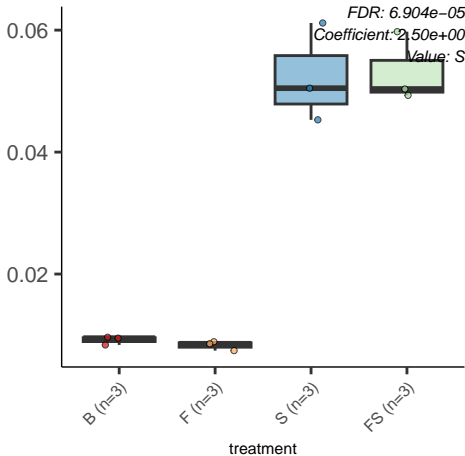
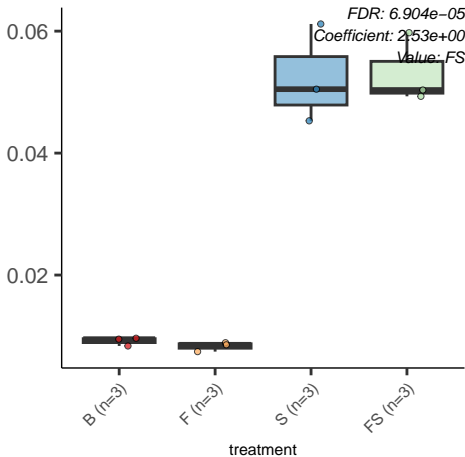


Competence.in.Streptococci



Competence.in.Streptococci



Late.competence

FDR: $6.904e-05$

Coefficient: $2.63e+00$

value: S

0.05

0.04

0.03

0.02

0.01

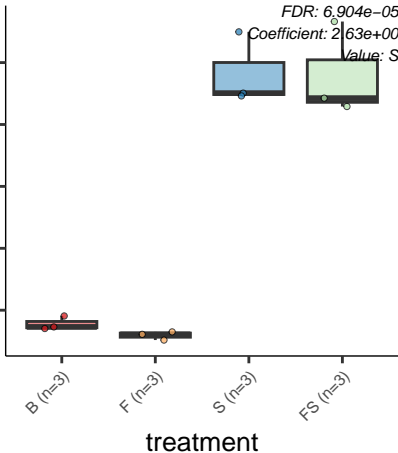
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Late.competence

FDR: 6.904e-05

Coefficient: 2.62e+00

Value: FS

0.05

0.04

0.03

0.02

0.01

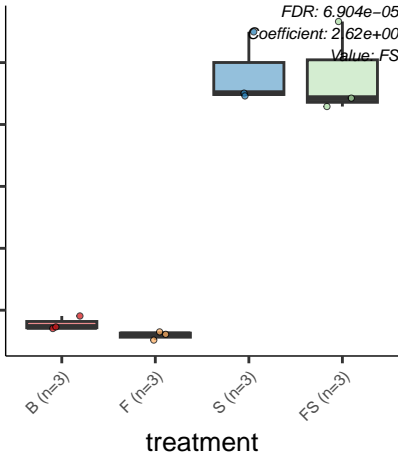
B (n=3)

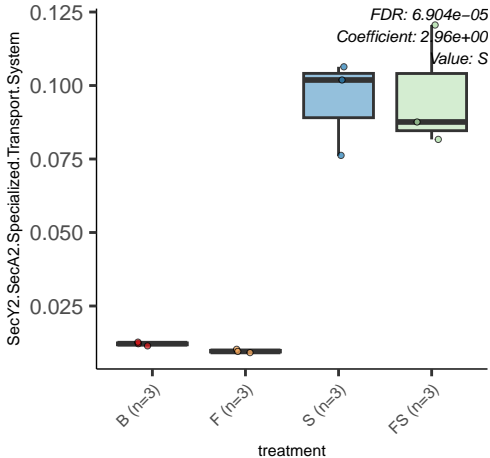
F (n=3)

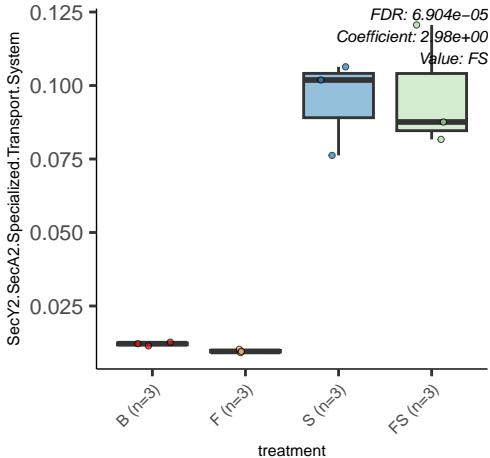
S (n=3)

FS (n=3)

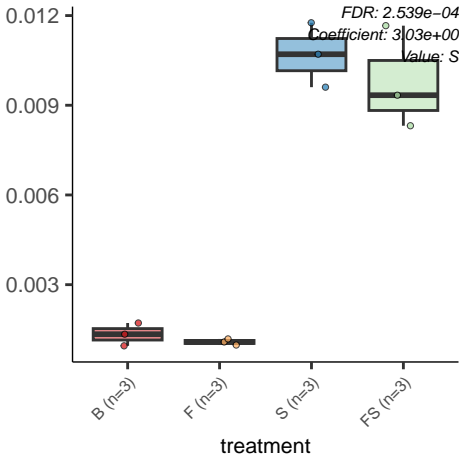
treatment



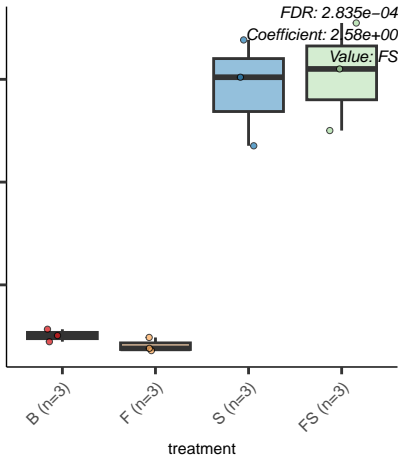




Sucrose.specific.PTS



Beta.lactamase.cluster.in.Streptococcus



Sucrose.specific.PTS

0.012
0.009
0.006
0.003

B (n=3)

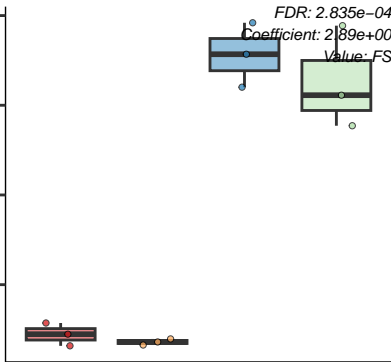
F (n=3)

S (n=3)

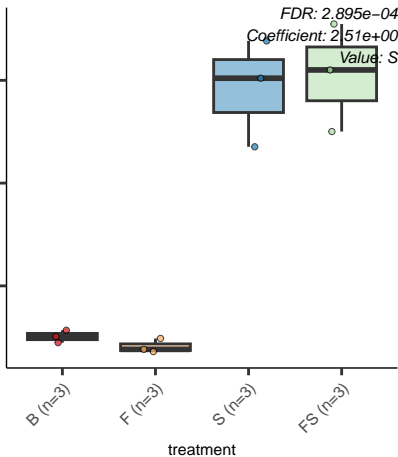
FS (n=3)

treatment

FDR: 2.835e-04
Coefficient: 2.89e+00
Value: FS



Beta.lactamase.cluster.in.Streptococcus



Urea.decomposition

0.05
0.04
0.03
0.02

B (n=3)

F (n=3)

S (n=3)

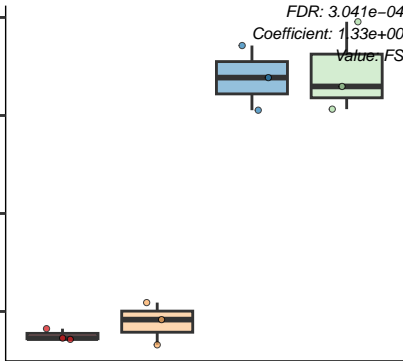
FS (n=3)

treatment

FDR: 3.041e-04

Coefficient: 1.33e+00

Value.FS



Urea.decomposition

0.05
0.04
0.03
0.02

B (n=3)

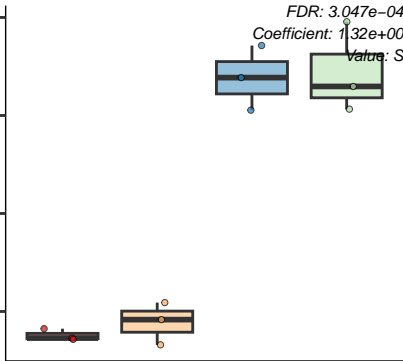
F (n=3)

S (n=3)

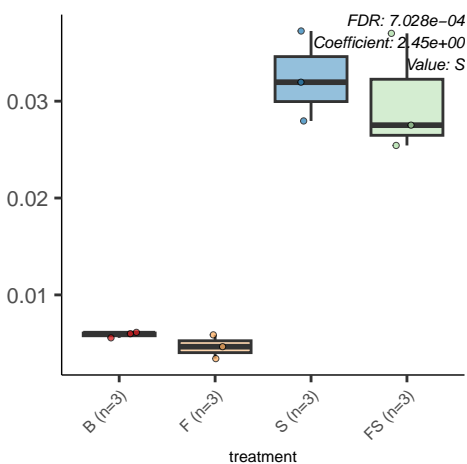
FS (n=3)

treatment

FDR: $3.047e-04$
Coefficient: $1.32e+00$
Value: S



Glutamate.transporter.involved.in.acid.tolerance.in.Streptococcus



Urease.subunits

FDR: 7.730e-04

Coefficient: 1.57e+00

Value: S

0.03

0.02

0.01

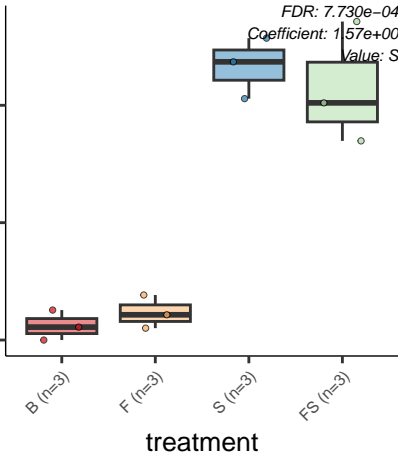
B (n=3)

F (n=3)

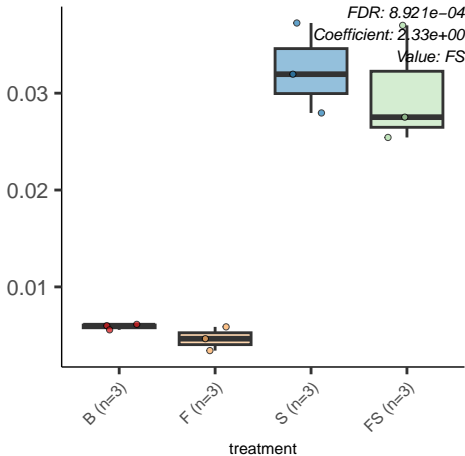
S (n=3)

FS (n=3)

treatment



Glutamate.transporter.involved.in.acid.tolerance.in.Streptococcus



Gram.Positive.Competence

0.06

0.04

0.02

B (n=3)

F (n=3)

S (n=3)

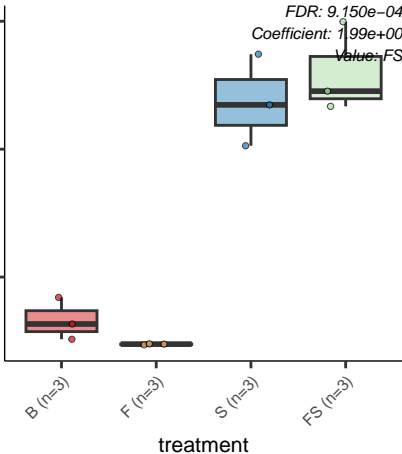
FS (n=3)

treatment

FDR: 9.150e-04

Coefficient: 1.99e+00

Value: FS



Urease.subunits

FDR: 1.013e-03
Coefficient: 1.48e+00
Value: FS

0.03

0.02

0.01

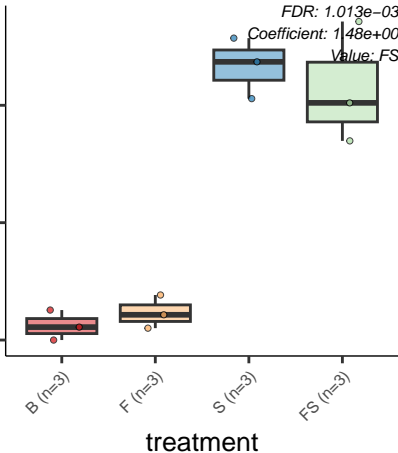
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Gram.Positive.Competence

0.06

0.04

0.02

B (n=3)

F (n=3)

S (n=3)

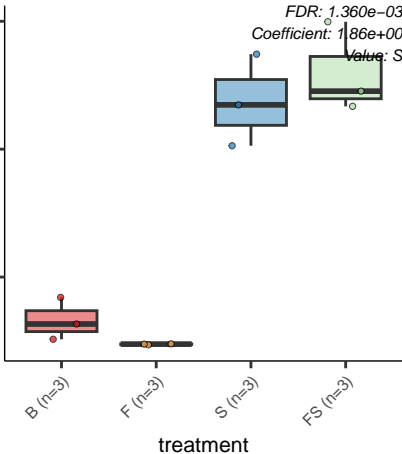
FS (n=3)

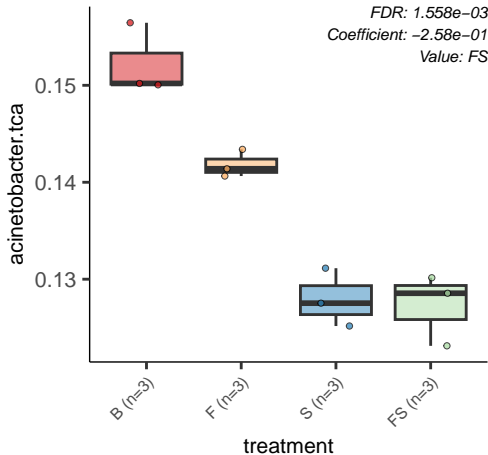
treatment

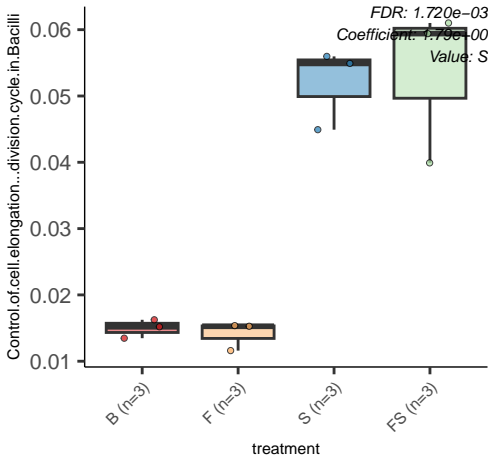
FDR: 1.360e-03

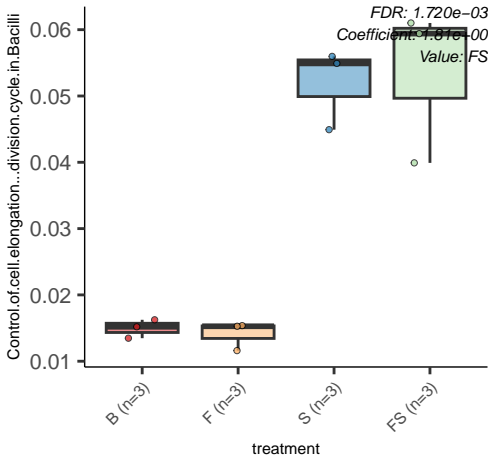
Coefficient: 1.86e+00

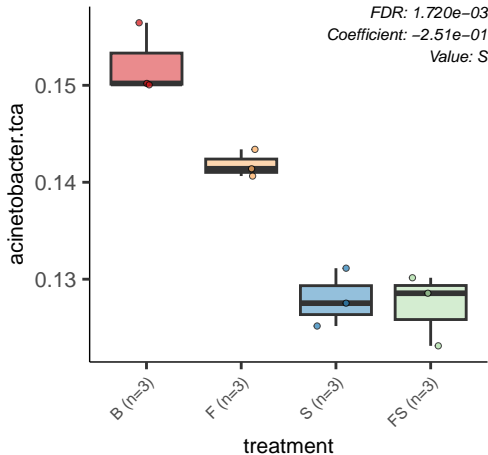
Value: S



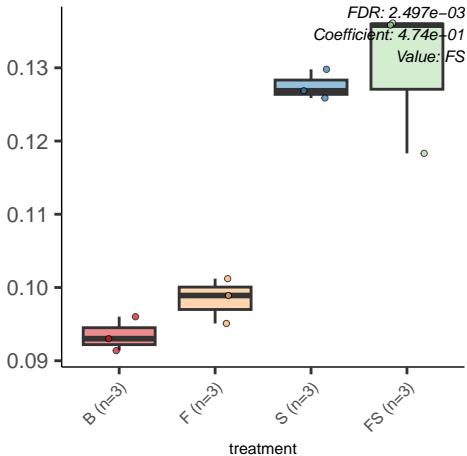








n, positive.cluster.that.relates.ribosomal.protein.L28P.to.a.set.of.unch



Archaeal.lipids

0.030

0.025

0.020

0.015

0.010

B (n=3)

F (n=3)

S (n=3)

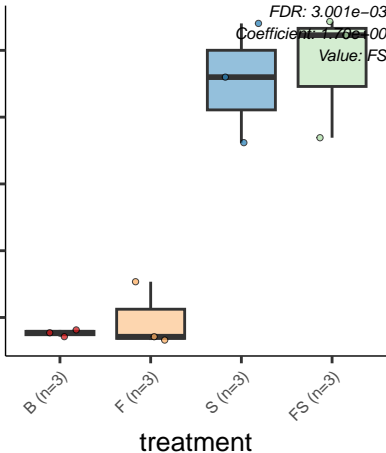
FS (n=3)

treatment

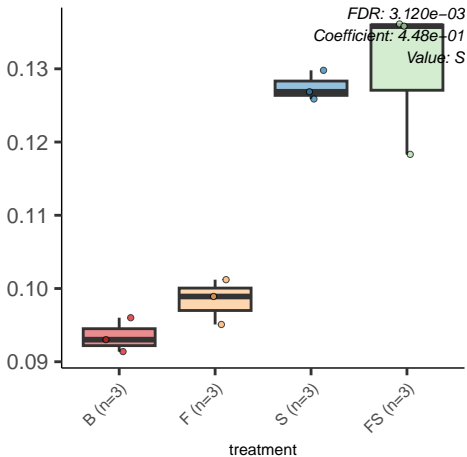
FDR: $3.001e-03$

Coefficient: $1.70e+00$

Value: FS



n, positive.cluster.that.relates.ribosomal.protein.L28P.to.a.set.of.unch



HtrA.and.Sec.secretion

0.05

0.04

0.03

0.02

B (n=3)

F (n=3)

S (n=3)

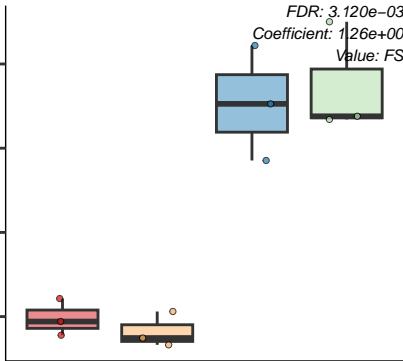
FS (n=3)

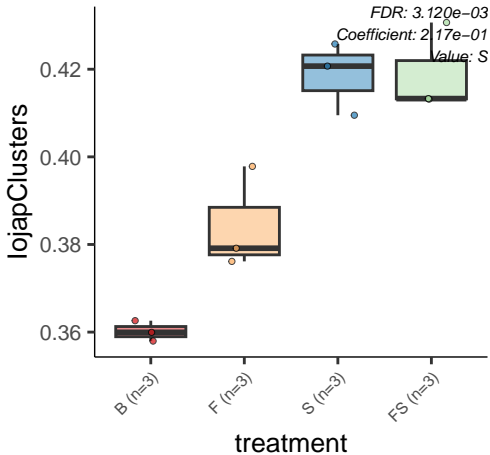
treatment

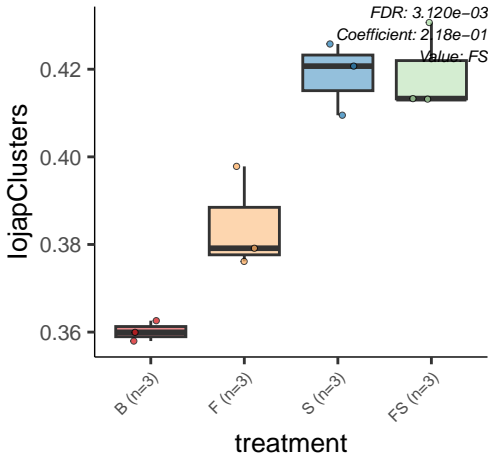
FDR: 3.120e-03

Coefficient: 1.26e+00

Value: FS







Archaeal.lipids

FDR: $3.167e-03$

Coefficient: $1.64e+00$

Value: S

0.030

0.025

0.020

0.015

0.010

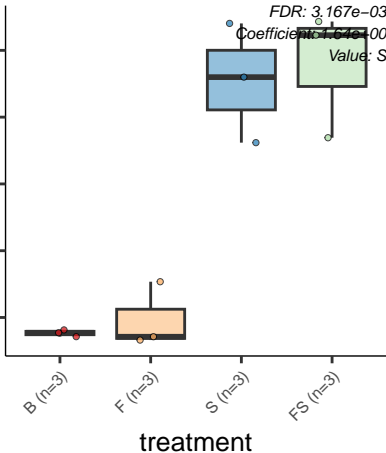
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



CBSS.262719.3.peg.410

FDR: 3.167e-03

Coefficient: 4.18e-01

Value: S

0.13
0.12
0.11
0.10

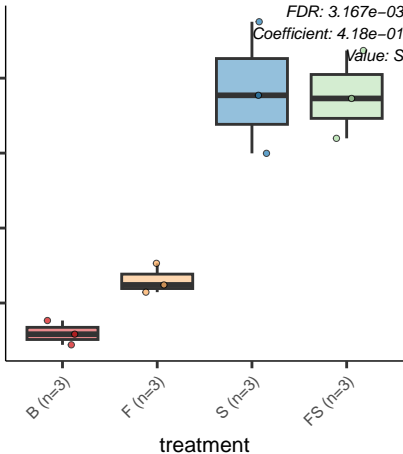
B (n=3)

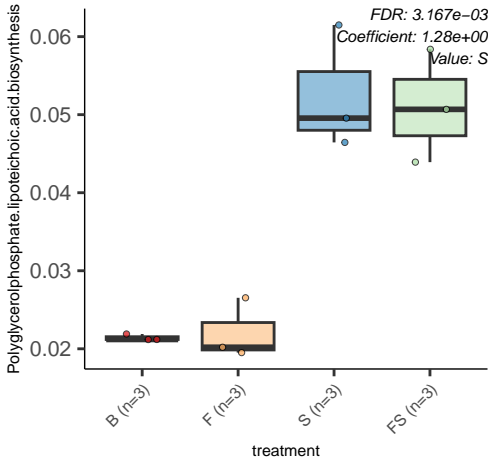
F (n=3)

S (n=3)

FS (n=3)

treatment





CBSS.262719.3.peg.410

FDR: 3.402e-03
Coefficient: 4.11e-01
Value: FS

0.13
0.12
0.11
0.10

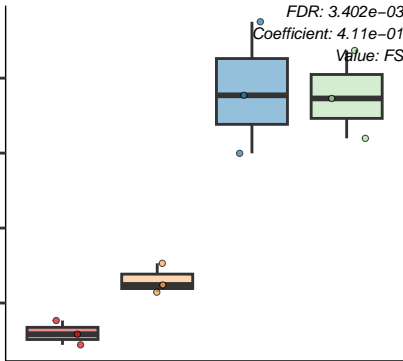
B (n=3)

F (n=3)

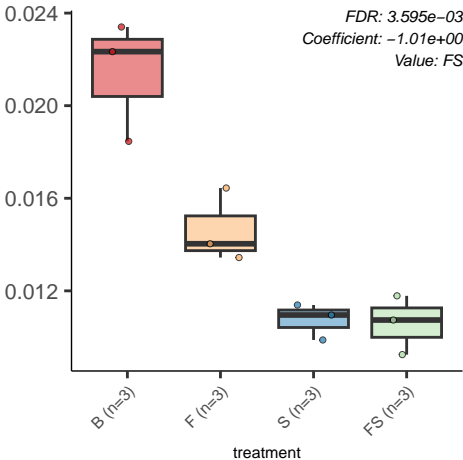
S (n=3)

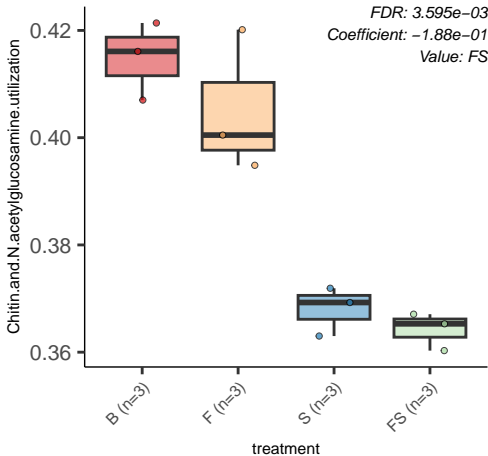
FS (n=3)

treatment



Capsular.surface.virulence.antigen.loci





HtrA.and.Sec.secretion

0.05

0.04

0.03

0.02

B (n=3)

F (n=3)

S (n=3)

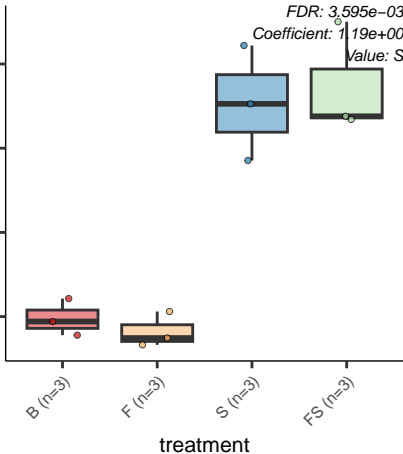
FS (n=3)

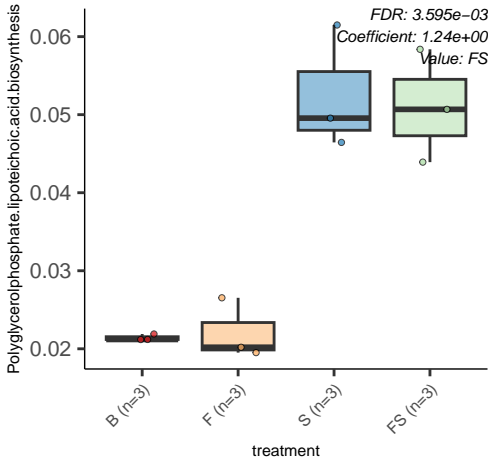
treatment

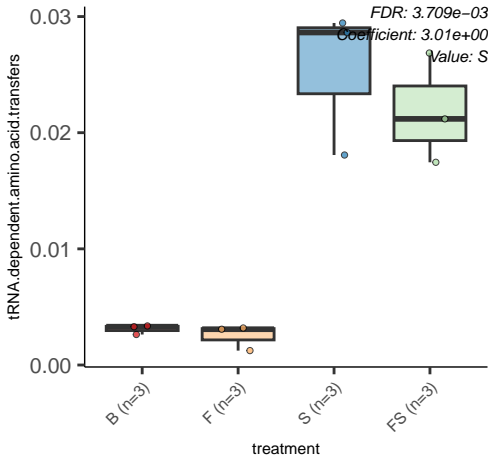
FDR: 3.595e-03

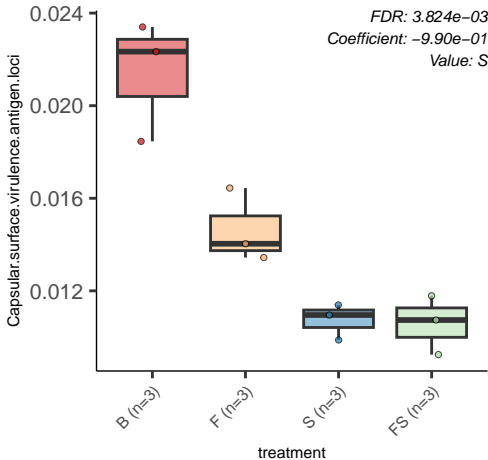
Coefficient: 1.19e+00

Value: S

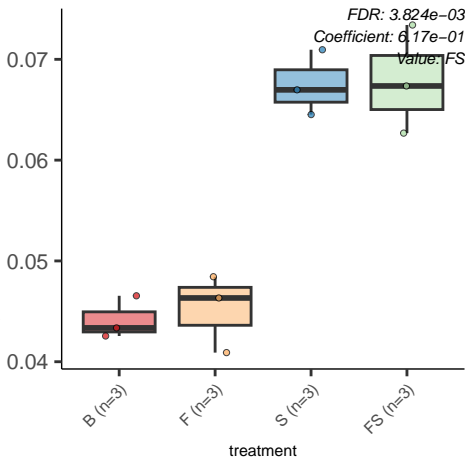


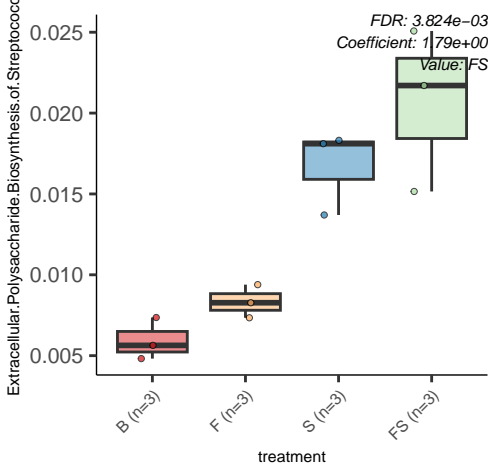




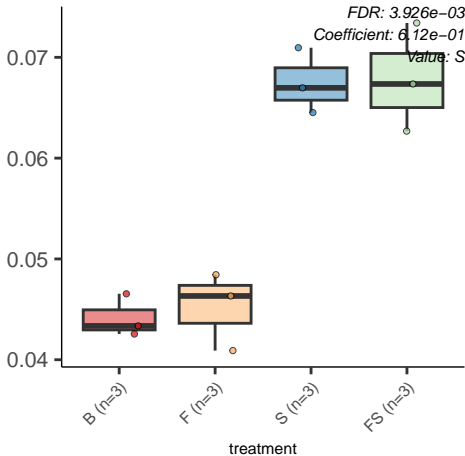


Conserved.gene.cluster.possibly.involved.in.RNA.metabolism

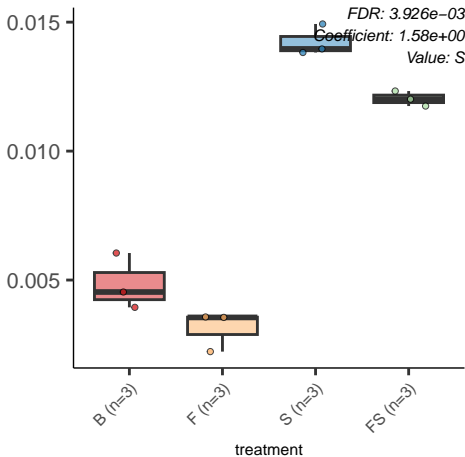




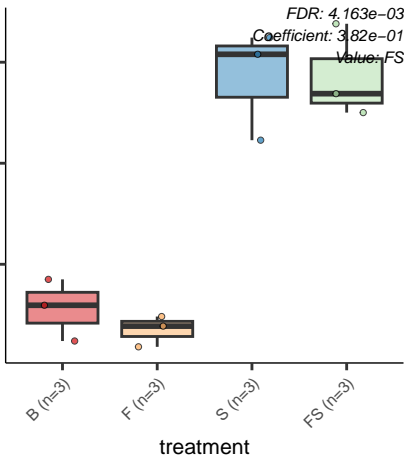
Conserved.gene.cluster.possibly.involved.in.RNA.metabolism



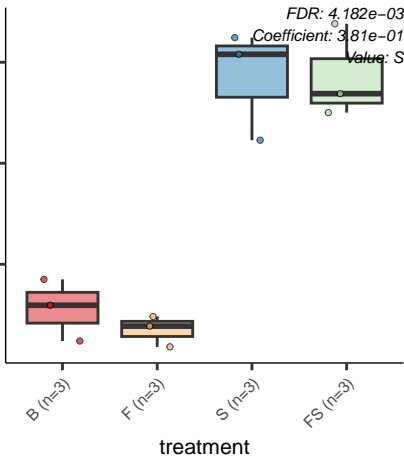
Single.Rhodanese.domain.proteins



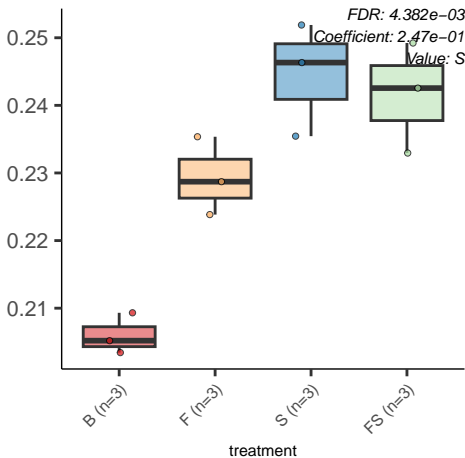
pyrimidine.conversions

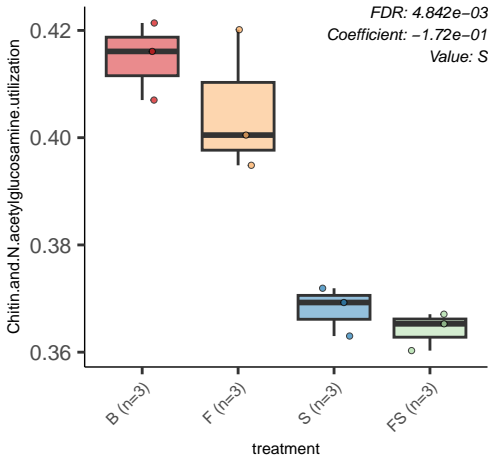


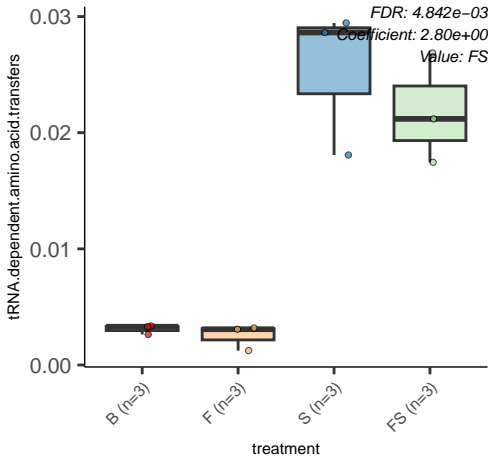
pyrimidine.conversions



tRNA.aminoacylation..Asp.and.Asn







Histidine.Biosynthesis

FDR: 4.895e-03

Coefficient: 1.47e-01

Value: S

B (n=3)

F (n=3)

S (n=3)

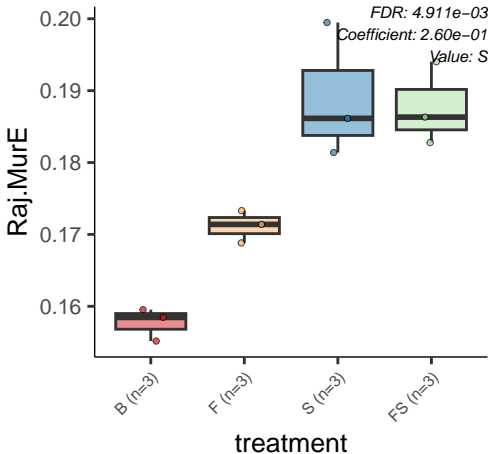
FS (n=3)

treatment

0.525

0.550

0.575



Cell.Division.Cluster

FDR: $5.053e-03$

Coefficient: $6.34e-01$

Value: S

0.08

0.07

0.06

0.05

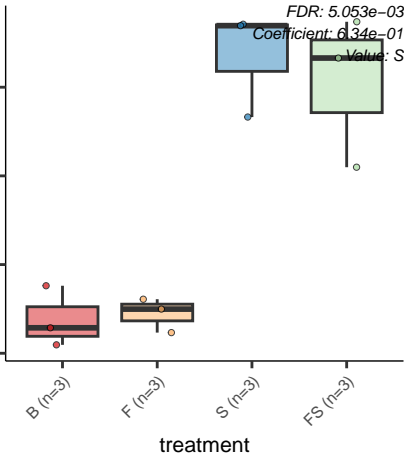
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



At4g10620.At3g57180.At3g47450

FDR: $5.174e-03$
Coefficient: $6.30e-01$
Value: FS

0.06

0.05

0.04

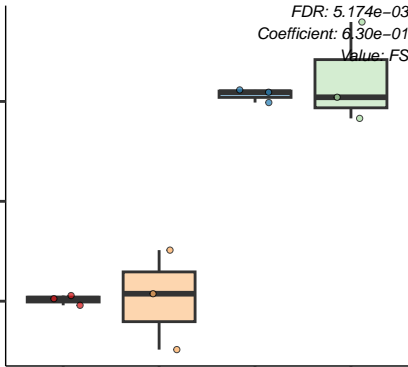
B (n=3)

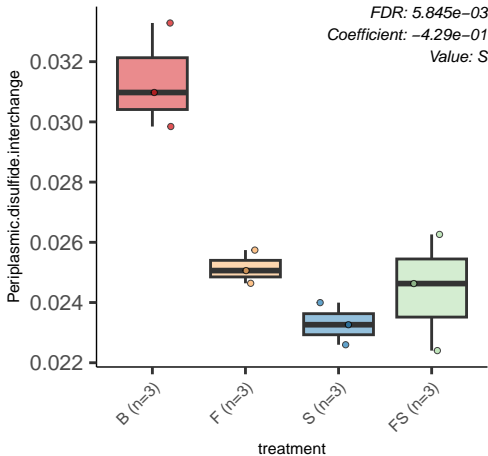
F (n=3)

S (n=3)

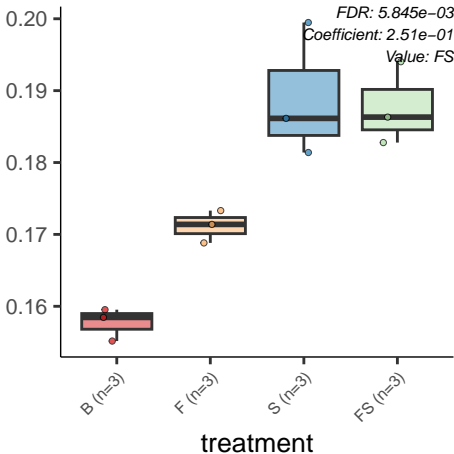
FS (n=3)

treatment

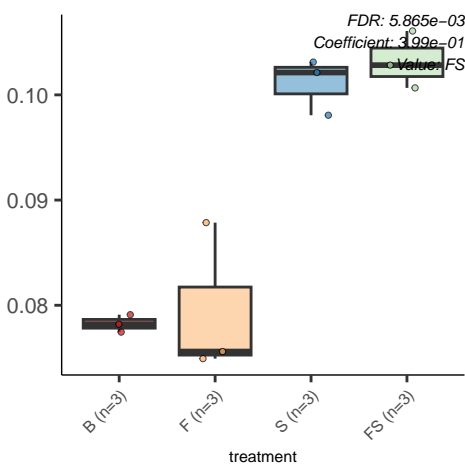




Raj.MurE

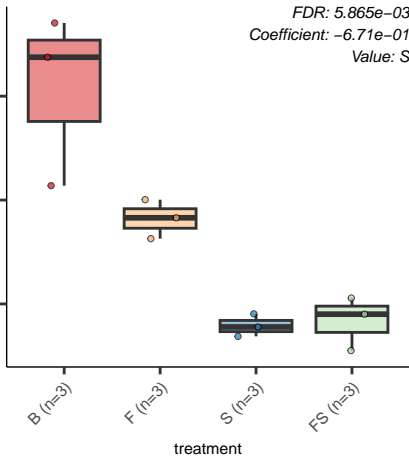


Cell.envelope.associated.LytR.CpsA.Psr.transcriptional.attenuation

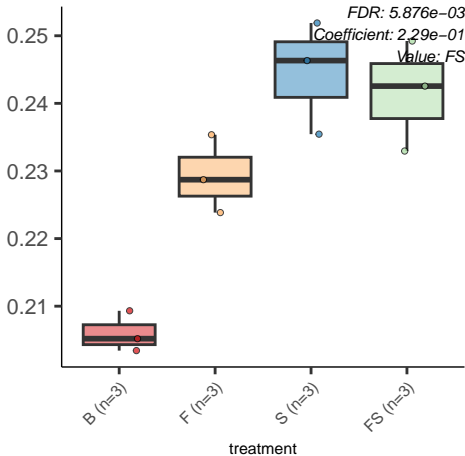


Threonine.anaerobic.catabolism.gene.cluster

FDR: 5.865e-03
Coefficient: -6.71e-01
Value: S



tRNA.aminoacylation..Asp.and.Asn



tRNA.aminoacylation..Thr

FDR: 5.876e-03

Coefficient: 3.75e-01

Value: S

0.070

0.065

0.060

0.055

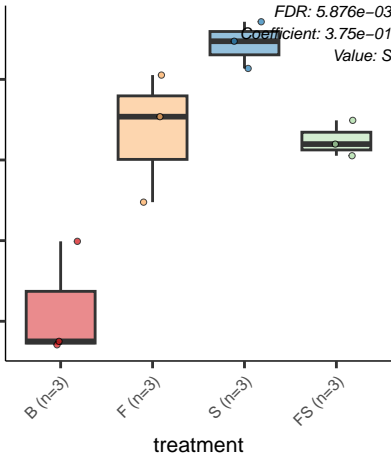
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Streptococcus.agalactiae.virulome

0.006

0.004

0.002

B (n=3)

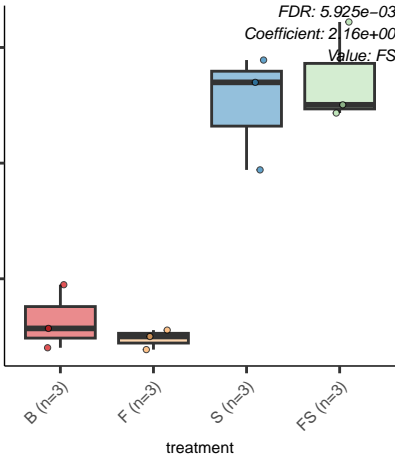
F (n=3)

S (n=3)

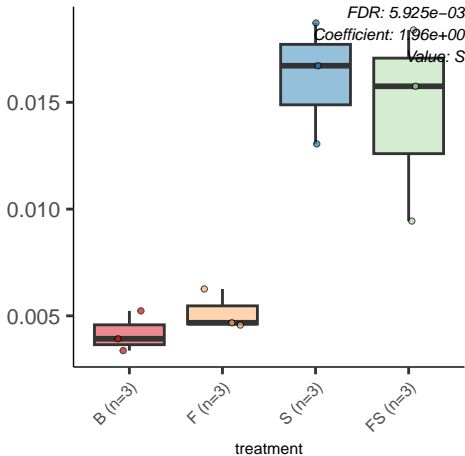
FS (n=3)

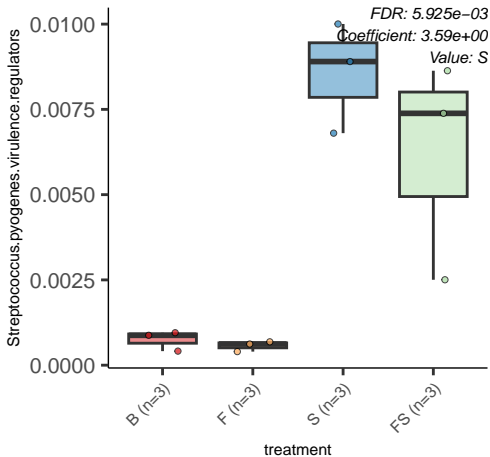
treatment

FDR: 5.925e-03
Coefficient: 2.16e+00
Value: FS



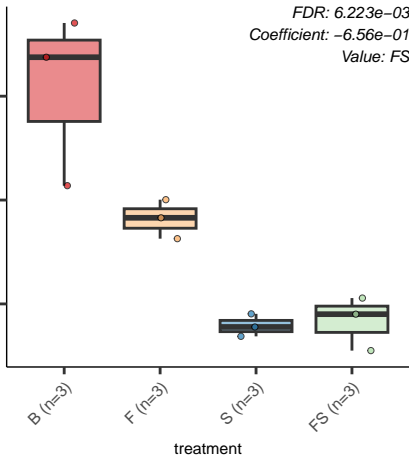
Streptococcus.pyogenes. Virulome





Threonine.anaerobic.catabolism.gene.cluster

FDR: 6.223e-03
Coefficient: -6.56e-01
Value: FS



At4g10620.At3g57180.At3g47450

FDR: 6.238e-03
Coefficient: 5.96e-01
Value: S

0.06
0.05
0.04

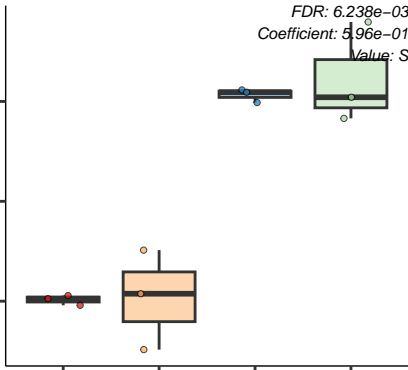
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



CBSS.393121.3.peg.2760

FDR: 6.238e-03

Coefficient: 2.71e-01

Value: S

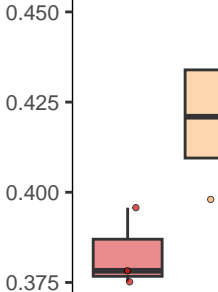
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Acetoin..butanediol.metabolism

0.14
0.13
0.12
0.11
0.10
0.09

B (n=3)

F (n=3)

S (n=3)

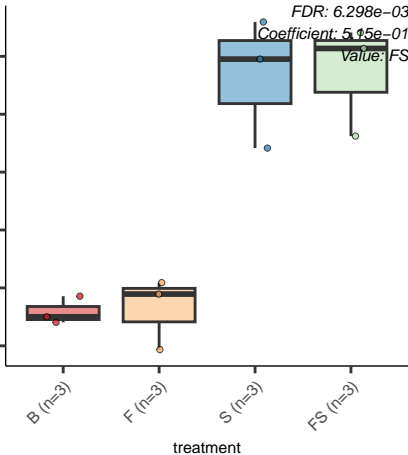
FS (n=3)

treatment

FDR: 6.298e-03

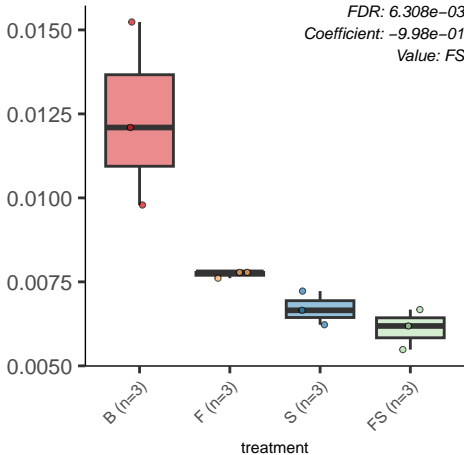
Coefficient: 5.45e-01

Value: FS



X4.Hydroxyphenylacetic.acid.catabolic.pathway

FDR: 6.308e-03
Coefficient: -9.98e-01
Value: FS



Glycerol.fermentation.to.1.3.propanediol

FDR: 6.308e-03
Coefficient: -4.71e-01
Value: S

0.027

0.024

0.021

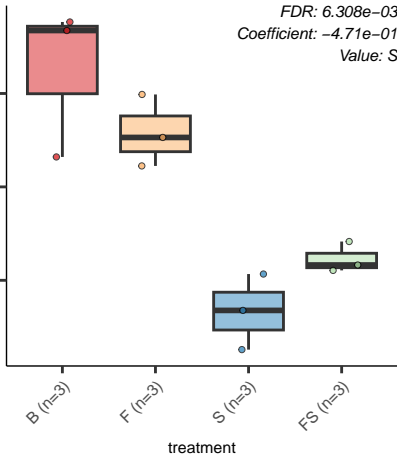
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



KDO2.Lipid.A.biosynthesis

FDR: 6.308e-03
Coefficient: -2.62e-01
Value: S

0.28
0.26
0.24

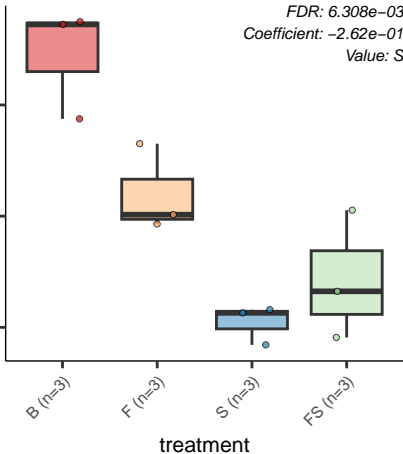
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Histidine.Biosynthesis

FDR: 6.310e-03

Coefficient: 1.35e-01

Value: FS

B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment

0.525

0.550

0.575

Acetoin..butanediol.metabolism

0.14
0.13
0.12
0.11
0.10
0.09

B (n=3)

F (n=3)

S (n=3)

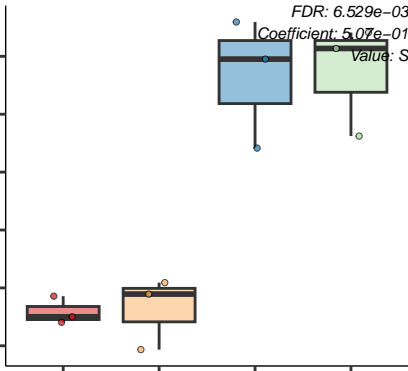
FS (n=3)

treatment

FDR: 6.529e-03

Coefficient: 5.07e-01

Value: S



Thiamin.biosynthesis.in.plants

FDR: 6.572e-03
Coefficient: -1.26e+00
Value: S

0.0030
0.0025
0.0020
0.0015
0.0010

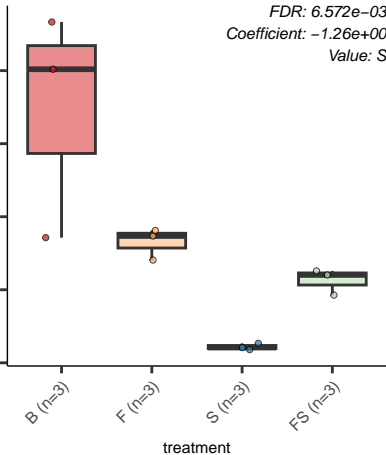
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Cell.Division.Cluster

0.08

0.07

0.06

0.05

B (n=3)

F (n=3)

S (n=3)

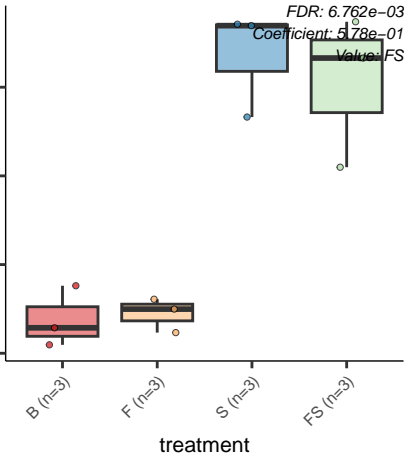
FS (n=3)

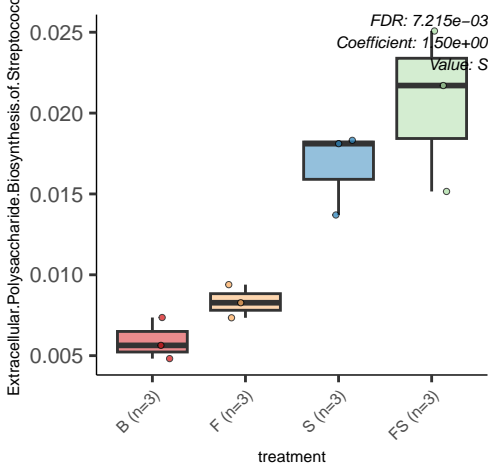
treatment

FDR: $6.762e-03$

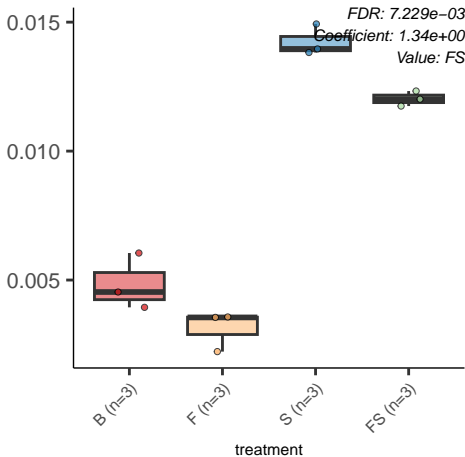
Coefficient: $5.78e-01$

Value: FS





Single.Rhodanese.domain.proteins



Streptococcus.agalactiae.virulome

0.006

0.004

0.002

B (n=3)

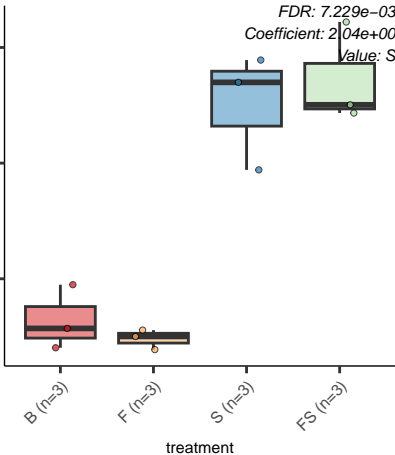
F (n=3)

S (n=3)

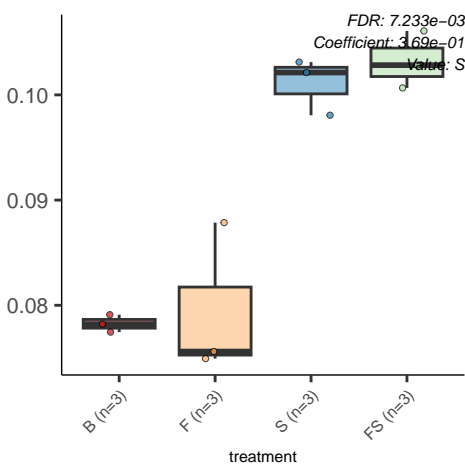
FS (n=3)

treatment

FDR: 7.229e-03
Coefficient: 2.04e+00
Value: S



Cell.envelope.associated.LytR.CpsA.Psr.transcriptional.atten



Unspecified.monosaccharide.transport.cluster

FDR: $7.954e-03$
Coefficient: $5.86e-01$
Value: FS

0.05

0.04

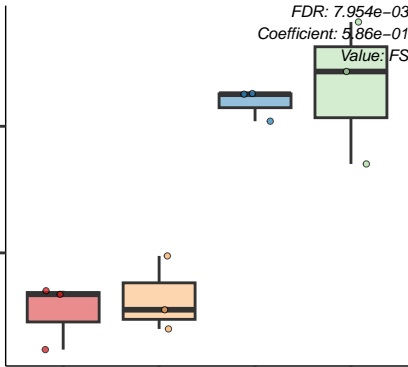
B (n=3)

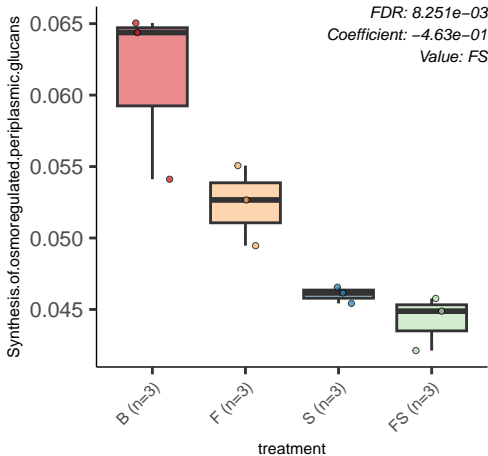
F (n=3)

S (n=3)

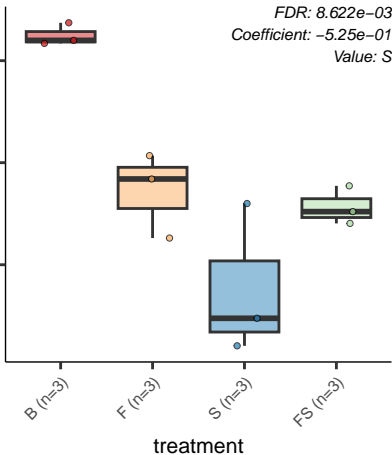
FS (n=3)

treatment





CBSS.320372.3.peg.6046

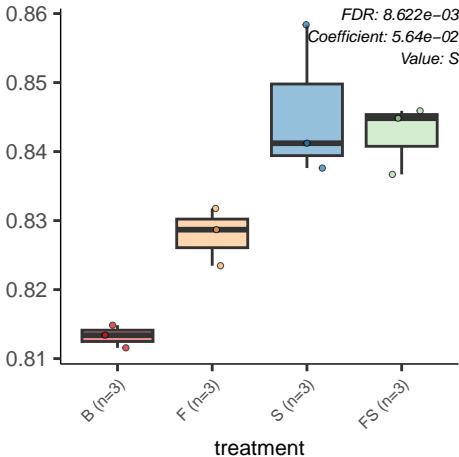


DNA.repair..bacterial

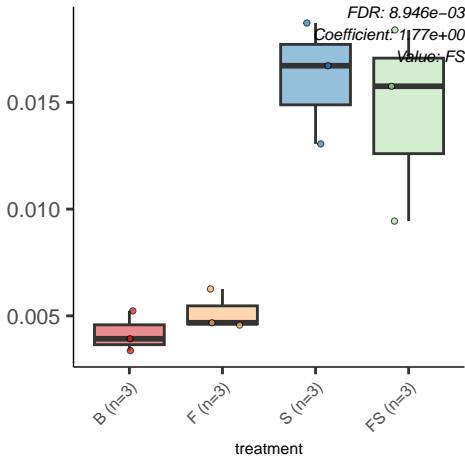
FDR: 8.622e-03

Coefficient: 5.64e-02

Value: S



Streptococcus.pyogenes. Virulome



D,Alanyl.Lipoteichoic.Acid.Biosynthesis

0.010

0.008

0.006

0.004

B (n=3)

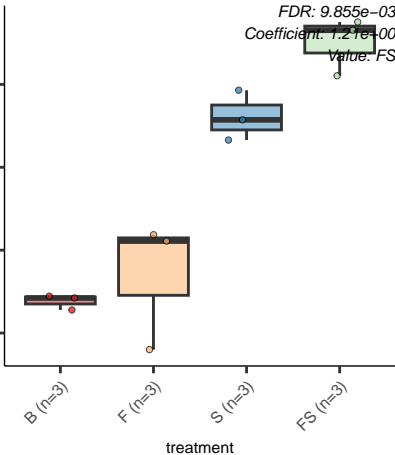
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: $9.855e-03$
Coefficient: $1.21e-00$
Value: FS



Methionine.Degradation

FDR: 9.855e-03
Coefficient: 9.26e-02
Value.FS

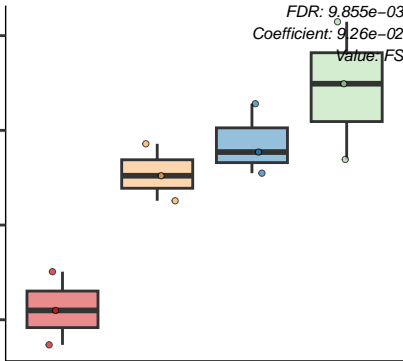
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Unspecified.monosaccharide.transport.cluster

FDR: 1.062e-02
Coefficient: 5.54e-01
Value: S

0.05

0.04

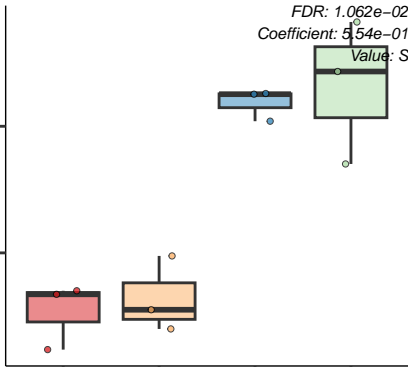
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Copper.homeostasis

FDR: 1.133e-02

Coefficient: 1.29e-01

Value: S

0.50

0.48

0.46

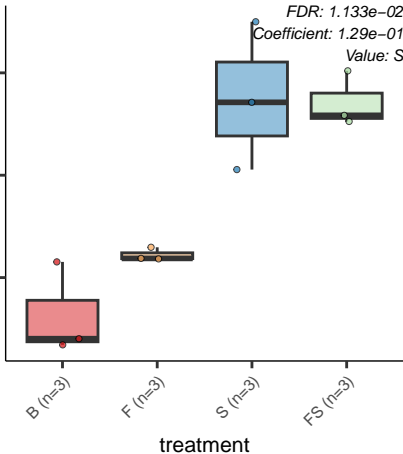
B (n=3)

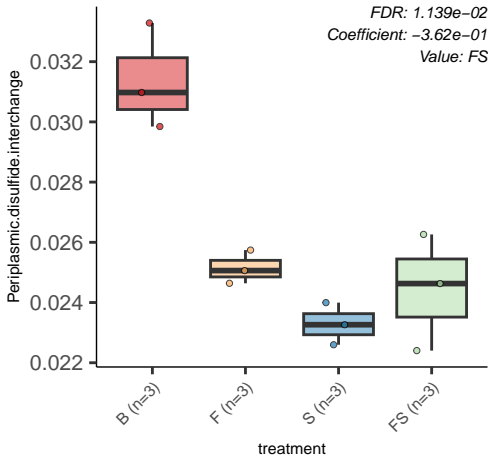
F (n=3)

S (n=3)

FS (n=3)

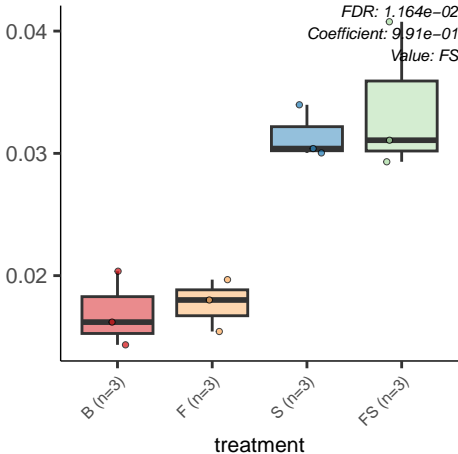
treatment

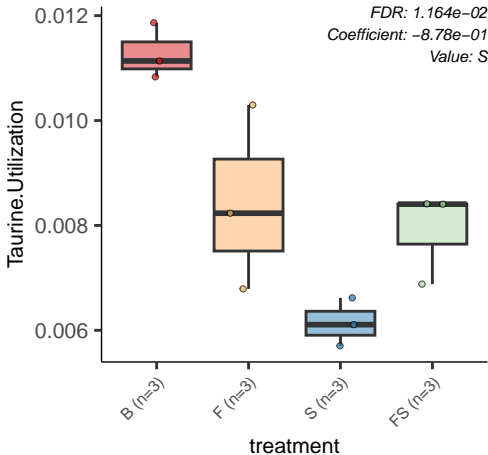




CBSS.222523.1.pcg.1311

FDR: 1.164e-02
Coefficient: 9.91e-01
Value: FS





Copper.homeostasis

FDR: 1.218e-02

Coefficient: 1.27e-01

Value: FS

0.50

0.48

0.46

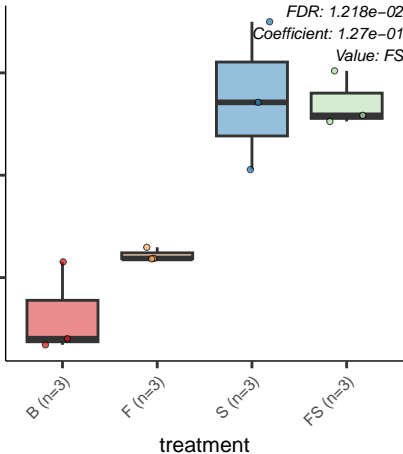
B (n=3)

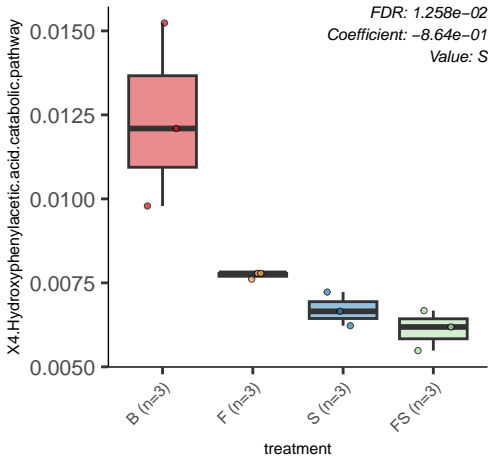
F (n=3)

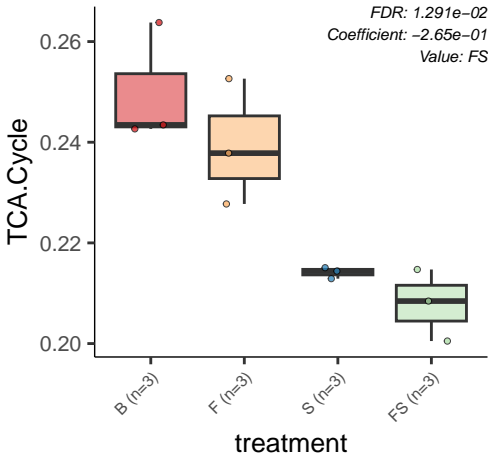
S (n=3)

FS (n=3)

treatment







ATP.dependent.Nuclease

FDR: 1.324e-02
Coefficient: 5.08e-01
Value: FS

0.18

0.16

0.14

0.12

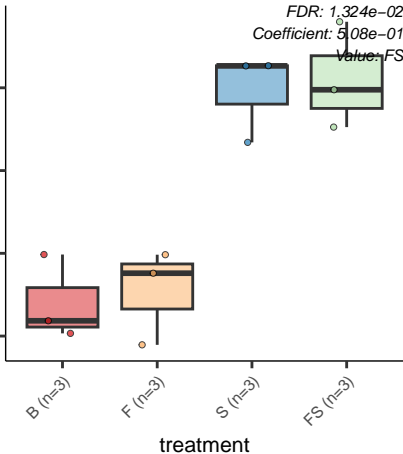
B (n=3)

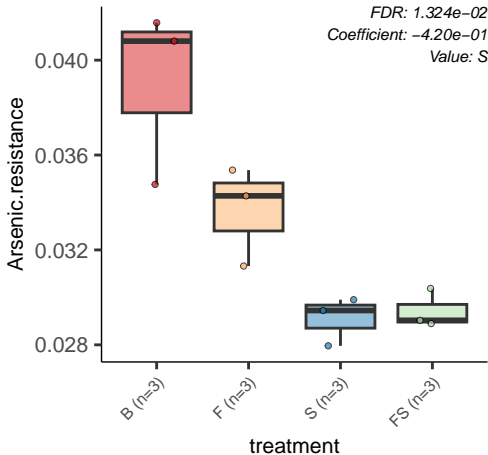
F (n=3)

S (n=3)

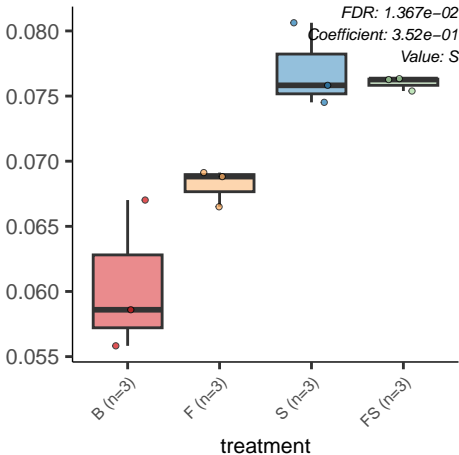
FS (n=3)

treatment





LMPTP.YwIE.cluster



Omega.amidase

FDR: 1.367e-02
Coefficient: 9.73e-01
Value: FS

0.008

0.006

0.004

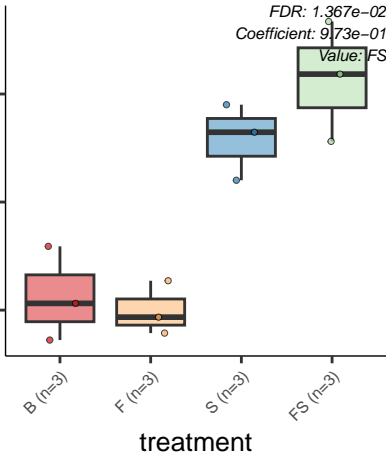
B (n=3)

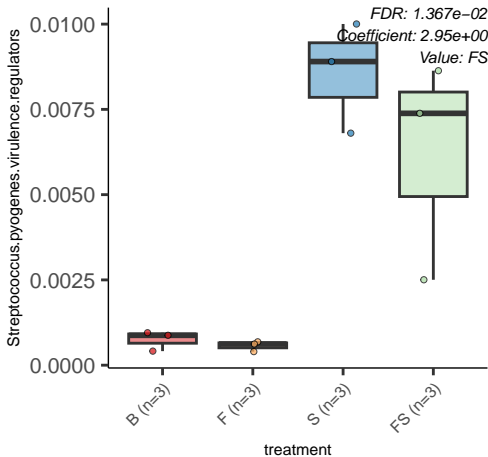
F (n=3)

S (n=3)

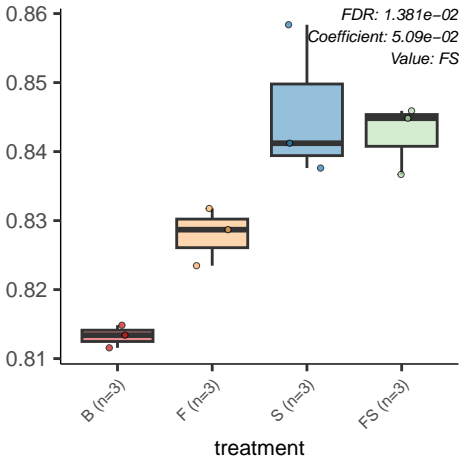
FS (n=3)

treatment





DNA.repair..bacterial



L.Arabinose.utilization

FDR: $1.381e-02$
Coefficient: $-1.96e-01$
Value: S

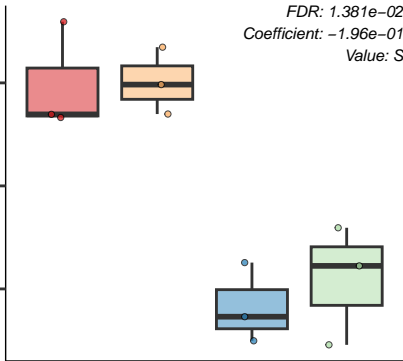
B (n=3)

F (n=3)

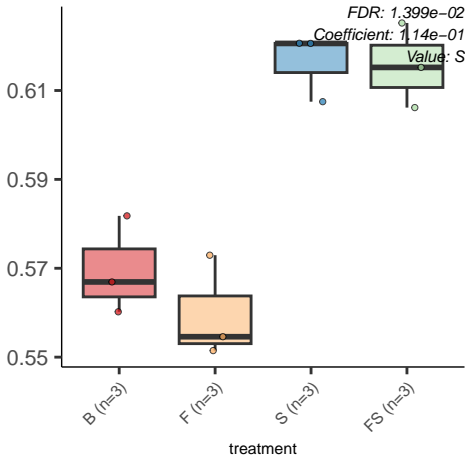
S (n=3)

FS (n=3)

treatment

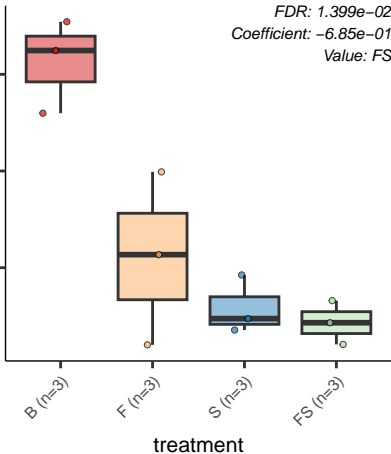


Glycerolipid.and.Glycerophospholipid.Metabolism.in.Bacte



Transposase.in.enteries

FDR: 1.399e-02
Coefficient: -6.85e-01
Value: FS



KDO2.Lipid.A.biosynthesis

FDR: $1.467\text{e-}02$
Coefficient: $-2.18\text{e-}01$
Value: FS

0.28
0.26
0.24

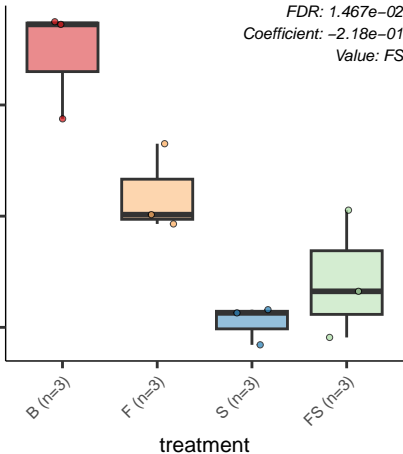
B (n=3)

F (n=3)

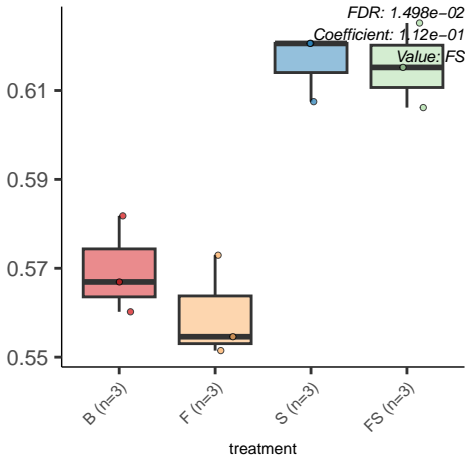
S (n=3)

FS (n=3)

treatment



Glycerolipid.and.Glycerophospholipid.Metabolism.in.Bacte



Iron.III..dicitrate.transport.system.Fec

FDR: $1.498e-02$
Coefficient: $-1.34e+00$
Value: S

B (n=3)

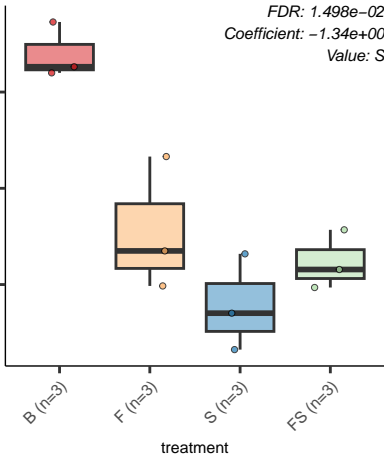
F (n=3)

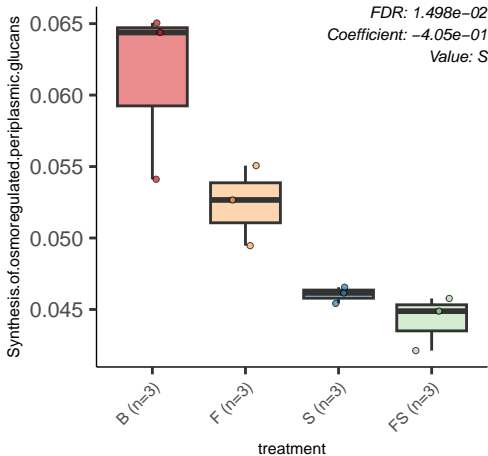
S (n=3)

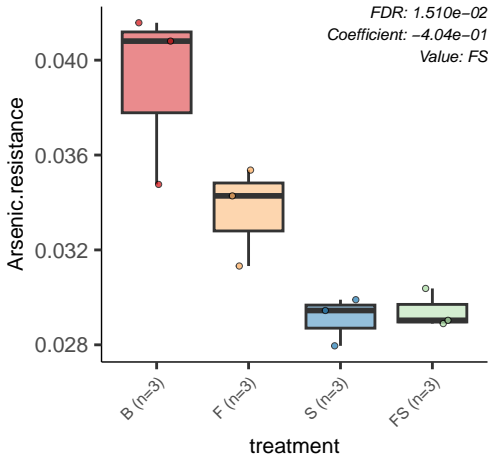
FS (n=3)

treatment

0.0100
0.0075
0.0050







Carnitine.Metabolism.in.Microorganisms

FDR: $1.510e-02$
Coefficient: $-8.62e-01$
Value: S

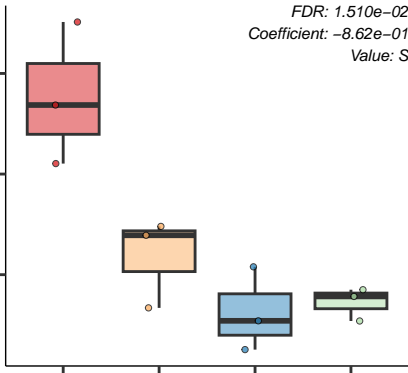
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



ATP.dependent.Nuclease

FDR: 1.532e-02
Coefficient: 4.86e-01
Value: S

0.18

0.16

0.14

0.12

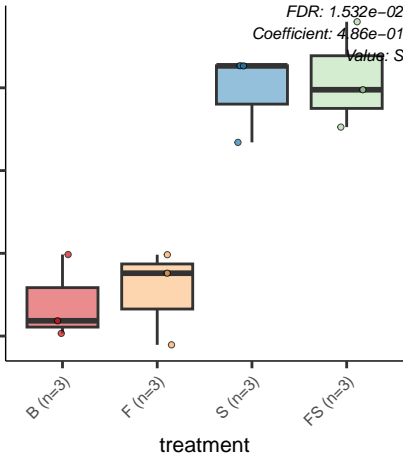
B (n=3)

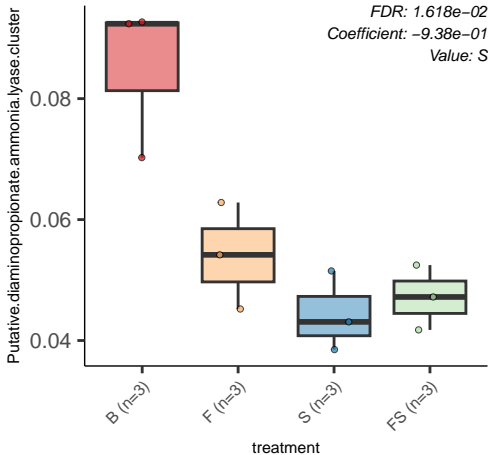
F (n=3)

S (n=3)

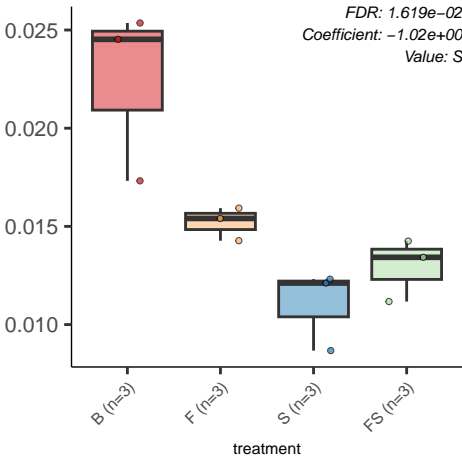
FS (n=3)

treatment



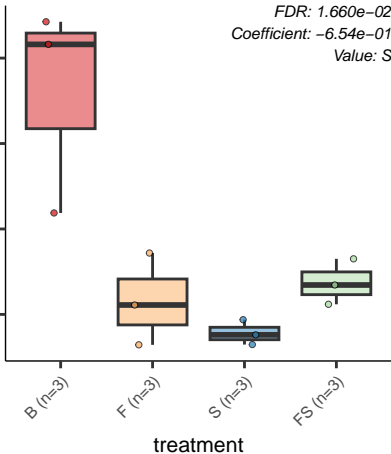


Accessory.colonization.factor

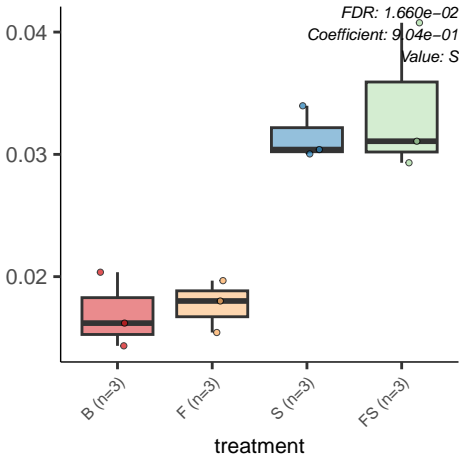


Bacterial.hemoglobins

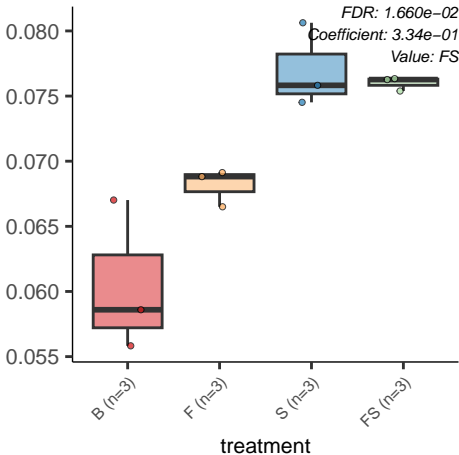
FDR: 1.660e-02
Coefficient: -6.54e-01
Value: S



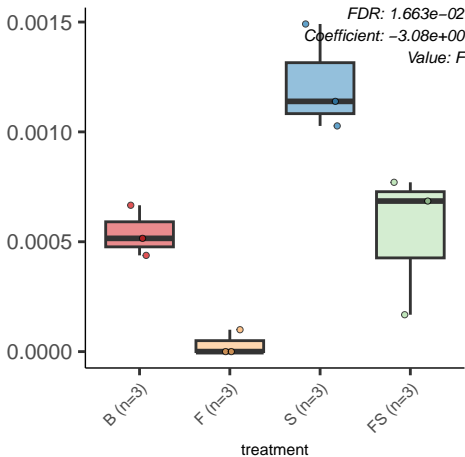
CBSS.222523.1.pcg.1311



LMPTP.YwIE.cluster

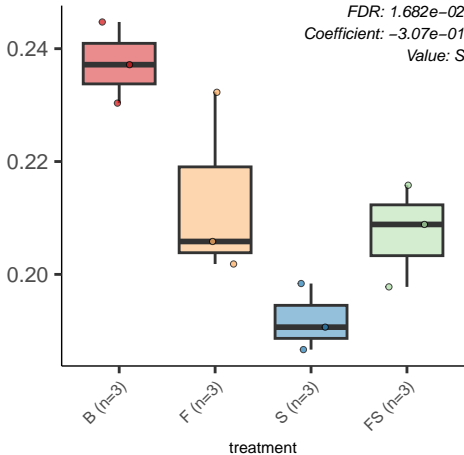


Fratricide.in.Streptococcus



N.Acetyl.l.Galactosamine.and.Galactosamine.Utilization

FDR: 1.682e-02
Coefficient: -3.07e-01
Value: S



Glyoxylate.bypass

FDR: 1.699e-02
Coefficient: -9.34e-01
Value: FS

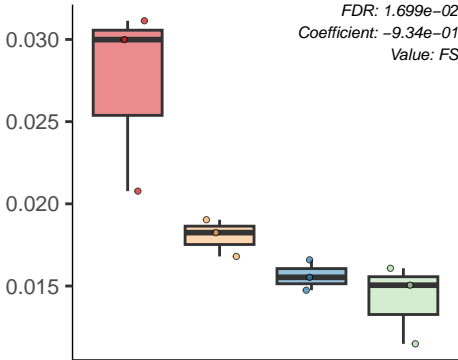
B (n=3)

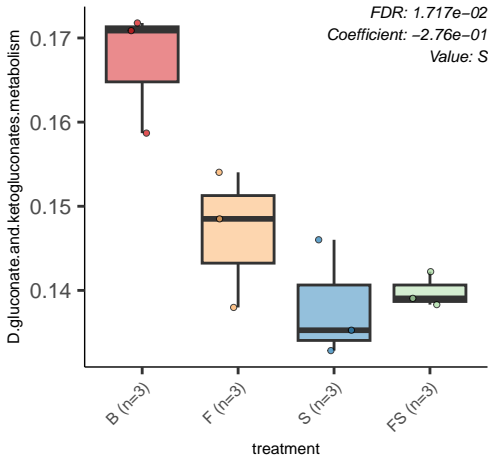
F (n=3)

S (n=3)

FS (n=3)

treatment





CBSS.393121.3.peg.2760

FDR: 1.768e-02

Coefficient: 2.11e-01

Value: FS

0.450

0.425

0.400

0.375

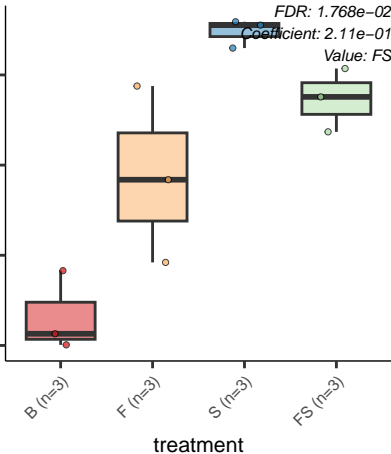
B (n=3)

F (n=3)

S (n=3)

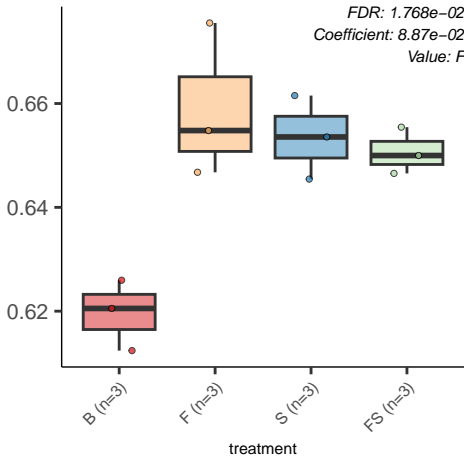
FS (n=3)

treatment



Glycolysis.and.Gluconeogenesis

FDR: 1.768e-02
Coefficient: 8.87e-02
Value: F



Phenylacetyl-CoA.catabolic.pathway..core.

FDR: $1.775e-02$
Coefficient: $-1.20e+00$
Value: S

0.020

0.015

0.010

0.005

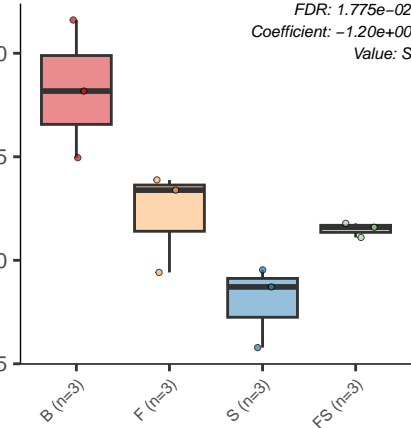
B (n=3)

F (n=3)

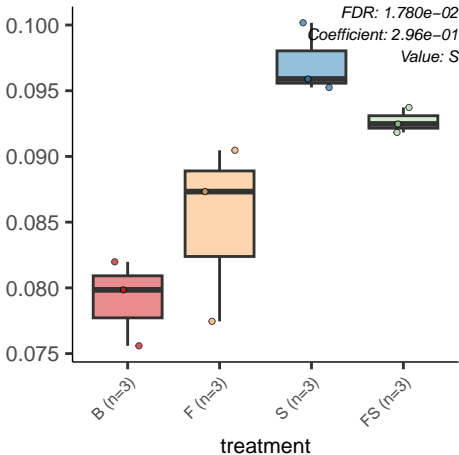
S (n=3)

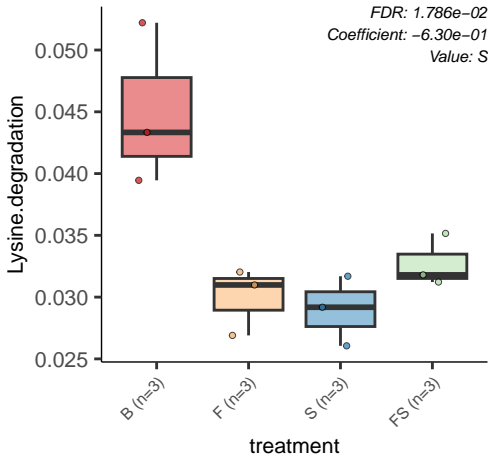
FS (n=3)

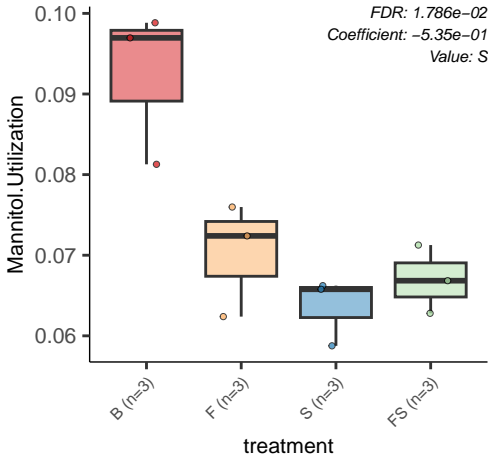
treatment



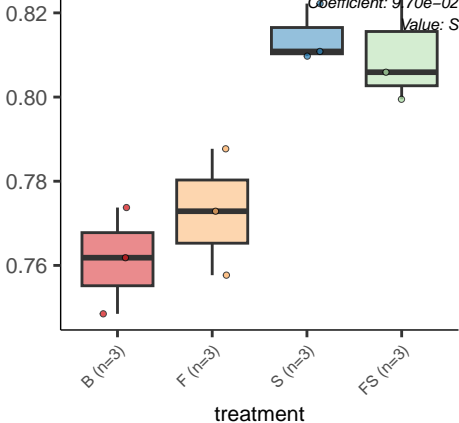
CBSS.84588.1.pcg.1247







Methionine.Biosynthesis



Multidrug.efflux.pump.in.Campylobacter.jejuni..CmeABC.op

FDR: $1.786e-02$
Coefficient: $-9.71e-01$
Value: S

0.04

0.03

0.02

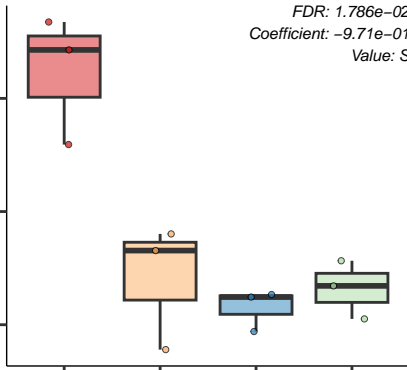
B (n=3)

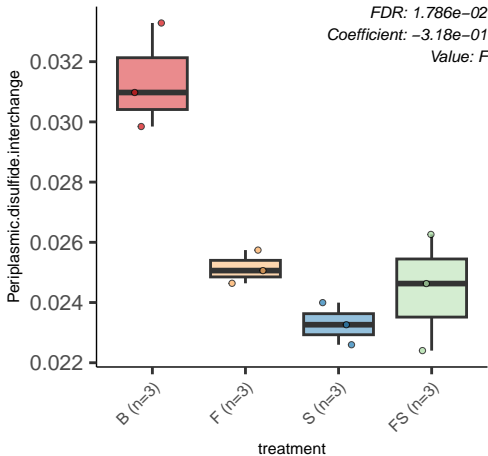
F (n=3)

S (n=3)

FS (n=3)

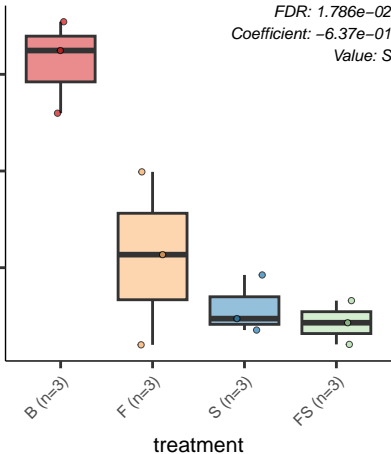
treatment





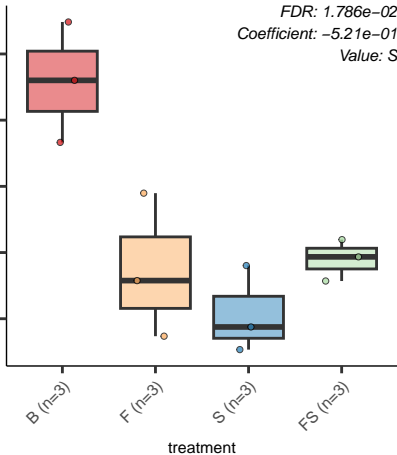
Transposase.in.enteries

FDR: 1.786e-02
Coefficient: -6.37e-01
Value: S



Unknown.sugar.utilization...cluster.yphABCDEFG.

FDR: 1.786e-02
Coefficient: -5.21e-01
Value: S

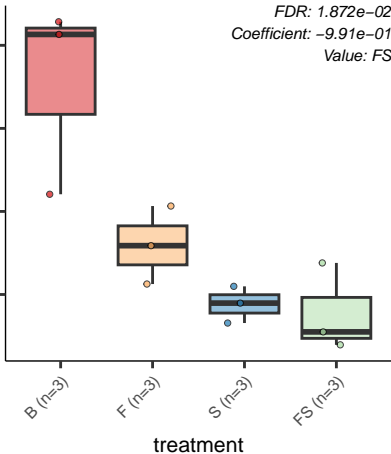


Cinnamic.Acid.Degradation

FDR: 1.872e-02

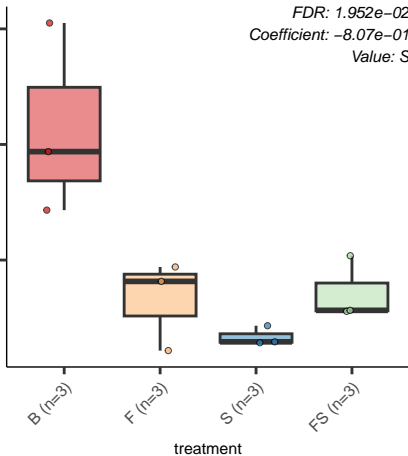
Coefficient: -9.91e-01

Value: FS



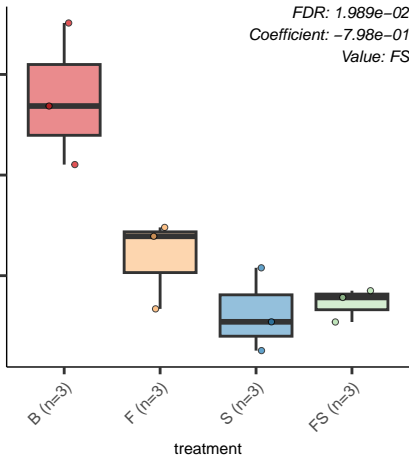
Major.Outer.Membrane.Proteins

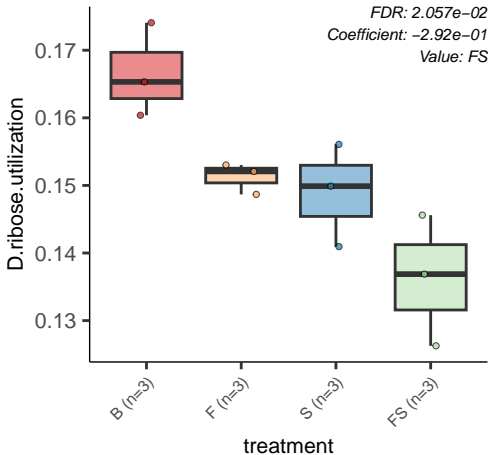
FDR: $1.952e-02$
Coefficient: $-8.07e-01$
Value: S



Carnitine.Metabolism.in.Microorganisms

FDR: 1.989e-02
Coefficient: -7.98e-01
Value: FS





EC.3.4.11...Aminopeptidases

0.29

0.28

0.27

B (n=3)

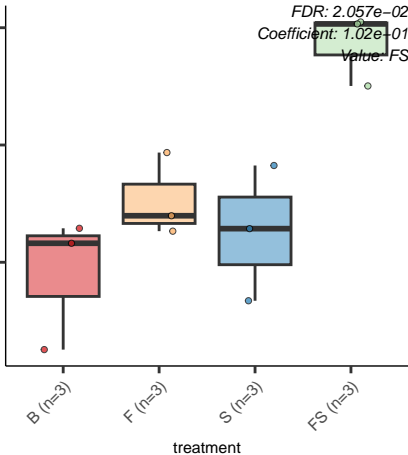
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 2.057e-02
Coefficient: 1.02e-01
Value: FS



Biotin.biosynthesis

FDR: 2.080e-02
Coefficient: -2.33e-01
Value: S

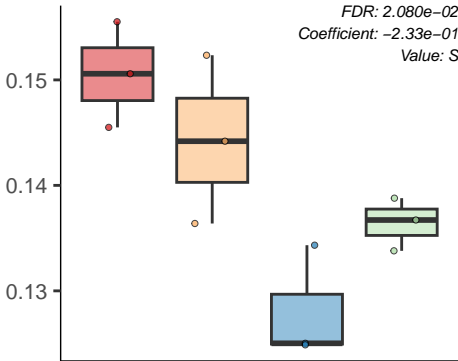
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Glycerol.fermentation.to.1.3.propanediol

FDR: 2.080e-02
Coefficient: -3.53e-01
Value: FS

0.027

0.024

0.021

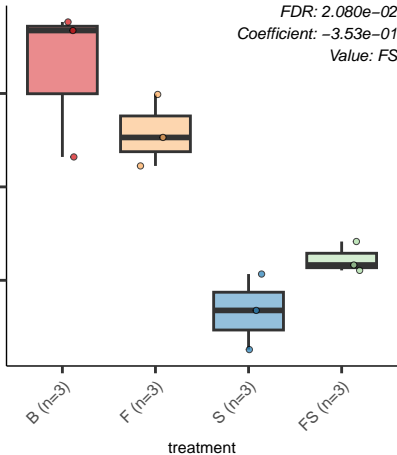
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Glycine.Biosynthesis

FDR: 2.161e-02
Coefficient: -1.46e-01
Value: FS

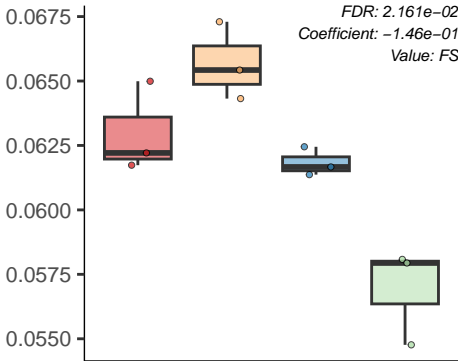
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



CbiZ.Main

FDR: 2.213e-02
Coefficient: -9.69e-01
Value: S

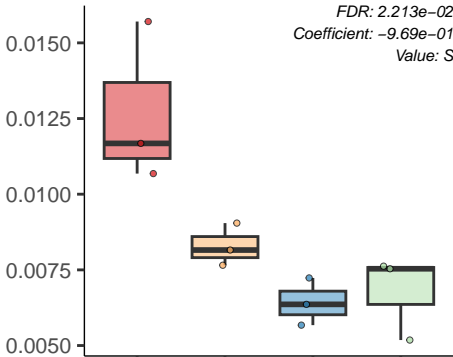
B (n=3)

F (n=3)

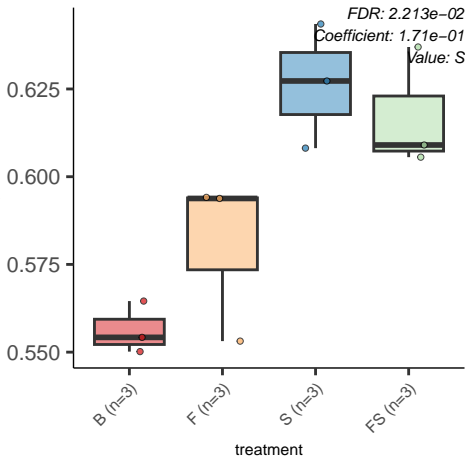
S (n=3)

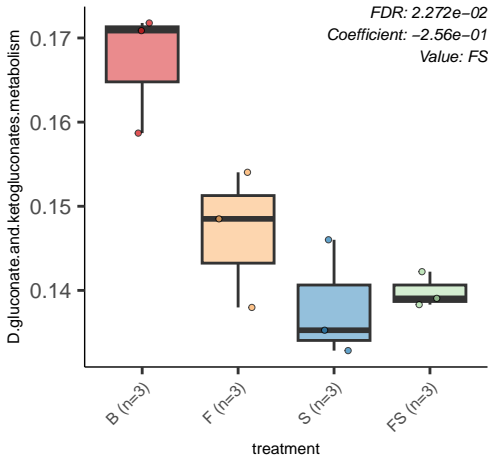
FS (n=3)

treatment



Heat.shock.dnaK.gene.cluster.extended





L.Arabinose.utilization

FDR: 2.272e-02
Coefficient: -1.71e-01
Value: FS

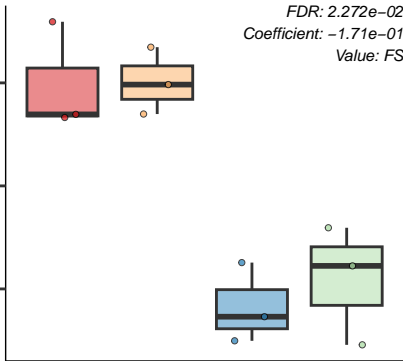
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Peptidoglycan.Biosynthesis

0.84
0.82
0.80

B (n=3)

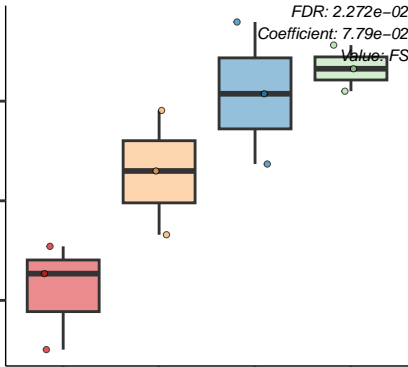
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 2.272e-02
Coefficient: 7.79e-02
Value: FS



Chloroaromatic.degradation.pathway

FDR: 2.276e-02
Coefficient: 1.07e+00
Value: F

0.00125

0.00100

0.00075

0.00050

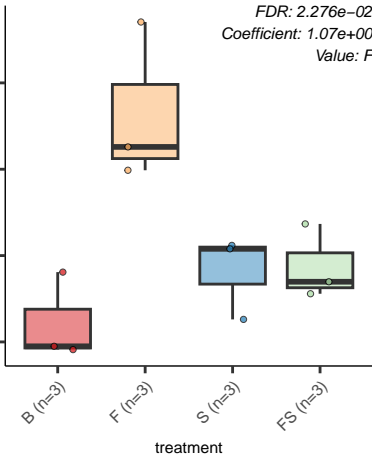
B (n=3)

F (n=3)

S (n=3)

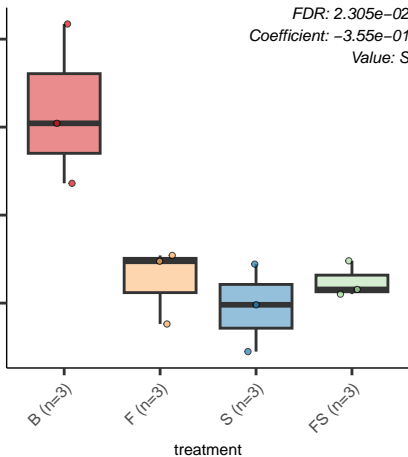
FS (n=3)

treatment



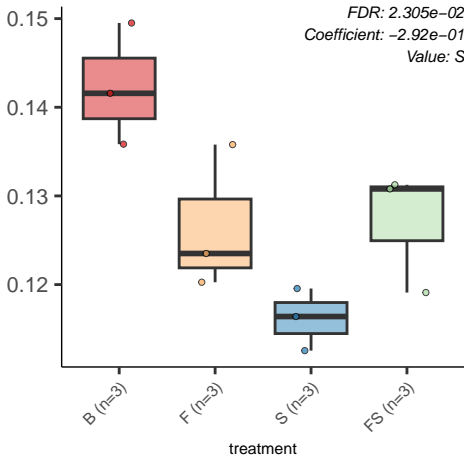
Capsular.Polysaccharides.Biosynthesis.and.Assembly

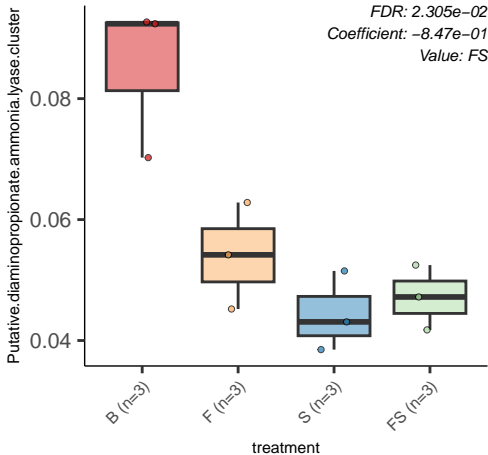
FDR: $2.305e-02$
Coefficient: $-3.55e-01$
Value: S



Lipid.A.Ara4N.pathway...Polymyxin..resistance..

