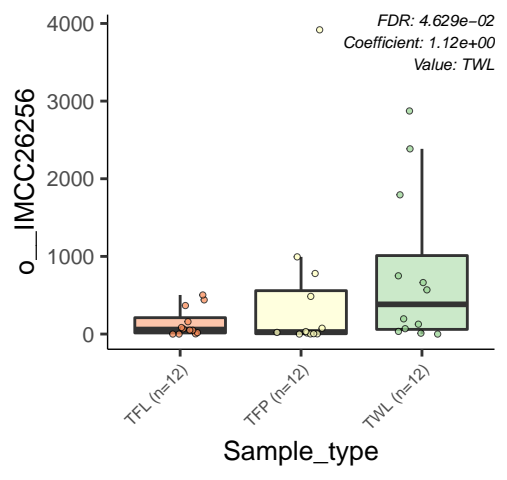
FDR: 4.629e-02
Coefficient: 1.12e+00
Value: TWL

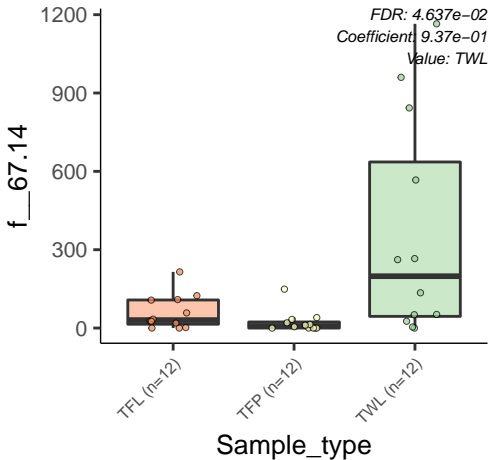
TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type





f_Ruminococcaceae

FDR: 4.675e-02
Coefficient: 8.53e-01
Value: TWL

400

200

0

TFL (n=12)

TFP (n=12)

TWL (n=12)

Sample_type