FDR: 2.305e-02
Coefficient: -2.92e-01
Value: S





Osmoregulation

FDR: 2.349e-02
Coefficient: -2.90e-01
Value: S

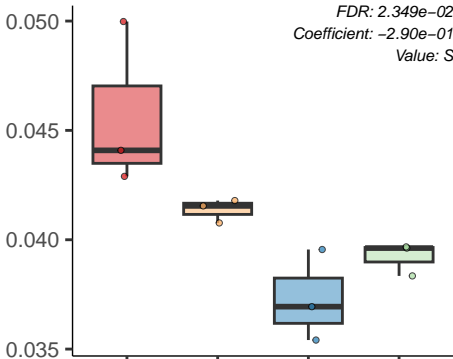
B (n=3)

F (n=3)

S (n=3)

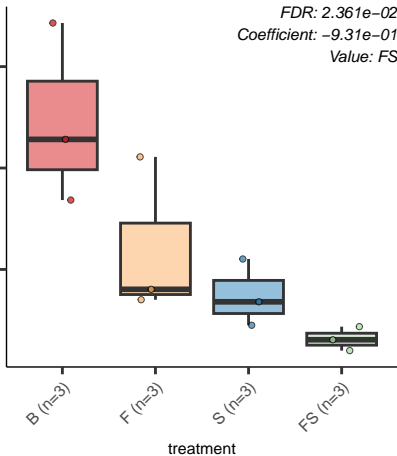
FS (n=3)

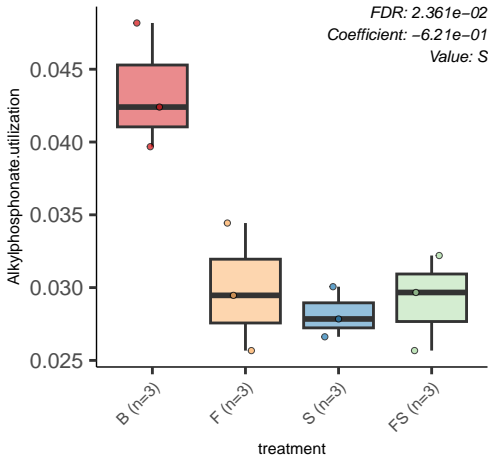
treatment

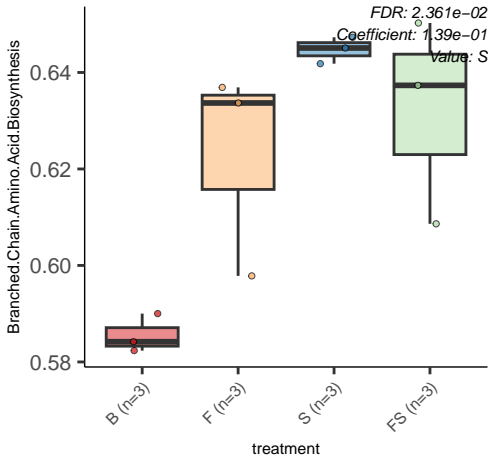


Acetone.Butanol.Ethanol.Synthesis

FDR: 2.361e-02
Coefficient: -9.31e-01
Value: FS







Cinnamic.Acid.Degradation

FDR: 2.361e-02
Coefficient: -9.22e-01
Value: S

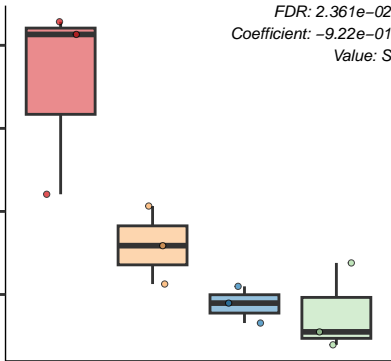
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



D,Alanyl.Lipoteichoic.Acid.Biosynthesis

0.010

0.008

0.006

0.004

B (n=3)

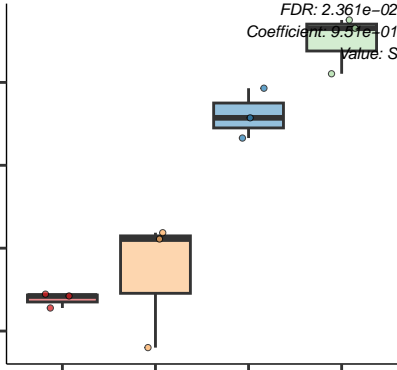
F (n=3)

S (n=3)

FS (n=3)

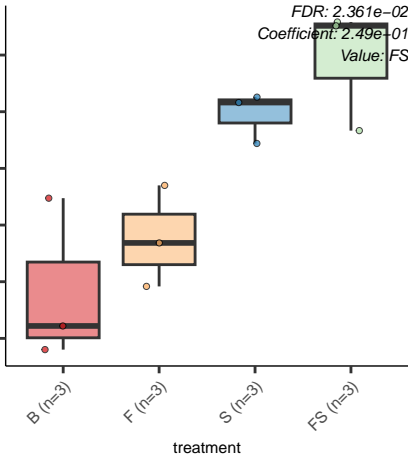
treatment

FDR: 2.361e-02
Coefficient: 9.51e-01
value: S



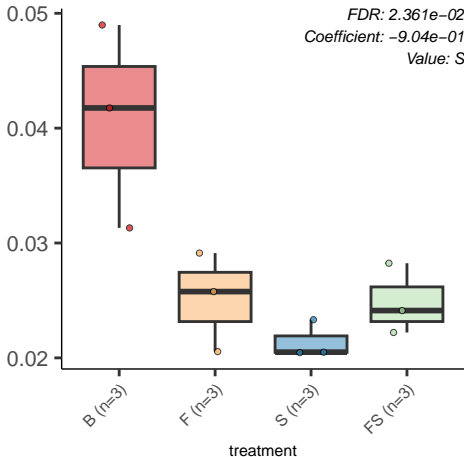
DNA.repair..bacterial.MutL.MutS.system

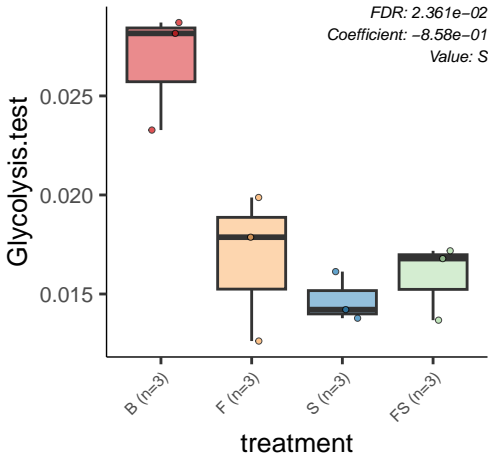
FDR: 2.361e-02
Coefficient: 2.49e-01
Value: FS



FOL.Commensurate.regulon.activation

FDR: 2.361e-02
Coefficient: -9.04e-01
Value: S



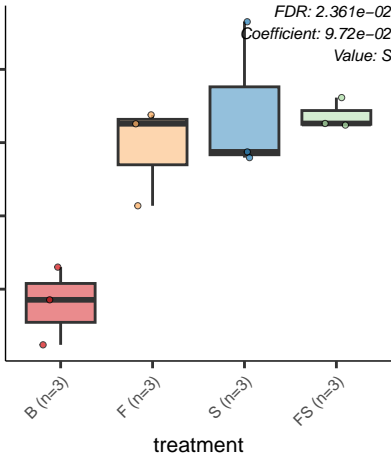


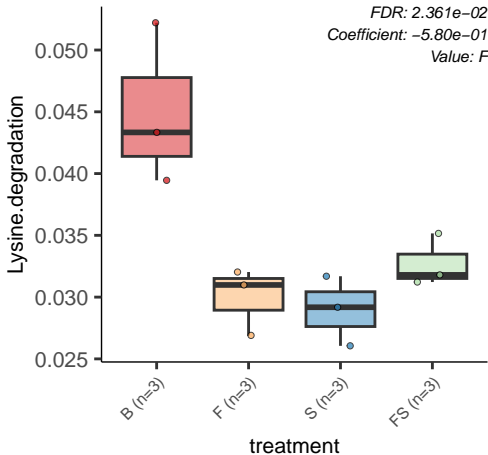
Isoprenoid.Biosynthesis

FDR: 2.361e-02

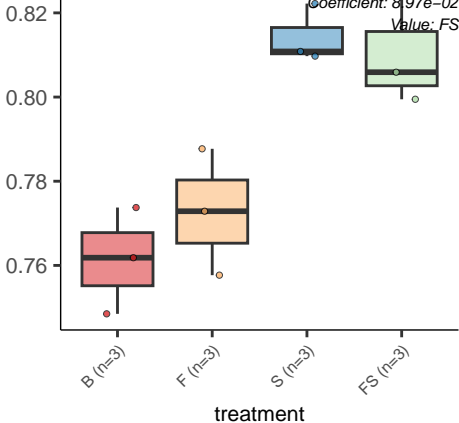
Coefficient: 9.72e-02

Value: S

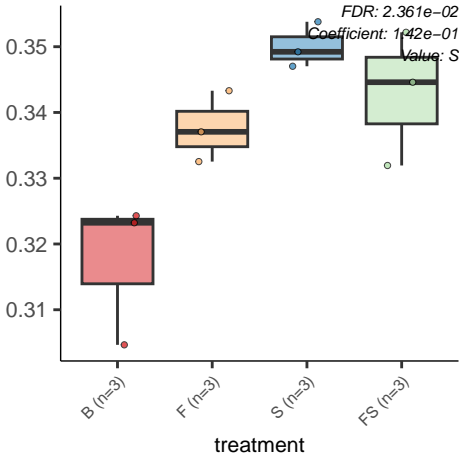




Methionine.Biosynthesis

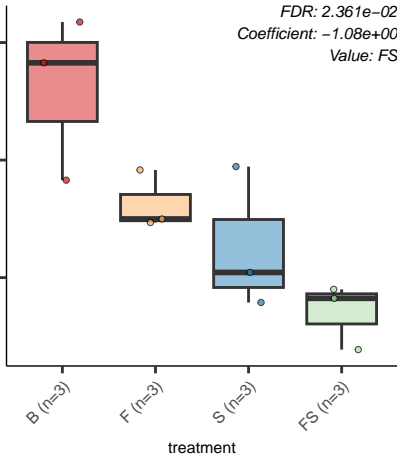


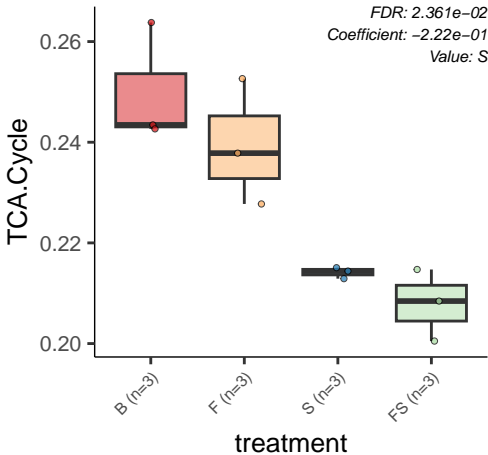
Ribosome.SSU.bacterial



Siderophore. Yersiniabactin. Biosynthesis

FDR: 2.361e-02
Coefficient: -1.08e+00
Value: FS





Tryptophan.synthesis

0.40
0.38
0.36

B (n=3)

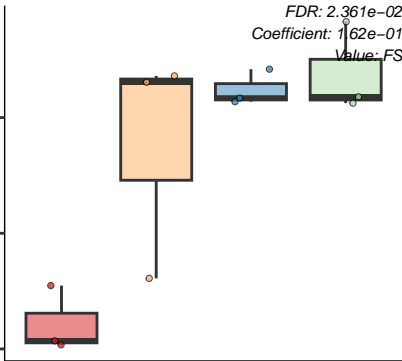
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 2.361e-02
Coefficient: 1.62e-01
Value: FS



tRNA.aminoacylation..Thr

FDR: 2.361e-02

Coefficient: 2.61e-01

Value: F

0.070

0.065

0.060

0.055

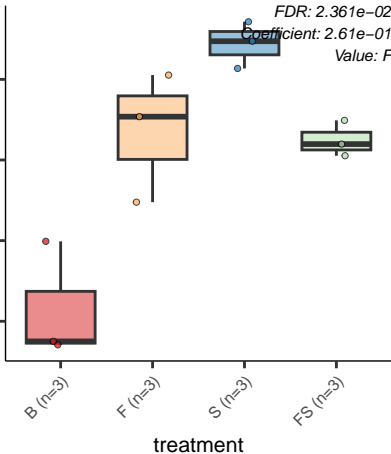
B (n=3)

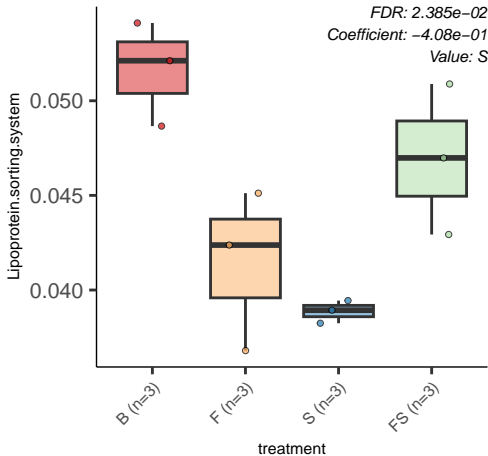
F (n=3)

S (n=3)

FS (n=3)

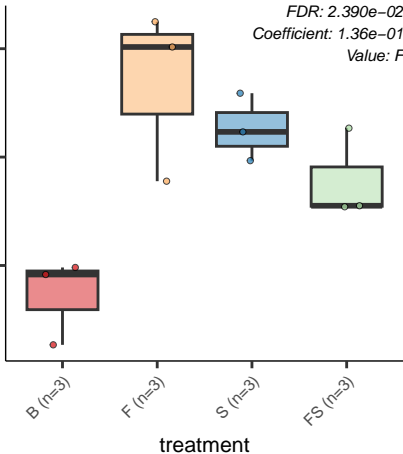
treatment





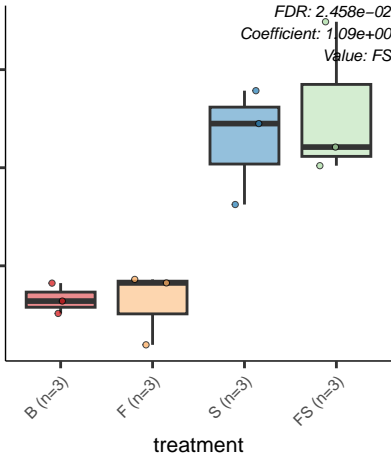
Leucine.Biosynthesis

FDR: 2.390e-02
Coefficient: 1.36e-01
Value: F



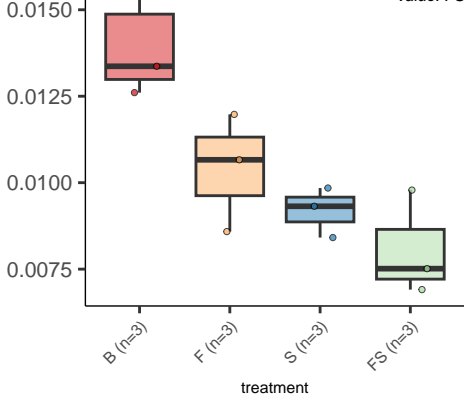
CBSS.261594.1.pcg.788

FDR: 2.458e-02
Coefficient: 1.09e+00
Value: FS



A.Gammaproteobacteria.Cluster.Relating.to.Translation

FDR: 2.527e-02
Coefficient: -8.14e-01
Value: FS



Isoprenoid.Biosynthesis

FDR: 2.527e-02

Coefficient: 9.51e-02

Value: FS

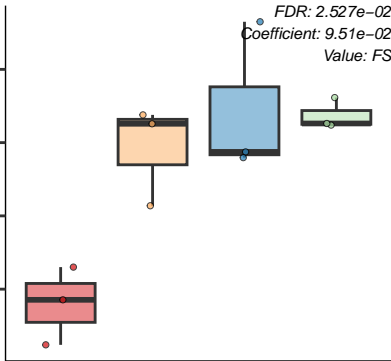
B (n=3)

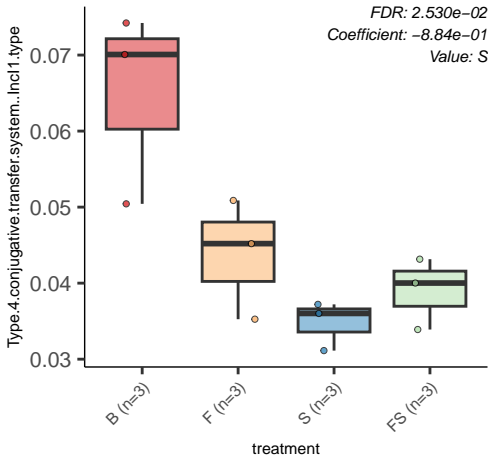
F (n=3)

S (n=3)

FS (n=3)

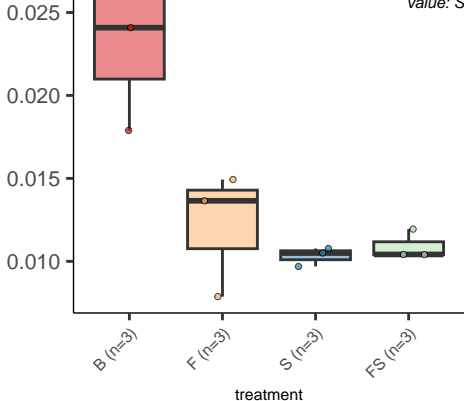
treatment





Biofilm.Adhesin.Biosynthesis

FDR: 2.604e-02
Coefficient: -1.15e+00
Value: S



CbiZ.Main

FDR: $2.604e-02$
Coefficient: $-9.06e-01$
Value: FS

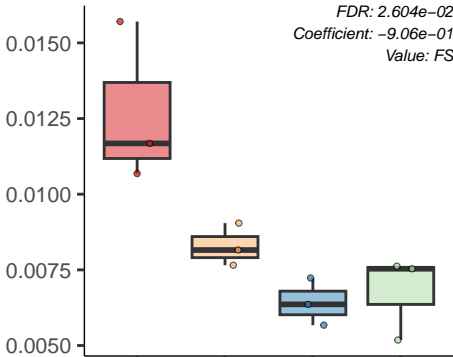
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



ECF.class.transporters

0.32
0.30
0.28
0.26

B (n=3)

F (n=3)

S (n=3)

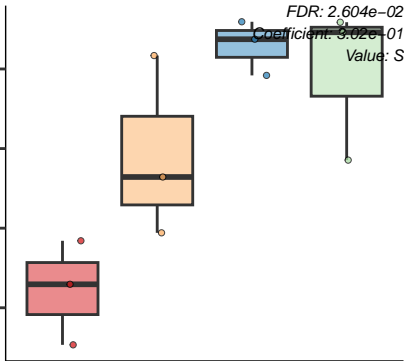
FS (n=3)

treatment

FDR: $2.604e-02$

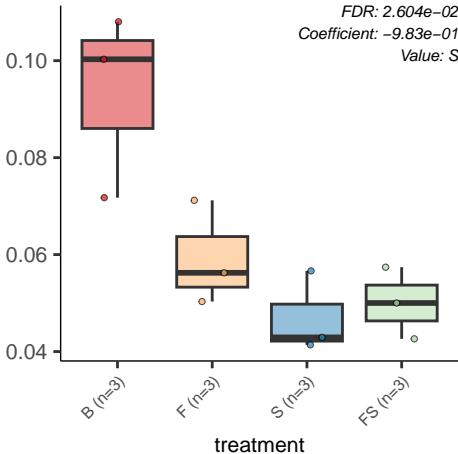
Coefficient: $3.02e-01$

Value: S

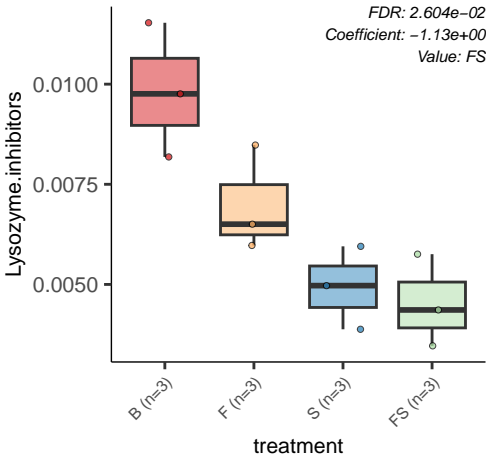


General.Secretion.Pathway

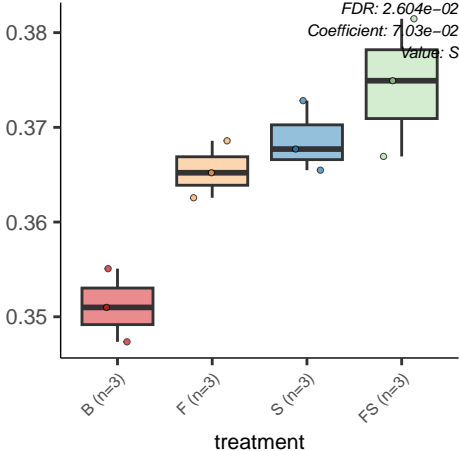
FDR: 2.604e-02
Coefficient: -9.83e-01
Value: S



Lysozyme.inhibitors

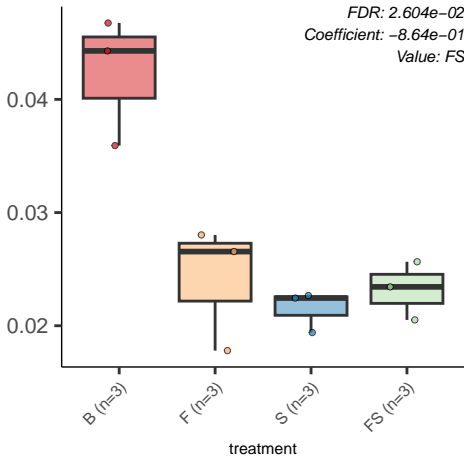


Methionine.Degradation



Multidrug.efflux.pump.in.Campylobacter.jejuni..CmeABC.op

FDR: $2.604e-02$
Coefficient: $-8.64e-01$
Value: FS



Orphan.regulatory.proteins

FDR: 2.604e-02
Coefficient: -7.65e-01
Value: S

0.10

0.08

0.06

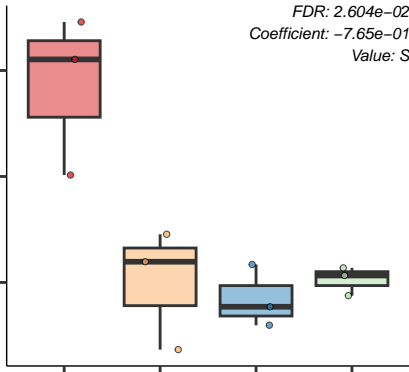
B (n=3)

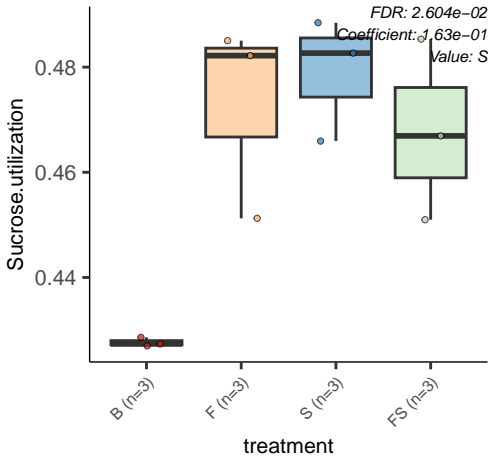
F (n=3)

S (n=3)

FS (n=3)

treatment





Two.partner.secretion.pathway..TPS.

FDR: 2.604e-02
Coefficient: -9.70e-01
Value: S

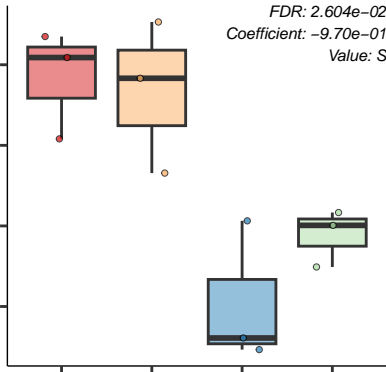
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



tRNA.aminoacylation..Arg

FDR: $2.604e-02$
Coefficient: $2.32e-01$
Value: FS

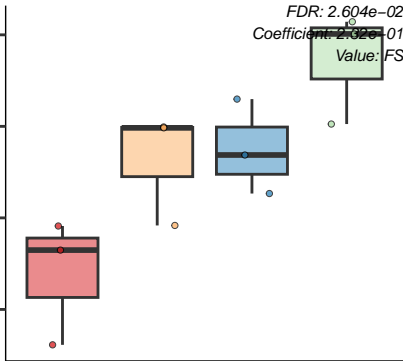
B (n=3)

F (n=3)

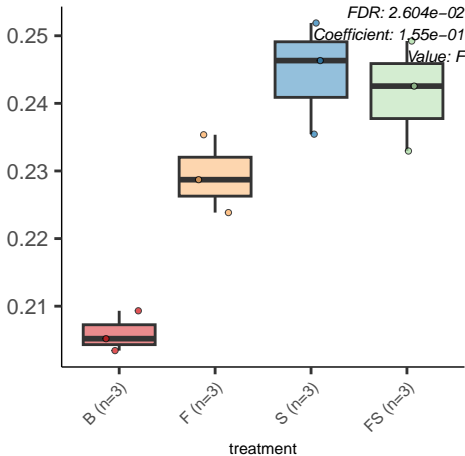
S (n=3)

FS (n=3)

treatment



tRNA.aminoacylation..Asp.and.Asn



tRNA.aminoacylation..Thr

FDR: 2.604e-02

Coefficient: 2.51e-01

Value: FS

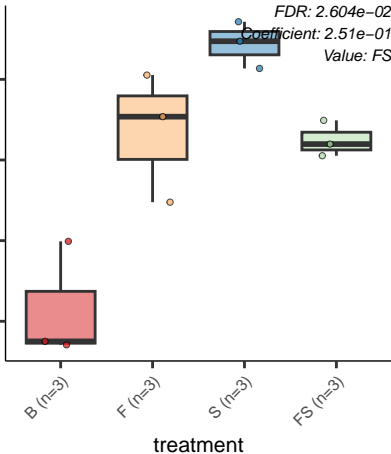
B (n=3)

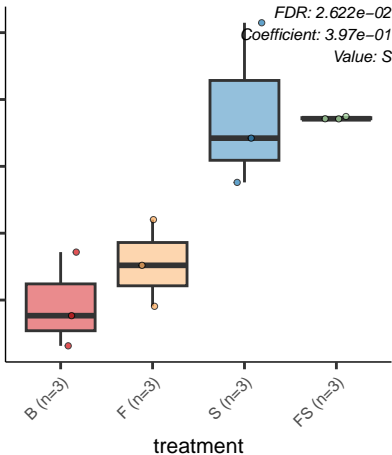
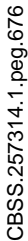
F (n=3)

S (n=3)

FS (n=3)

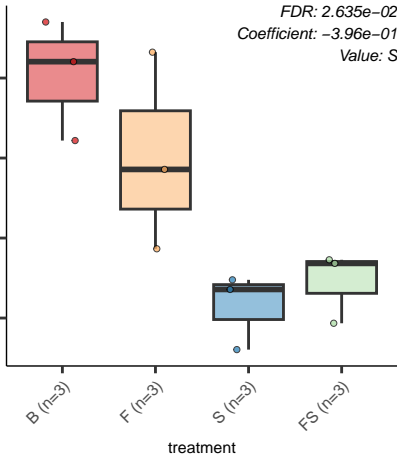
treatment

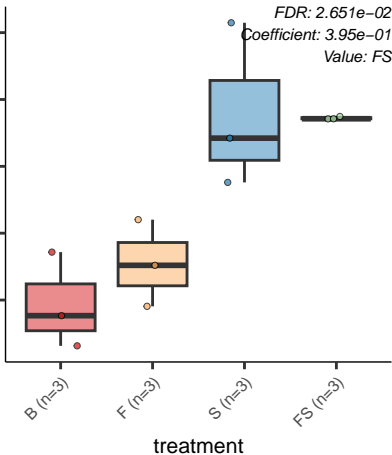
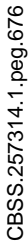




Broadly distributed proteins, not in subsystems

FDR: $2.635e-02$
Coefficient: $-3.96e-01$
Value: S





Nitrate.and.nitrite.ammonification

0.11
0.10
0.09
0.08
0.07

FDR: 2.663e-02
Coefficient: -5.06e-01
Value: FS

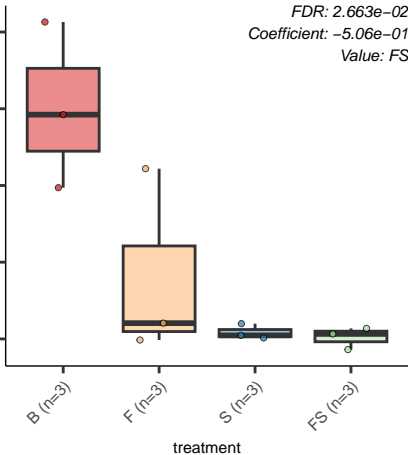
B (n=3)

F (n=3)

S (n=3)

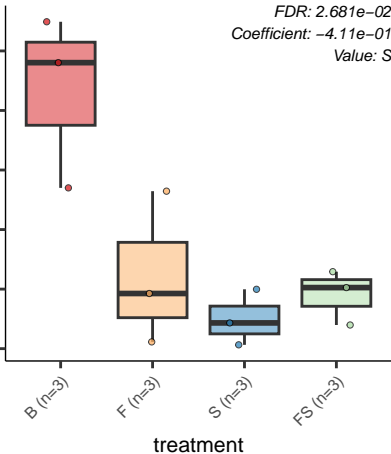
FS (n=3)

treatment



CBSS.326442.4.peg.1852

FDR: 2.681e-02
Coefficient: -4.11e-01
Value: S



Glycolysis.and.Gluconeogenesis

FDR: 2.692e-02

Coefficient: 7.68e-02

Value: S

0.66

0.64

0.62

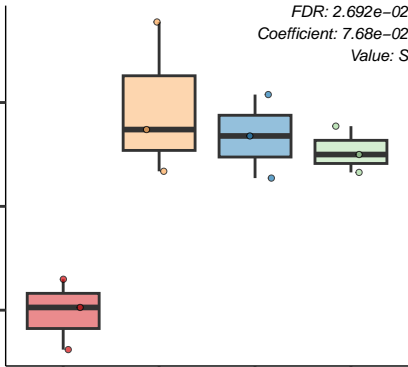
B (n=3)

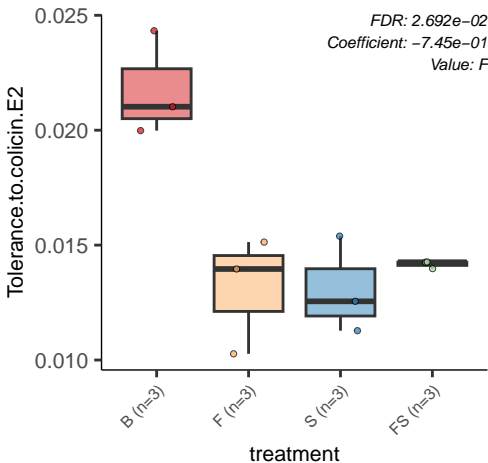
F (n=3)

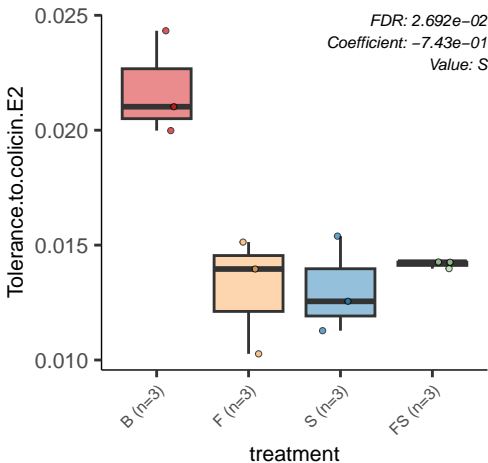
S (n=3)

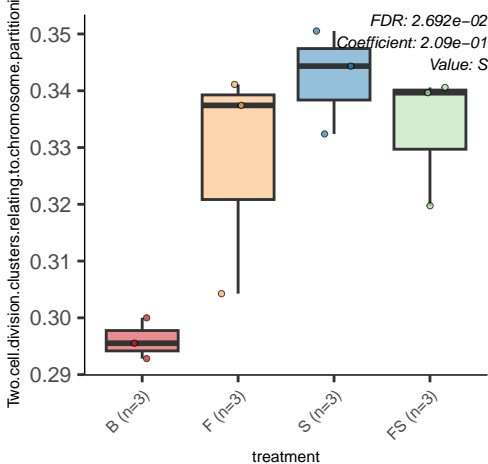
FS (n=3)

treatment

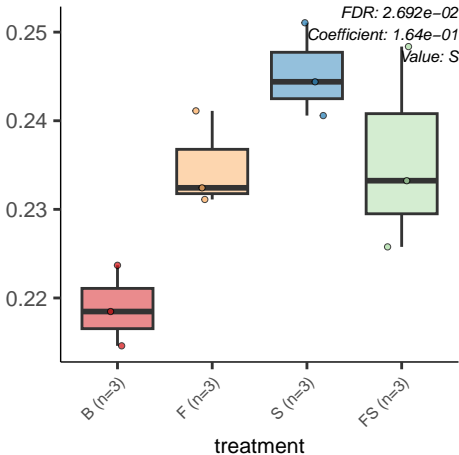






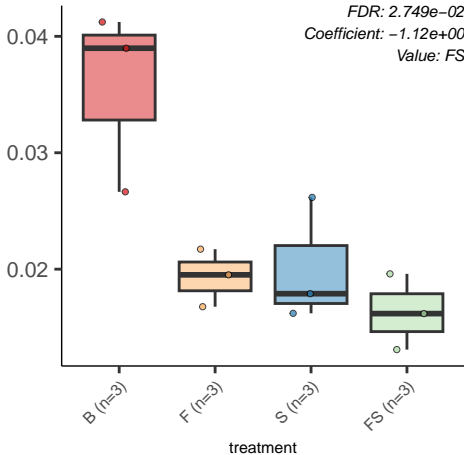


tRNA.aminoacylation..Val



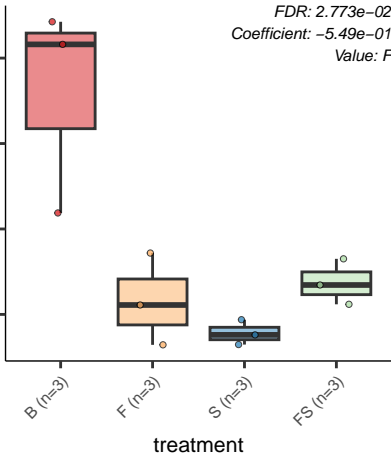
Peptide.ABC.transport.system.Sap

FDR: 2.749e-02
Coefficient: -1.12e+00
Value: FS



Bacterial.hemoglobins

FDR: 2.773e-02
Coefficient: -5.49e-01
Value: F



O.antigen.capsule.important.for.environmental.persistence

FDR: 2.773e-02
Coefficient: -9.69e-01
Value: S

0.04

0.03

0.02

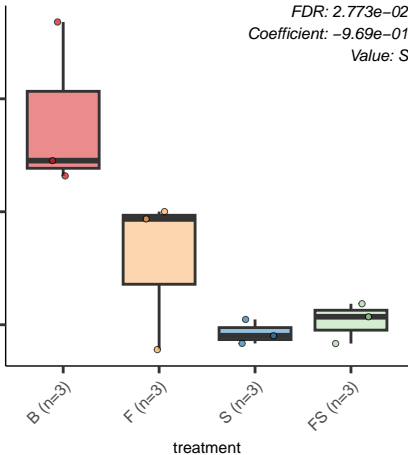
B (n=3)

F (n=3)

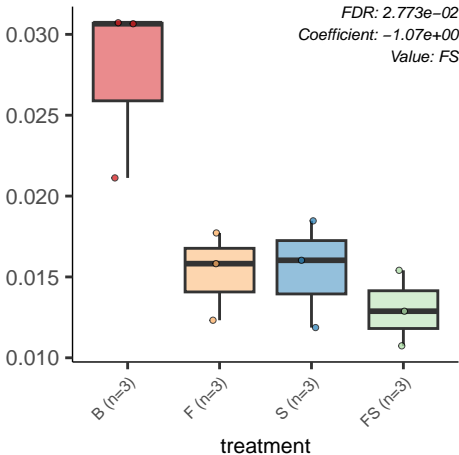
S (n=3)

FS (n=3)

treatment



The.fimbral.Stf.cluster



Tryptophan.synthesis

0.40
0.38
0.36

B (n=3)

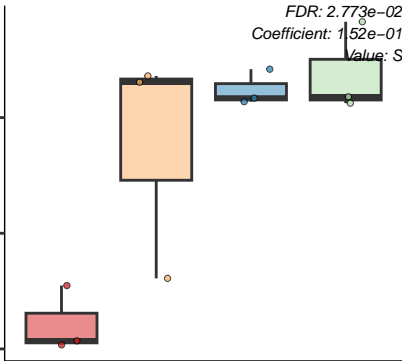
F (n=3)

S (n=3)

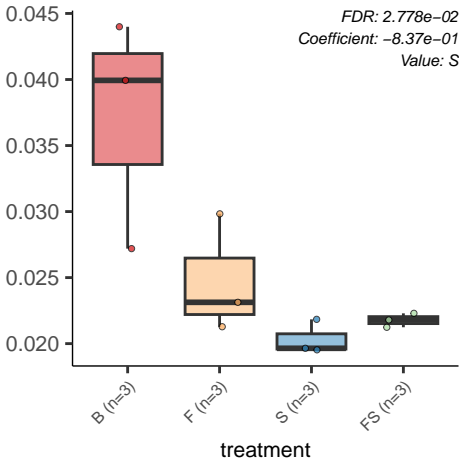
FS (n=3)

treatment

FDR: 2.773e-02
Coefficient: 1.52e-01
value: S



Siderophore.assembly.kit



Arginine.and.Ornithine.Degradation

FDR: 2.790e-02
Coefficient: -1.76e-01
Value: FS

0.28
0.27
0.26
0.25
0.24

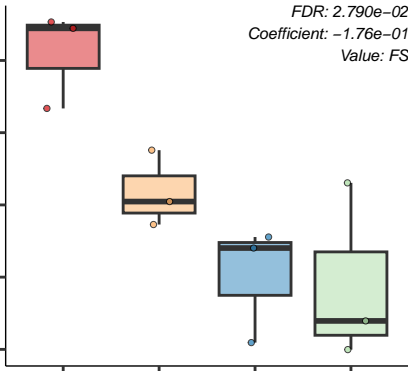
B (n=3)

F (n=3)

S (n=3)

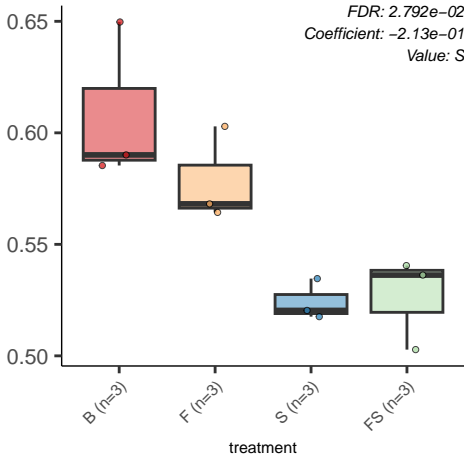
FS (n=3)

treatment

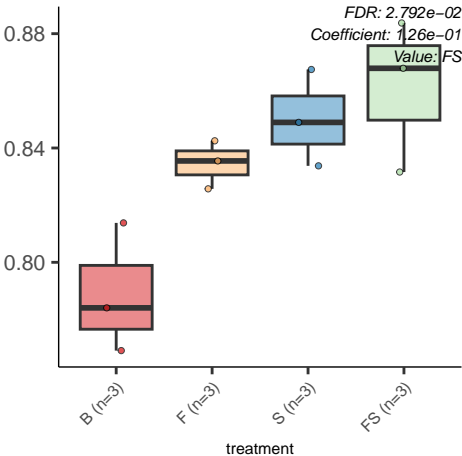


D.Galacturonate.and.D.Glucuronate.Utilization

FDR: 2.792e-02
Coefficient: -2.13e-01
Value: S



De.Novo.Purine.Biosynthesis



Omega.amidase

FDR: 2.792e-02
Coefficient: 7.69e-01
Value: S

0.008

0.006

0.004

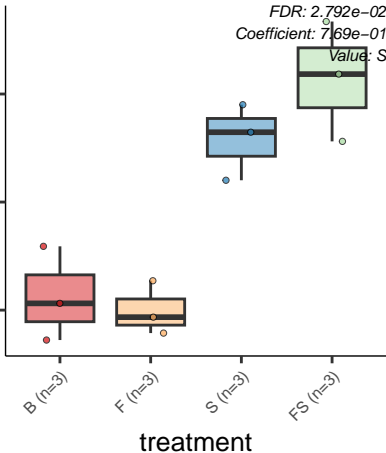
B (n=3)

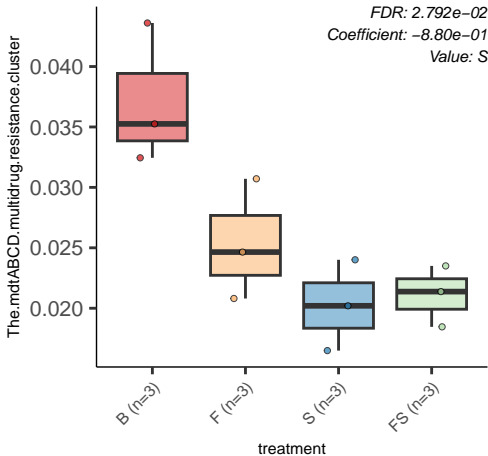
F (n=3)

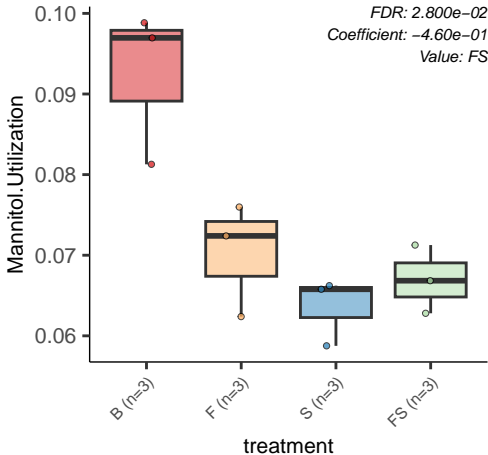
S (n=3)

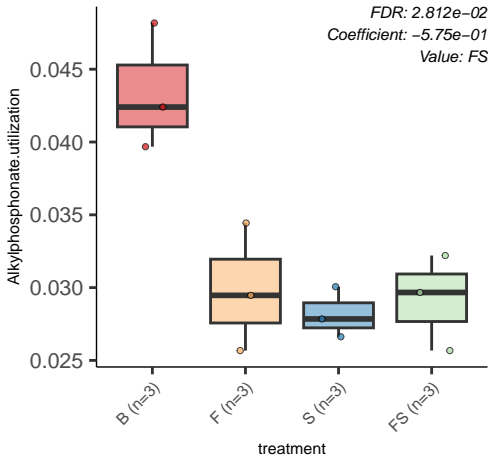
FS (n=3)

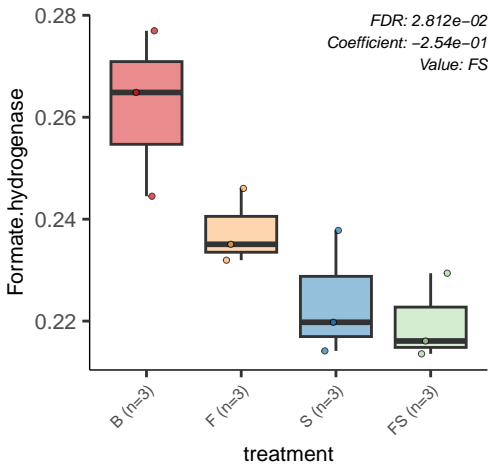
treatment









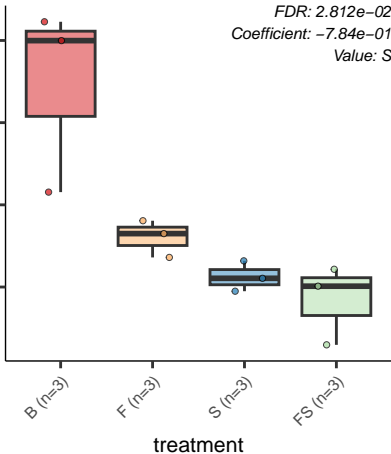


Glyoxylate.bypass

FDR: 2.812e-02

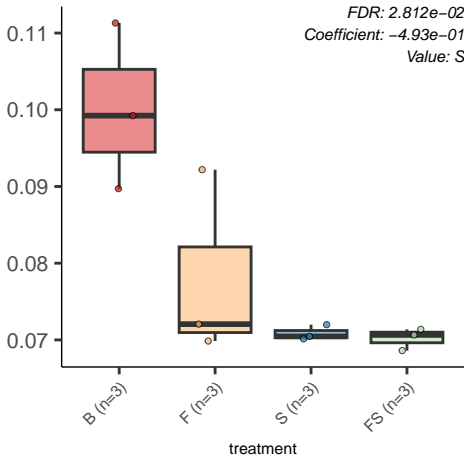
Coefficient: -7.84e-01

Value: S



Nitrate.and.nitrite.ammonification

FDR: 2.812e-02
Coefficient: -4.93e-01
Value: S



Phenylpropionate.Degradation

0.007
0.006
0.005
0.004
0.003

B (n=3)

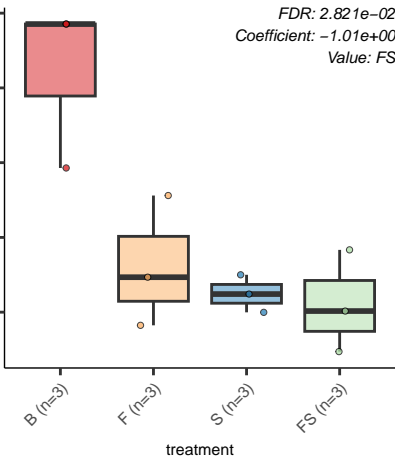
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 2.821e-02
Coefficient: -1.01e+00
Value: FS



Multidrug.efflux.pump.in.Campylobacter.jejuni..CmeABC.op

FDR: 2.829e-02
Coefficient: -8.30e-01
Value: F

0.04

0.03

0.02

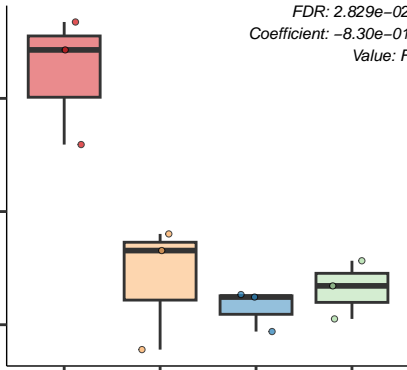
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Colonization.factor.antigen.l.fimbriae

FDR: 2.865e-02
Coefficient: -8.17e-01
Value: FS

0.030
0.025
0.020
0.015

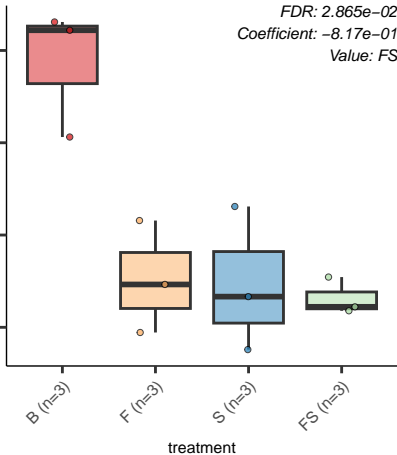
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Inorganic.Sulfur.Assimilation

FDR: 2.883e-02
Coefficient: -4.59e-01
Value: S

0.060

0.055

0.050

0.045

0.040

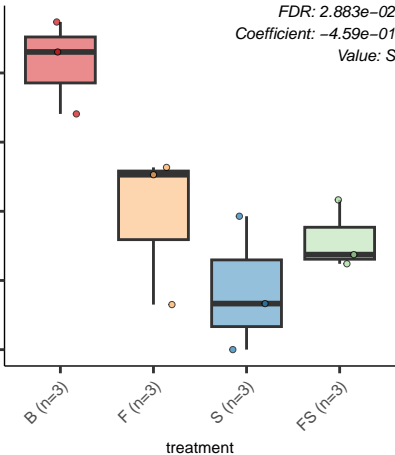
B (n=3)

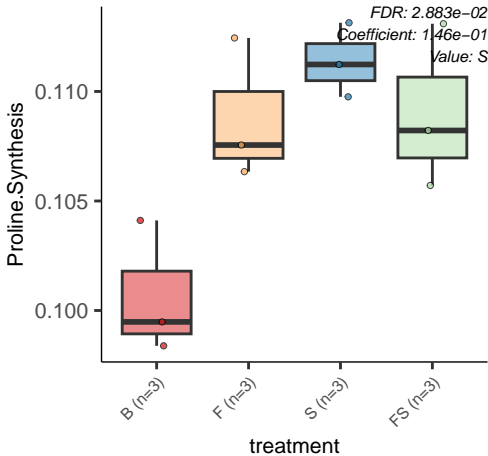
F (n=3)

S (n=3)

FS (n=3)

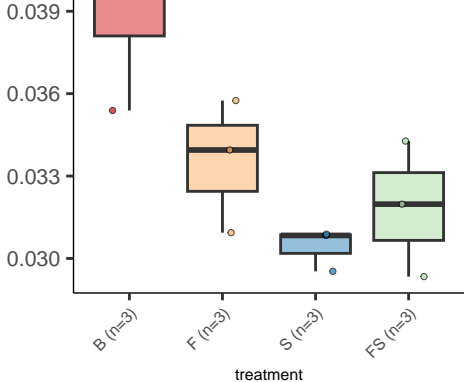
treatment





Ubiquinone.biosynthesis.....gjo

FDR: 2.893e-02
Coefficient: -3.61e-01
Value: S

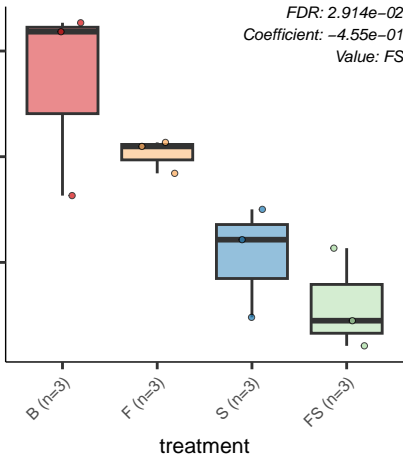


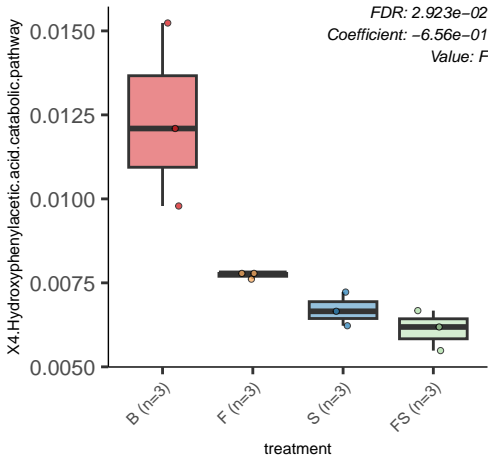
Phage.tail.proteins.2

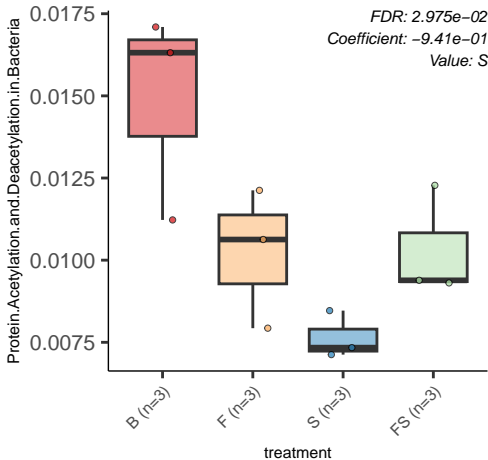
FDR: 2.914e-02

Coefficient: -4.55e-01

Value: FS







Peptidoglycan.Biosynthesis

0.84
0.82
0.80

B (n=3)

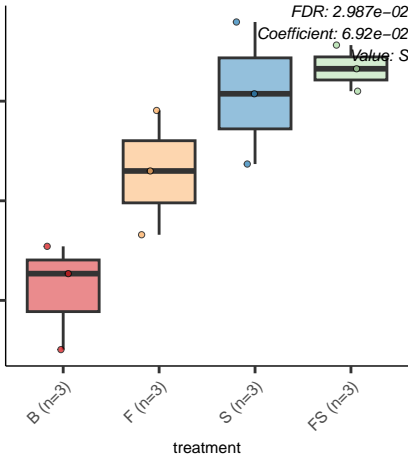
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 2.987e-02
Coefficient: 6.92e-02
Value: S



Outer.membrane

FDR: 2.987e-02

Coefficient: -4.44e-01

Value: S

0.045

0.040

0.035

0.030

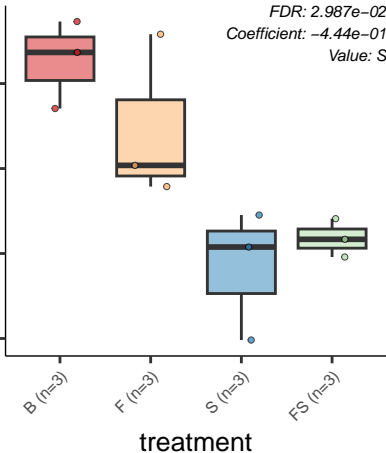
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment

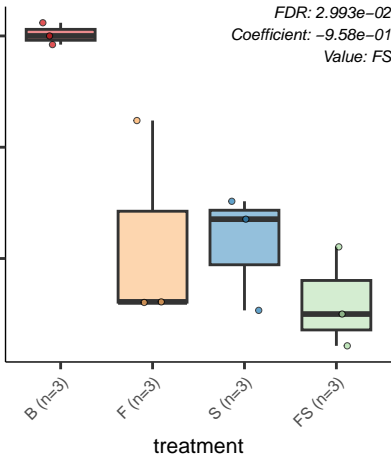


CBSS.584.1.pcg.841

FDR: 2.993e-02

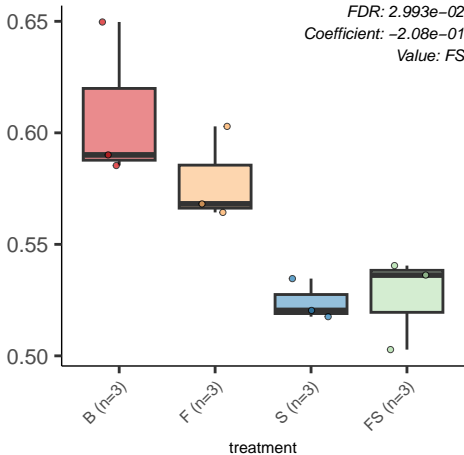
Coefficient: -9.58e-01

Value: FS

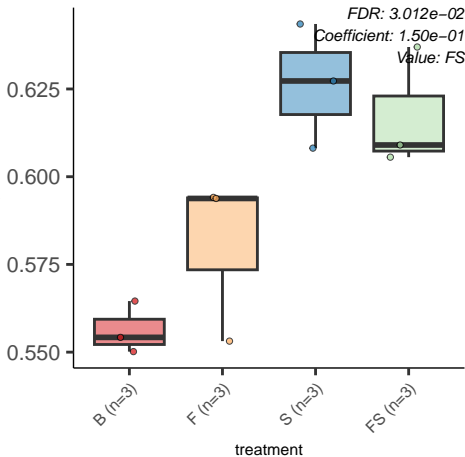


D.Galacturonate.and.D.Glucuronate.Utilization

FDR: 2.993e-02
Coefficient: -2.08e-01
Value: FS



Heat.shock.dnaK.gene.cluster.extended



Quinone.disambiguation

FDR: 3.012e-02
Coefficient: -5.80e-01
Value: FS

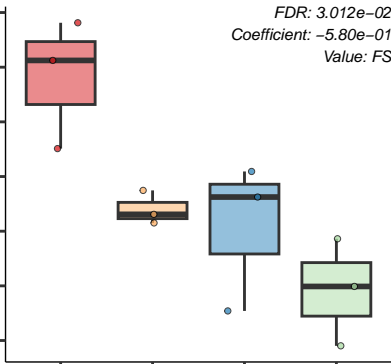
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



RNA.pseudouridine.syntheses

FDR: 3.012e-02
Coefficient: 2.08e-01
Value: FS

0.080

0.075

0.070

0.065

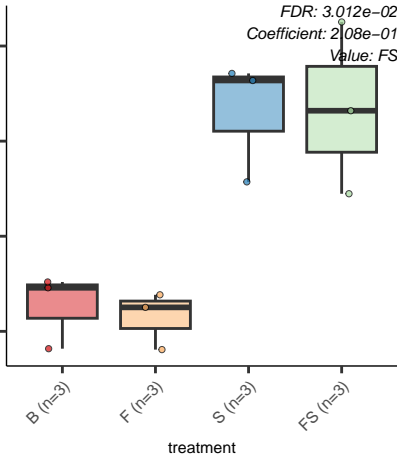
B (n=3)

F (n=3)

S (n=3)

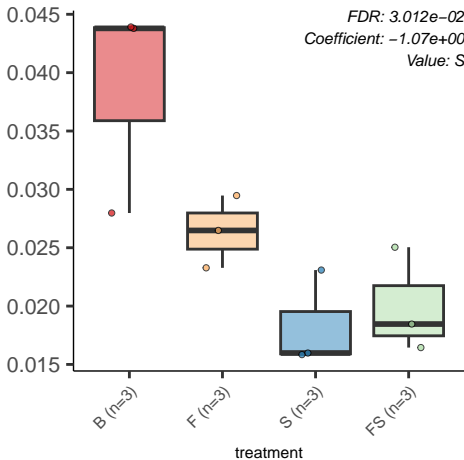
FS (n=3)

treatment



The.usher.protein.HtrE.fimbrial.cluster

FDR: 3.012e-02
Coefficient: -1.07e+00
Value: S



Oxygen.stress.response...Human.gut.microbiome

FDR: 3.024×10^{-2}
Coefficient: -2.04×10^{-1}
Value: FS

0.14

0.13

0.12

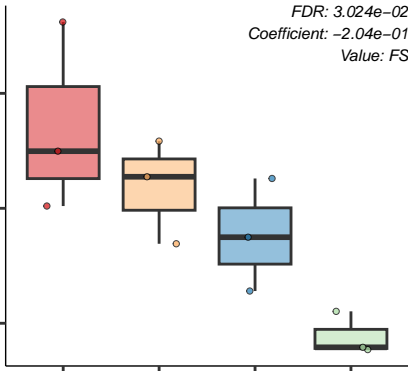
B (n=3)

F (n=3)

S (n=3)

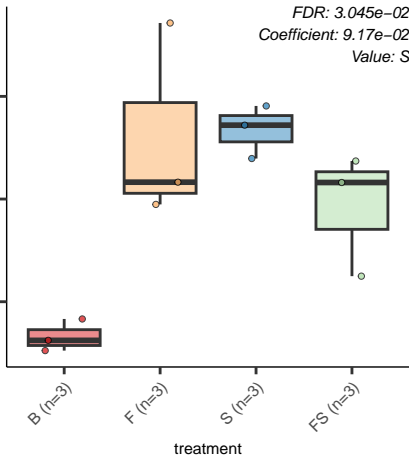
FS (n=3)

treatment



Single.copy.ribosomal.proteins

FDR: 3.045e-02
Coefficient: 9.17e-02
Value: S



Glutaredoxins

FDR: 3.046e-02
Coefficient: -9.20e-02
Value: S

0.225

0.220

0.215

0.210

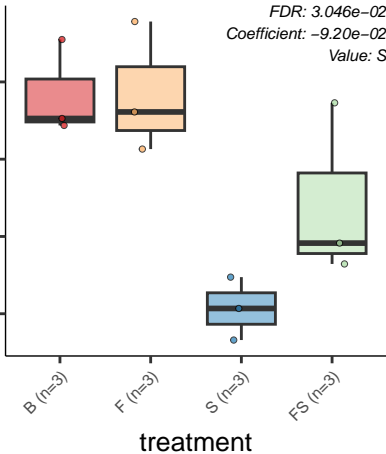
B (n=3)

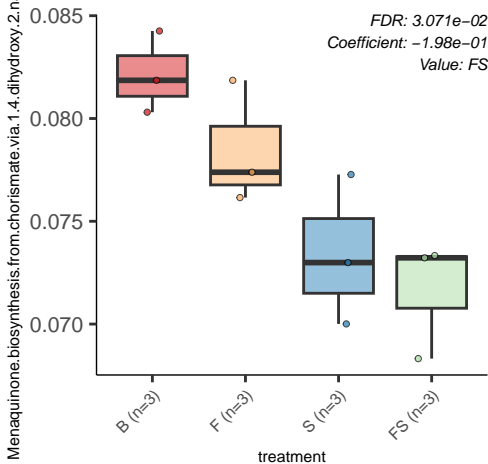
F (n=3)

S (n=3)

FS (n=3)

treatment





Pyrimidine.utilization

FDR: $3.071e-02$
Coefficient: $-7.97e-01$
Value: FS

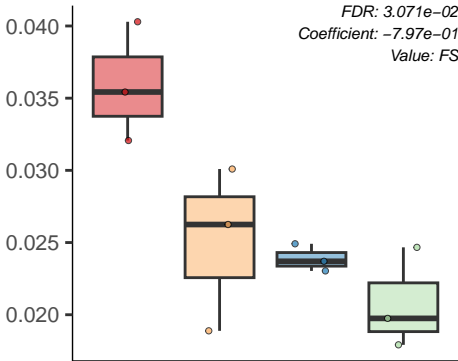
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Phosphorylcholine.incorporation.in.LPS

0.016
0.014
0.012
0.010

B (n=3)

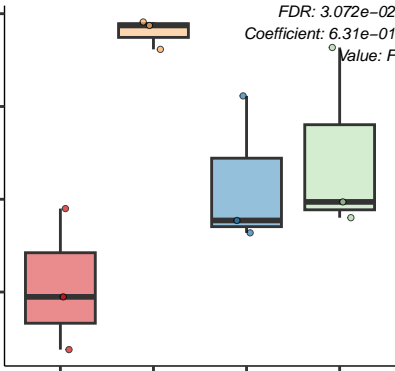
F (n=3)

S (n=3)

FS (n=3)

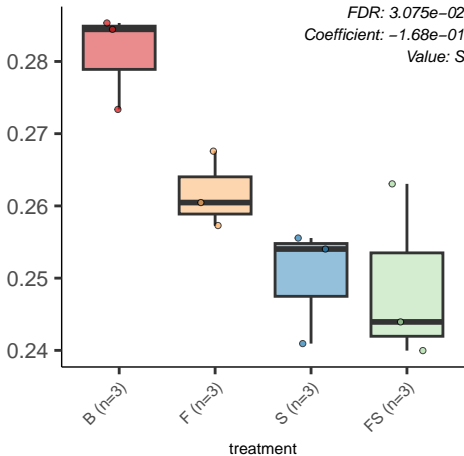
treatment

FDR: 3.072e-02
Coefficient: 6.31e-01
Value: F



Arginine.and.Ornithine.Degradation

FDR: 3.075e-02
Coefficient: -1.68e-01
Value: S



RNA.pseudouridine.syntheses

0.080
0.075
0.070
0.065

B (n=3)

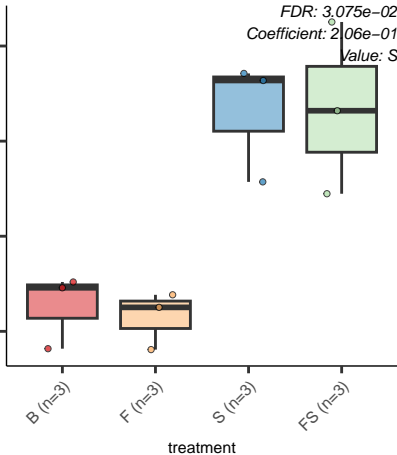
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 3.075e-02
Coefficient: 2.106e-01
value: S



Biofilm.Adhesin.Biosynthesis

FDR: $3.085e-02$
Coefficient: $-1.07e+00$
Value: FS

0.025

0.020

0.015

0.010

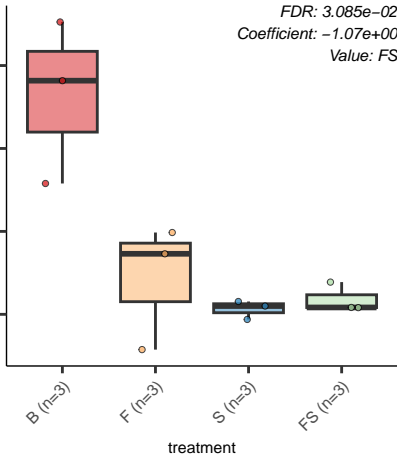
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Peptidoglycan.biosynthesis..gjo

0.23

0.22

0.21

B (n=3)

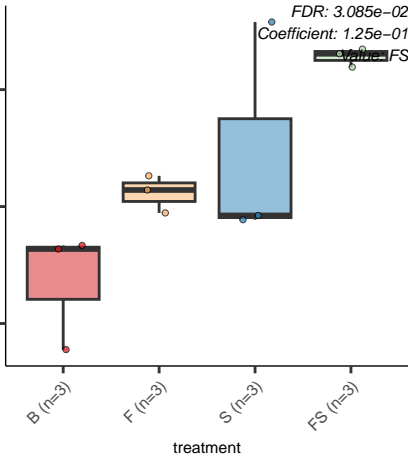
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 3.085e-02
Coefficient: 1.25e-01
Value FS



tRNA.aminoacylation..Gly

FDR: 3.085e-02

Coefficient: 1.96e-01

Value: FS

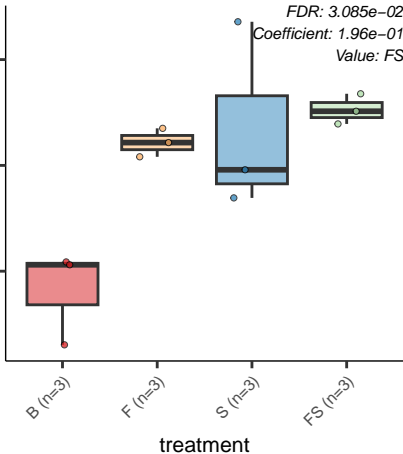
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Hemin.transport.system

FDR: $3.124e-02$
Coefficient: $-4.67e-01$
Value: S

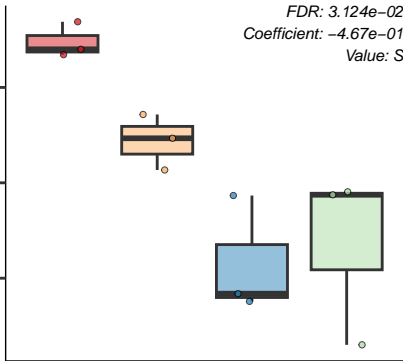
B (n=3)

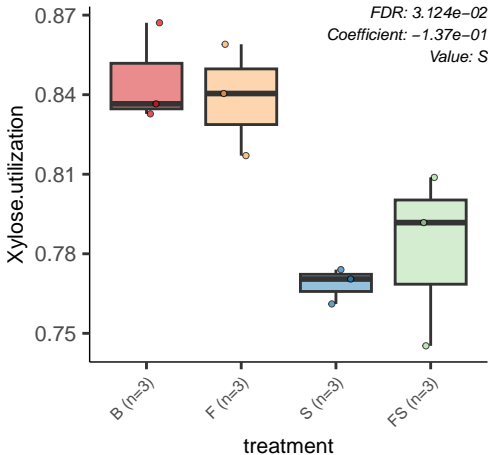
F (n=3)

S (n=3)

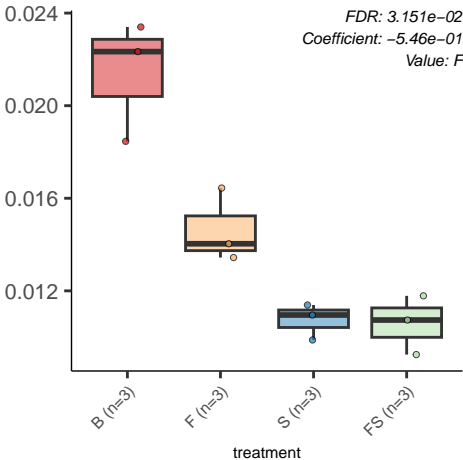
FS (n=3)

treatment





Capsular.surface.virulence.antigen.loci



Diadenylate.cyclase.cluster

0.008
0.006
0.004

B (n=3)

F (n=3)

S (n=3)

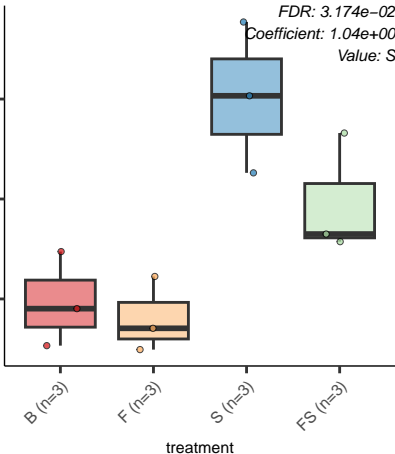
FS (n=3)

treatment

FDR: 3.174e-02

Coefficient: 1.04e+00

Value: S



Lipopolysaccharide.assembly

FDR: 3.174e-02
Coefficient: -6.41e-01
Value: S

0.10
0.09
0.08
0.07
0.06

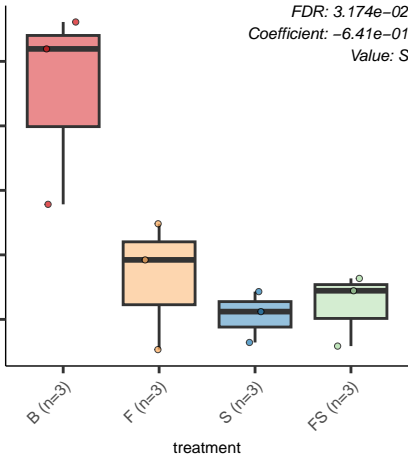
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Orphan.regulatory.proteins

0.10

0.08

0.06

B (n=3)

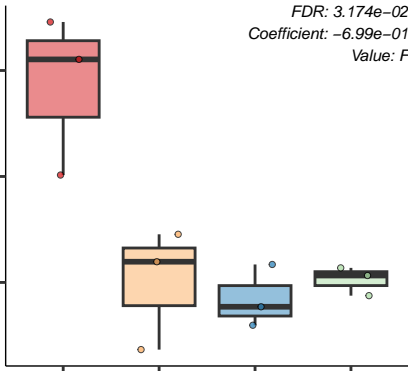
F (n=3)

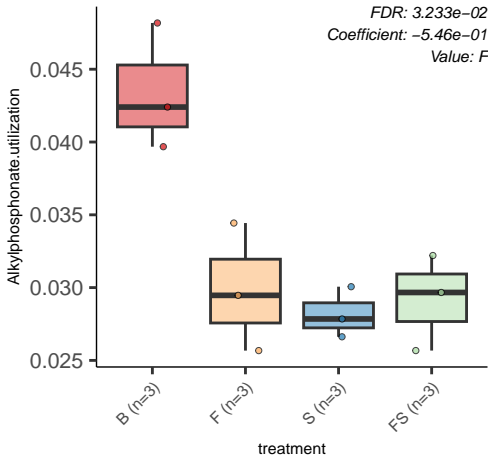
S (n=3)

FS (n=3)

treatment

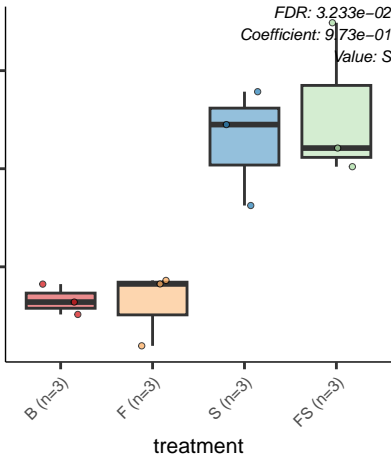
FDR: 3.174e-02
Coefficient: -6.99e-01
Value: F

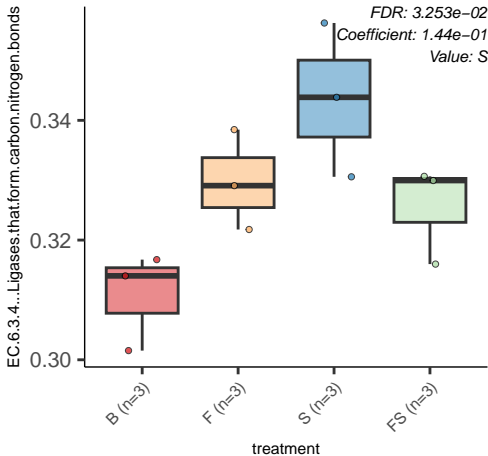


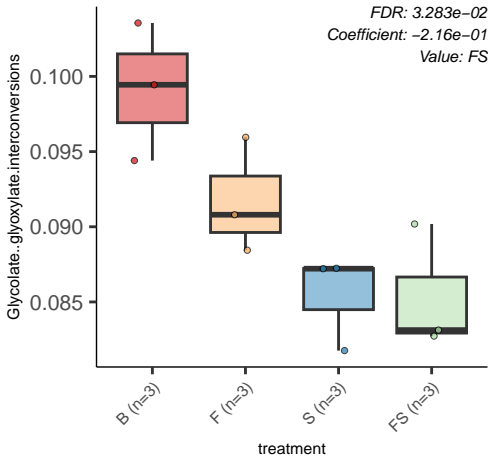


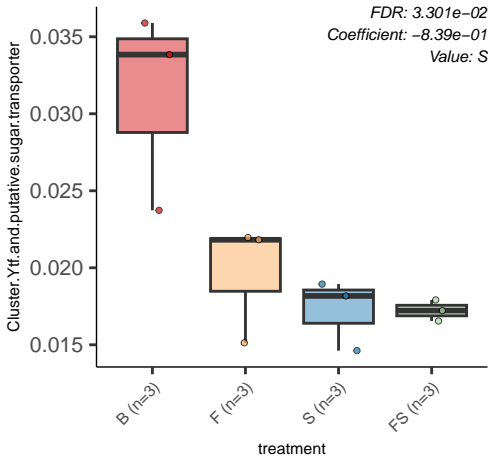
CBSS.261594.1.pcg.788

FDR: 3.233e-02
Coefficient: 9.73e-01
Value: S









Colonization.factor.antigen.l.fimbriae

FDR: 3.301e-02
Coefficient: -7.75e-01
Value: S

0.030

0.025

0.020

0.015

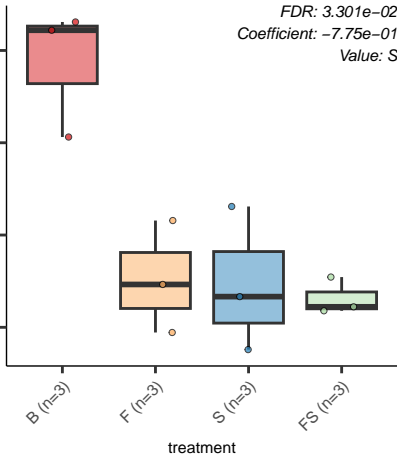
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



General.Secretion.Pathway

FDR: 3.301e-02
Coefficient: -8.89e-01
Value: FS

0.10
0.08
0.06
0.04

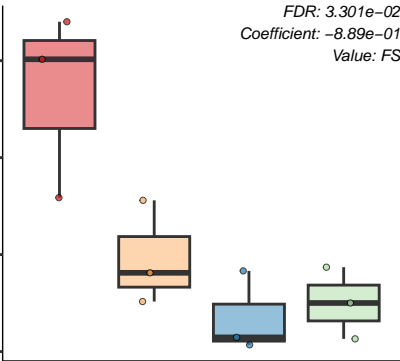
B (n=3)

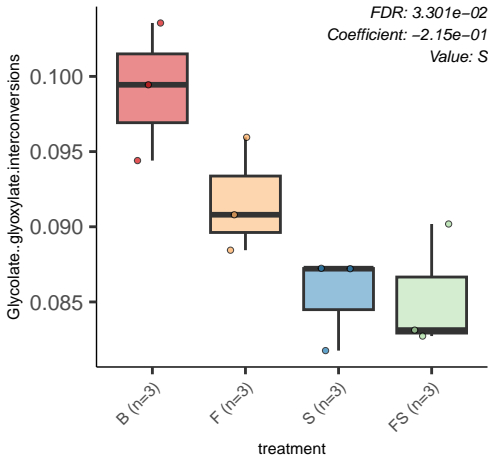
F (n=3)

S (n=3)

FS (n=3)

treatment





Glycolysis.and.Gluconeogenesis

FDR: 3.301e-02
Coefficient: 7.05e-02
Value: FS

0.66
0.64
0.62

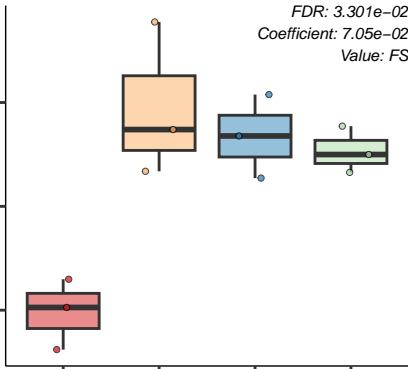
B (n=3)

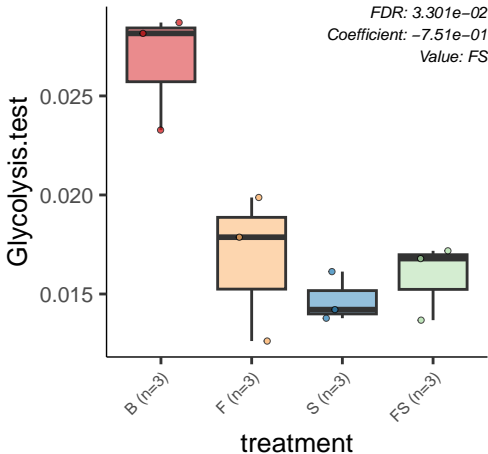
F (n=3)

S (n=3)

FS (n=3)

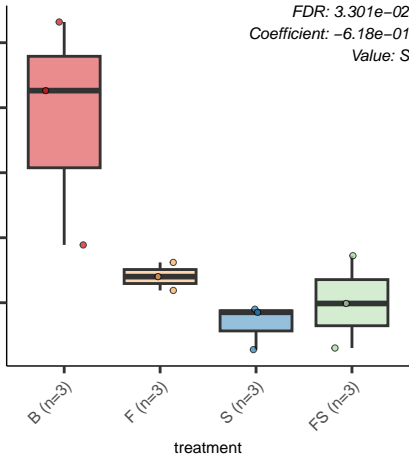
treatment

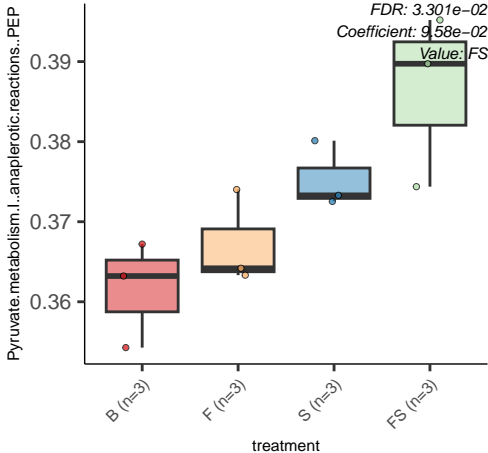




L.ascorbate.utilization..and.related.gene.clusters.

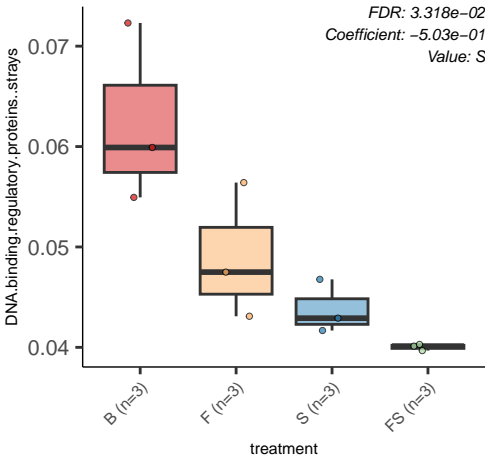
FDR: 3.301e-02
Coefficient: -6.18e-01
Value: S





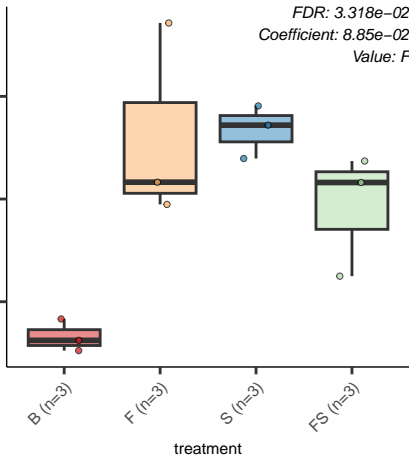
DNA.binding.regulatory.proteins...strays

FDR: 3.318e-02
Coefficient: -5.03e-01
Value: S



Single.copy.ribosomal.proteins

FDR: 3.318e-02
Coefficient: 8.85e-02
Value: F



O.antigen.capsule.important.for.environmental.persistence

FDR: $3.322e-02$
Coefficient: $-8.97e-01$
Value: FS

0.04

0.03

0.02

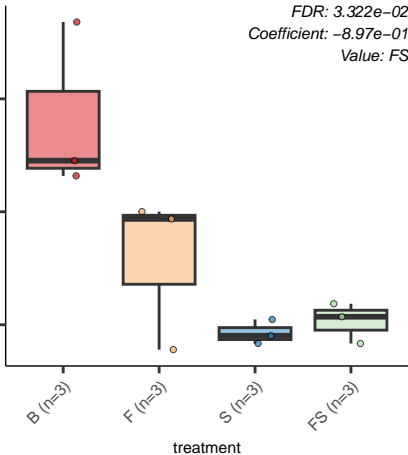
B (n=3)

F (n=3)

S (n=3)

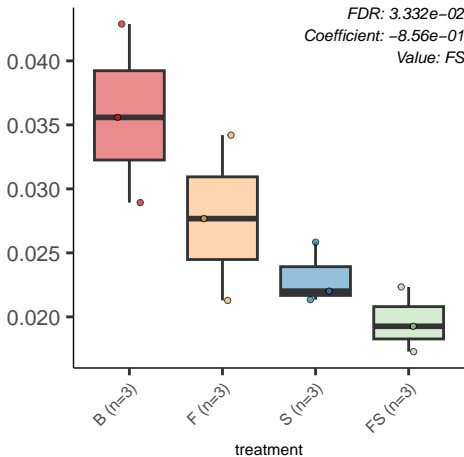
FS (n=3)

treatment



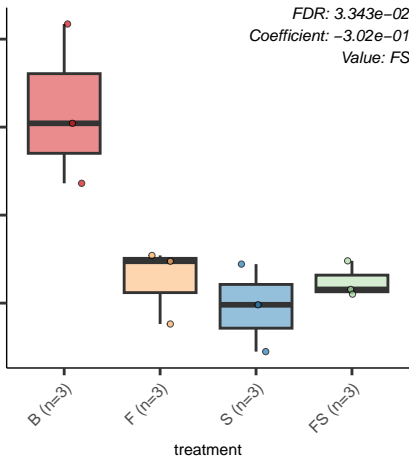
Inner.membrane.protein.YhjD.and.conservd.cluster.involved.in.LPS

FDR: $3.332e-02$
Coefficient: $-8.56e-01$
Value: FS

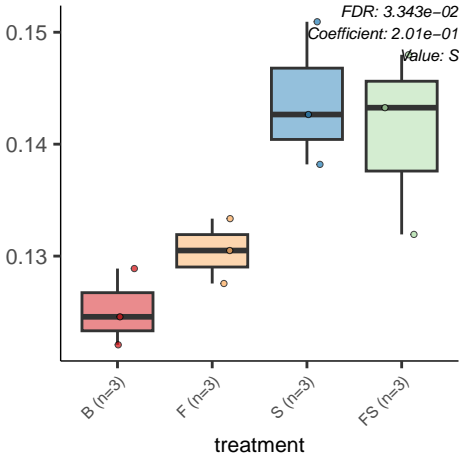


Capsular.Polysaccharides.Biosynthesis.and.Assembly

FDR: $3.343e-02$
Coefficient: $-3.02e-01$
Value: FS



Fe.S.cluster:assembly



Carbon.Starvation

FDR: 3.355e-02
Coefficient: -2.37e-01
Value: S

0.15

0.14

0.13

0.12

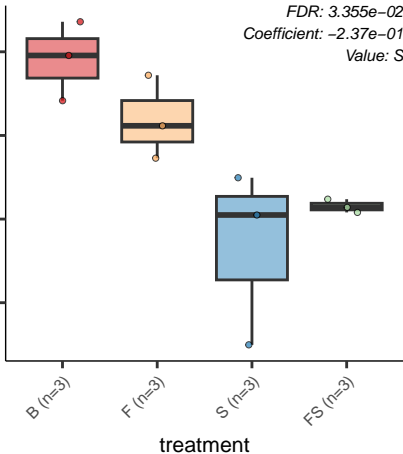
B (n=3)

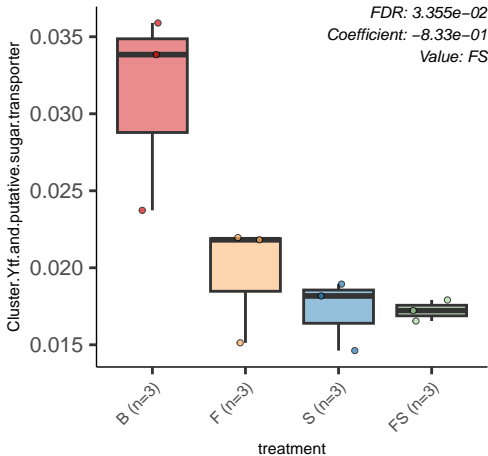
F (n=3)

S (n=3)

FS (n=3)

treatment





ECF.class.transporters

0.32
0.30
0.28
0.26

B (n=3)

F (n=3)

S (n=3)

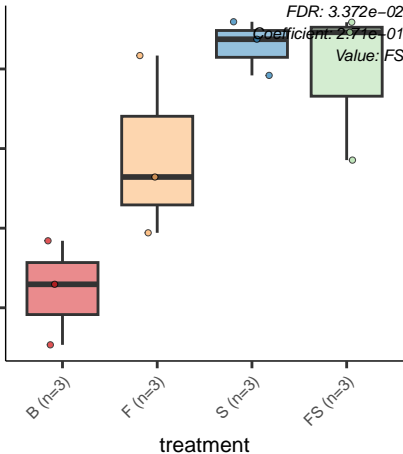
FS (n=3)

treatment

FDR: 3.372e-02

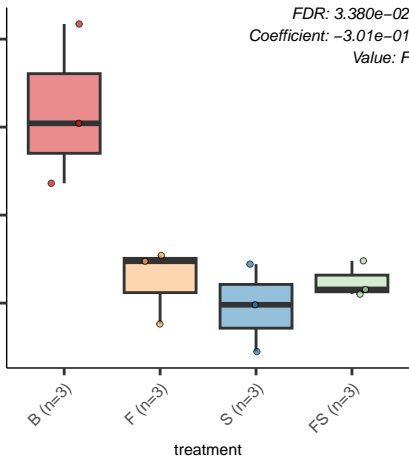
Coefficient: 2.71e-01

Value: FS

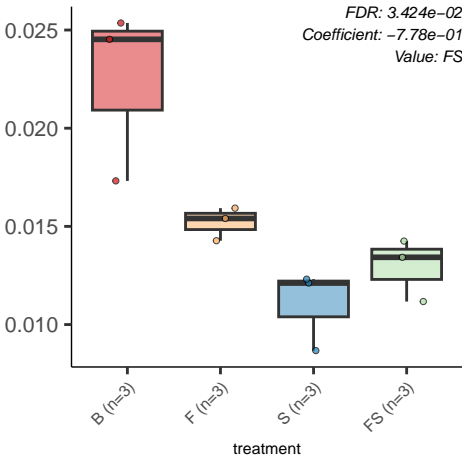


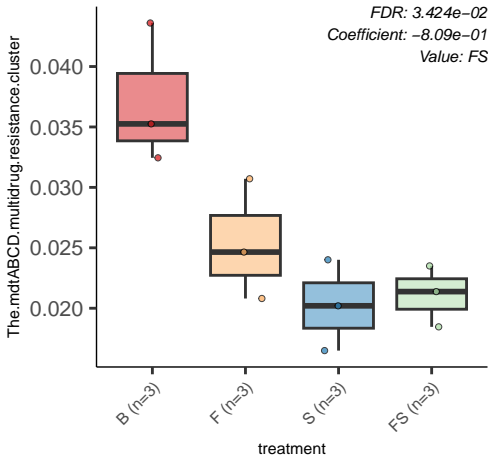
Capsular.Polysaccharides.Biosynthesis.and.Assembly

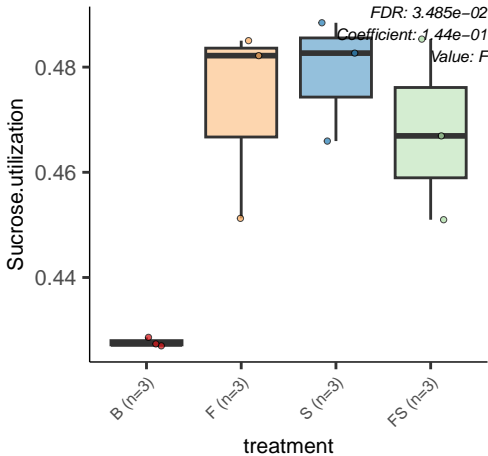
FDR: 3.380e-02
Coefficient: -3.01e-01
Value: F



Accessory.colonization.factor







Lysozyme.inhibitors

FDR: 3.516e-02
Coefficient: -1.00e+00
Value: S

B (n=3)

F (n=3)

S (n=3)

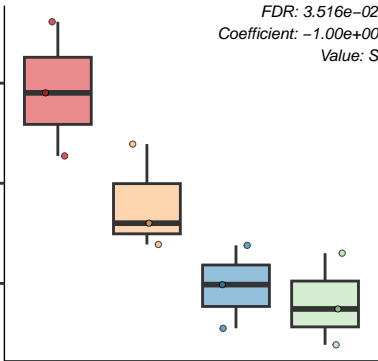
FS (n=3)

treatment

0.0100

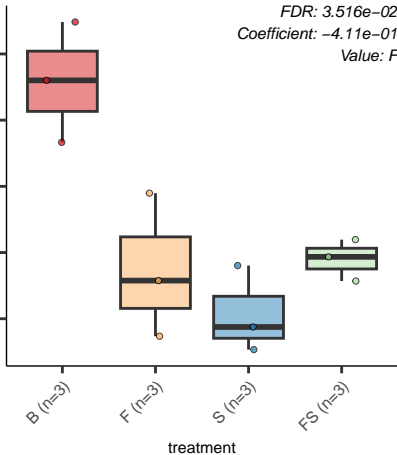
0.0075

0.0050

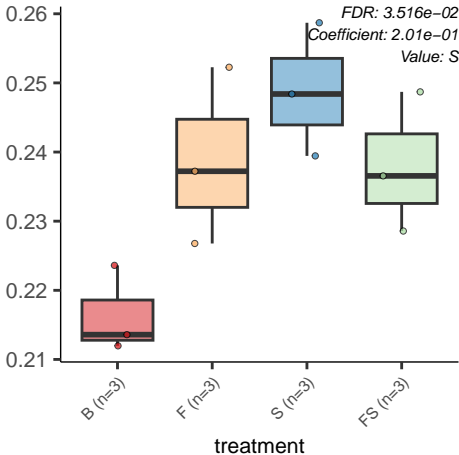


Unknown.sugar.utilization...cluster.yphABCDEFG.

FDR: 3.516e-02
Coefficient: -4.11e-01
Value: F



tRNA.aminoacylation..Phe



Orphan.regulatory.proteins

0.10

0.08

0.06

B (n=3)

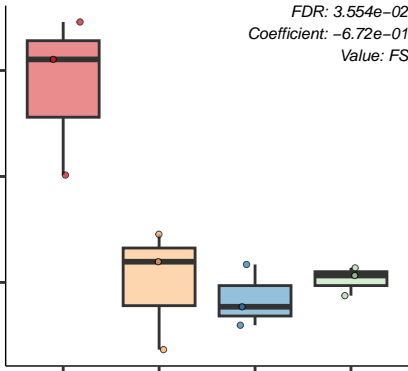
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 3.554e-02
Coefficient: -6.72e-01
Value: FS



Periplasmic.Stress.Response

0.094

0.090

0.086

B (n=3)

F (n=3)

S (n=3)

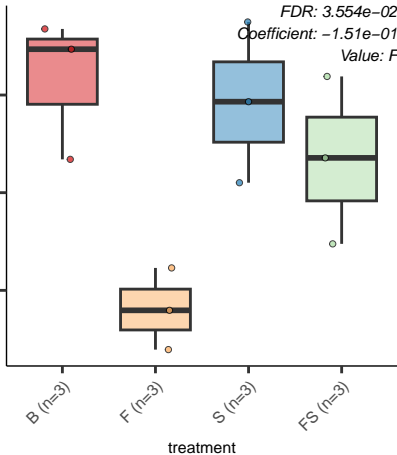
FS (n=3)

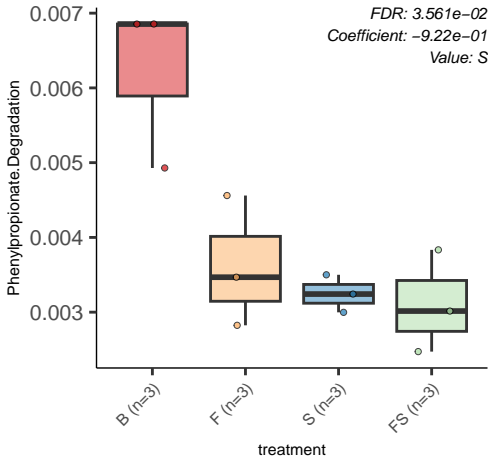
treatment

FDR: 3.554e-02

Coefficient: -1.51e-01

Value: F





Histidine.Biosynthesis

FDR: 3.622e-02

Coefficient: 8.21e-02

Value: F

B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment

0.525

0.550

0.575

Iron.III..dicitrate.transport.system.Fec

FDR: 3.625e-02
Coefficient: -9.85e-01
Value: FS

B (n=3)

F (n=3)

S (n=3)

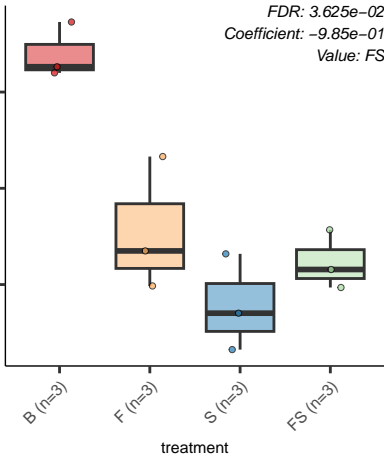
FS (n=3)

treatment

0.0100

0.0075

0.0050



CBSS.84588.1.pcg.1247

0.100
0.095
0.090
0.085
0.080
0.075

B (n=3)

F (n=3)

S (n=3)

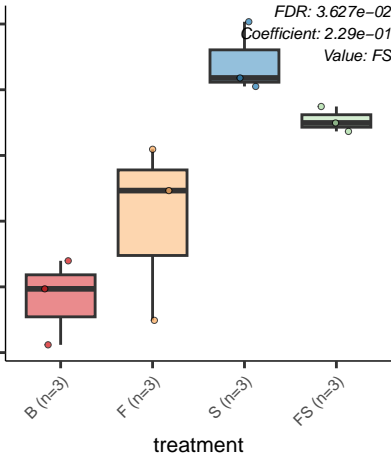
FS (n=3)

treatment

FDR: 3.627e-02

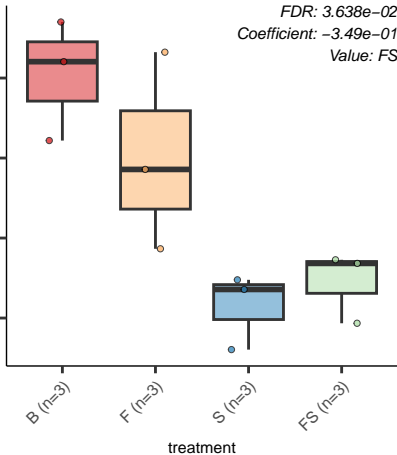
Coefficient: 2.29e-01

Value: FS



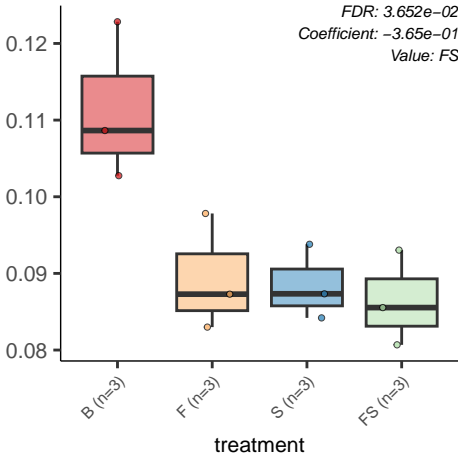
Broadly distributed proteins, not in subsystems

FDR: 3.638e-02
Coefficient: -3.49e-01
Value: FS



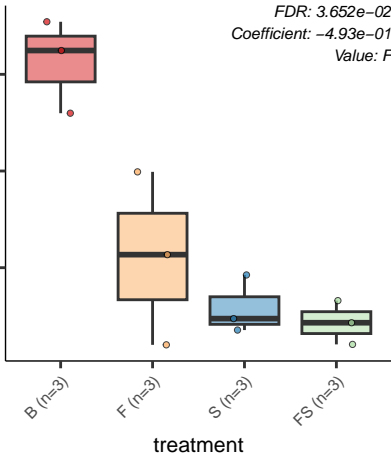
Flavo haemoglobin

FDR: 3.652e-02
Coefficient: -3.65e-01
Value: FS

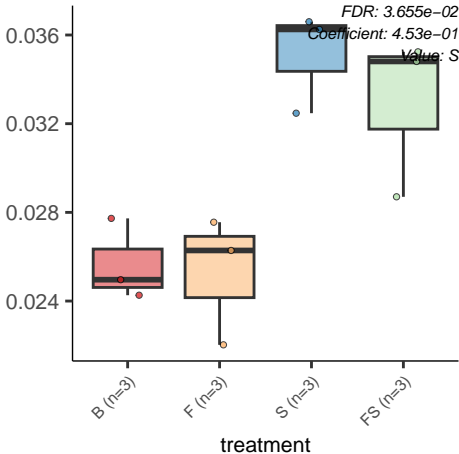


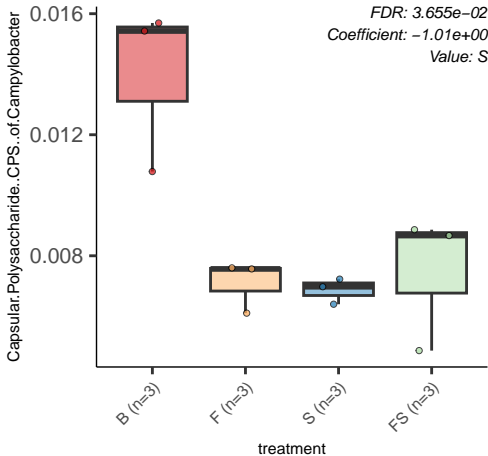
Transposase.in.entrics

FDR: 3.652e-02
Coefficient: -4.93e-01
Value: F



Adhesion.of.Campylobacter





Siderophore.Enterobactin

FDR: 3.655e-02
Coefficient: -9.65e-01
Value: S

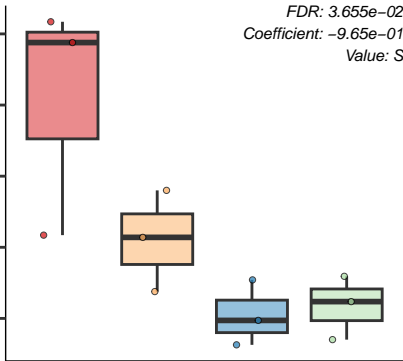
B (n=3)

F (n=3)

S (n=3)

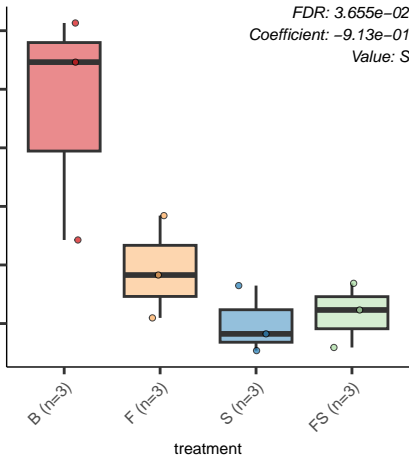
FS (n=3)

treatment



Type.1.pili..mannose.sensitive.fimbriae.

FDR: $3.655e-02$
Coefficient: $-9.13e-01$
Value: S



Copper.homeostasis..copper.tolerance

FDR: 3.662e-02
Coefficient: -2.74e-01
Value: F

0.050

0.045

0.040

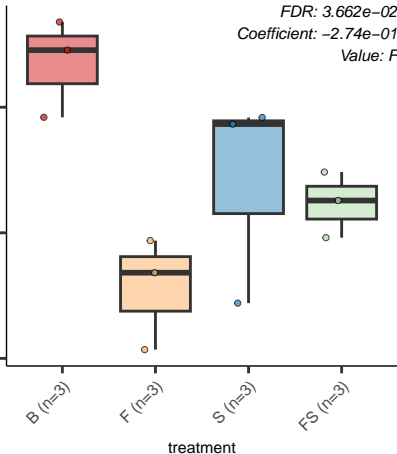
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Colonization.factor.antigen.l.fimbriae

FDR: 3.666e-02
Coefficient: -7.43e-01
Value: F

0.030
0.025
0.020
0.015

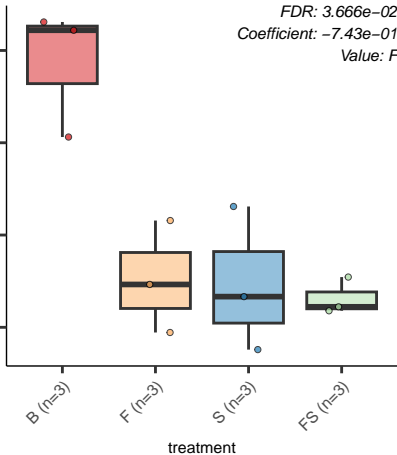
B (n=3)

F (n=3)

S (n=3)

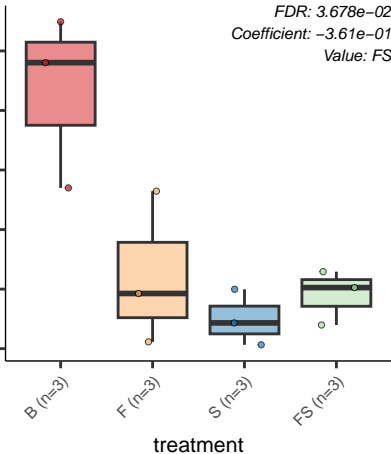
FS (n=3)

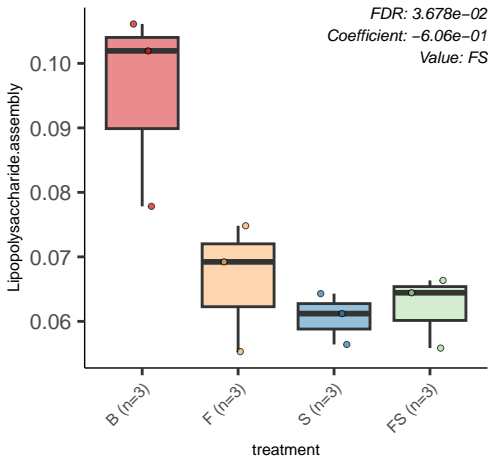
treatment

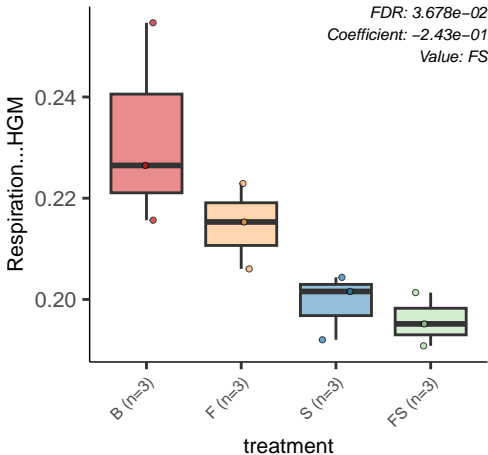


CBSS.326442.4.peg.1852

FDR: 3.678e-02
Coefficient: -3.61e-01
Value: FS





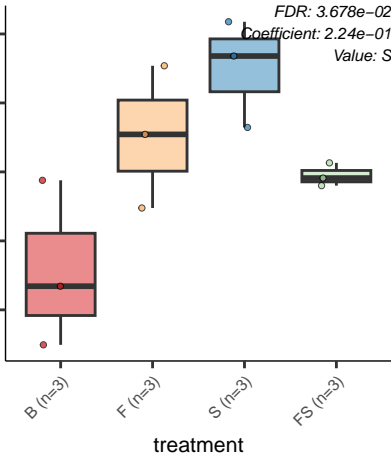


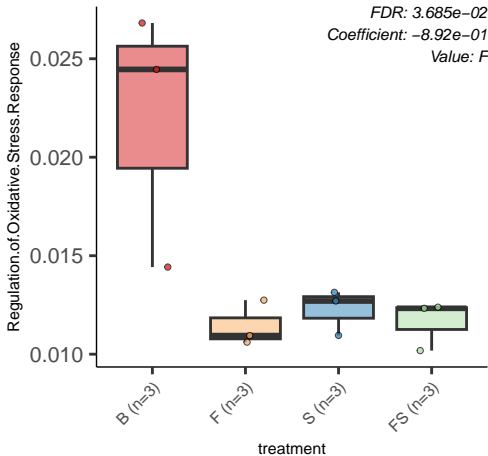
tRNA.aminoacylation..Trp

FDR: 3.678e-02

Coefficient: 2.24e-01

Value: S





Thiamin.biosynthesis.in.plants

FDR: 3.695e-02
Coefficient: -7.62e-01
Value: FS

0.0030
0.0025
0.0020
0.0015
0.0010

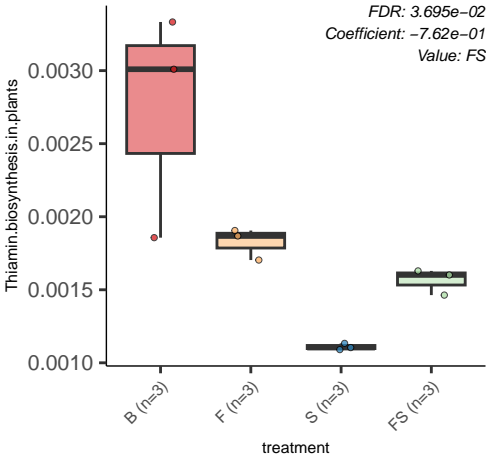
B (n=3)

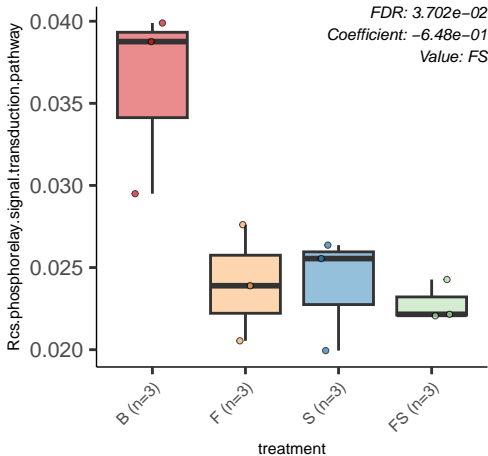
F (n=3)

S (n=3)

FS (n=3)

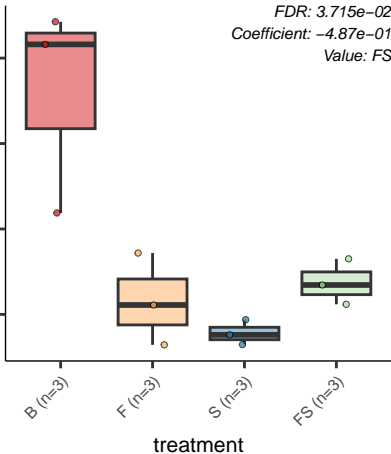
treatment





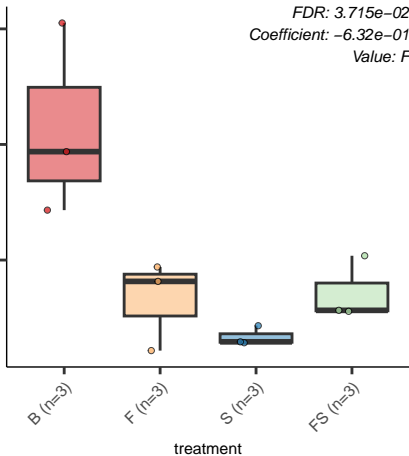
Bacterial.hemoglobins

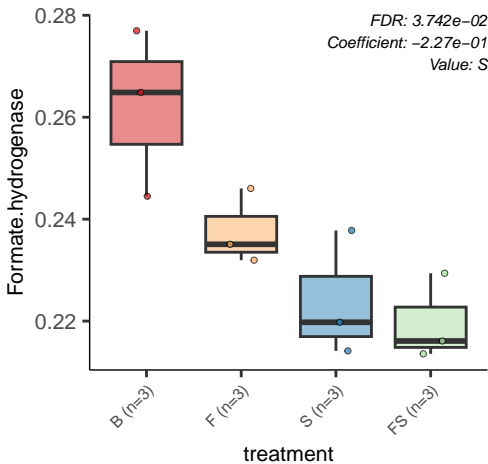
FDR: 3.715e-02
Coefficient: -4.87e-01
Value: FS



Major.Outer.Membrane.Proteins

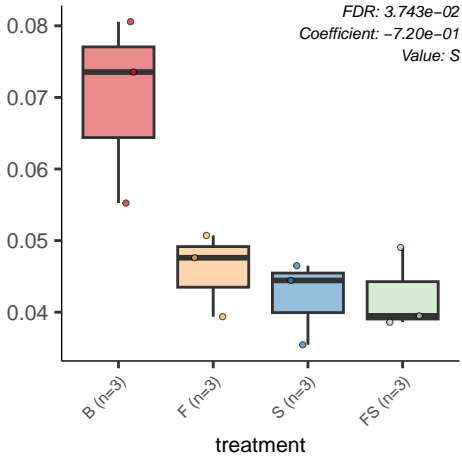
FDR: 3.715e-02
Coefficient: -6.32e-01
Value: F





Phage.tail.fiber.proteins

FDR: 3.743e-02
Coefficient: -7.20e-01
Value: S



CBSS.216592.1.pcg.3937

FDR: 3.743e-02
Coefficient: -7.57e-01
Value: S

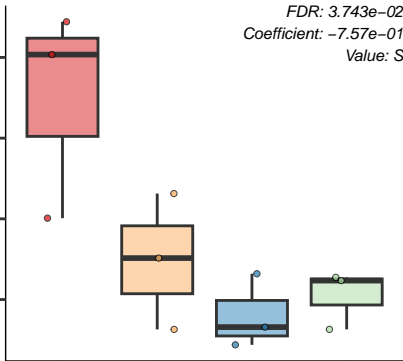
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Glycogen.metabolism

FDR: 3.745e-02

Coefficient: 1.17e-01

Value: S

1.00

0.96

0.92

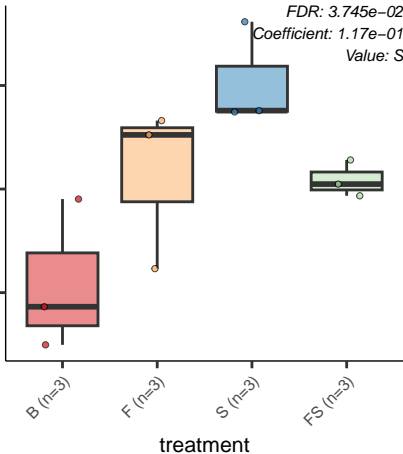
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Tricarboxylate.transport.system

0.012

0.011

0.010

0.009

0.008

B (n=3)

F (n=3)

S (n=3)

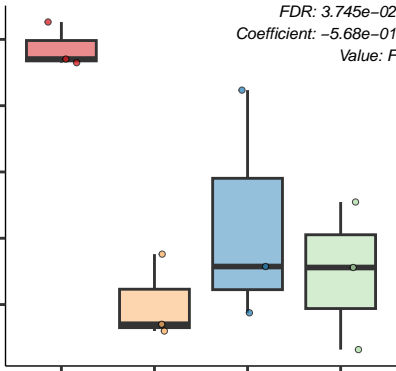
FS (n=3)

treatment

FDR: 3.745e-02

Coefficient: -5.68e-01

Value: F



Polysaccharide.deacetylases

0.06

0.05

B (n=3)

F (n=3)

S (n=3)

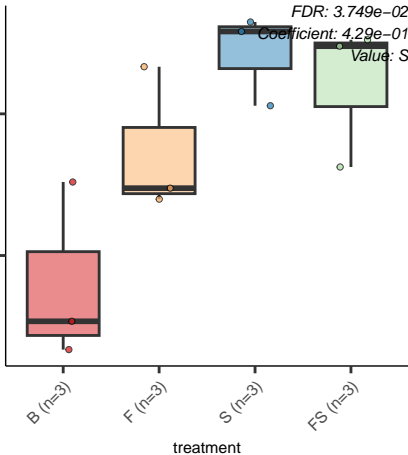
FS (n=3)

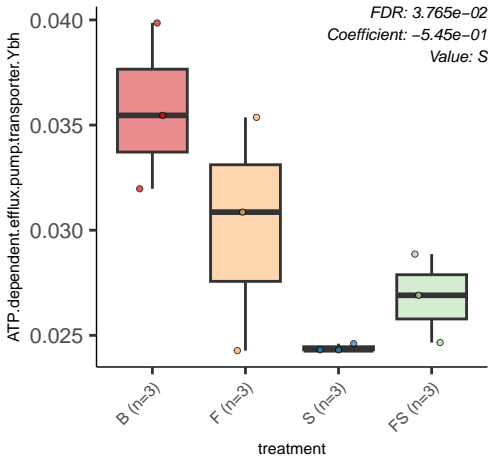
treatment

FDR: 3.749e-02

Coefficient: 4.29e-01

Value: S





Siderophore.assembly.kit

FDR: 3.773e-02
Coefficient: -7.37e-01
Value: FS

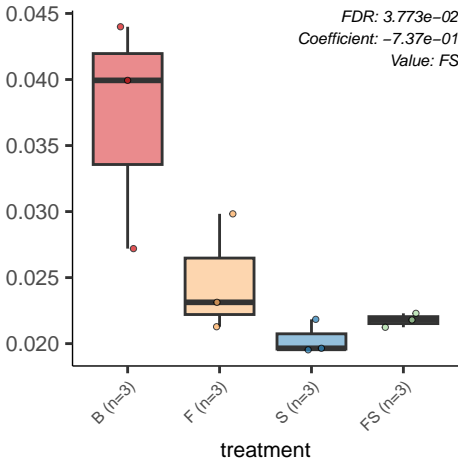
B (n=3)

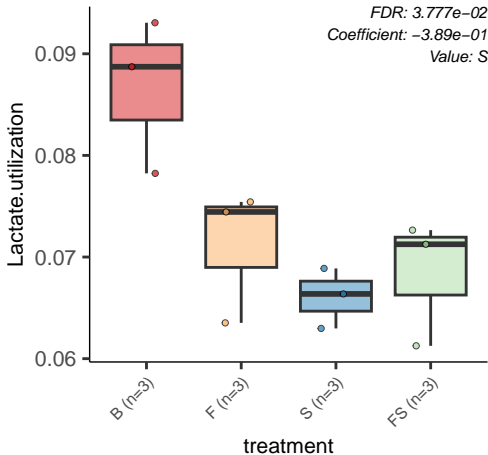
F (n=3)

S (n=3)

FS (n=3)

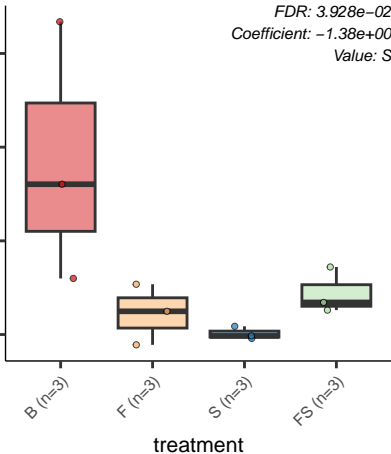
treatment





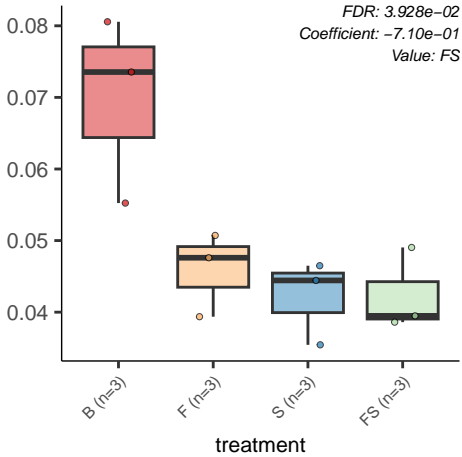
CBSS.194948.1.pcg.143

FDR: 3.928e-02
Coefficient: -1.38e+00
Value: S

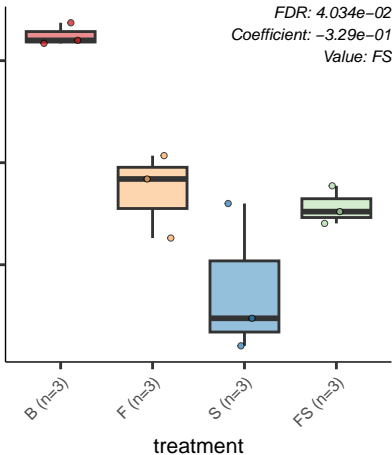


Phage.tail.fiber.proteins

FDR: 3.928e-02
Coefficient: -7.10e-01
Value: FS



CBSS.320372.3.peg.6046



Isoprenoid.Biosynthesis

FDR: 4.038e-02

Coefficient: 7.89e-02

Value: F

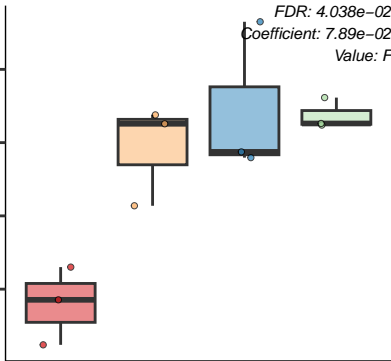
B (n=3)

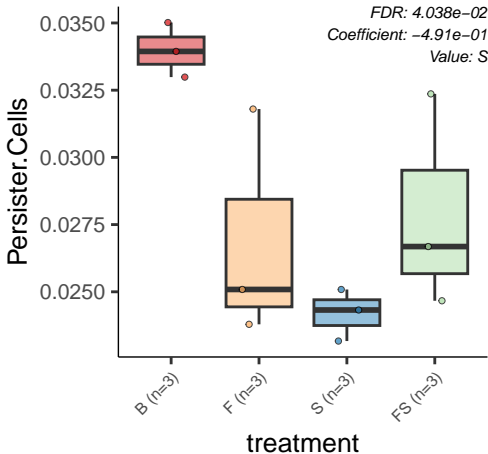
F (n=3)

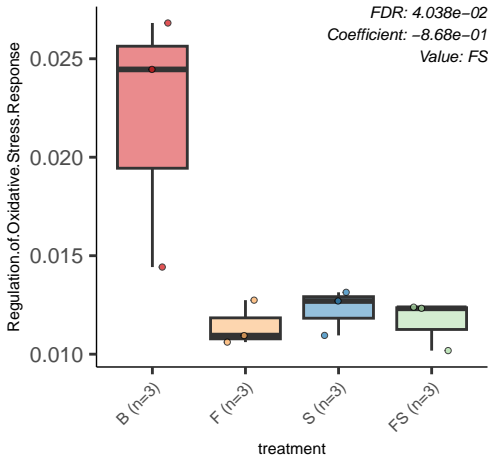
S (n=3)

FS (n=3)

treatment







Hemin.transport.system

FDR: 4.053e-02
Coefficient: -4.25e-01
Value: FS

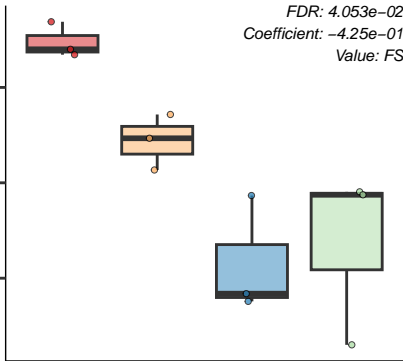
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Siderophore.Aerobactin

FDR: 4.053e-02
Coefficient: -8.92e-01
Value: S

B (n=3)

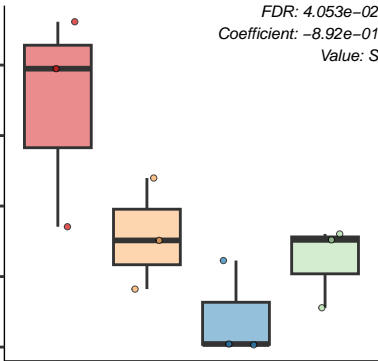
F (n=3)

S (n=3)

FS (n=3)

treatment

0.0175
0.0150
0.0125
0.0100
0.0075



CBSS.279010.5.peg.3195

B (n=3)

F (n=3)

S (n=3)

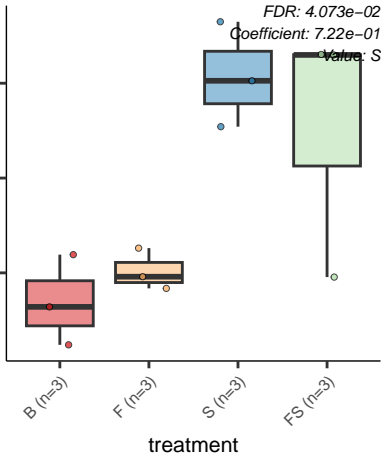
FS (n=3)

treatment

FDR: 4.073e-02

Coefficient: 7.22e-01

Value: S



Biofilm.Adhesin.Biosynthesis

FDR: 4.093e-02
Coefficient: -9.64e-01
Value: F

0.025

0.020

0.015

0.010

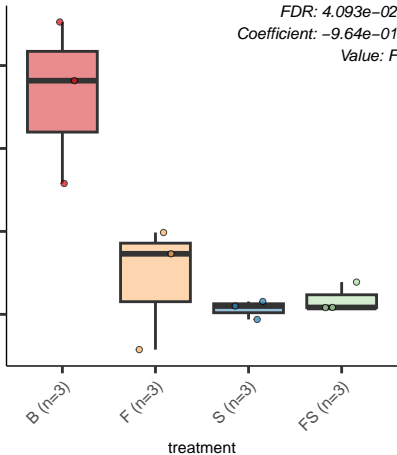
B (n=3)

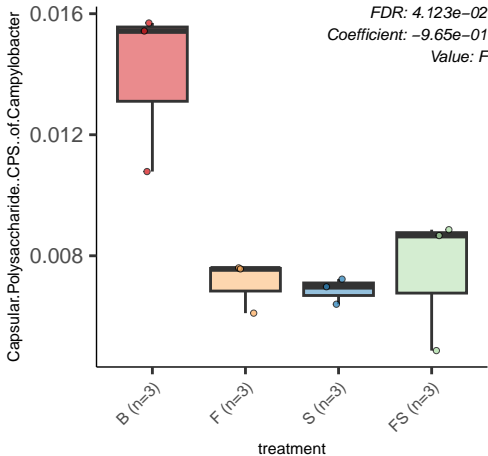
F (n=3)

S (n=3)

FS (n=3)

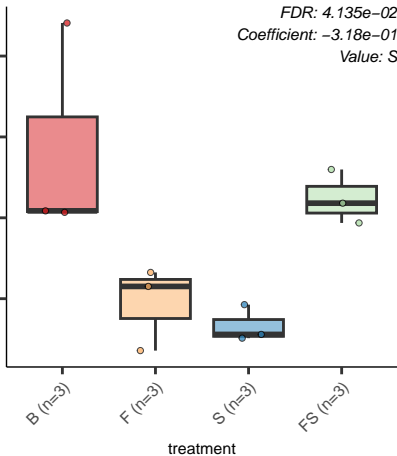
treatment

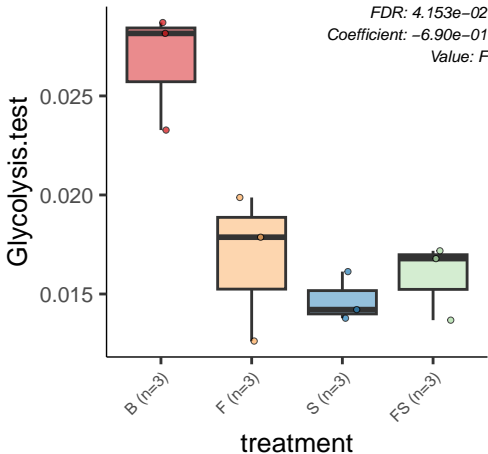




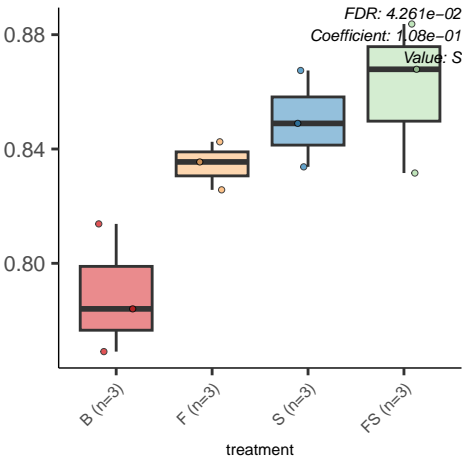
Twin.arginine.translocation.system

FDR: 4.135e-02
Coefficient: -3.18e-01
Value: S





De.Novo.Purine.Biosynthesis



GABA.and.putrescine.metabolism.from.clusters

FDR: 4.261e-02
Coefficient: -7.98e-01
Value: FS

0.020
0.016
0.012
0.008

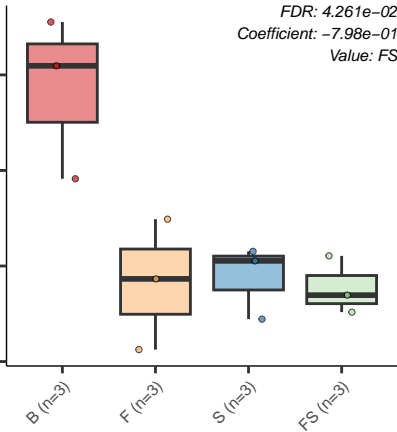
B (n=3)

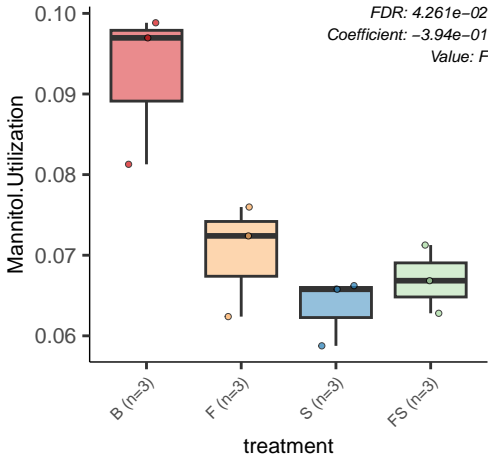
F (n=3)

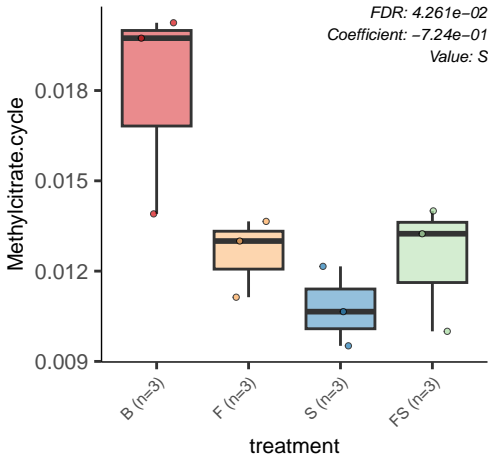
S (n=3)

FS (n=3)

treatment







Mycobacterium.jamboree

FDR: 4.261e-02
Coefficient: -1.30e+00
Value: S

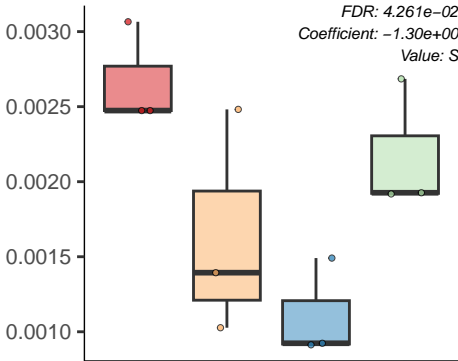
B (n=3)

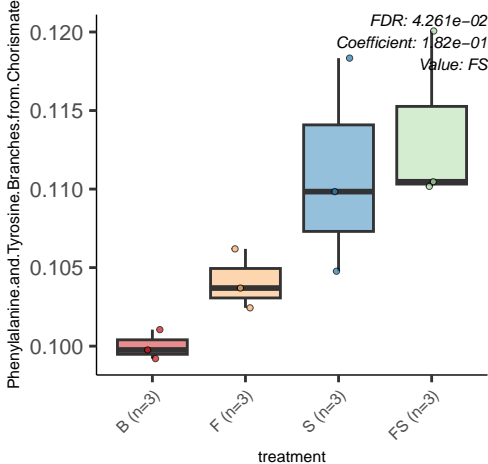
F (n=3)

S (n=3)

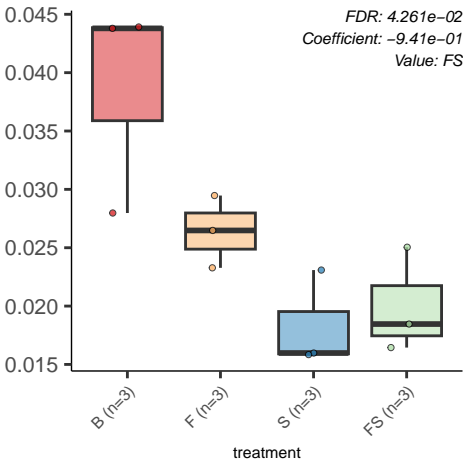
FS (n=3)

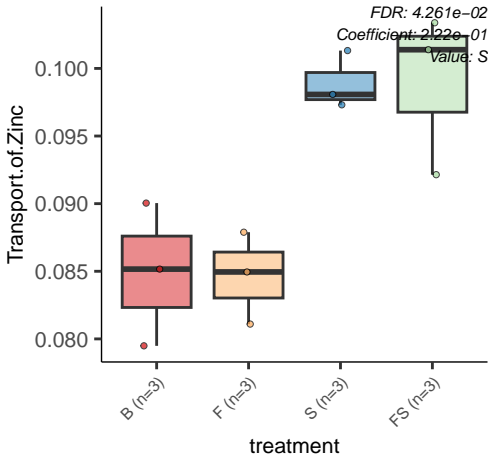
treatment

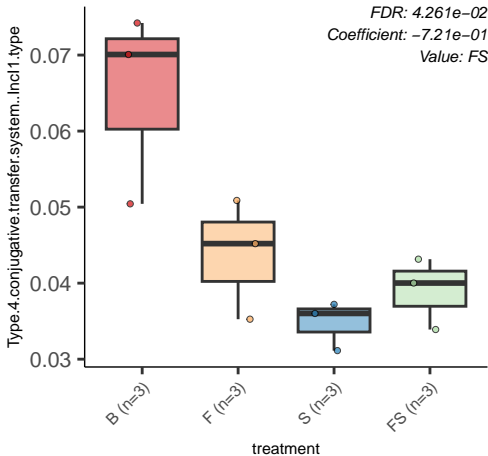




The.usher.protein.HtrE.fimbrial.cluster







Universal.GTPases

0.775
0.750
0.725
0.700

B (n=3)

F (n=3)

S (n=3)

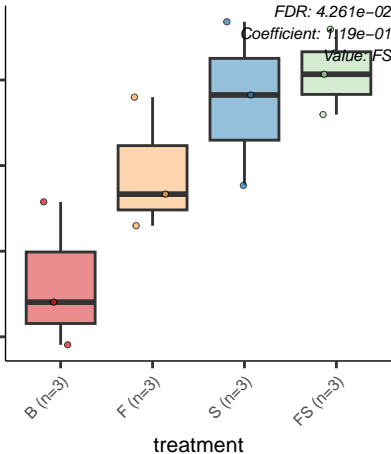
FS (n=3)

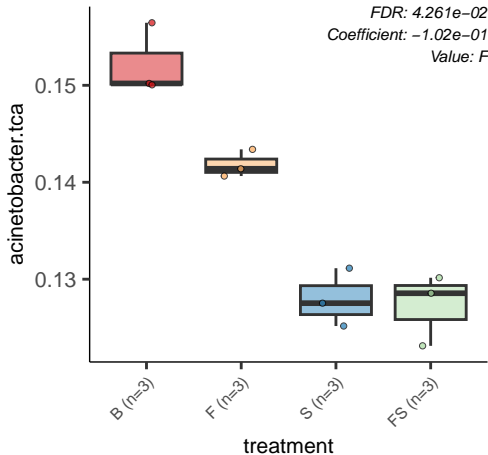
treatment

FDR: 4.261e-02

Coefficient: 1.19e-01

Value: FS





Ribosome.SSU.bacterial

FDR: 4.275e-02

Coefficient: 1.12e-01

Value: FS

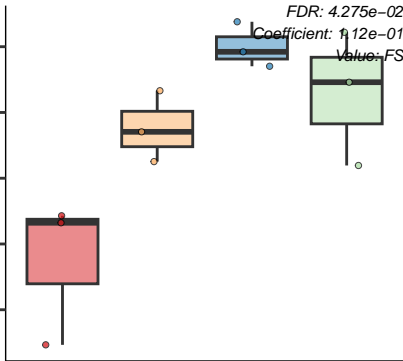
B (n=3)

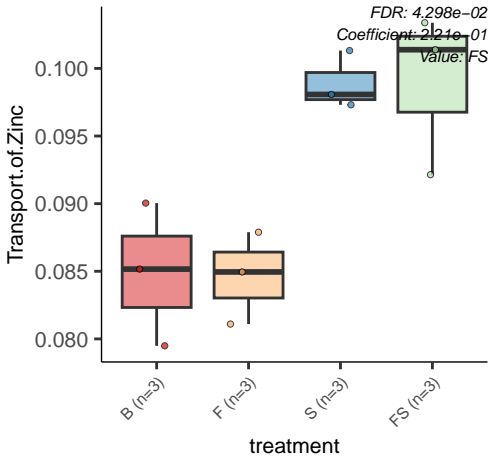
F (n=3)

S (n=3)

FS (n=3)

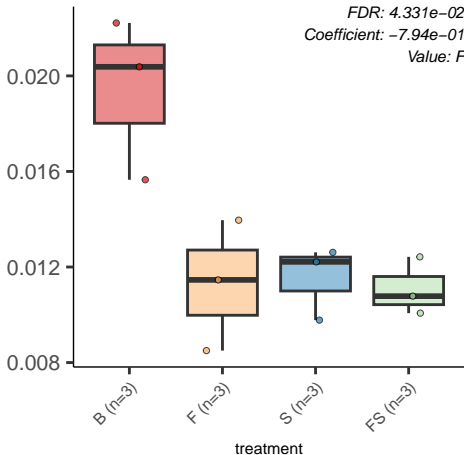
treatment





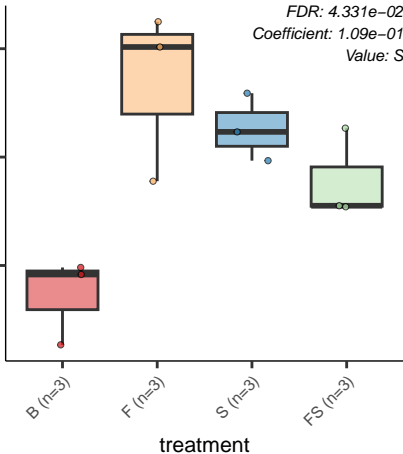
GABA.and.putrescine.metabolism.from.clusters

FDR: 4.331e-02
Coefficient: -7.94e-01
Value: F

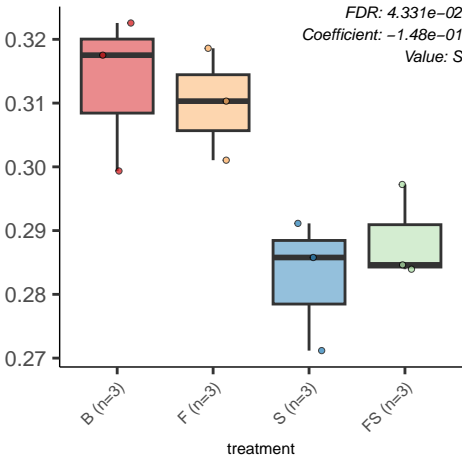


Leucine.Biosynthesis

FDR: 4.331e-02
Coefficient: 1.09e-01
Value: S



mislocating.NADH.quinone.oxidoreductase.and.rnf.like.group.of.electro



tRNA.aminoacylation..Gly

FDR: 4.331e-02
Coefficient: 1.73e-01
Value: S

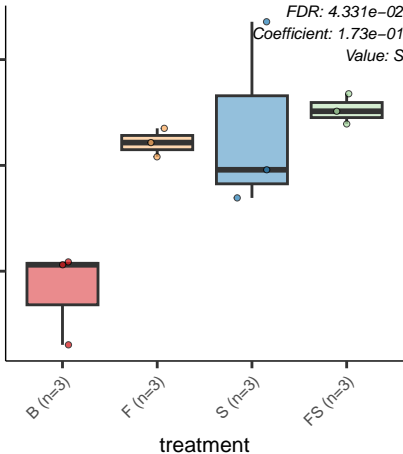
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Methionine.Degradation

FDR: 4.373e-02
Coefficient: 5.76e-02
value: F

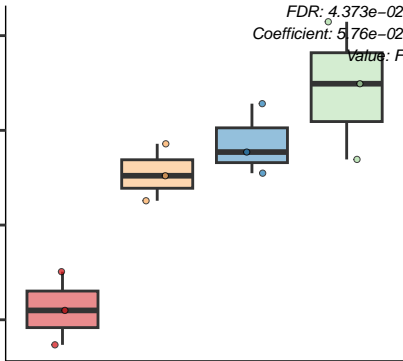
B (n=3)

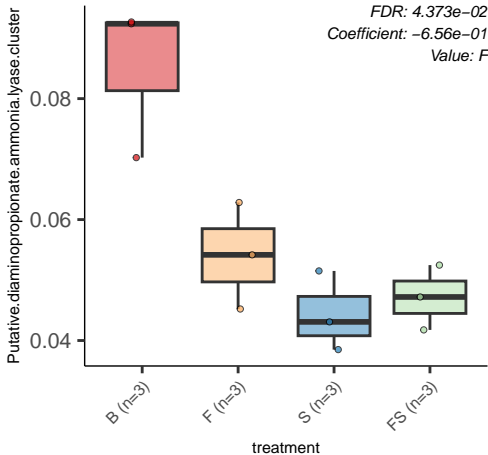
F (n=3)

S (n=3)

FS (n=3)

treatment





Siderophore.Enterobactin

FDR: 4.373e-02

Coefficient: -9.04e-01

Value: FS

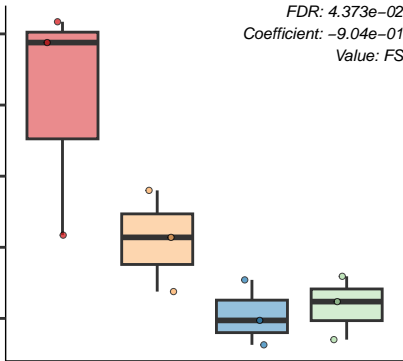
B (n=3)

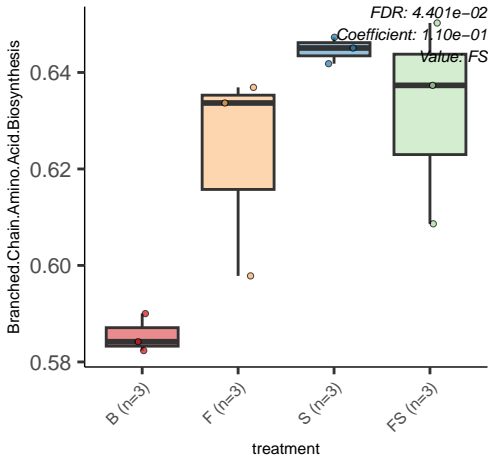
F (n=3)

S (n=3)

FS (n=3)

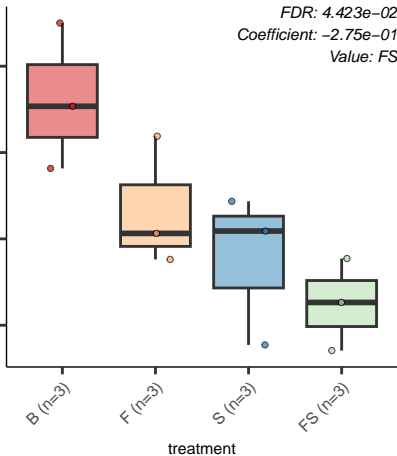
treatment



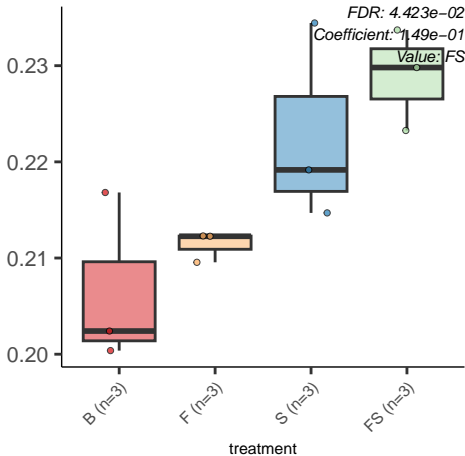


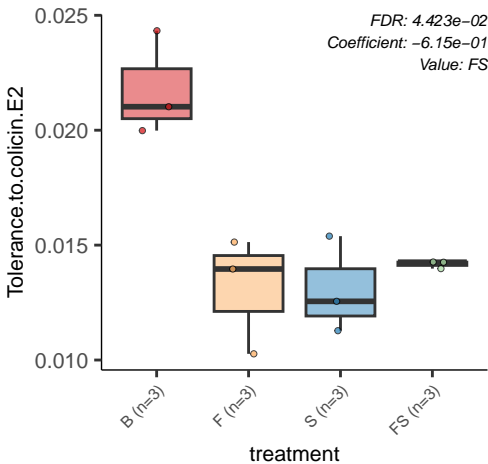
Acetyl.CoA.fermentation.to.Butyrate

FDR: $4.423e-02$
Coefficient: $-2.75e-01$
Value: FS



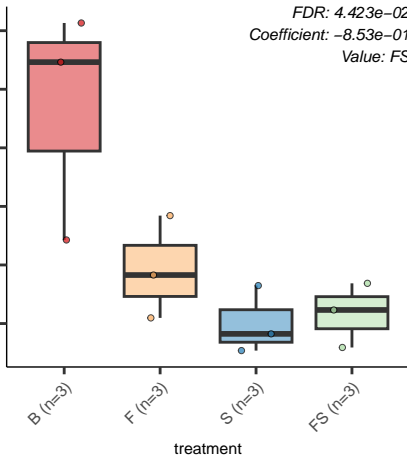
Mycobacterium.virulence.operon.involved.in.DNA.transcrip





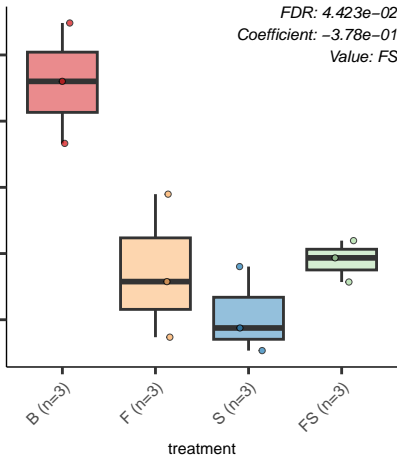
Type.1.pili..mannose.sensitive.fimbriae.

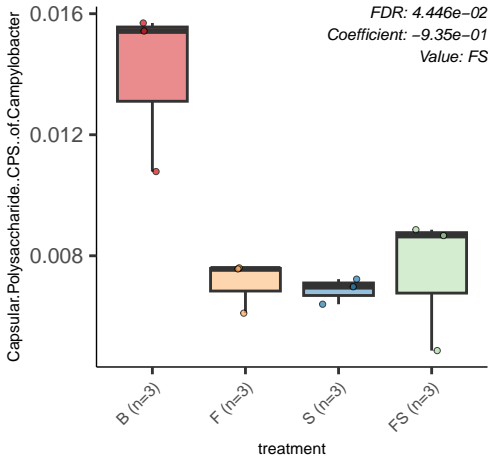
FDR: 4.423e-02
Coefficient: -8.53e-01
Value: FS

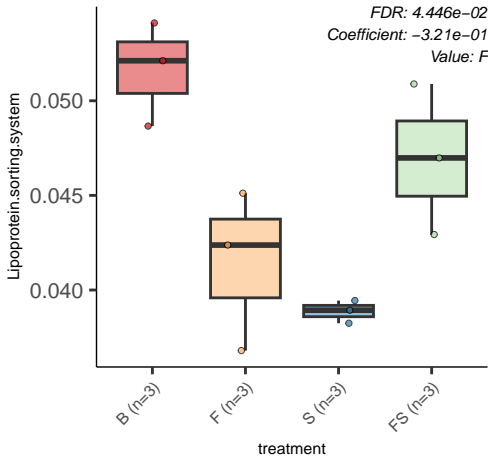


Unknown.sugar.utilization...cluster.yphABCDEFG.

FDR: 4.423e-02
Coefficient: -3.78e-01
Value: FS

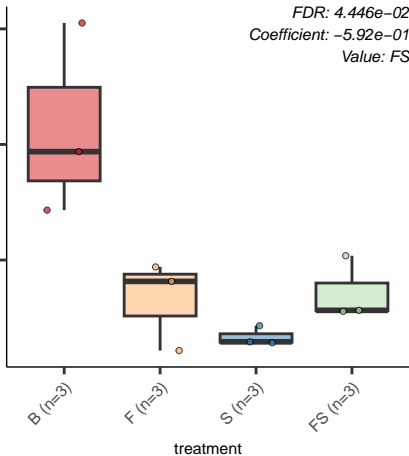


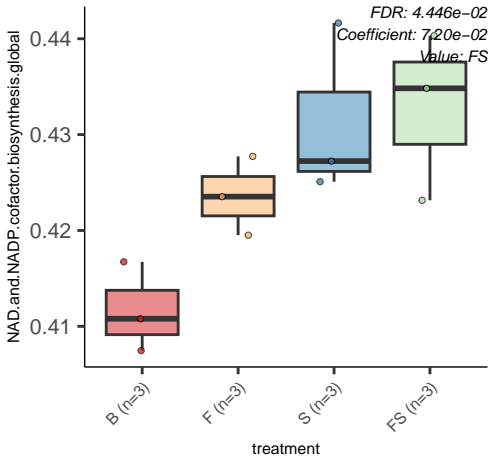




Major.Outer.Membrane.Proteins

FDR: $4.446e-02$
Coefficient: $-5.92e-01$
Value: FS





Streptococcal.Mga.Regulon

0.010

0.005

B (n=3)

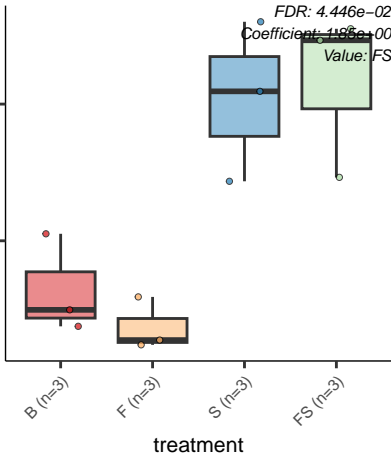
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: $4.446e-02$
Coefficient: $1.85e+00$
Value: FS



t.6.A.synthesis.in.bacteria

0.030
0.028
0.026

B (n=3)

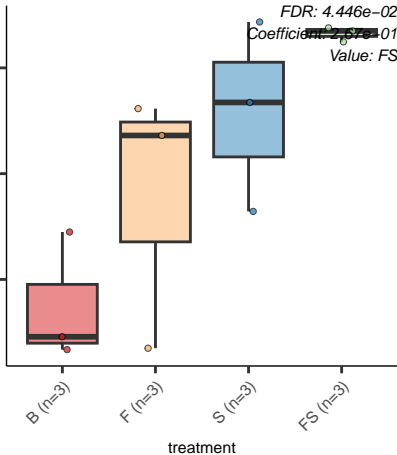
F (n=3)

S (n=3)

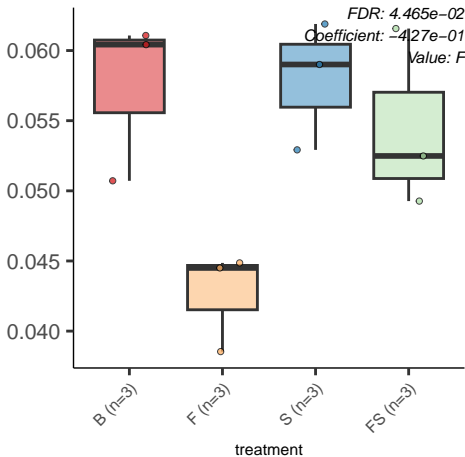
FS (n=3)

treatment

FDR: 4.446e-02
Coefficient: 2.67e-01
Value: FS

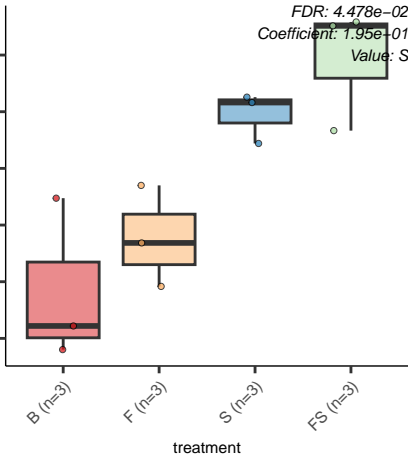


Glutathione..Non.redox.reactions

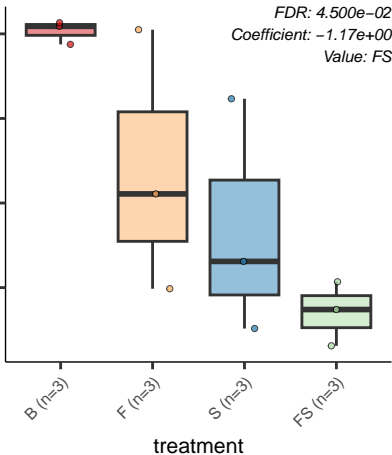


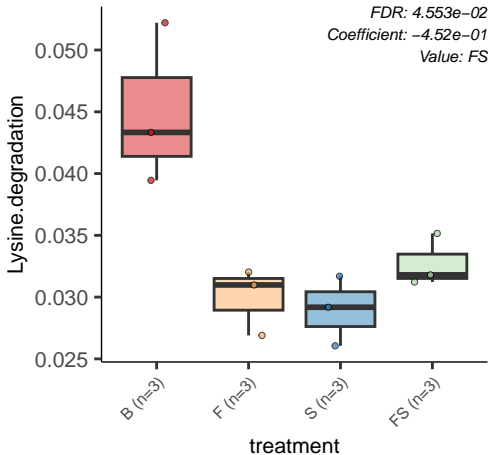
DNA.repair..bacterial.MutL.MutS.system

FDR: 4.478e-02
Coefficient: 1.95e-01
Value: S



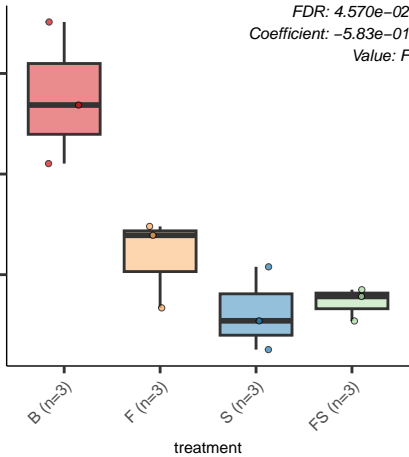
CBSS.502800.3.peg.2785

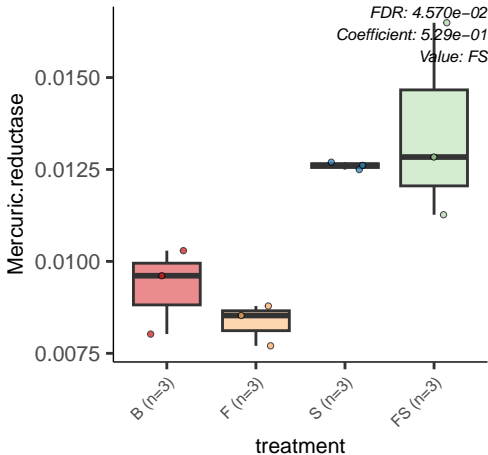


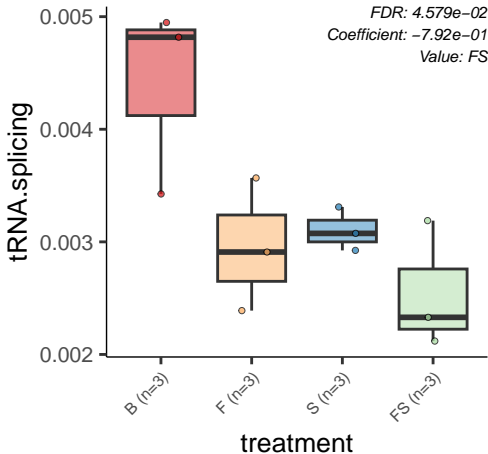


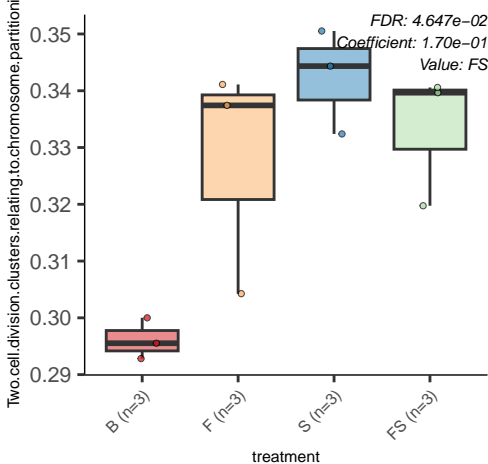
Carnitine.Metabolism.in.Microorganisms

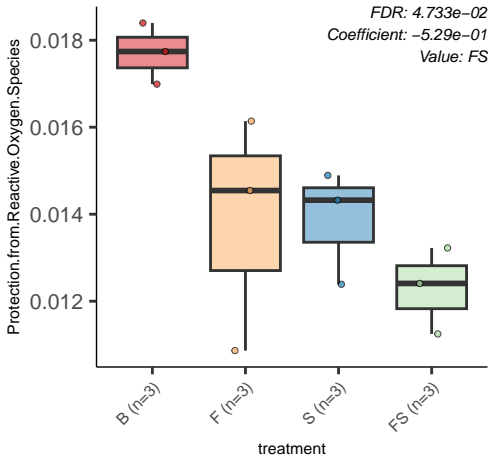
FDR: 4.570e-02
Coefficient: -5.83e-01
Value: F





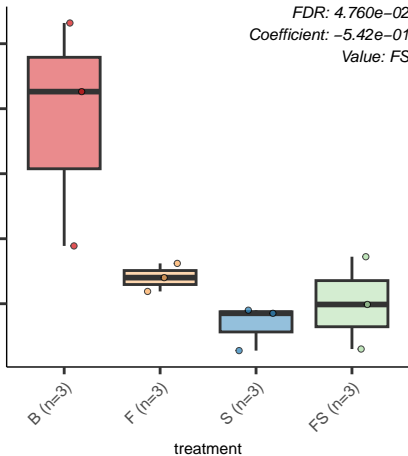






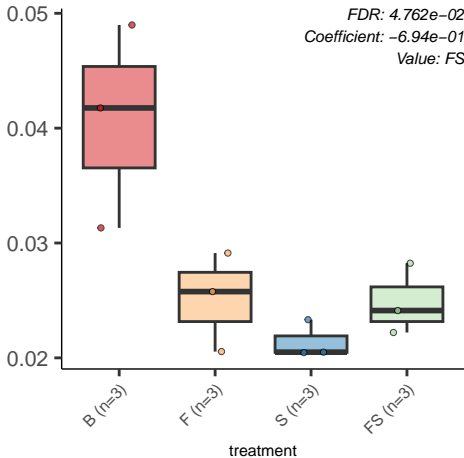
L.ascorbate.utilization..and.related.gene.clusters.

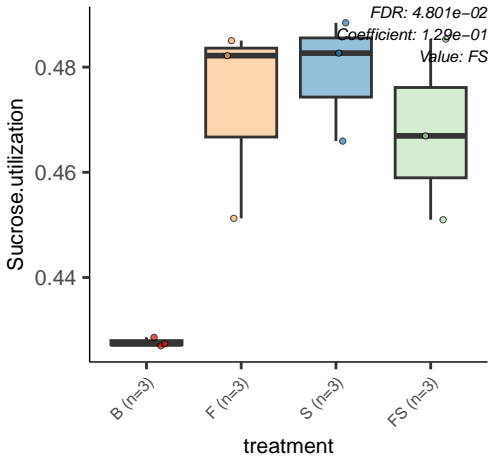
FDR: 4.760e-02
Coefficient: -5.42e-01
Value: FS

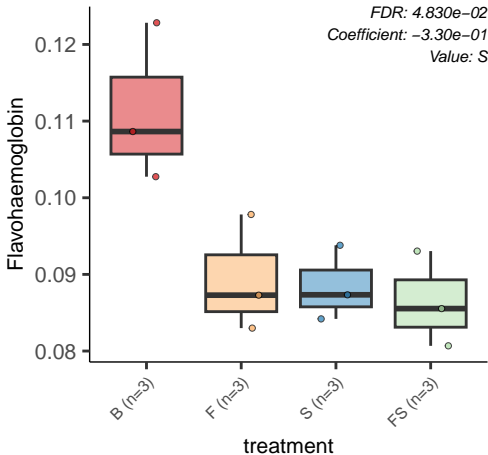


FOL.Commensurate.regulon.activation

FDR: 4.762e-02
Coefficient: -6.94e-01
Value: FS







Dehydrogenase.complexes

0.06
0.05
0.04
0.03

B (n=3)

F (n=3)

S (n=3)

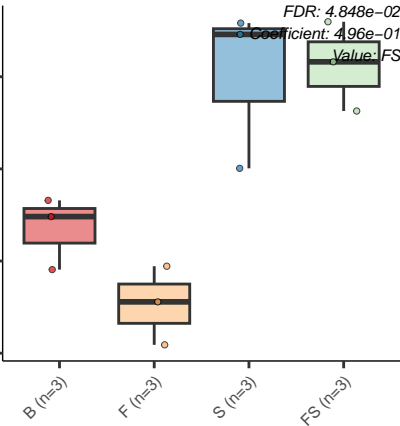
FS (n=3)

treatment

FDR: 4.848e-02

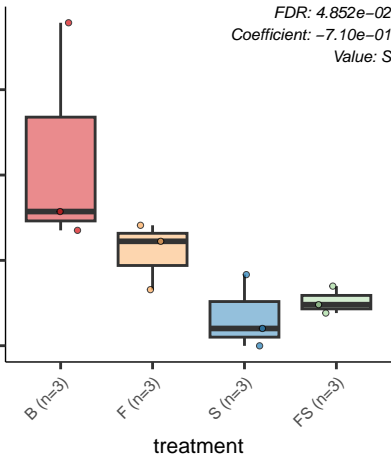
Coefficient: 4.96e-01

Value: FS



CBSS.211586.1.pcg.3133

FDR: 4.852e-02
Coefficient: -7.10e-01
Value: S



Hexose.Phosphate.Uptake.System

FDR: $4.908e-02$
Coefficient: $-7.42e-01$
Value: S

0.024

0.020

0.016

0.012

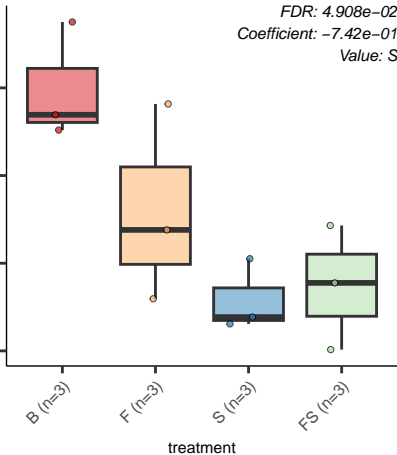
B (n=3)

F (n=3)

S (n=3)

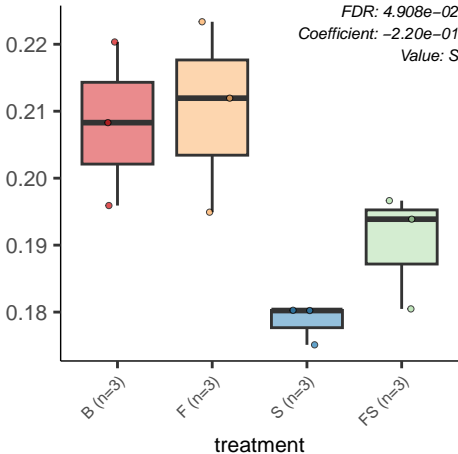
FS (n=3)

treatment



L.fucose.utilization

FDR: 4.908e-02
Coefficient: -2.20e-01
Value: S



Respiration...Human.gut.microbiome

FDR: 4.908e-02
Coefficient: -2.57e-01
Value: FS

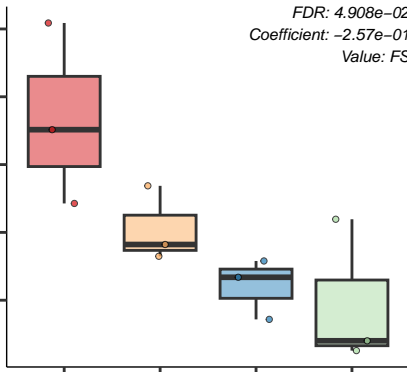
B (n=3)

F (n=3)

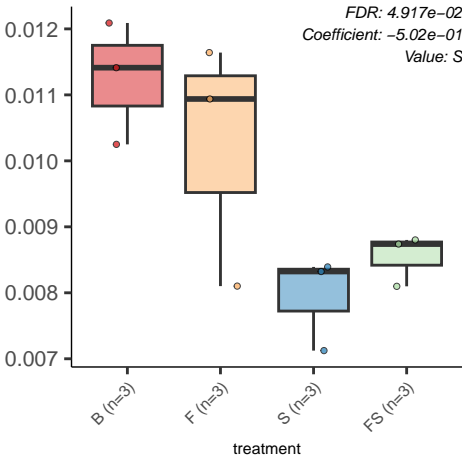
S (n=3)

FS (n=3)

treatment

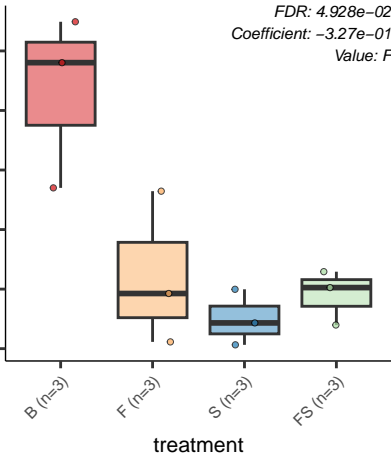


n.Phenylalkanoic.acid.degradation



CBSS.326442.4.peg.1852

FDR: 4.928e-02
Coefficient: -3.27e-01
Value: F



Osmoregulation

FDR: 4.928e-02
Coefficient: -2.16e-01
Value: FS

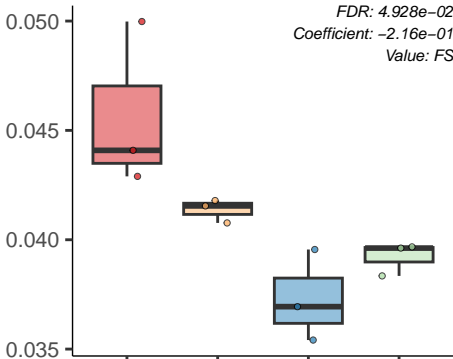
B (n=3)

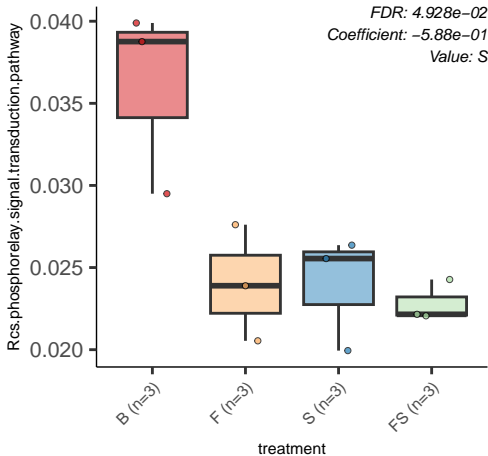
F (n=3)

S (n=3)

FS (n=3)

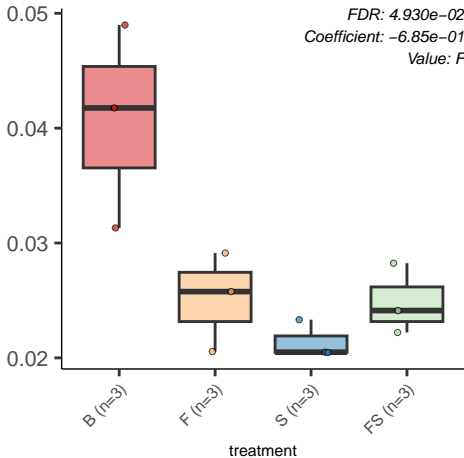
treatment

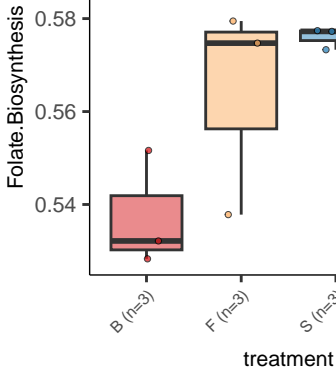




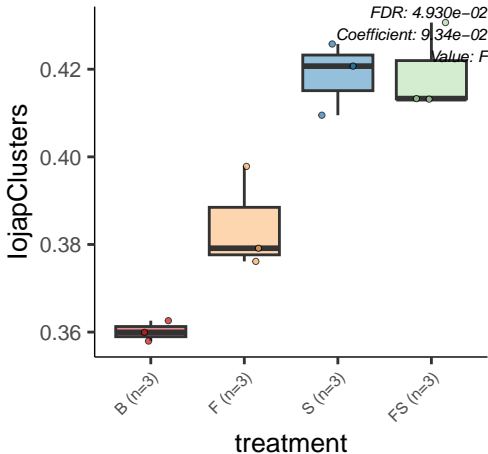
FOL.Commensurate.regulon.activation

FDR: 4.930e-02
Coefficient: -6.85e-01
Value: F





FDR: 4.930×10^{-2}
Coefficient: 1.15×10^{-1}
Value: FS



Outer.membrane

FDR: $4.930e-02$

Coefficient: $-3.67e-01$

Value: FS

0.045

0.040

0.035

0.030

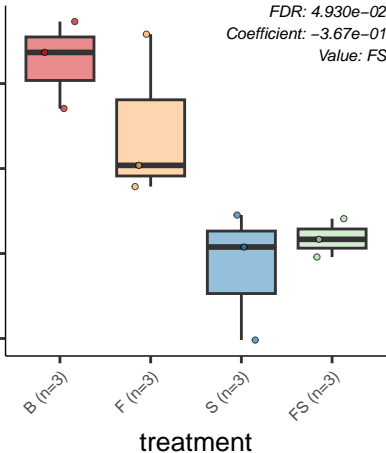
B (n=3)

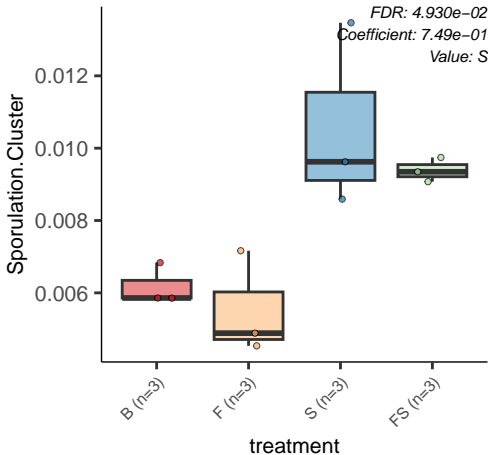
F (n=3)

S (n=3)

FS (n=3)

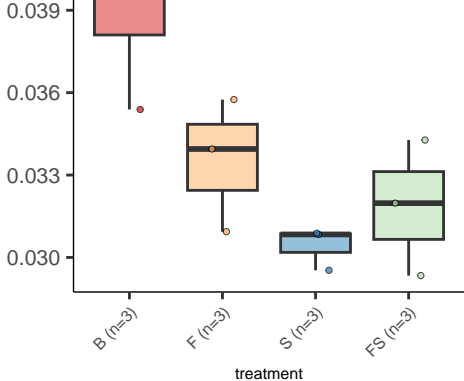
treatment





Ubiquinone.biosynthesis.....gjo

FDR: 4.930e-02
Coefficient: -2.97e-01
Value: FS



Respiratory.dehydrogenases.1

FDR: 4.961e-02
Coefficient: -1.32e-01
Value: S

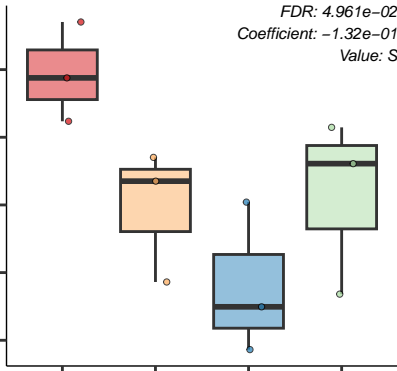
B (n=3)

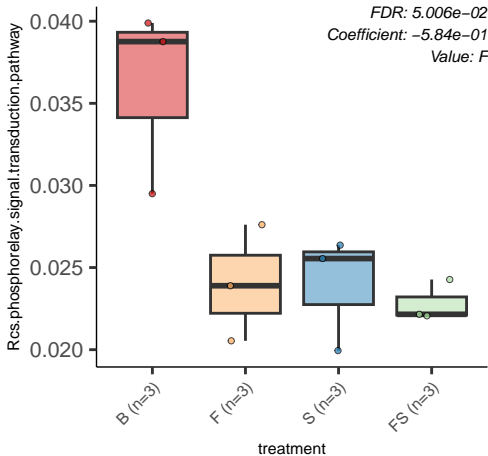
F (n=3)

S (n=3)

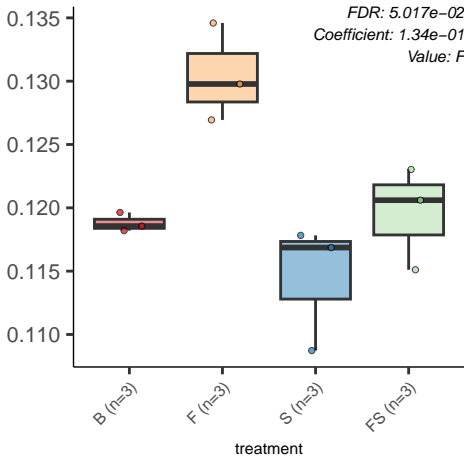
FS (n=3)

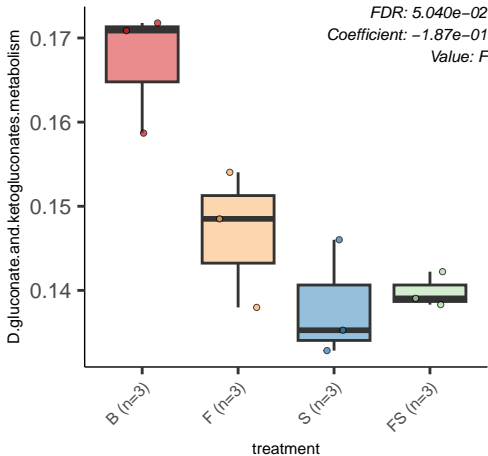
treatment





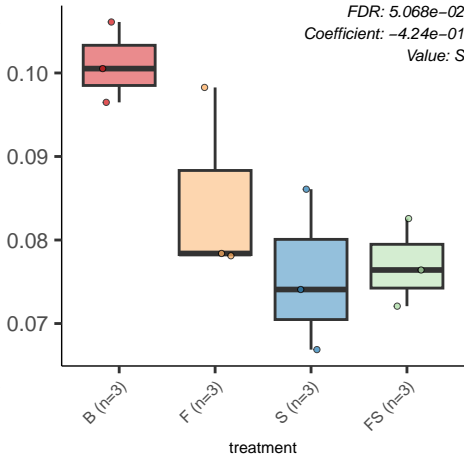
FDR: 5.017e-02
Coefficient: 1.34e-01
Value: F

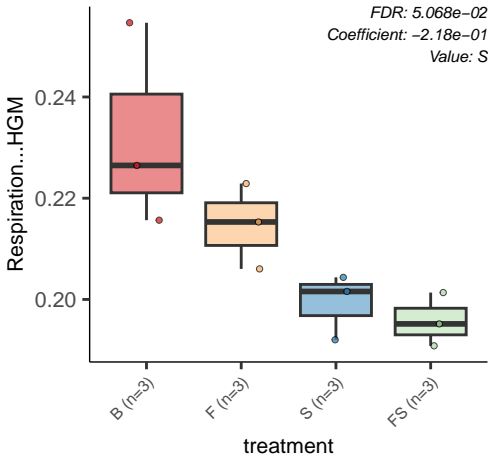




Multidrug.Resistance..Tripartite.Systems.Found.in.Gram.Negative

FDR: $5.068e-02$
Coefficient: $-4.24e-01$
Value: S





Streptococcal.Mga.Regulon

0.010

0.005

B (n=3)

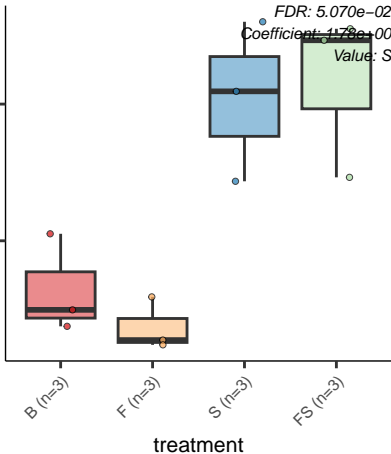
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 5.070e-02
Coefficient: 1.178e+00
Value: S



The.fimbral.Sfm.cluster

0.035
0.030
0.025
0.020
0.015

FDR: 5.204e-02
Coefficient: -8.37e-01
Value: S

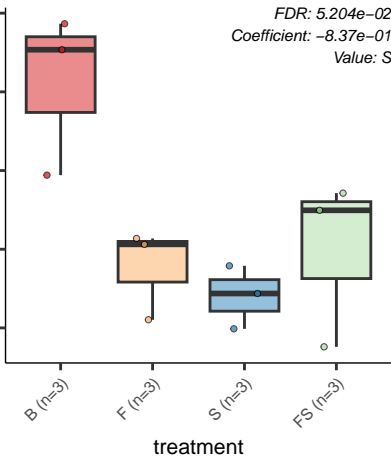
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



GABA.and.putrescine.metabolism.from.clusters

FDR: $5.211e-02$
Coefficient: $-7.45e-01$
Value: S

0.020
0.016
0.012
0.008

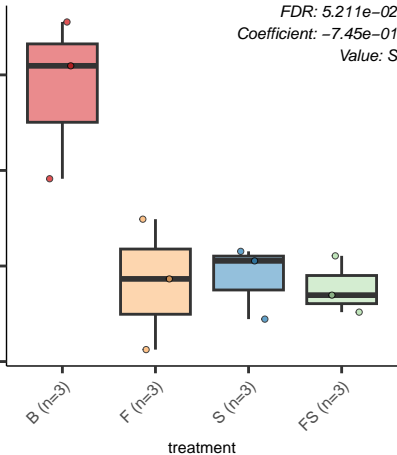
B (n=3)

F (n=3)

S (n=3)

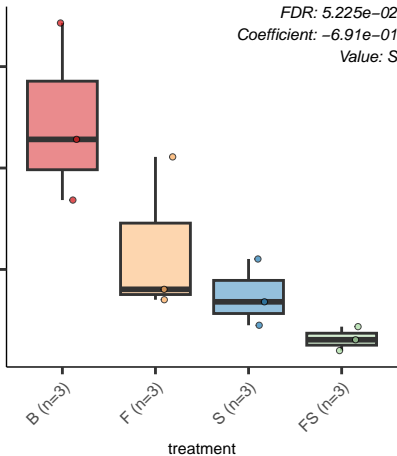
FS (n=3)

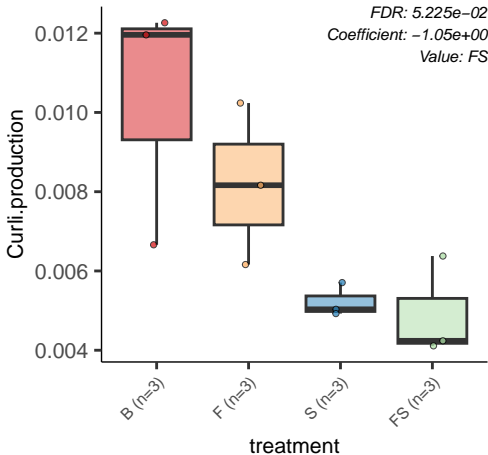
treatment



Acetone.Butanol.Ethanol.Synthesis

FDR: 5.225e-02
Coefficient: -6.91e-01
Value: S





Pyrroloquinoline.Quinone.biosynthesis

0.0015
0.0010
0.0005
0.0000

B (n=3)

F (n=3)

S (n=3)

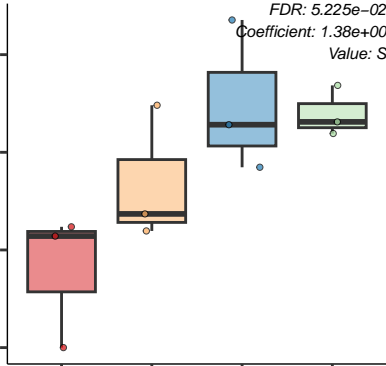
FS (n=3)

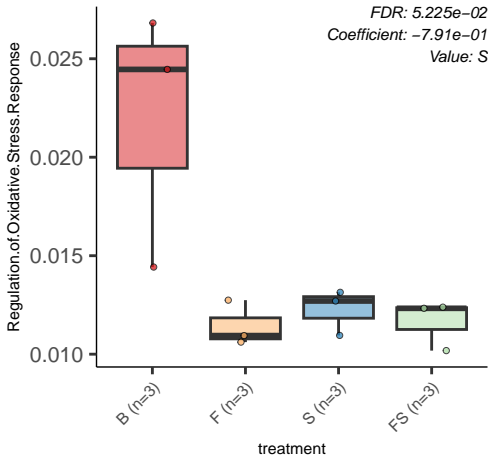
treatment

FDR: 5.225e-02

Coefficient: 1.38e+00

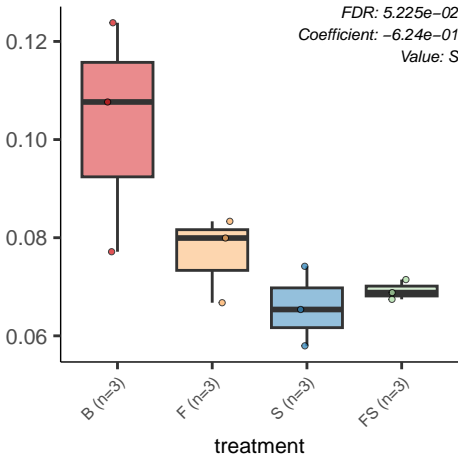
Value: S

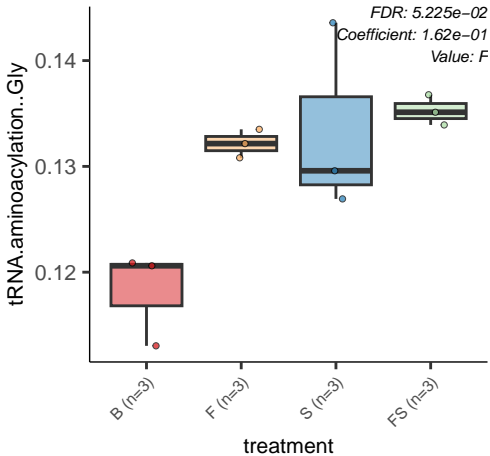




Type.VI.secretion.systems

FDR: 5.225e-02
Coefficient: -6.24e-01
Value: S





DNA.repair..UvrABC.system

FDR: 5.265e-02

Coefficient: 9.32e-02

Value: S

0.66

0.64

0.62

0.60

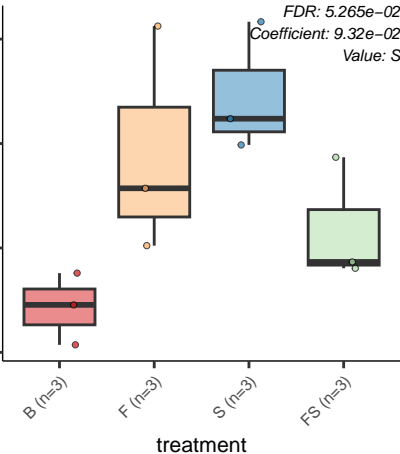
B (n=3)

F (n=3)

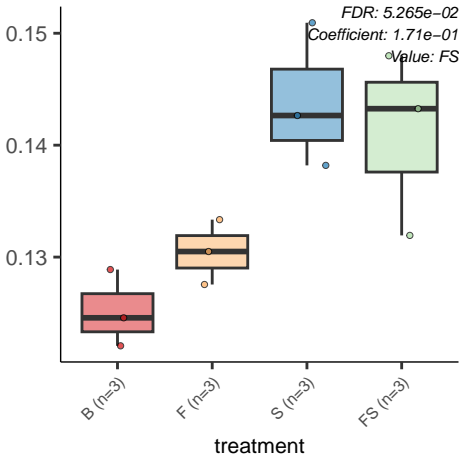
S (n=3)

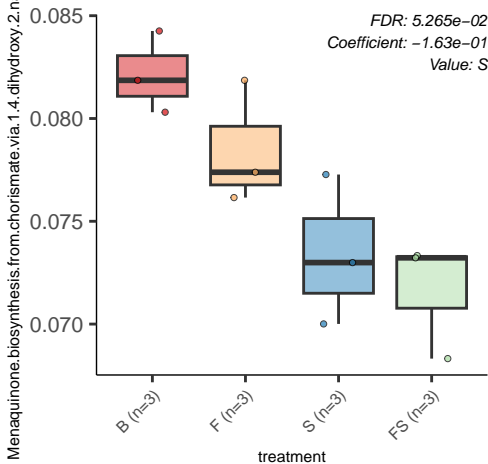
FS (n=3)

treatment



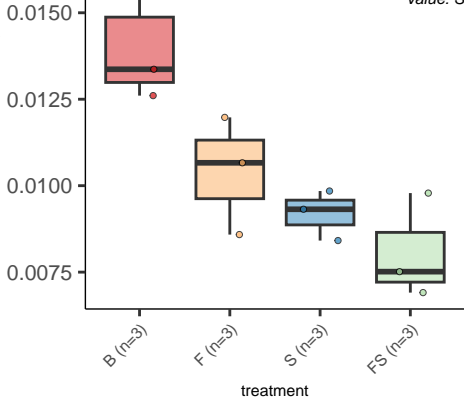
Fe.S.cluster.assembly

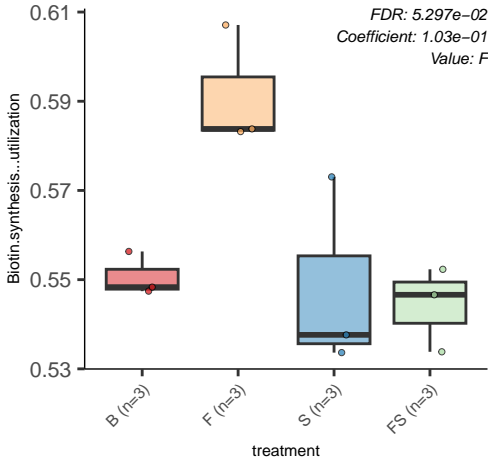




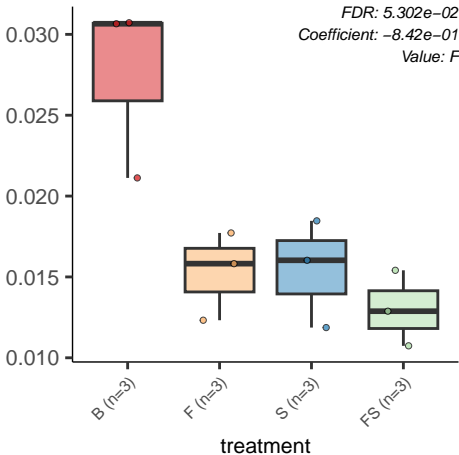
A.Gammaproteobacteria.Cluster.Relating.to.Translation

FDR: 5.267e-02
Coefficient: -6.13e-01
Value: S





The.fimbral.Stf.cluster



Aromatic.amino.acid.degradation

FDR: 5.310e-02
Coefficient: -5.48e-01
Value: S

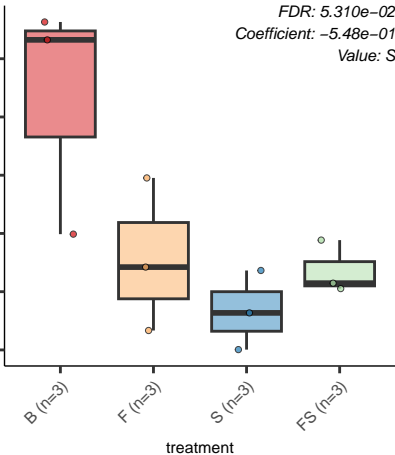
B (n=3)

F (n=3)

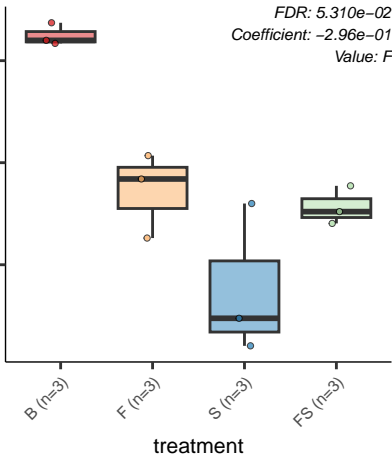
S (n=3)

FS (n=3)

treatment

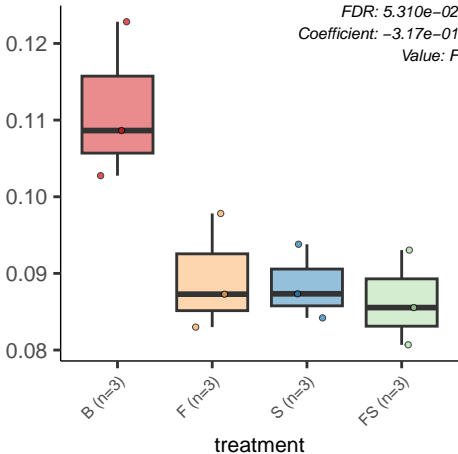


CBSS.320372.3.peg.6046



Flavo haemoglobin

FDR: 5.310e-02
Coefficient: -3.17e-01
Value: F



Murein.Hydrolases

0.15
0.14
0.13

B (n=3)

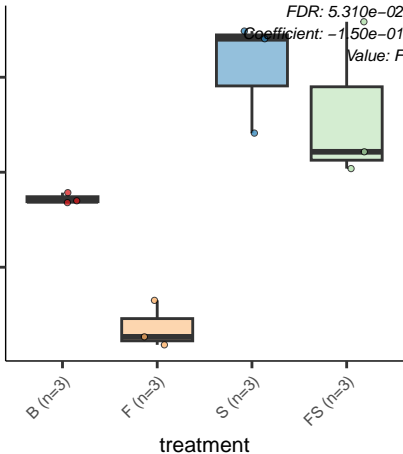
F (n=3)

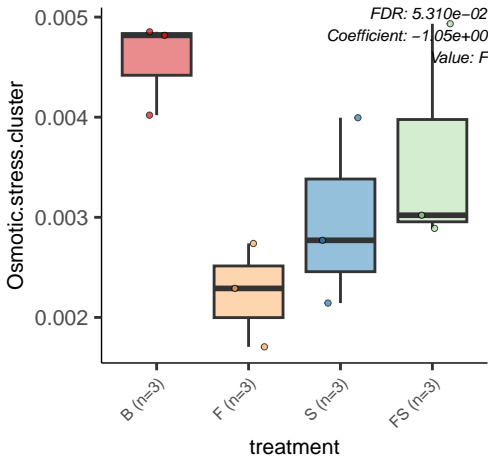
S (n=3)

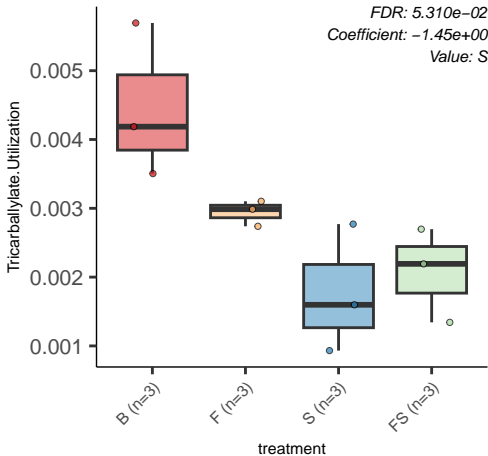
FS (n=3)

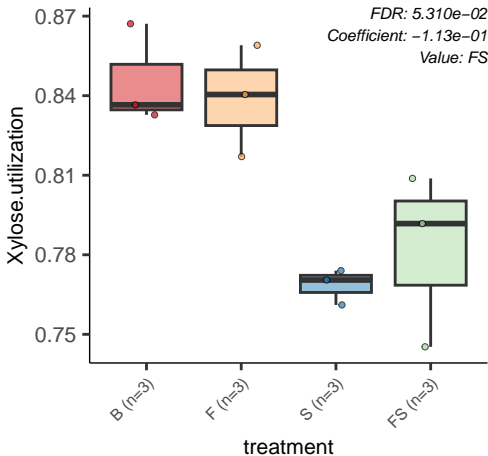
treatment

FDR: 5.310e-02
Coefficient: -1.50e-01
Value: F

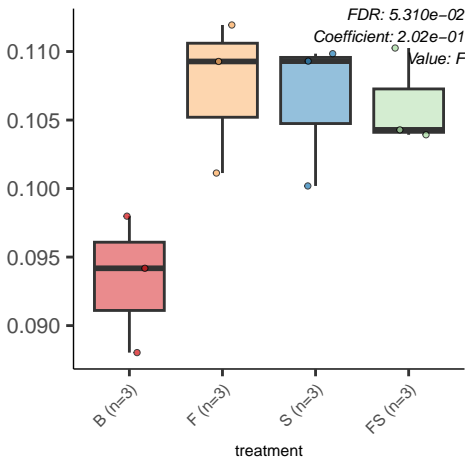






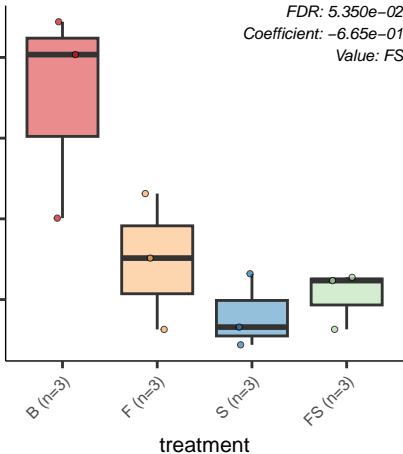


pVir.Plasmid.of.Campylobacter



CBSS.216592.1.peg.3937

FDR: 5.350e-02
Coefficient: -6.65e-01
Value: FS



CBSS.342610.3.peg.1536

FDR: 5.350e-02
Coefficient: -3.38e-01
Value: FS

0.040
0.035

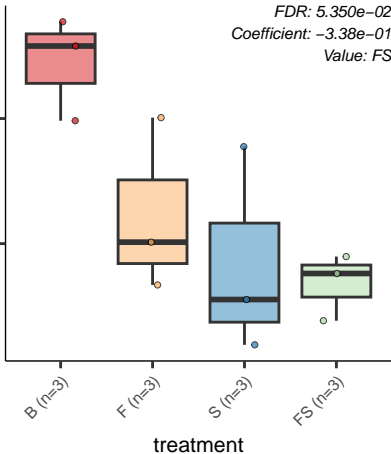
B (n=3)

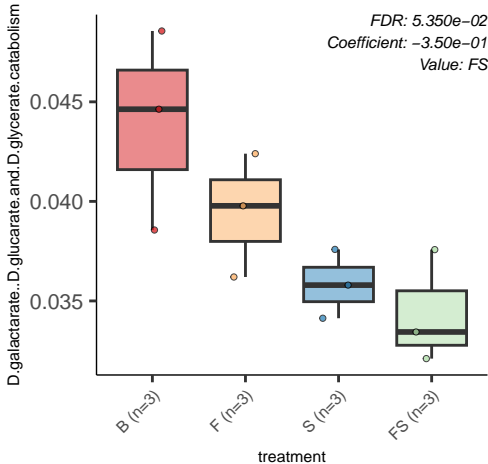
F (n=3)

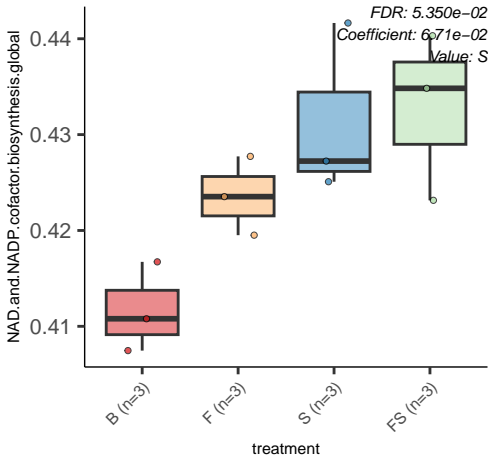
S (n=3)

FS (n=3)

treatment







Phenylpropionate.Degradation

0.007
0.006
0.005
0.004
0.003

B (n=3)

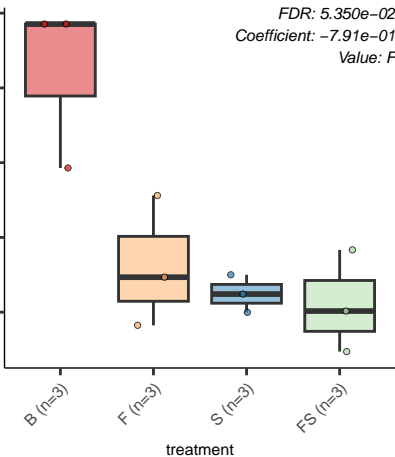
F (n=3)

S (n=3)

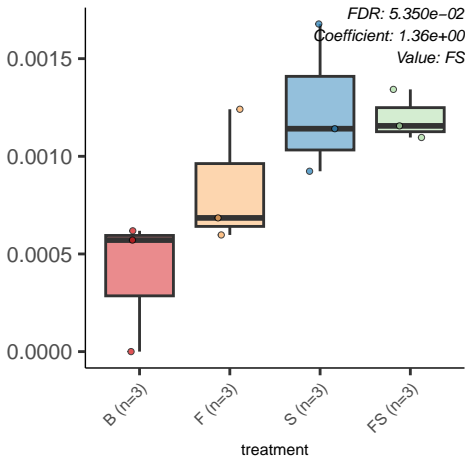
FS (n=3)

treatment

FDR: 5.350e-02
Coefficient: -7.91e-01
Value: F



Pyrroloquinoline.Quinone.biosynthesis

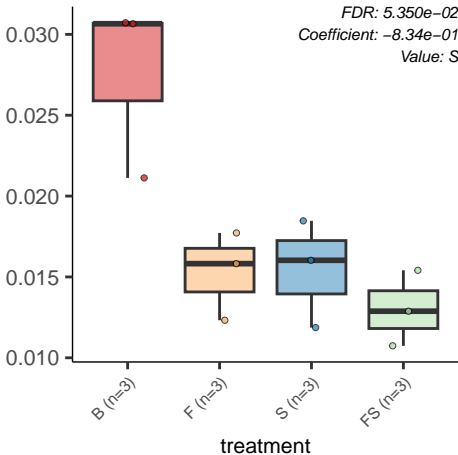


The.fimbral.Stf.cluster

FDR: 5.350e-02

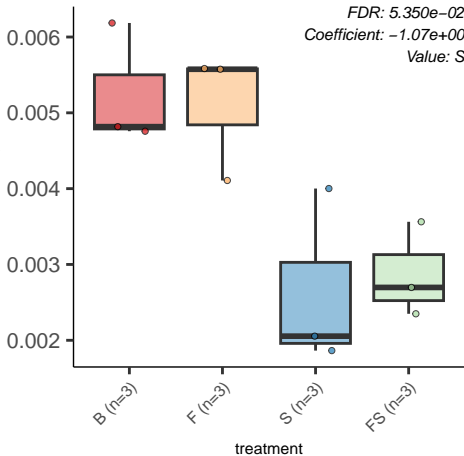
Coefficient: -8.34e-01

Value: S

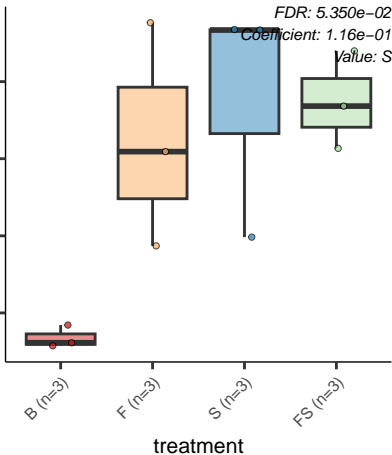


Unknown.carbohydrate.utilization.containing.Fructose.bisphosphatase

FDR: 5.350e-02
Coefficient: -1.07e+00
Value: S



tRNA.aminoacylation..Leu



Alkanesulfonates.Utilization

FDR: 5.382e-02
Coefficient: -5.00e-01
Value: S

0.009

0.008

0.007

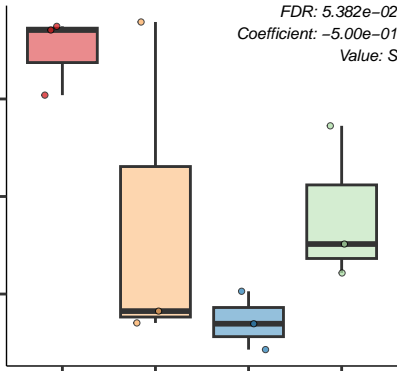
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



CBSS.393130.3.pcg.794

FDR: 5.382e-02
Coefficient: 4.95e-01
Value: S

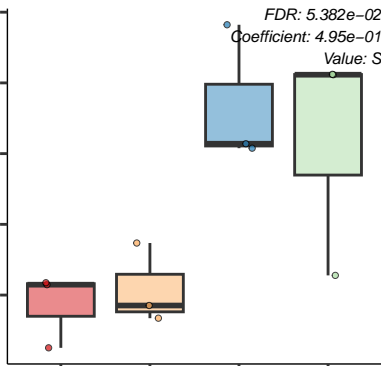
B (n=3)

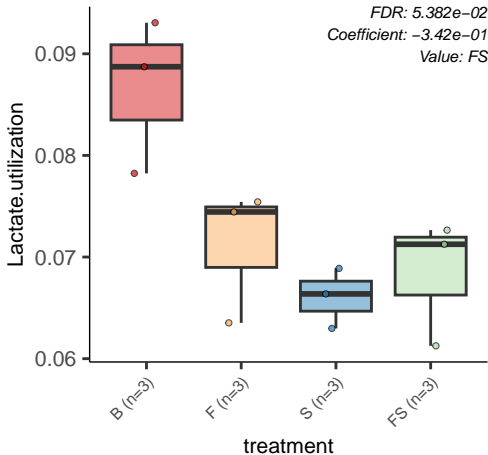
F (n=3)

S (n=3)

FS (n=3)

treatment





Peptide.ABC.transport.system.Sap

0.04

0.03

0.02

B (n=3)

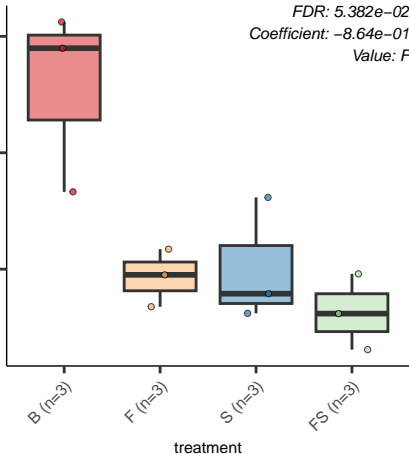
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 5.382e-02
Coefficient: -8.64e-01
Value: F



Polysaccharide.deacetylases

0.06

0.05

B (n=3)

F (n=3)

S (n=3)

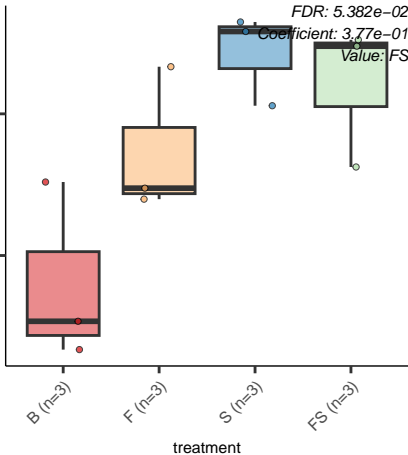
FS (n=3)

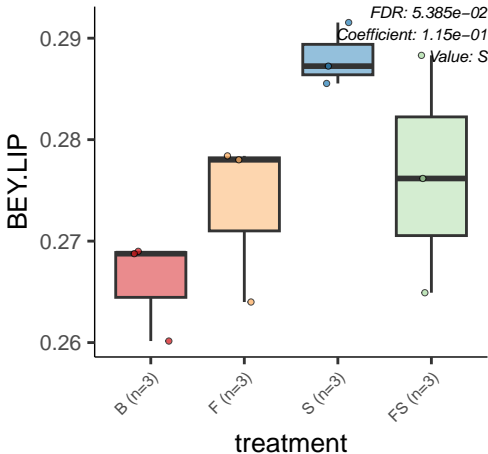
treatment

FDR: 5.382e-02

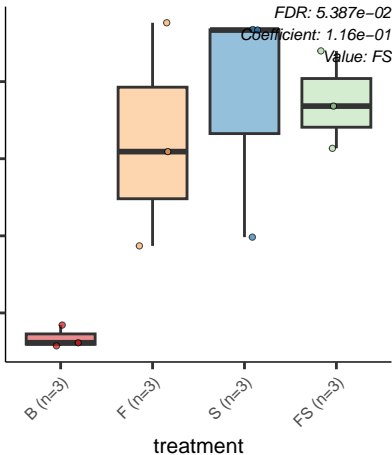
Coefficient: 3.77e-01

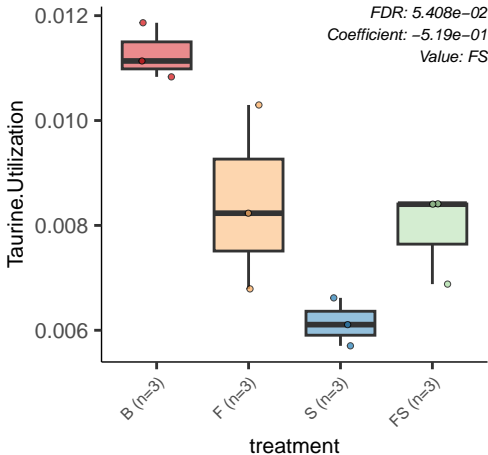
Value: FS

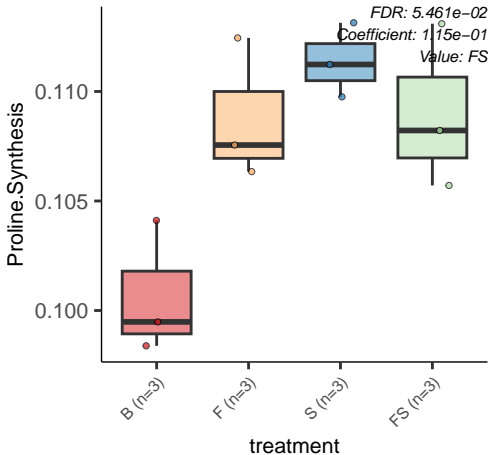




tRNA.aminoacylation..Leu







Lipid.A.modifications

FDR: $5.499\text{e-}02$
Coefficient: $-7.54\text{e-}01$
Value: S

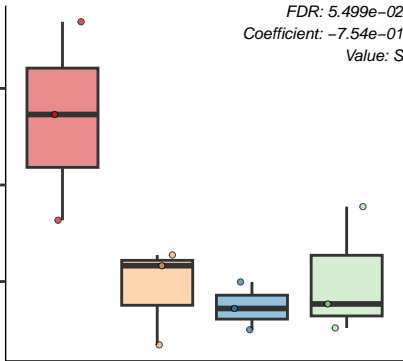
B (n=3)

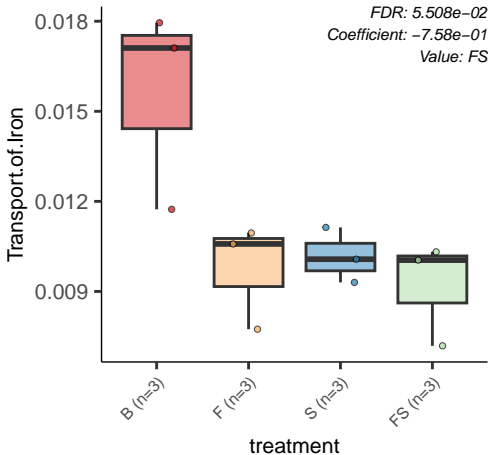
F (n=3)

S (n=3)

FS (n=3)

treatment





Tricarboxylate.transport.system

0.012

0.011

0.010

0.009

0.008

B (n=3)

F (n=3)

S (n=3)

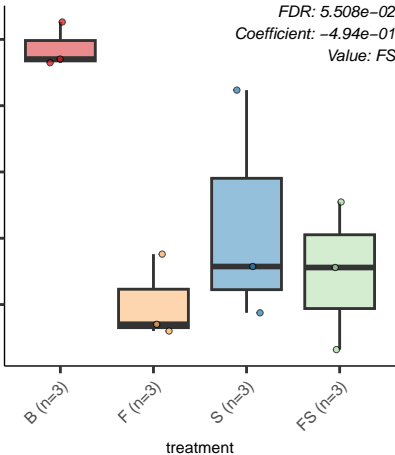
FS (n=3)

treatment

FDR: 5.508e-02

Coefficient: -4.94e-01

Value: FS



CBSS.393121.3.peg.2760

FDR: 5.526e-02

Coefficient: 1.38e-01

Value: F

0.450

0.425

0.400

0.375

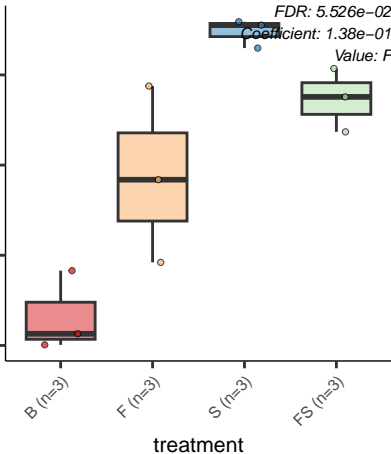
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Alpha.Amylase.locus.in.Streptococcus

0.08
0.07
0.06

B (n=3)

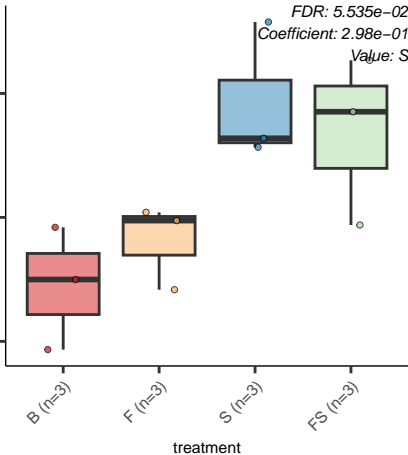
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 5.535e-02
Coefficient: 2.98e-01
Value: S



Tryptophan.synthesis

FDR: 5.555e-02
Coefficient: 1.16e-01
Value: F

0.40

0.38

0.36

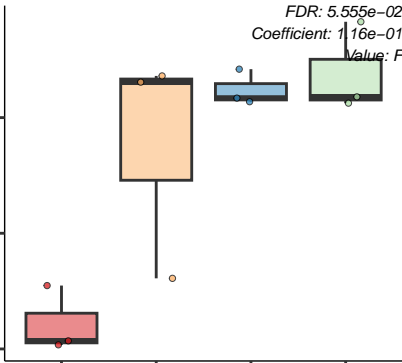
B (n=3)

F (n=3)

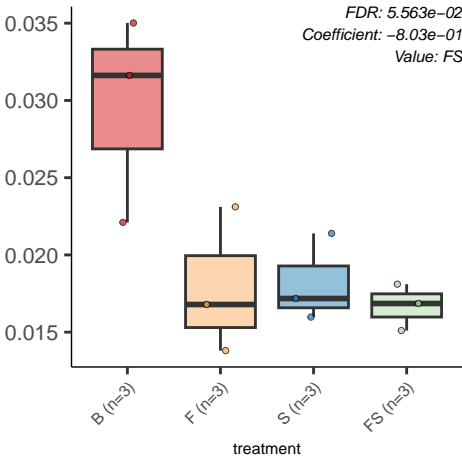
S (n=3)

FS (n=3)

treatment

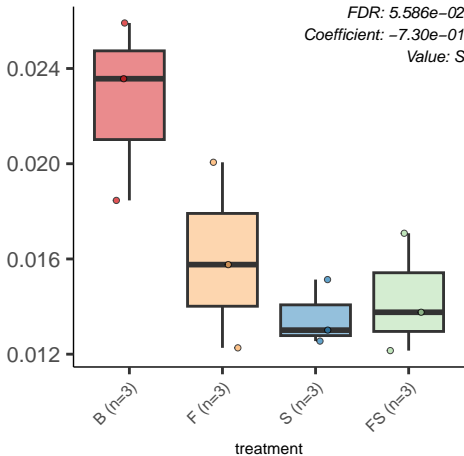


Putrescine.utilization.paths



Glutathionylspermidine.and.Tryptanothione

FDR: 5.586e-02
Coefficient: -7.30e-01
Value: S



GroEL.GroES

FDR: 5.586e-02

Coefficient: 1.02e-01

Value: S

0.115

0.110

0.105

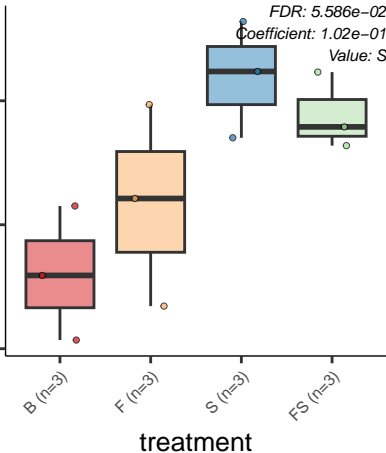
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Lipopolysaccharide.assembly

FDR: 5.586e-02
Coefficient: -5.18e-01
Value: F

0.10
0.09
0.08
0.07
0.06

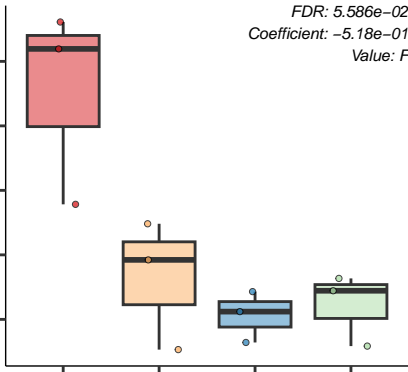
B (n=3)

F (n=3)

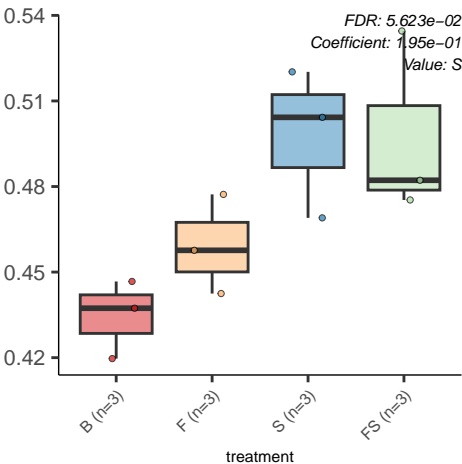
S (n=3)

FS (n=3)

treatment



ABC.transporter.oligopeptide..TC.3.A.1.5.1.



Translation.termination.factors.bacterial

FDR: 5.690e-02
Coefficient: 9.27e-02
Value: FS

0.34

0.33

0.32

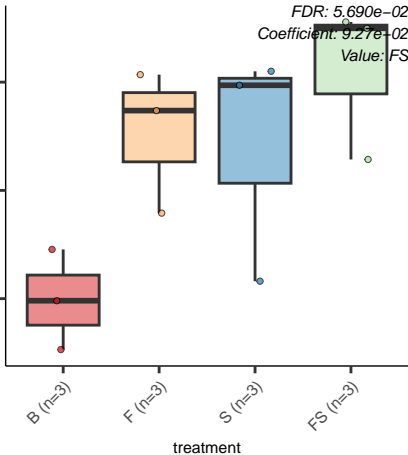
B (n=3)

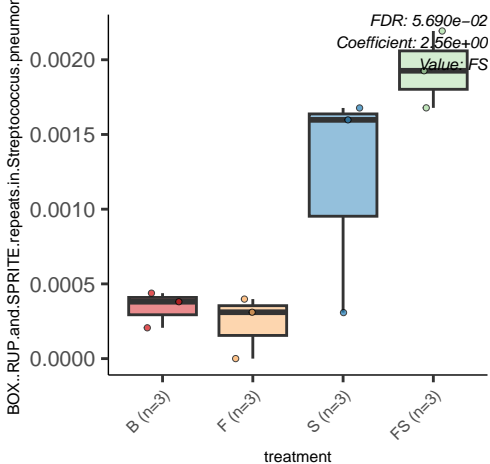
F (n=3)

S (n=3)

FS (n=3)

treatment





Colanic.acid.biosynthesis

FDR: 5.707e-02

Coefficient: -3.41e-01

Value: S

0.11

0.10

0.09

0.08

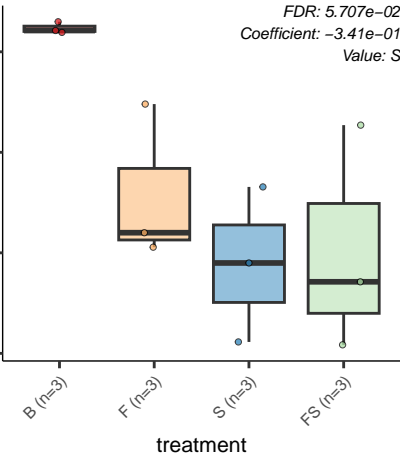
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Glycine.and.Serine.Utilization

FDR: 5.707e-02
Coefficient: -1.25e-01
Value: FS

0.23
0.22
0.21
0.20

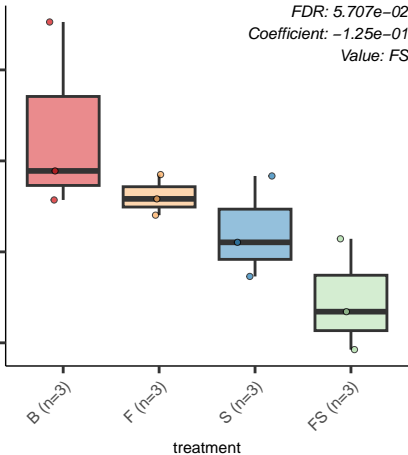
B (n=3)

F (n=3)

S (n=3)

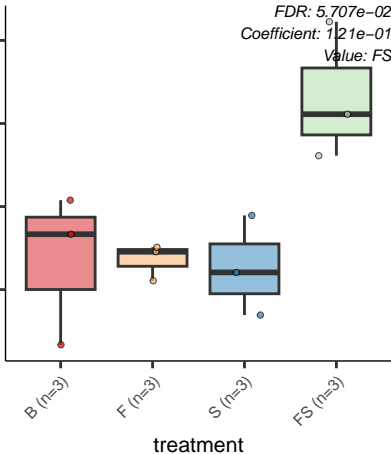
FS (n=3)

treatment



Glycine.cleavage.system

FDR: $5.707e-02$
Coefficient: $1.21e-01$
Value: FS



Rcs.negative.regulator.lgaA

0.025
0.020
0.015
0.010

B (n=3)

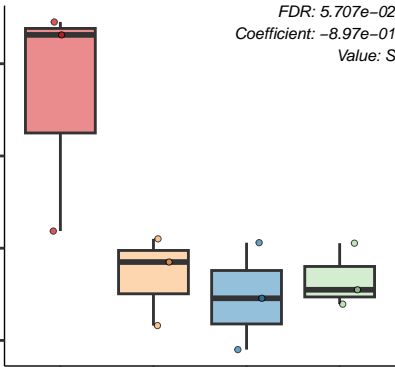
F (n=3)

S (n=3)

FS (n=3)

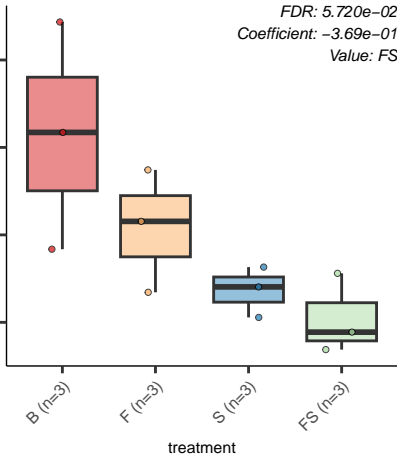
treatment

FDR: 5.707e-02
Coefficient: -8.97e-01
Value: S



D.galactarate..D.glucarate.and.D.glycerate.catabolism...g

FDR: $5.720e-02$
Coefficient: $-3.69e-01$
Value: FS



Small.multidrug.resistance.strays

0.004
0.003
0.002
0.001
0.000

FDR: 5.720e-02
Coefficient: -2.63e+00
Value: FS

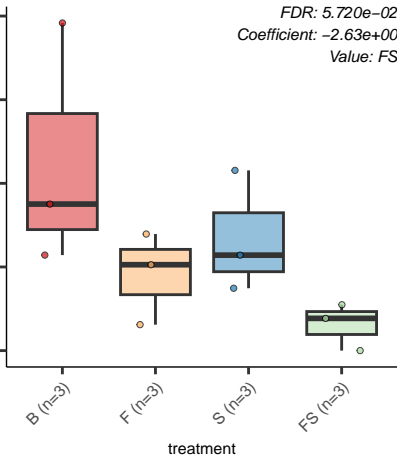
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Dehydrogenase.complexes

0.06
0.05
0.04
0.03

B (n=3)

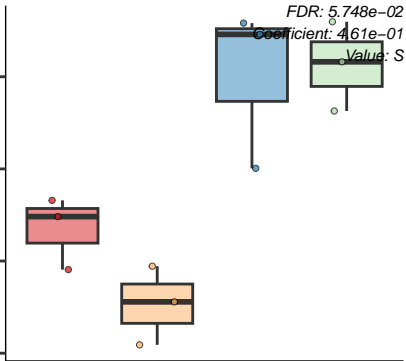
F (n=3)

S (n=3)

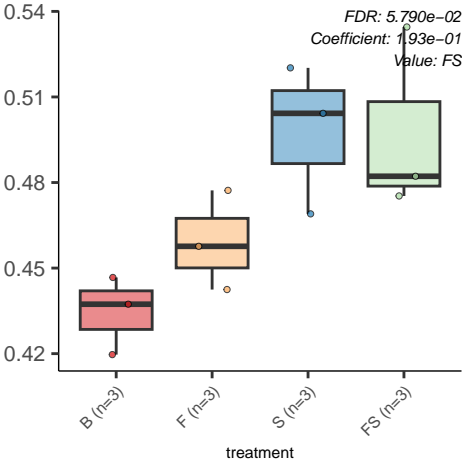
FS (n=3)

treatment

FDR: 5.748e-02
Coefficient: 4.61e-01
Value: S



ABC.transporter.oligopeptide..TC.3.A.1.5.1.



Hexose.Phosphate.Uptake.System

FDR: 5.790e-02
Coefficient: -6.91e-01
Value: FS

0.024
0.020
0.016
0.012

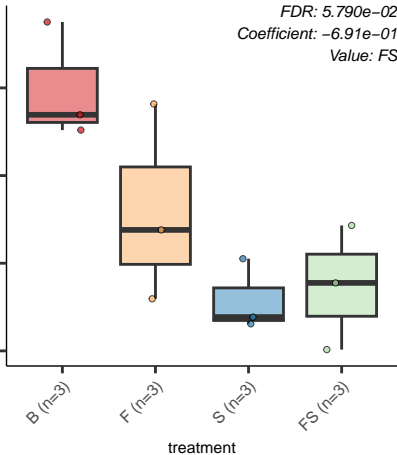
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



CBSS.323850.3.pcg.3269

FDR: 5.818e-02
Coefficient: -9.86e-01
Value: S

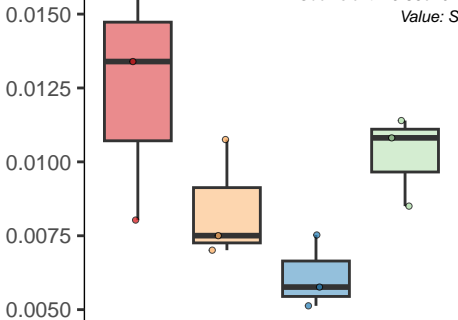
B (n=3)

F (n=3)

S (n=3)

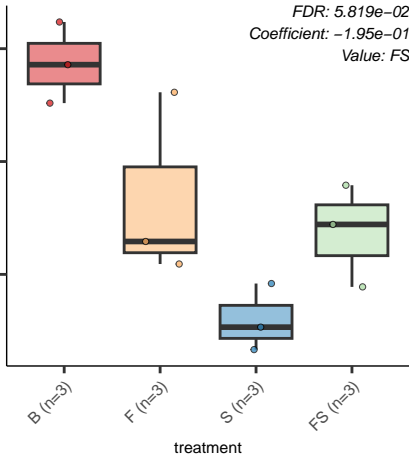
FS (n=3)

treatment



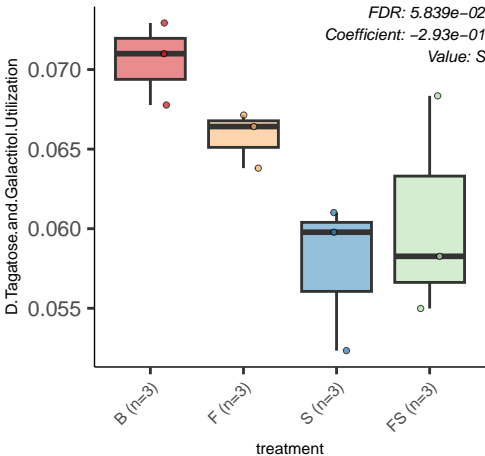
N.Acetyl.Galactosamine.and.Galactosamine.Utilization

FDR: $5.819\text{e-}02$
Coefficient: $-1.95\text{e-}01$
Value: FS



D. Tagatose.and.Galactitol.Utilization

FDR: 5.839e-02
Coefficient: -2.93e-01
Value: S



Fatty.Acid.Biosynthesis.FASII

FDR: 5.839e-02
Coefficient: 1.20e-01
Value: S

0.650
0.625
0.600
0.575

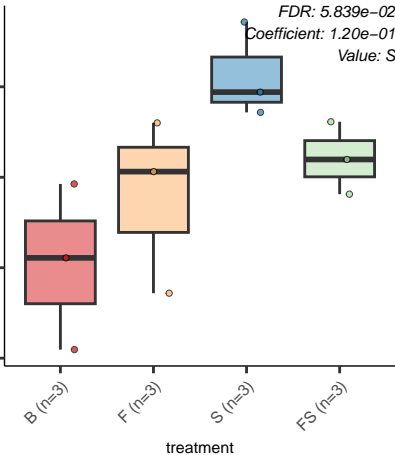
B (n=3)

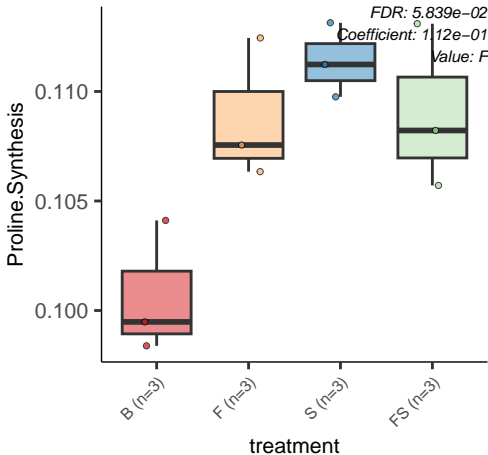
F (n=3)

S (n=3)

FS (n=3)

treatment





Phage.packaging.machinery

FDR: 5.840e-02
Coefficient: -3.26e-01
Value: FS

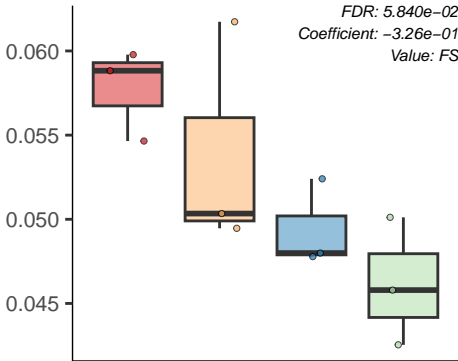
B (n=3)

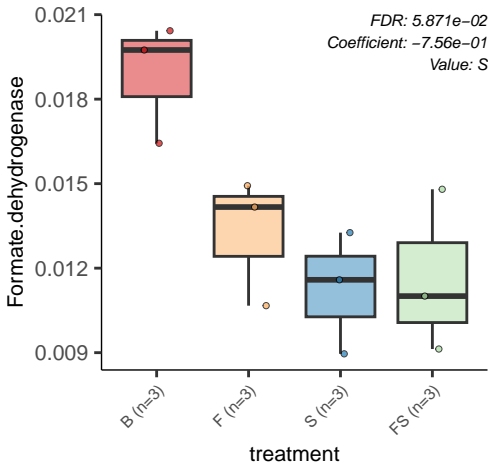
F (n=3)

S (n=3)

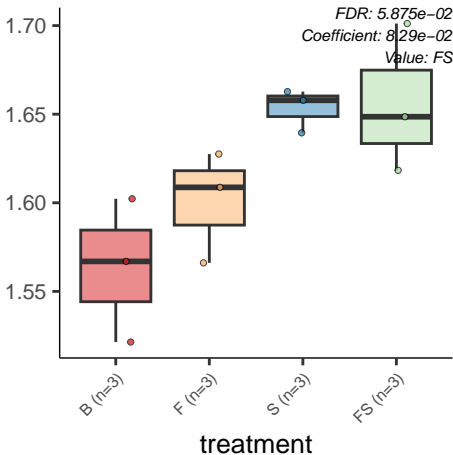
FS (n=3)

treatment



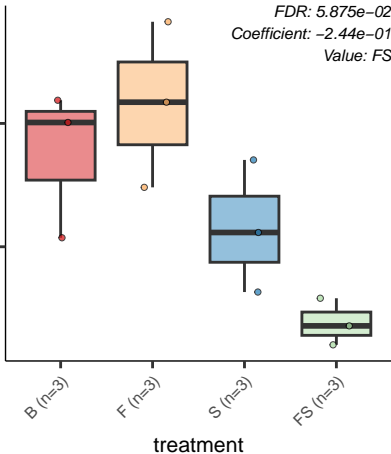


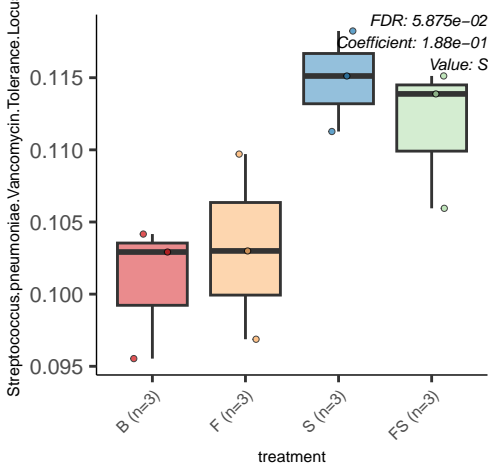
DNA.replication



Hydantoin.metabolism

FDR: $5.875e-02$
Coefficient: $-2.44e-01$
Value: FS





Iron.III..dicitrate.transport.system.Fec

FDR: 5.893e-02
Coefficient: -8.15e-01
Value: F

B (n=3)

F (n=3)

S (n=3)

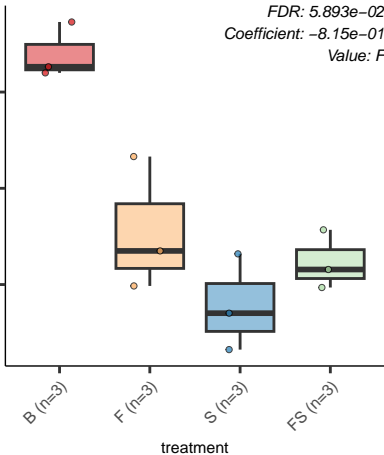
FS (n=3)

treatment

0.0100

0.0075

0.0050



Peptide.ABC.transport.system.Sap

0.04

0.03

0.02

B (n=3)

F (n=3)

S (n=3)

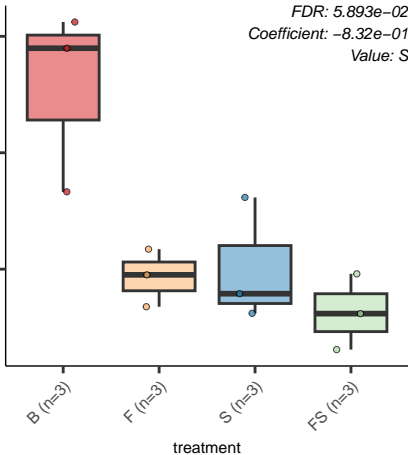
FS (n=3)

treatment

FDR: $5.893e-02$

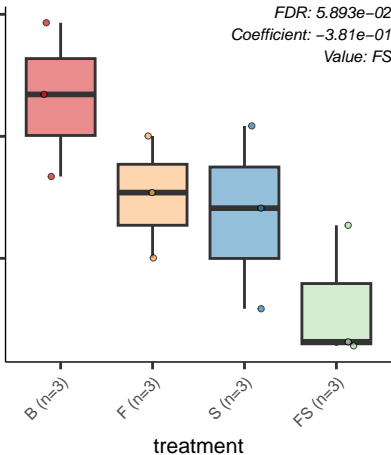
Coefficient: $-8.32e-01$

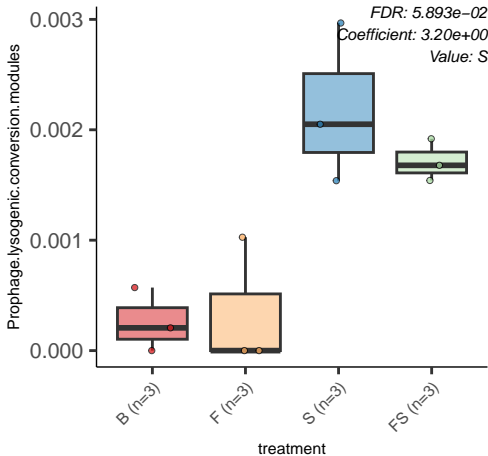
Value: S

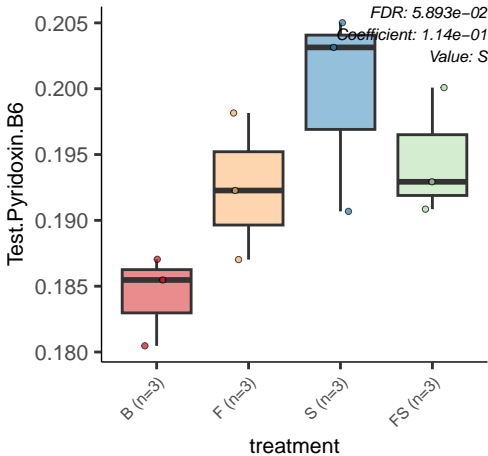


Propanediol.utilization

FDR: 5.893e-02
Coefficient: -3.81e-01
Value: FS

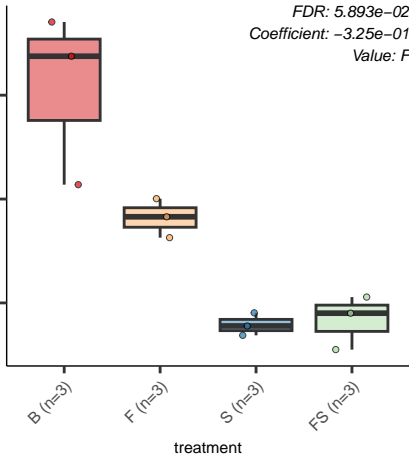


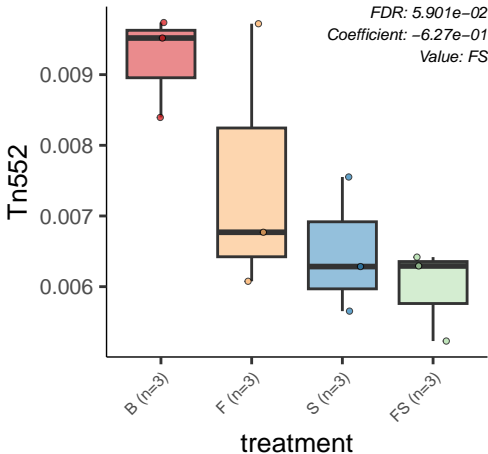




Threonine.anaerobic.catabolism.gene.cluster

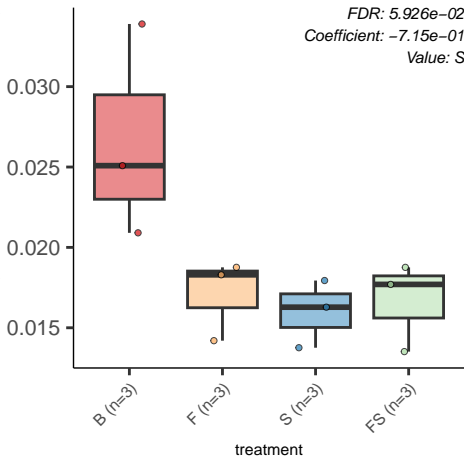
FDR: 5.893e-02
Coefficient: -3.25e-01
Value: F





Central.meta.cleavage.pathway.of.aromatic.compound.degra

FDR: $5.926e-02$
Coefficient: $-7.15e-01$
Value: S



Phage.shock.protein..psp..operon

0.008
0.006
0.004
0.002

B (n=3)

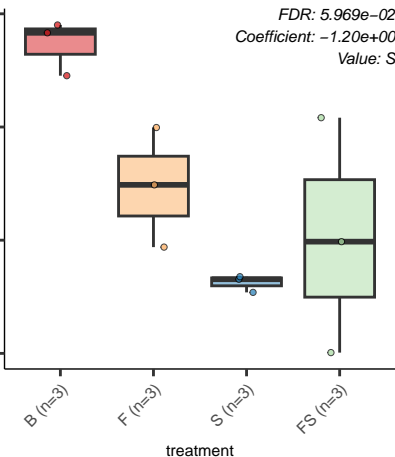
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 5.969e-02
Coefficient: -1.20e+00
Value: S



CBSS.205922.3.pcg.1809

FDR: 5.977e-02
Coefficient: -1.37e+00
Value: F

B (n=3)

F (n=3)

S (n=3)

FS (n=3)

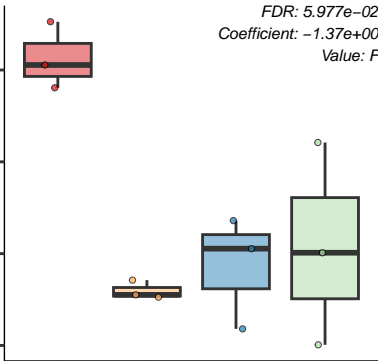
treatment

0.0020

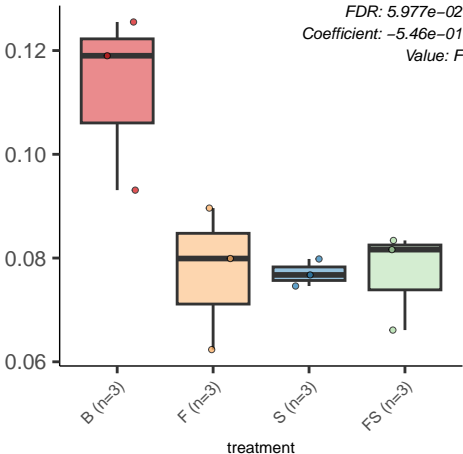
0.0015

0.0010

0.0005



rRNA.modification.bacteria



CBSS.269801.1.peg.2186

FDR: $6.008e-02$
Coefficient: $-6.84e-01$
Value: S

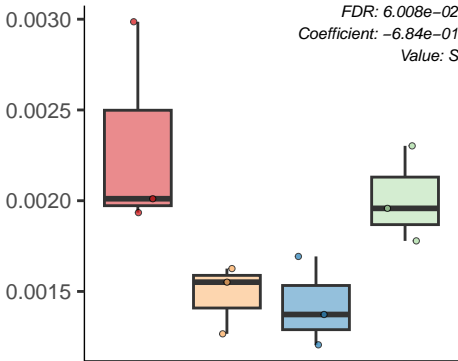
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Choline.and.Betaine.Uptake.and.Betaine.Biosynthesis

0.20
0.19
0.18
0.17
0.16

B (n=3)

F (n=3)

S (n=3)

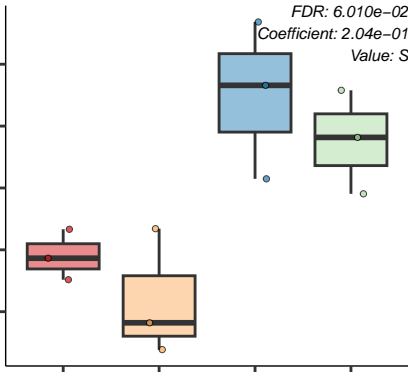
FS (n=3)

treatment

FDR: 6.010e-02

Coefficient: 2.04e-01

Value: S



KDO2.Lipid.A.biosynthesis

FDR: 6.010e-02
Coefficient: -1.31e-01
Value: F

0.28

0.26

0.24

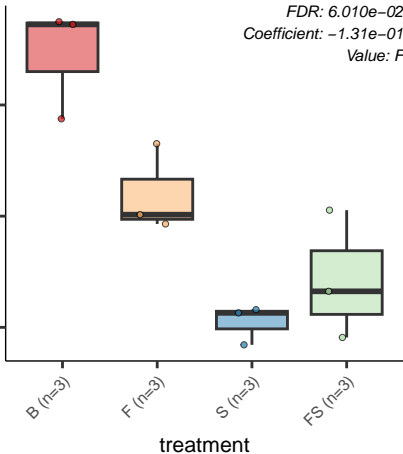
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Mercury.resistance.operon

FDR: $6.010e-02$
Coefficient: $4.93e-01$
Value: FS

0.0150
0.0125
0.0100
0.0075

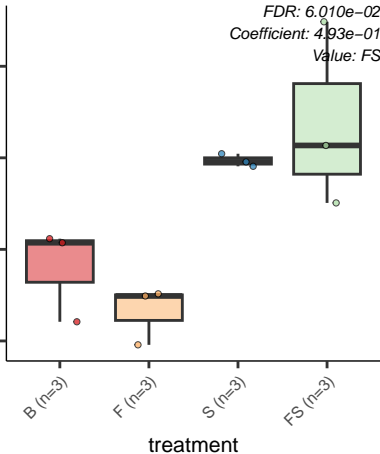
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Multidrug.Resistance..Tripartite.Systems.Found.in.Gram.Negative

FDR: $6.010e-02$
Coefficient: $-3.93e-01$
Value: FS

0.10
0.09
0.08
0.07

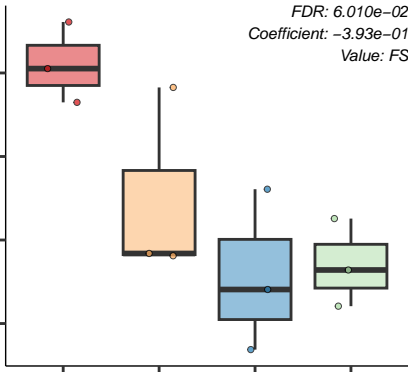
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Universal.GTPases

0.775
0.750
0.725
0.700

B (n=3)

F (n=3)

S (n=3)

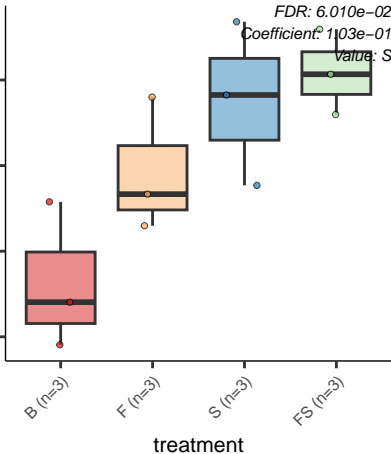
FS (n=3)

treatment

FDR: 6.010e-02

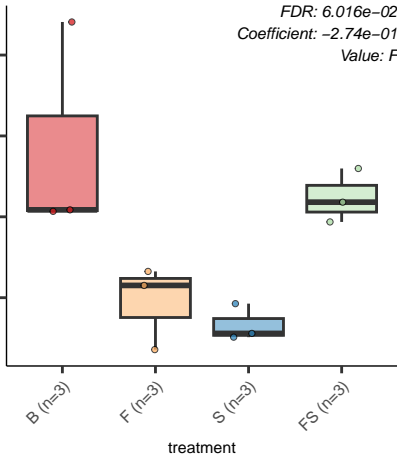
Coefficient: 1.03e-01

value: S



Twin.arginine.translocation.system

FDR: 6.016e-02
Coefficient: -2.74e-01
Value: F



rRNA.modification.bacteria

0.06

0.08

0.10

0.12

B (n=3)

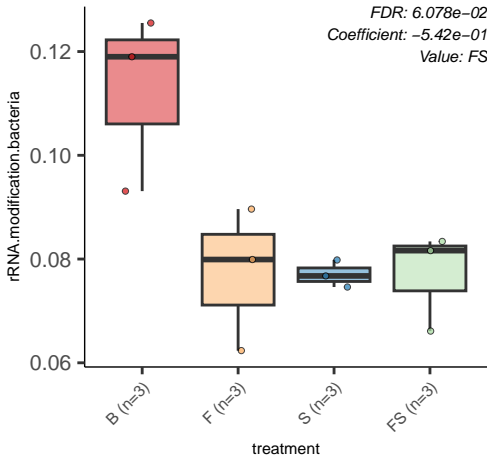
F (n=3)

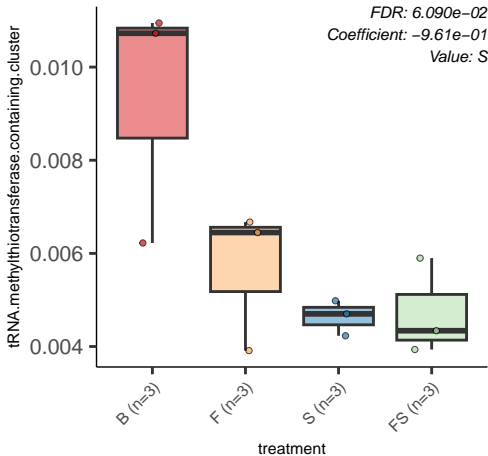
S (n=3)

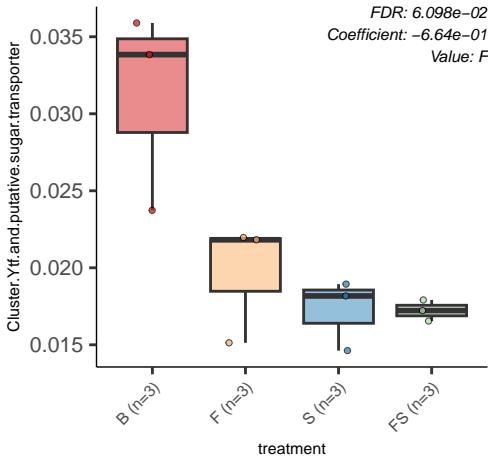
FS (n=3)

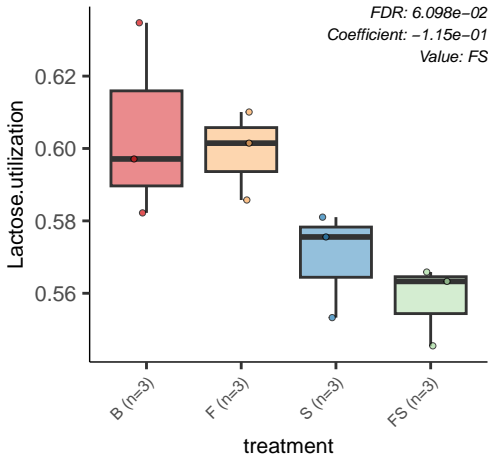
treatment

FDR: 6.078e-02
Coefficient: -5.42e-01
Value: FS



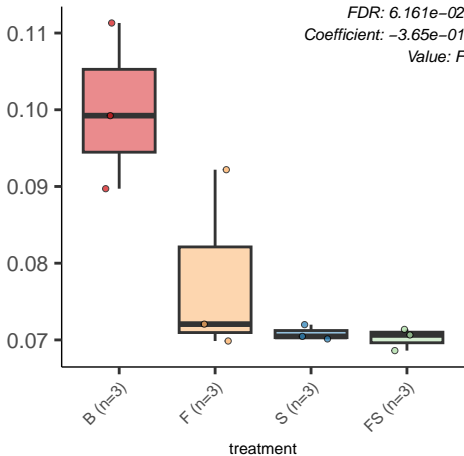






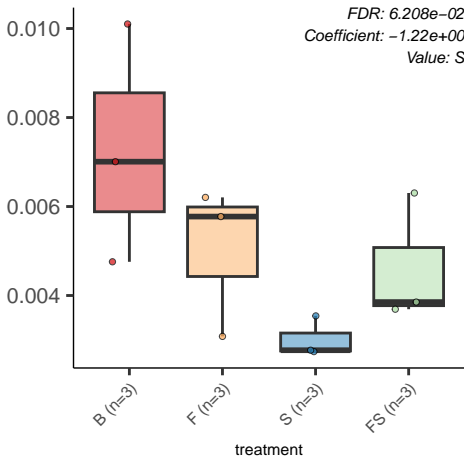
Nitrate.and.nitrite.ammonification

FDR: 6.161e-02
Coefficient: -3.65e-01
Value: F



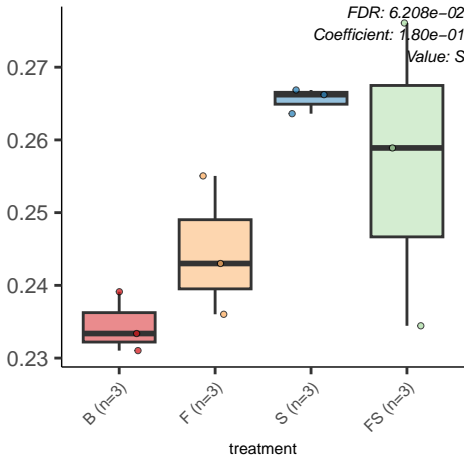
A.conserved.operon.linked.to.TyrR.and.possibly.involved.in.vir

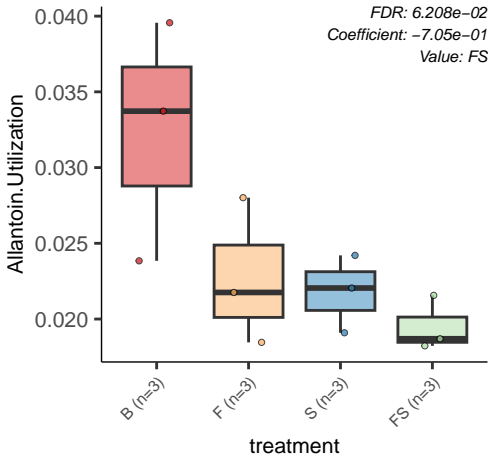
FDR: 6.208e-02
Coefficient: -1.22e+00
Value: S



ABC.transporter.branched.chain.amino.acid..TC.3.A.1.4.

FDR: 6.208e-02
Coefficient: 1.80e-01
Value: S





At5g63290

0.46
0.44
0.42

B (n=3)

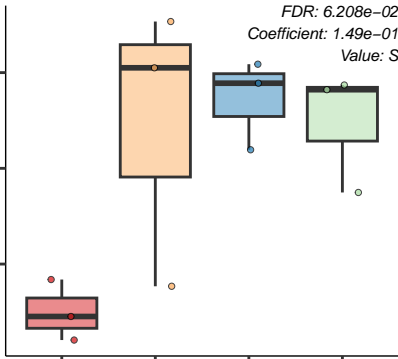
F (n=3)

S (n=3)

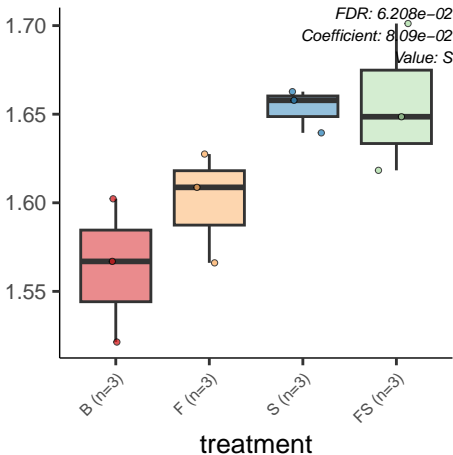
FS (n=3)

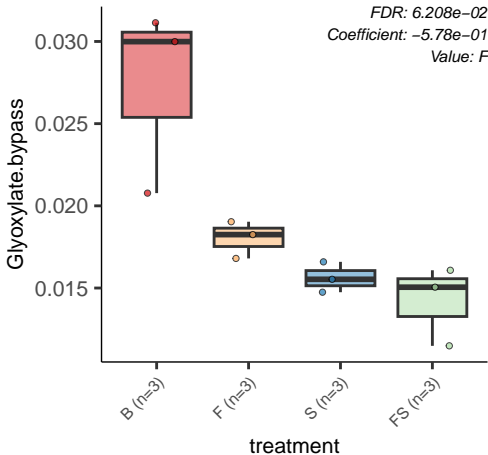
treatment

FDR: 6.208e-02
Coefficient: 1.49e-01
Value: S



DNA.replication





Inorganic.Sulfur.Assimilation

0.060
0.055
0.050
0.045
0.040

B (n=3)

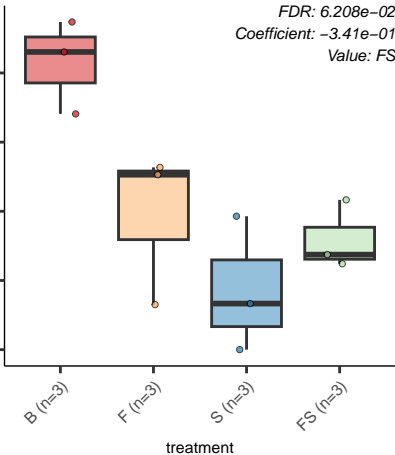
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 6.208e-02
Coefficient: -3.41e-01
Value: FS



Natural.DNA.Transformation.in.Vibrio

FDR: $6.208e-02$
Coefficient: $-1.56e+00$
Value: FS

0.003
0.002
0.001

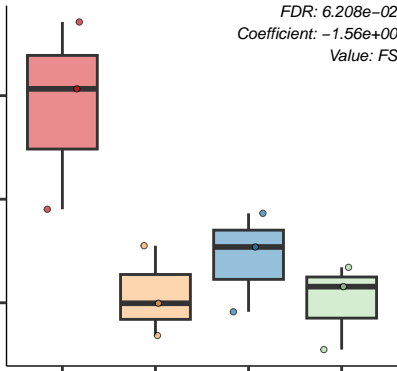
B (n=3)

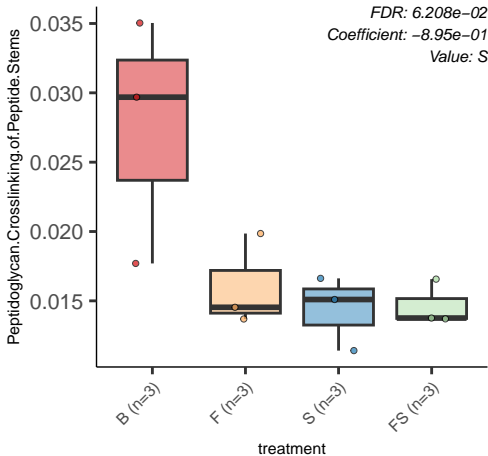
F (n=3)

S (n=3)

FS (n=3)

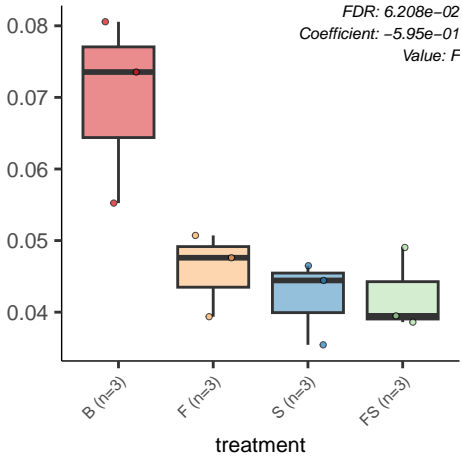
treatment





Phage.tail.fiber.proteins

FDR: 6.208e-02
Coefficient: -5.95e-01
Value: F

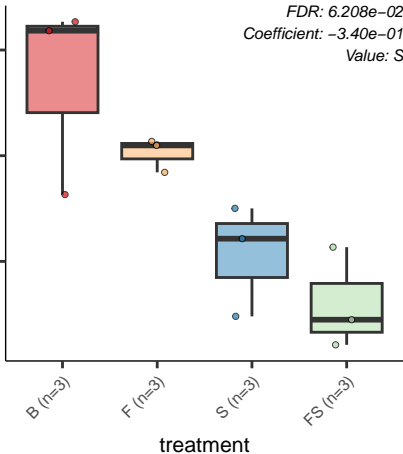


Phage.tail.proteins.2

FDR: 6.208e-02

Coefficient: -3.40e-01

Value: S



RNA.polymerase.bacterial

FDR: $6.208e-02$
Coefficient: $7.78e-02$
Value: S

0.57
0.56
0.55
0.54
0.53

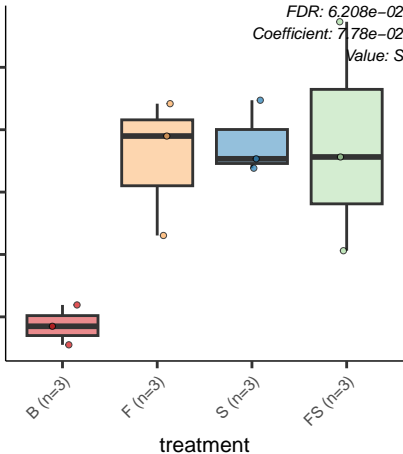
B (n=3)

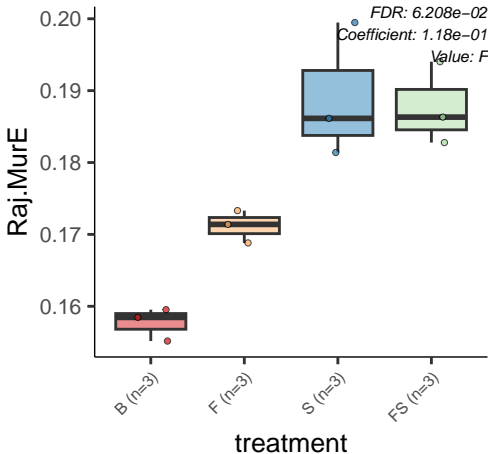
F (n=3)

S (n=3)

FS (n=3)

treatment





Type.4.secretion.and.conjugative.transfer

FDR: 6.208e-02
Coefficient: -6.67e-01
Value: F

0.004
0.003

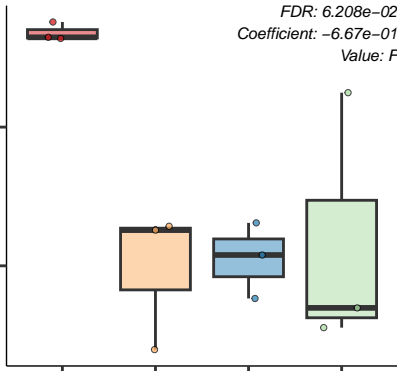
B (n=3)

F (n=3)

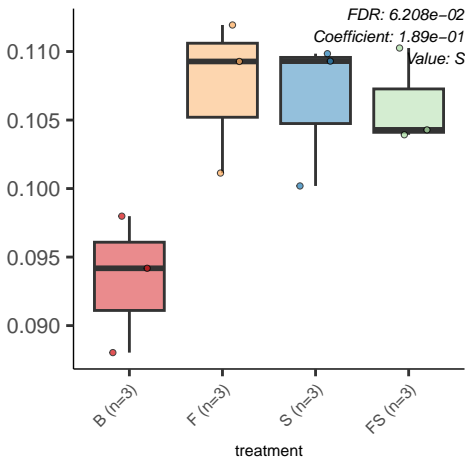
S (n=3)

FS (n=3)

treatment



pVir.Plasmid.of.Campylobacter



rRNA.modification.bacteria

0.12

0.10

0.08

0.06

B (n=3)

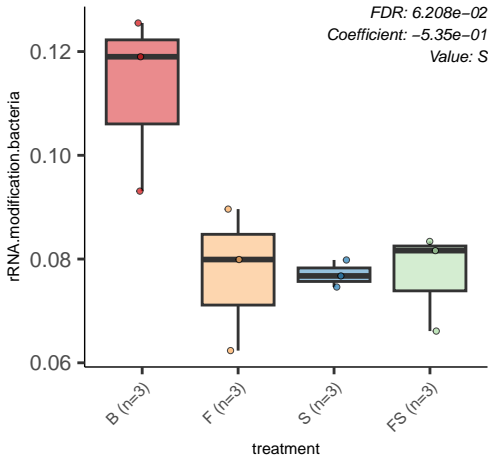
F (n=3)

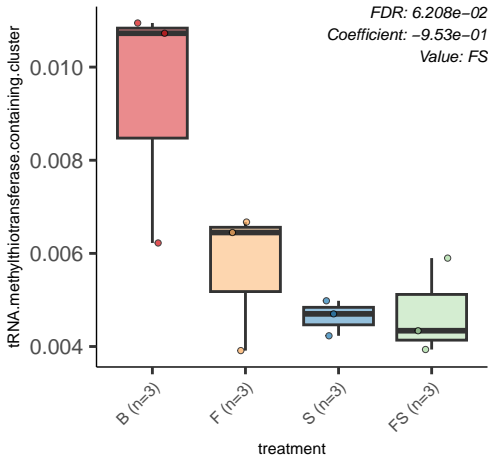
S (n=3)

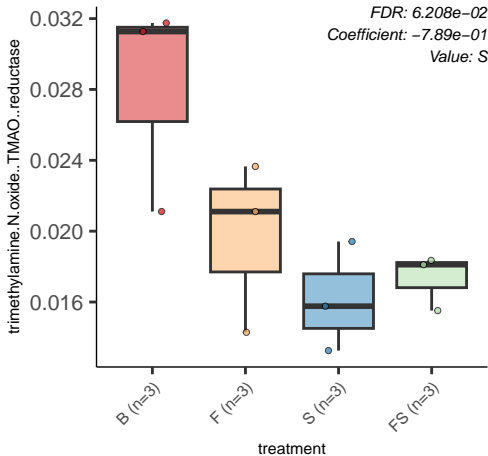
FS (n=3)

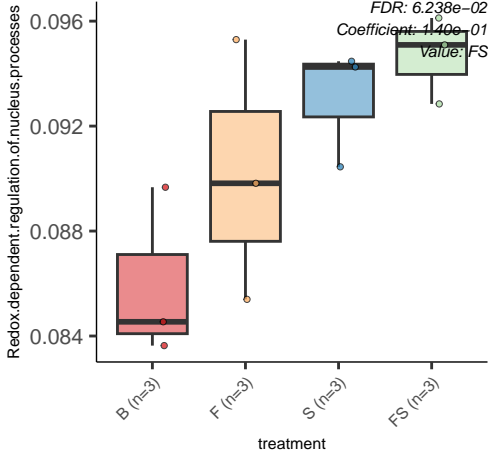
treatment

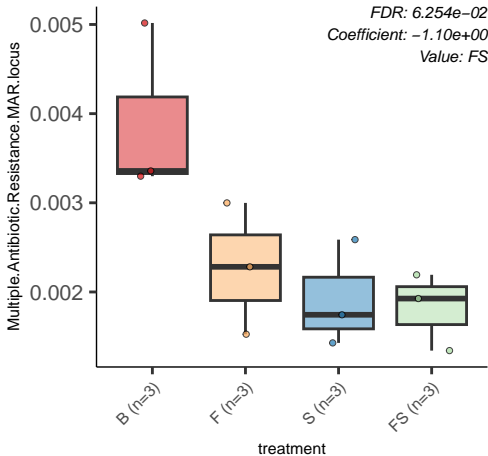
FDR: 6.208e-02
Coefficient: -5.35e-01
Value: S

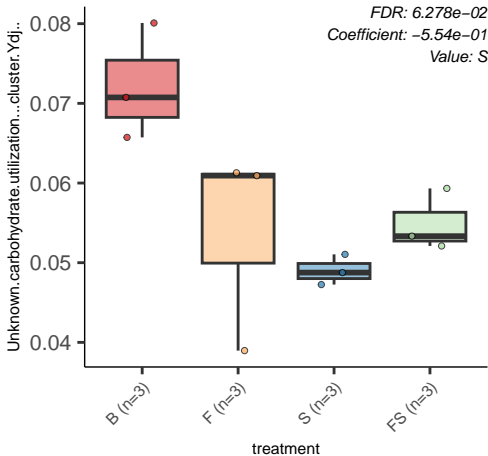












RNA.polymerase.bacterial

FDR: $6.386e-02$
Coefficient: $7.71e-02$
Value: FS

0.57
0.56
0.55
0.54
0.53

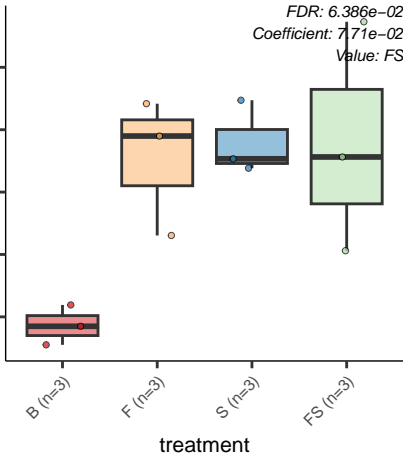
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



rRNA.modification.Archaea

FDR: 6.386e-02
Coefficient: -1.00e+00
Value: S

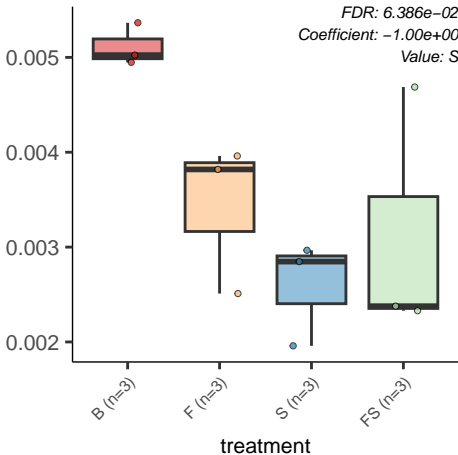
B (n=3)

F (n=3)

S (n=3)

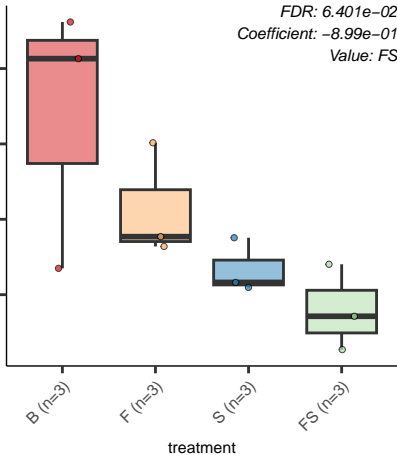
FS (n=3)

treatment



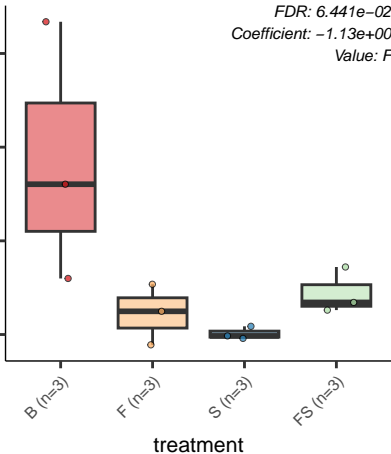
Molybdopterin.cytosine.dinucleotide

FDR: 6.401e-02
Coefficient: -8.99e-01
Value: FS

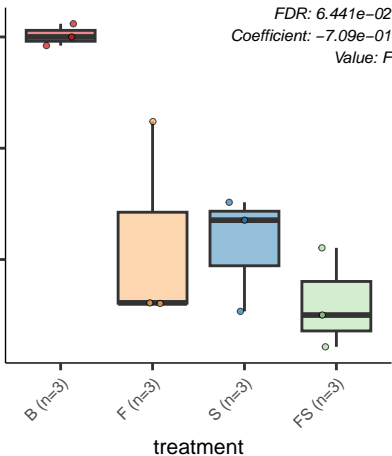


CBSS.194948.1.pcg.143

FDR: 6.441e-02
Coefficient: -1.13e+00
Value: F



CBSS.584.1.pcg.841



Colanic.acid.biosynthesis

FDR: 6.441e-02
Coefficient: -3.24e-01
Value: FS

0.11
0.10
0.09
0.08

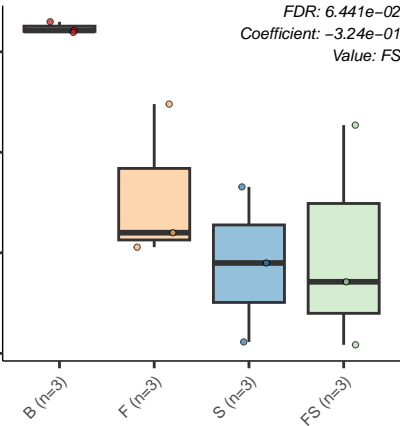
B (n=3)

F (n=3)

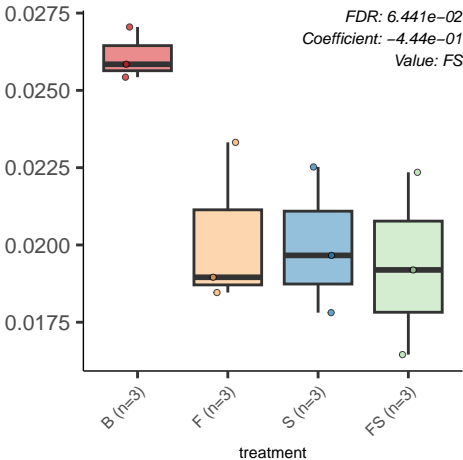
S (n=3)

FS (n=3)

treatment

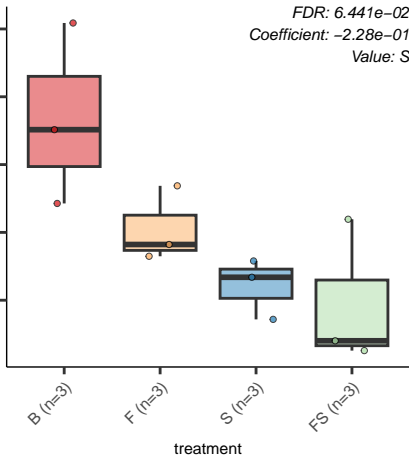


Khodge314.Isoleucine.Biosynthesis



Respiration...Human.gut.microbiome

FDR: 6.441e-02
Coefficient: -2.28e-01
Value: S



Trehalose.Biosynthesis

FDR: 6.441e-02
Coefficient: -1.49e-01
Value: FS

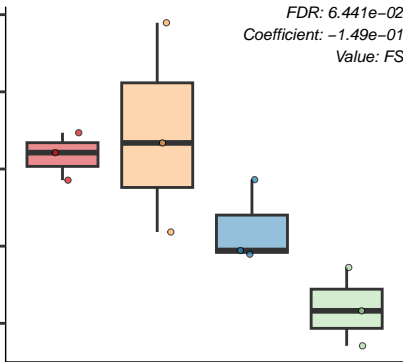
B (n=3)

F (n=3)

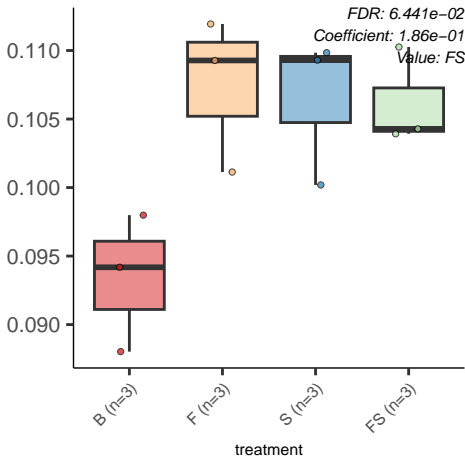
S (n=3)

FS (n=3)

treatment



pVir.Plasmid.of.Campylobacter



At1g69340.At2g40600

FDR: $6.509e-02$
Coefficient: $2.77e-01$
Value: FS

0.08

0.07

0.06

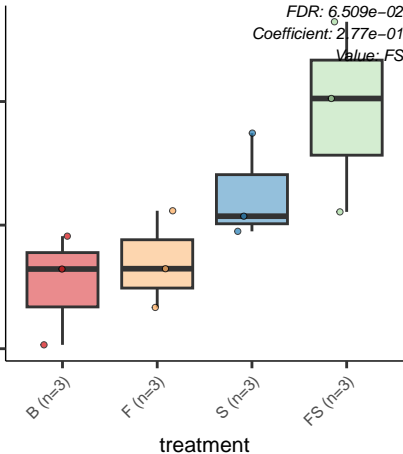
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Listeria.Pathogenicity.Island.LPI.1.extended

FDR: $6.509e-02$
Coefficient: $-3.71e-01$
Value: S

0.016
0.014
0.012
0.010

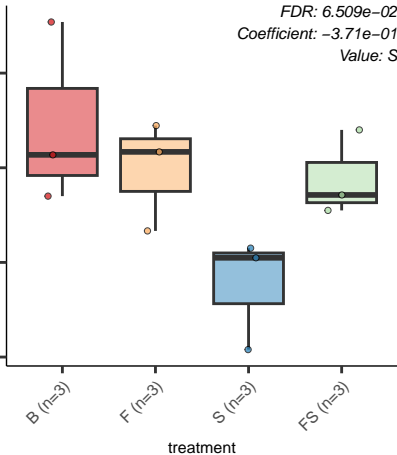
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Murein.Hydrolases

0.15
0.14
0.13

B (n=3)

F (n=3)

S (n=3)

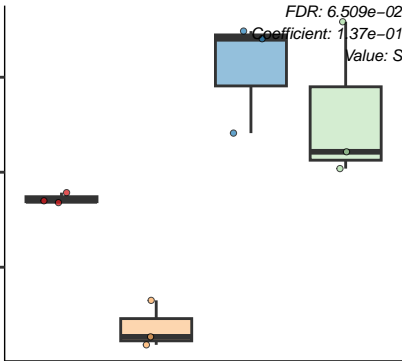
FS (n=3)

treatment

FDR: 6.509e-02

Coefficient: 1.37e-01

Value: S



Propionate.CoA.to.Succinate.Module

FDR: $6.509e-02$
Coefficient: $-6.74e-01$
Value: F

0.012
0.010
0.008
0.006

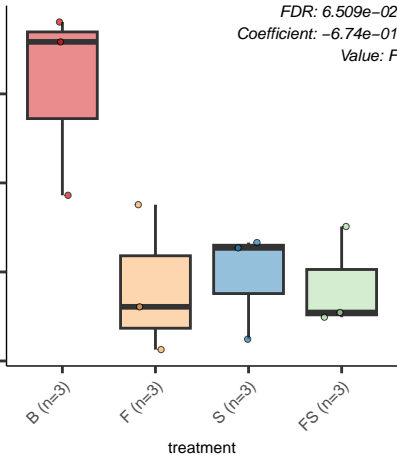
B (n=3)

F (n=3)

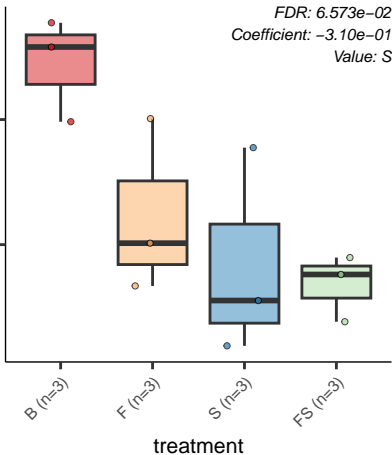
S (n=3)

FS (n=3)

treatment

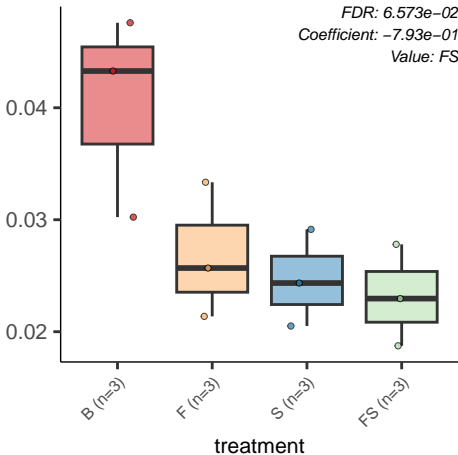


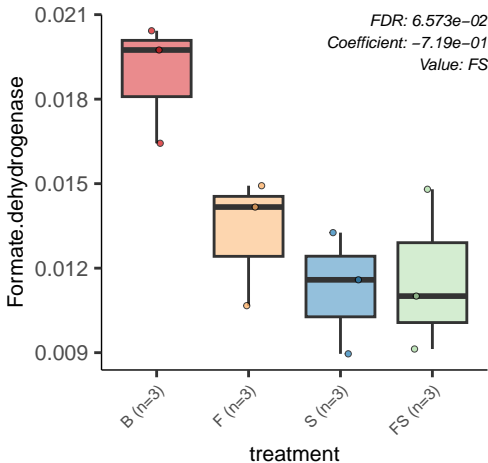
CBSS.342610.3.peg.1536



D.galactonate.catabolism

FDR: $6.573e-02$
Coefficient: $-7.93e-01$
Value: FS





Pentose.phosphate.pathway

FDR: 6.588e-02
Coefficient: 1.60e-01
Value: F

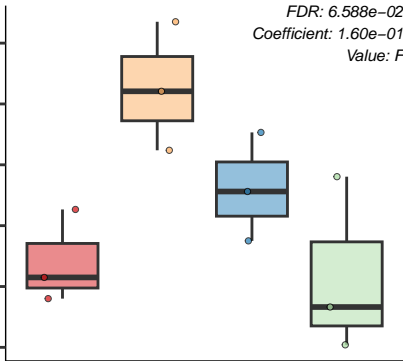
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Glutamine.synthetases

0.072

0.069

0.066

0.063

B (n=3)

F (n=3)

S (n=3)

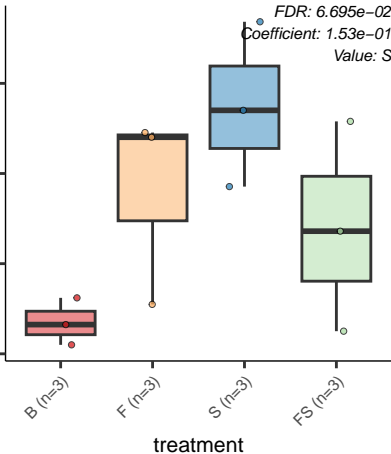
FS (n=3)

treatment

FDR: 6.695e-02

Coefficient: 1.53e-01

Value: S



Queuosine.Archaeosine.Biosynthesis

FDR: 6.695e-02
Coefficient: -1.24e-01
Value: S

0.180
0.175
0.170
0.165
0.160

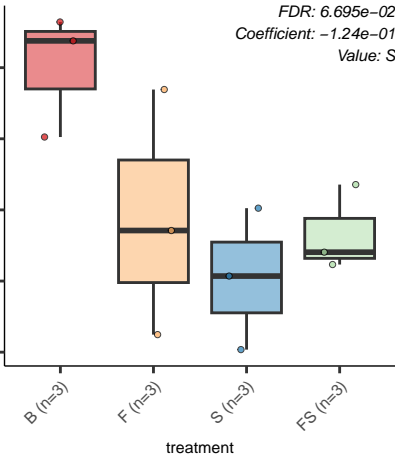
B (n=3)

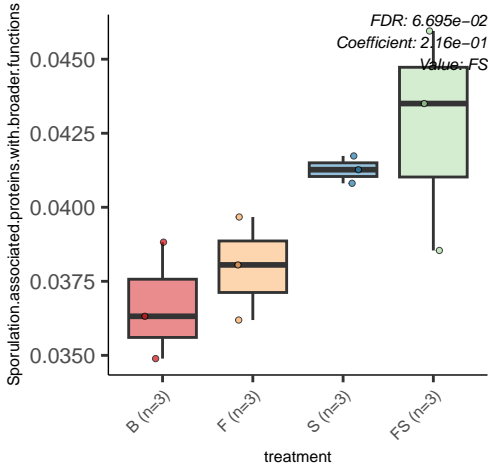
F (n=3)

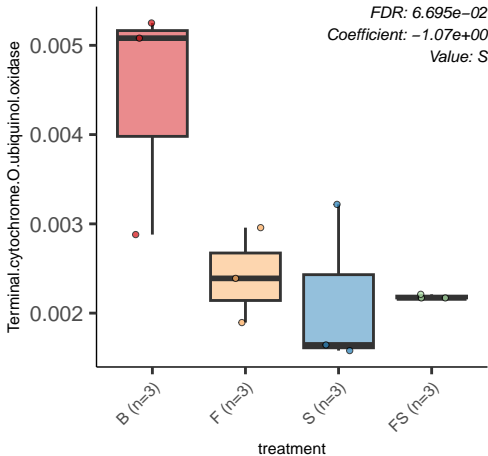
S (n=3)

FS (n=3)

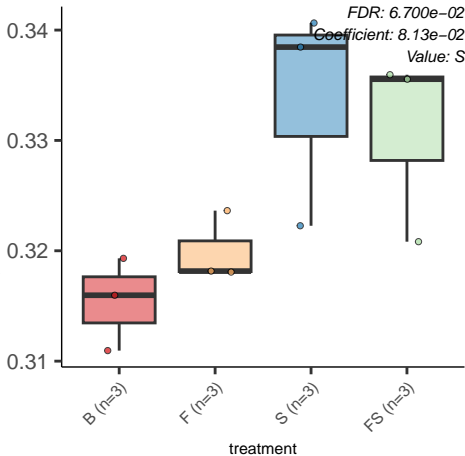
treatment

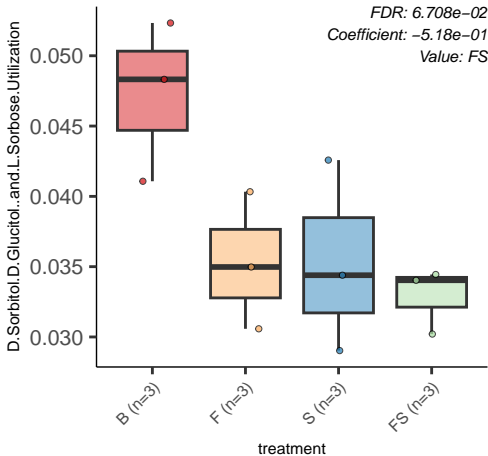


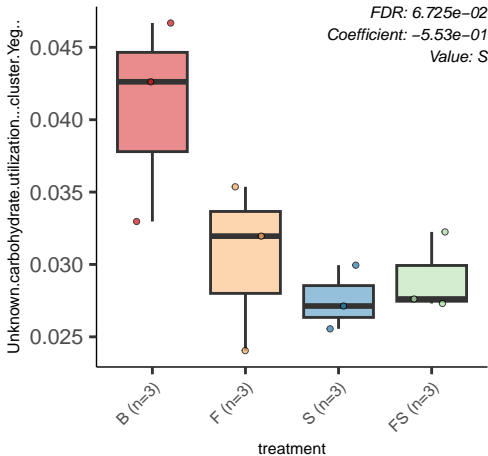




Competence.or.DNA.damage.inducible.protein.CinA.and.related.pro







Adhesion.of.Campylobacter

0.036

0.032

0.028

0.024

B (n=3)

F (n=3)

S (n=3)

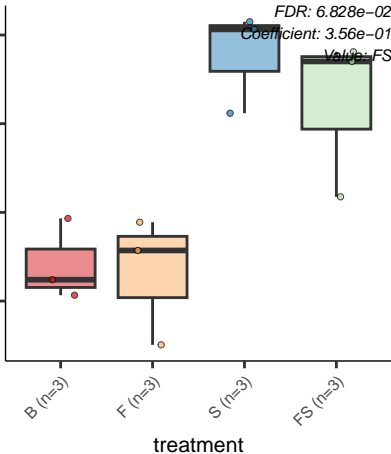
FS (n=3)

treatment

FDR: 6.828e-02

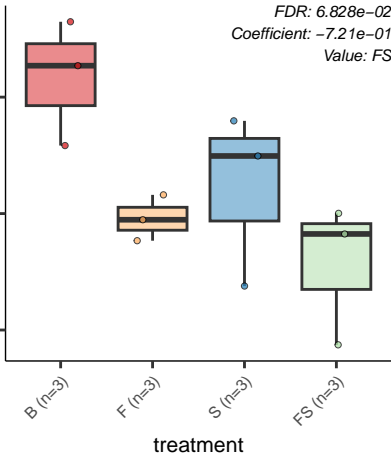
Coefficient: 3.56e-01

Value: FS



Aromatic.Amin.Catabolism

FDR: 6.828e-02
Coefficient: -7.21e-01
Value: FS



Carbon.Starvation

FDR: 6.828e-02
Coefficient: -1.81e-01
Value: FS

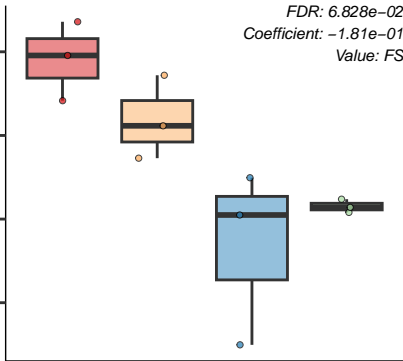
B (n=3)

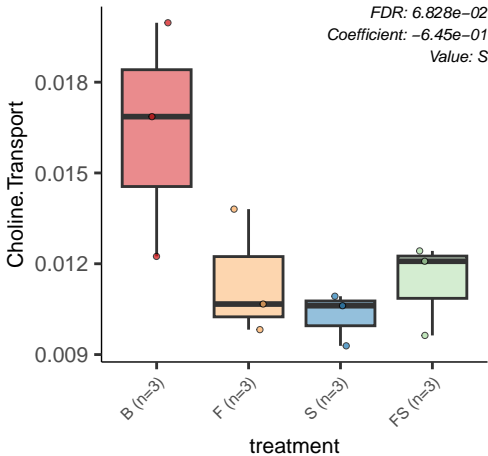
F (n=3)

S (n=3)

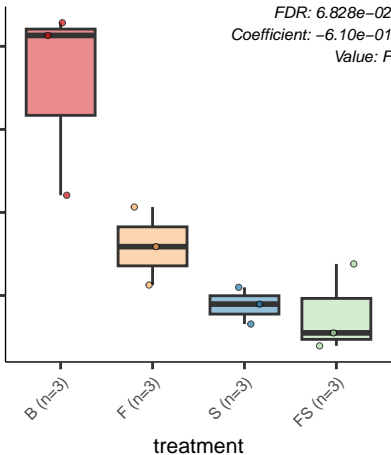
FS (n=3)

treatment





Cinnamic Acid Degradation



CBSS.211586.1.pcg.3133

FDR: 6.851e-02
Coefficient: -6.14e-01
Value: FS

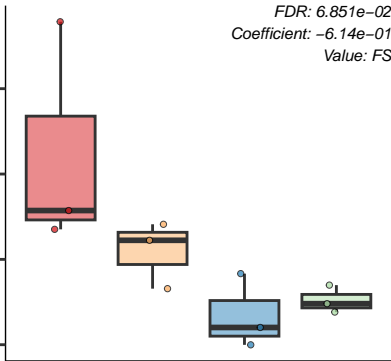
B (n=3)

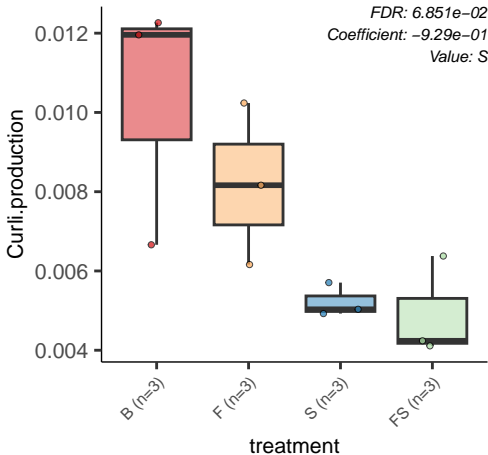
F (n=3)

S (n=3)

FS (n=3)

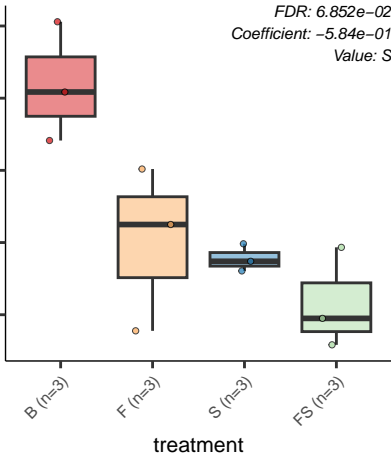
treatment

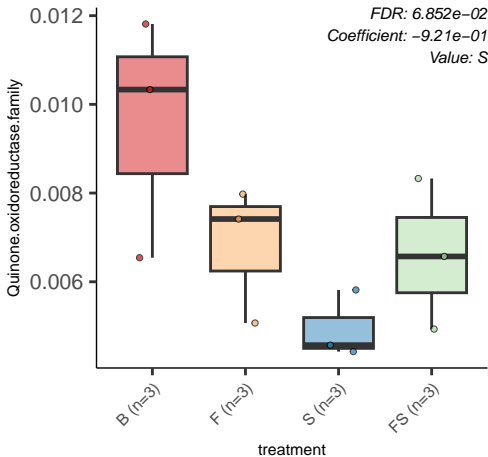


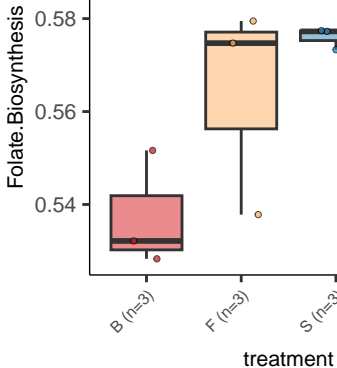


Pyrimidine.utilization

FDR: $6.852e-02$
Coefficient: $-5.84e-01$
Value: S







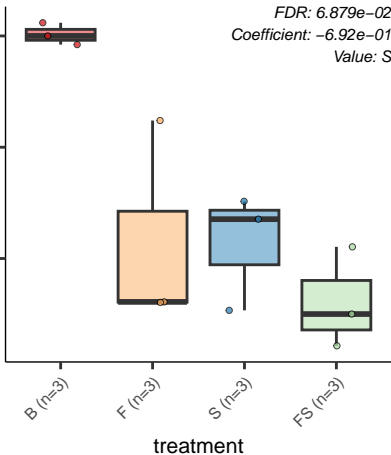
FDR: 6.865e-02
Coefficient: 1.00e-01
Value: S

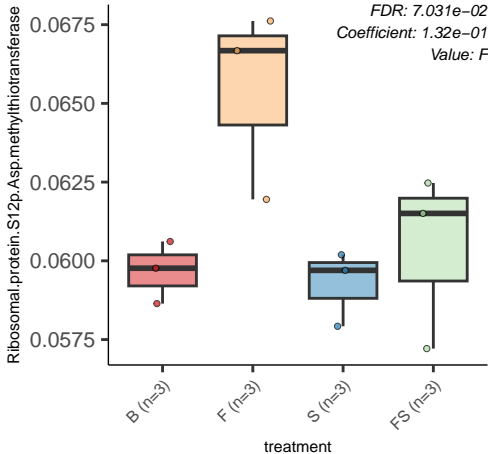
CBSS.584.1.pcg.841

FDR: 6.879e-02

Coefficient: -6.92e-01

Value: S





Putrescine.utilization.pathways

0.035
0.030
0.025
0.020
0.015

FDR: 7.052e-02
Coefficient: -7.31e-01
Value: F

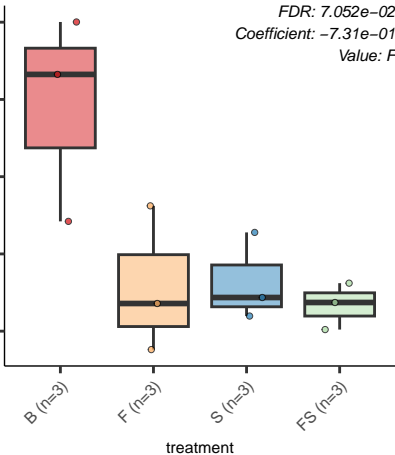
B (n=3)

F (n=3)

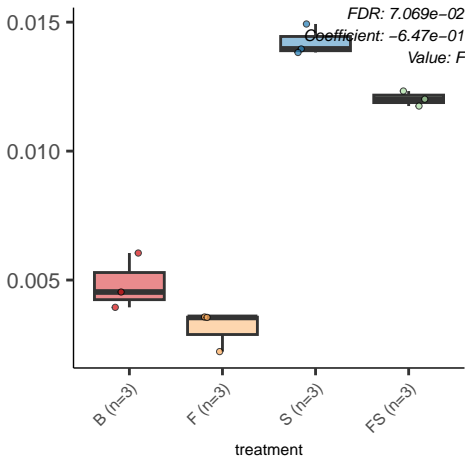
S (n=3)

FS (n=3)

treatment



Single.Rhodanese.domain.proteins



Propionate.CoA.to.Succinate.Module

FDR: 7.082e-02
Coefficient: -6.55e-01
Value: FS

0.012
0.010
0.008
0.006

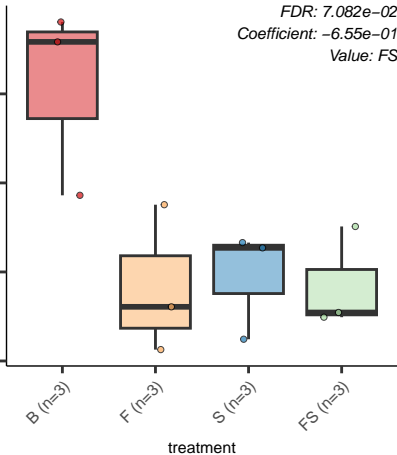
B (n=3)

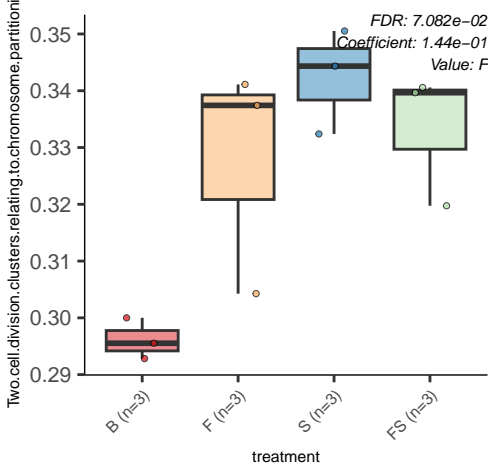
F (n=3)

S (n=3)

FS (n=3)

treatment





Mercuric.reductase

FDR: $7.117e-02$
Coefficient: $4.45e-01$
Value: S

0.0150
0.0125
0.0100
0.0075

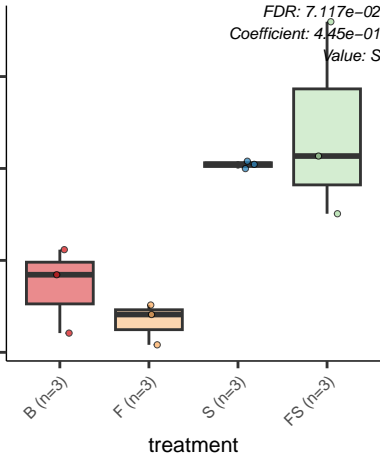
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



tRNA.mods.Archaea

FDR: 7.117e-02
Coefficient: 7.38e-02
Value: F

0.43

0.42

0.41

0.40

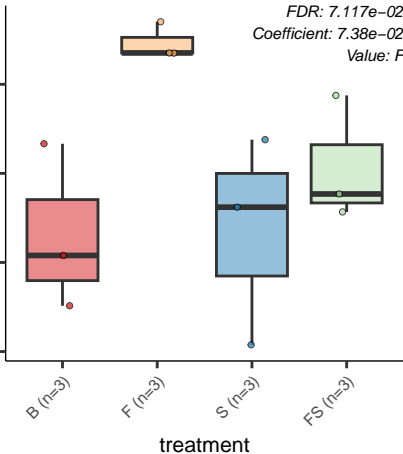
B (n=3)

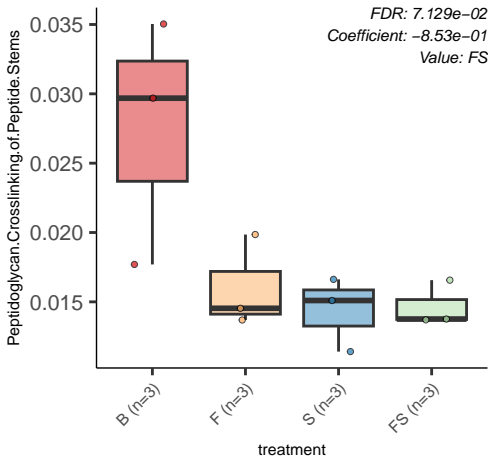
F (n=3)

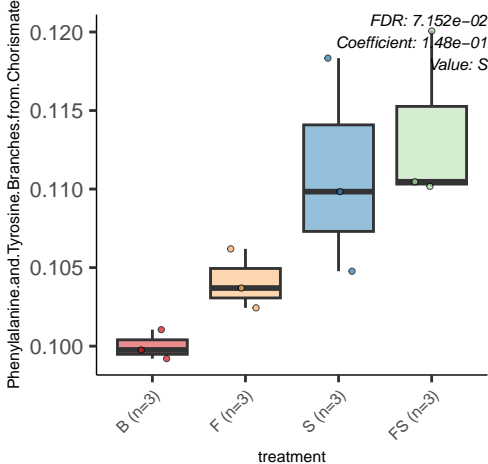
S (n=3)

FS (n=3)

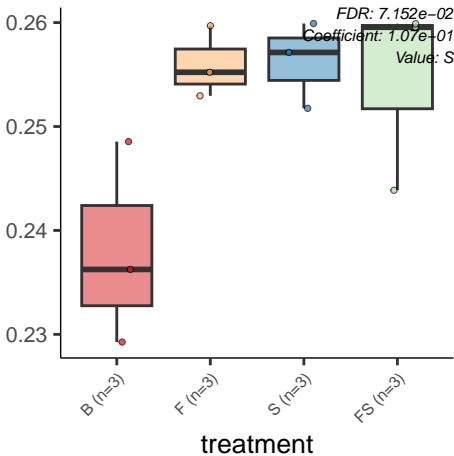
treatment







tRNA.processing



Glutathionylspermidine.and.Tryptanothione

FDR: 7.201e-02
Coefficient: -6.60e-01
Value: FS

0.024
0.020
0.016
0.012

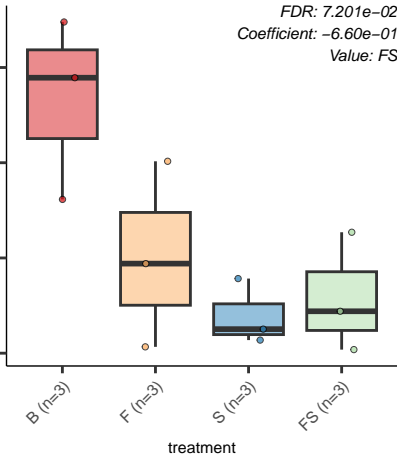
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Central.meta.cleavage.pathway.of.aromatic.compound.degra

FDR: $7.223e-02$
Coefficient: $-6.62e-01$
Value: FS

0.030
0.025
0.020
0.015

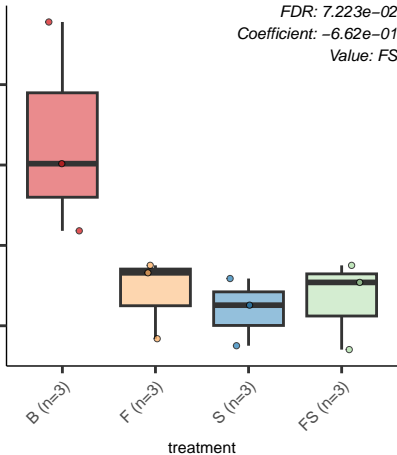
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



LOS.core.oligosaccharide.biosynthesis

FDR: $7.223e-02$
Coefficient: $-1.43e-01$
Value: FS

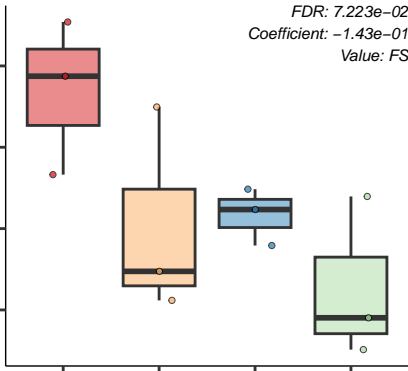
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Respiratory.Complex.I

FDR: 7.223e-02
Coefficient: -2.34e-01
Value: FS

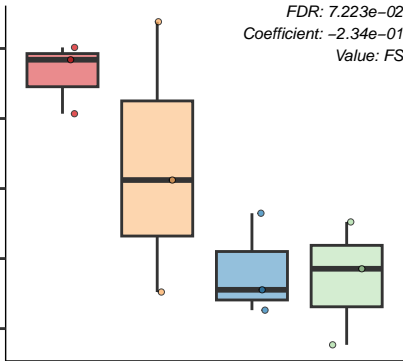
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Type.VI.secretion.systems

FDR: 7.223e-02

Coefficient: -5.44e-01

Value: FS

0.12

0.10

0.08

0.06

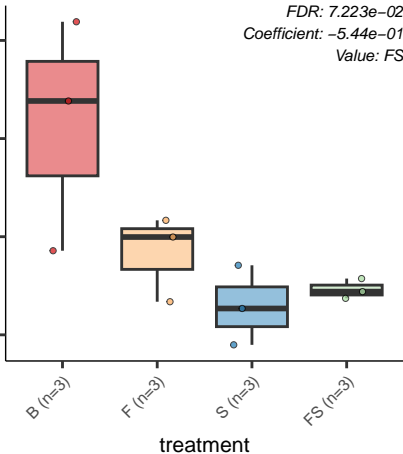
B (n=3)

F (n=3)

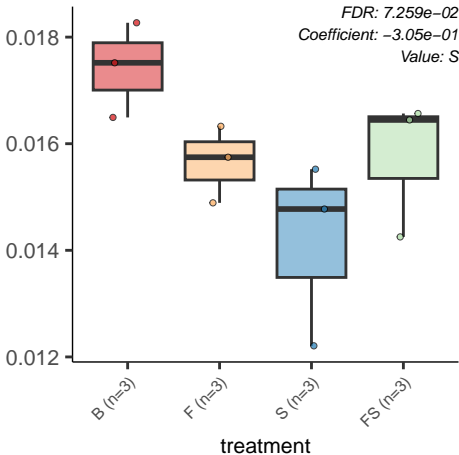
S (n=3)

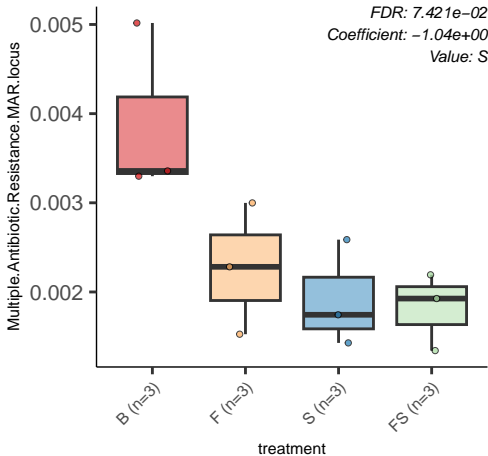
FS (n=3)

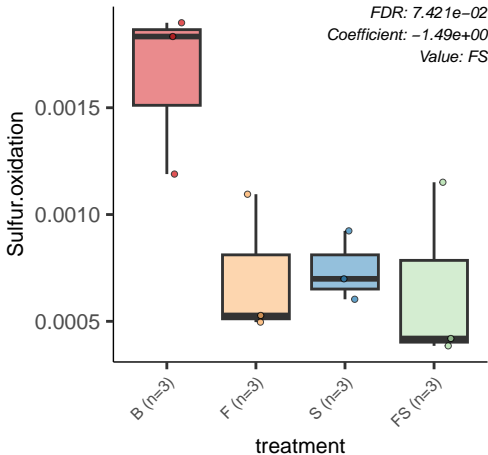
treatment



CBSS.316057.3.peg.659







Unsaturated.Fatty.Acid.Metabolism

0.018
0.015
0.012
0.009
0.006

FDR: 7.428e-02
Coefficient: -7.55e-01
Value: FS

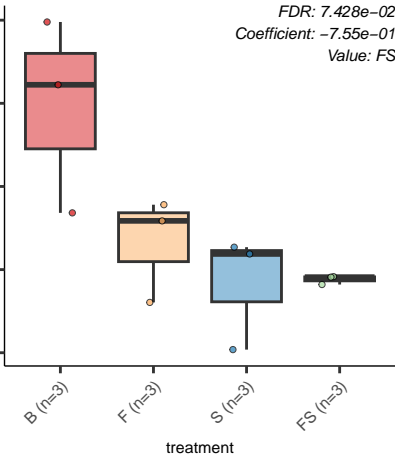
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Lipid.A.modifications

FDR: 7.440e-02
Coefficient: -6.70e-01
Value: F

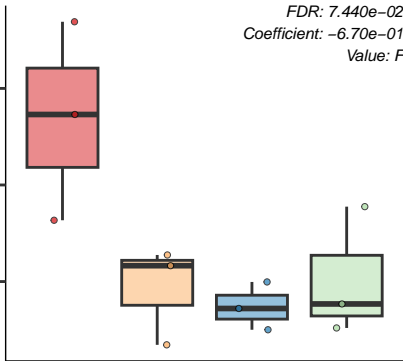
B (n=3)

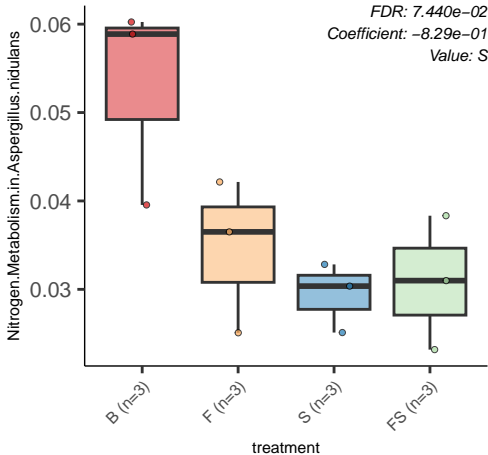
F (n=3)

S (n=3)

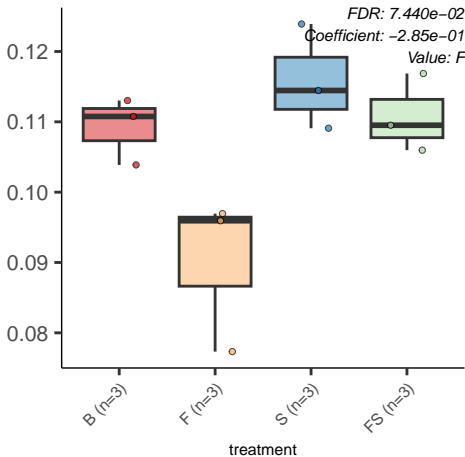
FS (n=3)

treatment



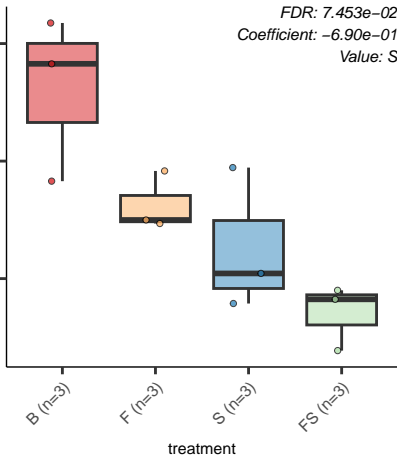


Trehalose.Uptake.and.Utilization



Siderophore. Yersiniabactin. Biosynthesis

FDR: 7.453e-02
Coefficient: -6.90e-01
Value: S



Type.4.secretion.and.conjugative.transfer

FDR: $7.462e-02$
Coefficient: $-6.22e-01$
Value: S

0.004
0.003

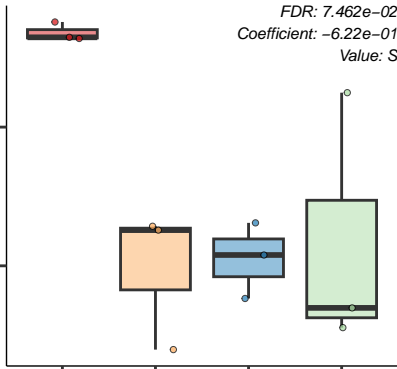
B (n=3)

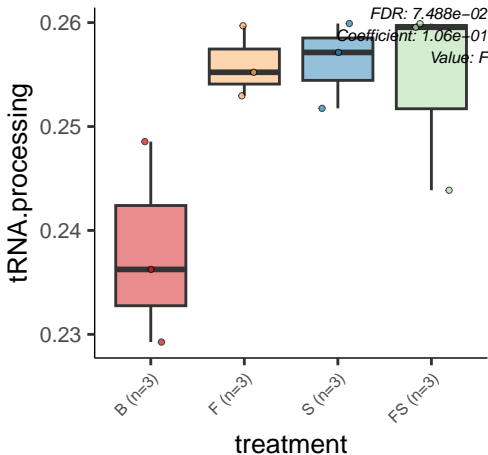
F (n=3)

S (n=3)

FS (n=3)

treatment





CbiZ.Main

FDR: 7.528e-02
Coefficient: -5.98e-01
Value: F

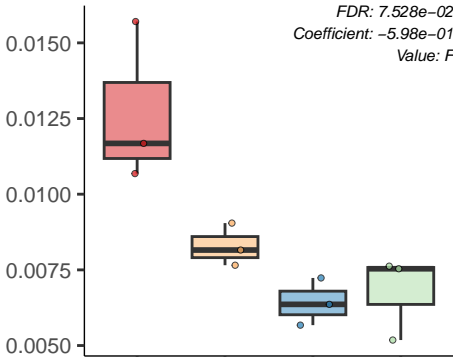
B (n=3)

F (n=3)

S (n=3)

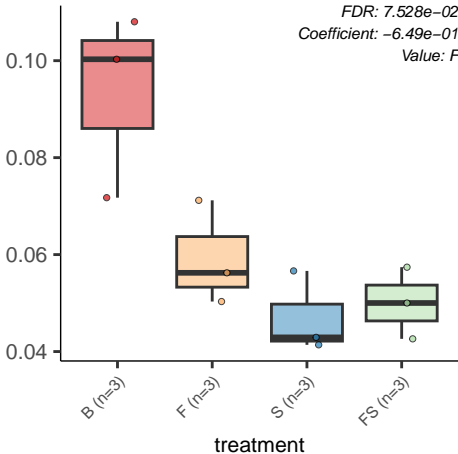
FS (n=3)

treatment



General.Secretion.Pathway

FDR: 7.528e-02
Coefficient: -6.49e-01
Value: F



Natural.DNA.Transformation.in.Vibrio

FDR: 7.528e-02
Coefficient: -1.45e+00
Value: F

0.003
0.002
0.001

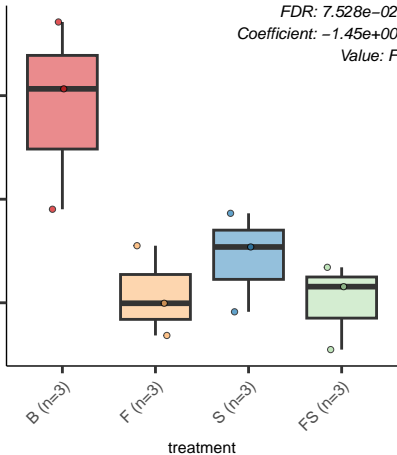
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Ribosome.SSU.bacterial

FDR: 7.528e-02

Coefficient: 8.96e-02

Value: F

0.35

0.34

0.33

0.32

0.31

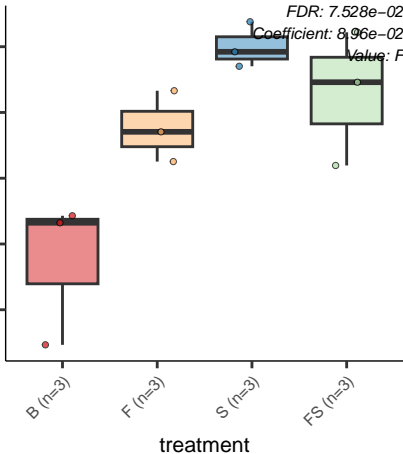
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



HPr.catabolite.repression.system

0.065
0.060
0.055
0.050
0.045

B (n=3)

F (n=3)

S (n=3)

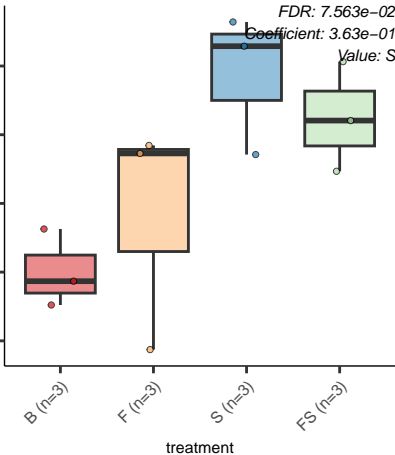
FS (n=3)

treatment

FDR: 7.563e-02

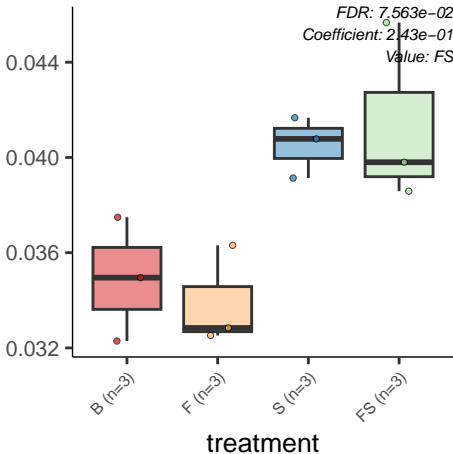
Coefficient: 3.63e-01

Value: S



Monika.MRSA

FDR: $7.563e-02$
Coefficient: $2.43e-01$
Value: FS



Siderophore.assembly.kit

FDR: 7.563e-02
Coefficient: -5.67e-01
Value: F

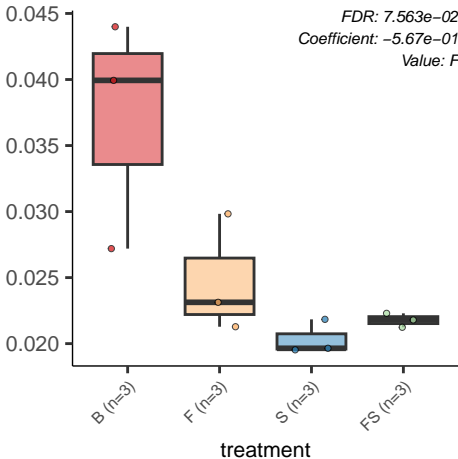
B (n=3)

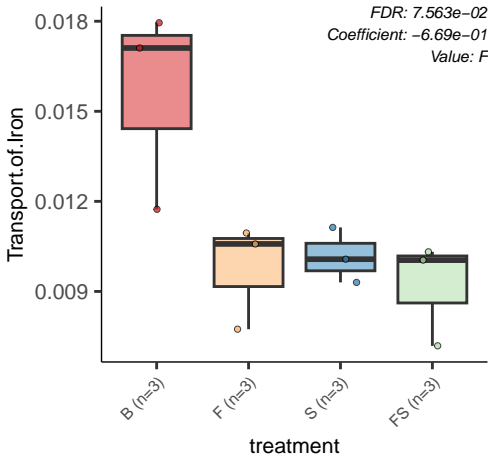
F (n=3)

S (n=3)

FS (n=3)

treatment





Biotin.biosynthesis

FDR: $7.596e-02$

Coefficient: $-1.42e-01$

Value: FS

0.15

0.14

0.13

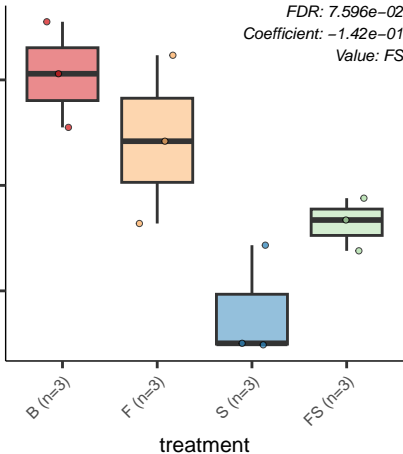
B (n=3)

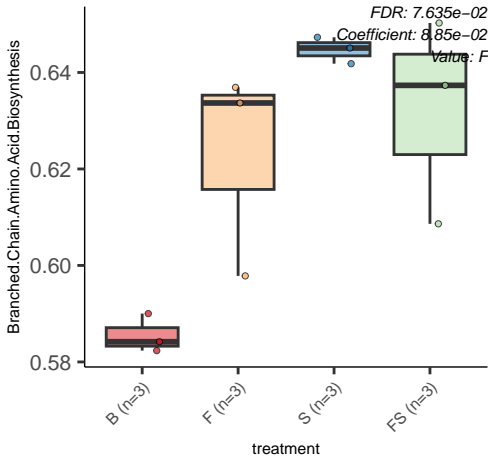
F (n=3)

S (n=3)

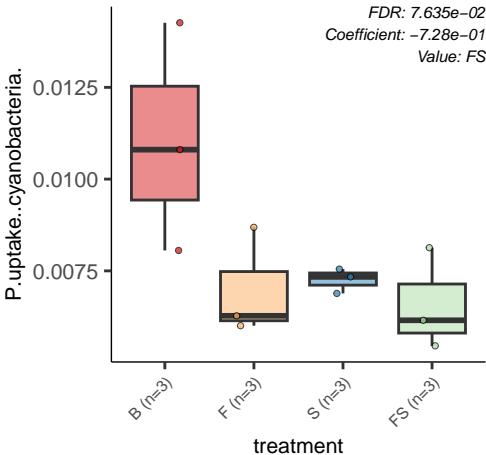
FS (n=3)

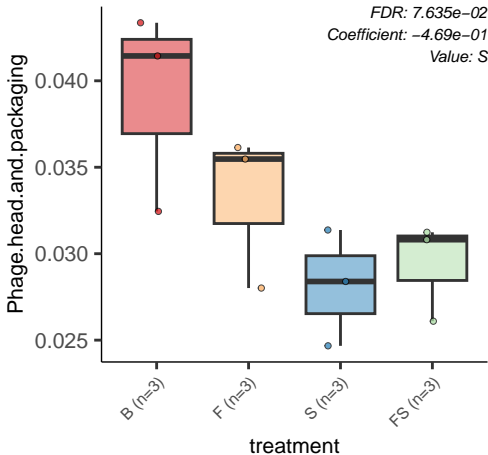
treatment

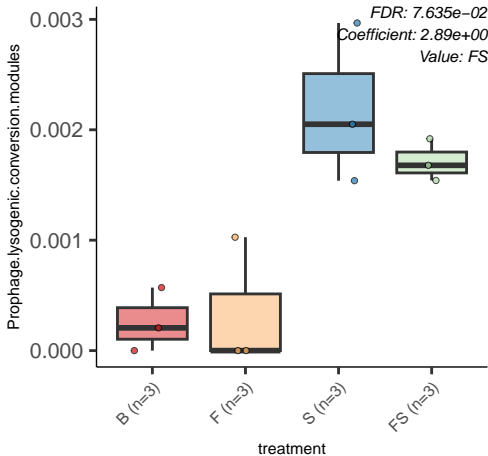




P.uptake..cyanobacteria.







CBSS.350688.3.pcg.1509

FDR: 7.658e-02
Coefficient: 2.10e-01
Value: F

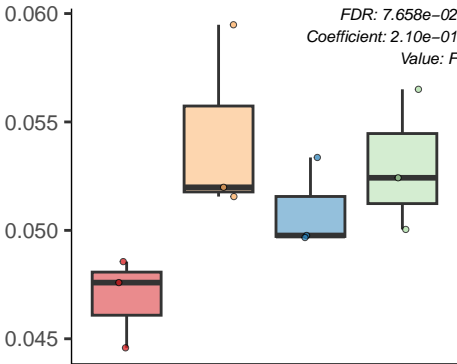
B (n=3)

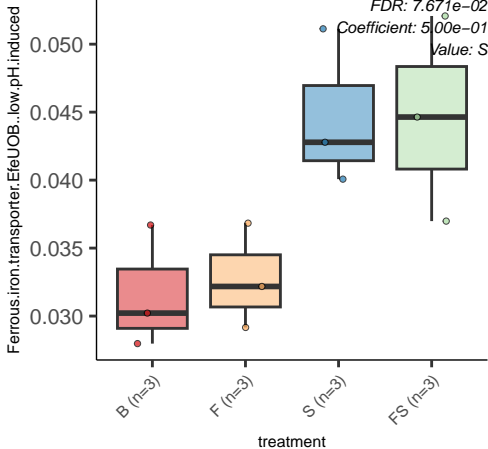
F (n=3)

S (n=3)

FS (n=3)

treatment





CBSS.269801.1.peg.2186

FDR: 7.700e-02
Coefficient: -6.21e-01
Value: F

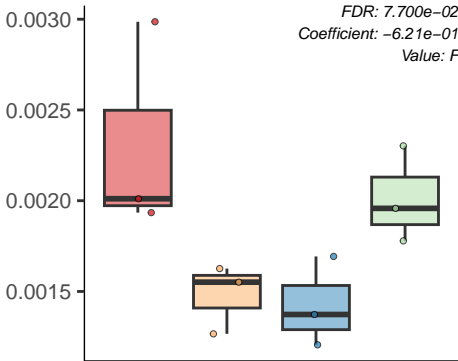
B (n=3)

F (n=3)

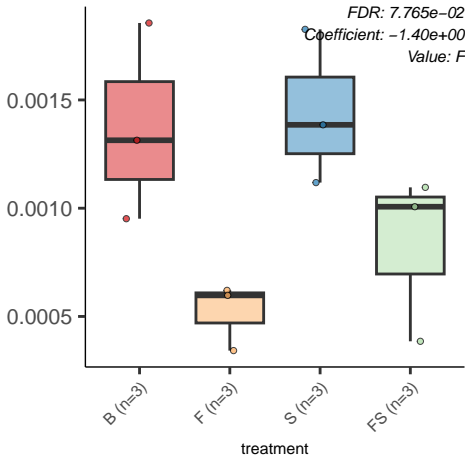
S (n=3)

FS (n=3)

treatment

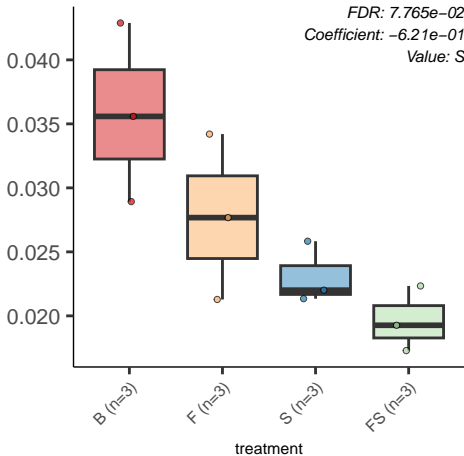


Bacterial.cyanide.production.and.tolerance.mechanisms

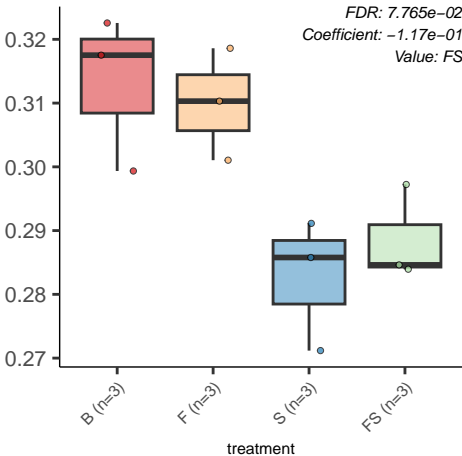


Inner.membrane.protein.YhjD.and.conservd.cluster.involved.in.LPS

FDR: 7.765e-02
Coefficient: -6.21e-01
Value: S



mislocating.NADH.quinone.oxidoreductase.and.rnf.like.group.of.electro



Beta.Glucoside.Metabolism

FDR: 7.814e-02

Coefficient: 7.95e-02

Value: S

B (n=3)

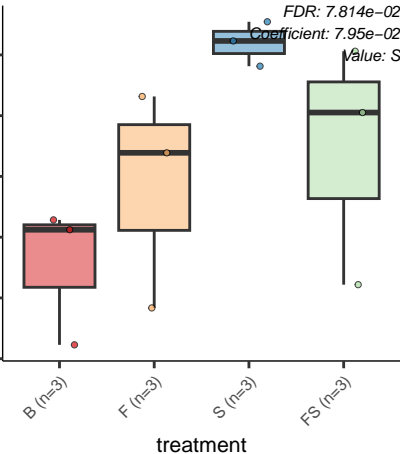
F (n=3)

S (n=3)

FS (n=3)

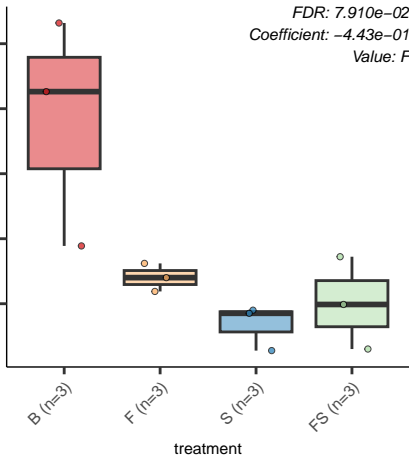
treatment

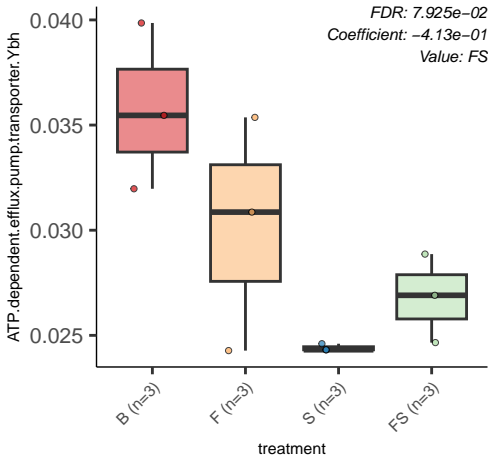
0.63
0.64
0.65
0.66
0.67
0.68



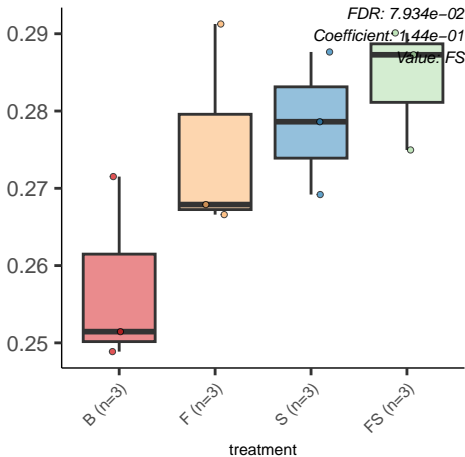
L.ascorbate.utilization..and.related.gene.clusters.

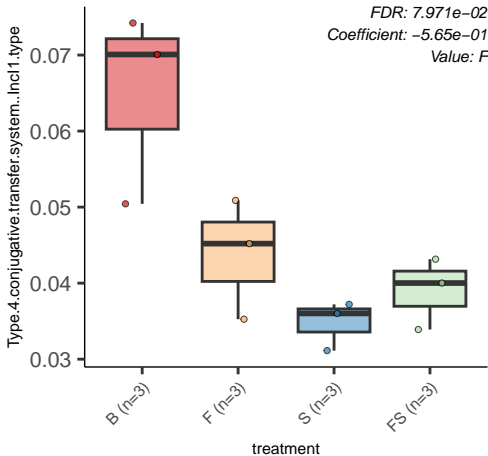
FDR: 7.910e-02
Coefficient: -4.43e-01
Value: F





Exopolysaccharide.Biosynthesis





Alpha.acetolactate.operon

0.008

0.006

0.004

0.002

B (n=3)

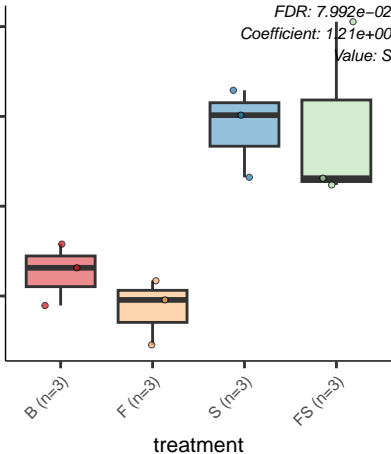
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: $7.992e-02$
Coefficient: $1.21e+00$
Value: S



RNA.polymerase.bacterial

FDR: 7.992×10^{-2}
Coefficient: 7.11×10^{-2}
Value: F

0.57
0.56
0.55
0.54
0.53

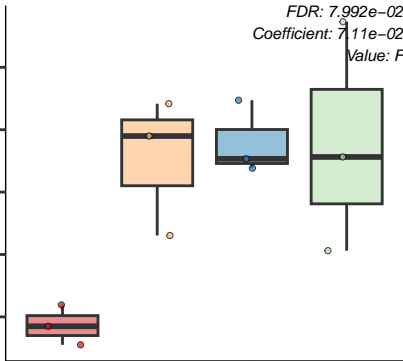
B (n=3)

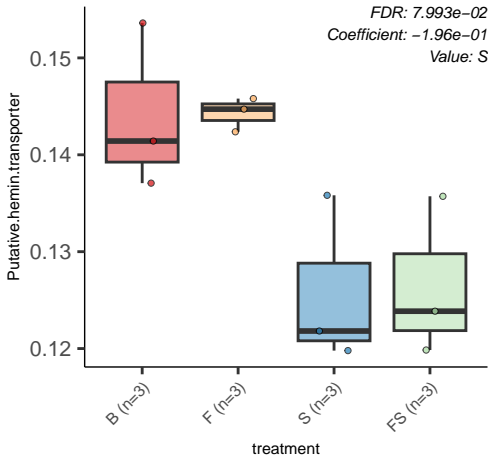
F (n=3)

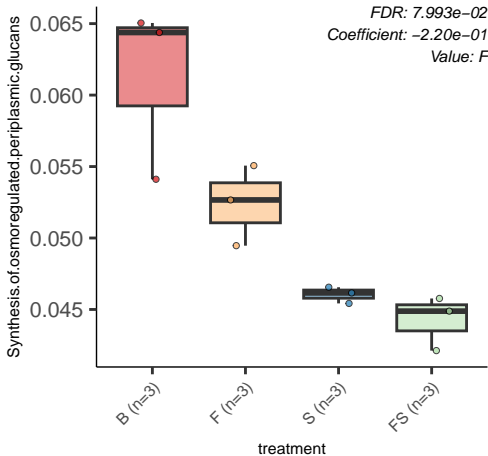
S (n=3)

FS (n=3)

treatment







CBSS.279010.5.peg.3195

B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 8.010e-02

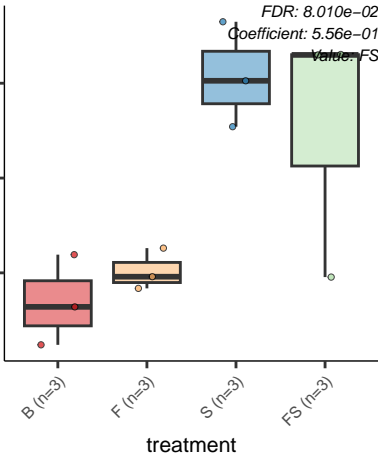
Coefficient: 5.56e-01

Value: FS

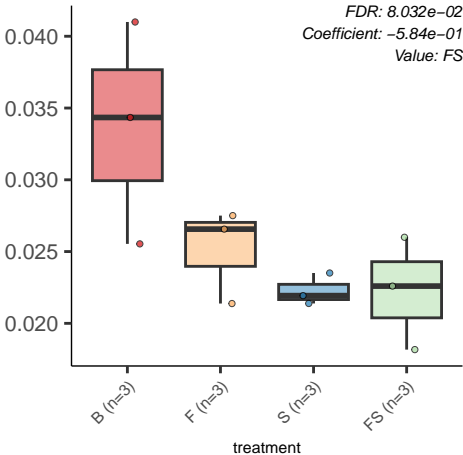
0.0150

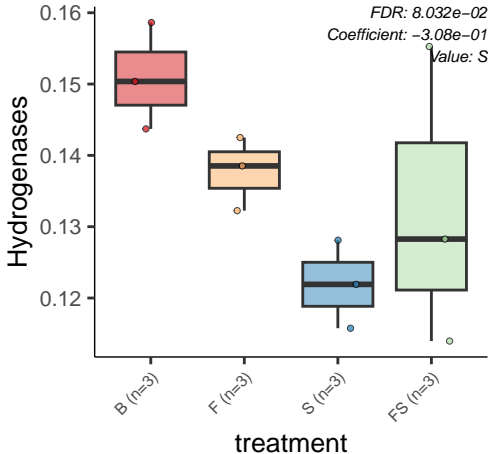
0.0125

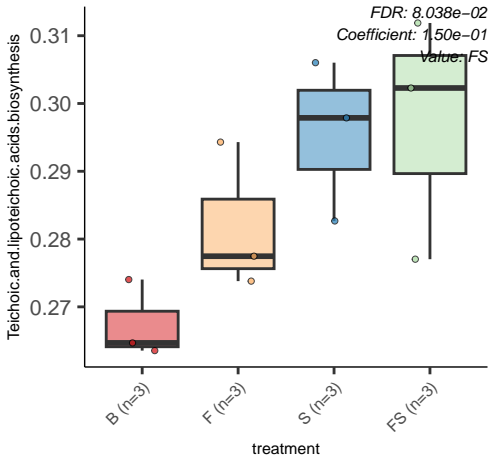
0.0100



Fatty.acid.degradation.regulons







Type.4.secretion.and.conjugative.transfer

FDR: $8.077e-02$
Coefficient: $-6.03e-01$
Value: FS

0.004
0.003

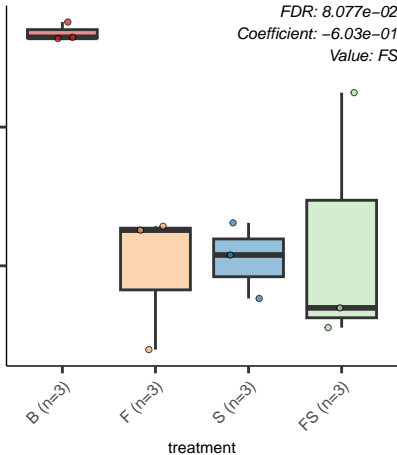
B (n=3)

F (n=3)

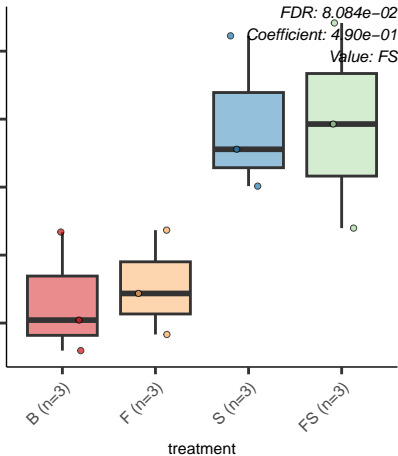
S (n=3)

FS (n=3)

treatment



Ferrous.iron.transporter.EfeUOB..low.pH.induced



Respiratory.Complex.I

FDR: 8.084e-02
Coefficient: -2.24e-01
Value: S

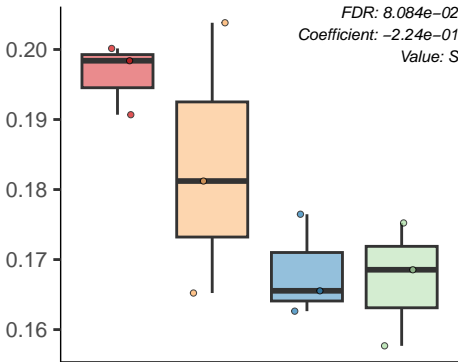
B (n=3)

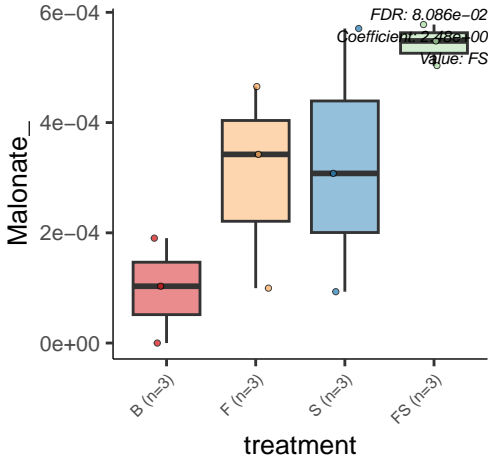
F (n=3)

S (n=3)

FS (n=3)

treatment





The.fimbrial.Sfm.cluster

0.035
0.030
0.025
0.020
0.015

FDR: 8.158e-02
Coefficient: -6.96e-01
Value: F

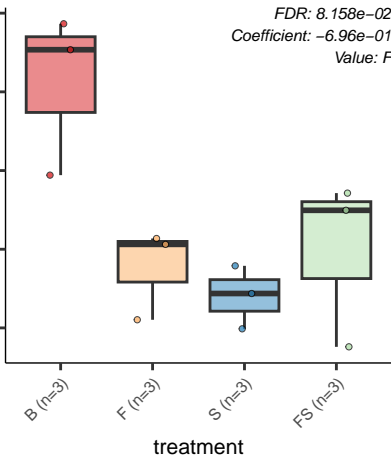
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Propionate.CoA.to.Succinate.Module

FDR: $8.206e-02$
Coefficient: $-6.20e-01$
Value: S

0.012

0.010

0.008

0.006

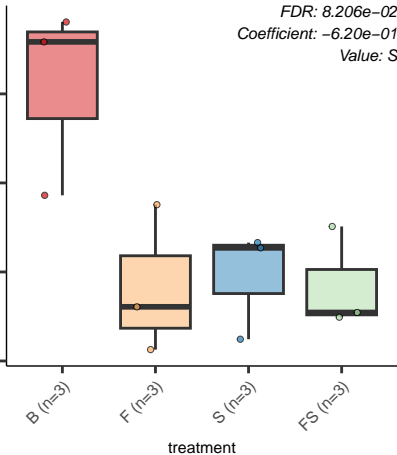
B (n=3)

F (n=3)

S (n=3)

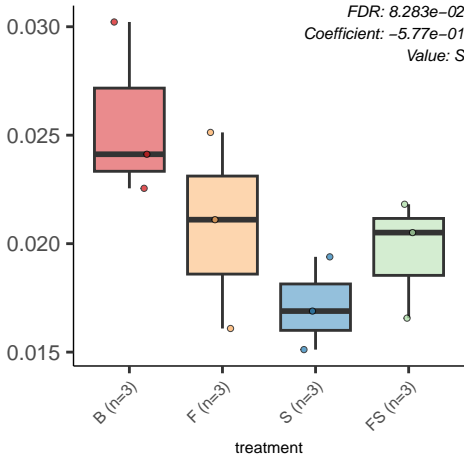
FS (n=3)

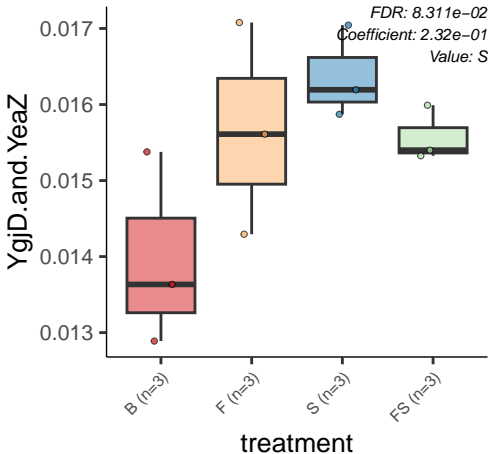
treatment



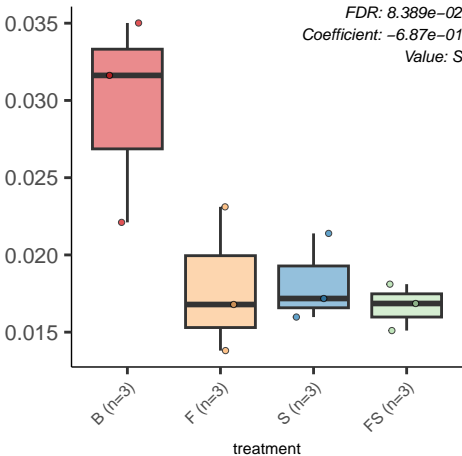
p.Aminobenzoyl.Glutamate.Utilization

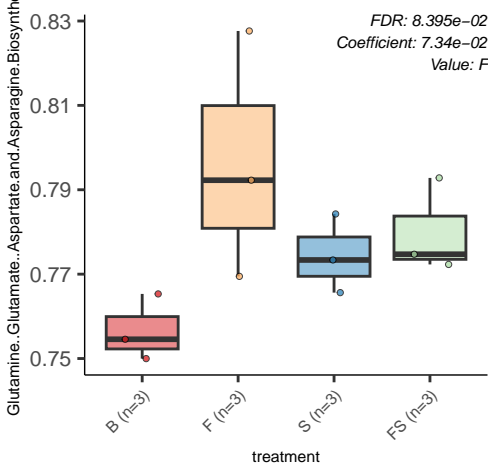
FDR: 8.283e-02
Coefficient: -5.77e-01
Value: S



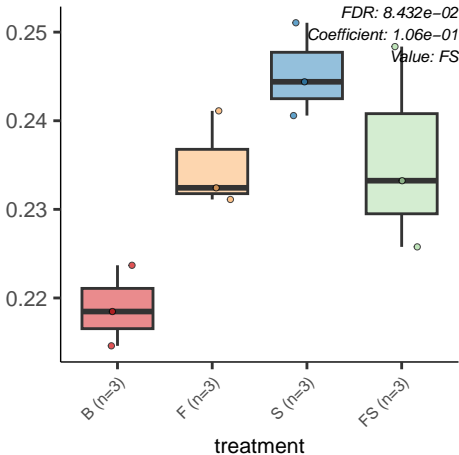


Putrescine.utilization.paths





tRNA.aminoacylation.. Val



CBSS.205922.3.pcg.1809

FDR: 8.440e-02
Coefficient: -1.20e+00
Value: S

B (n=3)

F (n=3)

S (n=3)

FS (n=3)

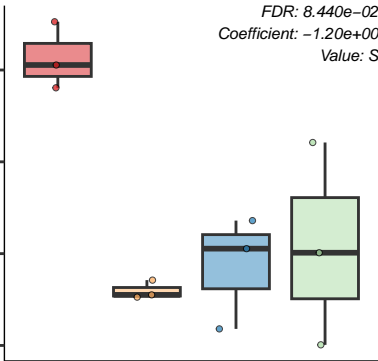
treatment

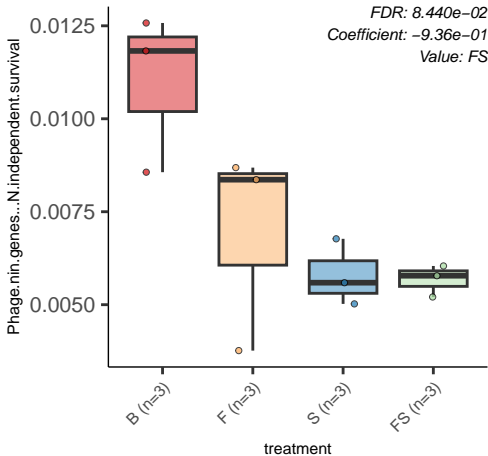
0.0020

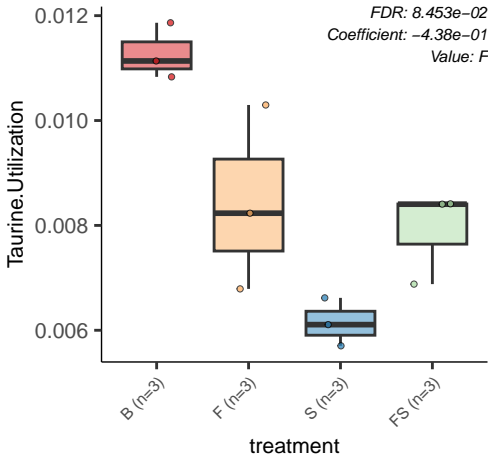
0.0015

0.0010

0.0005

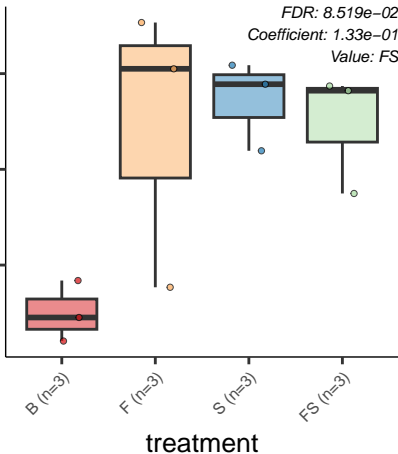


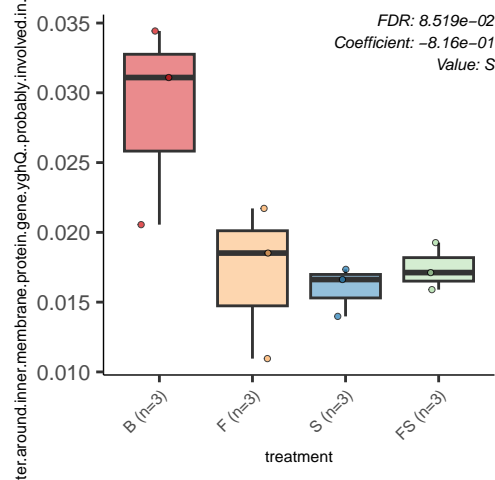




At5g63290

FDR: 8.519e-02
Coefficient: 1.33e-01
Value: FS





Rcs.negative.regulator.lgaA

0.025

0.020

0.015

0.010

B (n=3)

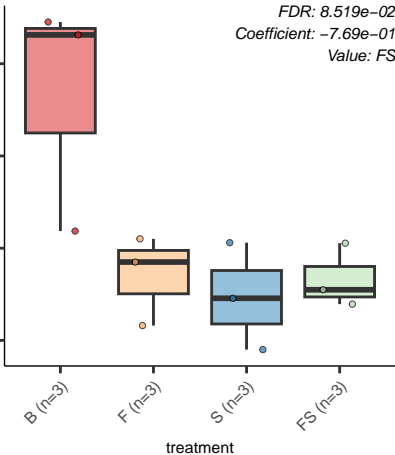
F (n=3)

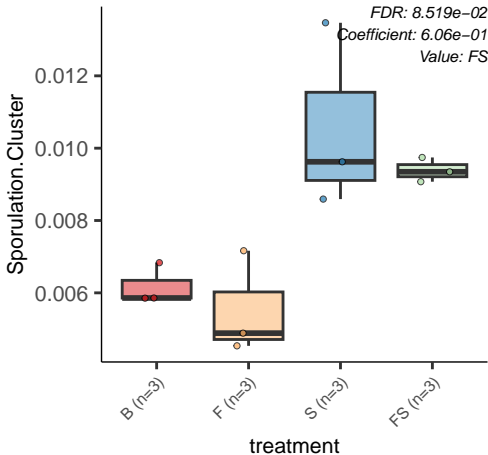
S (n=3)

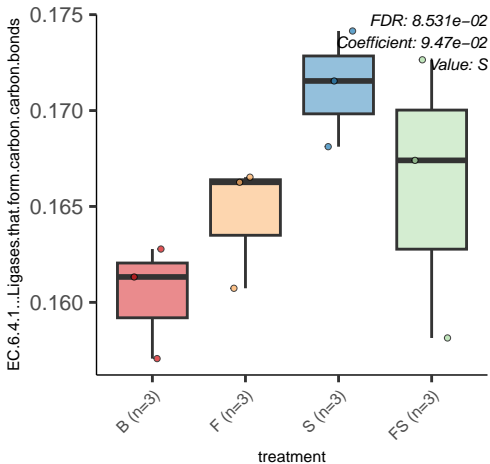
FS (n=3)

treatment

FDR: 8.519e-02
Coefficient: -7.69e-01
Value: FS







Alpha.Amylase.locus.in.Streptococcus

0.08
0.07
0.06

B (n=3)

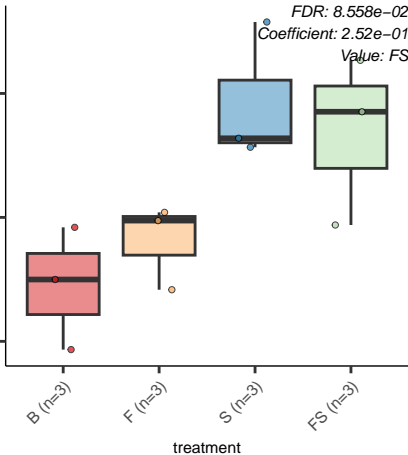
F (n=3)

S (n=3)

FS (n=3)

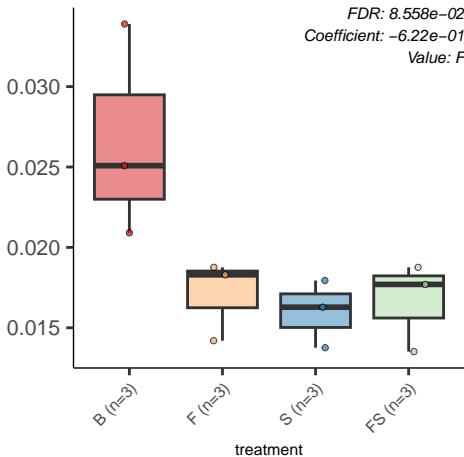
treatment

FDR: 8.558e-02
Coefficient: 2.52e-01
Value: FS



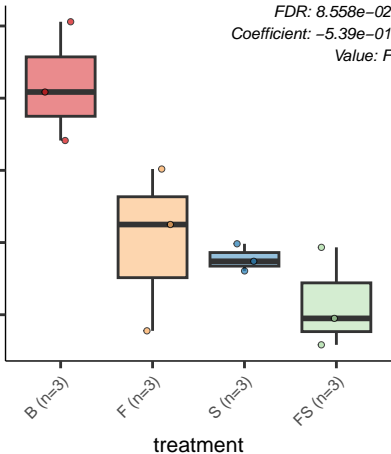
Central.meta.cleavage.pathway.of.aromatic.compound.degra

FDR: 8.558e-02
Coefficient: -6.22e-01
Value: F



Pyrimidine.utilization

FDR: 8.558e-02
Coefficient: -5.39e-01
Value: F



tRNA.aminoacylation..Leu

FDR: $8.558e-02$

Coefficient: $9.69e-02$

Value: F

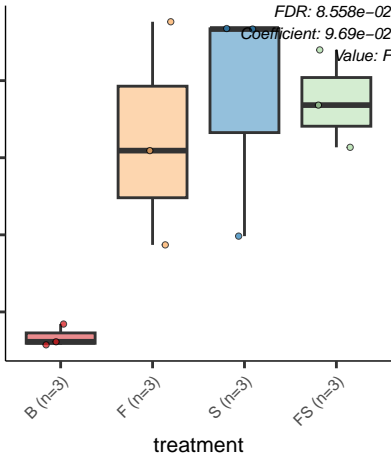
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



cell.division.cluster.containing.FtsQ

0.06
0.05

B (n=3)

F (n=3)

S (n=3)

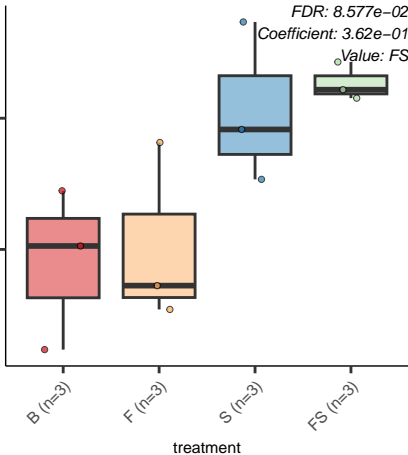
FS (n=3)

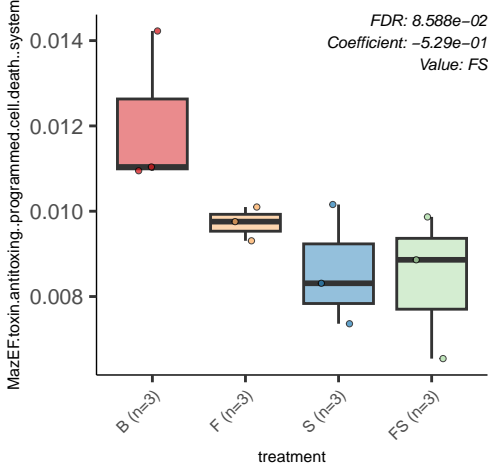
treatment

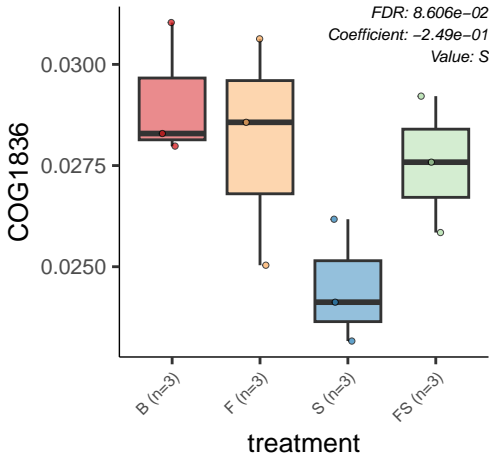
FDR: $8.577e-02$

Coefficient: $3.62e-01$

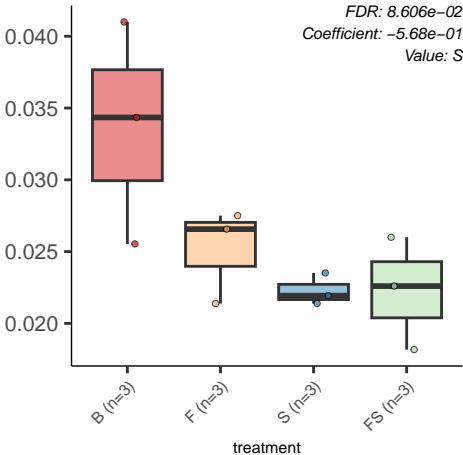
Value: FS







Fatty.acid.degradation.regulons



Fructooligosaccharides.FOS..and.Raffinose.Utilization

FDR: 8.606e-02
Coefficient: -7.92e-02
Value: S

1.04
1.00
0.96

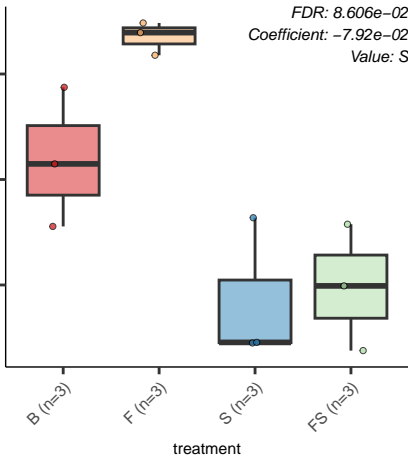
B (n=3)

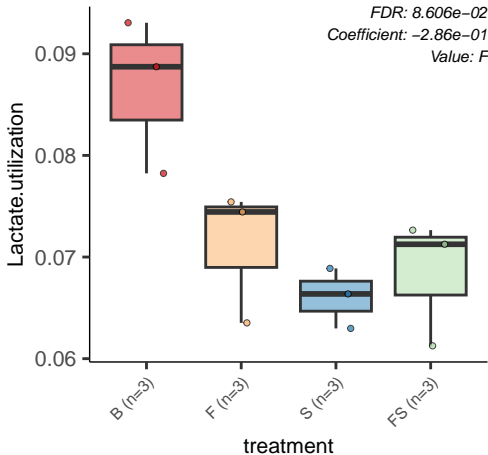
F (n=3)

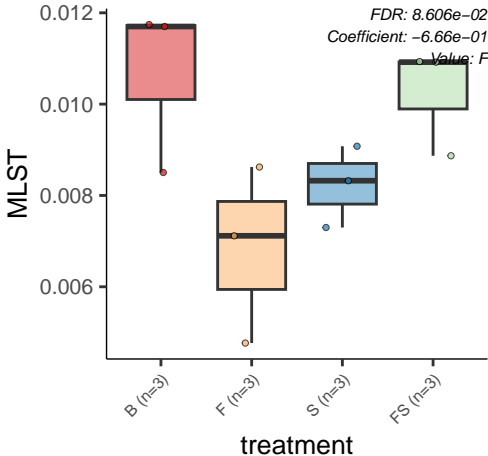
S (n=3)

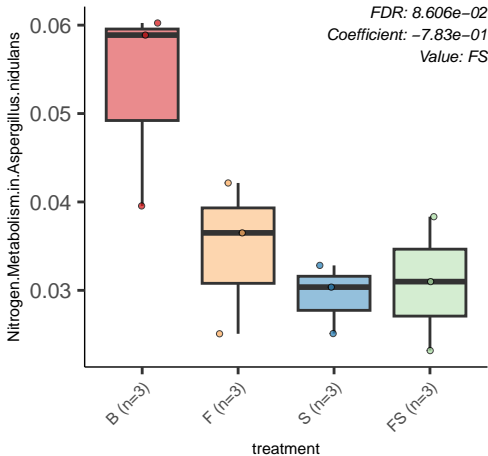
FS (n=3)

treatment









Polyadenylation.bacterial

0.19
0.18
0.17
0.16

B (n=3)

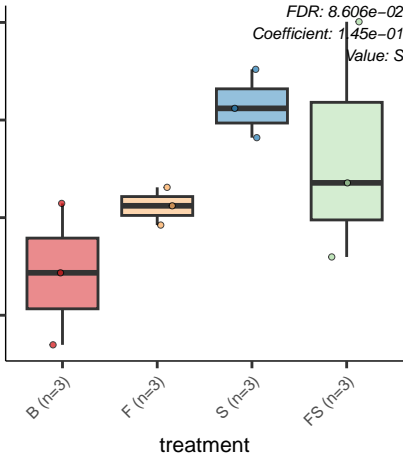
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: $8.606e-02$
Coefficient: $1.45e-01$
Value: S



RNA.3..terminal.phosphate.cyclase

0.015
0.012
0.009
0.006

B (n=3)

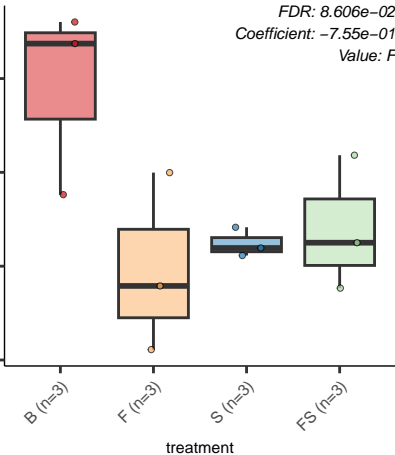
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: $8.606e-02$
Coefficient: $-7.55e-01$
Value: F



Lipid.A.modifications

FDR: 8.667e-02
Coefficient: -6.31e-01
Value: FS

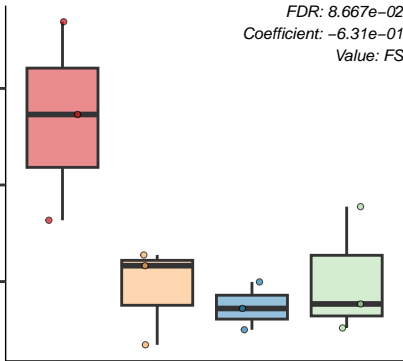
B (n=3)

F (n=3)

S (n=3)

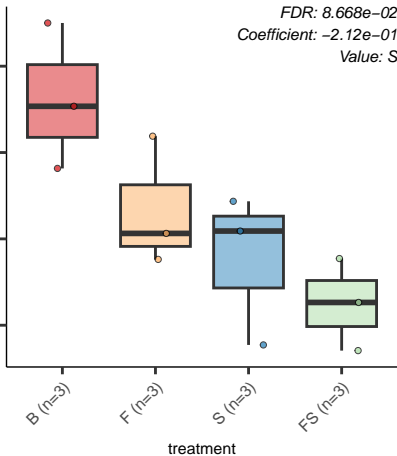
FS (n=3)

treatment

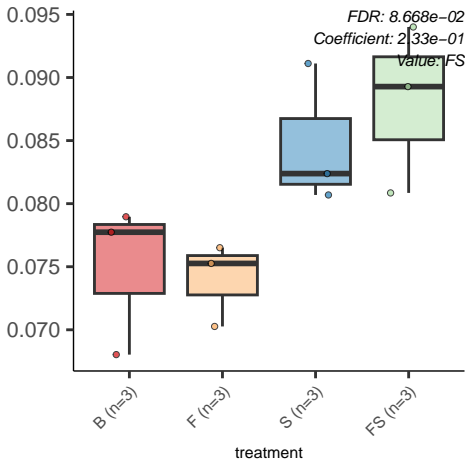


Acetyl.CoA.fermentation.to.Butyrate

FDR: $8.668e-02$
Coefficient: $-2.12e-01$
Value: S

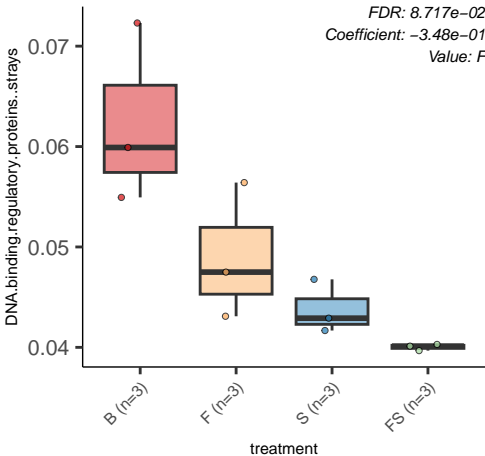


DNA.repair..bacterial.DinG.and.relative

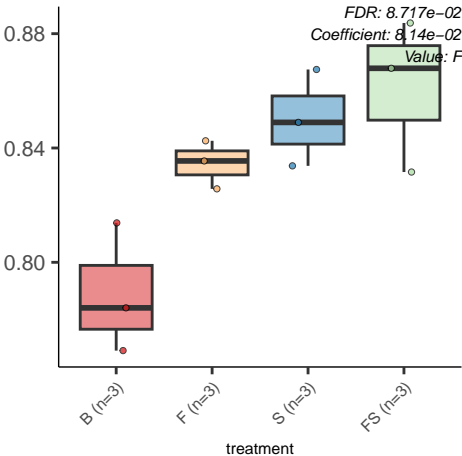


DNA.binding.regulatory.proteins...strays

FDR: 8.717e-02
Coefficient: -3.48e-01
Value: F

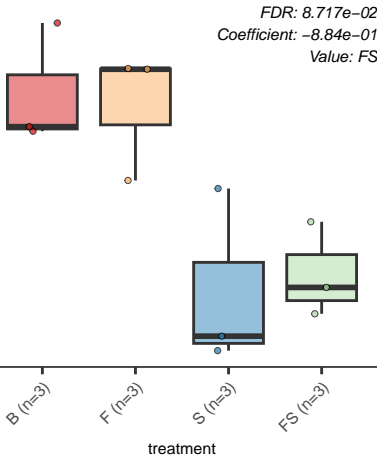


De.Novo.Purine.Biosynthesis



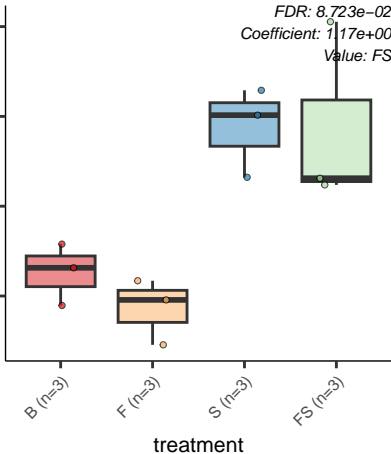
Unknown.carbohydrate.utilization.containing.Fructose.bisphosphatase

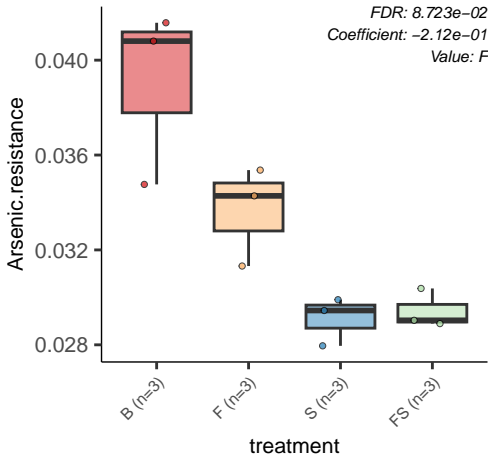
FDR: $8.717e-02$
Coefficient: $-8.84e-01$
Value: FS

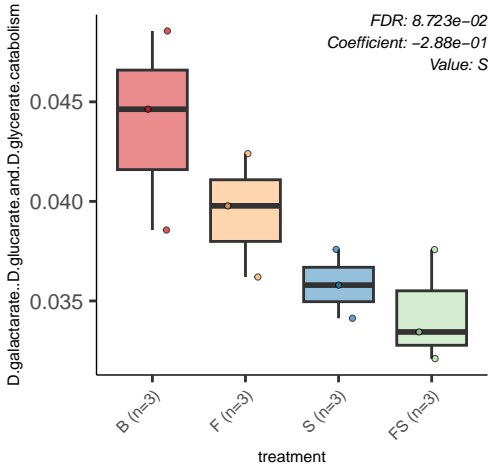


Alpha.acetolactate.operon

FDR: $8.723e-02$
Coefficient: $1.117e+00$
Value: FS







Listeria.surface.proteins..Internalin.like.proteins

FDR: $8.723e-02$
Coefficient: $-1.26e+00$
Value: S

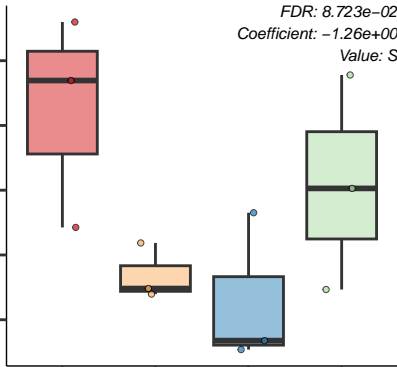
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Proline..4.hydroxyproline.uptake.and.utilization

FDR: 8.723e-02
Coefficient: -2.23e-01
Value: FS

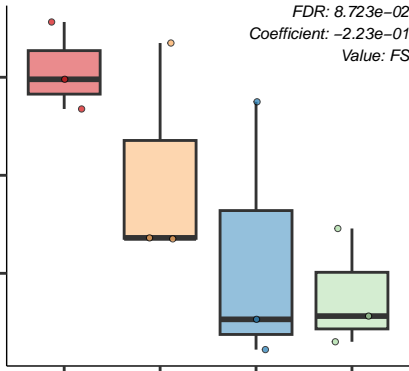
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Quinone.disambiguation

FDR: 8.723e-02
Coefficient: -3.85e-01
Value: S

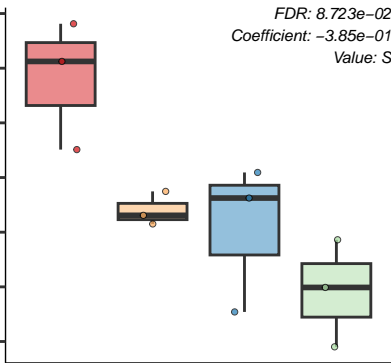
B (n=3)

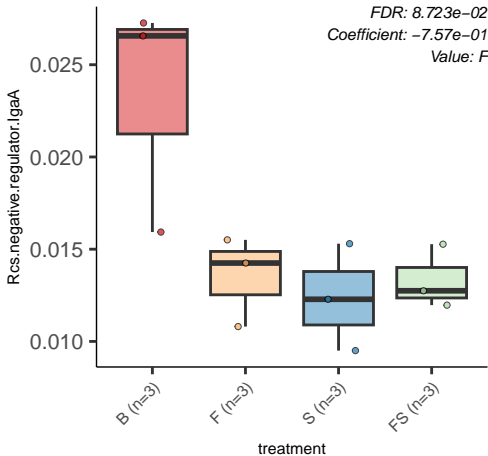
F (n=3)

S (n=3)

FS (n=3)

treatment





Serine.Biosynthesis

FDR: 8.723e-02

Coefficient: 1.47e-01

Value: S

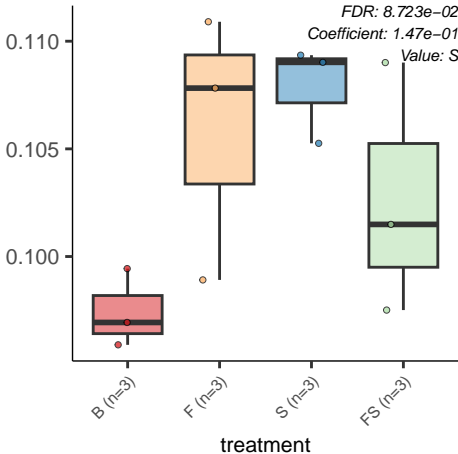
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Deoxyribose.and.Deoxynucleoside.Catabolism

0.18
0.16
0.14

FDR: 8.744e-02

Coefficient: 1.89e-01

Value: S

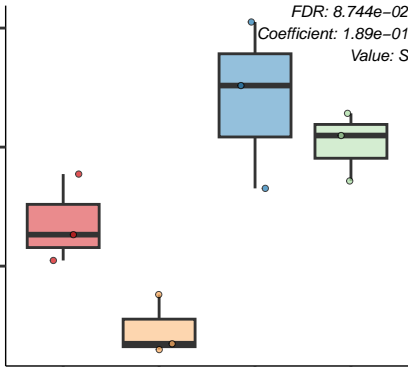
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Glutathione..Redox.cycle

FDR: $8.744e-02$
Coefficient: $3.75e-01$
Value: S

0.05
0.04

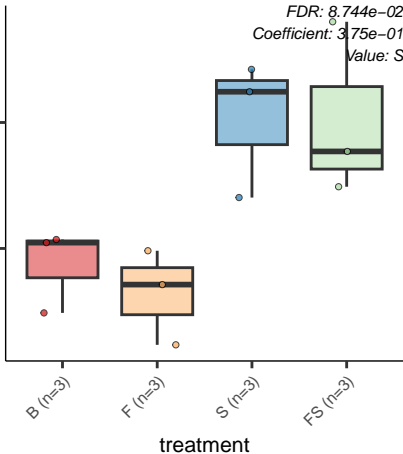
B (n=3)

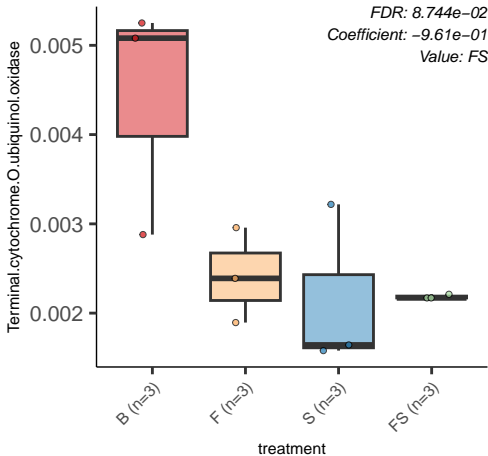
F (n=3)

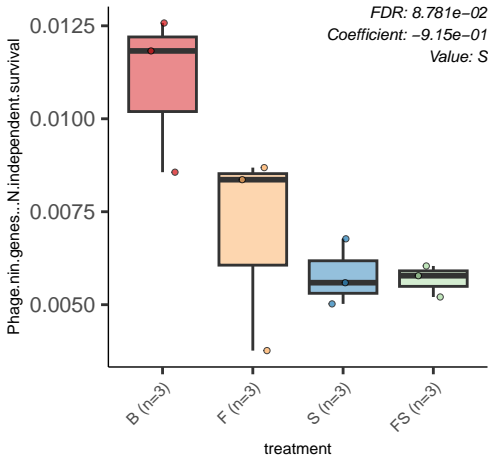
S (n=3)

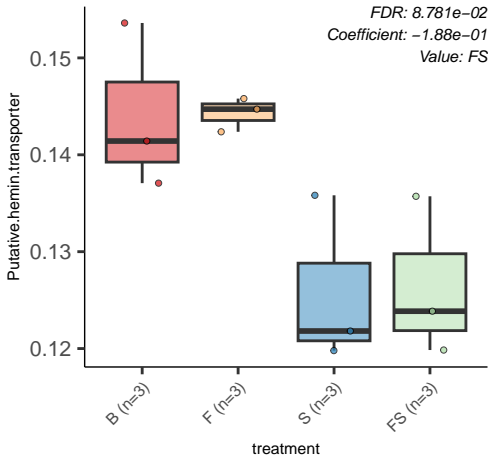
FS (n=3)

treatment

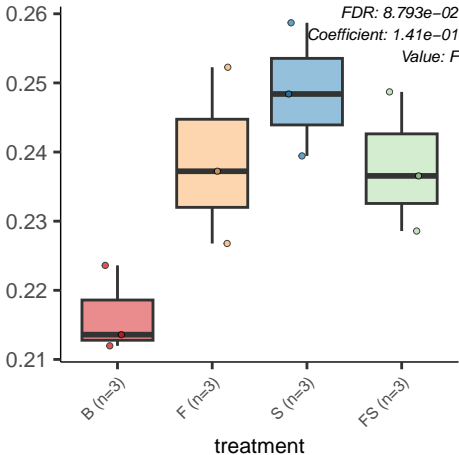




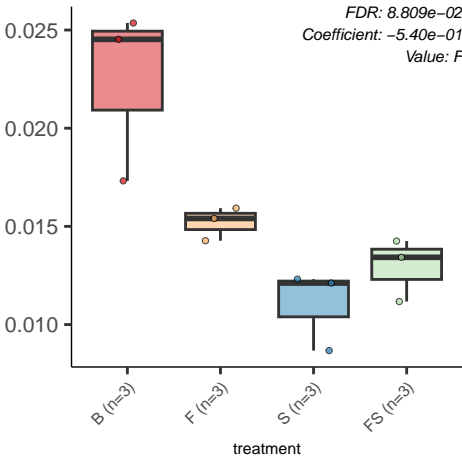




tRNA.aminoacylation..Phe



Accessory.colonization.factor



CBSS.243265.1.pcg.198

FDR: 8.868e-02

Coefficient: 3.28e-01

Value: S

0.030

0.025

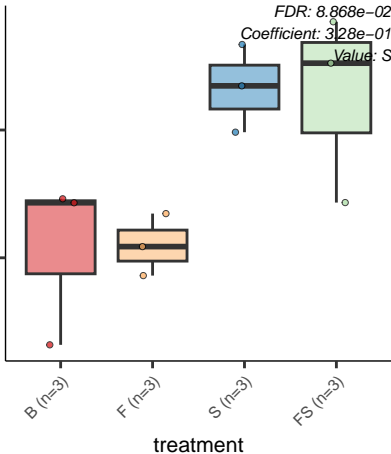
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment

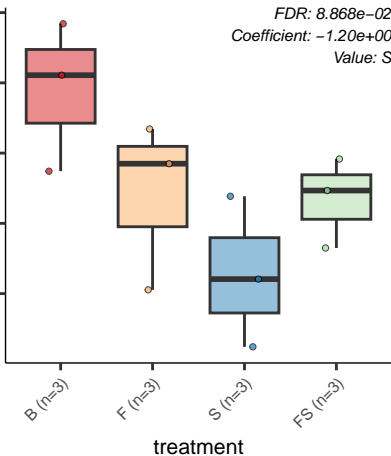


CBSS.316275.9.pcg.382

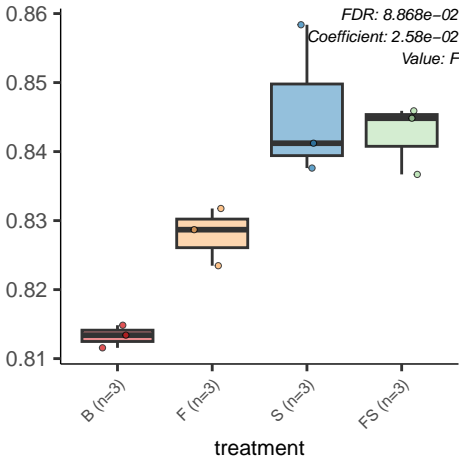
FDR: 8.868e-02

Coefficient: -1.20e+00

Value: S



DNA.repair..bacterial



CBSS.393130.3.pcg.794

FDR: 8.872e-02

Coefficient: 4.05e-01

Value: FS

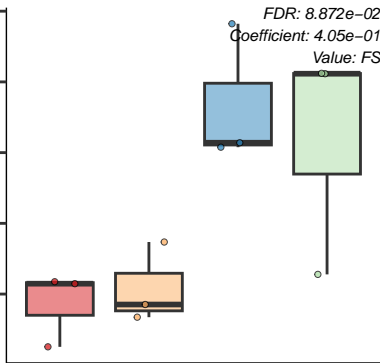
B (n=3)

F (n=3)

S (n=3)

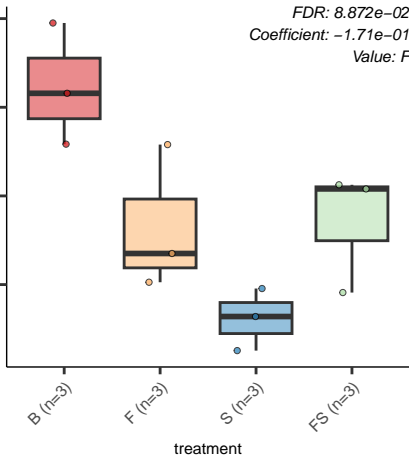
FS (n=3)

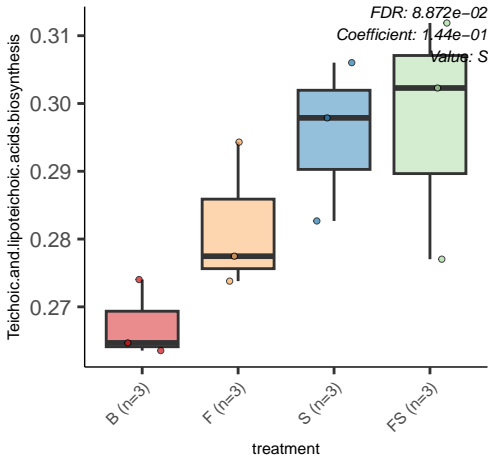
treatment



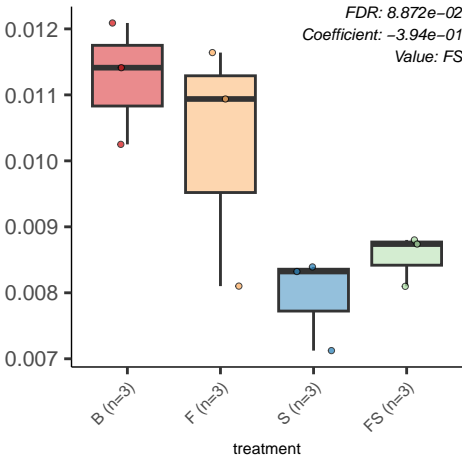
Lipid.A.Ara4N.pathway...Polymyxin..resistance..

FDR: 8.872e-02
Coefficient: -1.71e-01
Value: F

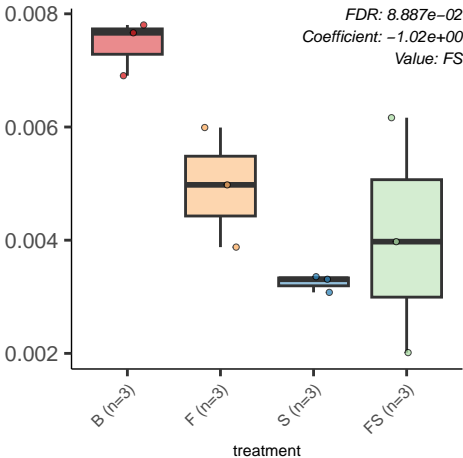




n.Phenylalkanoic.acid.degradation



Phage.shock.protein..psp..operon



At5g63290

0.46
0.44
0.42

B (n=3)

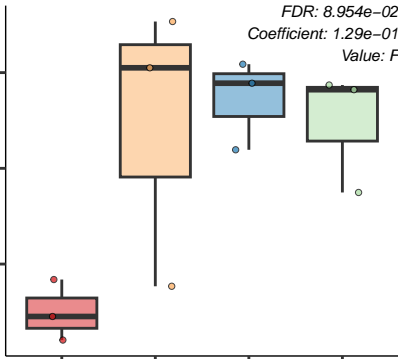
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 8.954e-02
Coefficient: 1.29e-01
Value: F



Glutathione..Redox.cycle

FDR: $8.954e-02$
Coefficient: $3.71e-01$
Value: FS

0.05
0.04

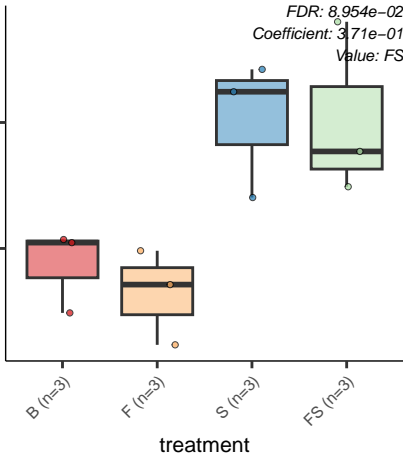
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Khodge314.Isoleucine.Biosynthesis

0.0275

0.0250

0.0225

0.0200

0.0175

B (n=3)

F (n=3)

S (n=3)

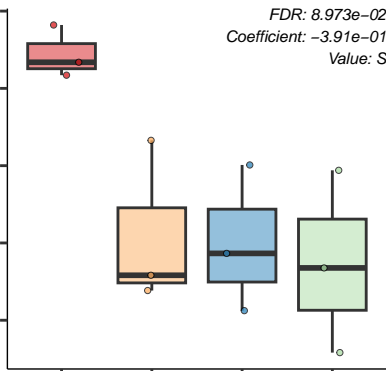
FS (n=3)

treatment

FDR: $8.973e-02$

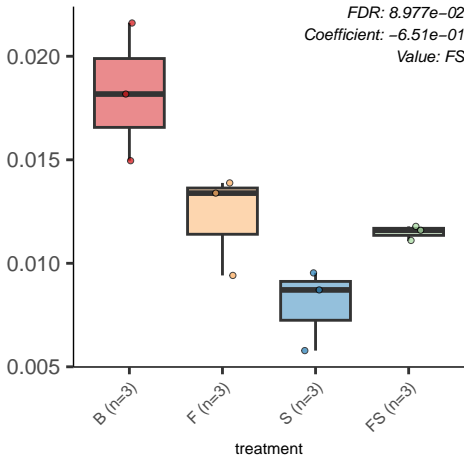
Coefficient: $-3.91e-01$

Value: S



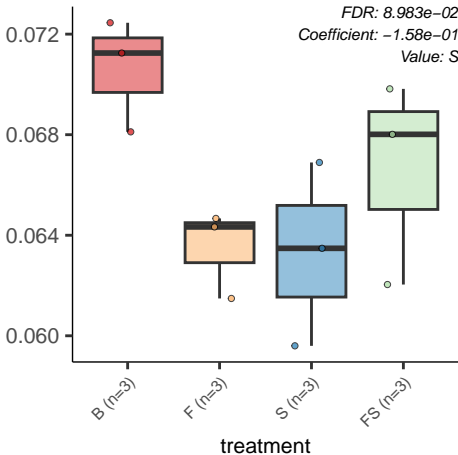
Phenylacetyl-CoA.catabolic.pathway..core.

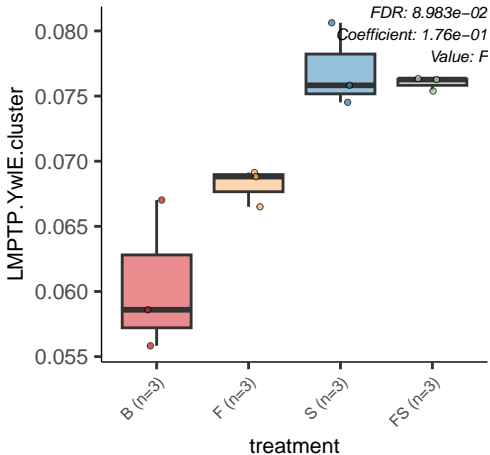
FDR: $8.977\text{e-}02$
Coefficient: $-6.51\text{e-}01$
Value: FS



CBSS.354.1.peg.2917

FDR: $8.983e-02$
Coefficient: $-1.58e-01$
Value: S





Inorganic.Sulfur.Assimilation

FDR: 9.013e-02
Coefficient: -2.95e-01
Value: F

0.060
0.055
0.050
0.045
0.040

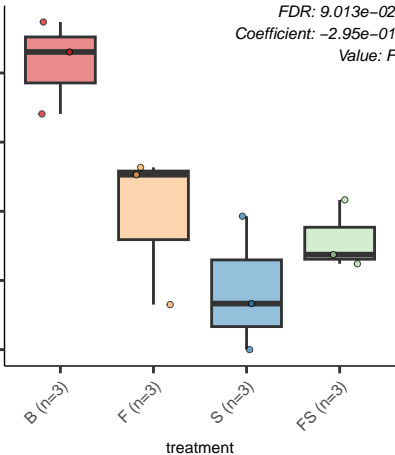
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Thiamin.biosynthesis.in.plants

FDR: $9.013e-02$
Coefficient: $-5.40e-01$
Value: F

0.0030

0.0025

0.0020

0.0015

0.0010

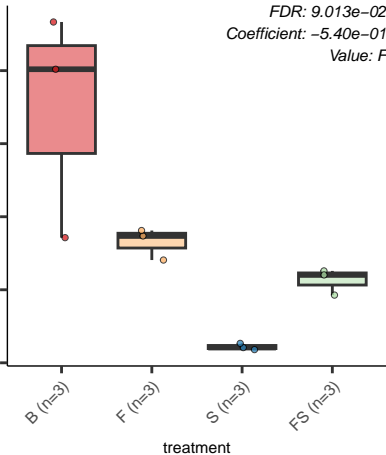
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



D.galactonate.catabolism

FDR: $9.086e-02$
Coefficient: $-6.99e-01$
Value: S

B (n=3)

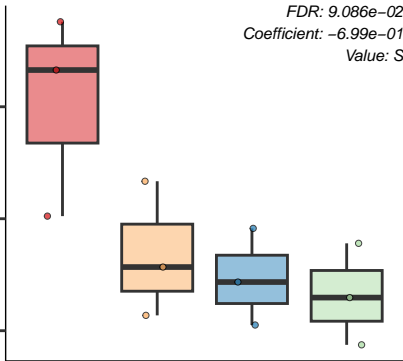
F (n=3)

S (n=3)

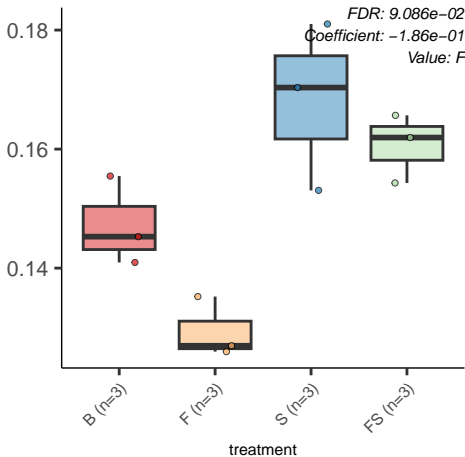
FS (n=3)

treatment

0.04
0.03
0.02

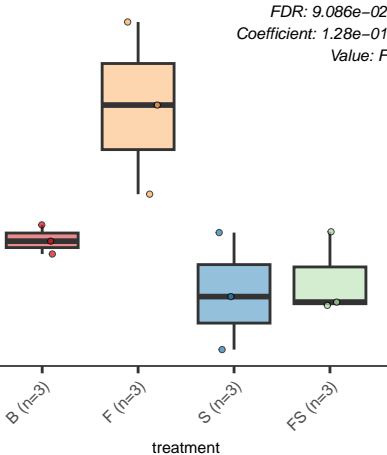


Deoxyribose.and.Deoxynucleoside.Catabolism



Lacto.N.Biose.l.and.Galacto.N.Biose.Metabolic.Pathway

FDR: 9.086e-02
Coefficient: 1.28e-01
Value: F



Rhamnose.containing.glycans

0.62

0.60

0.58

0.56

B (n=3)

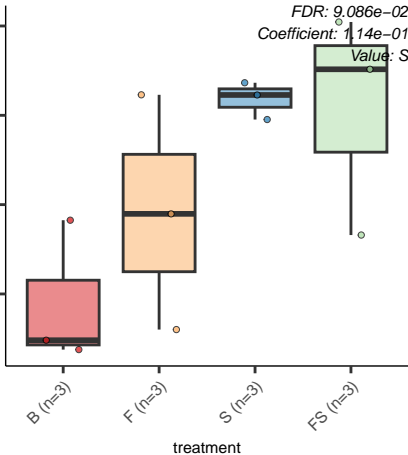
F (n=3)

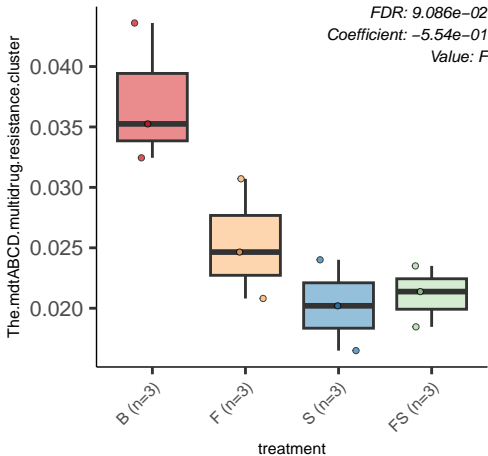
S (n=3)

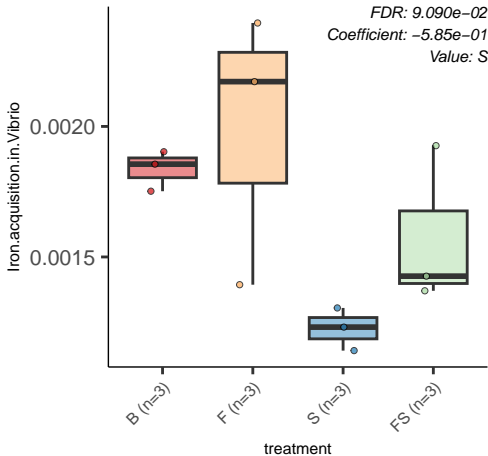
FS (n=3)

treatment

FDR: $9.086e-02$
Coefficient: $1.14e-01$
Value: S

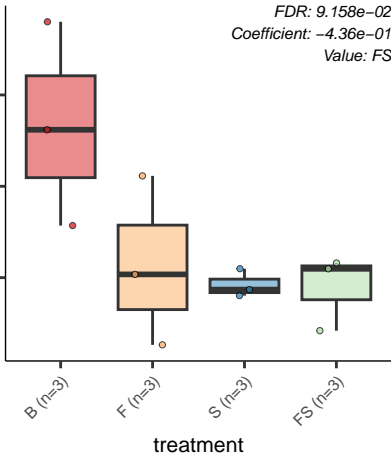






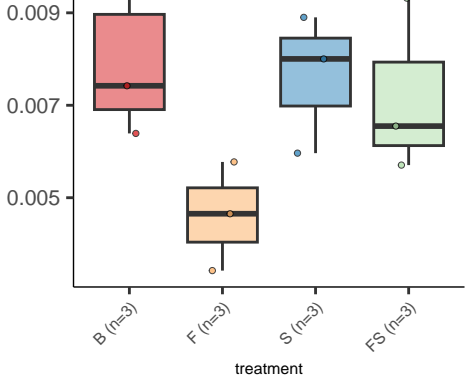
RpoS.Regulators.SG1

FDR: 9.158e-02
Coefficient: -4.36e-01
Value: FS

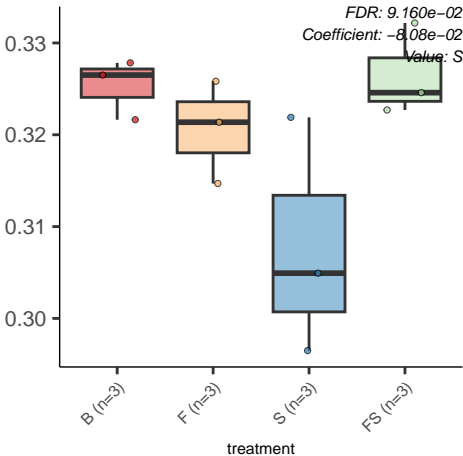


Toxin.antitoxin.replicon.stabilization.systems

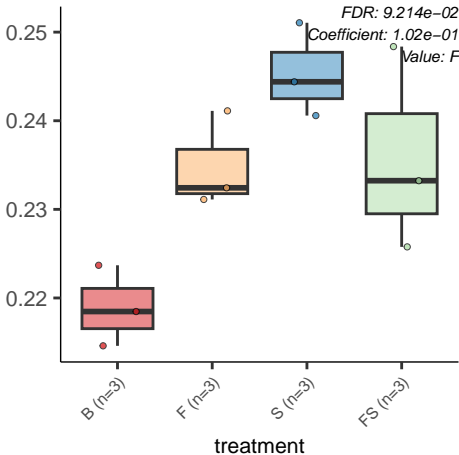
FDR: $9.158e-02$
Coefficient: $-8.13e-01$
Value: F



Glutathione.regulated.potassium.ATPase.system.and.associated.f

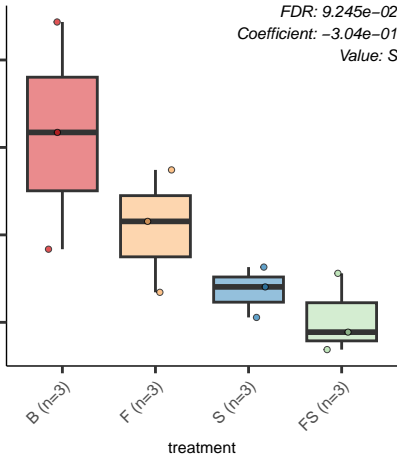


tRNA.aminoacylation..Val



D.galactarate..D.glucarate.and.D.glycerate.catabolism...g

FDR: $9.245e-02$
Coefficient: $-3.04e-01$
Value: S



L.rhamnose.utilization

FDR: $9.245e-02$
Coefficient: $-2.19e-01$
Value: S

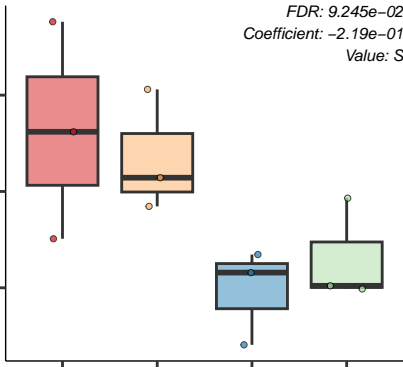
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Putative.TldE.TldD.proteolytic.complex

FDR: 9.245e-02
Coefficient: -4.13e-01
Value: S

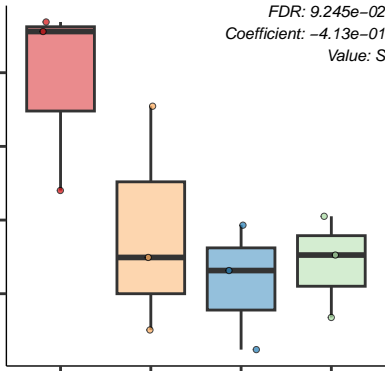
B (n=3)

F (n=3)

S (n=3)

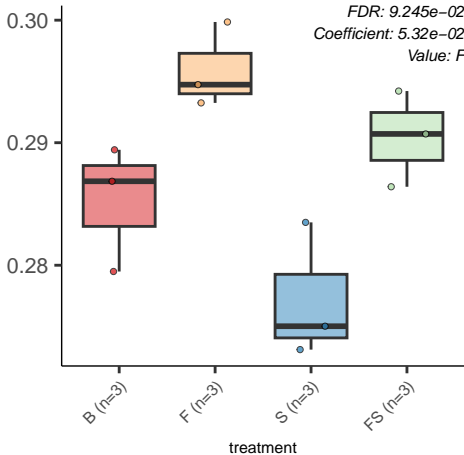
FS (n=3)

treatment

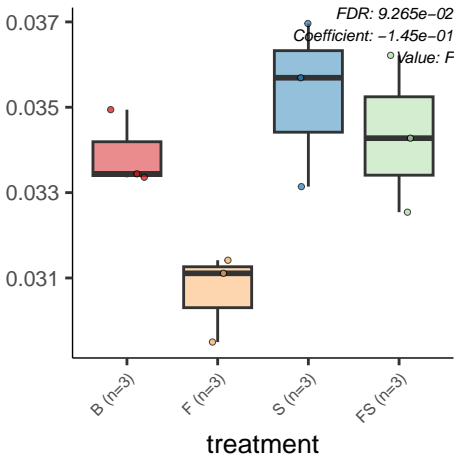


Type.I.Restriction.Modification

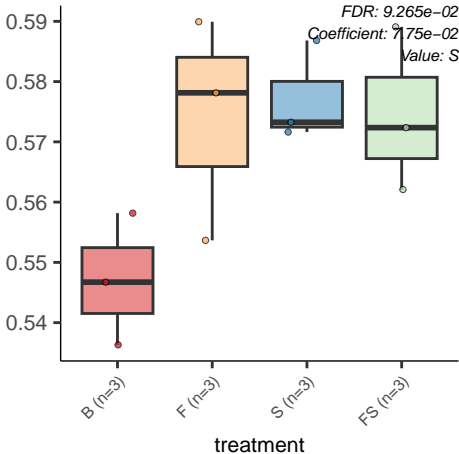
FDR: 9.245e-02
Coefficient: 5.32e-02
Value: F

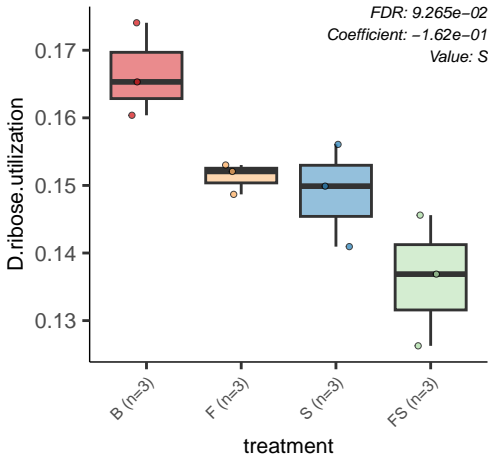


At1g21350



Bacterial.Cell.Division





GroEL.GroES

FDR: $9.265e-02$

Coefficient: $8.34e-02$

Value: FS

0.115

0.110

0.105

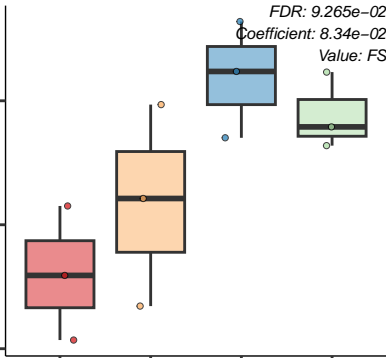
B (n=3)

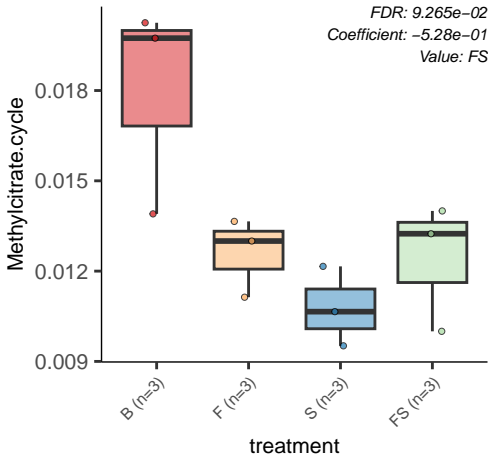
F (n=3)

S (n=3)

FS (n=3)

treatment





Proton.dependent.Peptide.Transporters

FDR: 9.265e-02
Coefficient: -3.39e-01
Value: S

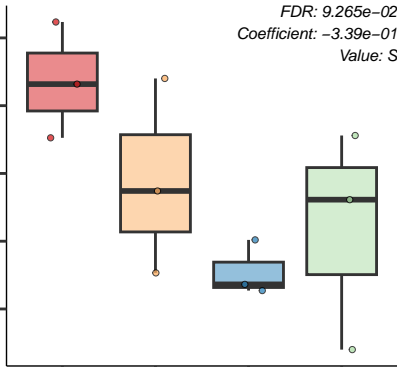
B (n=3)

F (n=3)

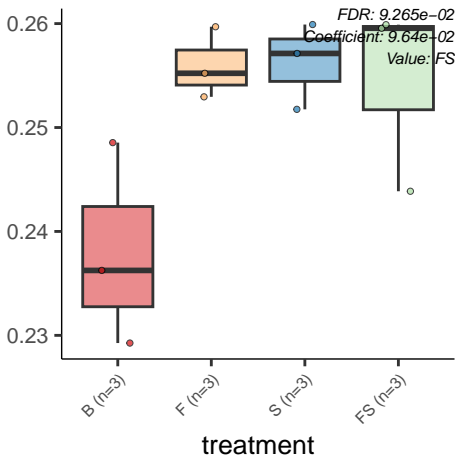
S (n=3)

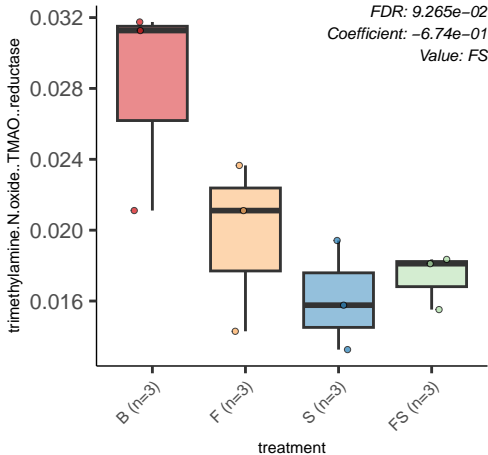
FS (n=3)

treatment



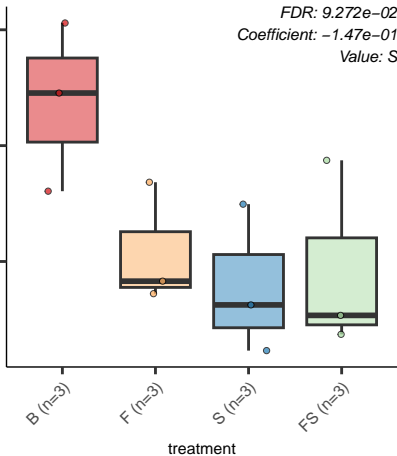
tRNA.processing



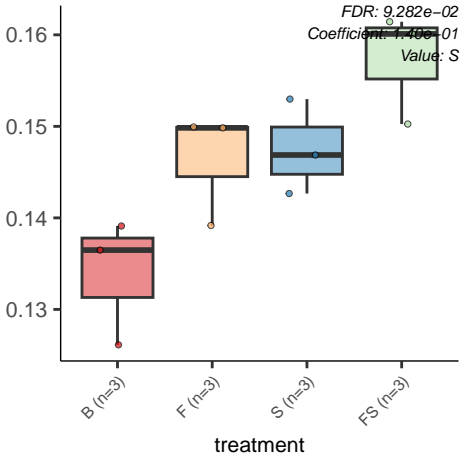


Terminal.cytochrome.oxidases

FDR: 9.272e-02
Coefficient: -1.47e-01
Value: S



tRNA.aminoacylation..Arg



CBSS.205922.3.peg.1809

FDR: $9.312e-02$
Coefficient: $-1.14e+00$
Value: FS

B (n=3)

F (n=3)

S (n=3)

FS (n=3)

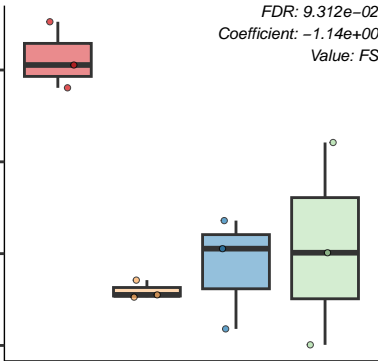
treatment

0.0020

0.0015

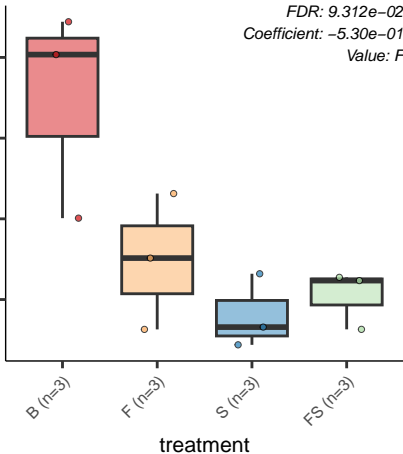
0.0010

0.0005



CBSS.216592.1.pcg.3937

FDR: 9.312e-02
Coefficient: -5.30e-01
Value: F



Two.partner.secretion.pathway..TPS.

FDR: $9.312e-02$
Coefficient: $-5.85e-01$
Value: FS

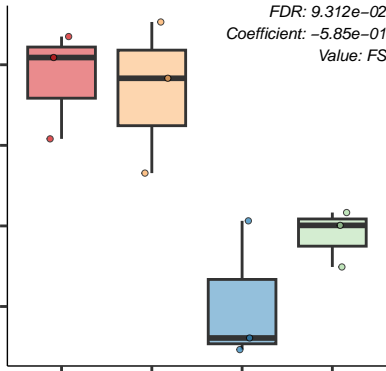
B (n=3)

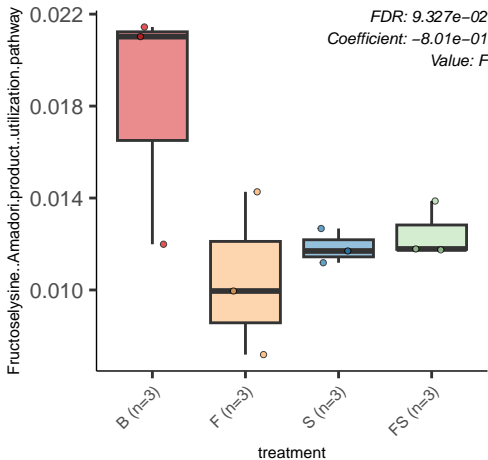
F (n=3)

S (n=3)

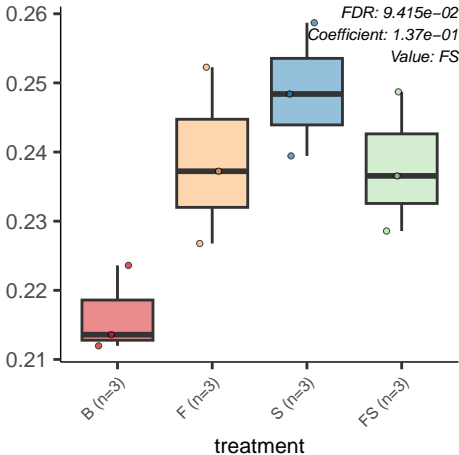
FS (n=3)

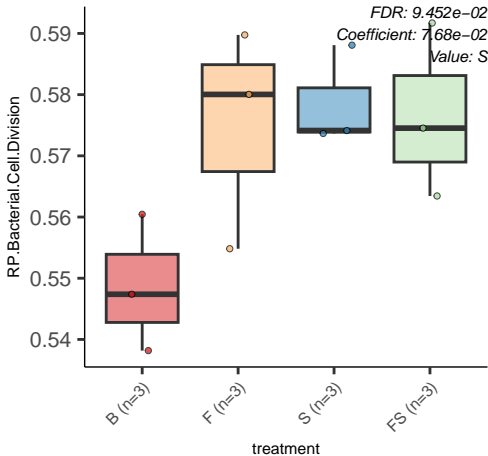
treatment

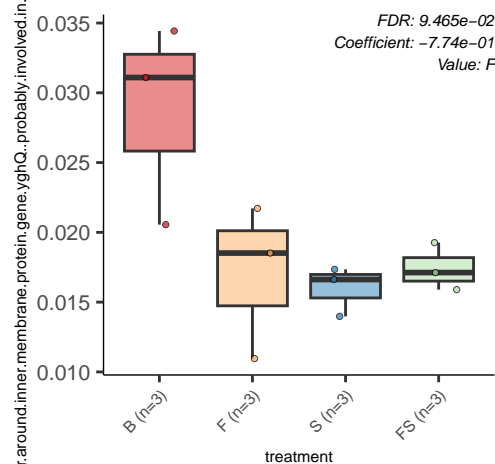


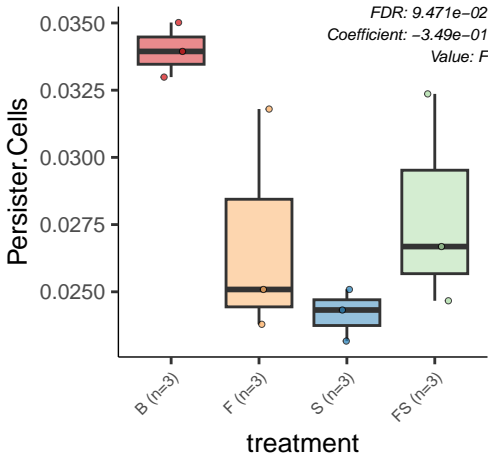


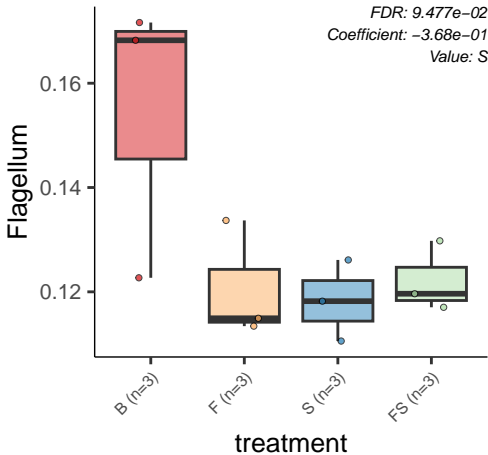
tRNA.aminoacylation..Phe

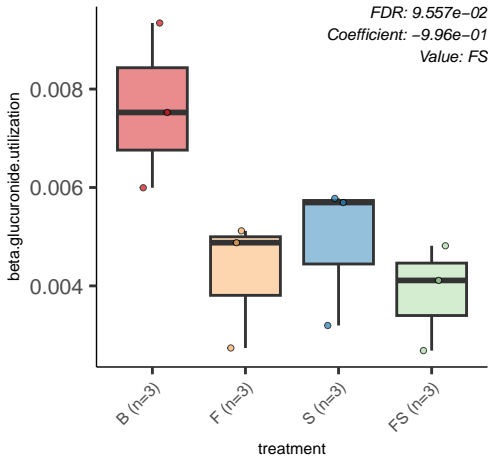




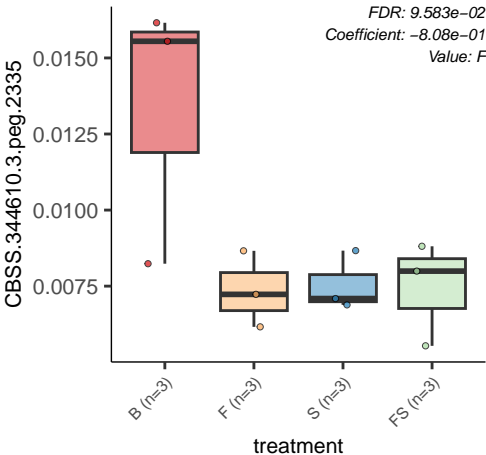






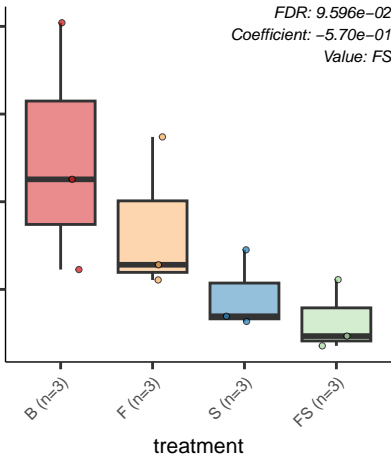


CBSS.344610.3.peg.2335



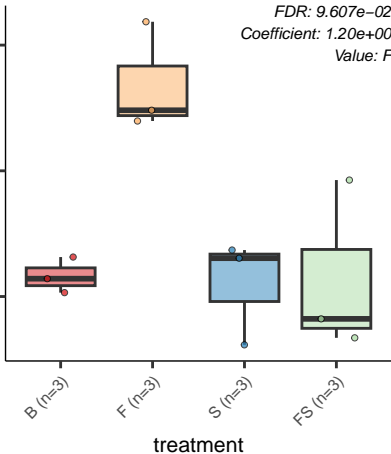
At2g33980.At1g28960

FDR: $9.596e-02$
Coefficient: $-5.70e-01$
Value: FS



Streptothricin.resistance

FDR: 9.607e-02
Coefficient: 1.20e+00
Value: F



dcernst.CoA.Salvage

0.180
0.175
0.170
0.165

B (n=3)

F (n=3)

S (n=3)

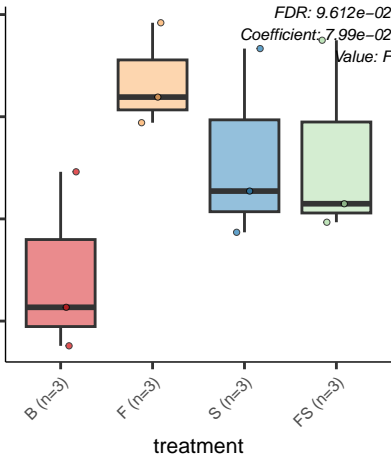
FS (n=3)

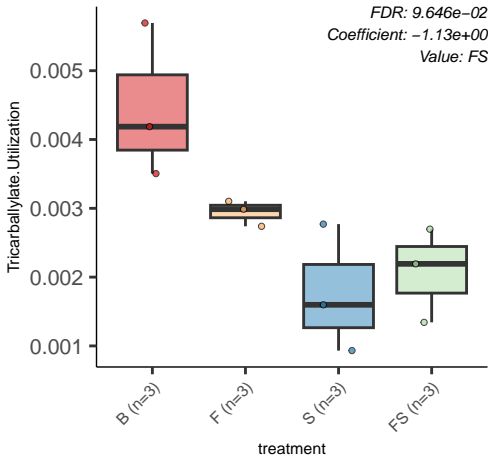
treatment

FDR: 9.612e-02

Coefficient: 7.99e-02

Value: F





CBSS.354.1.peg.2917

FDR: 9.655e-02
Coefficient: -1.53e-01
Value: F

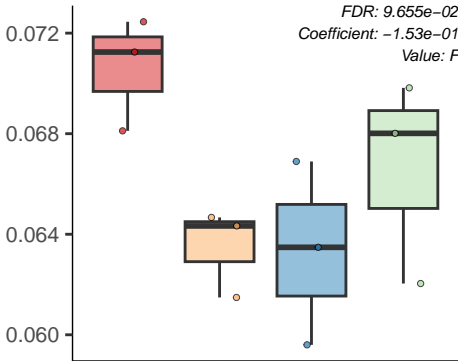
B (n=3)

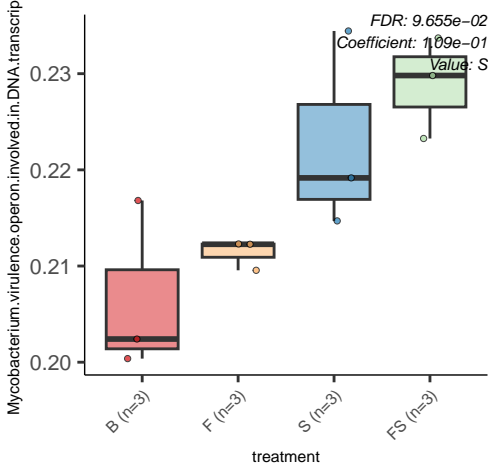
F (n=3)

S (n=3)

FS (n=3)

treatment





O.antigen.capsule.important.for.environmental.persistence

FDR: $9.655e-02$
Coefficient: $-5.91e-01$
Value: F

0.04

0.03

0.02

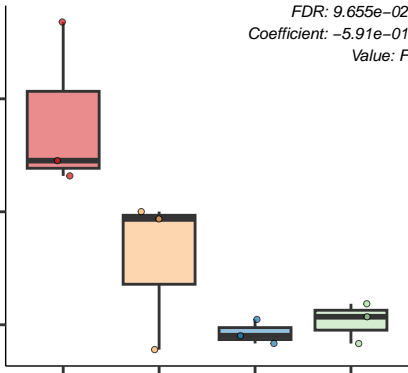
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Pseudomonas.quinolone.signal.PQS

FDR: $9.655e-02$
Coefficient: $-1.68e+00$
Value: S

B (n=3)

F (n=3)

S (n=3)

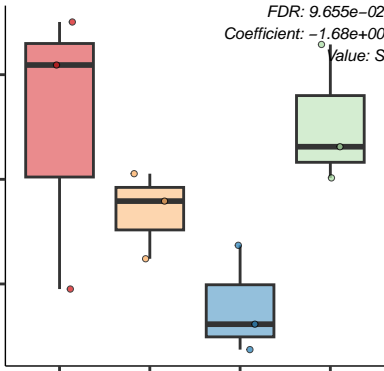
FS (n=3)

treatment

0.0015

0.0010

0.0005



Single.copy.ribosomal.proteins

FDR: 9.655e-02
Coefficient: 5.82e-02
Value: FS

0.66
0.64
0.62

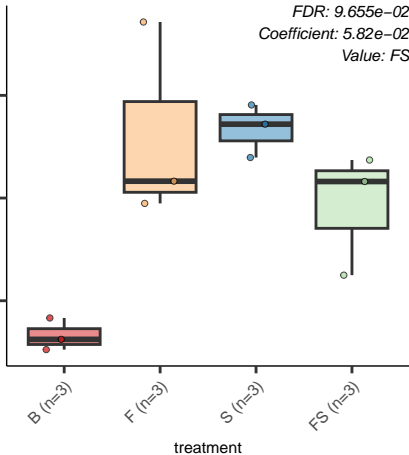
B (n=3)

F (n=3)

S (n=3)

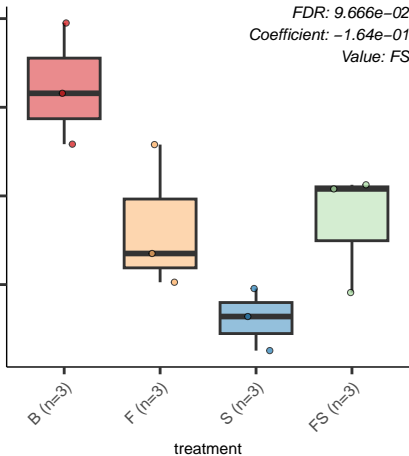
FS (n=3)

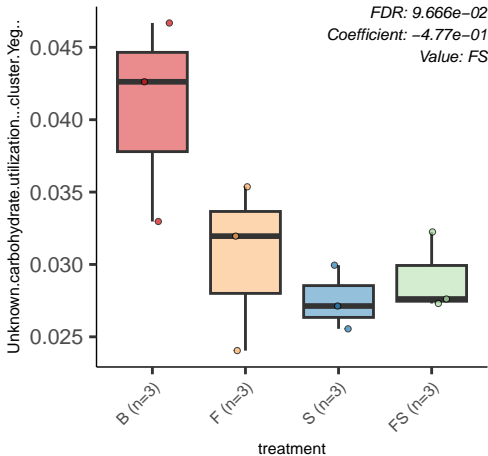
treatment



Lipid.A.Ara4N.pathway...Polymyxin..resistance..

FDR: $9.666e-02$
Coefficient: $-1.64e-01$
Value: FS





CBSS.344610.3.peg.2335

B (n=3)

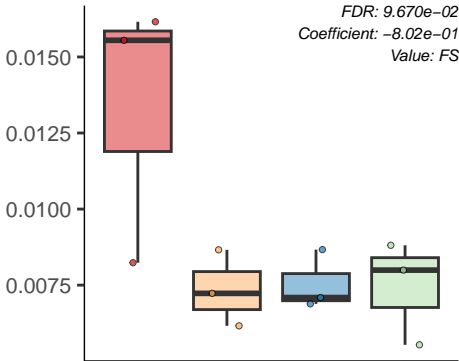
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: $9.670e-02$
Coefficient: $-8.02e-01$
Value: FS



Osmoprotectant.ABC.transporter.YehZYXW.of.Enterobacter

FDR: 9.675e-02
Coefficient: -7.88e-01
Value: S

0.010
0.008
0.006
0.004

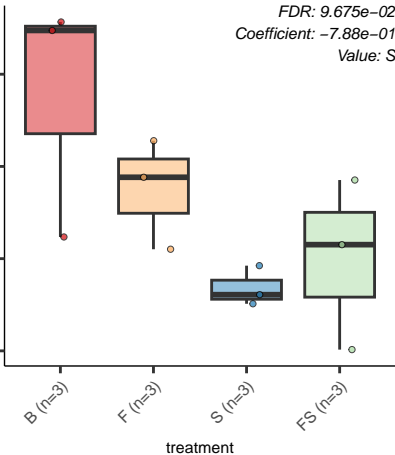
B (n=3)

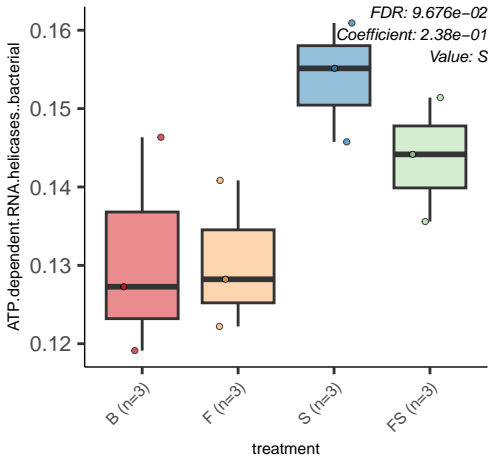
F (n=3)

S (n=3)

FS (n=3)

treatment





RpoS.Regulators.SG1

FDR: $9.684e-02$

Coefficient: $-4.23e-01$

Value: S

0.028

0.024

0.020

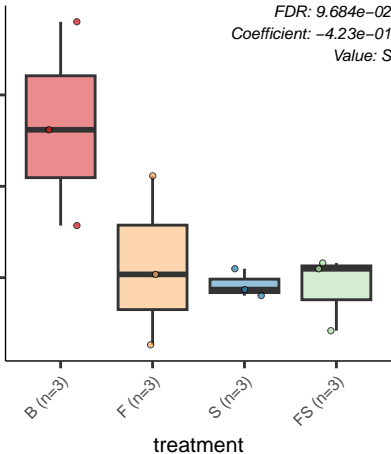
B (n=3)

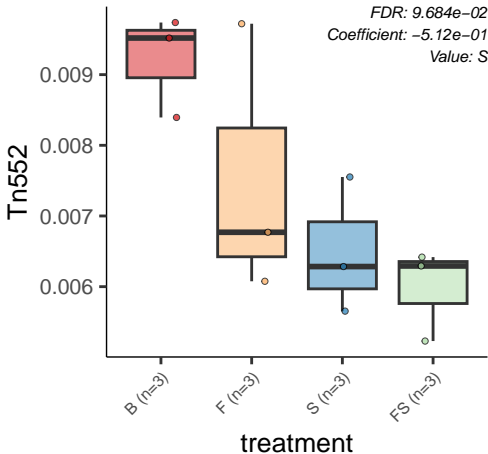
F (n=3)

S (n=3)

FS (n=3)

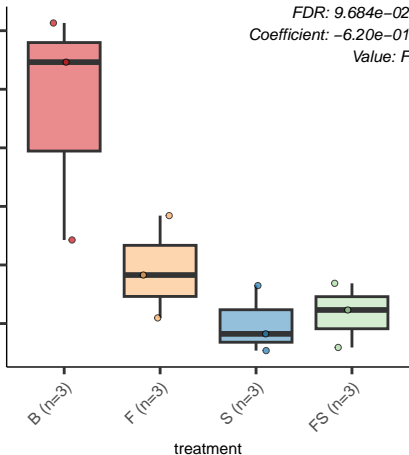
treatment





Type.1.pili..mannose.sensitive.fimbriae.

FDR: 9.684e-02
Coefficient: -6.20e-01
Value: F

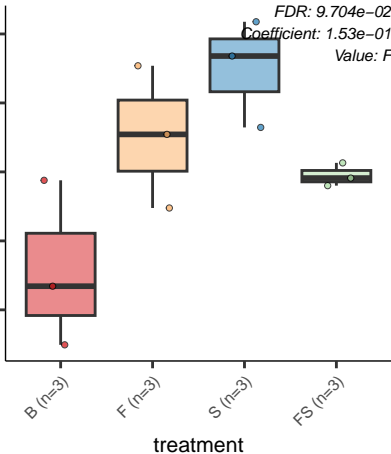


tRNA.aminoacylation..Trp

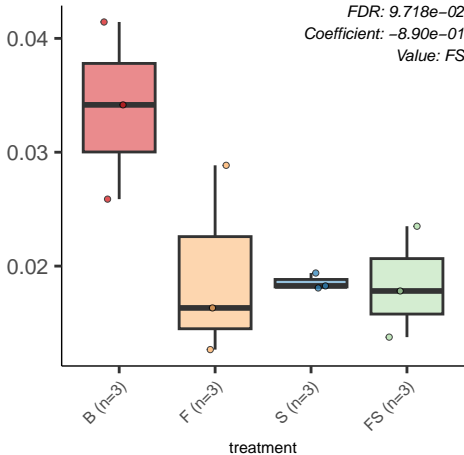
FDR: 9.704e-02

Coefficient: 1.53e-01

Value: F



FDR: $9.718e-02$
Coefficient: $-8.90e-01$
Value: FS



The.fimbral.Sfm.cluster

FDR: 9.718e-02
Coefficient: -6.41e-01
Value: FS

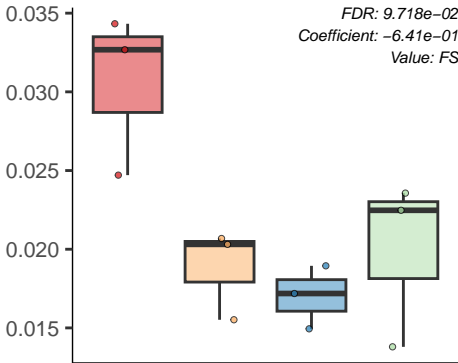
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Monika.MRSA

FDR: $9.723e-02$
Coefficient: $2.17e-01$
Value: S

0.044
0.040
0.036
0.032

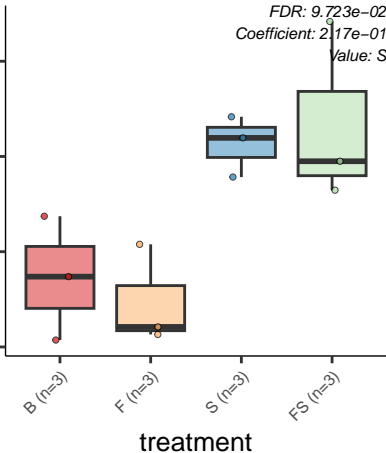
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Restriction.Modification.System

FDR: 9.723e-02
Coefficient: 7.08e-02
Value: F

0.43

0.42

0.41

0.40

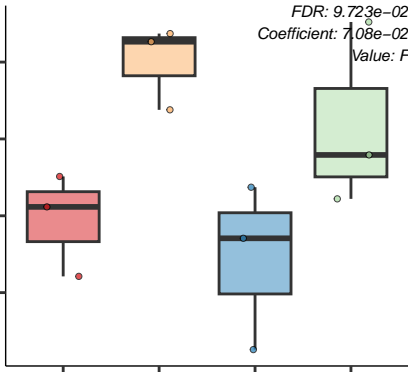
B (n=3)

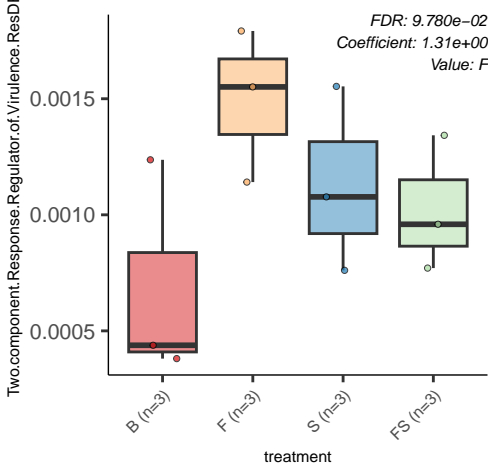
F (n=3)

S (n=3)

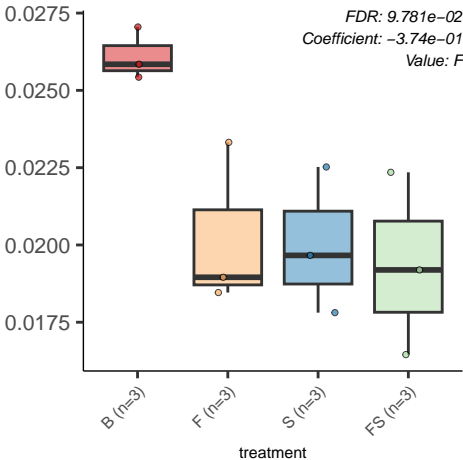
FS (n=3)

treatment



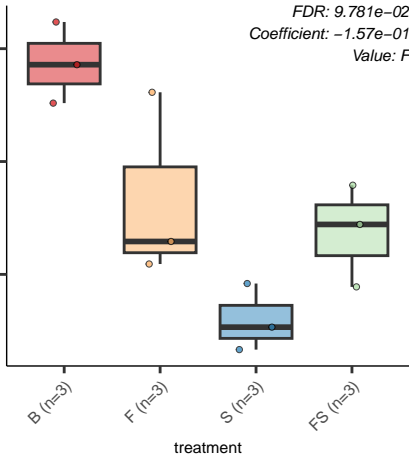


Khodge314.Isoleucine.Biosynthesis



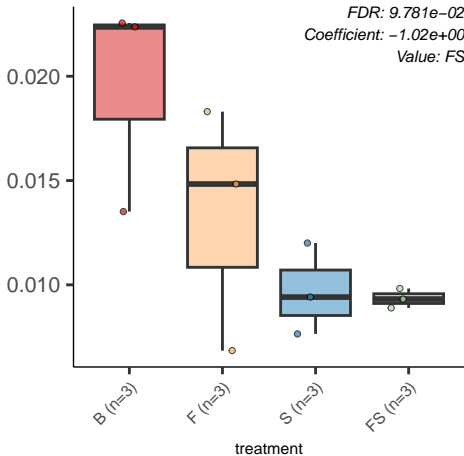
N.Acetyl.l.Galactosamine.and.Galactosamine.Utilization

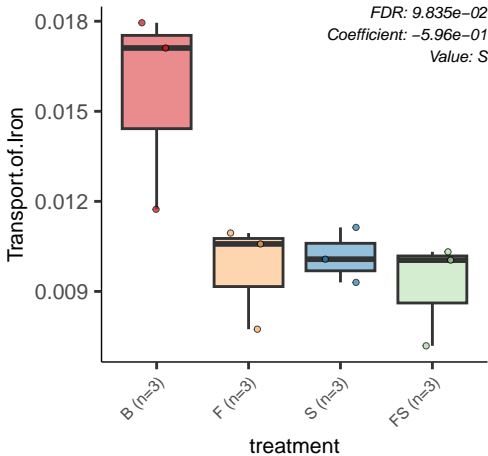
FDR: $9.781\text{e-}02$
Coefficient: $-1.57\text{e-}01$
Value: F

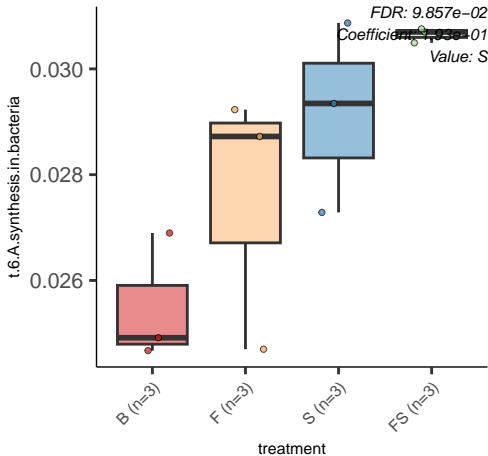


YjbEFGH.Locus.Involved.in.Exopolysaccharide.Production

FDR: $9.781e-02$
Coefficient: $-1.02e+00$
Value: FS

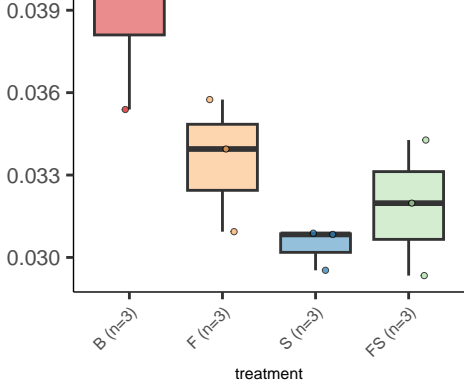






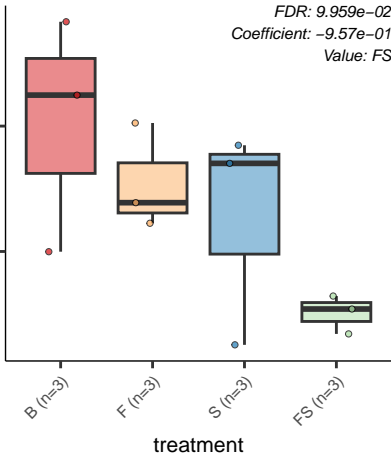
Ubiquinone.biosynthesis.....gjo

FDR: $9.890e-02$
Coefficient: $-2.22e-01$
Value: F



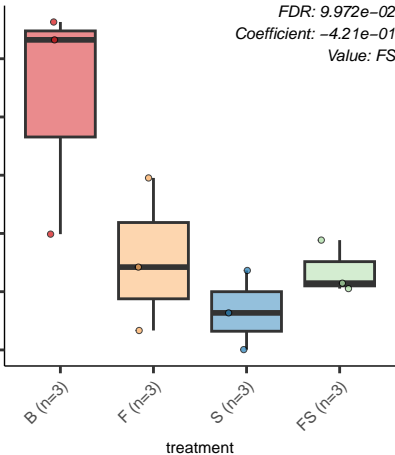
Citrate.Metabolism.KE2

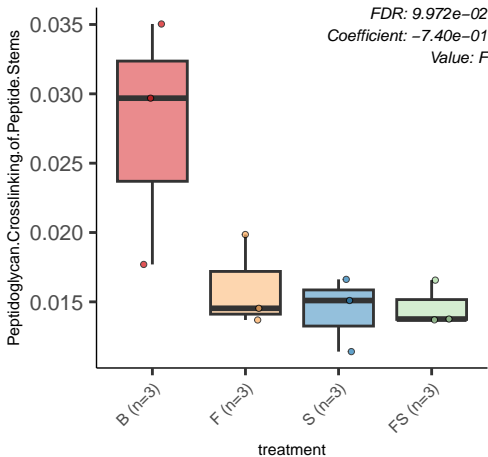
FDR: $9.959e-02$
Coefficient: $-9.57e-01$
Value: FS

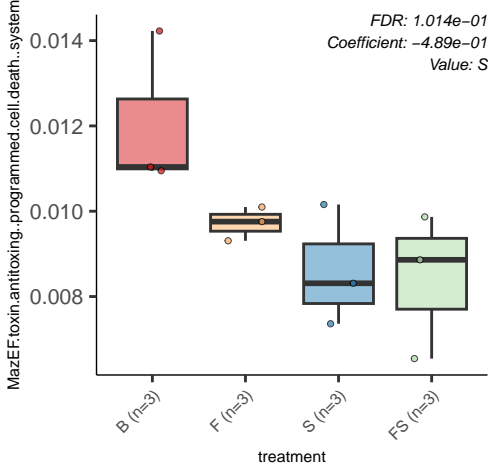


Aromatic.amino.acid.degradation

FDR: 9.972e-02
Coefficient: -4.21e-01
Value: FS







Test...Riboflavin

FDR: 1.018e-01
Coefficient: 8.13e-02
Value: F

0.54
0.52
0.50

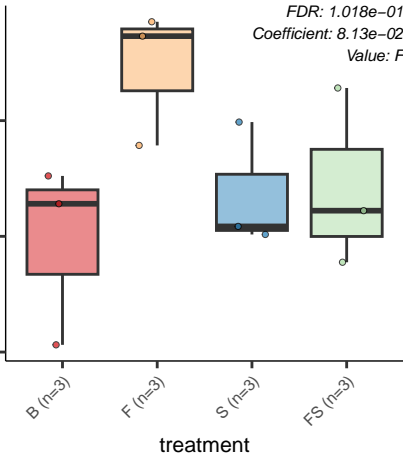
B (n=3)

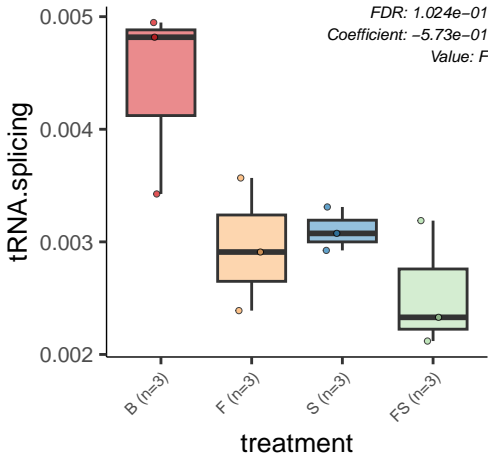
F (n=3)

S (n=3)

FS (n=3)

treatment





CBSS.243265.1.pcg.198

0.030

0.025

B (n=3)

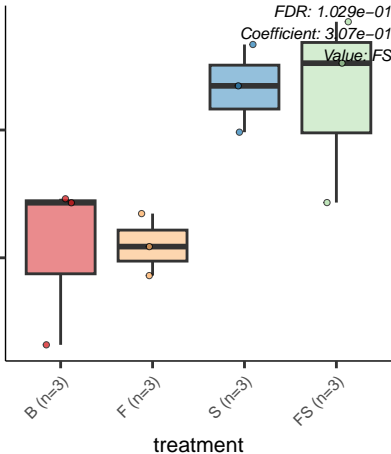
F (n=3)

S (n=3)

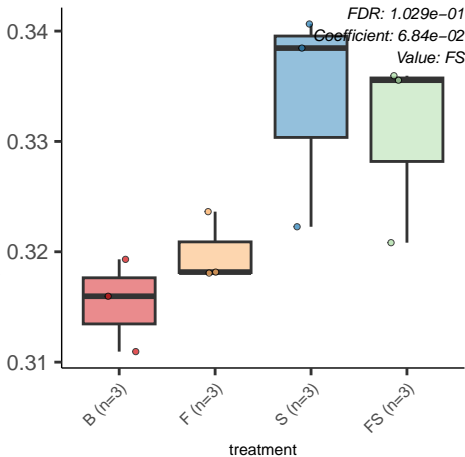
FS (n=3)

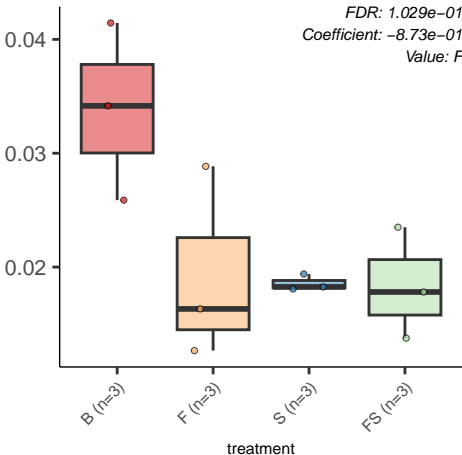
treatment

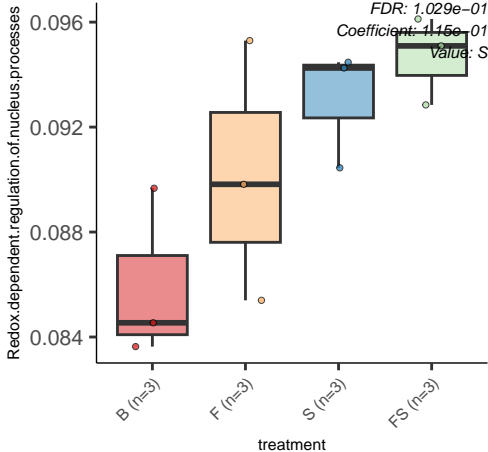
FDR: 1.029e-01
Coefficient: 3.07e-01
Value: FS



Competence.or.DNA.damage.inducible.protein.CinA.and.related.pro







Rhamnose.containing.glycans

0.62

0.60

0.58

0.56

B (n=3)

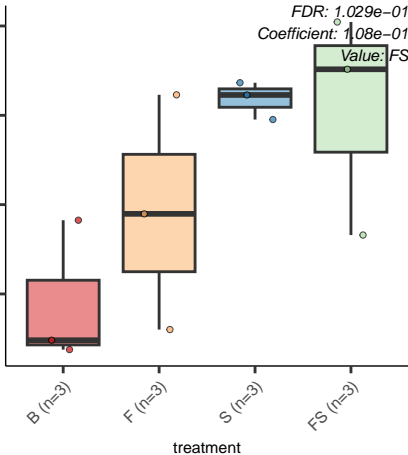
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 1.029e-01
Coefficient: 1.08e-01
Value: FS



Mercury.resistance.operon

FDR: 1.031e-01
Coefficient: 3.96e-01
Value: S

0.0150
0.0125
0.0100
0.0075

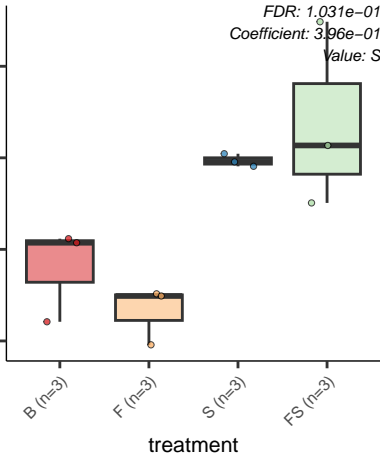
B (n=3)

F (n=3)

S (n=3)

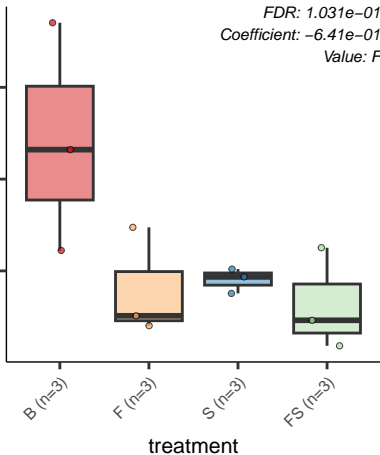
FS (n=3)

treatment



P.uptake..cyanobacteria.

FDR: 1.031e-01
Coefficient: -6.41e-01
Value: F



cAMP.signaling.in.bacteria

FDR: 1.044e-01
Coefficient: -1.81e-01
Value: S

0.16
0.15
0.14
0.13

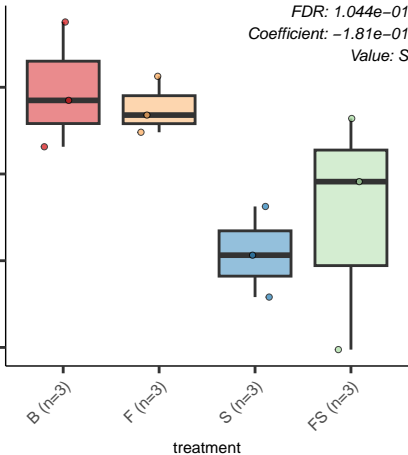
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



At3g21300

0.15
0.14
0.13
0.12

B (n=3)

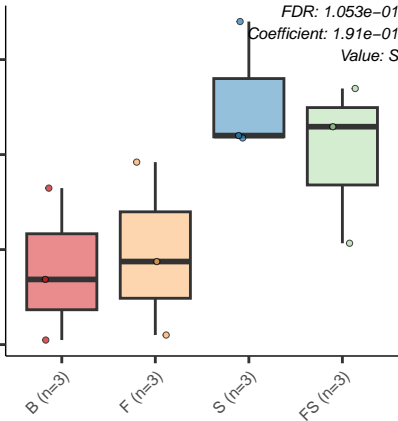
F (n=3)

S (n=3)

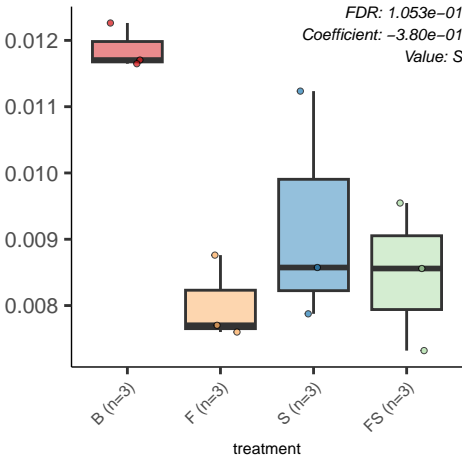
FS (n=3)

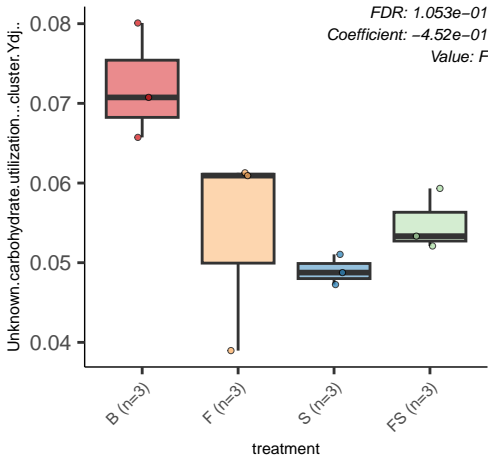
treatment

FDR: 1.053e-01
Coefficient: 1.91e-01
Value: S



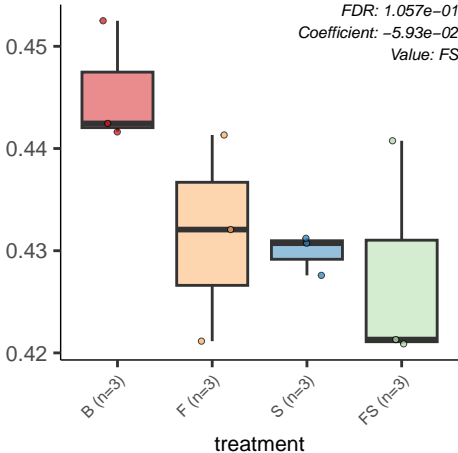
Tricarboxylate.transport.system





Polyamine.Metabolism

FDR: 1.057e-01
Coefficient: -5.93e-02
Value: FS



Cyanobacterial.Circadian.Clock

FDR: 1.060e-01
Coefficient: 3.48e-01
Value: FS

0.020

0.018

0.016

0.014

0.012

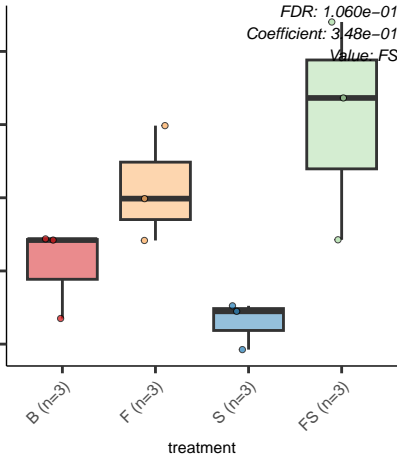
B (n=3)

F (n=3)

S (n=3)

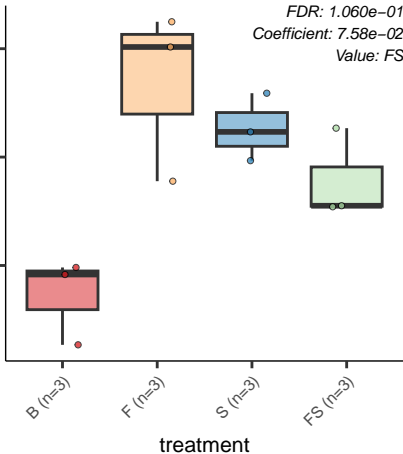
FS (n=3)

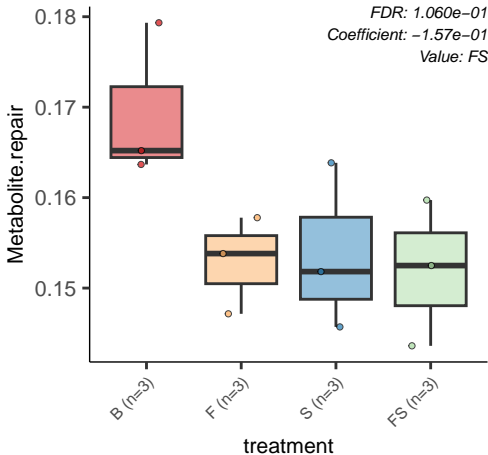
treatment

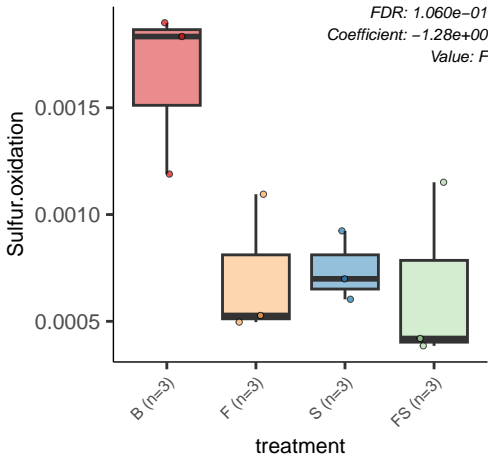


Leucine.Biosynthesis

FDR: 1.060e-01
Coefficient: 7.58e-02
Value: FS







YjbEFGH.Locus.Involved.in.Exopolysaccharide.Production

FDR: 1.062e-01
Coefficient: -9.93e-01
Value: S

0.020
0.015
0.010

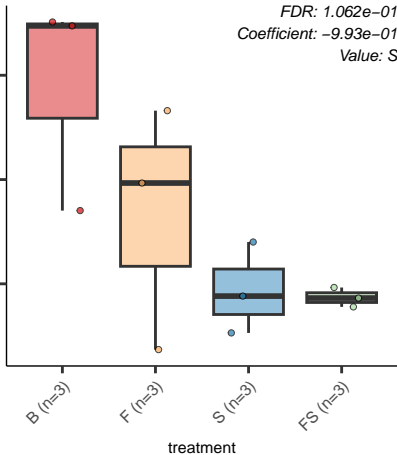
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



DNA.processing.cluster

FDR: 1.062e-01
Coefficient: 6.35e-02
Value: F

0.31

0.30

0.29

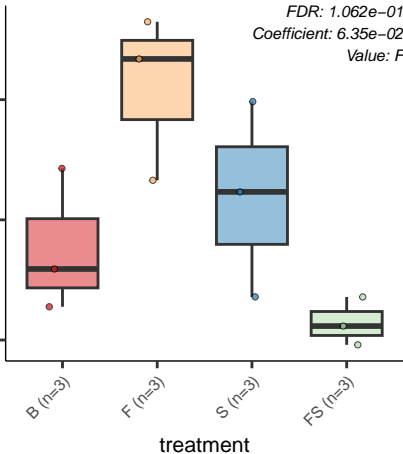
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Peptidoglycan.Biosynthesis

0.84
0.82
0.80

B (n=3)

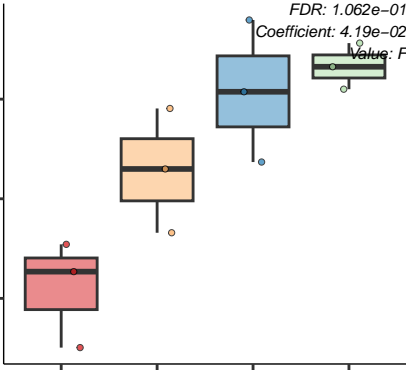
F (n=3)

S (n=3)

FS (n=3)

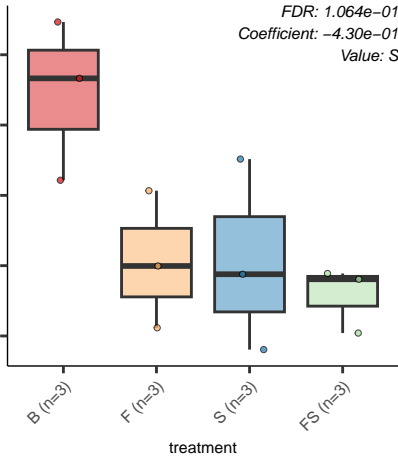
treatment

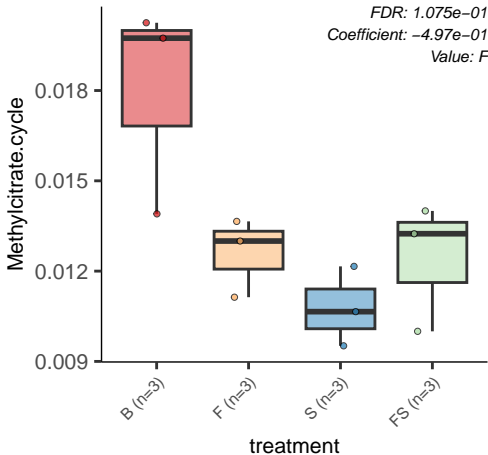
FDR: 1.062e-01
Coefficient: 4.19e-02
Value: F



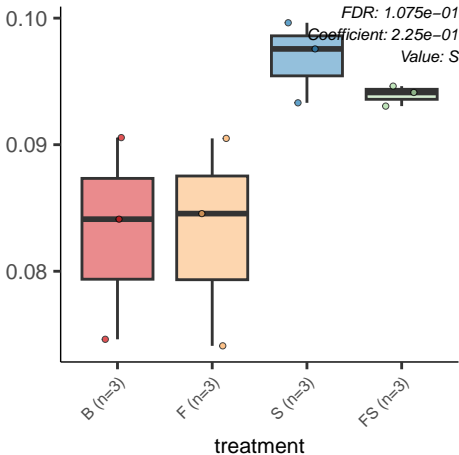
D.Sorbitol.D.Glucitol...and.L.Sorbose.Utilization

FDR: 1.064e-01
Coefficient: -4.30e-01
Value: S





CBSS.176299.4.peg.1292



ECF.class.transporters

0.32
0.30
0.28
0.26

B (n=3)

F (n=3)

S (n=3)

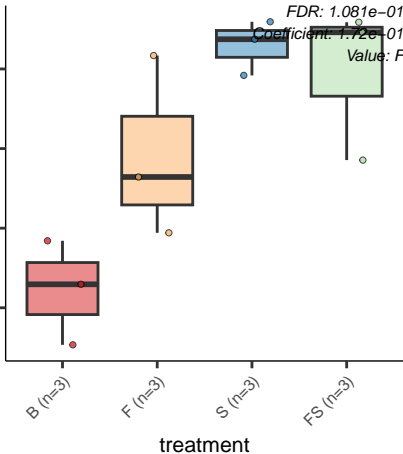
FS (n=3)

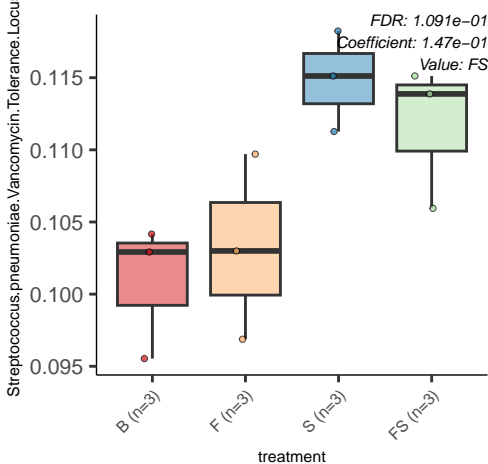
treatment

FDR: 1.081e-01

Coefficient: 1.72e-01

Value: F





Phage.head.and.packaging

FDR: 1.093e-01
Coefficient: -4.05e-01
Value: FS

0.040

0.035

0.030

0.025

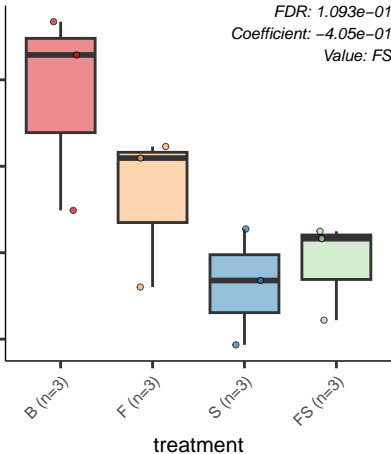
B (n=3)

F (n=3)

S (n=3)

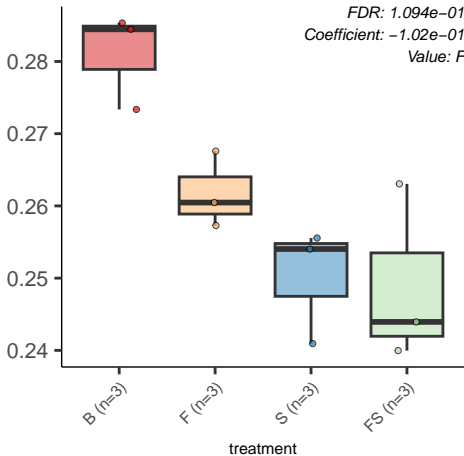
FS (n=3)

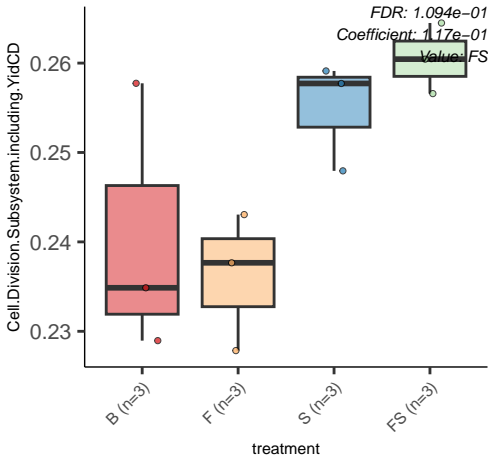
treatment

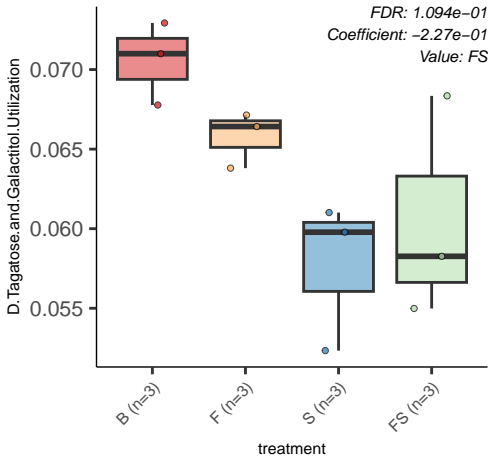


Arginine.and.Ornithine.Degradation

FDR: 1.094e-01
Coefficient: -1.02e-01
Value: F







CBSS.344610.3.peg.2335

FDR: 1.108e-01
Coefficient: -7.63e-01
Value: S

B (n=3)

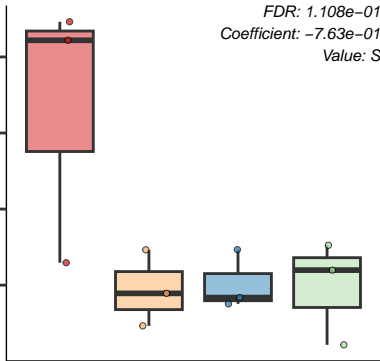
F (n=3)

S (n=3)

FS (n=3)

treatment

0.0150
0.0125
0.0100
0.0075



Fructooligosaccharides.FOS..and.Raffinose.Utilization

FDR: 1.116e-01
Coefficient: -7.10e-02
Value: FS

1.04
1.00
0.96

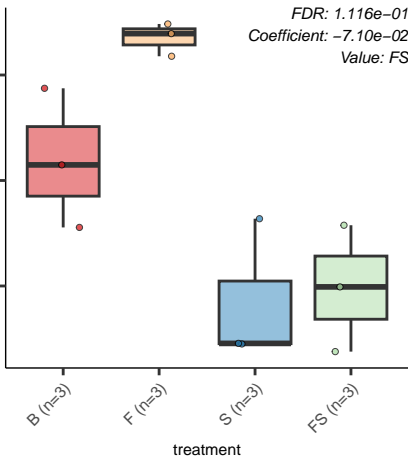
B (n=3)

F (n=3)

S (n=3)

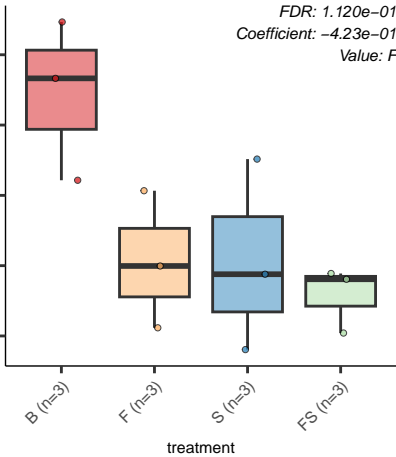
FS (n=3)

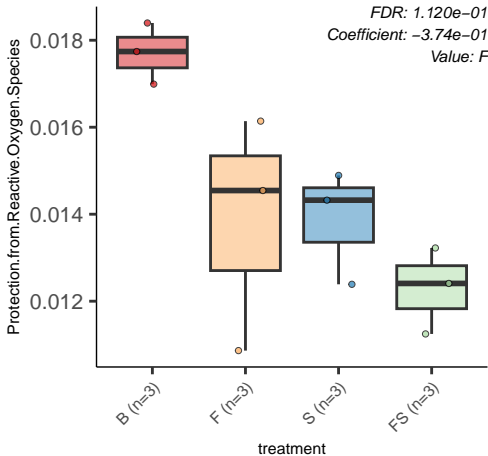
treatment



D.Sorbitol.D.Glucitol...and.L.Sorbose.Utilization

FDR: 1.120e-01
Coefficient: -4.23e-01
Value: F





p.Hydroxybenzoate.degradation

FDR: 1.127e-01
Coefficient: -1.00e+00
Value: S

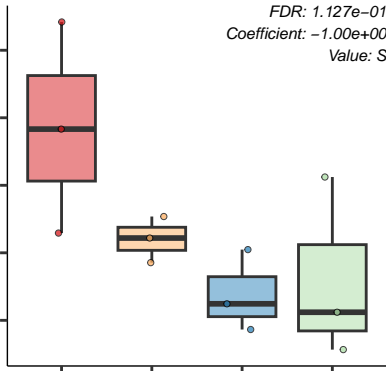
B (n=3)

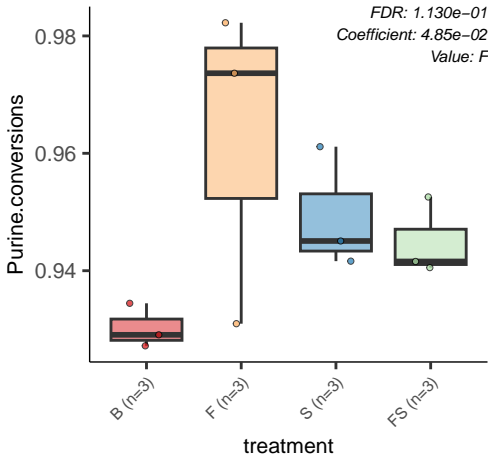
F (n=3)

S (n=3)

FS (n=3)

treatment





Streptococcus.pyogenes.recombinatorial.zone

0.030
0.025
0.020
0.015

B (n=3)

F (n=3)

S (n=3)

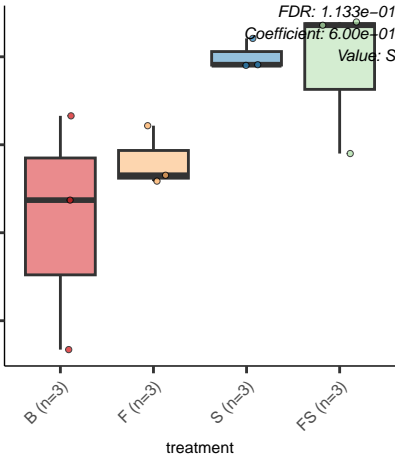
FS (n=3)

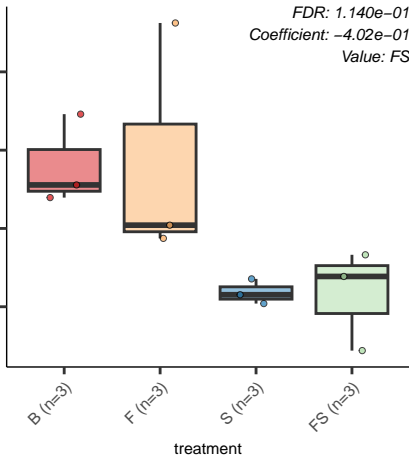
treatment

FDR: 1.133e-01

Coefficient: 6.00e-01

Value: S





A.toxin.antitoxin.module.cotranscribed.with.DinB

FDR: $1.144e-01$
Coefficient: $-1.58e+00$
Value: S

0.004
0.003
0.002
0.001

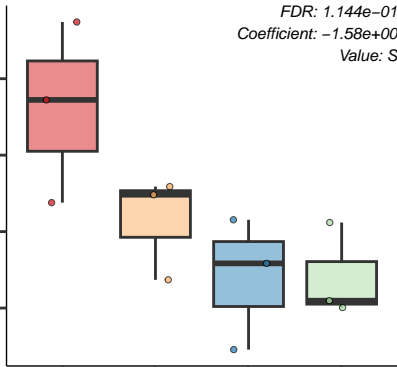
B (n=3)

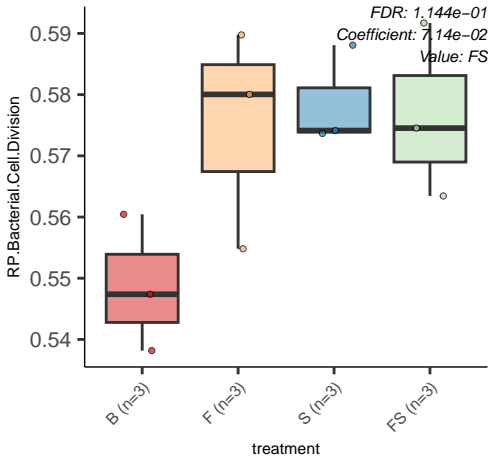
F (n=3)

S (n=3)

FS (n=3)

treatment





DNA.repair..UvrABC.system

FDR: 1.146e-01

Coefficient: 6.79e-02

Value: F

0.66

0.64

0.62

0.60

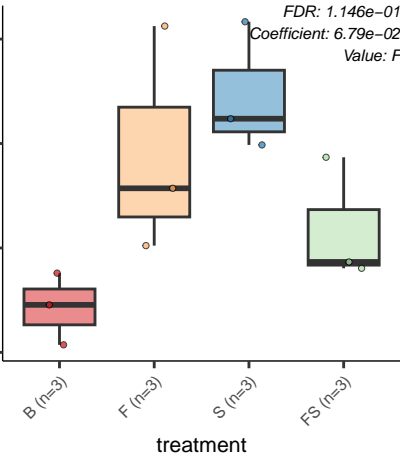
B (n=3)

F (n=3)

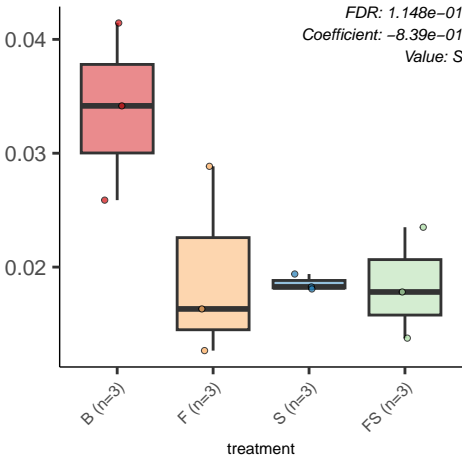
S (n=3)

FS (n=3)

treatment



Mediator.of.hyperadherence.YidE.in.Enterobacteria.and.its.conse



Synechocystis.experimental

FDR: 1.151e-01
Coefficient: -2.75e-01
Value: FS

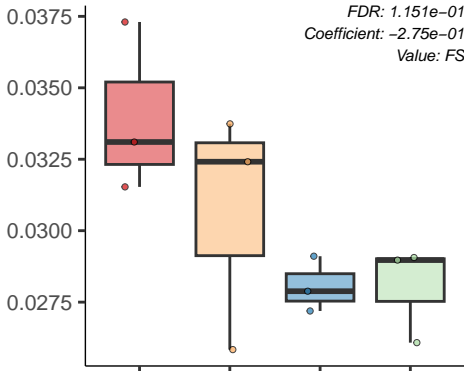
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



EC699.706

FDR: 1.160e-01
Coefficient: -3.42e-01
Value: S

B (n=3)

F (n=3)

S (n=3)

FS (n=3)

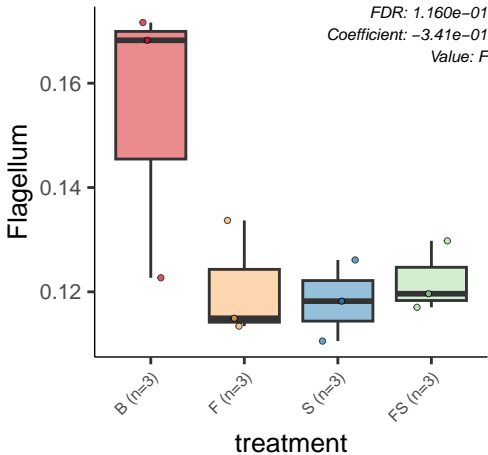
treatment

0.055

0.050

0.045

0.040



Aromatic.amino.acid.interconversions.with.aryl.acids

FDR: 1.161e-01
Coefficient: -2.04e-01
Value: FS

0.09
0.08

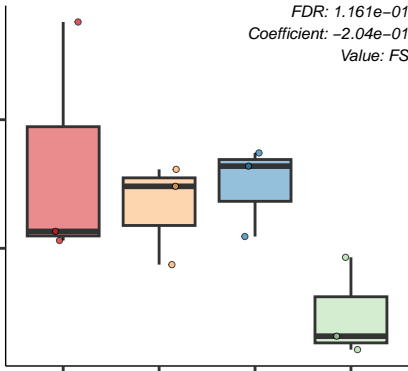
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Transport.of.Manganese

0.070
0.065
0.060
0.055
0.050
0.045

B (n=3)

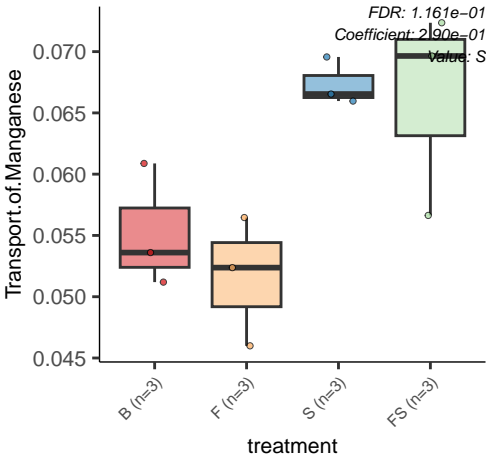
F (n=3)

S (n=3)

FS (n=3)

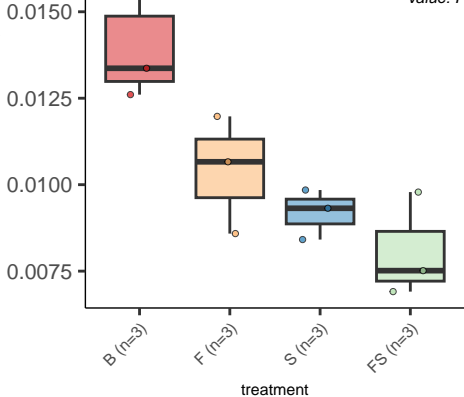
treatment

FDR: 1.161e-01
Coefficient: 2.190e-01
Value: S



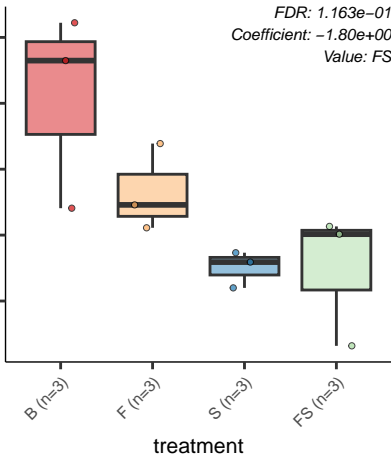
A.Gammaproteobacteria.Cluster.Relating.to.Translation

FDR: 1.162e-01
Coefficient: -4.44e-01
Value: F



X..945..Fimbriae

FDR: 1.163e-01
Coefficient: -1.80e+00
Value: FS



Bacterial.Cytoskeleton

FDR: 1.164e-01
Coefficient: 7.09e-02
Value: F

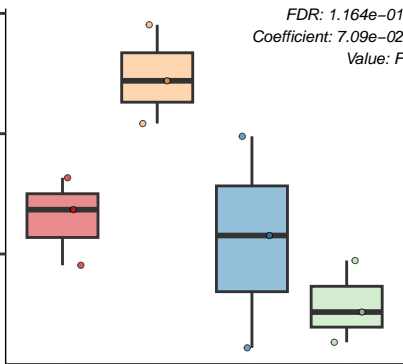
B (n=3)

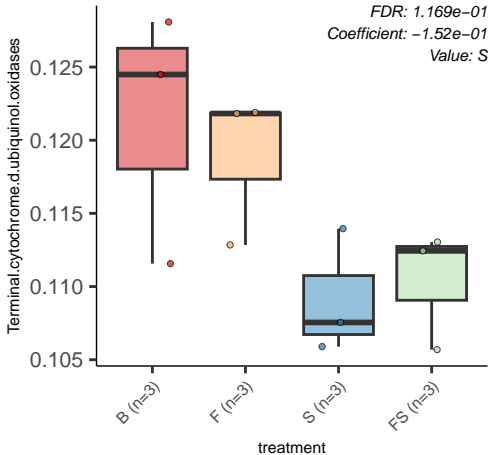
F (n=3)

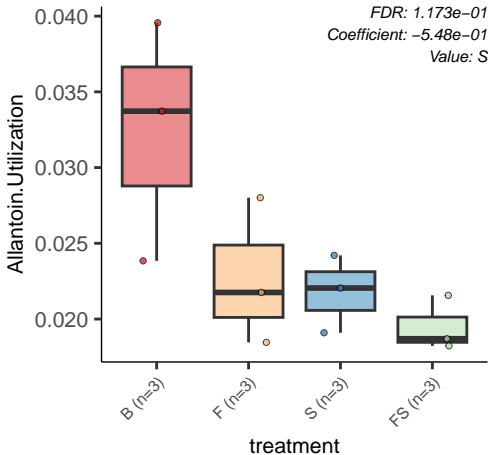
S (n=3)

FS (n=3)

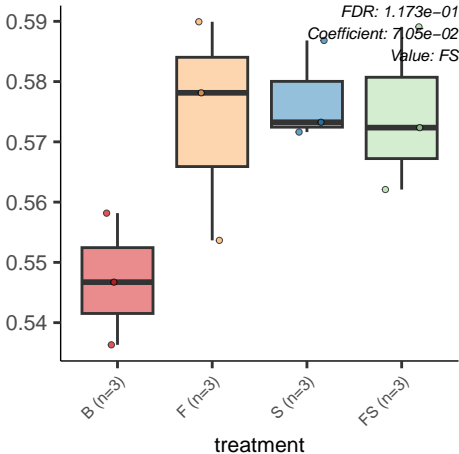
treatment







Bacterial.Cell.Division



CBSS.216592.1.peg.3534

FDR: 1.173e-01
Coefficient: -3.60e-01
Value: FS

B (n=3)

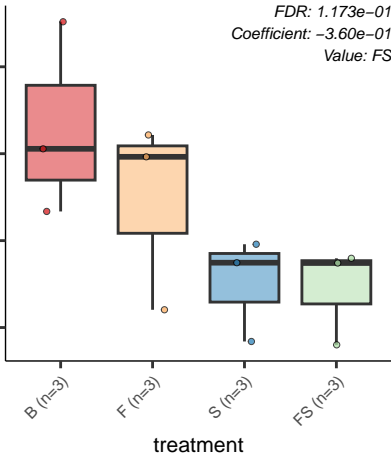
F (n=3)

S (n=3)

FS (n=3)

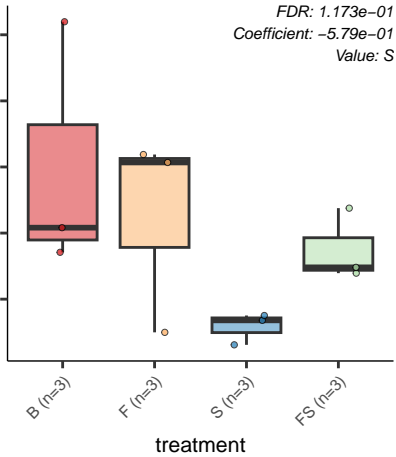
treatment

0.018
0.016
0.014
0.012



CBSS.52598.3.peg.2843

FDR: 1.173e-01
Coefficient: -5.79e-01
Value: S



Coenzyme.B.synthesis

FDR: 1.173e-01
Coefficient: 2.18e+00
Value: F

0.0015
0.0010
0.0005
0.0000

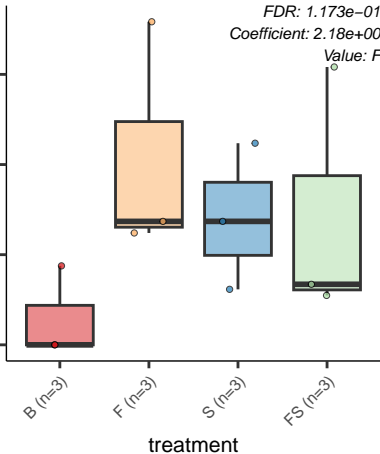
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Late.competence

FDR: 1.173e-01

Coefficient: -3.95e-01

Value: F

0.05

0.04

0.03

0.02

0.01

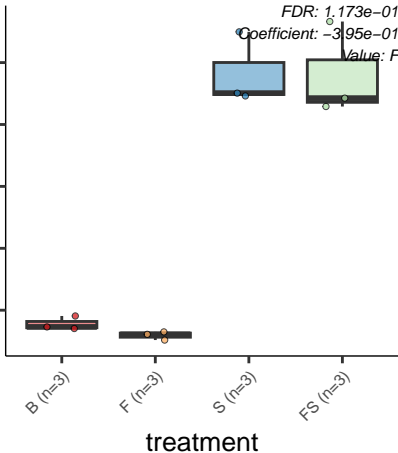
B (n=3)

F (n=3)

S (n=3)

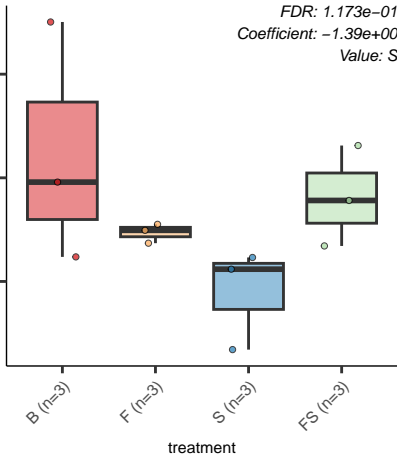
FS (n=3)

treatment

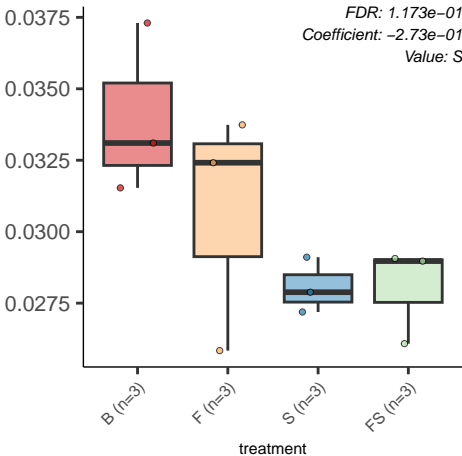


Purine.nucleotide.synthesis.regulator

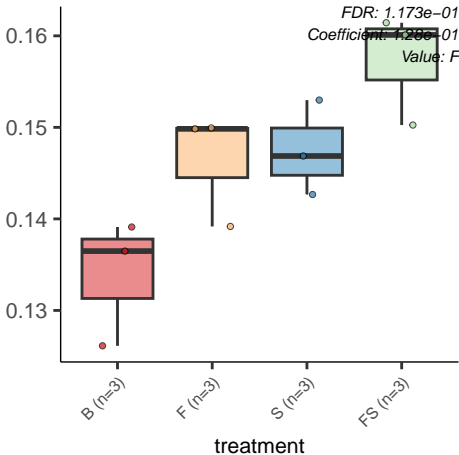
FDR: 1.173e-01
Coefficient: -1.39e+00
Value: S



Synechocystis.experimental



tRNA.aminoacylation..Arg



rRNA.modification.Archaea

FDR: 1.176e-01
Coefficient: -7.87e-01
Value: FS

B (n=3)

F (n=3)

S (n=3)

FS (n=3)

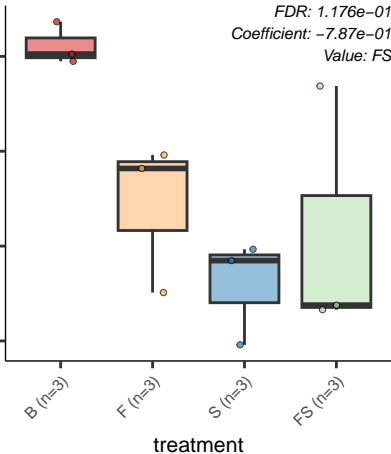
treatment

0.005

0.004

0.003

0.002



Siderophore.Aerobactin

FDR: 1.177e-01
Coefficient: -5.83e-01
Value: FS

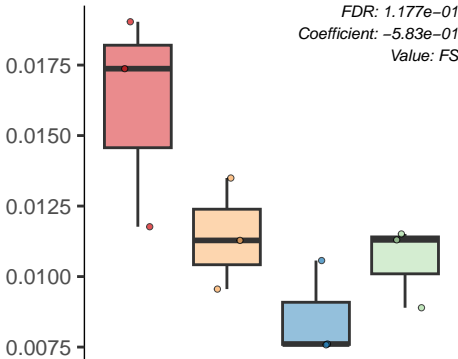
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Aromatic.amino.acid.degradation

FDR: 1.180e-01
Coefficient: -3.95e-01
Value: F

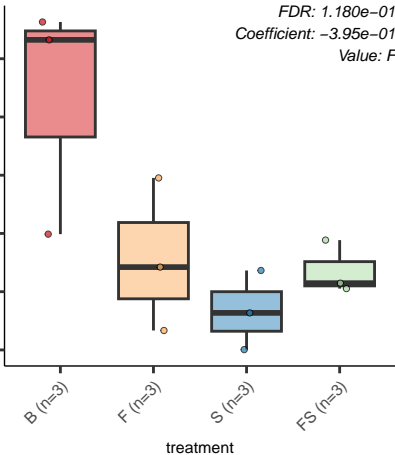
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Phenylacetyl-CoA.catabolic.pathway..core.

FDR: 1.180e-01
Coefficient: -5.82e-01
Value: F

0.020

0.015

0.010

0.005

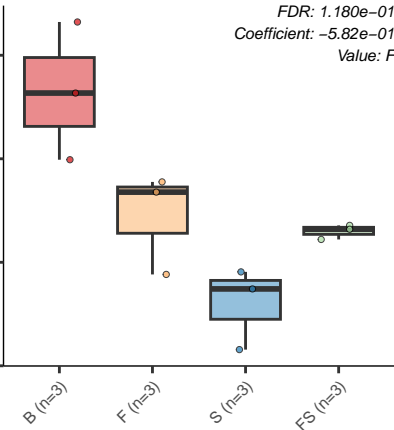
B (n=3)

F (n=3)

S (n=3)

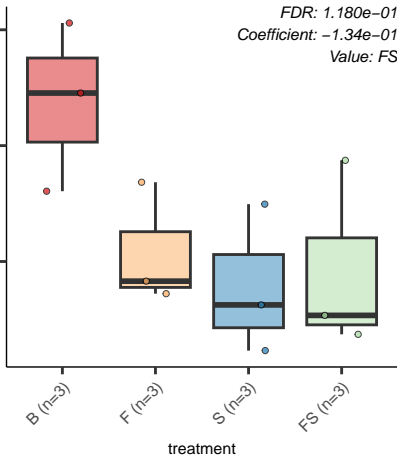
FS (n=3)

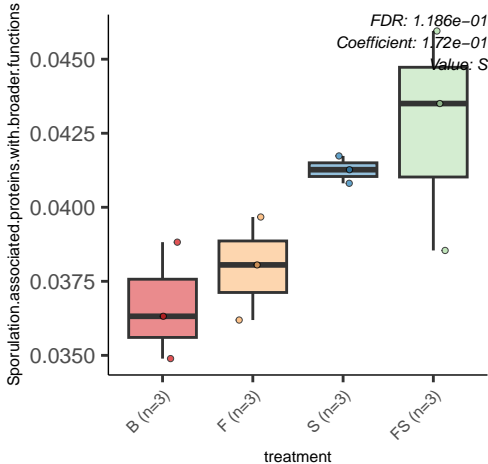
treatment



Terminal.cytochrome.oxidases

FDR: 1.180e-01
Coefficient: -1.34e-01
Value: FS





CBSS.350688.3.pcg.1509

FDR: 1.199e-01
Coefficient: 1.75e-01
Value: FS

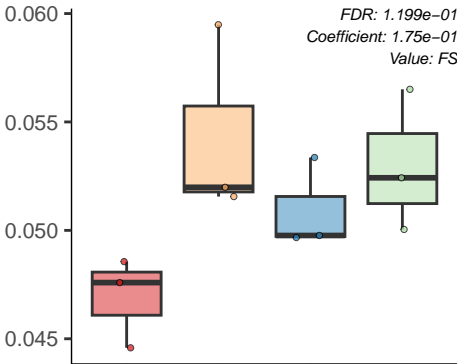
B (n=3)

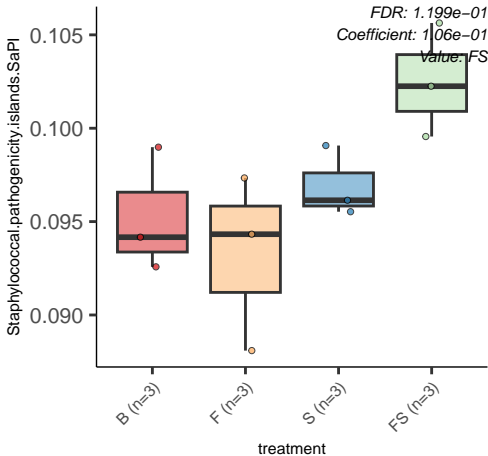
F (n=3)

S (n=3)

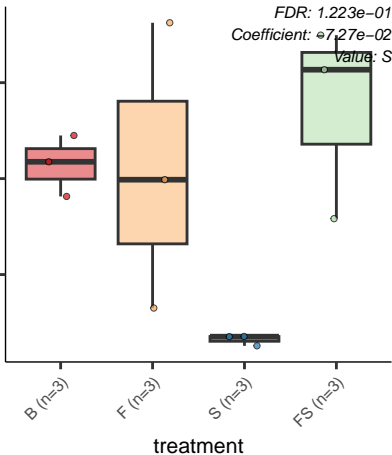
FS (n=3)

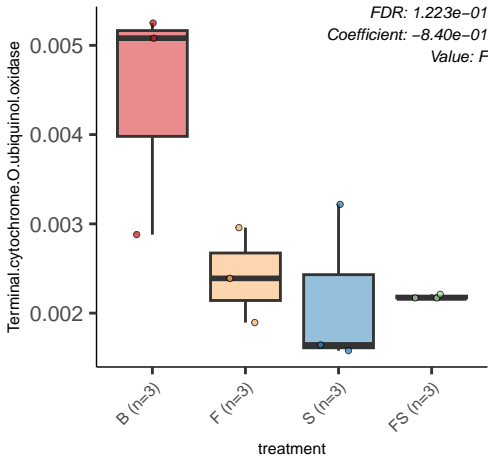
treatment





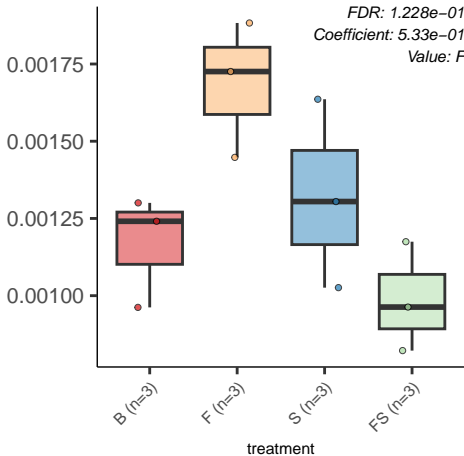
Succinate.dehydrogenase





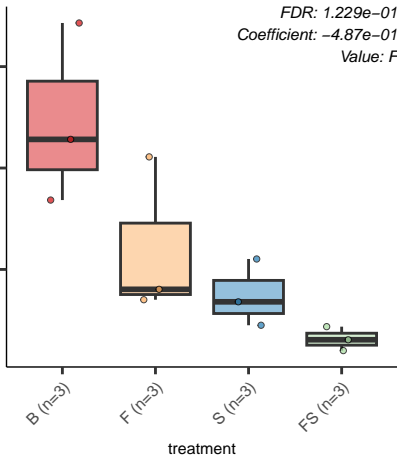
L.2.amino.thiazoline.4.carboxylic.acid.Lcysteine.conversion

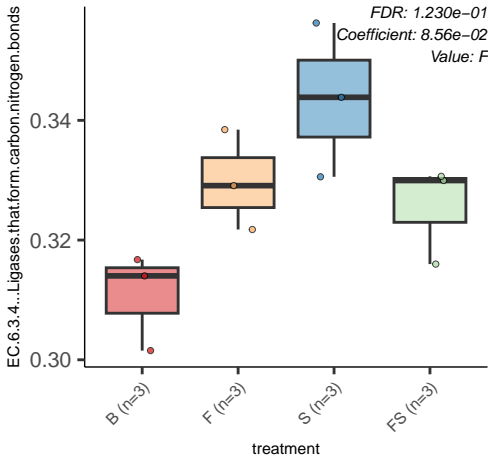
FDR: 1.228e-01
Coefficient: 5.33e-01
Value: F

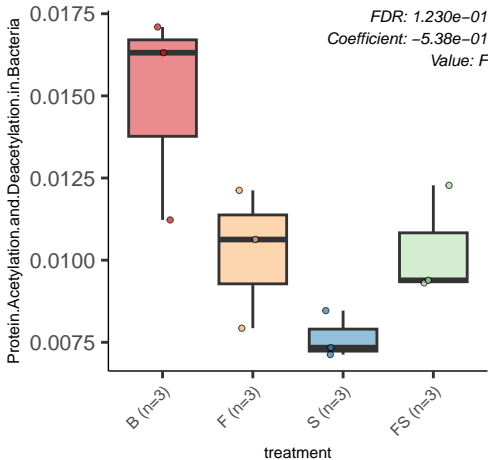


Acetone.Butanol.Ethanol.Synthesis

FDR: 1.229e-01
Coefficient: -4.87e-01
Value: F







Translation.termination.factors.bacterial

FDR: 1.230e-01
Coefficient: 6.79e-02
Value: F

0.34

0.33

0.32

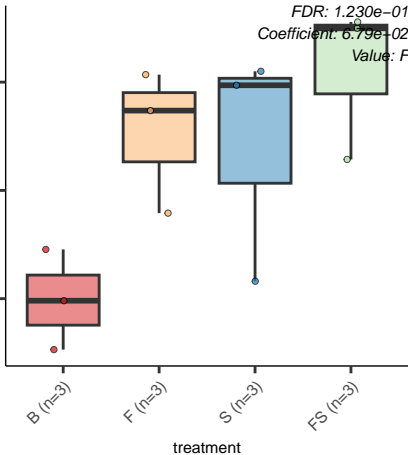
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Transport.of.Molybdenum

FDR: 1.230e-01
Coefficient: -5.19e-01
Value: FS

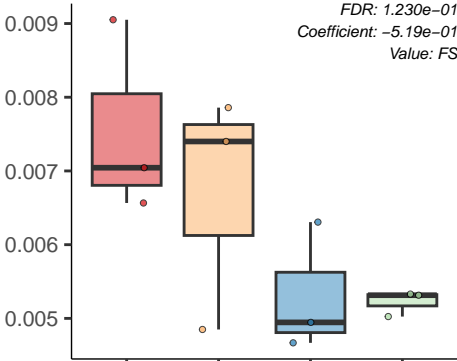
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



p.Hydroxybenzoate.degradation

FDR: 1.230e-01
Coefficient: -9.66e-01
Value: FS

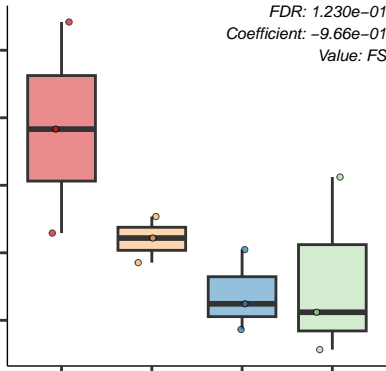
B (n=3)

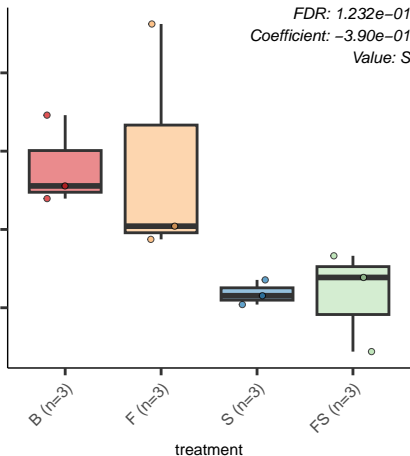
F (n=3)

S (n=3)

FS (n=3)

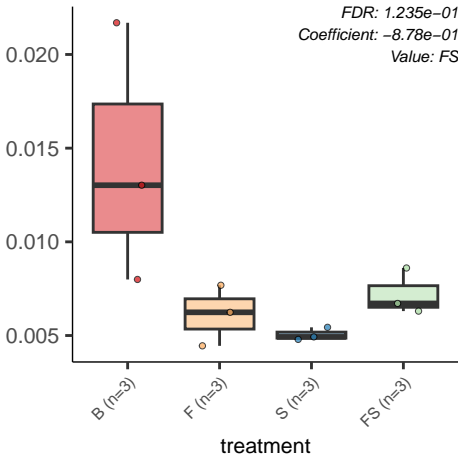
treatment

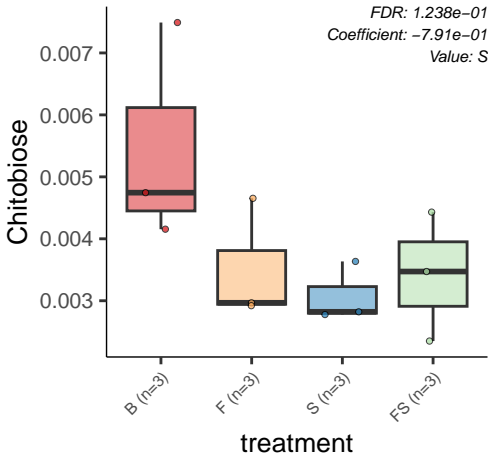




CBSS.194948.1.peg.143

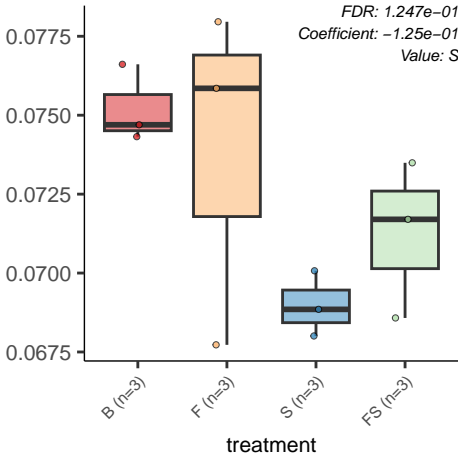
FDR: 1.235e-01
Coefficient: -8.78e-01
Value: FS





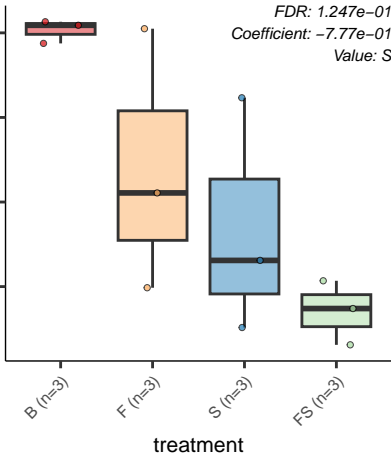
Butanol.Biosynthesis

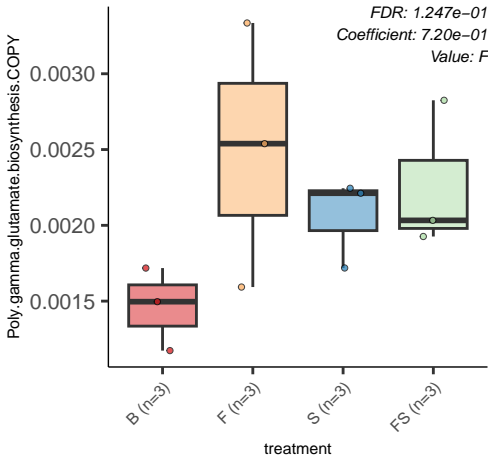
FDR: 1.247e-01
Coefficient: -1.25e-01
Value: S



CBSS.502800.3.pcg.2785

FDR: 1.247e-01
Coefficient: -7.77e-01
Value: S





Putative.TldE.TldD.proteolytic.complex

FDR: 1.247e-01
Coefficient: -3.67e-01
Value: FS

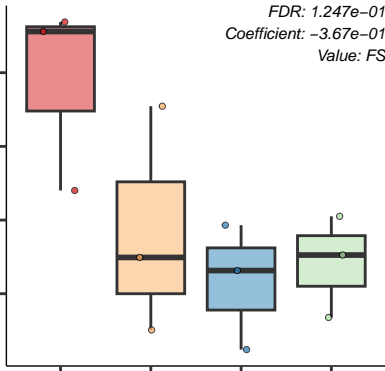
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Queuosine.Archaeosine.Biosynthesis

FDR: 1.247e-01
Coefficient: -9.72e-02
Value: FS

0.180
0.175
0.170
0.165
0.160

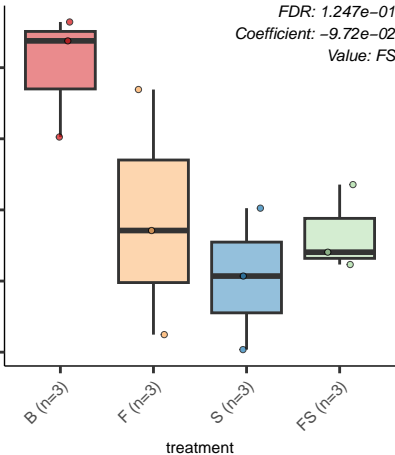
B (n=3)

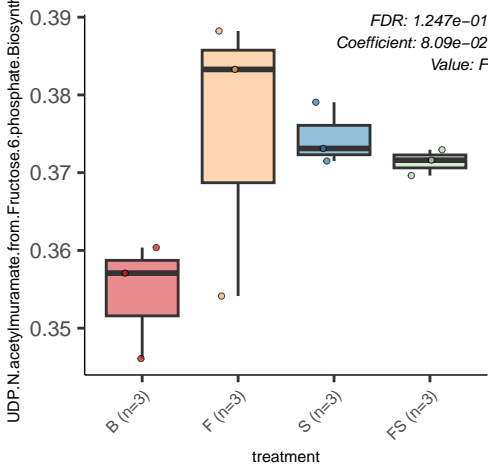
F (n=3)

S (n=3)

FS (n=3)

treatment





cell.division.cluster.containing.FtsQ

0.06
0.05

B (n=3)

F (n=3)

S (n=3)

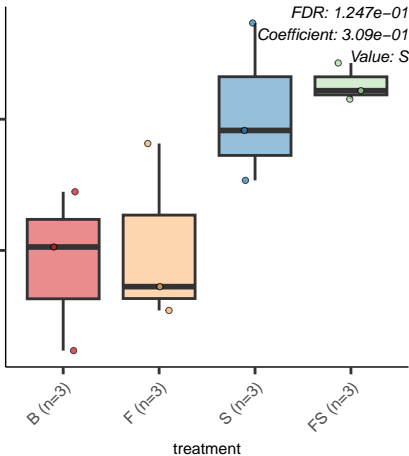
FS (n=3)

treatment

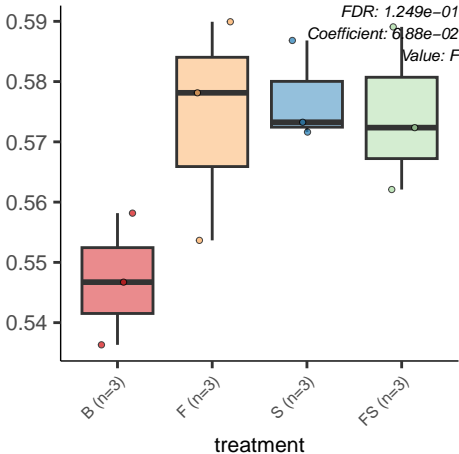
FDR: 1.247e-01

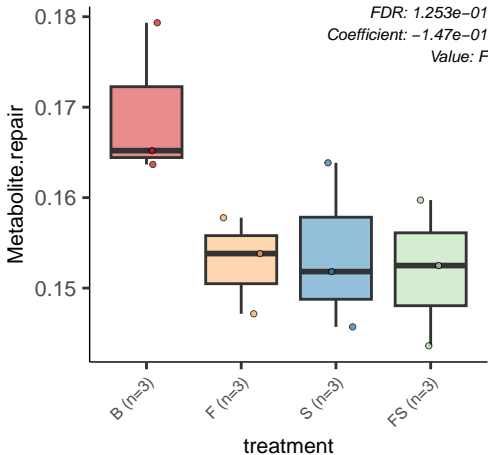
Coefficient: 3.09e-01

Value: S



Bacterial.Cell.Division





Peptidoglycan.biosynthesis..gjo

0.23
0.22
0.21

B (n=3)

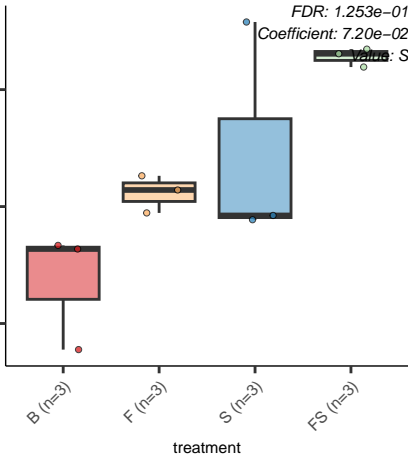
F (n=3)

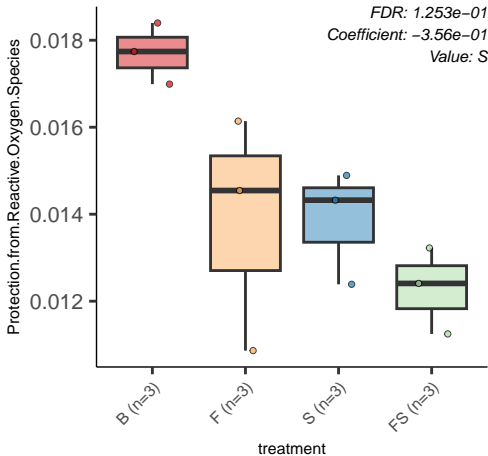
S (n=3)

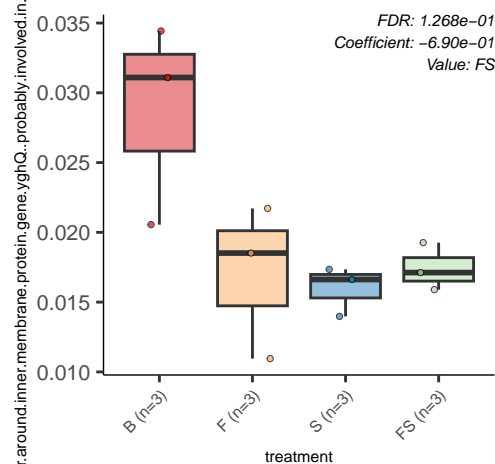
FS (n=3)

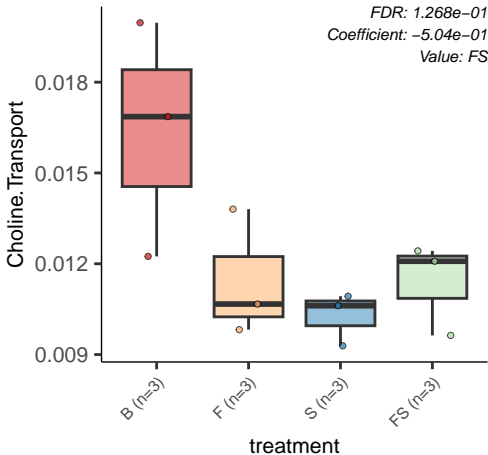
treatment

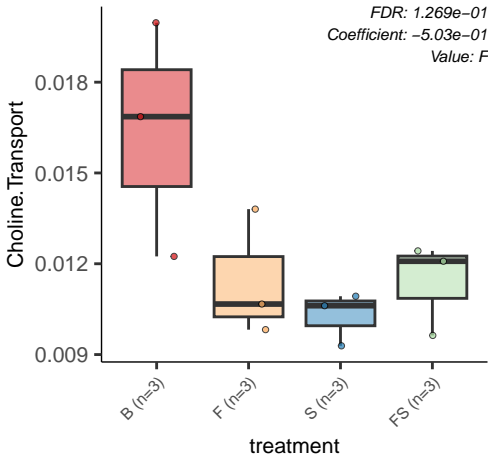
FDR: 1.253e-01
Coefficient: 7.20e-02
Value: S











At5g04520.AT1G06240

FDR: 1.272e-01
Coefficient: -1.09e-01
Value: F

0.084

0.080

0.076

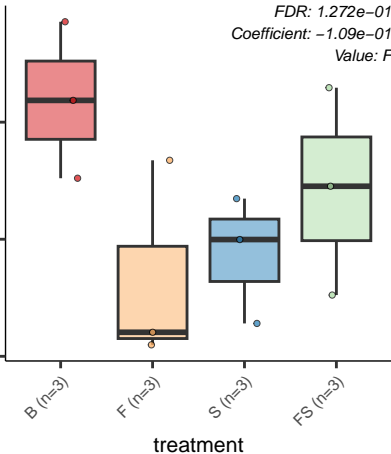
B (n=3)

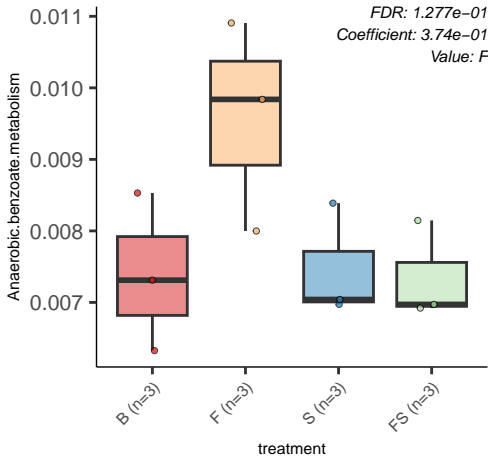
F (n=3)

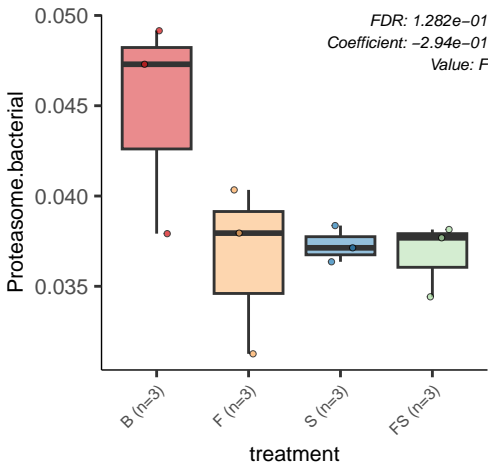
S (n=3)

FS (n=3)

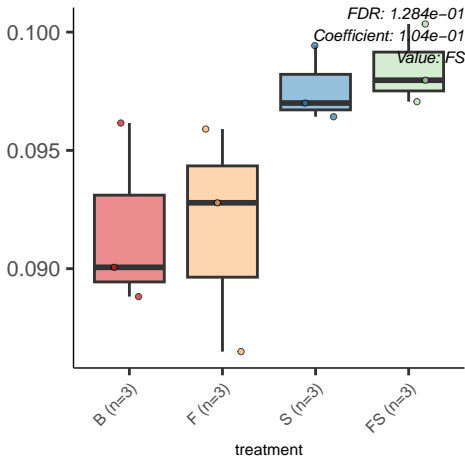
treatment



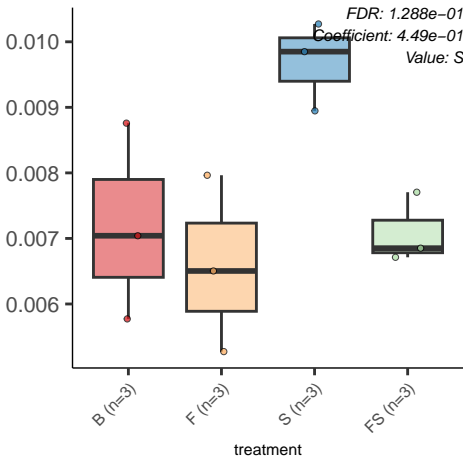




RuvABC.plus.a.hypothetical



ESAT.6.proteins.secretion.system.in.Firmicutes



Choline.and.Betaine.Uptake.and.Betaine.Biosynthesis

0.20
0.19
0.18
0.17
0.16

FDR: 1.292e-01
Coefficient: 1.50e-01
Value: FS

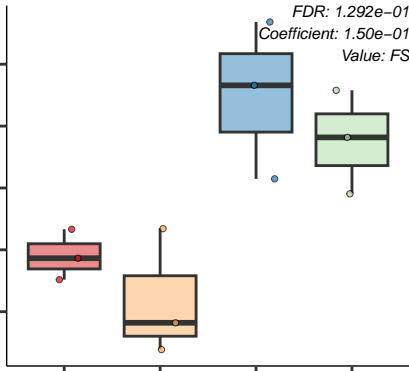
B (n=3)

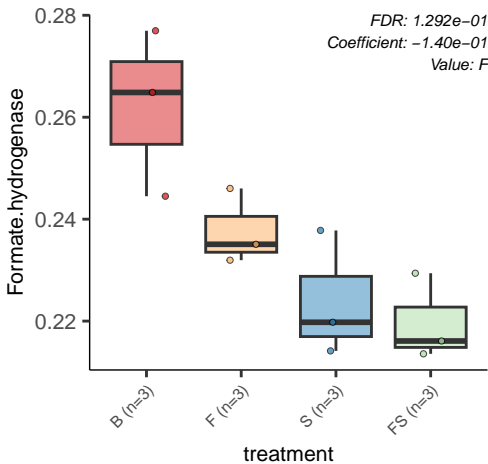
F (n=3)

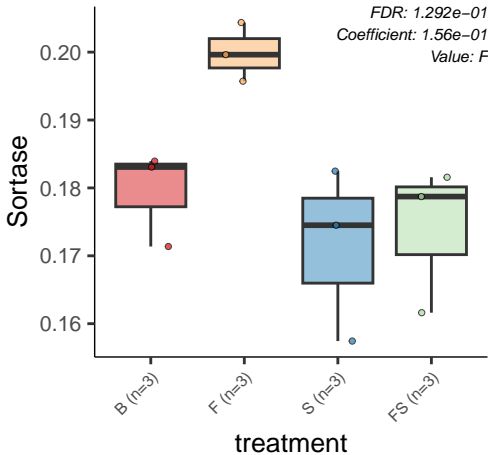
S (n=3)

FS (n=3)

treatment

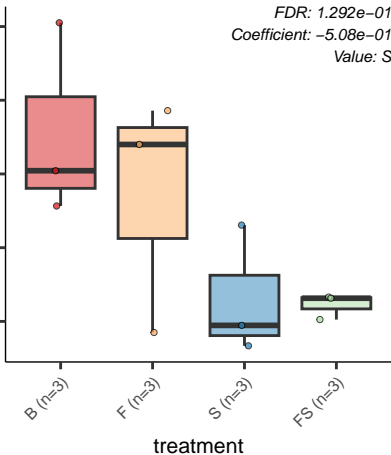






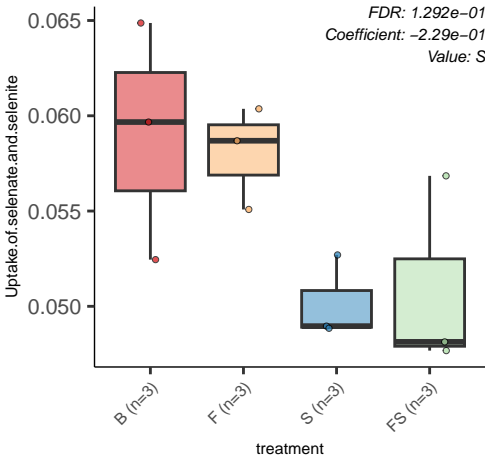
Transport.of.Molybdenum

FDR: 1.292e-01
Coefficient: -5.08e-01
Value: S



Uptake.of.selenate.and.selenite

FDR: 1.292e-01
Coefficient: -2.29e-01
Value: S



Menaquinone.Biosynthesis.via.Futalosine

0.011
0.010
0.009
0.008
0.007
0.006
0.005

B (n=3)

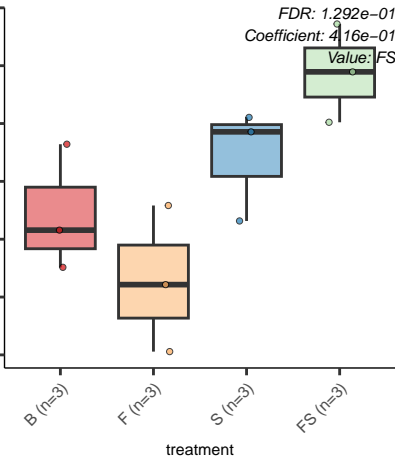
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 1.292e-01
Coefficient: 4.16e-01
Value: FS



CBSS.216592.1.peg.3534

FDR: 1.296e-01
Coefficient: -3.46e-01
Value: S

B (n=3)

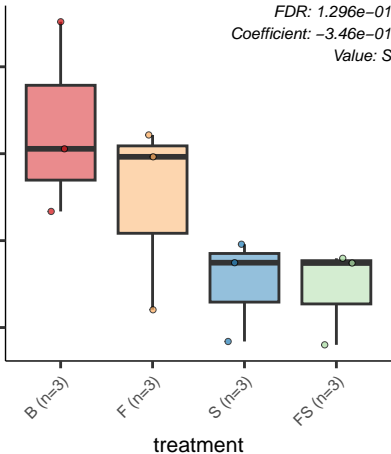
F (n=3)

S (n=3)

FS (n=3)

treatment

0.018
0.016
0.014
0.012



HPr.catabolite.repression.system

0.065
0.060
0.055
0.050
0.045

B (n=3)

F (n=3)

S (n=3)

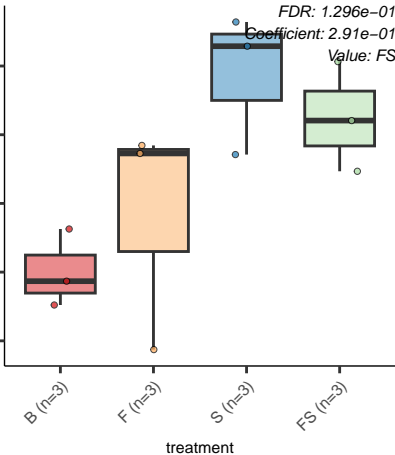
FS (n=3)

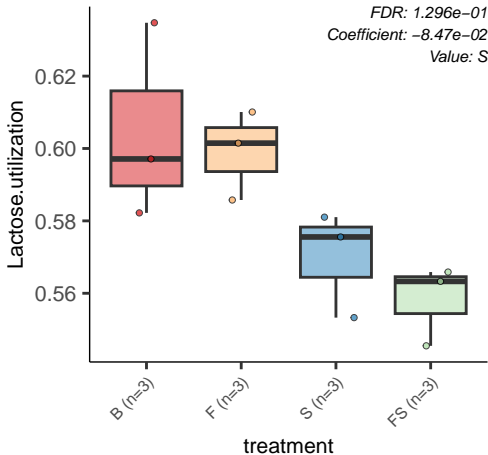
treatment

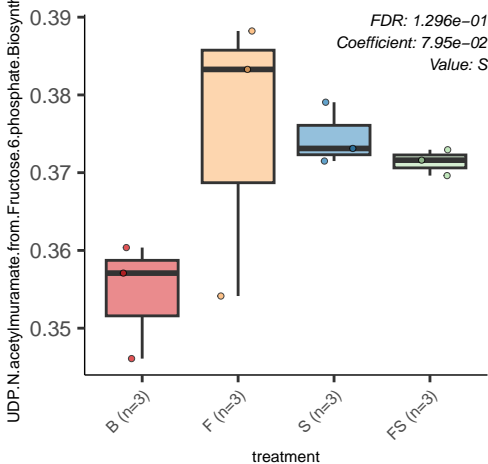
FDR: 1.296e-01

Coefficient: 2.91e-01

Value: FS







Diadenylate.cyclase.cluster

0.008
0.006
0.004

B (n=3)

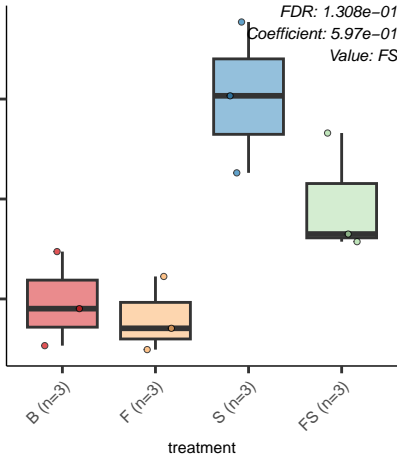
F (n=3)

S (n=3)

FS (n=3)

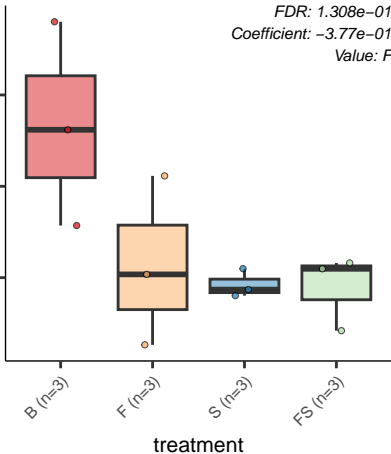
treatment

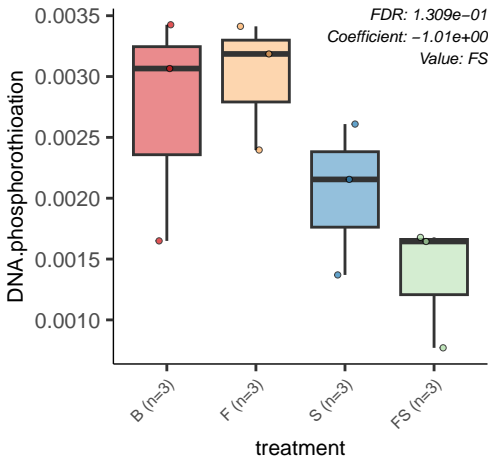
FDR: 1.308e-01
Coefficient: 5.97e-01
Value: FS

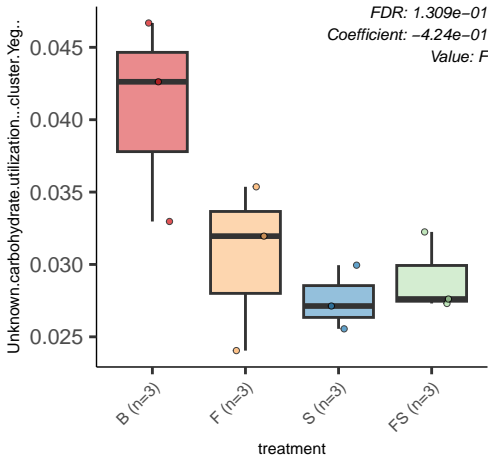


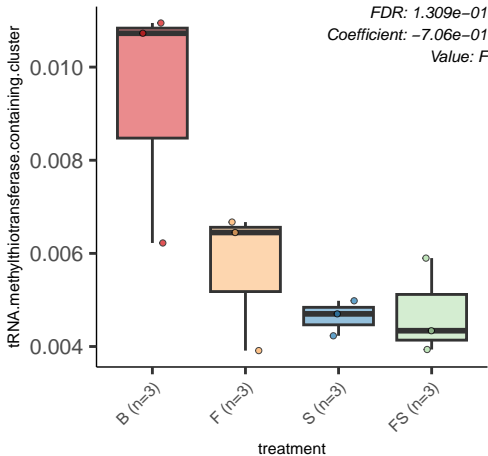
RpoS.Regulators.SG1

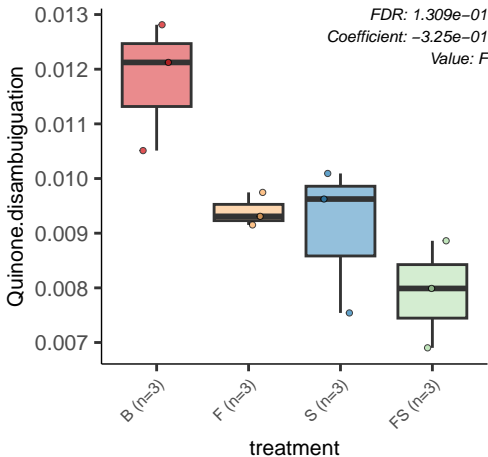
FDR: 1.308e-01
Coefficient: -3.77e-01
Value: F

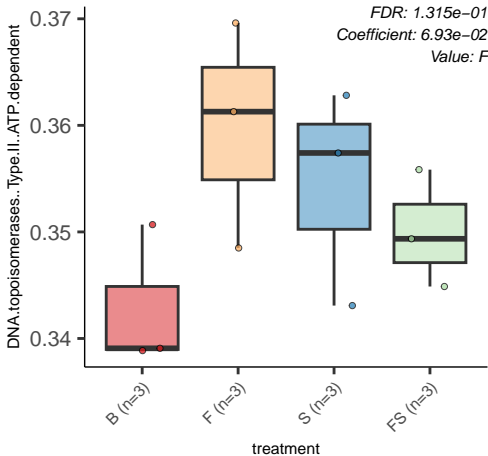












CBSS.203122.12.peg.188

B (n=3)

F (n=3)

S (n=3)

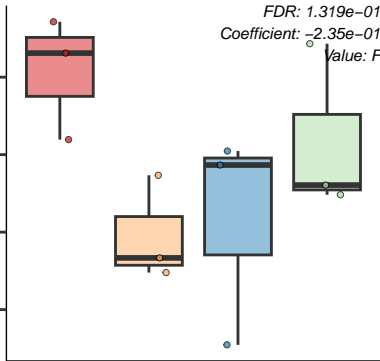
FS (n=3)

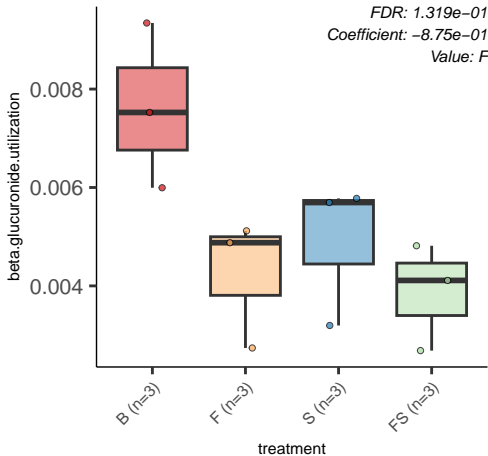
treatment

FDR: 1.319e-01

Coefficient: -2.35e-01

Value: F





Commensurate.regulon.activation

FDR: 1.322e-01
Coefficient: -1.07e+00
Value: FS

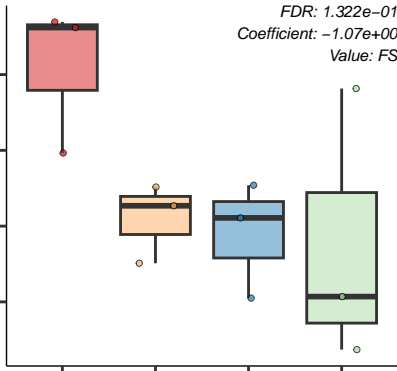
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Polysaccharide.deacetylases

0.06

0.05

B (n=3)

F (n=3)

S (n=3)

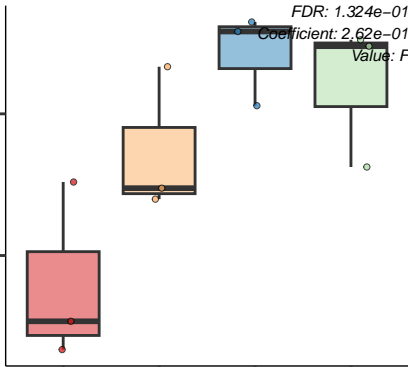
FS (n=3)

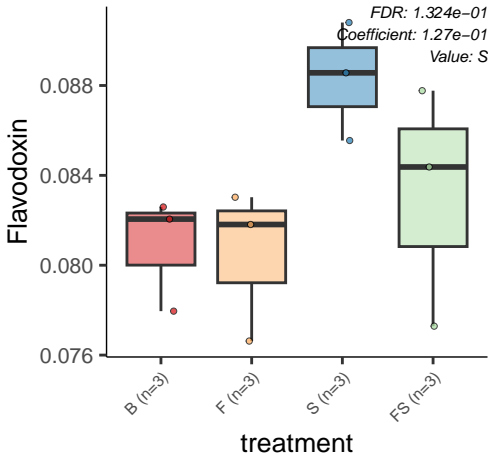
treatment

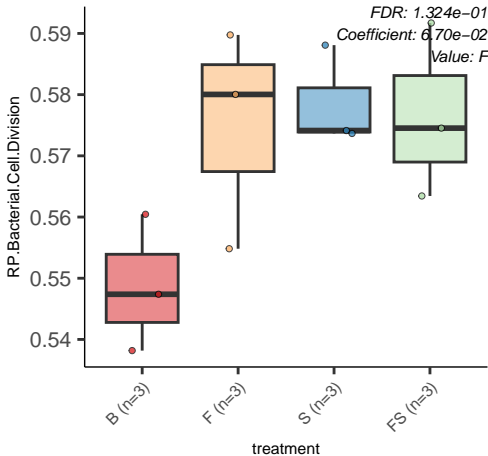
FDR: 1.324e-01

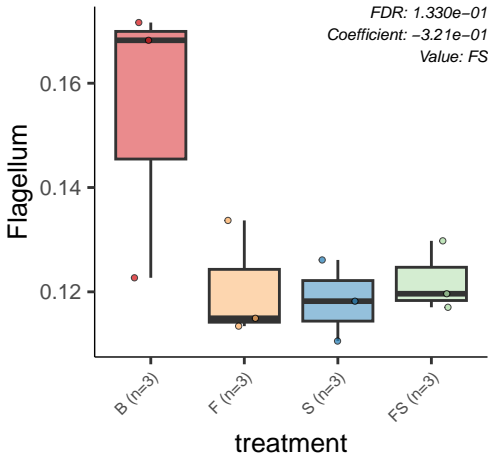
Coefficient: 2.62e-01

Value: F









Streptococcus.pyogenes.recombinatorial.zone

0.030
0.025
0.020
0.015

B (n=3)

F (n=3)

S (n=3)

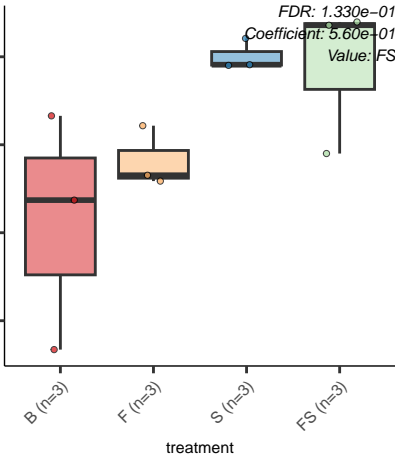
FS (n=3)

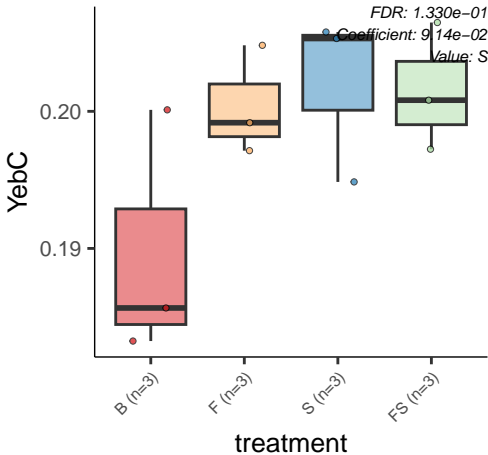
treatment

FDR: 1.330e-01

Coefficient: 5.60e-01

Value: FS





Copper.homeostasis..copper.tolerance

FDR: $1.330e-01$
Coefficient: $-1.64e-01$
Value: FS

0.050

0.045

0.040

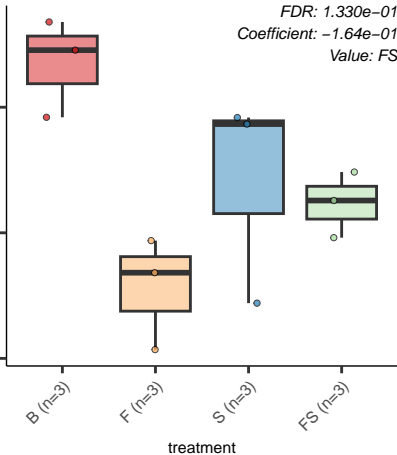
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Glutathionylspermidine.and.Tryptanothione

FDR: 1.330e-01
Coefficient: -5.13e-01
Value: F

0.024
0.020
0.016
0.012

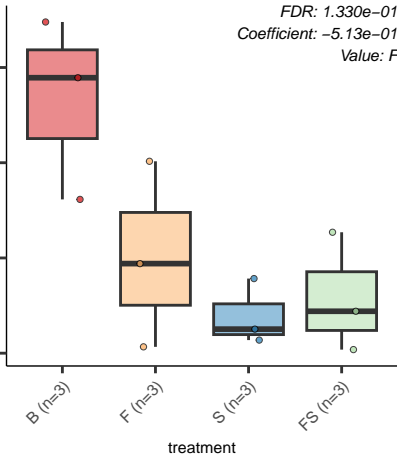
B (n=3)

F (n=3)

S (n=3)

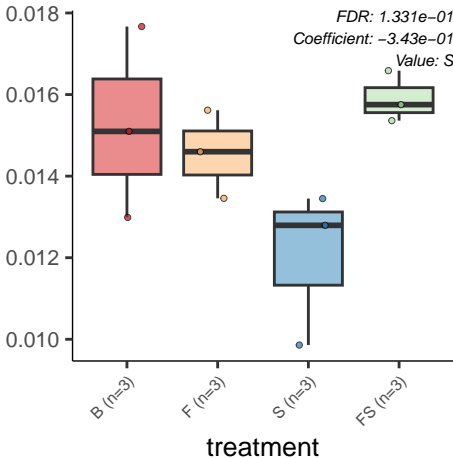
FS (n=3)

treatment



RecA.and.RecX

FDR: 1.331e-01
Coefficient: -3.43e-01
Value: S



Gram.Positive.Competence

0.06

0.04

0.02

B (n=3)

F (n=3)

S (n=3)

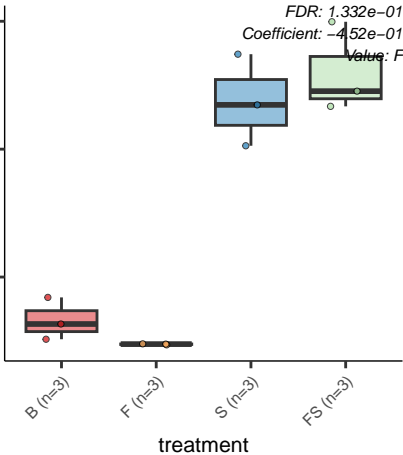
FS (n=3)

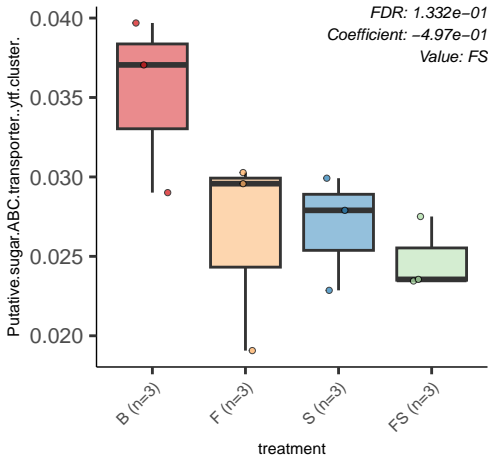
treatment

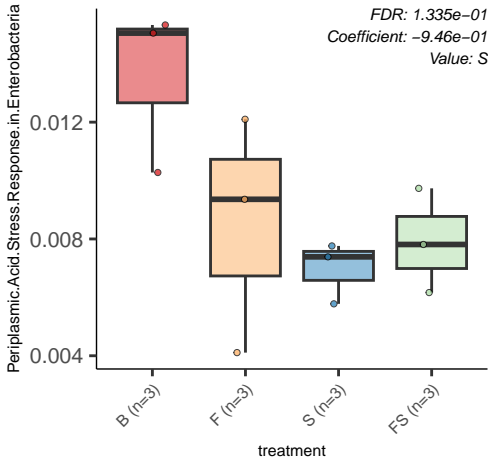
FDR: 1.332e-01

Coefficient: -4.52e-01

Value: F

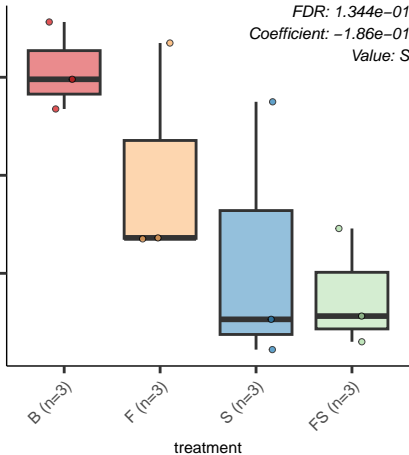


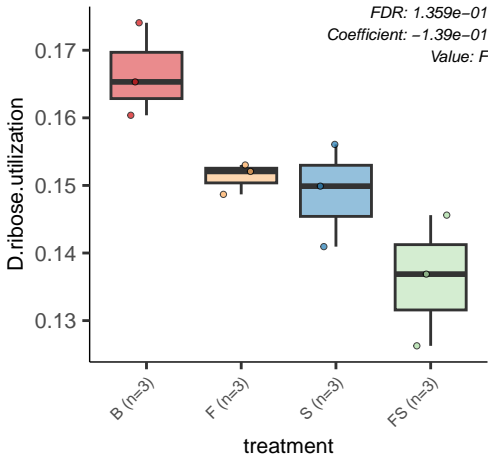


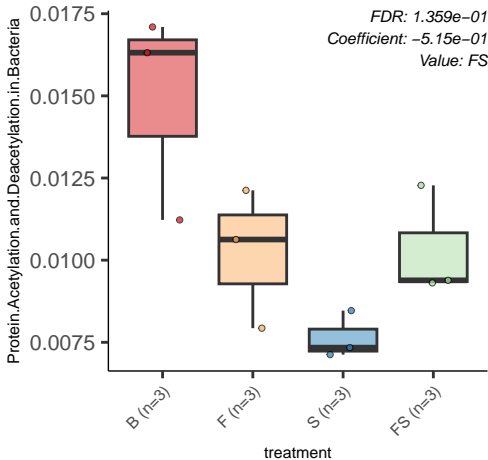


Proline..4.hydroxyproline.uptake.and.utilization

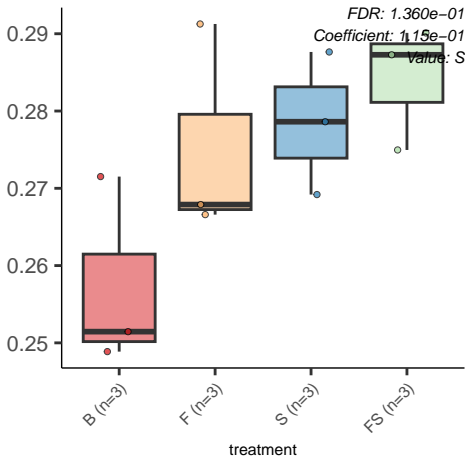
FDR: 1.344e-01
Coefficient: -1.86e-01
Value: S







Exopolysaccharide.Biosynthesis



Fructooligosaccharides.FOS..and.Raffinose.Utilization

FDR: 1.367e-01
Coefficient: 6.52e-02
Value: F

1.04
1.00
0.96

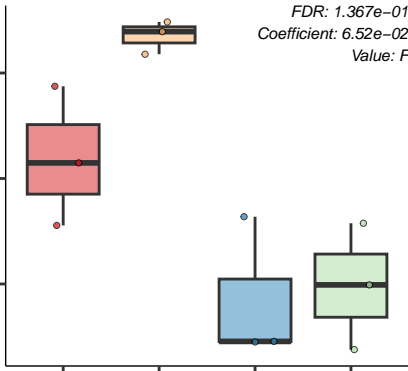
B (n=3)

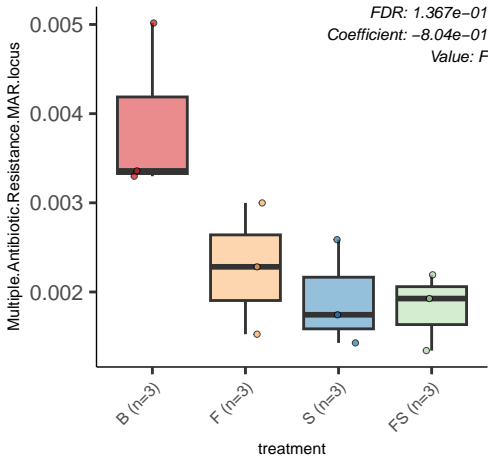
F (n=3)

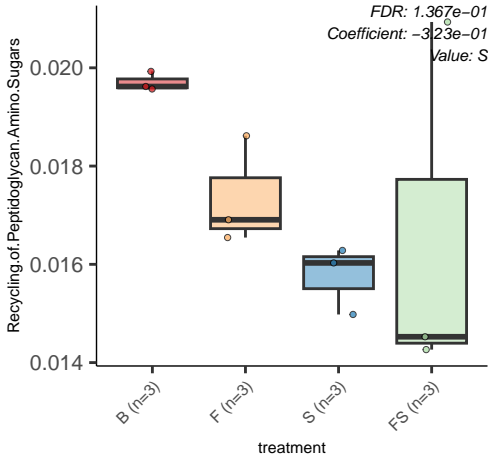
S (n=3)

FS (n=3)

treatment







Phosphorylcholine.incorporation.in.LPS

FDR: 1.367e-01
Coefficient: 3.50e-01
Value: FS

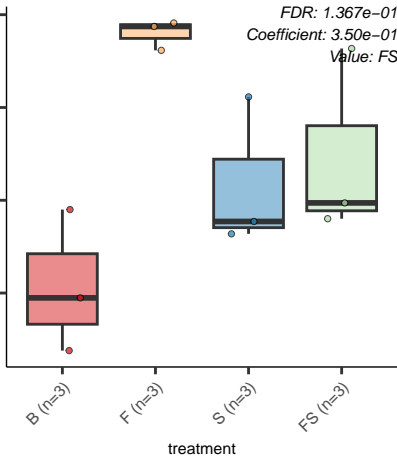
B (n=3)

F (n=3)

S (n=3)

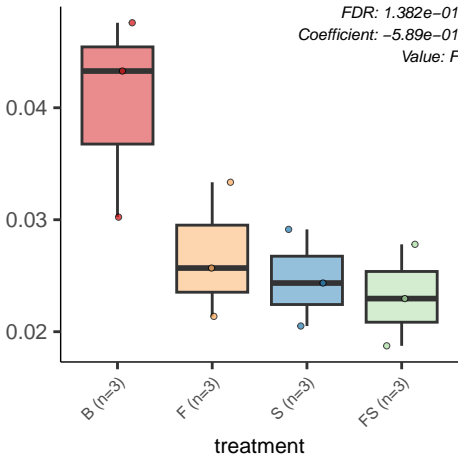
FS (n=3)

treatment



D.galactonate.catabolism

FDR: 1.382e-01
Coefficient: -5.89e-01
Value: F



FolateExerciseMaizeClassVDC

0.005

0.004

0.003

B (n=3)

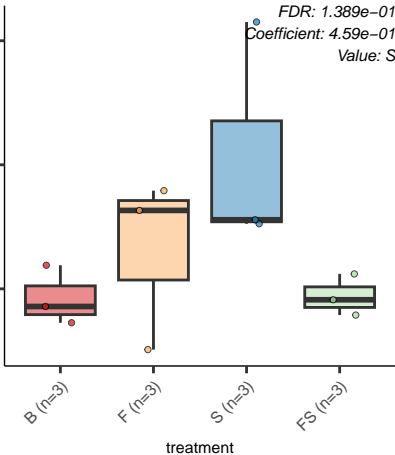
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 1.389e-01
Coefficient: 4.59e-01
Value: S



Methylthiotransferases

FDR: 1.402e-01
Coefficient: 1.54e-01
Value: F

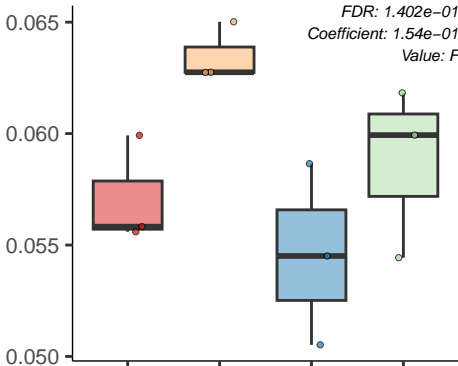
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Phage.capsid.proteins

0.013

0.011

0.009

0.007

B (n=3)

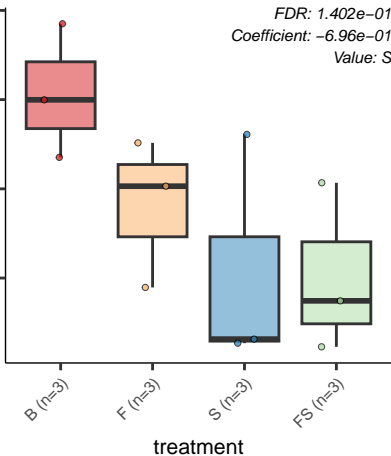
F (n=3)

S (n=3)

FS (n=3)

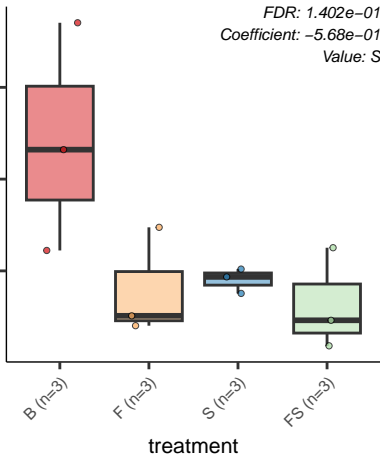
treatment

FDR: 1.402e-01
Coefficient: -6.96e-01
Value: S



P.uptake..cyanobacteria.

FDR: 1.402e-01
Coefficient: -5.68e-01
Value: S



Mycobacterium.jamboree

FDR: 1.409e-01
Coefficient: -8.00e-01
Value: F

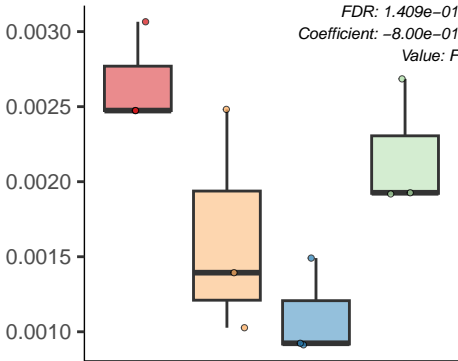
B (n=3)

F (n=3)

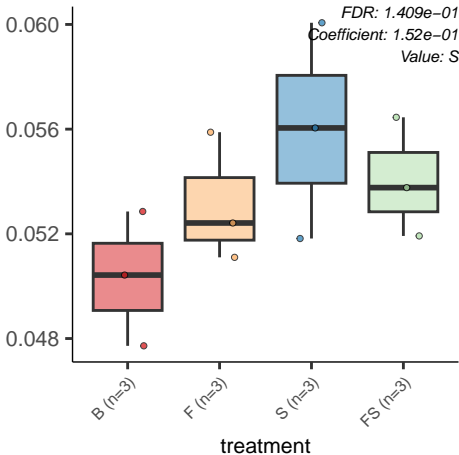
S (n=3)

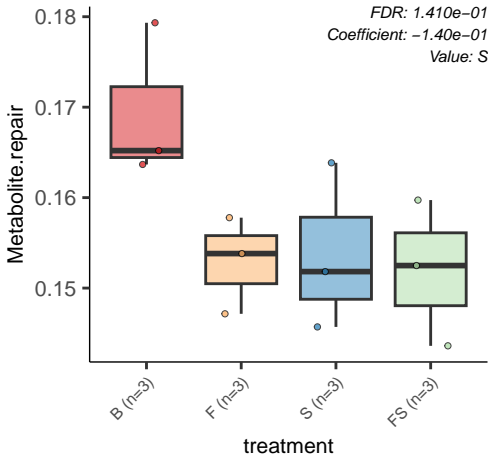
FS (n=3)

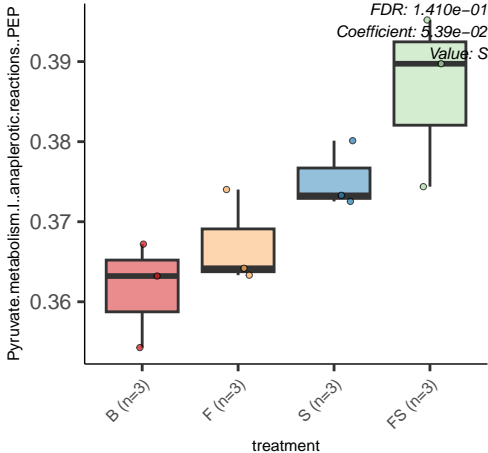
treatment



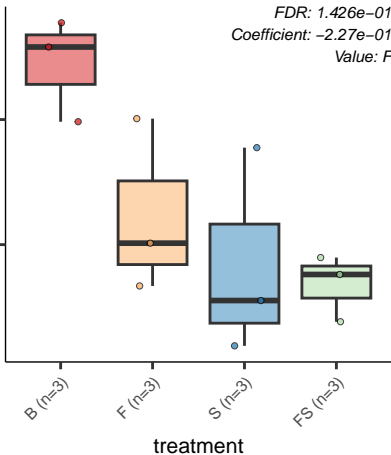
t6A.synthesis.in.bacteria

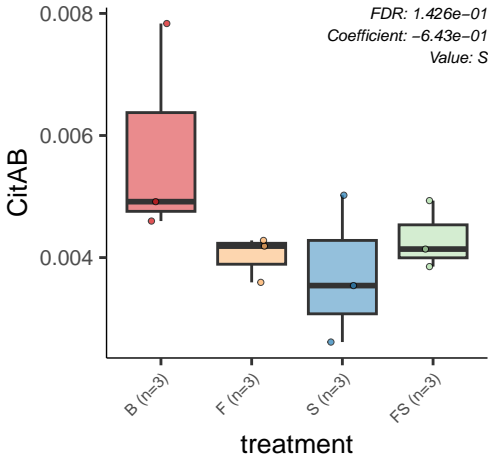


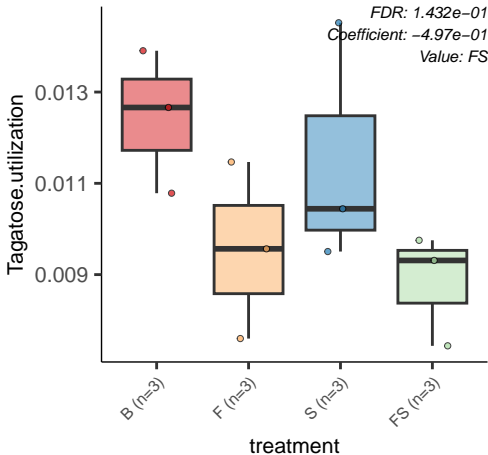




CBSS.342610.3.peg.1536







Translation.elongation.factors.bacterial

FDR: 1.435e-01
Coefficient: 9.92e-02
Value: FS

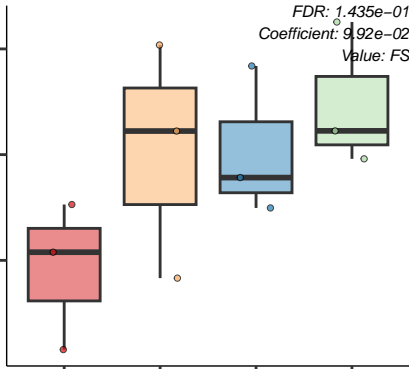
B (n=3)

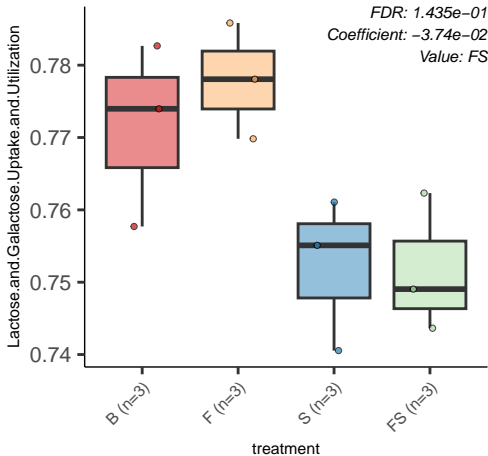
F (n=3)

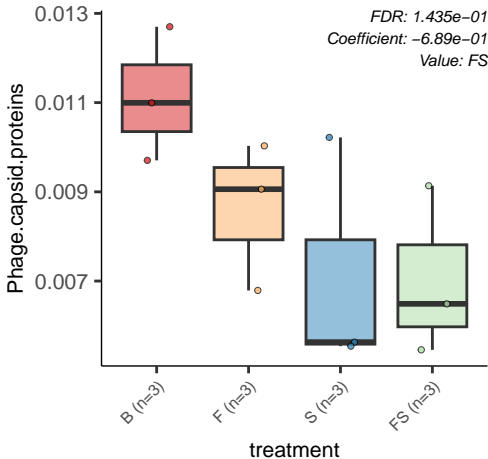
S (n=3)

FS (n=3)

treatment







Propionyl.CoA.to.Succinyl.CoA.Module

FDR: 1.435e-01
Coefficient: -2.38e-01
Value: S

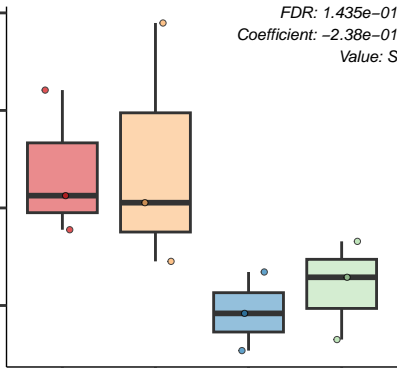
B (n=3)

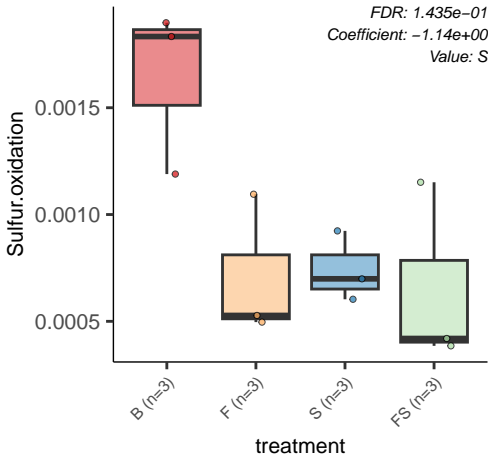
F (n=3)

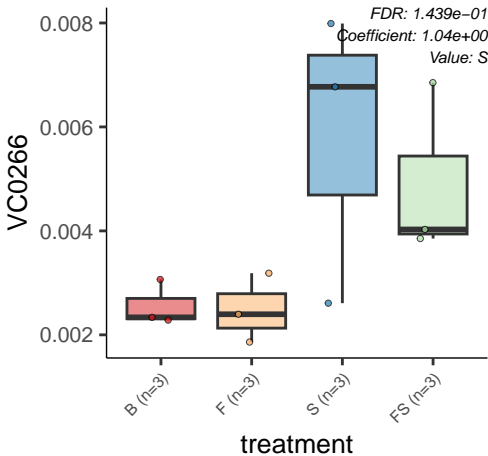
S (n=3)

FS (n=3)

treatment







Phage.packaging.machinery

FDR: 1.439e-01
Coefficient: -2.26e-01
Value: S

B (n=3)

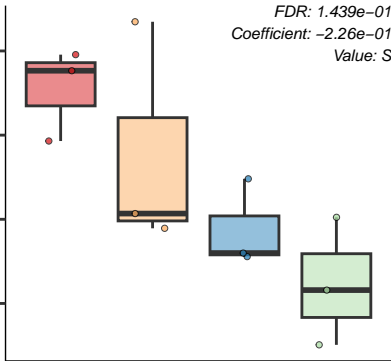
F (n=3)

S (n=3)

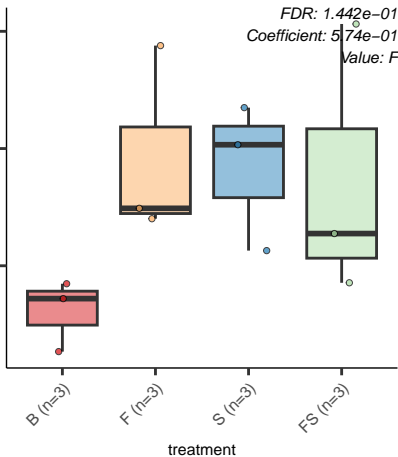
FS (n=3)

treatment

0.060
0.055
0.050
0.045

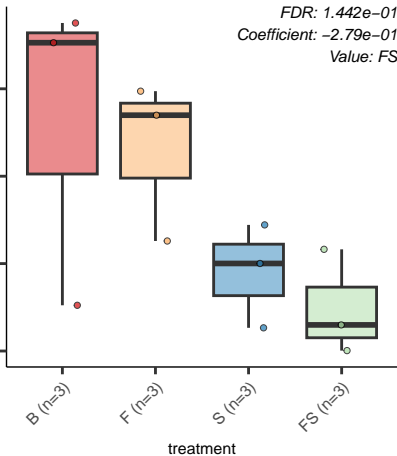


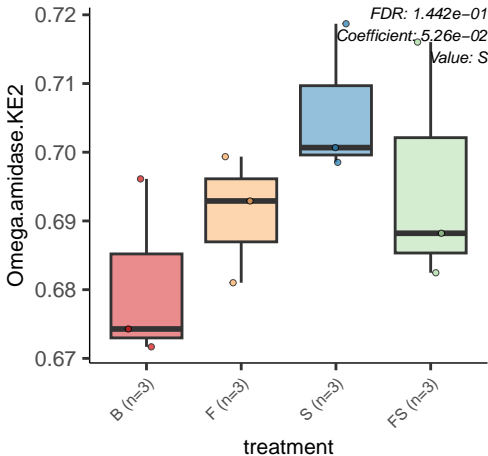
ABC.transporter.tungstate..TC.3.A.1.6.2.

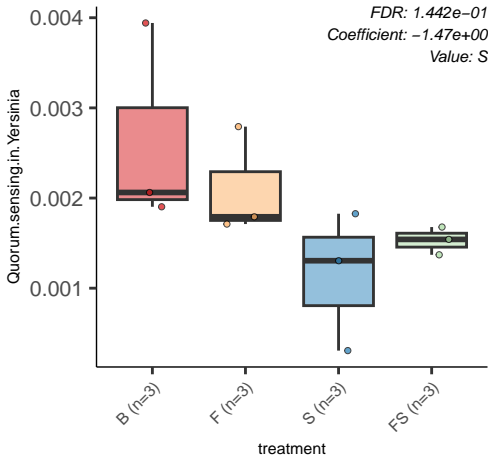


Homogenisate.pathway.of.aromatic.compound.degradation

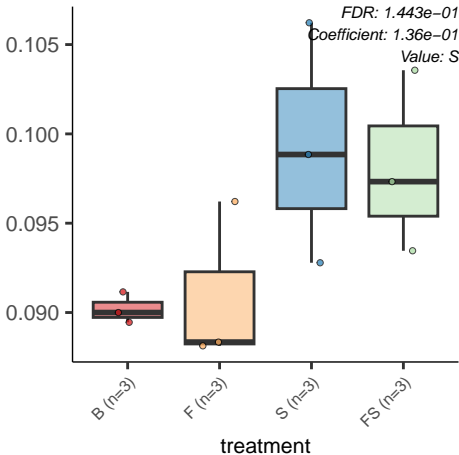
FDR: 1.442×10^{-1}
Coefficient: -2.79×10^{-1}
Value: FS





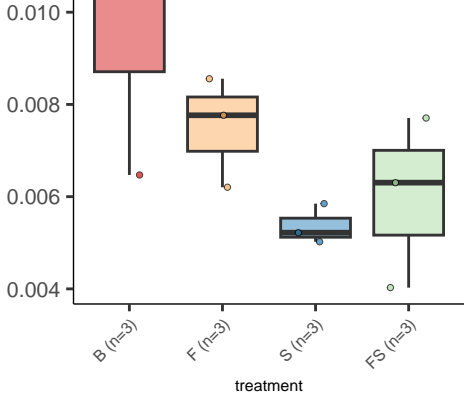


Alanine.biosynthesis



Osmoprotectant.ABC.transporter.YehZYXW.of.Enterobacter

FDR: 1.444e-01
Coefficient: -6.70e-01
Value: FS



Osmoregulation

FDR: 1.444e-01
Coefficient: -1.39e-01
Value: F

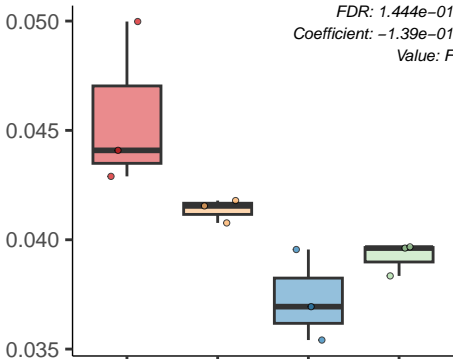
B (n=3)

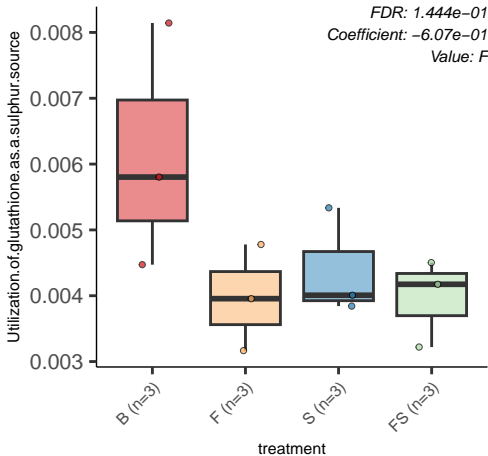
F (n=3)

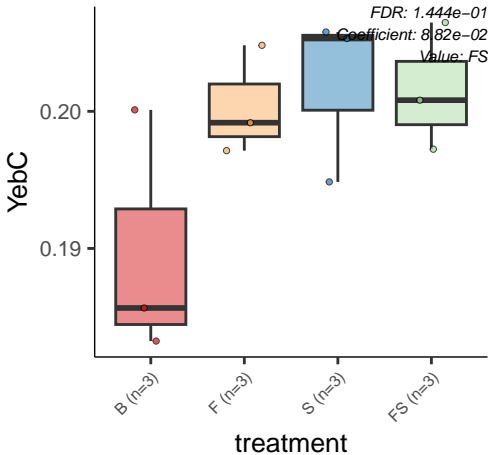
S (n=3)

FS (n=3)

treatment







Calvin.Benson.cycle

0.20

0.19

0.18

B (n=3)

F (n=3)

S (n=3)

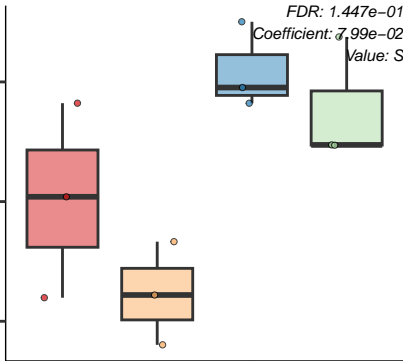
FS (n=3)

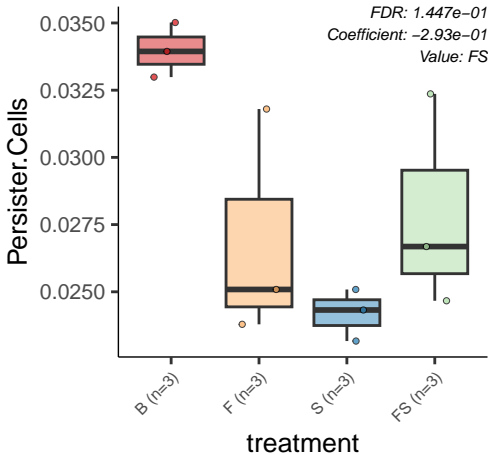
treatment

FDR: 1.447e-01

Coefficient: 7.99e-02

Value: S





Colanic.acid.biosynthesis

FDR: 1.447e-01
Coefficient: -2.33e-01
Value: F

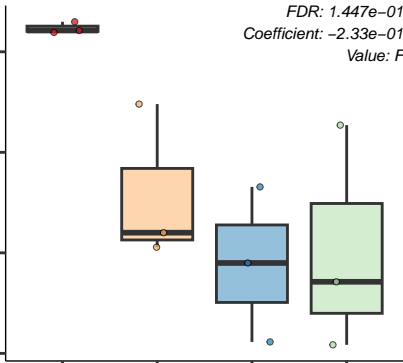
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Test...Thiamin

FDR: 1.447e-01
Coefficient: 6.46e-02
Value: F

0.30
0.29
0.28
0.27

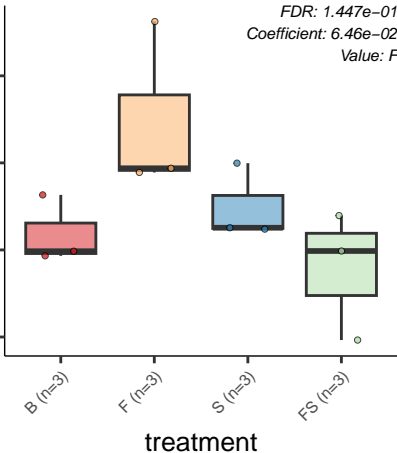
B (n=3)

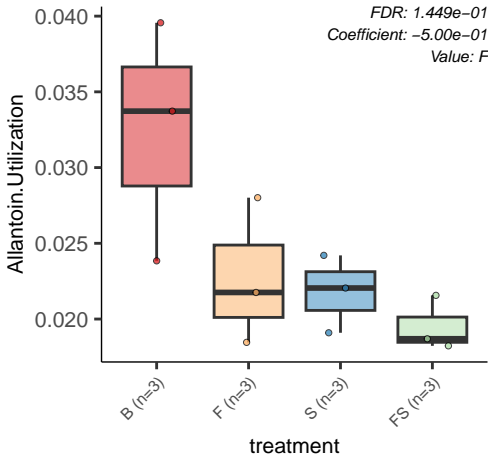
F (n=3)

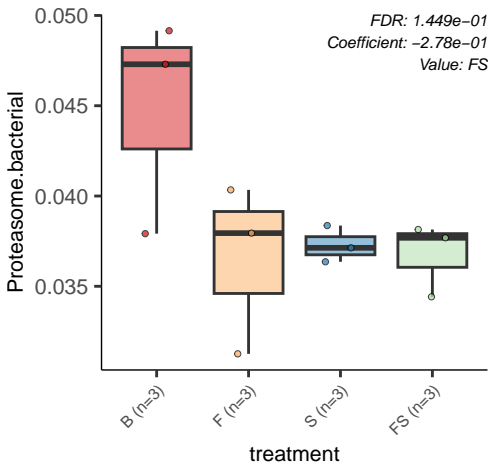
S (n=3)

FS (n=3)

treatment







Creatine.and.Creatinine.Degradation

FDR: 1.450e-01
Coefficient: -4.27e-01
Value: S

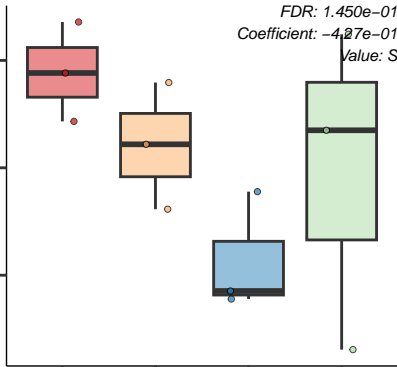
B (n=3)

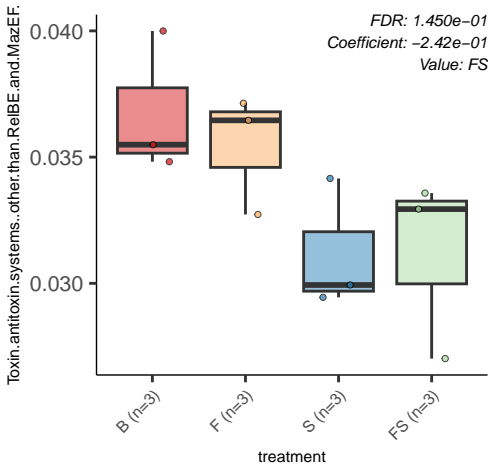
F (n=3)

S (n=3)

FS (n=3)

treatment





Nitric.oxide.synthase

0.003

0.002

0.001

B (n=3)

F (n=3)

S (n=3)

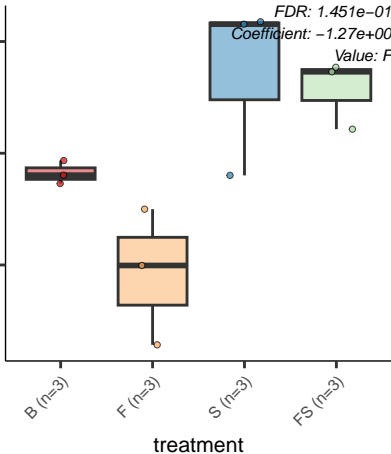
FS (n=3)

treatment

FDR: 1.451e-01

Coefficient: -1.27e+00

Value: F



Serine.Biosynthesis

FDR: 1.451e-01

Coefficient: 1.19e-01

Value: F

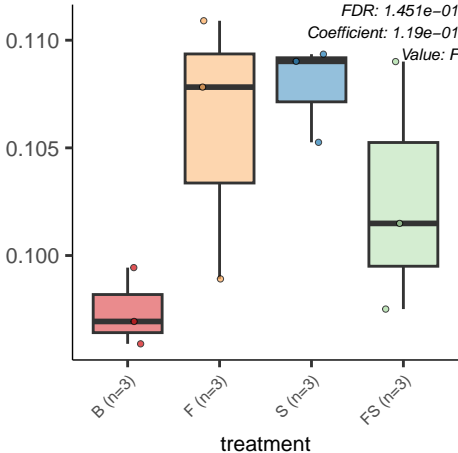
B (n=3)

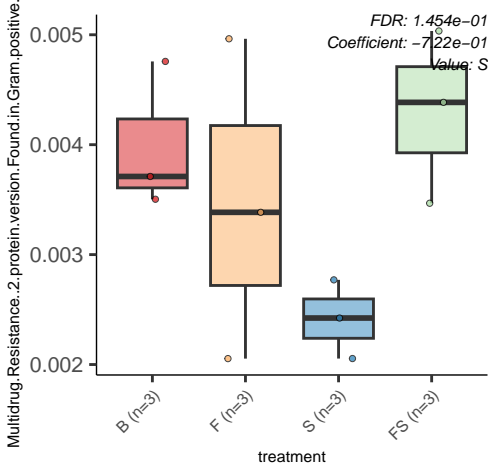
F (n=3)

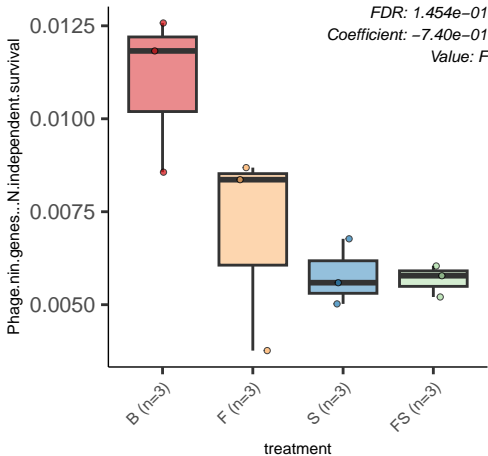
S (n=3)

FS (n=3)

treatment

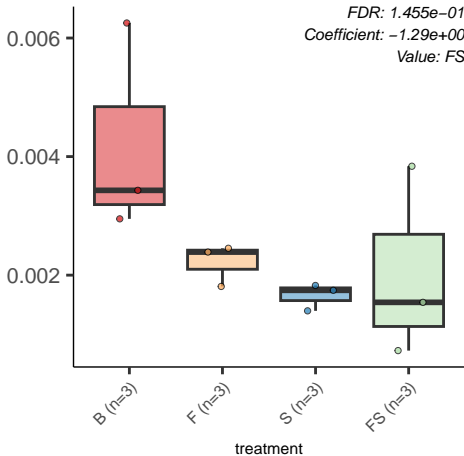






lutathione.dependent.Thiol.Reductase.Associated.with.a.Step.in.Lys

FDR: $1.455e-01$
Coefficient: $-1.29e+00$
Value: FS



MethanopterinAromatic

FDR: 1.455e-01
Coefficient: -4.96e-01
Value: F

0.0025

0.0020

0.0015

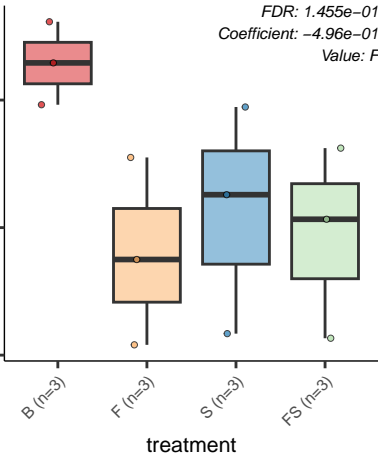
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Proteorhodopsin

B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment

0.00200

0.00175

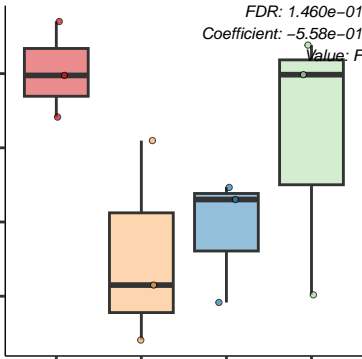
0.00150

0.00125

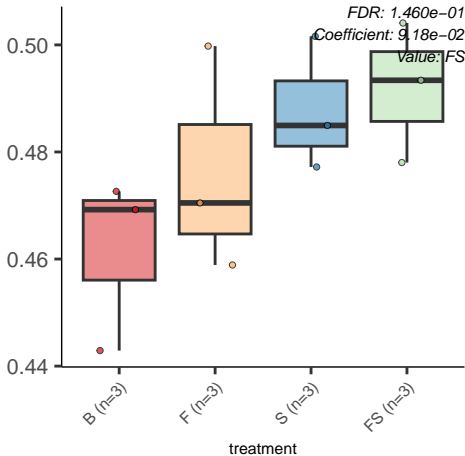
FDR: 1.460e-01

Coefficient: -5.58e-01

Value: F



Riboflavin...FMN.and.FAD.metabolism.Extended



Unsaturated.Fatty.Acid.Metabolism

0.018
0.015
0.012
0.009
0.006

FDR: 1.460e-01
Coefficient: -5.68e-01
Value: F

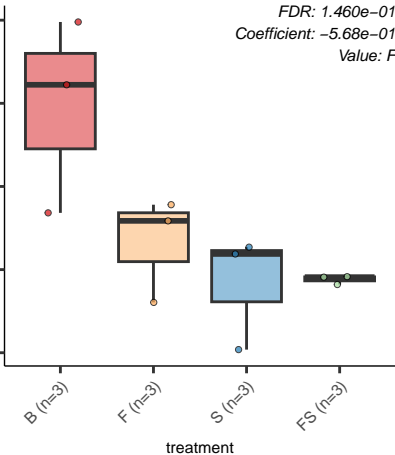
B (n=3)

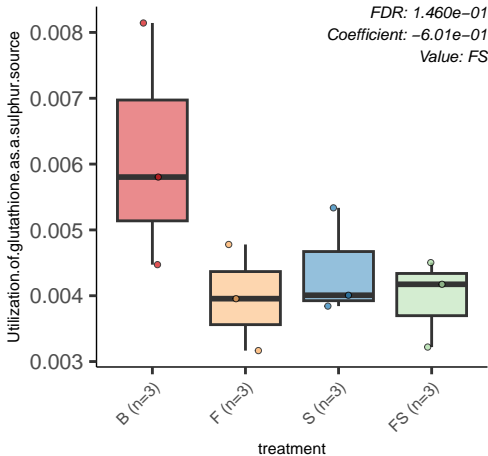
F (n=3)

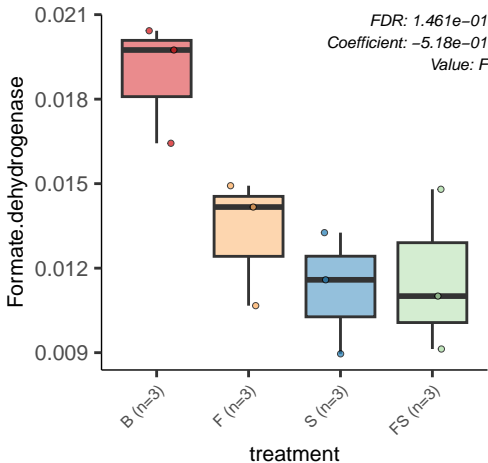
S (n=3)

FS (n=3)

treatment







CBSS.318161.14.peg.2599

FDR: 1.465e-01
Coefficient: -9.51e-01
Value: FS

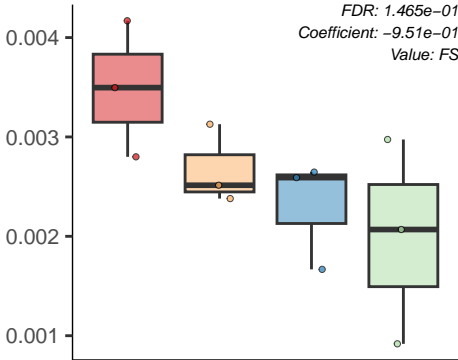
B (n=3)

F (n=3)

S (n=3)

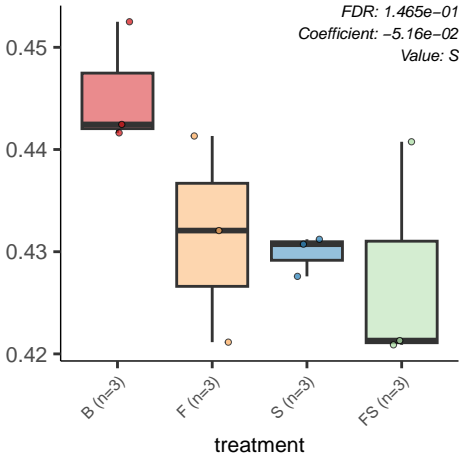
FS (n=3)

treatment



Polyamine.Metabolism

FDR: 1.465e-01
Coefficient: -5.16e-02
Value: S



lbrA.and.lbrB..co.actors.of.prophage.gene.expression

FDR: 1.469e-01
Coefficient: -2.98e-01
Value: FS

0.050
0.045
0.040
0.035

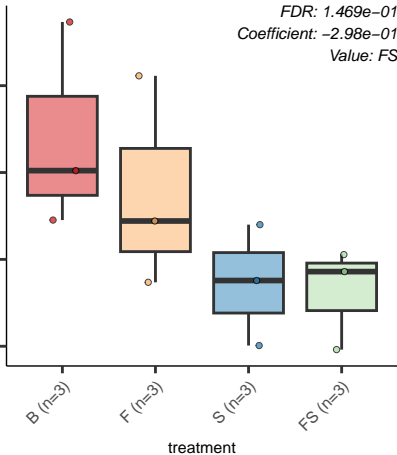
B (n=3)

F (n=3)

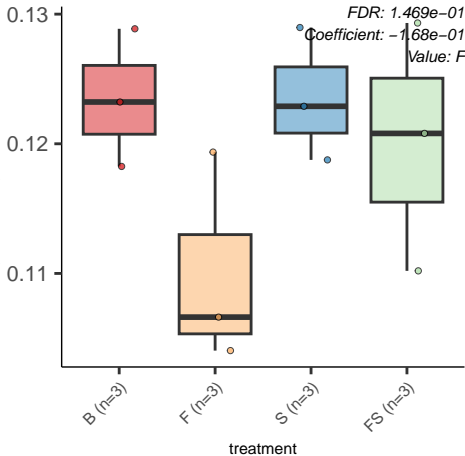
S (n=3)

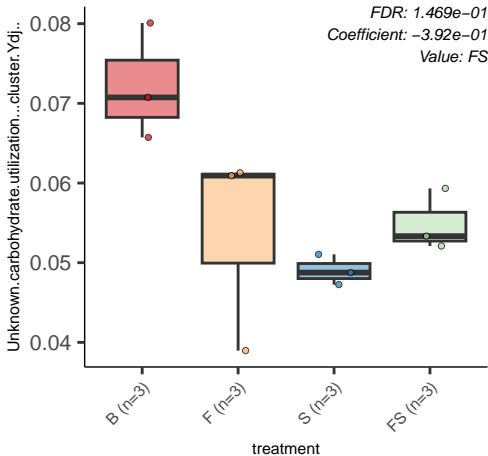
FS (n=3)

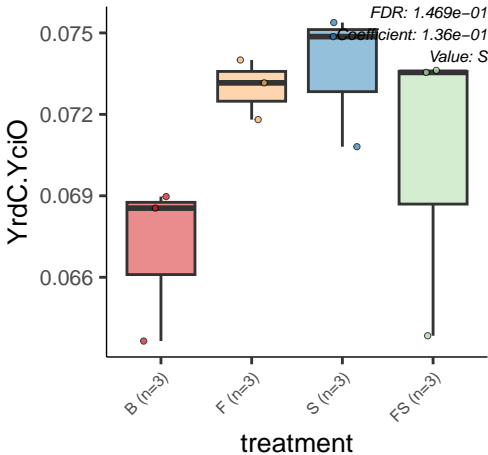
treatment



Recycling.of.Peptidoglycan.Amino.Acids







ABC.transporter.branched.chain.amino.acid..TC.3.A.1.4.

FDR: $1.471e-01$
Coefficient: $1.26e-01$
Value: FS

0.27
0.26
0.25
0.24
0.23

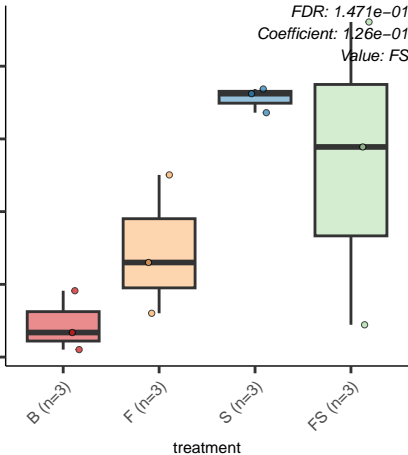
B (n=3)

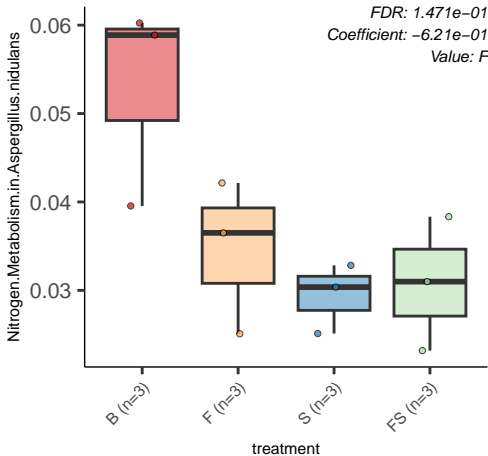
F (n=3)

S (n=3)

FS (n=3)

treatment





Translation.termination.factors.bacterial

FDR: $1.471e-01$
Coefficient: $6.23e-02$
Value: S

0.34

0.33

0.32

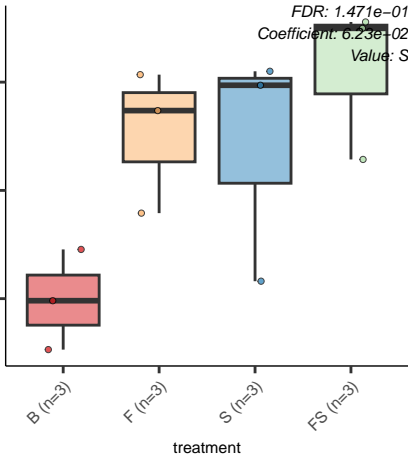
B (n=3)

F (n=3)

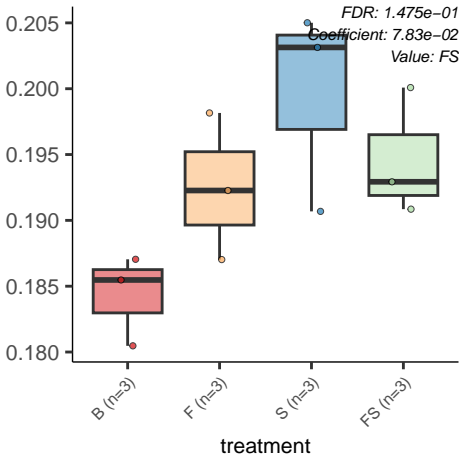
S (n=3)

FS (n=3)

treatment

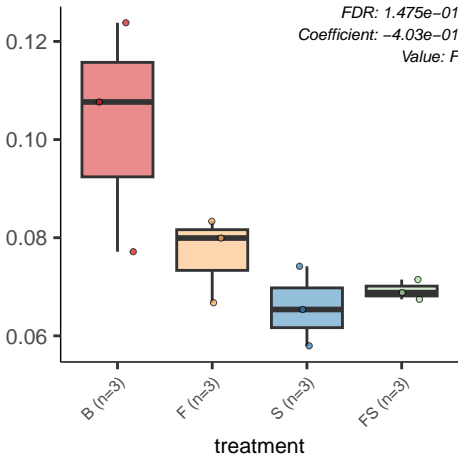


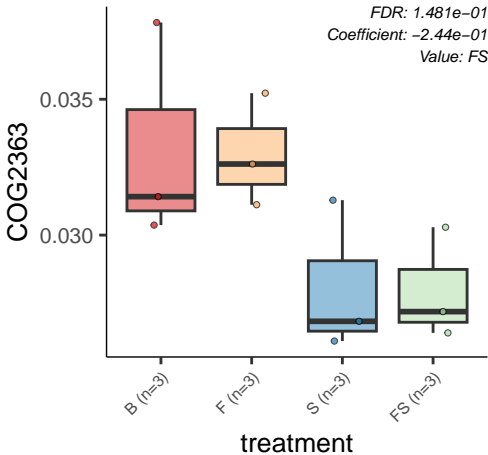
Test.Pyridoxin.B6



Type.VI.secretion.systems

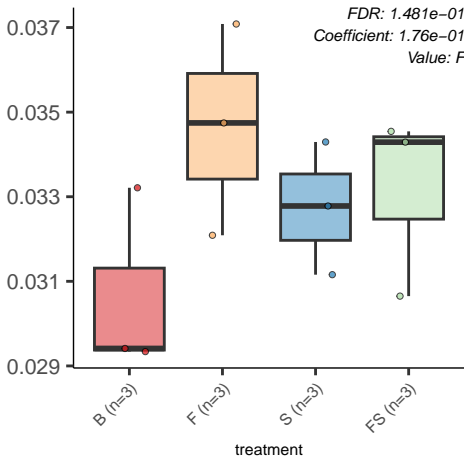
FDR: 1.475e-01
Coefficient: -4.03e-01
Value: F





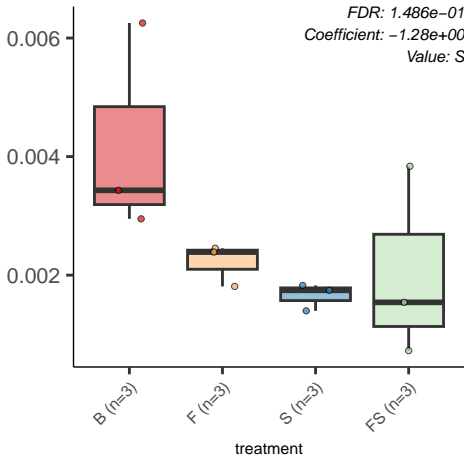
cobacterium.virulence.operon.involved.in.protein.synthesis..LSU.rib

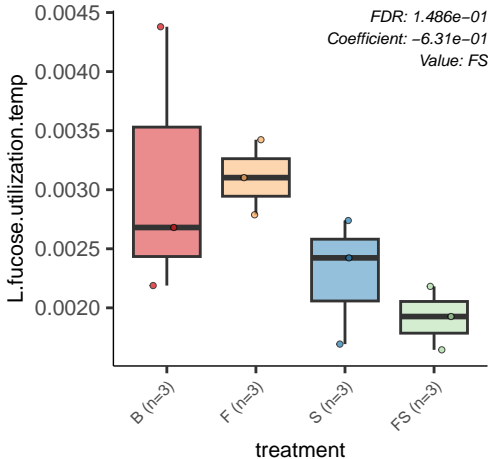
FDR: 1.481e-01
Coefficient: 1.76e-01
Value: F



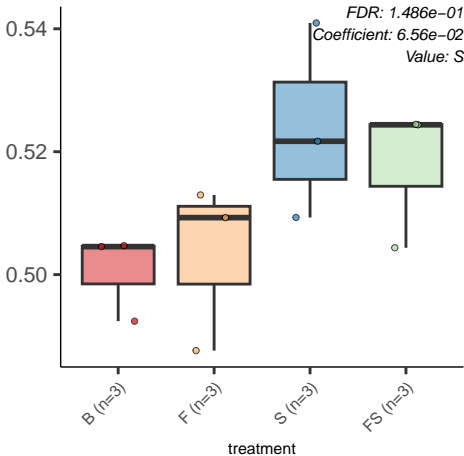
lutathione-dependent. Thiol.Reductase. Associated. with. a. Step. in. Lys

FDR: $1.486e-01$
Coefficient: $-1.28e+00$
Value: S





Proteolysis.in.bacteria..ATP.dependent



Quinate.degradation

FDR: 1.486e-01
Coefficient: 2.41e-01
Value: FS

B (n=3)

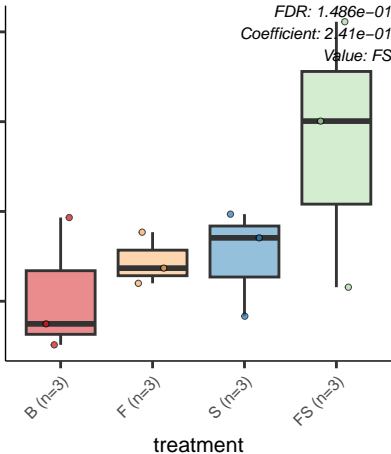
F (n=3)

S (n=3)

FS (n=3)

treatment

0.024
0.022
0.020
0.018



Test...DHFR

FDR: 1.486e-01
Coefficient: 9.29e-02
Value: FS

0.30
0.29
0.28
0.27
0.26

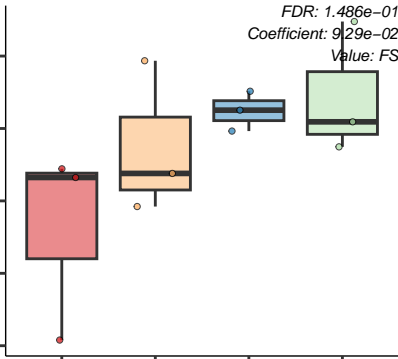
B (n=3)

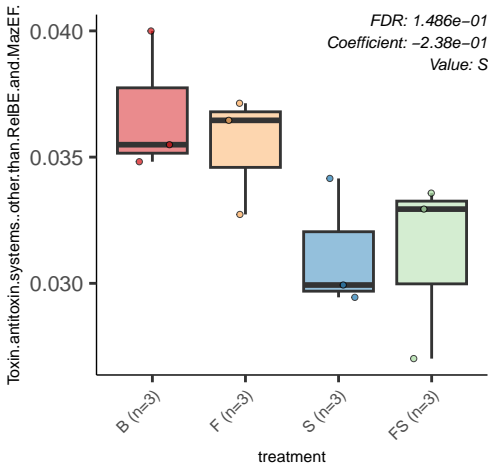
F (n=3)

S (n=3)

FS (n=3)

treatment





Legionaminic Acid Biosynthesis

0.0400
0.0375
0.0350
0.0325

B (n=3)

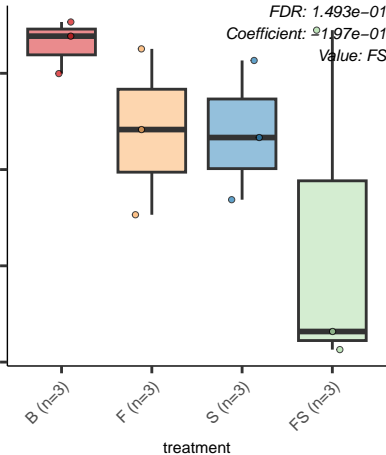
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 1.493e-01
Coefficient: 1.97e-01
Value: FS



Queuosine.Archaeosine.Biosynthesis

FDR: 1.498e-01
Coefficient: -8.90e-02
Value: F

0.180
0.175
0.170
0.165
0.160

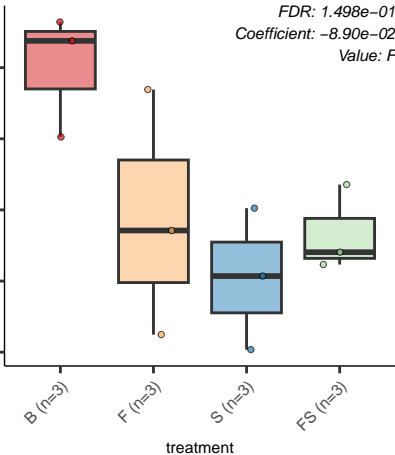
B (n=3)

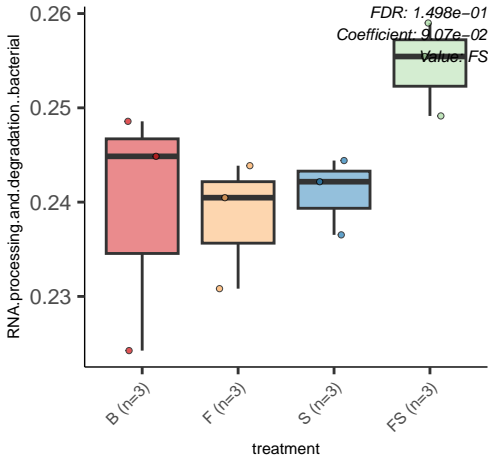
F (n=3)

S (n=3)

FS (n=3)

treatment





Bacterial.Chemotaxis

FDR: $1.498e-01$
Coefficient: $-1.54e-01$
Value: S

0.16
0.15
0.14

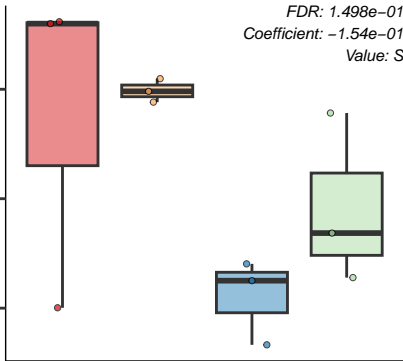
B (n=3)

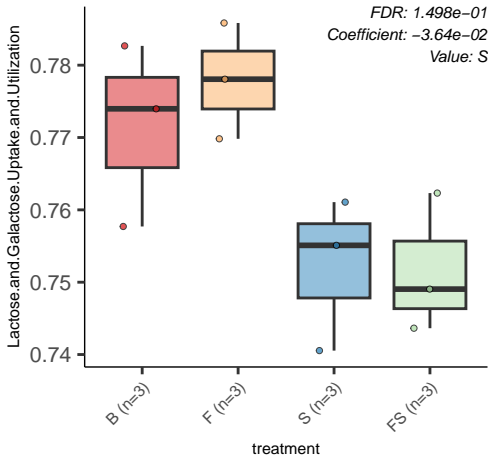
F (n=3)

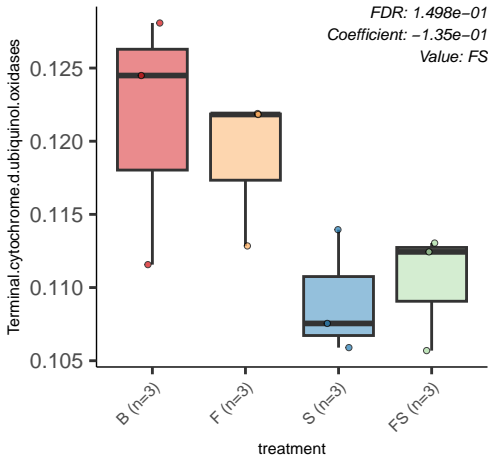
S (n=3)

FS (n=3)

treatment







Transport.of.Manganese

0.070
0.065
0.060
0.055
0.050
0.045

B (n=3)

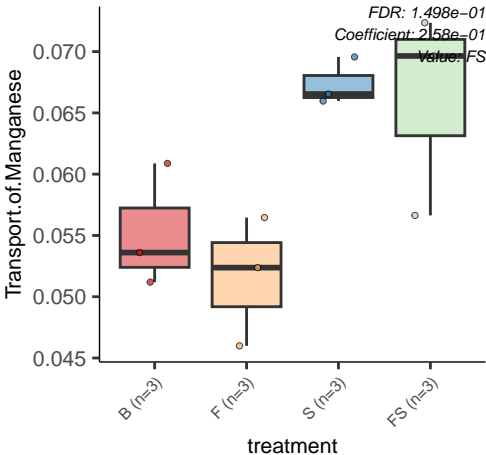
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 1.498e-01
Coefficient: 2.158e-01
Value: FS



Translation.elongation.factor.G.family

FDR: 1.501e-01
Coefficient: 1.10e-01
Value: F

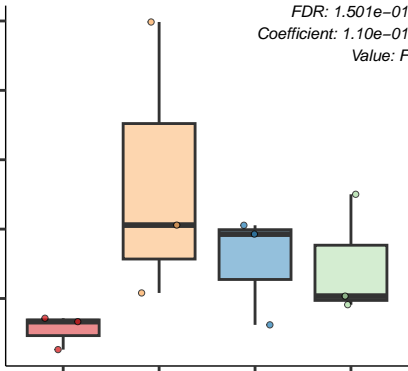
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Uptake.of.selenate.and.selenite

FDR: 1.501e-01
Coefficient: -2.13e-01
Value: FS

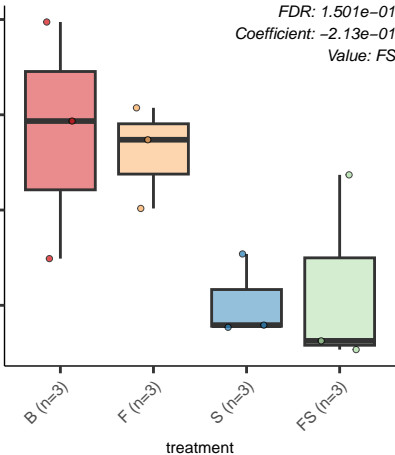
B (n=3)

F (n=3)

S (n=3)

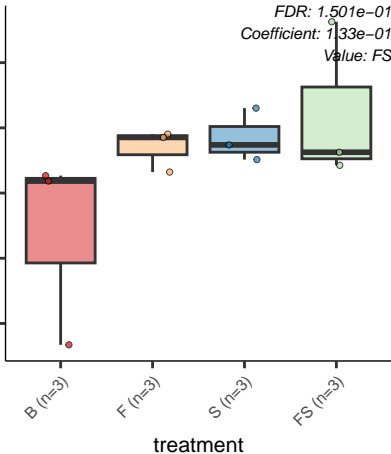
FS (n=3)

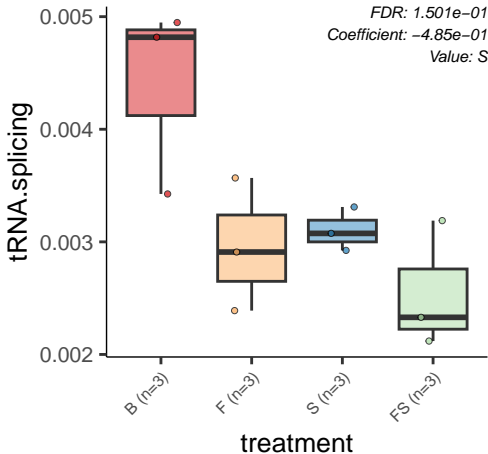
treatment



tRNA.aminoacylation..Tyr

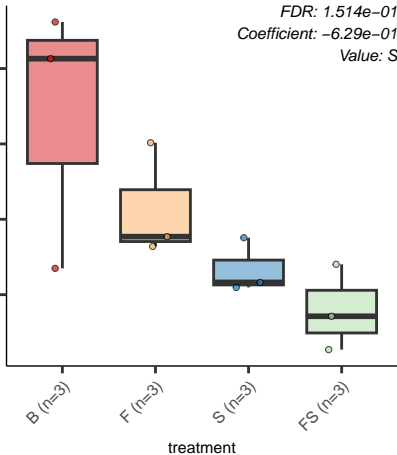
FDR: 1.501e-01
Coefficient: 1.33e-01
Value: FS





Molybdopterin.cytosine.dinucleotide

FDR: 1.514e-01
Coefficient: -6.29e-01
Value: S



A.toxin.antitoxin.module.cotranscribed.with.DinB

FDR: $1.522e-01$
Coefficient: $-1.39e+00$
Value: FS

0.004
0.003
0.002
0.001

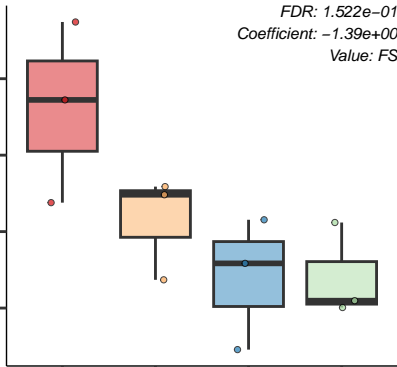
B (n=3)

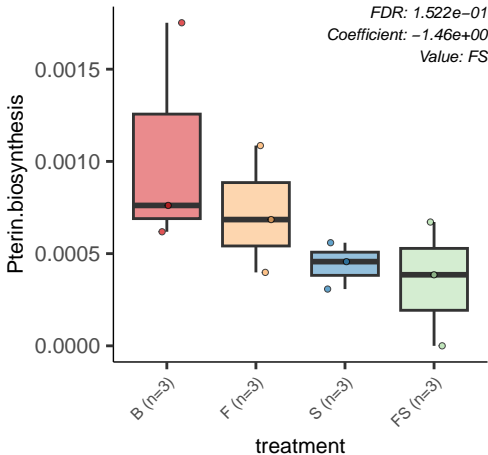
F (n=3)

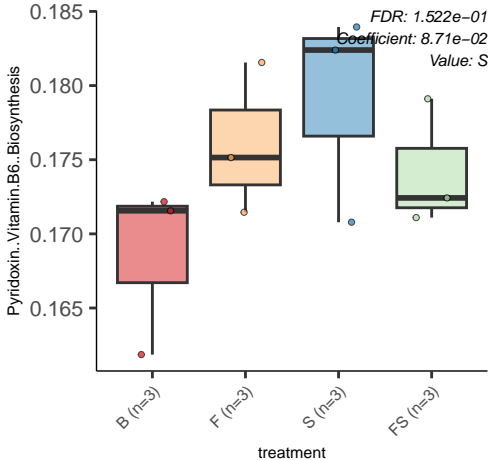
S (n=3)

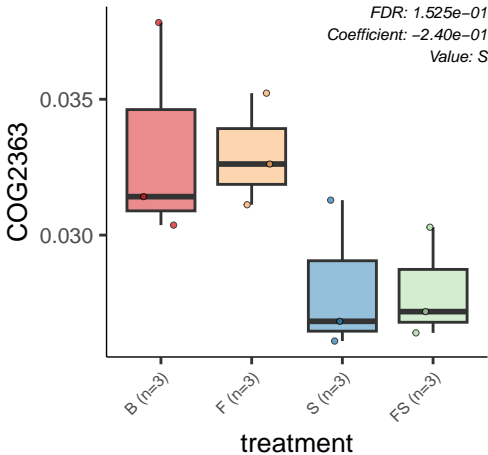
FS (n=3)

treatment



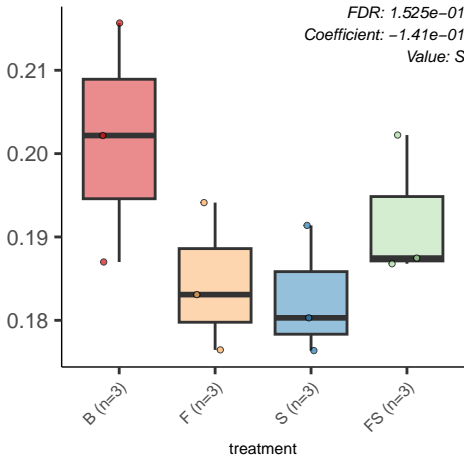






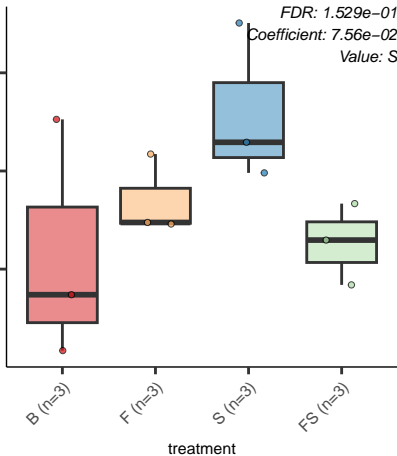
Glycerol.and.Glycerol.3.phosphate.Uptake.and.Utilization

FDR: 1.525e-01
Coefficient: -1.41e-01
Value: S



Translation.initiation.factors.bacterial

FDR: 1.529e-01
Coefficient: 7.56e-02
Value: S



Fructose.and.Mannose.Inducible.PTS

FDR: 1.534e-01
Coefficient: 2.02e-01
Value: F

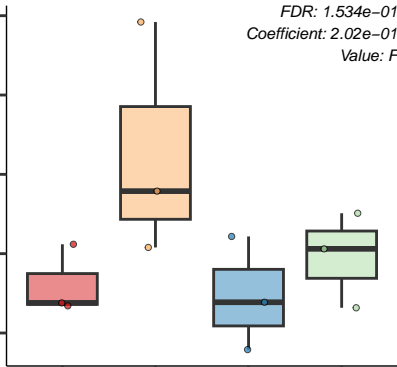
B (n=3)

F (n=3)

S (n=3)

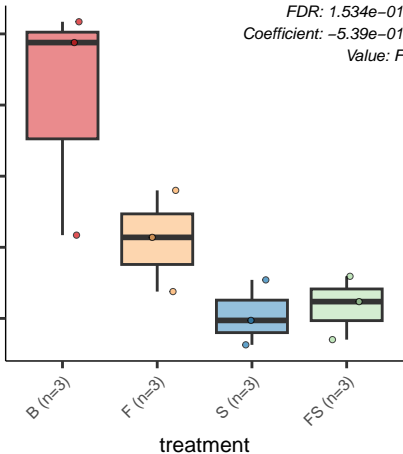
FS (n=3)

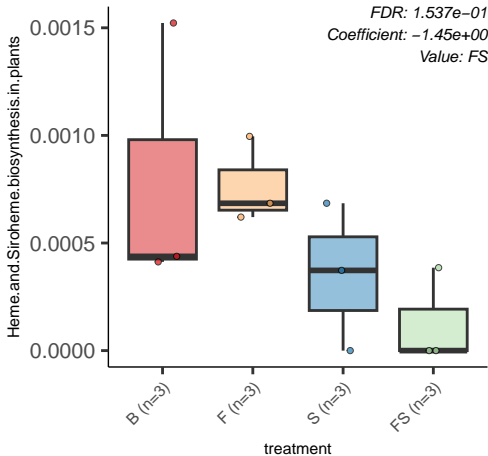
treatment



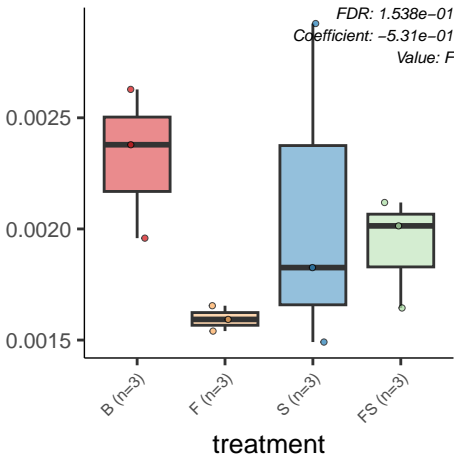
Siderophore.Enterobactin

FDR: 1.534e-01
Coefficient: -5.39e-01
Value: F



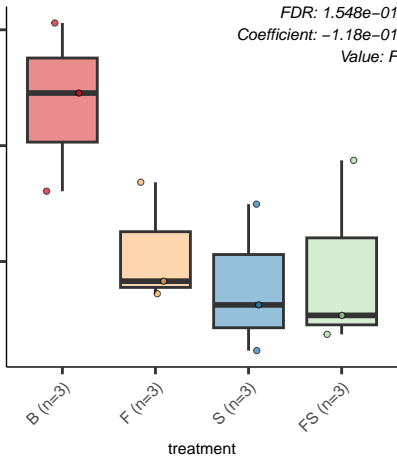


Selenoprotein.O



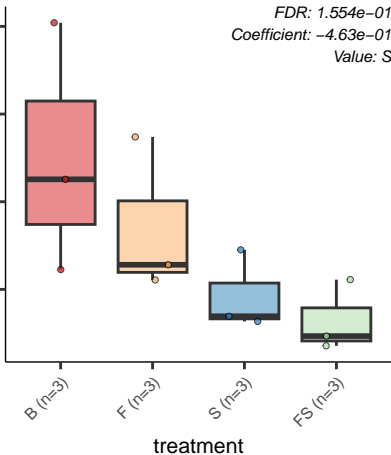
Terminal.cytochrome.oxidases

FDR: 1.548e-01
Coefficient: -1.18e-01
Value: F



At2g33980.At1g28960

FDR: 1.554e-01
Coefficient: -4.63e-01
Value: S



CBSS.203122.12.peg.188

B (n=3)

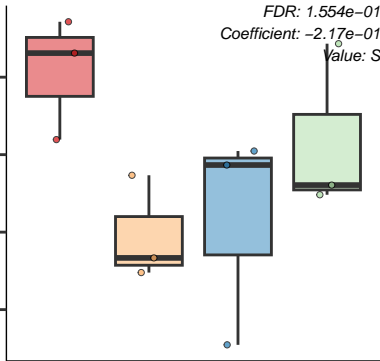
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: $1.554e-01$
Coefficient: $-2.17e-01$
Value: S



Dehydrogenase.complexes

0.06
0.05
0.04
0.03

B (n=3)

F (n=3)

S (n=3)

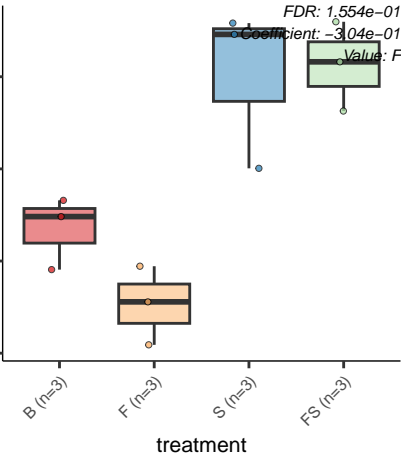
FS (n=3)

treatment

FDR: 1.554e-01

Coefficient: -3.04e-01

Value: F



Phosphate.metabolism

FDR: 1.554e-01
Coefficient: 3.74e-02
Value: F

1.18

1.16

1.14

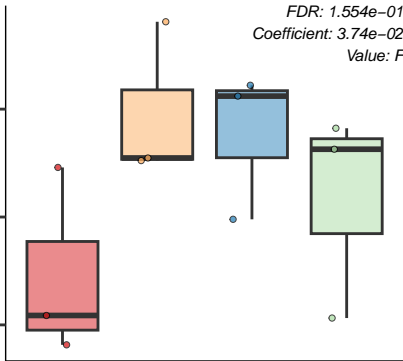
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Benzoate.degradation

FDR: 1.556e-01
Coefficient: -1.07e+00
Value: S

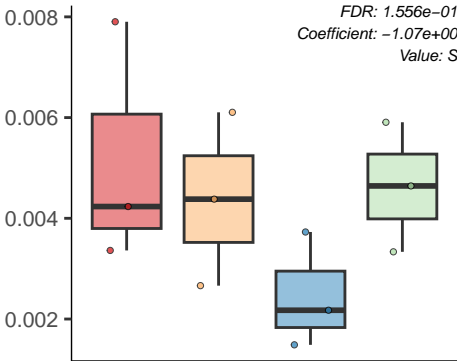
B (n=3)

F (n=3)

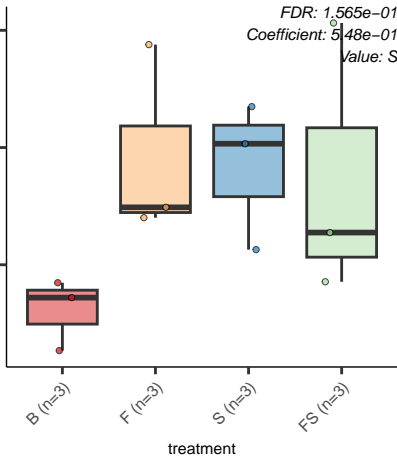
S (n=3)

FS (n=3)

treatment



ABC.transporter.tungstate..TC.3.A.1.6.2.



Cyanate.hydrolysis

0.040

0.035

0.030

B (n=3)

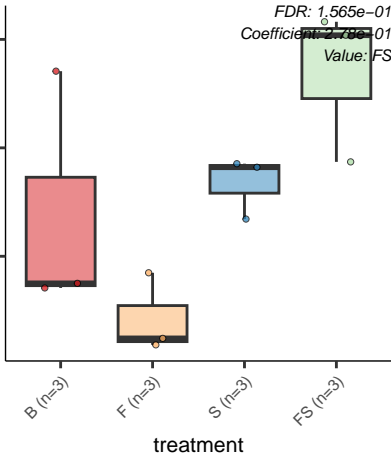
F (n=3)

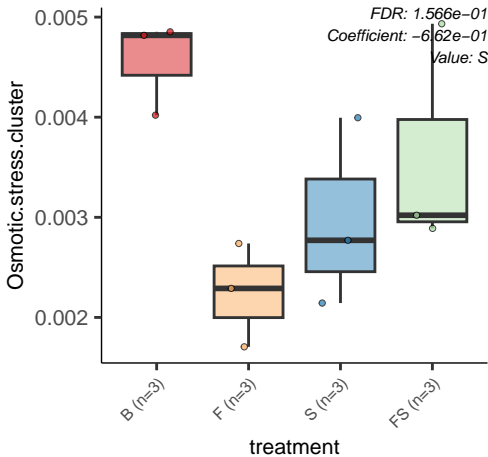
S (n=3)

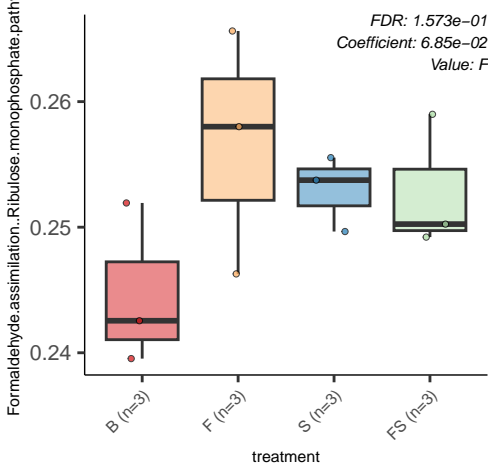
FS (n=3)

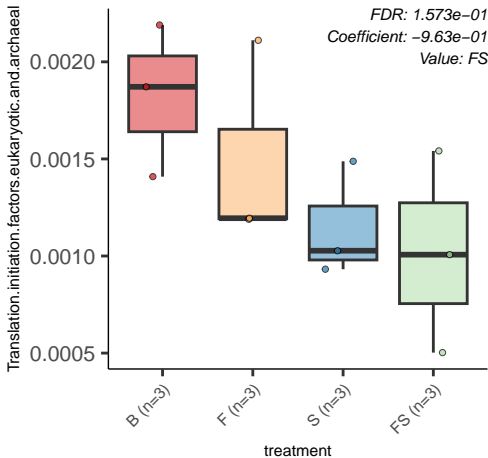
treatment

FDR: 1.565e-01
Coefficient: 2.78e-01
Value: FS









RNA.3..terminal.phosphate.cyclase

FDR: 1.581e-01
Coefficient: -5.79e-01
Value: S

0.015
0.012
0.009
0.006

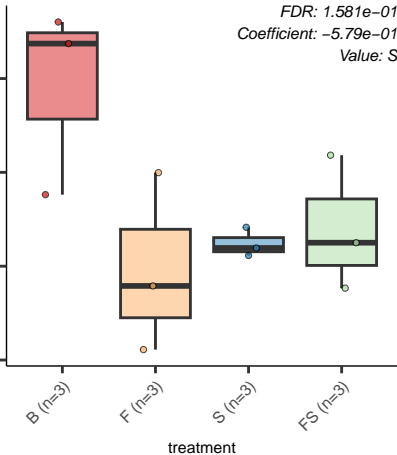
B (n=3)

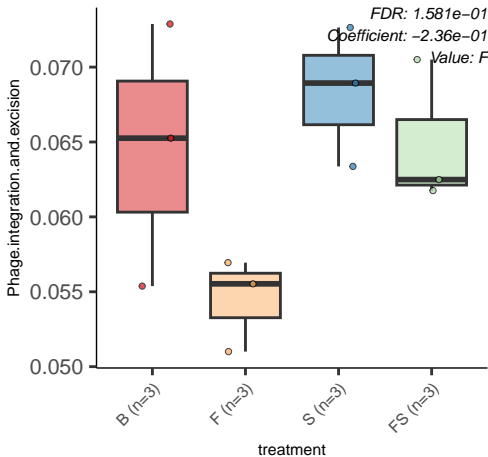
F (n=3)

S (n=3)

FS (n=3)

treatment





Respiratory.dehydrogenases.1

FDR: 1.581e-01
Coefficient: -8.14e-02
Value: F

0.180

0.175

0.170

0.165

0.160

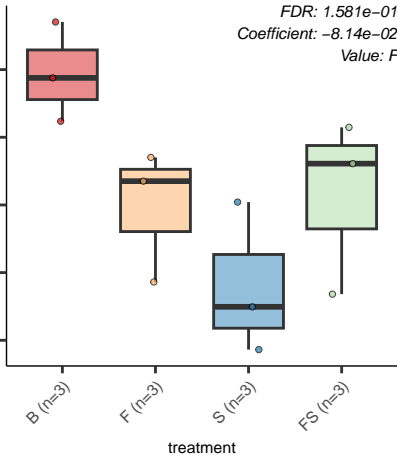
B (n=3)

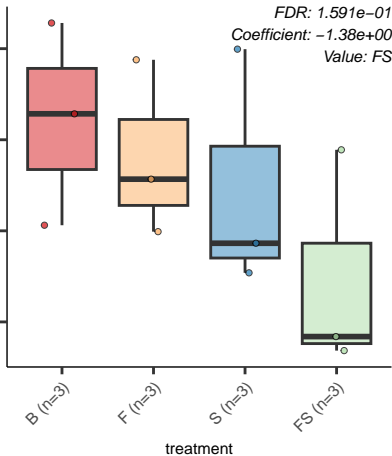
F (n=3)

S (n=3)

FS (n=3)

treatment





Cadmium.resistance

FDR: 1.597e-01
Coefficient: 3.64e-01
Value: S

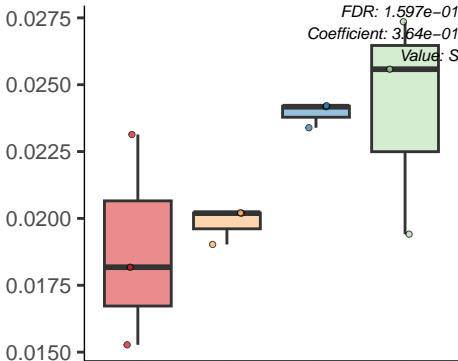
B (n=3)

F (n=3)

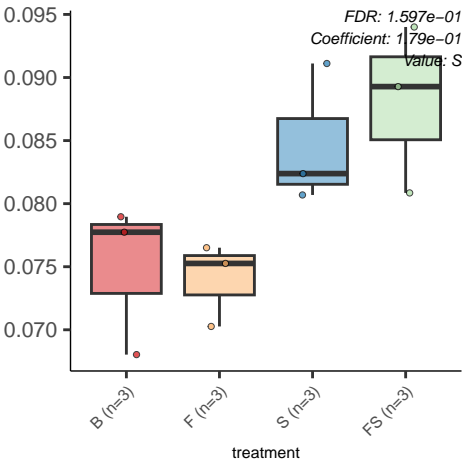
S (n=3)

FS (n=3)

treatment



DNA.repair..bacterial.DinG.and.relatives



De.Novo.Pyrimidine.Synthesis

0.82
0.80
0.78
0.76
0.74

B (n=3)

F (n=3)

S (n=3)

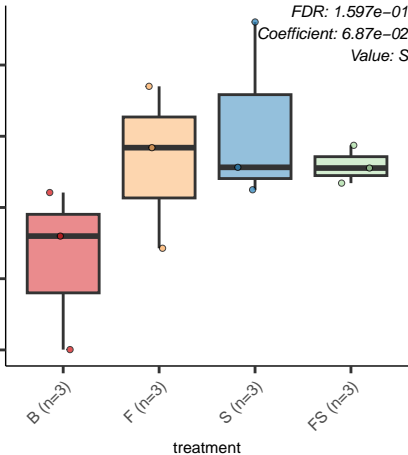
FS (n=3)

treatment

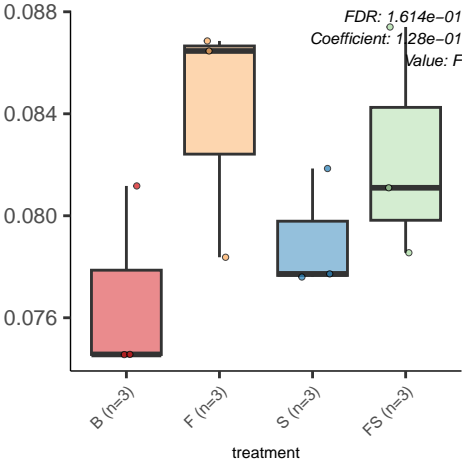
FDR: 1.597e-01

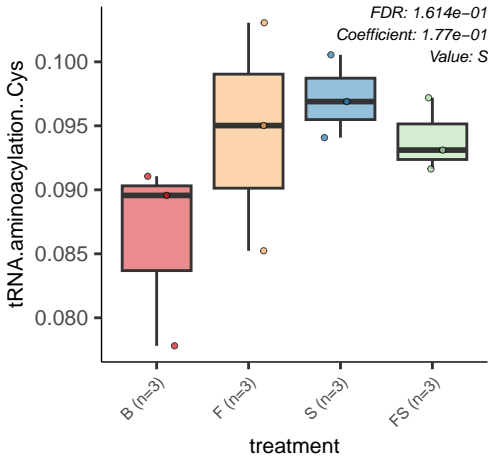
Coefficient: 6.87e-02

Value: S



Streptococcal.Hyaluronic.Acid.Capsule





Rrf2.family.transcriptional.regulators

FDR: 1.639e-01
Coefficient: -2.47e-01
Value: F

0.0300
0.0275
0.0250
0.0225
0.0200

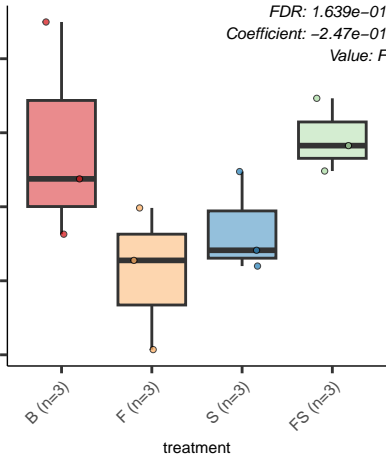
B (n=3)

F (n=3)

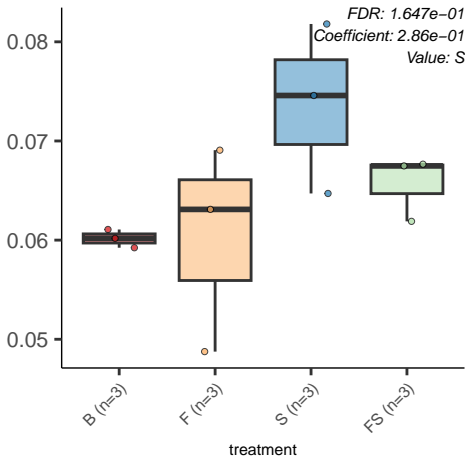
S (n=3)

FS (n=3)

treatment



Bacitracin.Stress.Response



Cadmium.resistance

FDR: 1.647e-01
Coefficient: 3.60e-01
Value: FS

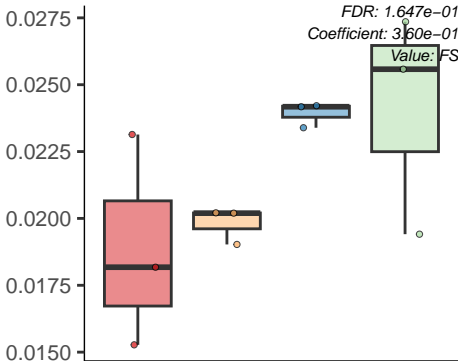
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



CytR.regulation

FDR: 1.647e-01
Coefficient: -7.56e-01
Value: S

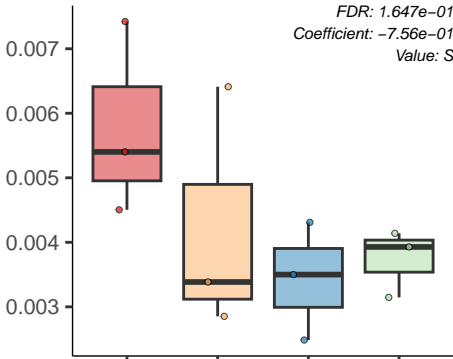
B (n=3)

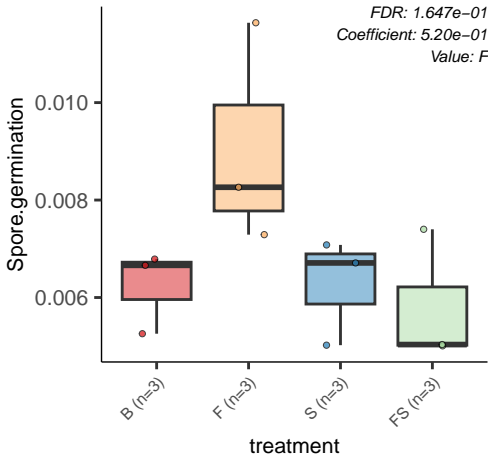
F (n=3)

S (n=3)

FS (n=3)

treatment



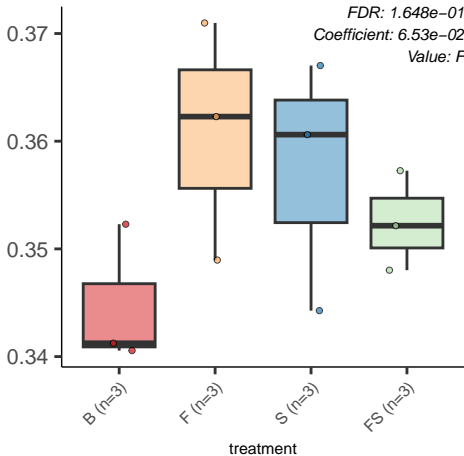


Resistance.to.fluoroquinolones

FDR: 1.648e-01

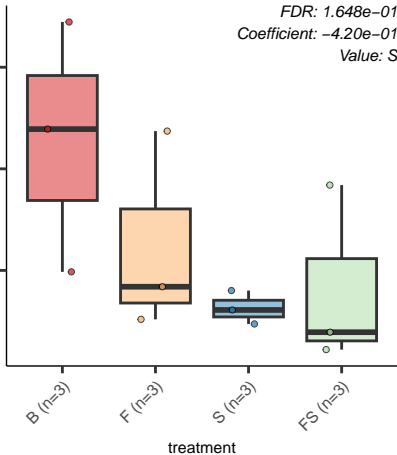
Coefficient: 6.53e-02

Value: F



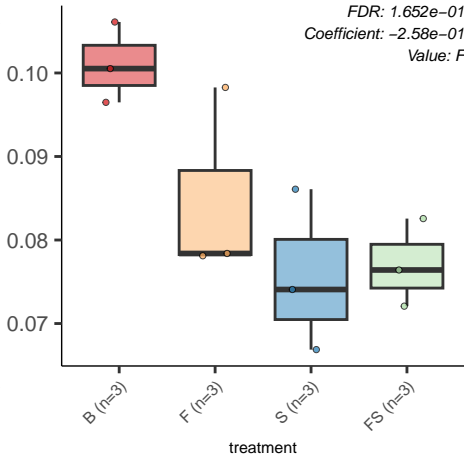
SeqA.and.Co.occuring.Genes

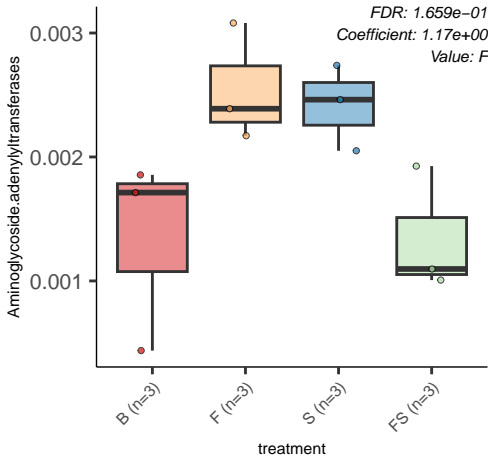
FDR: 1.648e-01
Coefficient: -4.20e-01
Value: S



Multidrug.Resistance..Tripartite.Systems.Found.in.Gram.Negative

FDR: 1.652e-01
Coefficient: -2.58e-01
Value: F





Entner.Doudoroff.Pathway

FDR: 1.662e-01
Coefficient: -9.05e-02
Value: S

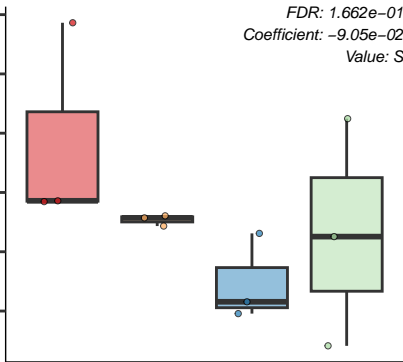
B (n=3)

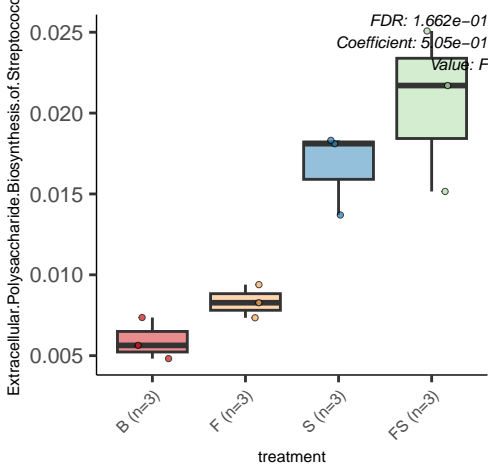
F (n=3)

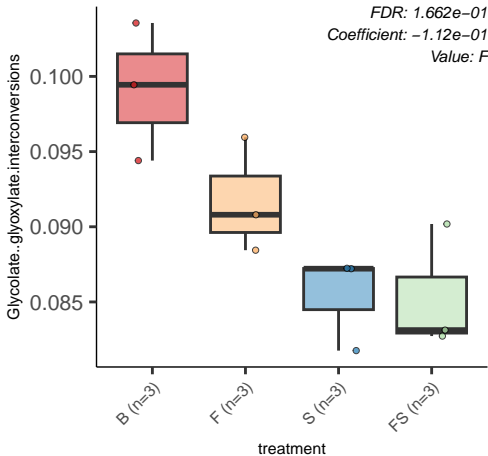
S (n=3)

FS (n=3)

treatment







L.rhamnose.utilization

FDR: 1.662e-01
Coefficient: -1.70e-01
Value: FS

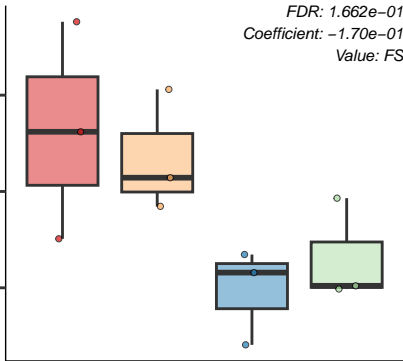
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Proton.dependent.Peptide.Transporters

FDR: 1.662e-01
Coefficient: -2.64e-01
Value: FS

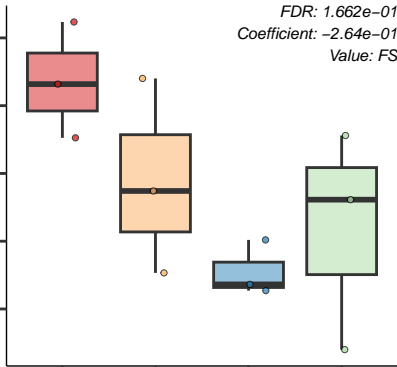
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Type.I.Restriction.Modification

0.30
0.29
0.28

FDR: 1.662e-01
Coefficient: -4.13e-02
Value: S

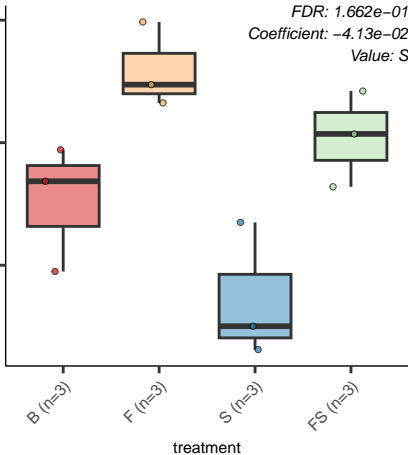
B (n=3)

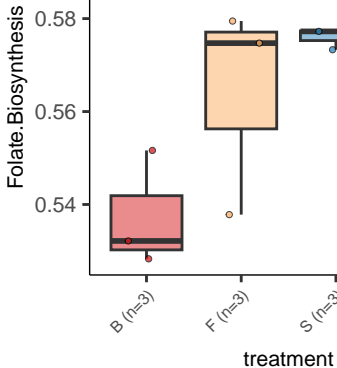
F (n=3)

S (n=3)

FS (n=3)

treatment





FDR: 1.663e-01
Coefficient: 6.93e-02
Value: F

Glutaredoxins

FDR: 1.663e-01
Coefficient: -4.63e-02
Value: FS

0.225

0.220

0.215

0.210

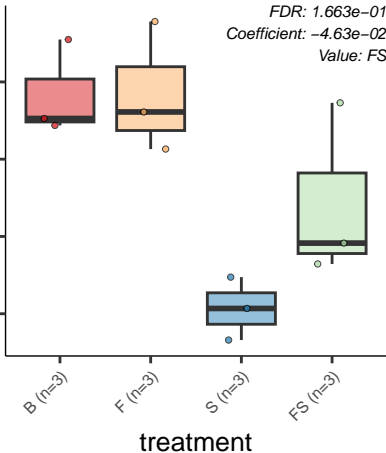
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Glycogen.metabolism

FDR: 1.663e-01

Coefficient: 6.42e-02

Value: F

1.00

0.96

0.92

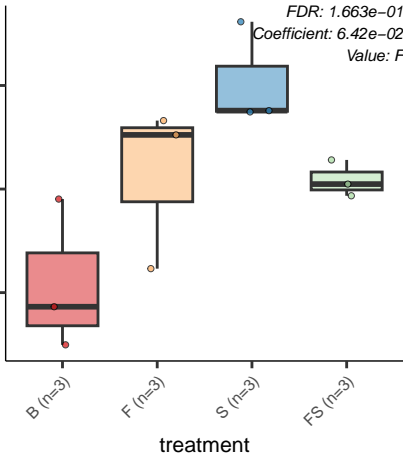
B (n=3)

F (n=3)

S (n=3)

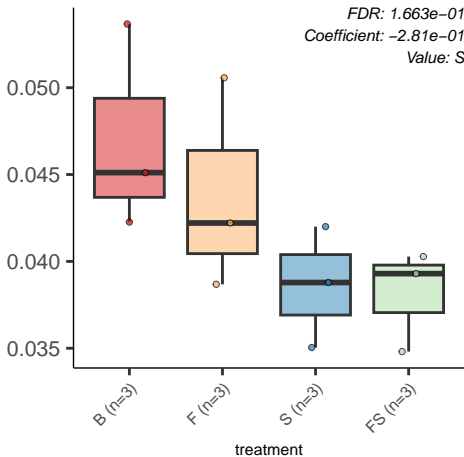
FS (n=3)

treatment



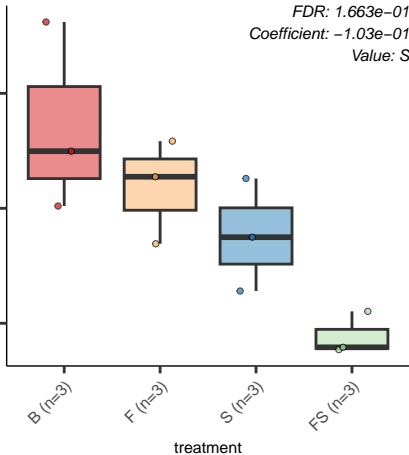
lbrA.and.lbrB..co.actors.of.prophage.gene.expression

FDR: 1.663e-01
Coefficient: -2.81e-01
Value: S



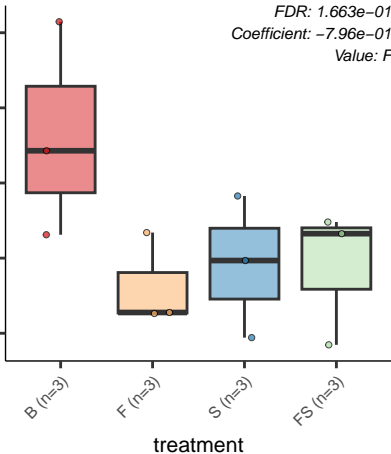
Oxygen.stress.response...Human.gut.microbiome

FDR: 1.663e-01
Coefficient: -1.03e-01
Value: S



Pseudouridine.Metabolism

FDR: 1.663e-01
Coefficient: -7.96e-01
Value: F



Alkanesulfonates.Utilization

FDR: 1.668e-01
Coefficient: -3.11e-01
Value: F

0.009

0.008

0.007

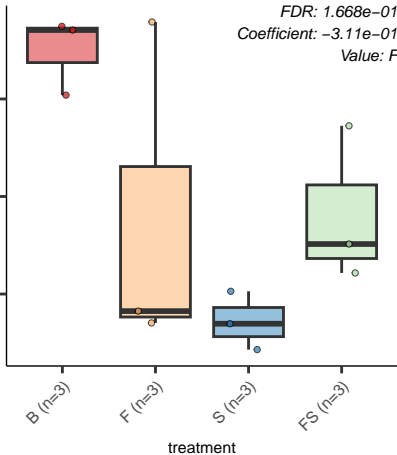
B (n=3)

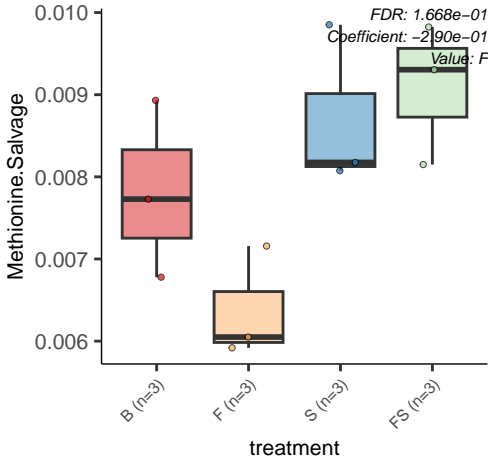
F (n=3)

S (n=3)

FS (n=3)

treatment





tRNA.aminoacylation..Glu.and.Gln

FDR: 1.671e-01
Coefficient: 9.30e-02
Value: F

0.30
0.29
0.28
0.27

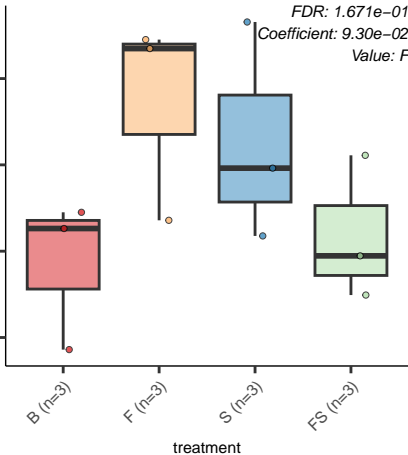
B (n=3)

F (n=3)

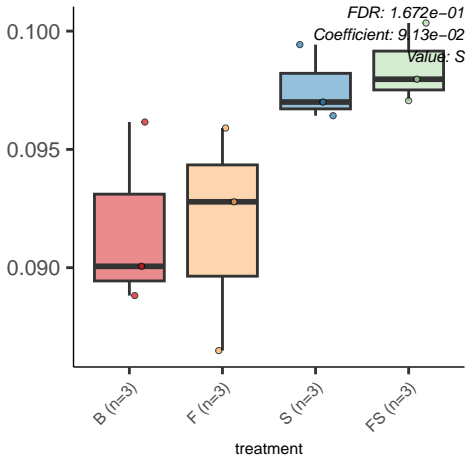
S (n=3)

FS (n=3)

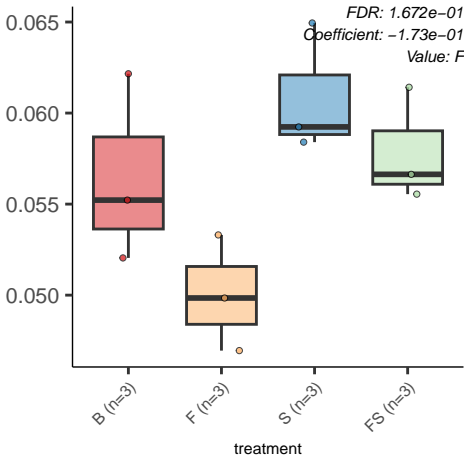
treatment

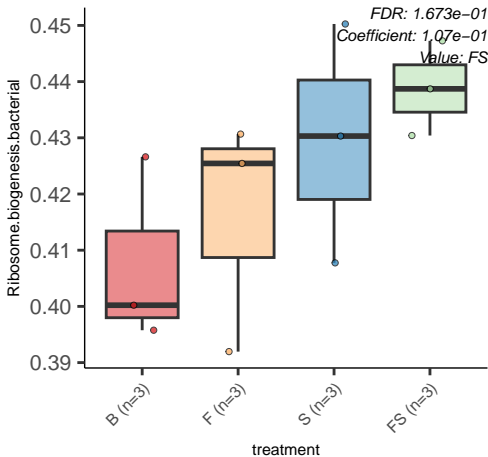


RuvABC.plus.a.hypothetical



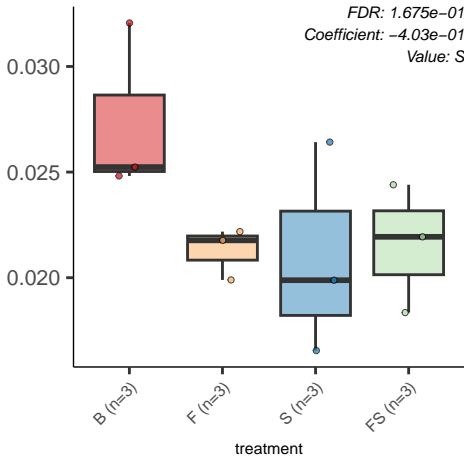
Transport of Nickel and Cobalt

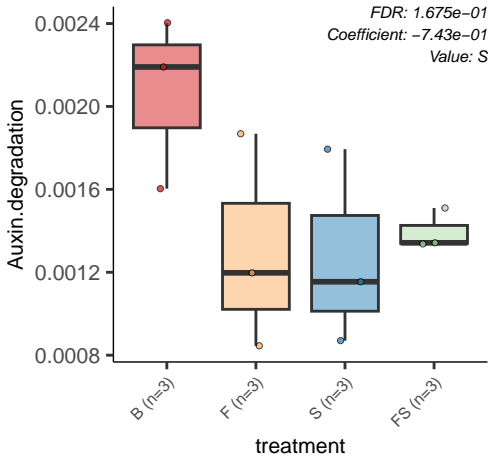


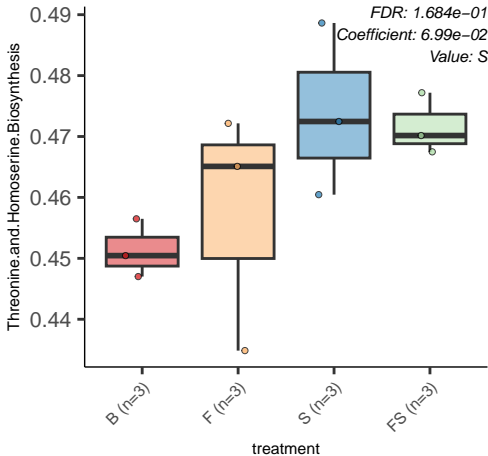


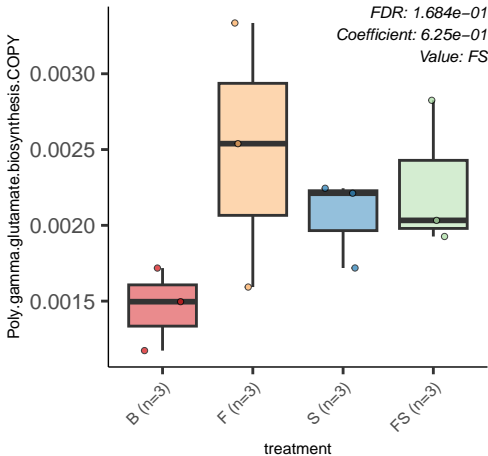
Autoinducer.2...Al.2...transport.and.processing..lsrACDBFGE.

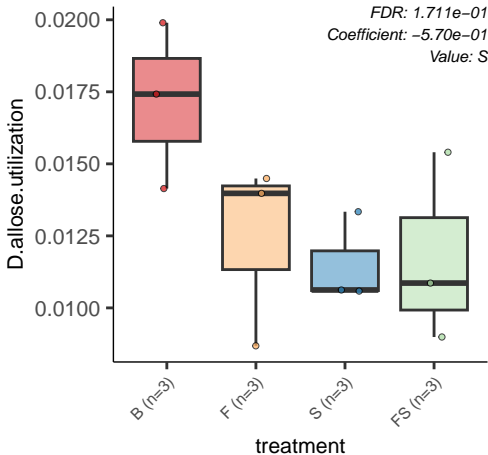
FDR: 1.675e-01
Coefficient: -4.03e-01
Value: S











Lysine.fermentation

FDR: 1.711e-01
Coefficient: 1.01e-01
Value: S

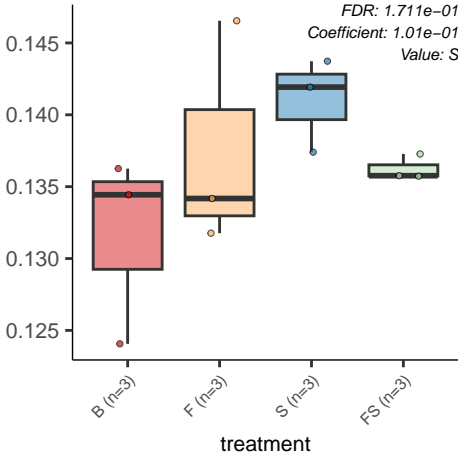
B (n=3)

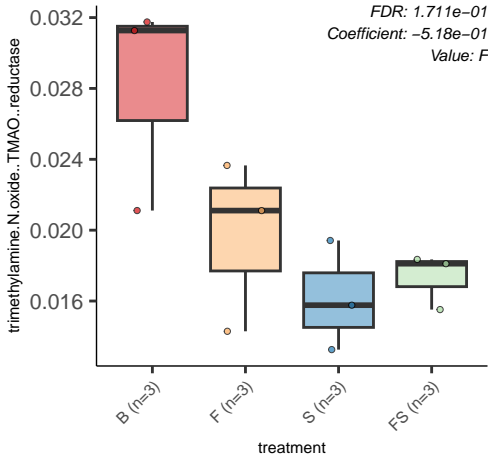
F (n=3)

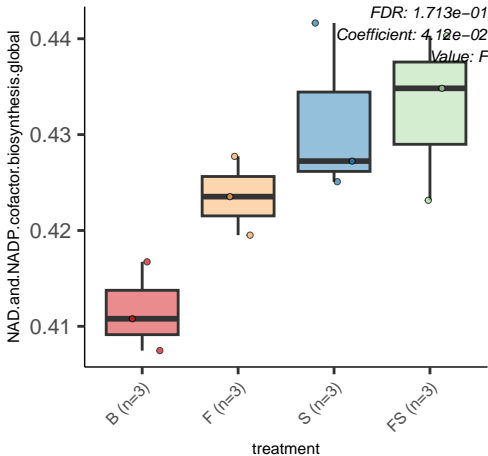
S (n=3)

FS (n=3)

treatment







Aromatic.Amin.Catabolism

FDR: 1.716e-01
Coefficient: -4.88e-01
Value: F

0.008

0.006

0.004

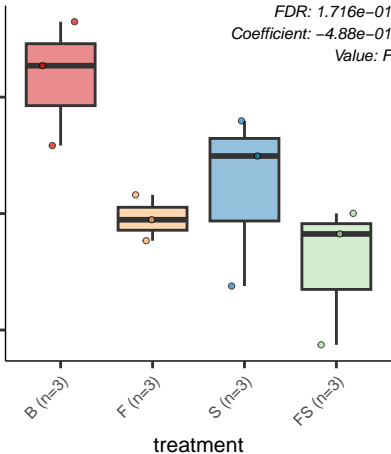
B (n=3)

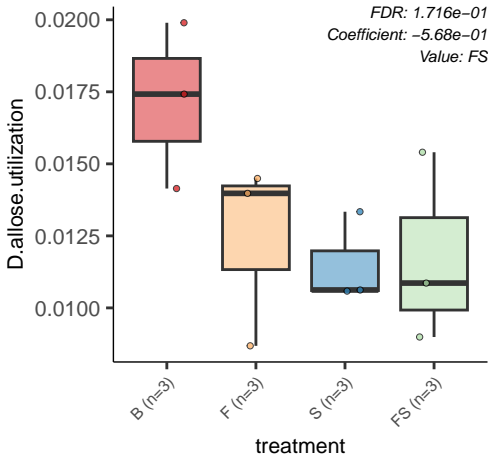
F (n=3)

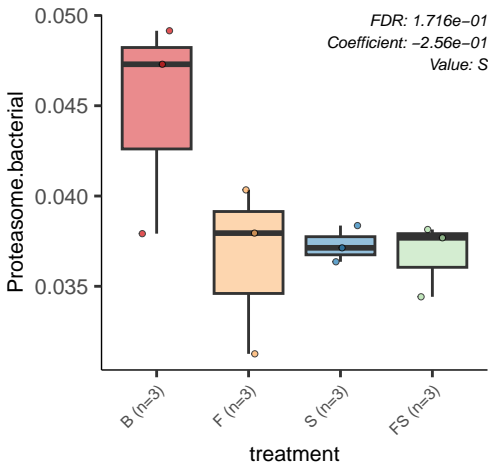
S (n=3)

FS (n=3)

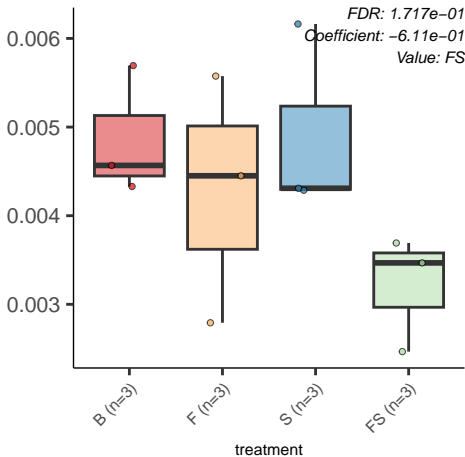
treatment



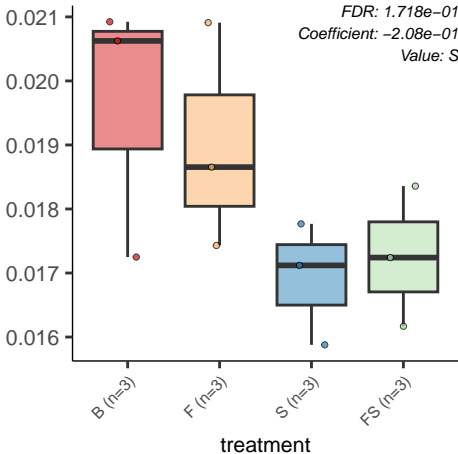




Inclusion.membrane.proteins.supporting.intracellular.life.styles.in.C



Ethanolamine.utilization



Natural.DNA.Transformation.in.Vibrio

FDR: $1.719\text{e-}01$
Coefficient: $-1.02\text{e}+00$
Value: S

0.003
0.002
0.001

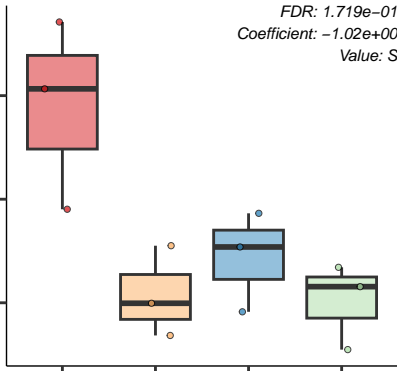
B (n=3)

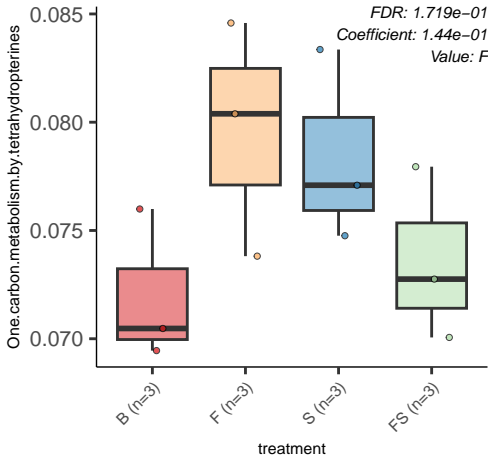
F (n=3)

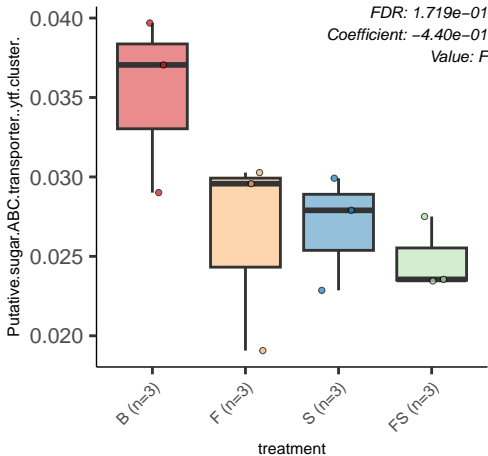
S (n=3)

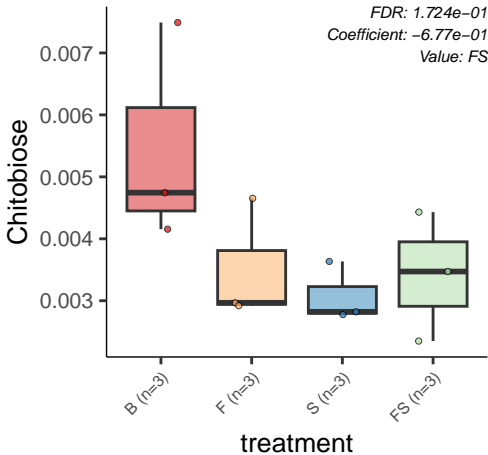
FS (n=3)

treatment



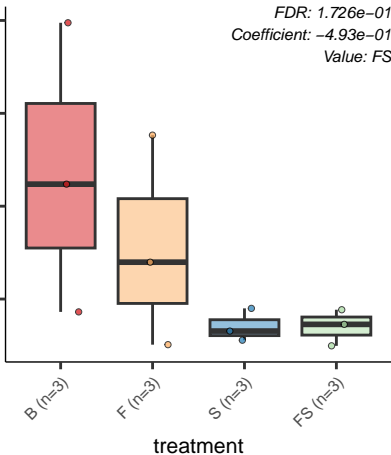






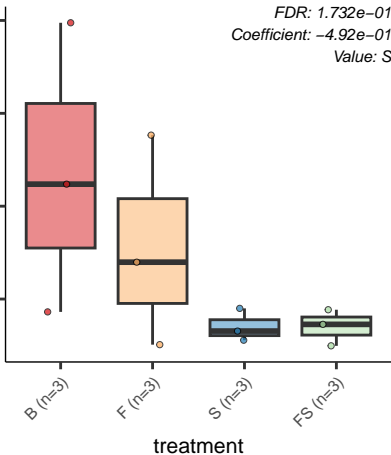
CBSS.316407.3.peg.1371

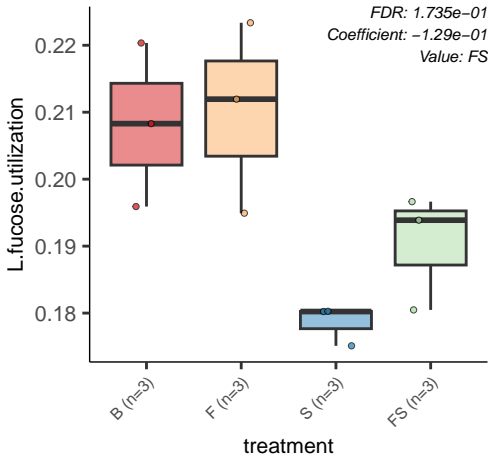
FDR: 1.726e-01
Coefficient: -4.93e-01
Value: FS



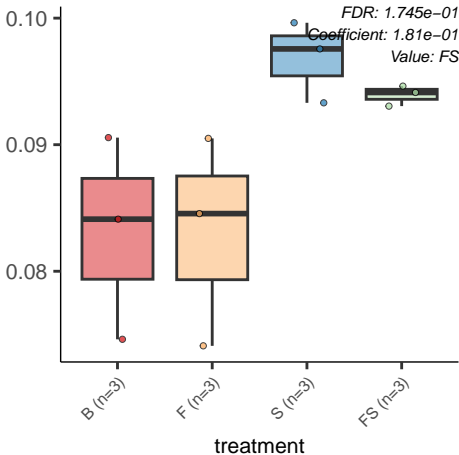
CBSS.316407.3.peg.1371

FDR: 1.732e-01
Coefficient: -4.92e-01
Value: S



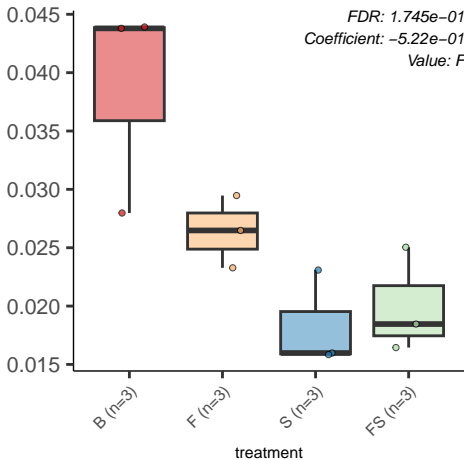


CBSS.176299.4.peg.1292



The.usher.protein.HtrE.fimbrial.cluster

FDR: 1.745e-01
Coefficient: -5.22e-01
Value: F



CBSS.246196.1.peg.364

FDR: 1.745e-01
Coefficient: -2.20e-01
Value: FS

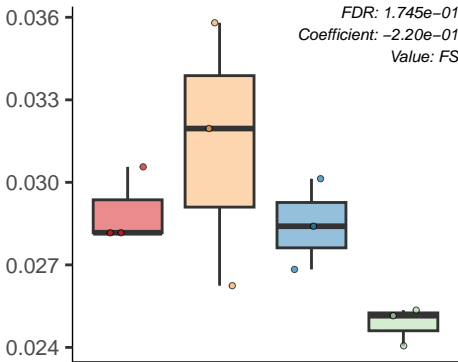
B (n=3)

F (n=3)

S (n=3)

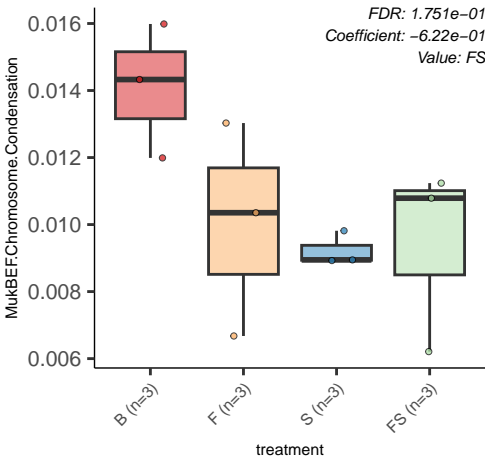
FS (n=3)

treatment



MukBEF:Chromosome.Condensation

FDR: 1.751e-01
Coefficient: -6.22e-01
Value: FS



Ribosome.LSU.bacterial

FDR: 1.751e-01

Coefficient: 7.06e-02

Value: F

0.53

0.52

0.51

0.50

0.49

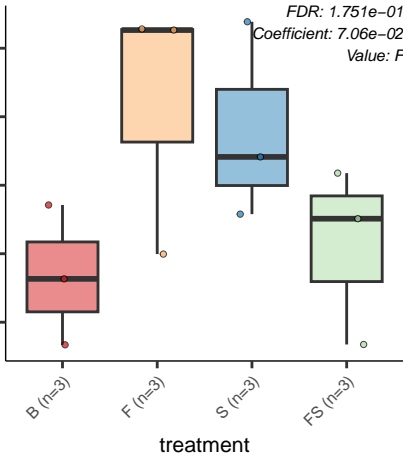
B (n=3)

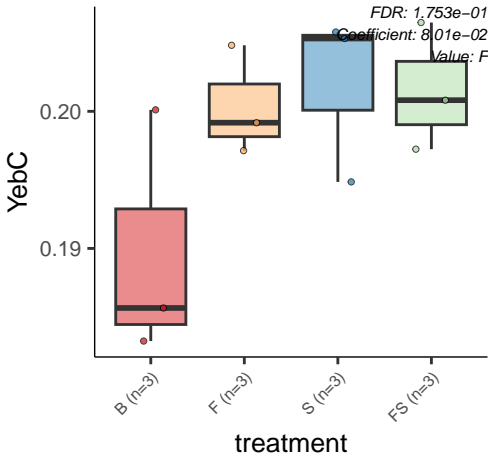
F (n=3)

S (n=3)

FS (n=3)

treatment





Listeria.surface.proteins..Internalin.like.proteins

FDR: 1.776e-01
Coefficient: -9.21e-01
Value: F

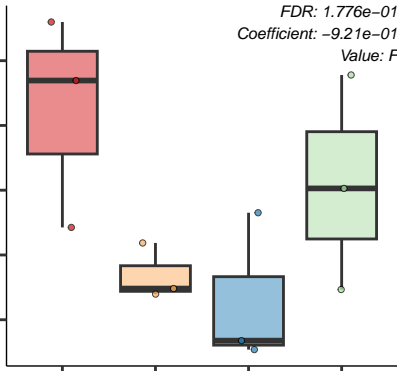
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



LOS.core.oligosaccharide.biosynthesis

FDR: 1.782e-01
Coefficient: -9.73e-02
Value: F

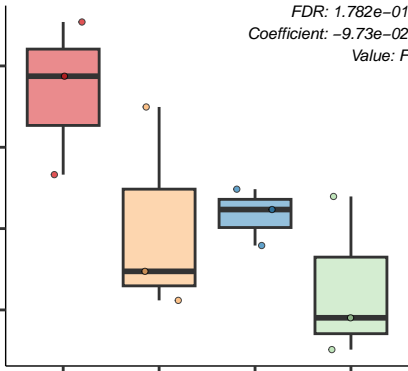
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Zinc.regulated.enzymes

FDR: 1.788e-01
Coefficient: -3.60e-01
Value: FS

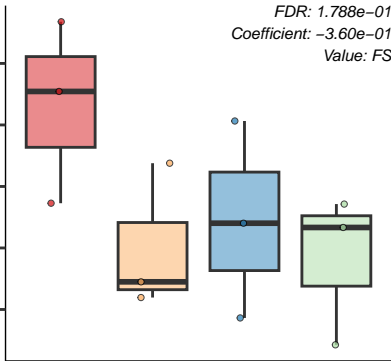
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



N.linked.Glycosylation.in.Bacteria

FDR: 1.796e-01
Coefficient: -1.11e-01
Value: FS

0.13
0.12

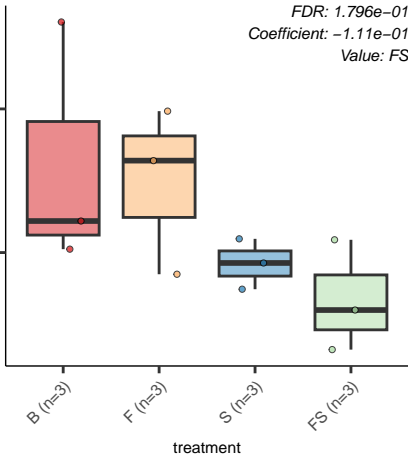
B (n=3)

F (n=3)

S (n=3)

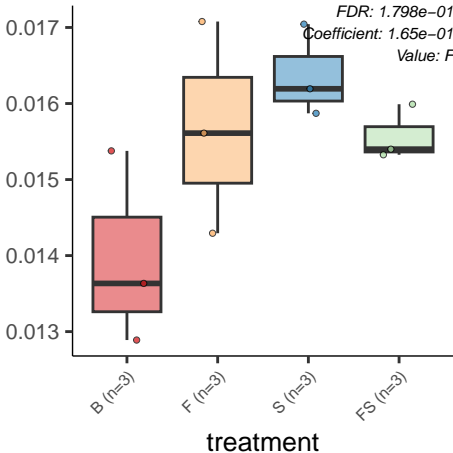
FS (n=3)

treatment



YgjD.and.YeaZ

FDR: 1.798e-01
Coefficient: 1.65e-01
Value: F



At5g04520.AT1G06240

FDR: 1.798e-01
Coefficient: -9.22e-02
Value: S

0.084

0.080

0.076

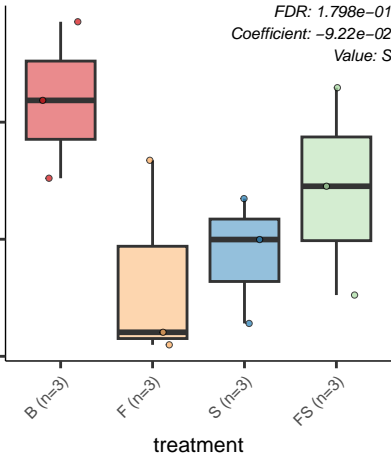
B (n=3)

F (n=3)

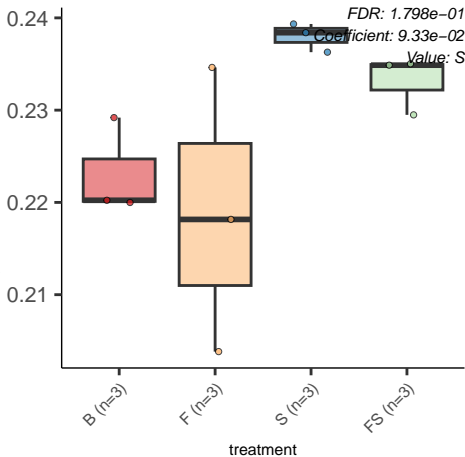
S (n=3)

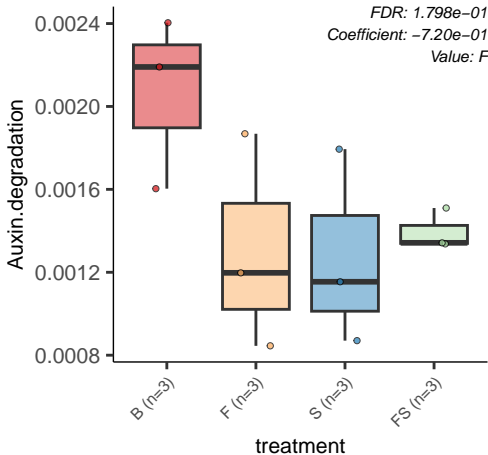
FS (n=3)

treatment



At5g37530..CsdL.protein.family.





Teichuronic.acid.biosynthesis

FDR: 1.798e-01
Coefficient: -2.46e-01
Value: S

0.045

0.040

0.035

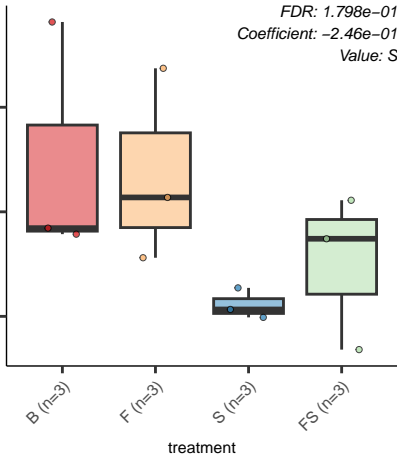
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



cAMP.signaling.in.bacteria

FDR: 1.798e-01
Coefficient: -1.42e-01
Value: FS

0.16
0.15
0.14
0.13

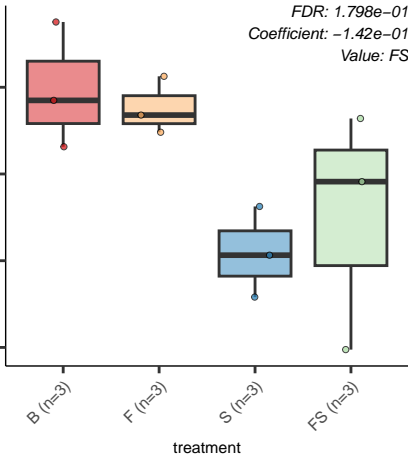
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Selenocysteine.metabolism

FDR: 1.800e-01
Coefficient: -2.17e-01
Value: S

0.08

0.07

0.06

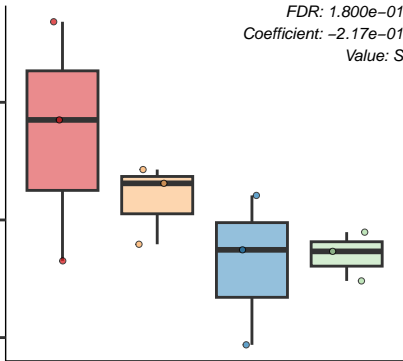
B (n=3)

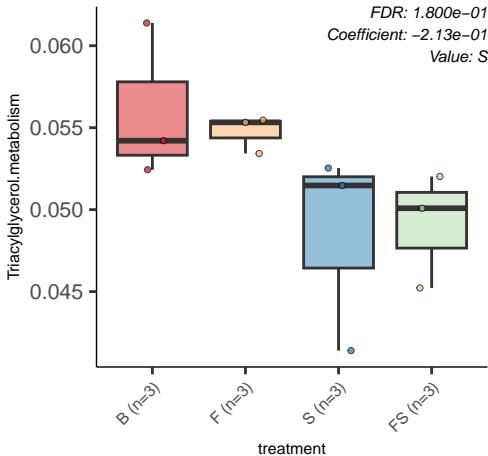
F (n=3)

S (n=3)

FS (n=3)

treatment





EC699.706

FDR: 1.802e-01
Coefficient: -2.79e-01
Value: FS

B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment

0.055

0.050

0.045

0.040

Lipoic acid metabolism

FDR: 1.802×10^{-1}
Coefficient: -1.80×10^{-1}
Value: F

0.0325

0.0300

0.0275

0.0250

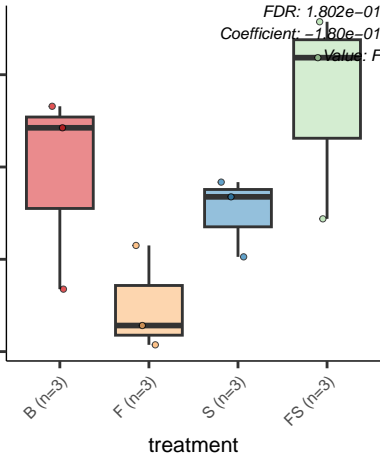
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Tenl.like.tautomerase

FDR: $1.807e-01$
Coefficient: $-8.72e-02$
Value: FS

0.130
0.125
0.120
0.115

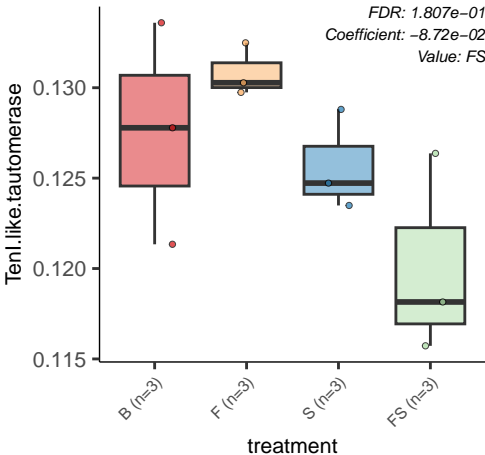
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Glycogen.metabolism

FDR: 1.809e-01

Coefficient: 6.16e-02

Value: FS

1.00

0.96

0.92

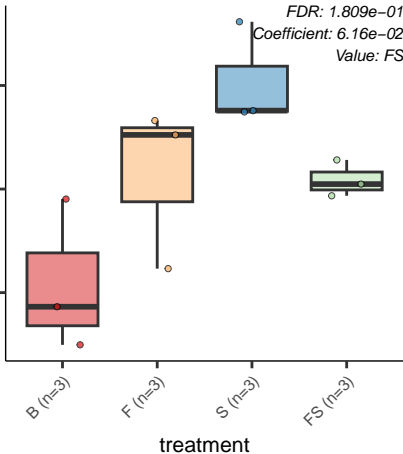
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Murein.Hydrolases

0.15
0.14
0.13

B (n=3)

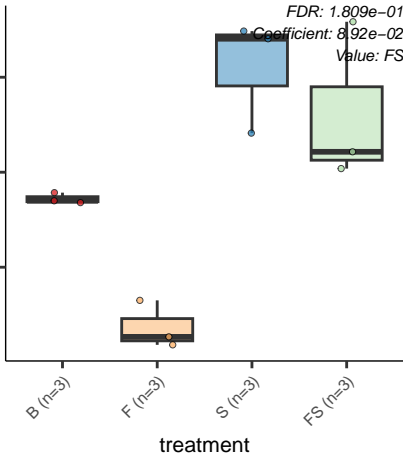
F (n=3)

S (n=3)

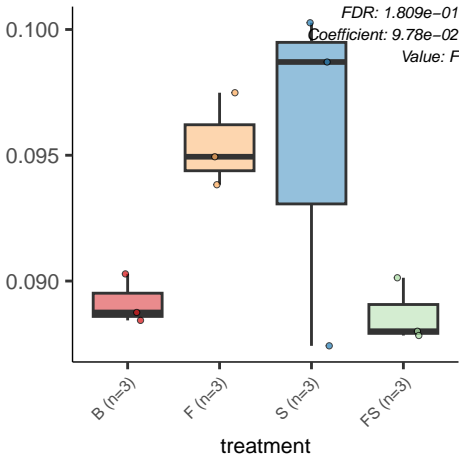
FS (n=3)

treatment

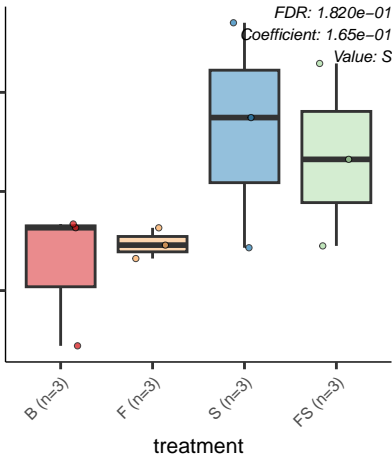
FDR: 1.809e-01
Coefficient: 8.92e-02
Value: FS

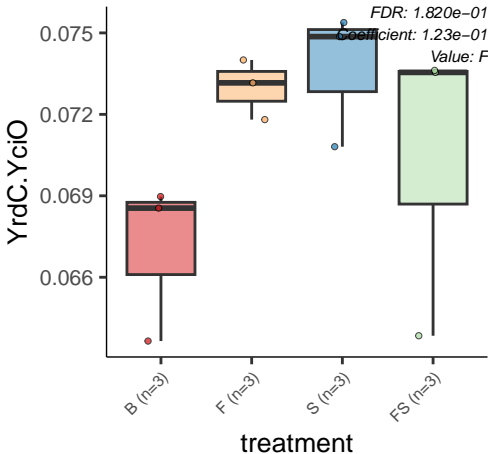


Omega.amidase.KE



CBSS.257314.1.peg.488





Glycine.Biosynthesis

FDR: 1.841e-01
Coefficient: 6.07e-02
Value: F

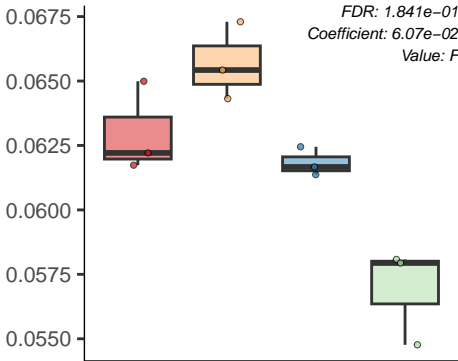
B (n=3)

F (n=3)

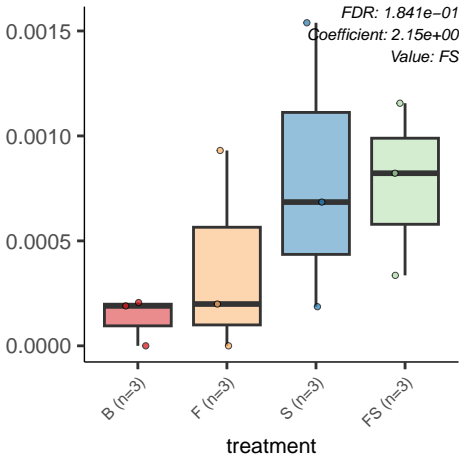
S (n=3)

FS (n=3)

treatment



Phenazine.biosynthesis



Putative.TldE.TldD.proteolytic.complex

FDR: 1.841e-01
Coefficient: -3.06e-01
Value: F

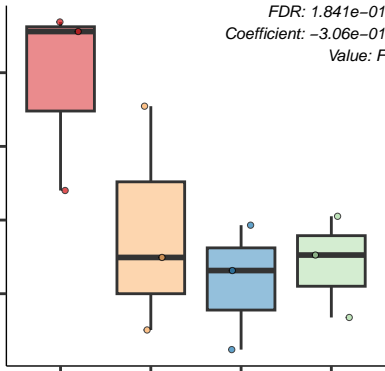
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Copper.homeostasis..copper.tolerance

FDR: 1.842e-01
Coefficient: -1.41e-01
Value: S

0.050

0.045

0.040

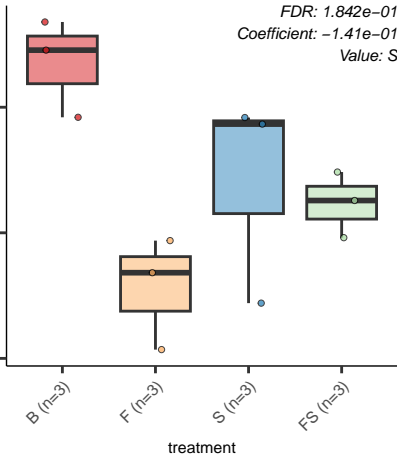
B (n=3)

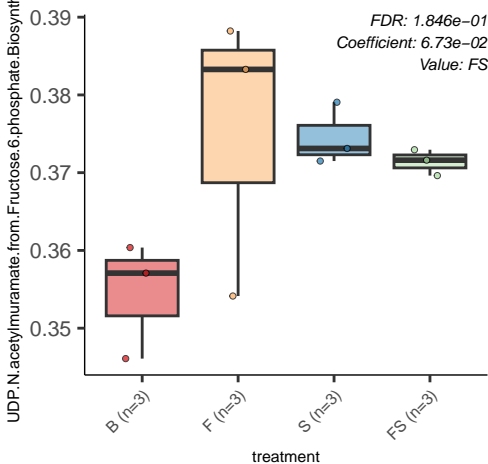
F (n=3)

S (n=3)

FS (n=3)

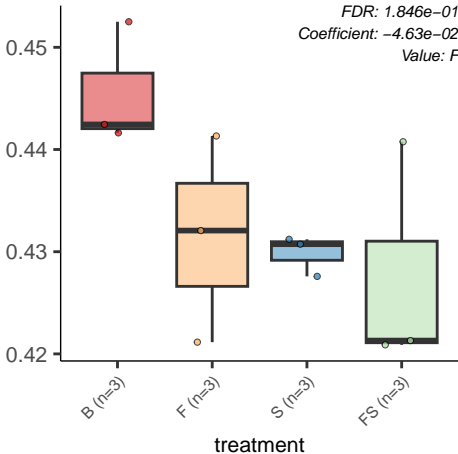
treatment





Polyamine.Metabolism

FDR: 1.846e-01
Coefficient: -4.63e-02
Value: F



CBSS.342610.3.pcg.283

FDR: 1.847e-01
Coefficient: 1.85e-01
Value.FS

0.022

0.020

0.018

0.016

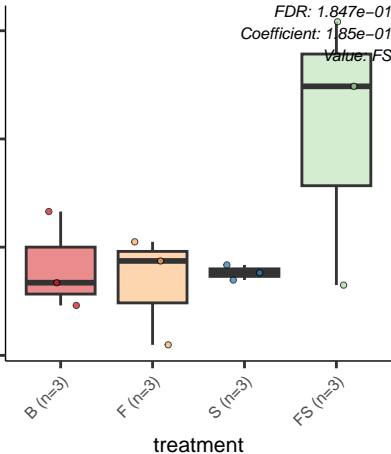
B (n=3)

F (n=3)

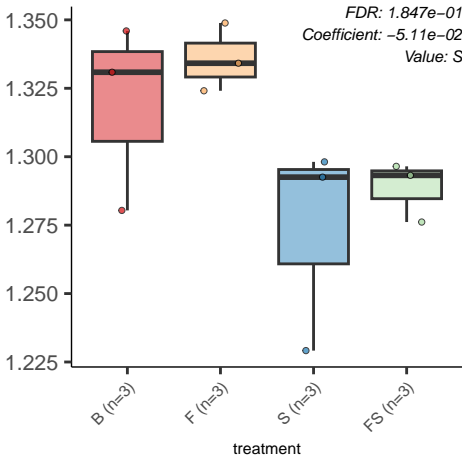
S (n=3)

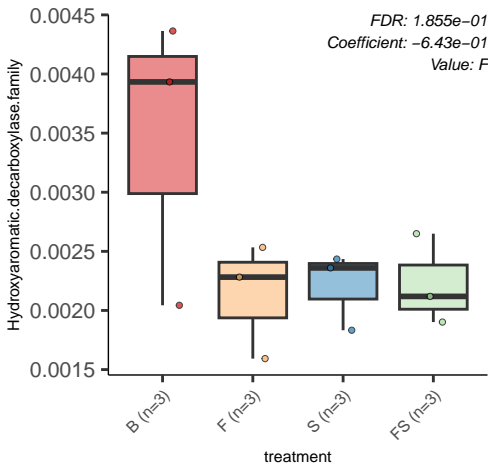
FS (n=3)

treatment



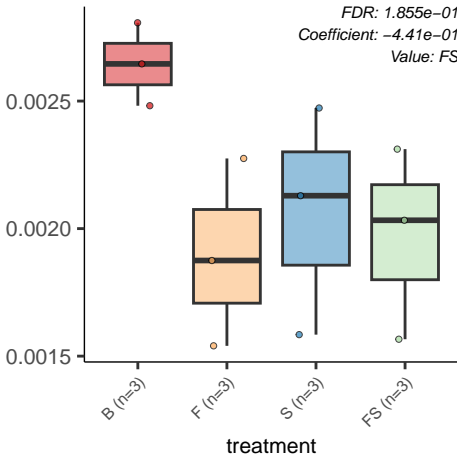
Maltose.and.Maltodextrin.Utilization





MethanopterinAromatic

FDR: $1.855e-01$
Coefficient: $-4.41e-01$
Value: FS



Siderophore.Aerobactin

FDR: 1.855e-01
Coefficient: -4.73e-01
Value: F

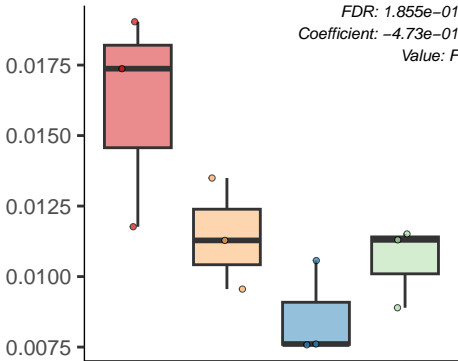
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Test...DHFR

FDR: 1.855e-01
Coefficient: 8.38e-02
Value: S

0.30
0.29
0.28
0.27
0.26

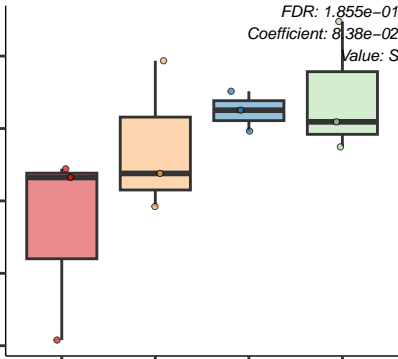
B (n=3)

F (n=3)

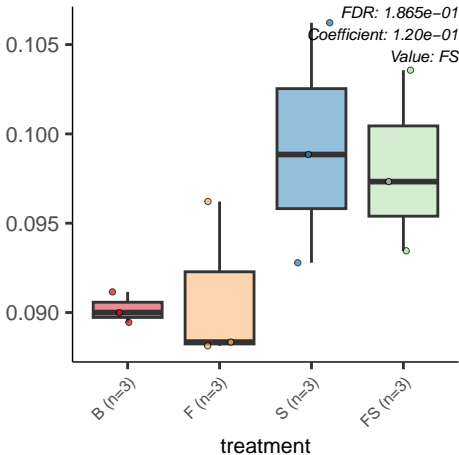
S (n=3)

FS (n=3)

treatment

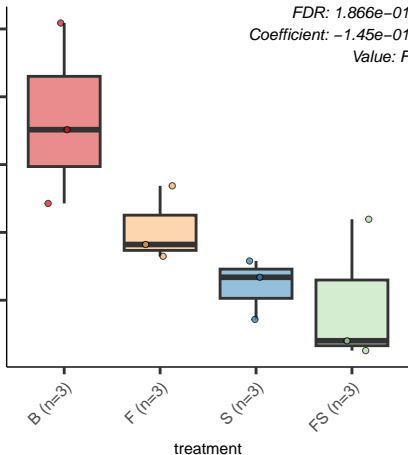


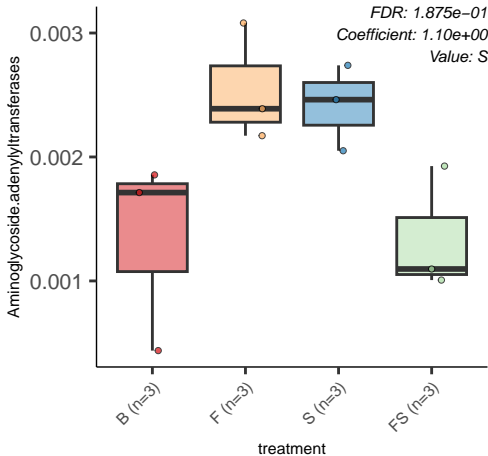
Alanine.biosynthesis



Respiration...Human.gut.microbiome

FDR: 1.866e-01
Coefficient: -1.45e-01
Value: F





MukBEF:Chromosome.Condensation

FDR: 1.875e-01
Coefficient: -6.03e-01
Value: S

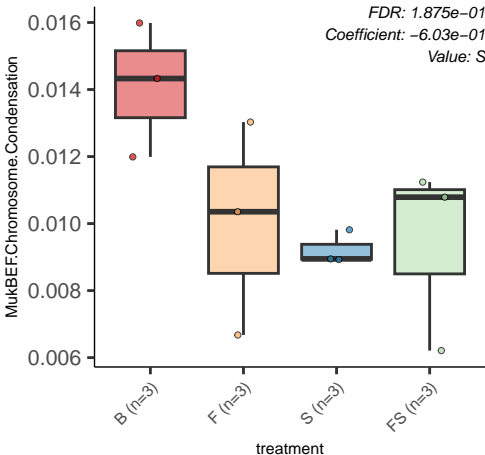
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Polyadenylation.bacterial

FDR: 1.875e-01
Coefficient: 1.03e-01
Value: FS

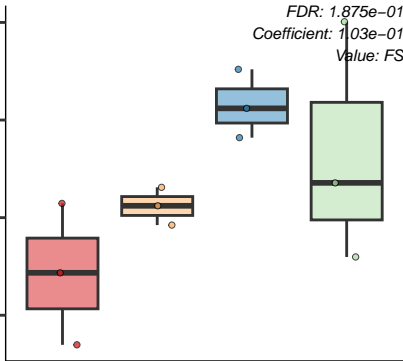
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Universal.GTPases

0.775
0.750
0.725
0.700

B (n=3)

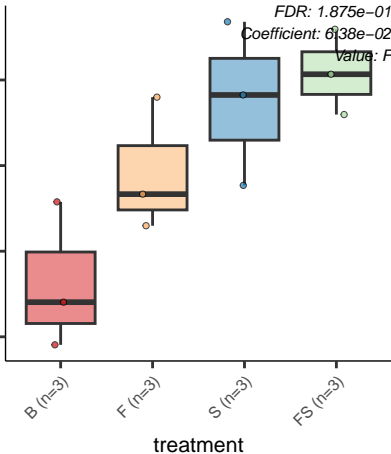
F (n=3)

S (n=3)

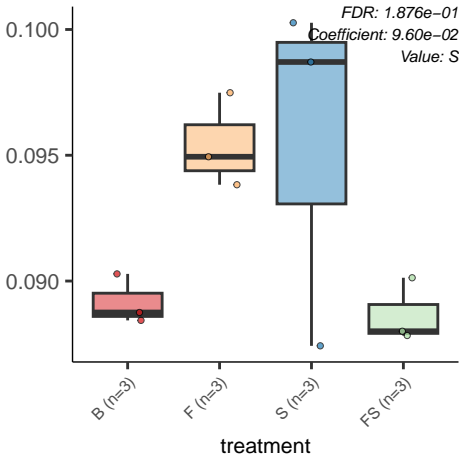
FS (n=3)

treatment

FDR: 1.875e-01
Coefficient: 6.38e-02
value: F



Omega.amidase.KE



Dihydroxyacetone.kinases

0.075

0.070

0.065

0.060

B (n=3)

F (n=3)

S (n=3)

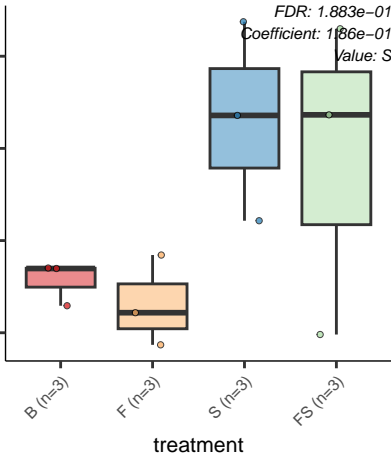
FS (n=3)

treatment

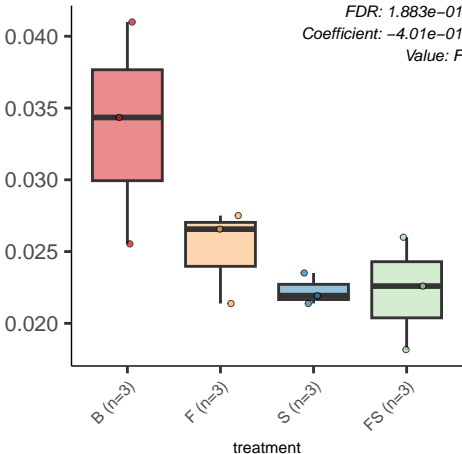
FDR: 1.883e-01

Coefficient: 1.86e-01

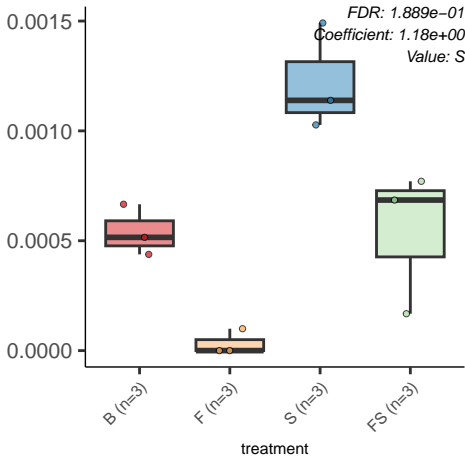
Value: S

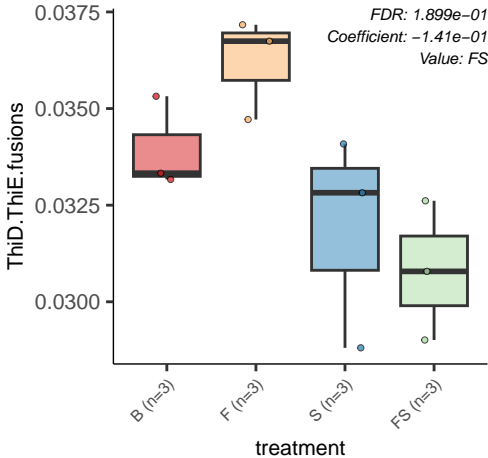


Fatty.acid.degradation.regulons



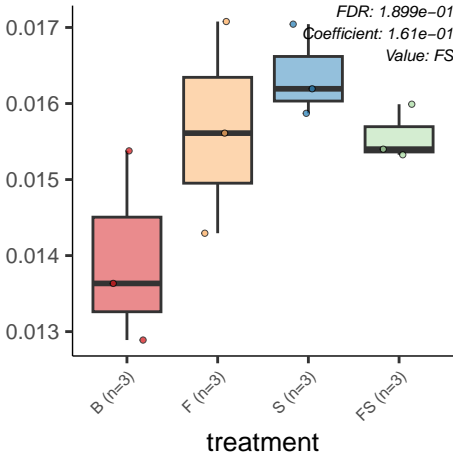
Fratricide.in.Streptococcus

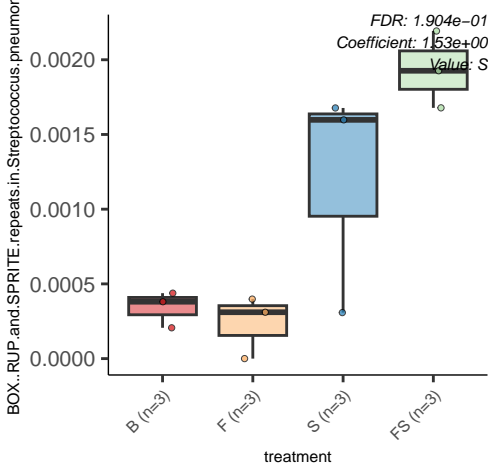




YgjD.and.YeaZ

FDR: 1.899e-01
Coefficient: 1.61e-01
Value: FS





RNA.3..terminal.phosphate.cyclase

FDR: 1.907e-01
Coefficient: -5.30e-01
Value: FS

0.015
0.012
0.009
0.006

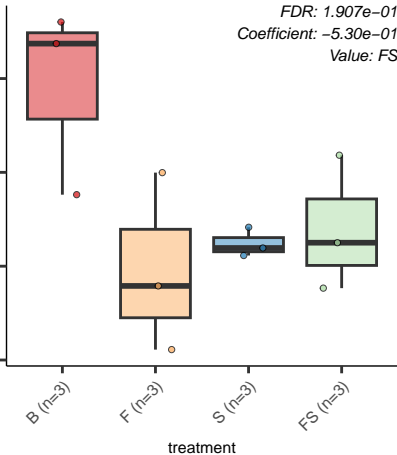
B (n=3)

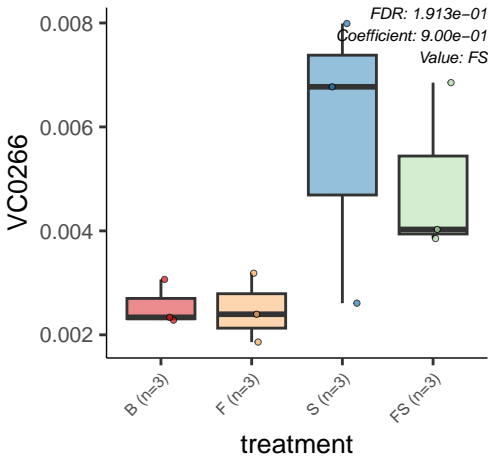
F (n=3)

S (n=3)

FS (n=3)

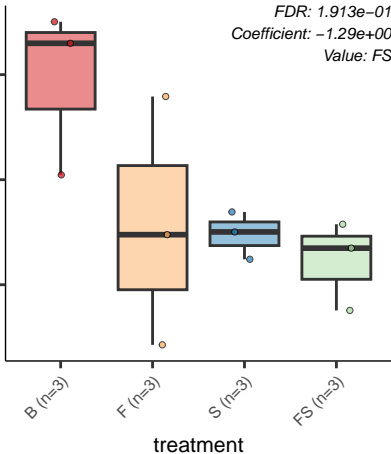
treatment

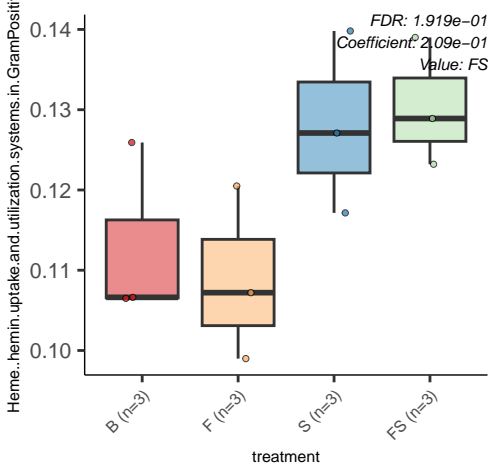




Salmonella.invasion.locus

FDR: 1.913e-01
Coefficient: -1.29e+00
Value: FS





Respiratory.dehydrogenases.1

FDR: 1.920e-01
Coefficient: -7.43e-02
Value: FS

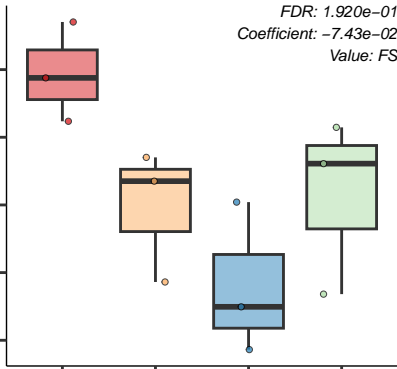
B (n=3)

F (n=3)

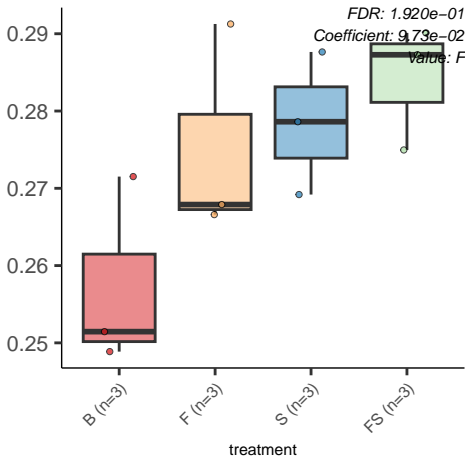
S (n=3)

FS (n=3)

treatment



Exopolysaccharide.Biosynthesis



Glycerol.and.Glycerol.3.phosphate.Uptake.and.Utilization

FDR: 1.924e-01
Coefficient: -1.26e-01
Value: F

0.21
0.20
0.19
0.18

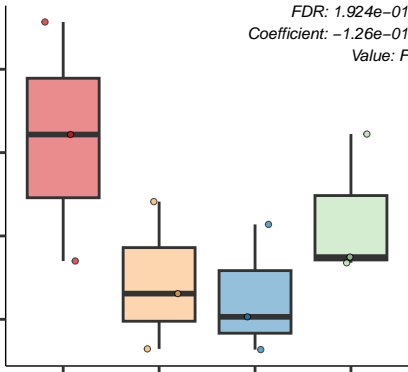
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Fatty.Acid.Biosynthesis.FASl

FDR: 1.925e-01
Coefficient: 2.86e-01
Value: F

0.18
0.16
0.14

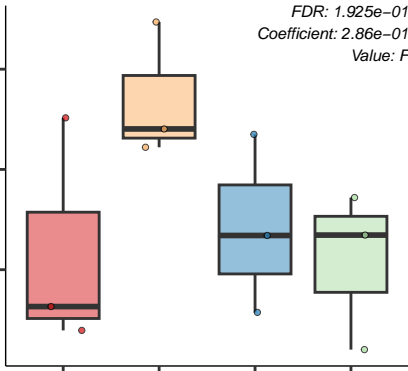
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



CBSS.262719.3.peg.410

FDR: 1.931e-01

Coefficient: 1.03e-01

Value: F

0.13
0.12
0.11
0.10

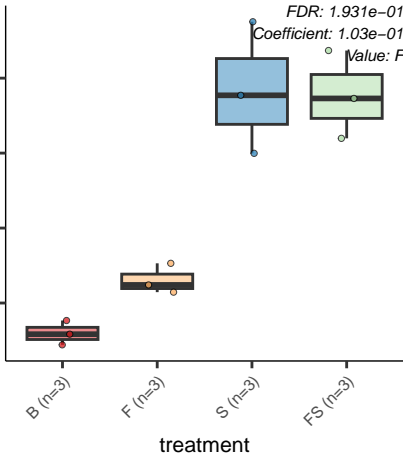
B (n=3)

F (n=3)

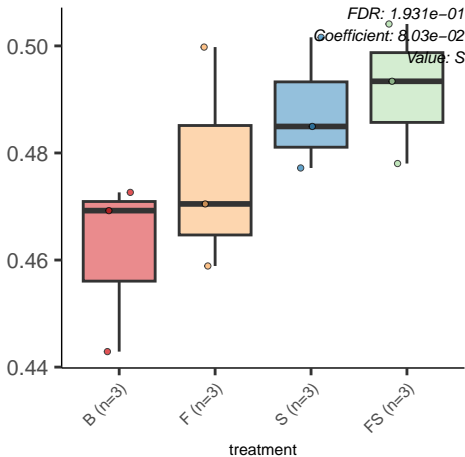
S (n=3)

FS (n=3)

treatment

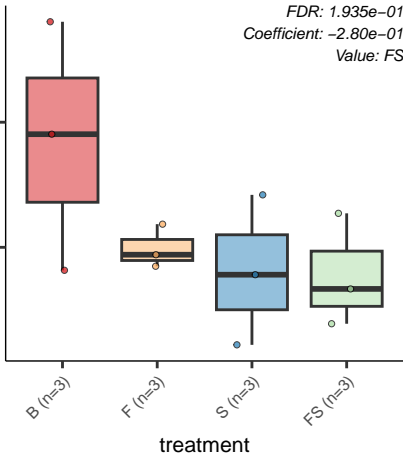


Riboflavin...FMN.and.FAD.metabolism.Extended



Ubiquinone.Biosynthesis

FDR: 1.935e-01
Coefficient: -2.80e-01
Value: FS



Lysozyme.inhibitors

B (n=3)

F (n=3)

S (n=3)

FS (n=3)

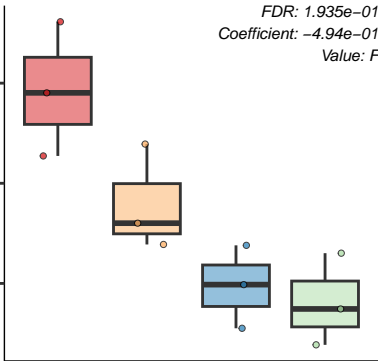
treatment

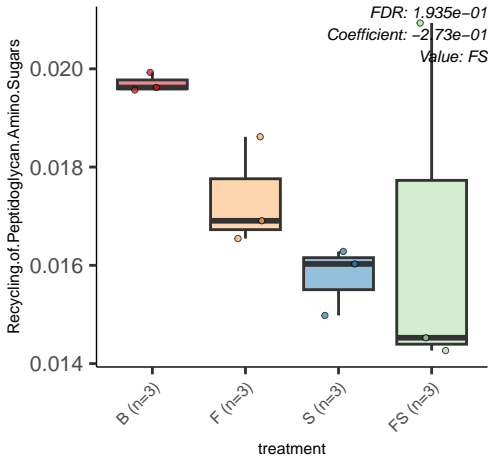
FDR: 1.935e-01
Coefficient: -4.94e-01
Value: F

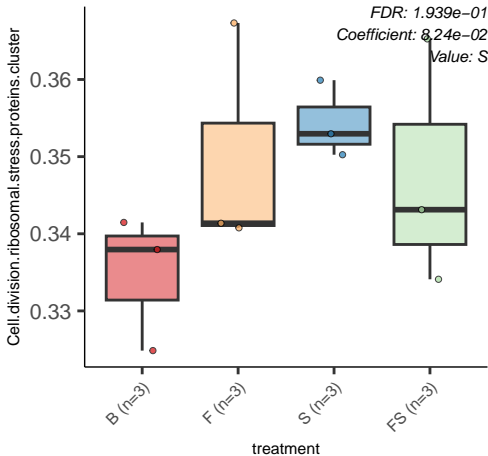
0.0100

0.0075

0.0050







Galactosylceramide.and.Sulfatide.metabolism

FDR: 1.969e-01
Coefficient: -1.03e-01
Value: FS

0.70
0.65

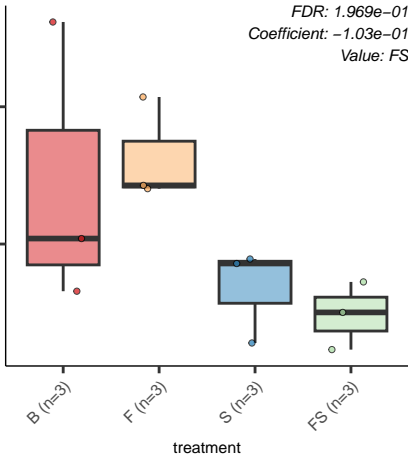
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Chorismate.Synthesis

0.26

0.25

0.24

B (n=3)

F (n=3)

S (n=3)

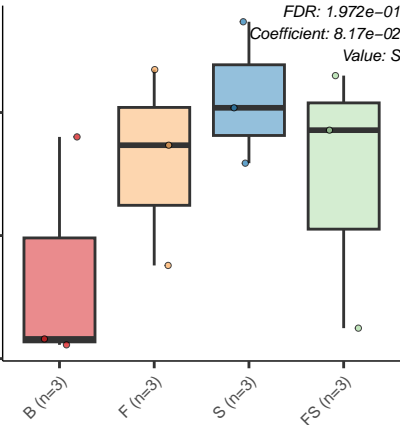
FS (n=3)

treatment

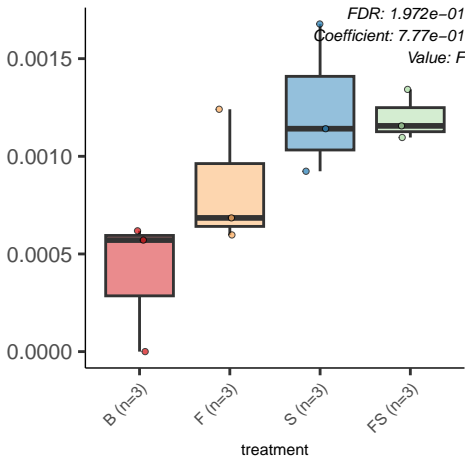
FDR: 1.972e-01

Coefficient: 8.17e-02

Value: S



Pyrroloquinoline.Quinone.biosynthesis



Catechol.branch.of.beta.ketoadipate.pathway

FDR: 2.006e-01

Coefficient: 9.10e-01

Value: F

B (n=3)

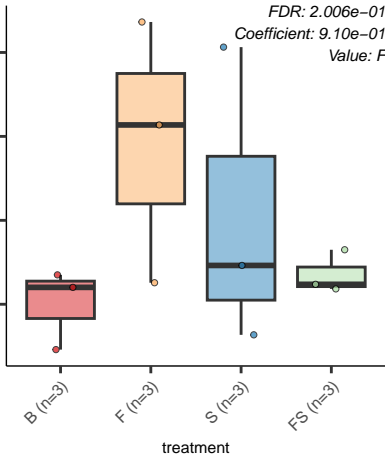
F (n=3)

S (n=3)

FS (n=3)

treatment

0.0025
0.0020
0.0015
0.0010



Periplasmic.Acid.Stress.Response.in.Enterobacteria

FDR: 2.006e-01
Coefficient: -7.83e-01
Value: F

0.012
0.008
0.004

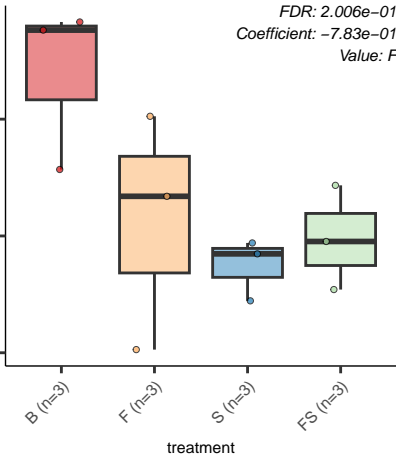
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment

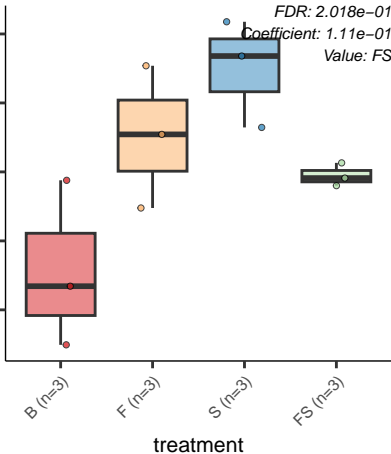


tRNA.aminoacylation..Trp

FDR: 2.018e-01

Coefficient: 1.11e-01

Value: FS



Alkanesulfonates.Utilization

FDR: 2.021e-01
Coefficient: -2.85e-01
Value: FS

0.009

0.008

0.007

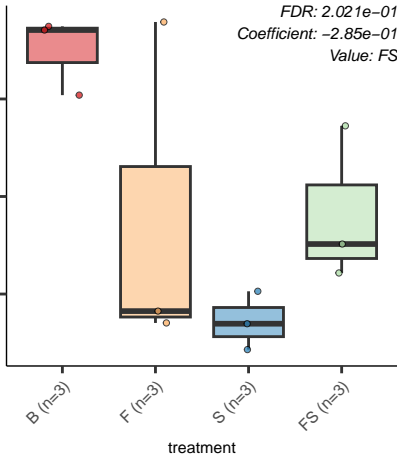
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Glycine.and.Serine.Utilization

FDR: 2.025e-01
Coefficient: -7.26e-02
Value: S

0.23
0.22
0.21
0.20

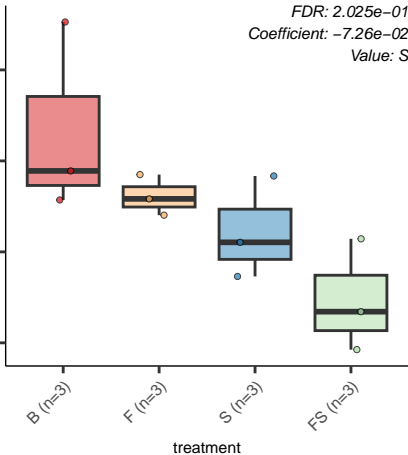
B (n=3)

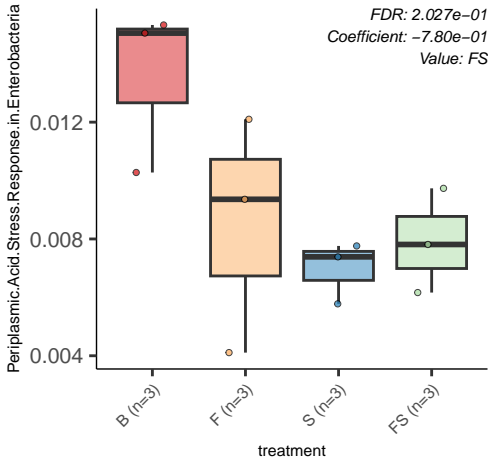
F (n=3)

S (n=3)

FS (n=3)

treatment





Hexose.Phosphate.Uptake.System

FDR: 2.027e-01
Coefficient: -4.04e-01
Value: F

0.024
0.020
0.016
0.012

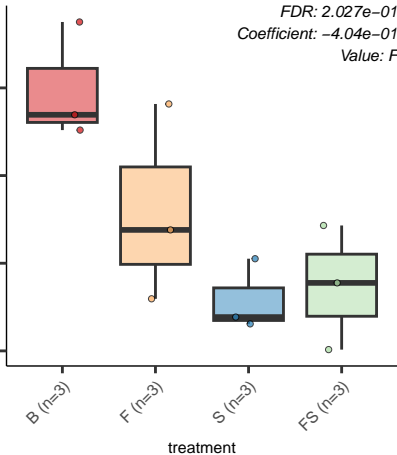
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Ubiquinone.Biosynthesis

FDR: 2.043e-01

Coefficient: -2.74e-01

Value: S

0.06

0.05

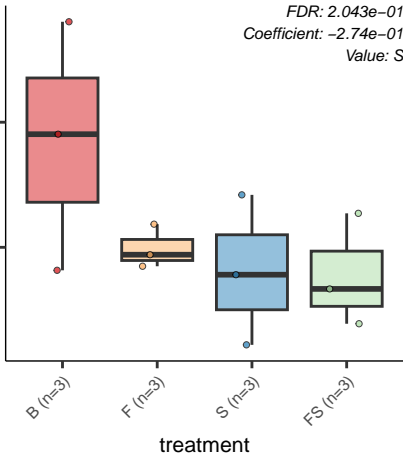
B (n=3)

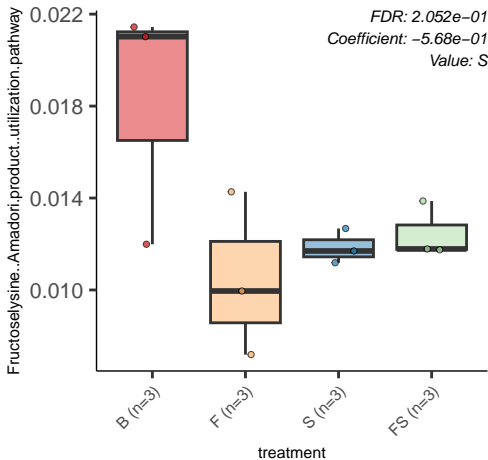
F (n=3)

S (n=3)

FS (n=3)

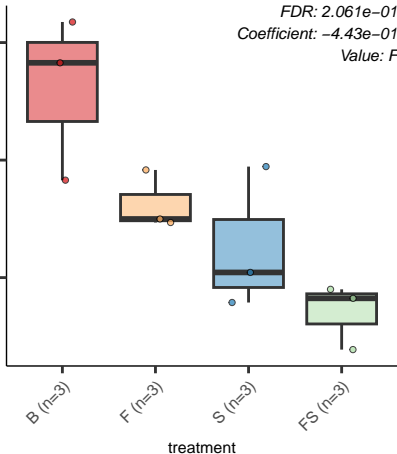
treatment

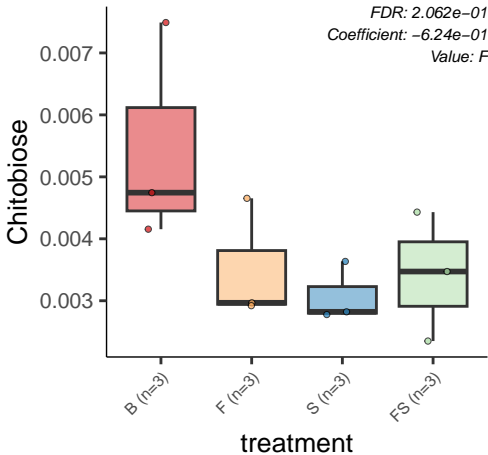


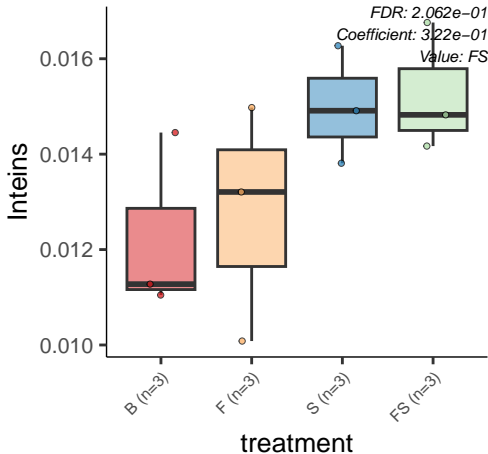


Siderophore. Yersiniabactin. Biosynthesis

FDR: 2.061e-01
Coefficient: -4.43e-01
Value: F







Phosphate.metabolism

FDR: 2.069e-01
Coefficient: 3.28e-02
Value: S

1.18

1.16

1.14

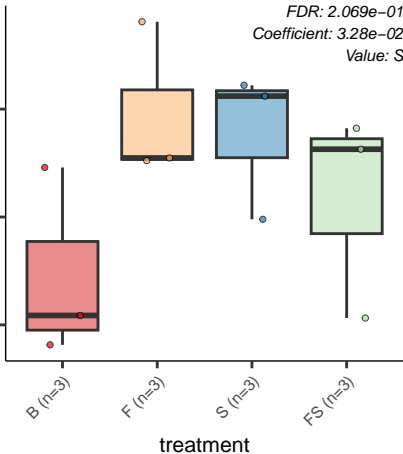
B (n=3)

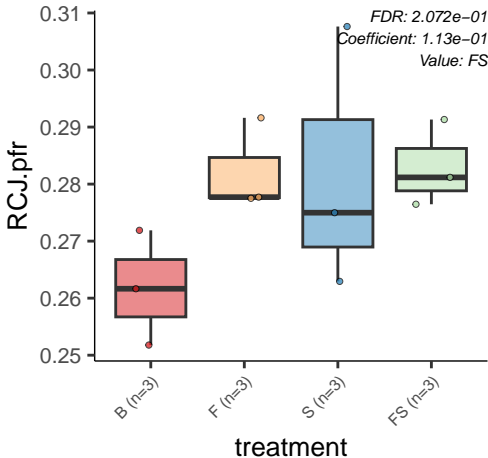
F (n=3)

S (n=3)

FS (n=3)

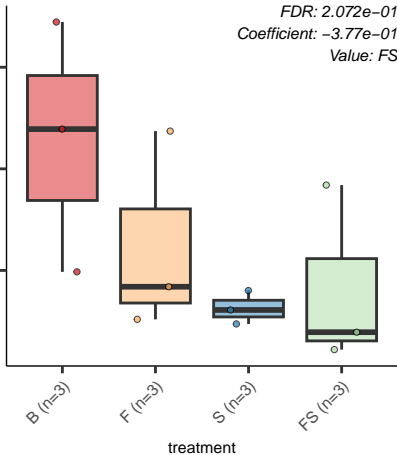
treatment





SeqA.and.Co.occuring.Genes

FDR: 2.072e-01
Coefficient: -3.77e-01
Value: FS

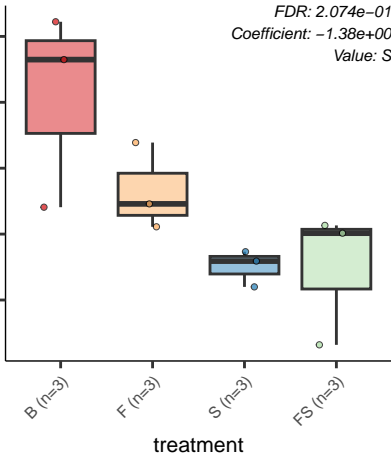


X..945..Fimbriae

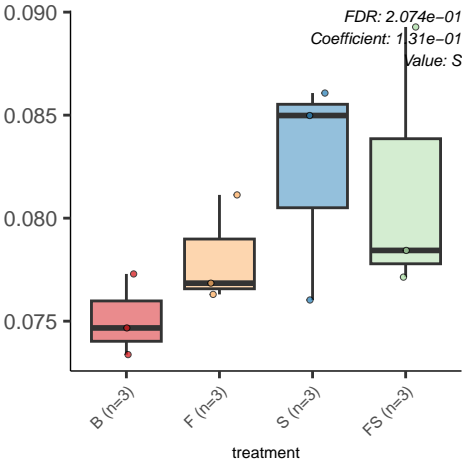
FDR: 2.074e-01

Coefficient: -1.38e+00

Value: S



Hyperosmotic.potassium.uptake



Iron.Scavenging.cluster.in.Thermus

FDR: 2.074e-01
Coefficient: -1.77e+00
Value: FS

0.00075
0.00050
0.00025
0.00000

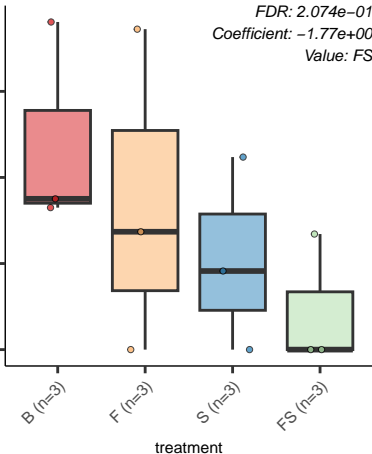
B (n=3)

F (n=3)

S (n=3)

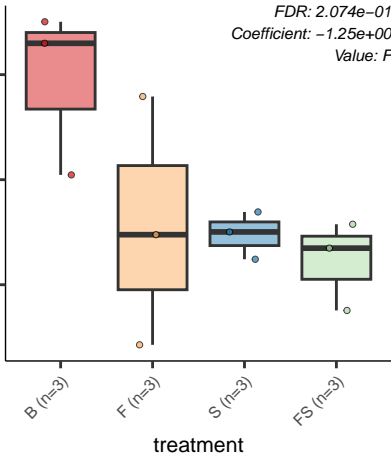
FS (n=3)

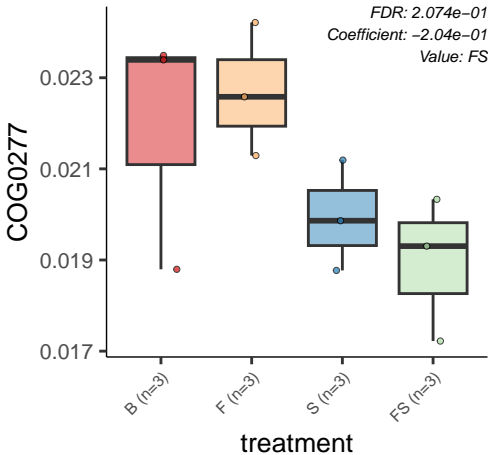
treatment

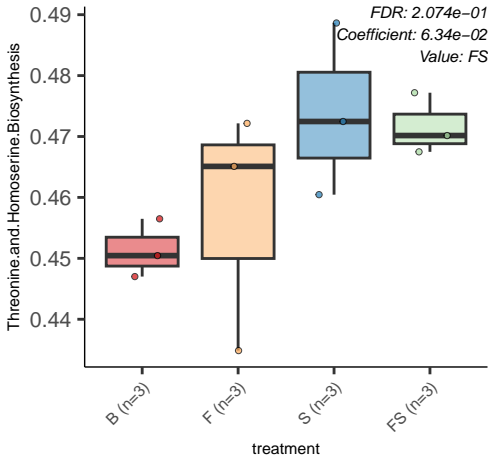


Salmonella.invasion.locus

FDR: 2.074e-01
Coefficient: -1.25e+00
Value: F

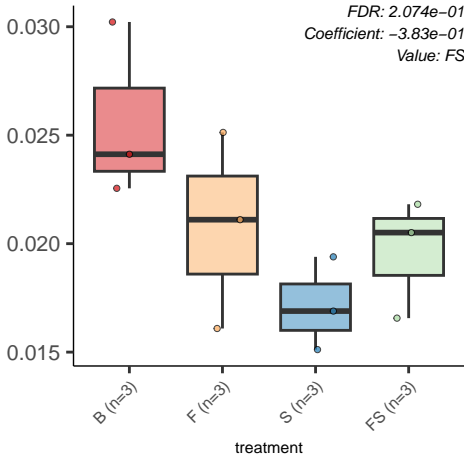






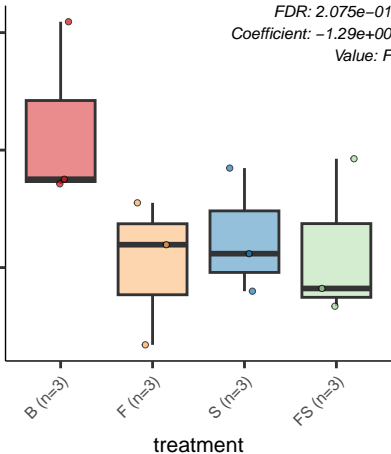
p.Aminobenzoyl.Glutamate.Utilization

FDR: 2.074e-01
Coefficient: -3.83e-01
Value: FS



CBSS.323850.3.peg.3284

FDR: 2.075e-01
Coefficient: -1.29e+00
Value: F



Glutamine.synthetases

FDR: 2.076e-01

Coefficient: 9.40e-02

Value: F

0.072

0.069

0.066

0.063

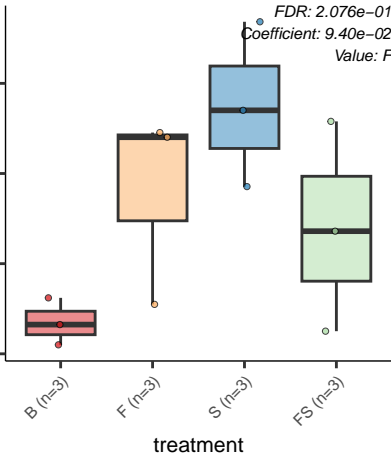
B (n=3)

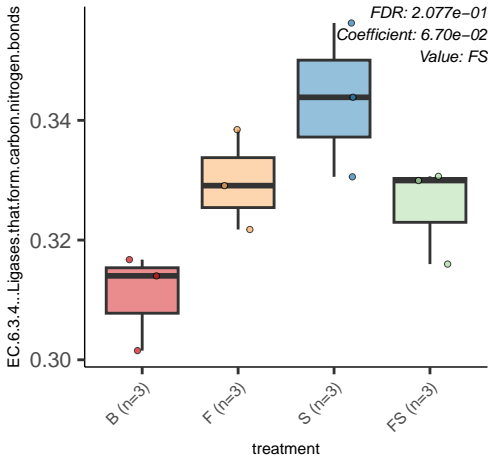
F (n=3)

S (n=3)

FS (n=3)

treatment





rRNA.modification.Archaea

FDR: 2.086e-01
Coefficient: -6.04e-01
Value: F

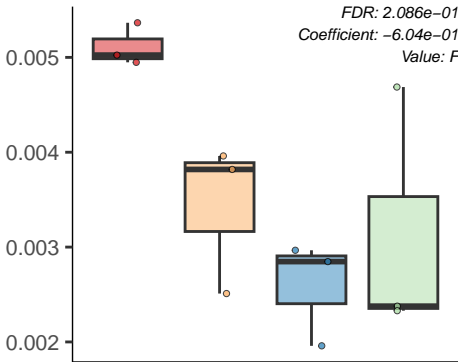
B (n=3)

F (n=3)

S (n=3)

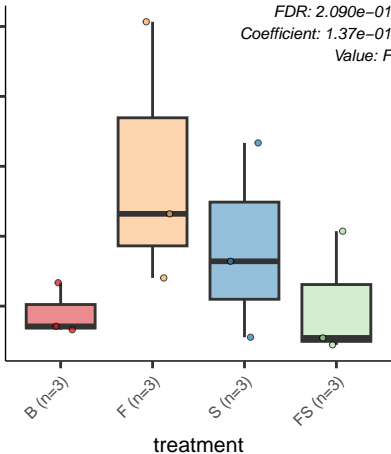
FS (n=3)

treatment



Glutamate.dehydrogenases

FDR: 2.090e-01
Coefficient: 1.37e-01
Value: F



Phosphorylcholine.incorporation.in.LPS

0.016
0.014
0.012
0.010

B (n=3)

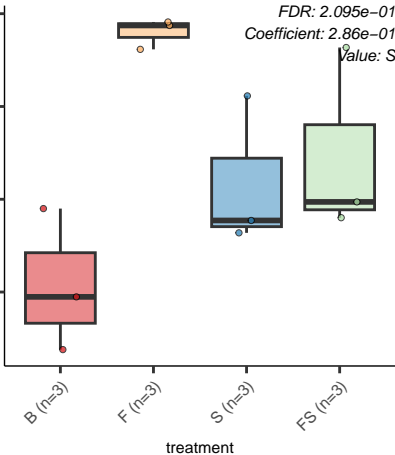
F (n=3)

S (n=3)

FS (n=3)

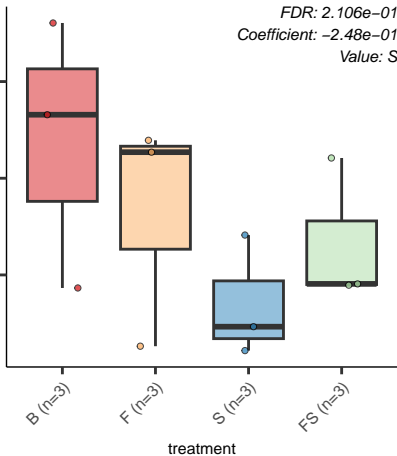
treatment

FDR: 2.095e-01
Coefficient: 2.86e-01
Value: S

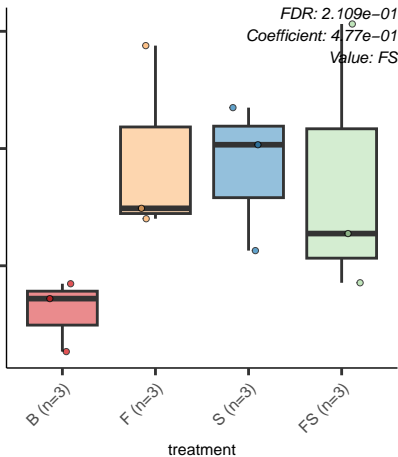


Small.acid.soluble.spore.proteins

FDR: 2.106e-01
Coefficient: -2.48e-01
Value: S



ABC.transporter.tungstate..TC.3.A.1.6.2.



DNA.Repair.Base.Excision

FDR: 2.109e-01

Coefficient: 5.66e-02

Value: FS

0.44

0.43

0.42

0.41

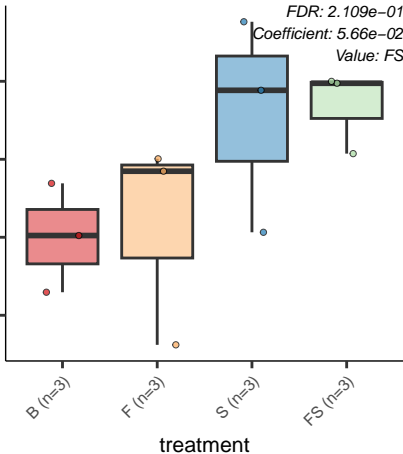
B (n=3)

F (n=3)

S (n=3)

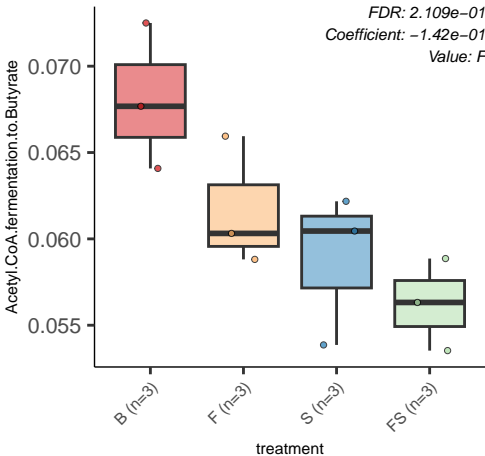
FS (n=3)

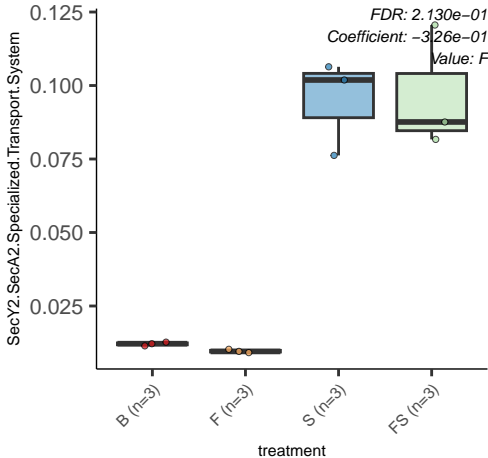
treatment



Acetyl.CoA.fermentation.to.Butyrate

FDR: 2.109e-01
Coefficient: -1.42e-01
Value: F





Fatty.Acid.Biosynthesis.FASII

FDR: 2.139e-01
Coefficient: 6.88e-02
Value: FS

0.650
0.625
0.600
0.575

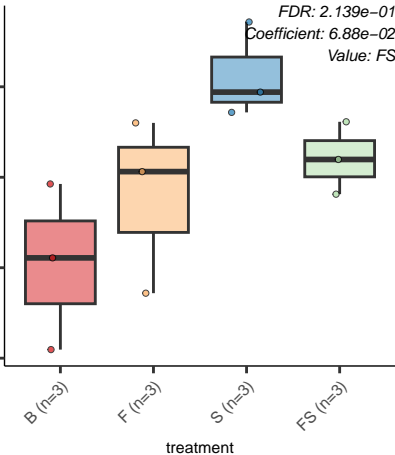
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Heme.biosynthesis.orphans

FDR: 2.139e-01
Coefficient: -1.58e-01
Value: FS

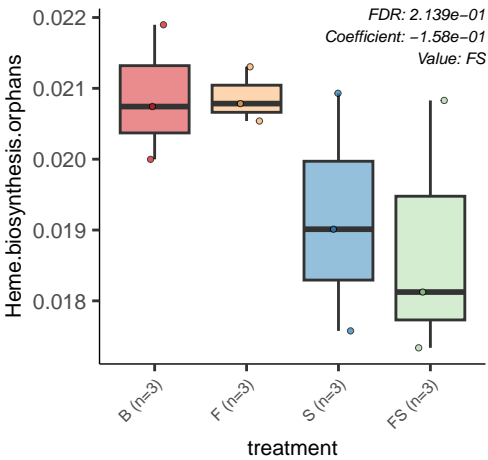
B (n=3)

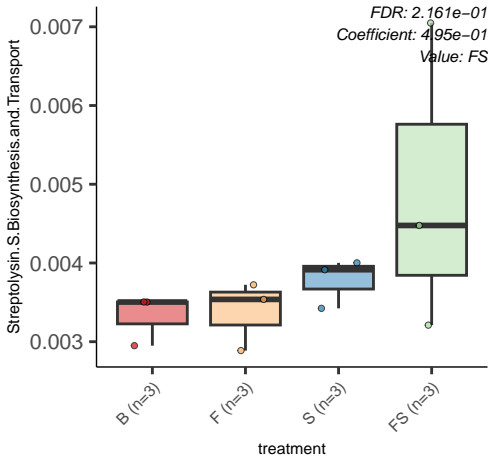
F (n=3)

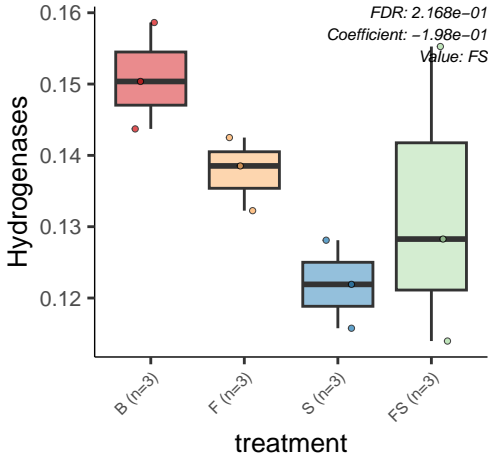
S (n=3)

FS (n=3)

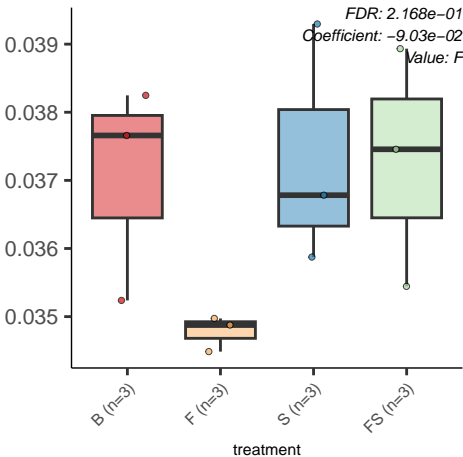
treatment







Ribosomal.protein.S5p.acylation



Zinc.regulated.enzymes

FDR: 2.168e-01
Coefficient: -3.29e-01
Value: F

B (n=3)

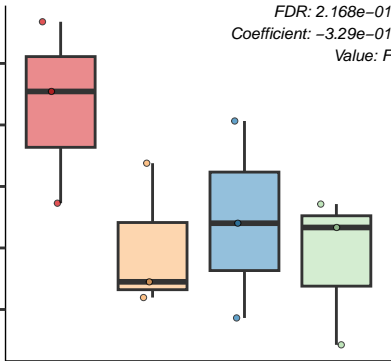
F (n=3)

S (n=3)

FS (n=3)

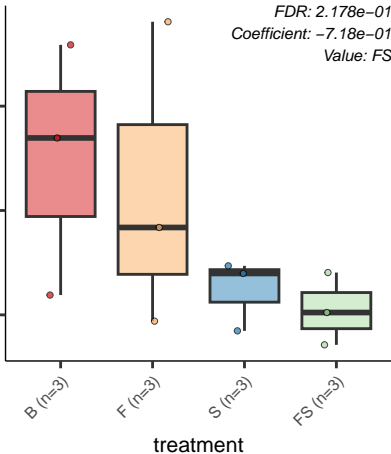
treatment

0.060
0.055
0.050
0.045
0.040

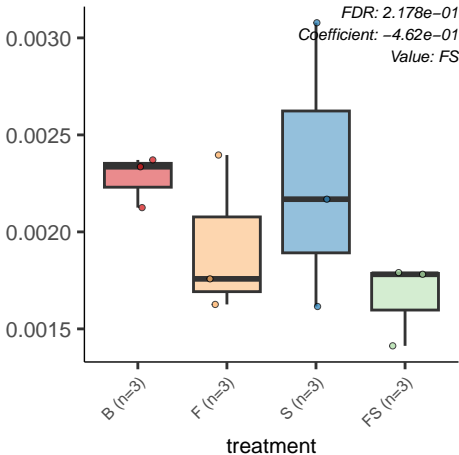


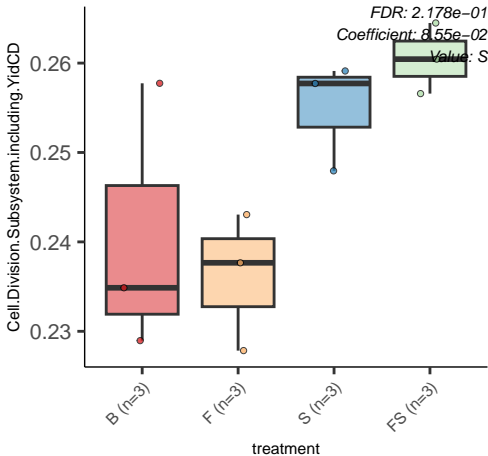
CBSS.211586.1.peg.2357

FDR: 2.178e-01
Coefficient: -7.18e-01
Value: FS



CBSS.323098.3.peg.2823





Deoxyribose.and.Deoxynucleoside.Catabolism

0.18
0.16
0.14

FDR: 2.178e-01

Coefficient: 1.26e-01

Value: FS

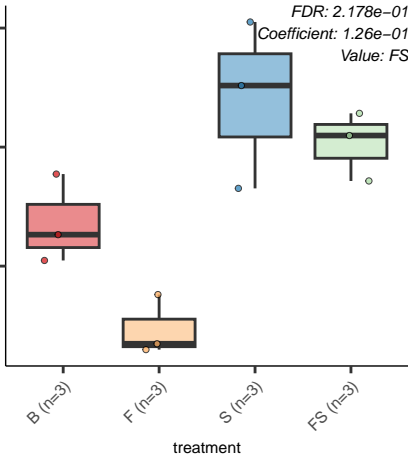
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



NusA.TFII.Cluster

FDR: 2.178e-01

Coefficient: 8.59e-02

Value: S

0.130

0.125

0.120

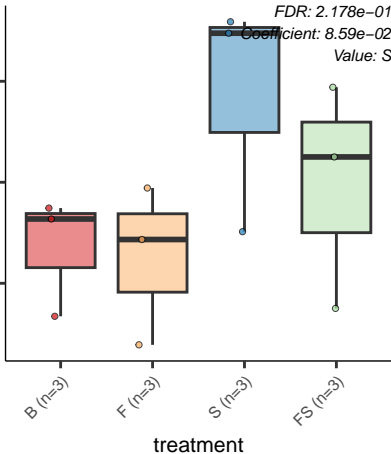
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Alkanesulfonate.assimilation

FDR: 2.194e-01
Coefficient: -2.15e-01
Value: FS

0.09
0.08

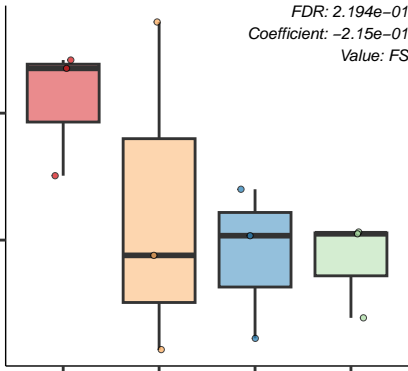
B (n=3)

F (n=3)

S (n=3)

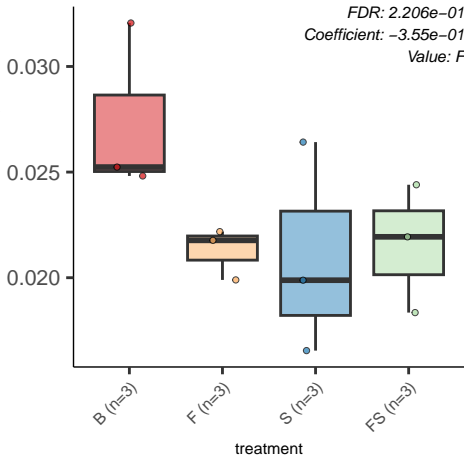
FS (n=3)

treatment



Autoinducer.2...Al.2...transport.and.processing..lsrACDBFGE.

FDR: 2.206e-01
Coefficient: -3.55e-01
Value: F



Periplasmic.Binding.Protein.Dependent.Transport.System.for...945.

FDR: 2.206e-01
Coefficient: -1.80e+00
Value: FS

0.00075
0.00050
0.00025
0.00000

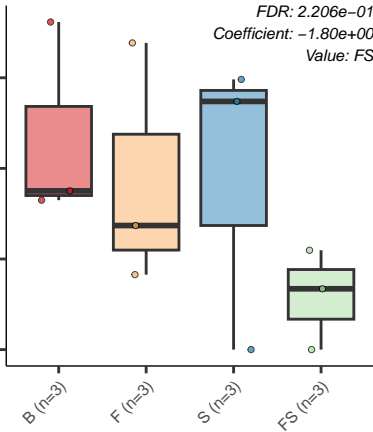
B (n=3)

F (n=3)

S (n=3)

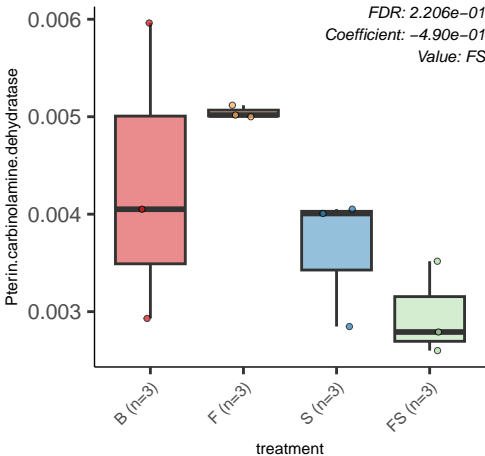
FS (n=3)

treatment

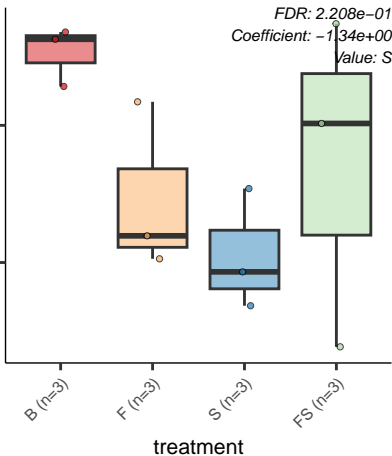


Pterin.carbinolamine.dehydratase

FDR: 2.206e-01
Coefficient: -4.90e-01
Value: FS



CBSS.265072.7.peg.546



Lipopolysaccharide.assembly.cluster

FDR: 2.208e-01
Coefficient: -4.51e-01
Value: FS

B (n=3)

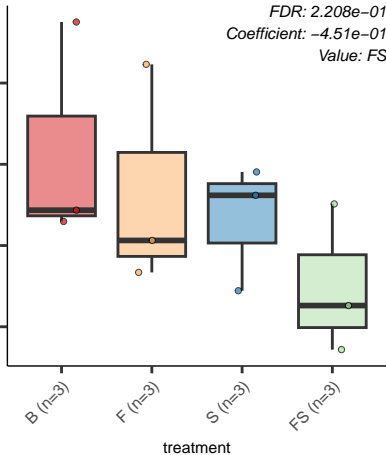
F (n=3)

S (n=3)

FS (n=3)

treatment

0.0175
0.0150
0.0125
0.0100



Selenocysteine.metabolism

FDR: 2.208e-01
Coefficient: -1.97e-01
Value: FS

0.08

0.07

0.06

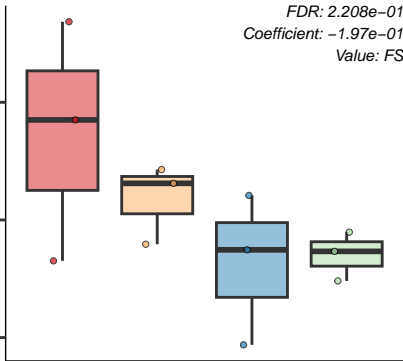
B (n=3)

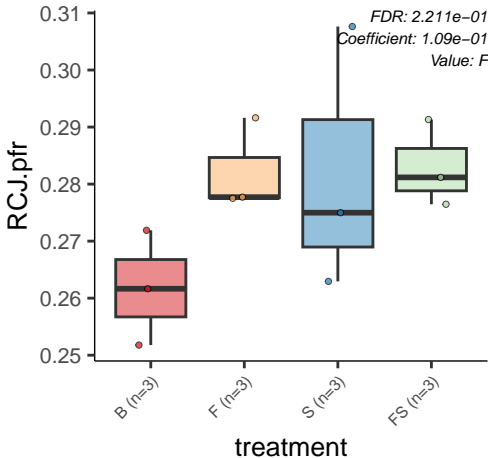
F (n=3)

S (n=3)

FS (n=3)

treatment





LOS.core.oligosaccharide.biosynthesis

FDR: 2.222e-01
Coefficient: -8.76e-02
Value: S

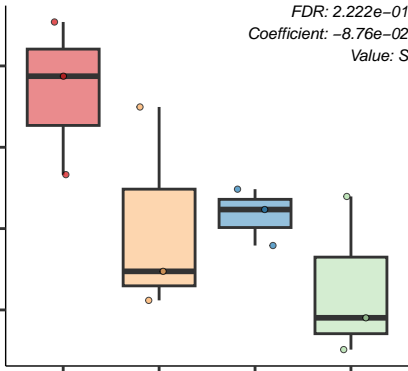
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Coenzyme.B.synthesis

FDR: 2.242e-01
Coefficient: 1.61e+00
Value: S

0.0015
0.0010
0.0005
0.0000

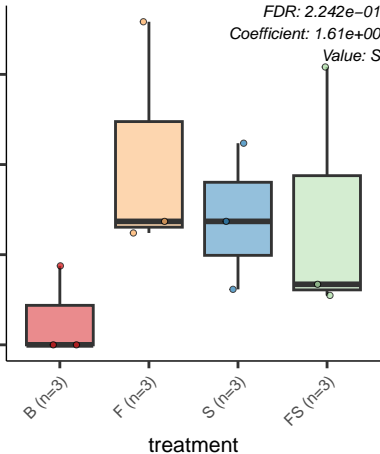
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Pseudouridine.Metabolism

FDR: 2.242e-01
Coefficient: -6.92e-01
Value: FS

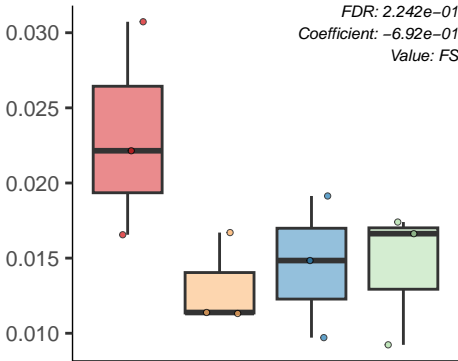
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



At1g54520

FDR: 2.253e-01
Coefficient: 3.80e-01
Value: F

0.006

0.005

0.004

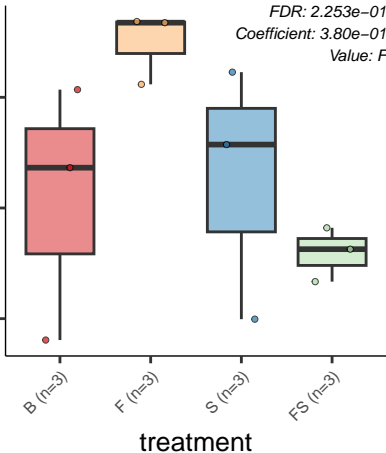
B (n=3)

F (n=3)

S (n=3)

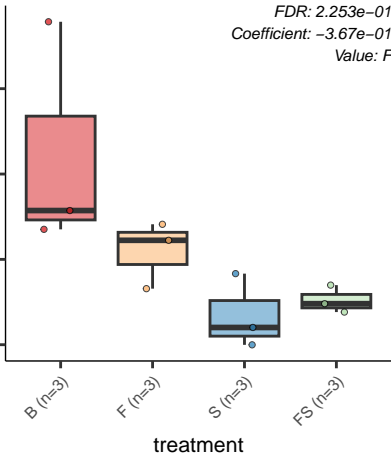
FS (n=3)

treatment



CBSS.211586.1.pcg.3133

FDR: 2.253e-01
Coefficient: -3.67e-01
Value: F



Flagellum.in.Campylobacter

FDR: 2.255e-01
Coefficient: 1.84e-01
Value: FS

0.060

0.055

0.050

0.045

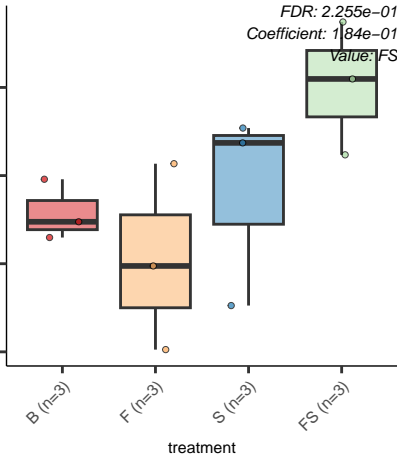
B (n=3)

F (n=3)

S (n=3)

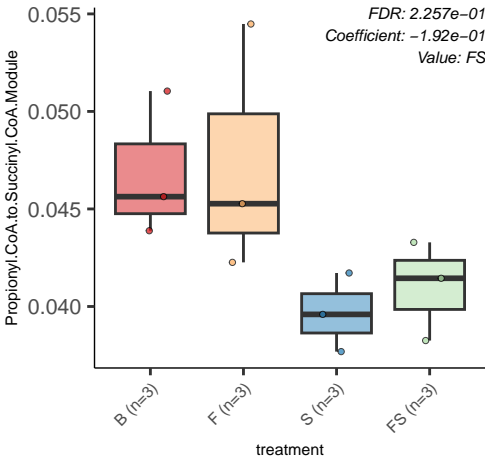
FS (n=3)

treatment



Propionyl.CoA.to.Succinyl.CoA.Module

FDR: 2.257e-01
Coefficient: -1.92e-01
Value: FS



Thiamin.Copy.RZ

FDR: 2.257e-01
Coefficient: 9.57e-02
Value: F

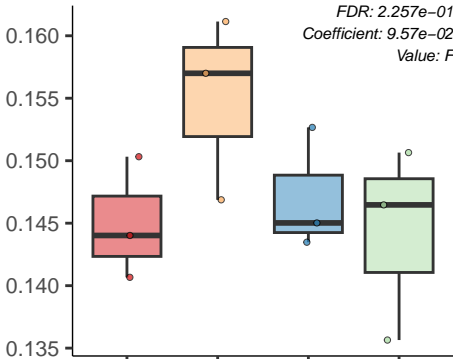
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Commensurate.regulon.activation

FDR: 2.263e-01
Coefficient: -8.31e-01
Value: S

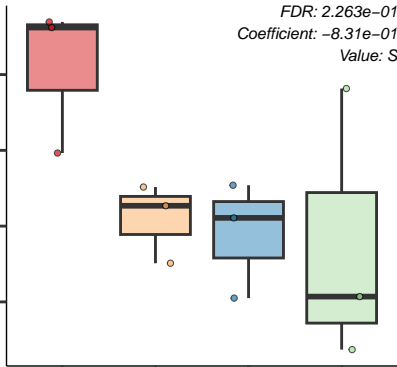
B (n=3)

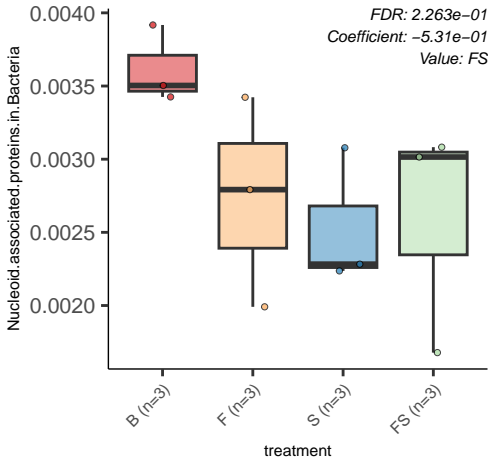
F (n=3)

S (n=3)

FS (n=3)

treatment





Proteorhodopsin

B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment

0.00200

0.00175

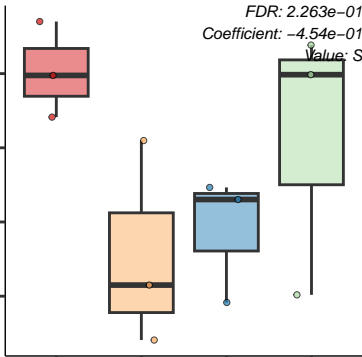
0.00150

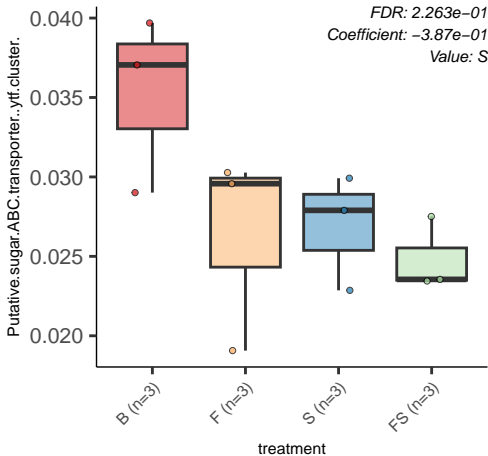
0.00125

FDR: 2.263e-01

Coefficient: -4.54e-01

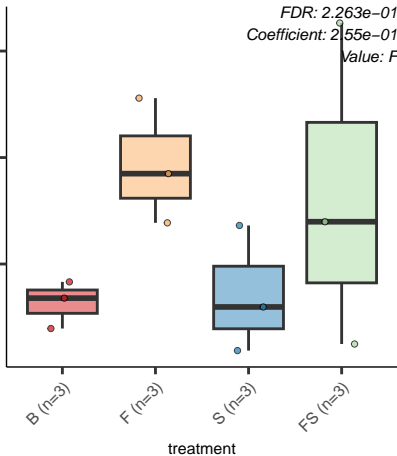
Value: S



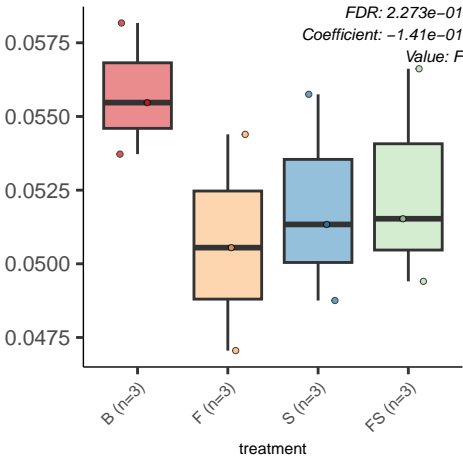


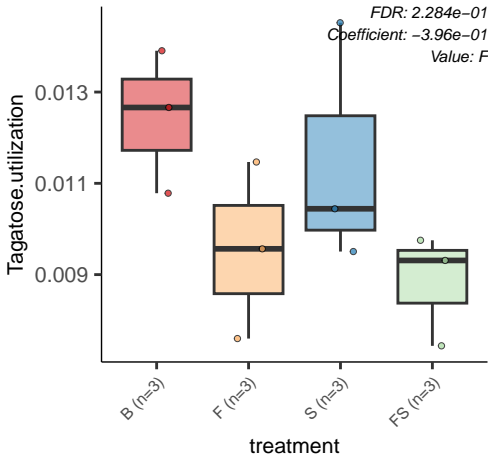
Ribosome.activity.modulation

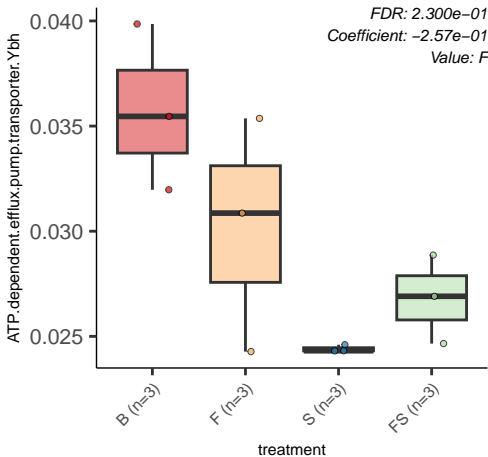
FDR: 2.263e-01
Coefficient: 2.55e-01
Value: F

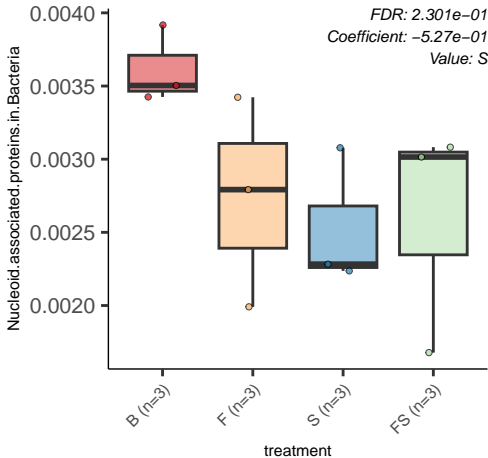


BlaR1.Family.Regulatory.Sensor.transducer.Disambiguation

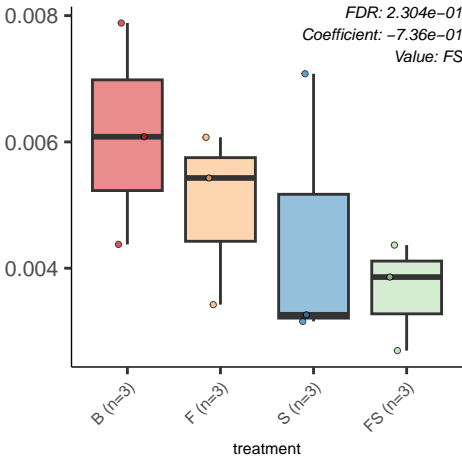








Glutathione.dependent.pathway.of.formaldehyde.detoxifica



Type.IV.pilus

0.0025

0.0020

0.0015

B (n=3)

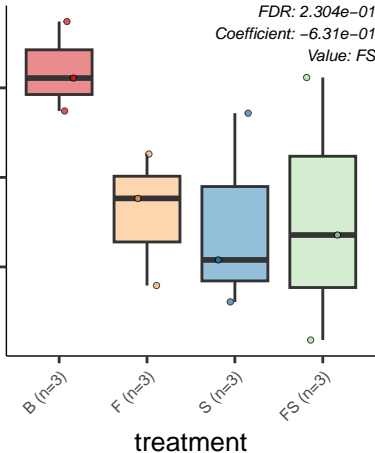
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 2.304e-01
Coefficient: -6.31e-01
Value: FS



Ribosome.LSU.eukaryotic.and.archaeal

FDR: 2.304e-01
Coefficient: 4.24e-01
Value: FS

0.006
0.005
0.004
0.003

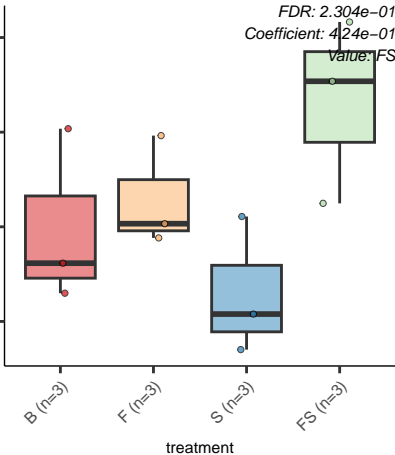
B (n=3)

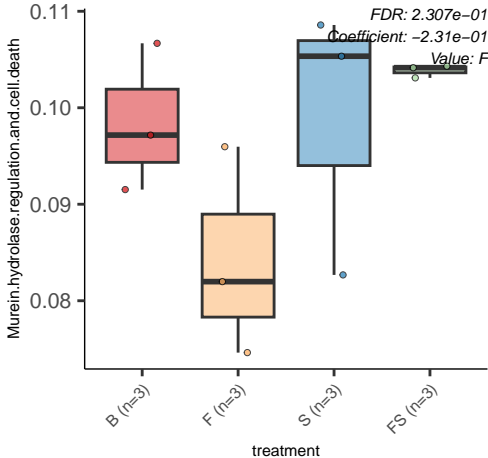
F (n=3)

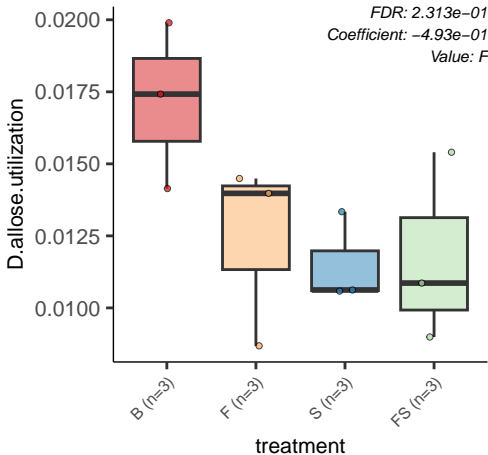
S (n=3)

FS (n=3)

treatment

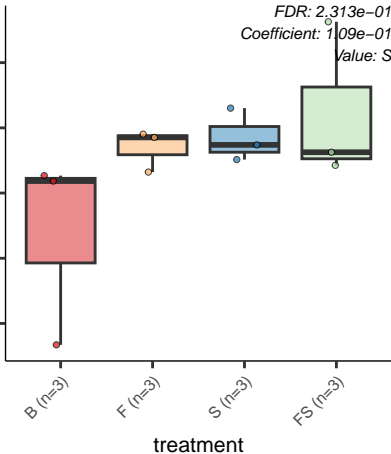


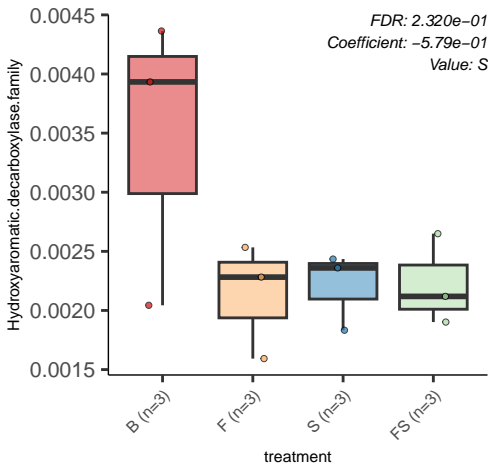




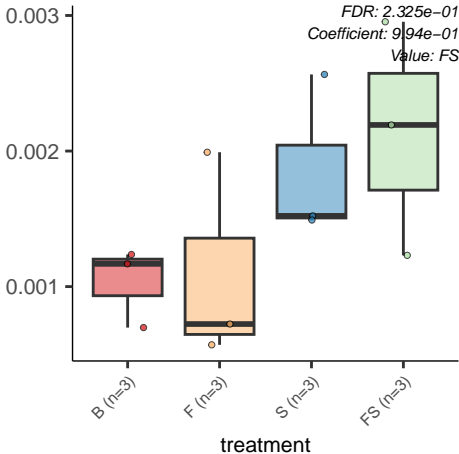
tRNA.aminoacylation..Tyr

FDR: 2.313e-01
Coefficient: 1.109e-01
Value: S





CoenzymeM.Archaea



Ethanolamine.utilization

FDR: 2.325e-01
Coefficient: -1.80e-01
Value: FS

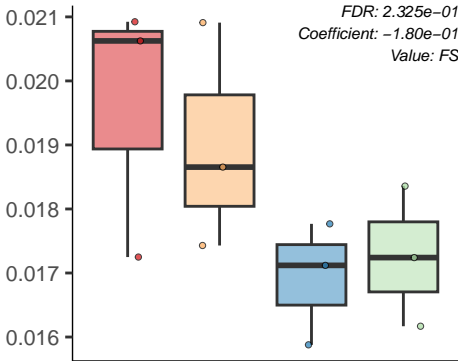
B (n=3)

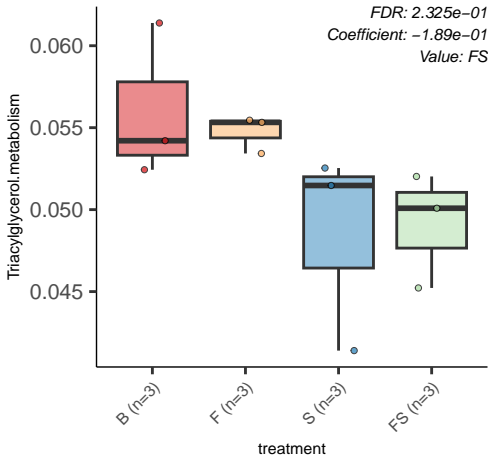
F (n=3)

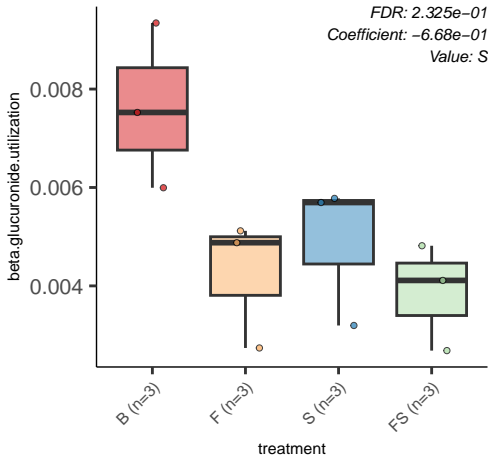
S (n=3)

FS (n=3)

treatment

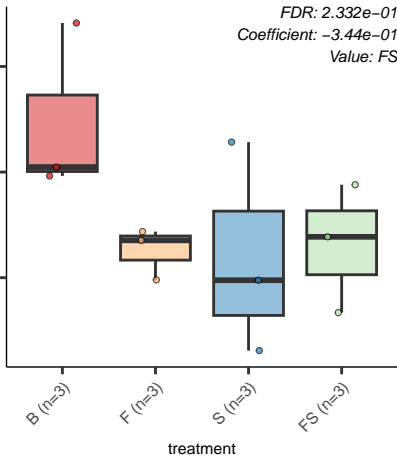




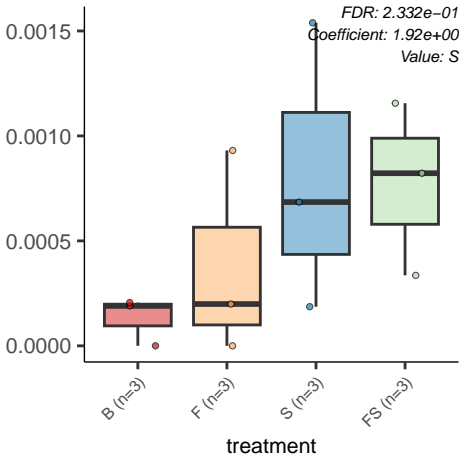


Autoinducer.2...Al.2...transport.and.processing..lsrACDBFGE.

FDR: 2.332e-01
Coefficient: -3.44e-01
Value: FS

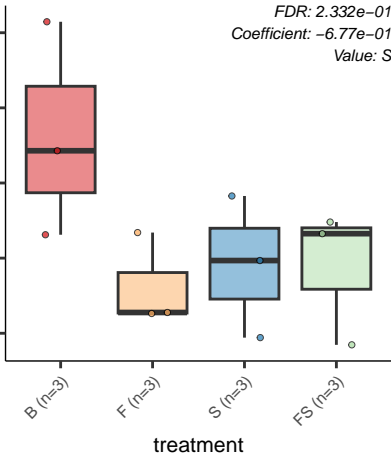


Phenazine.biosynthesis

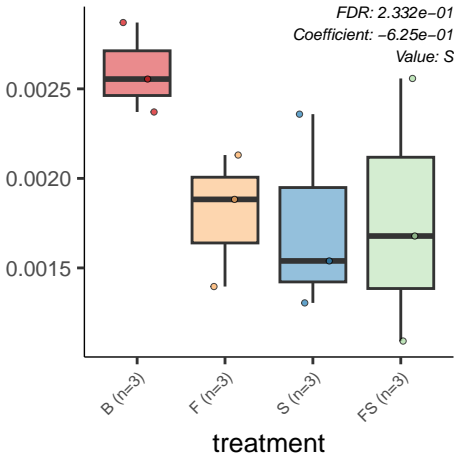


Pseudouridine.Metabolism

FDR: 2.332e-01
Coefficient: -6.77e-01
Value: S



Type.IV.pilus



CBSS.323850.3.pcg.3269

FDR: 2.341e-01
Coefficient: -5.37e-01
Value: F

B (n=3)

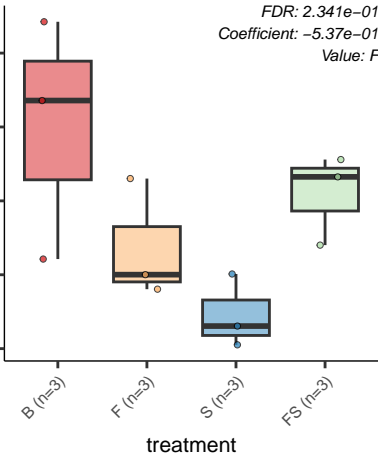
F (n=3)

S (n=3)

FS (n=3)

treatment

0.0150
0.0125
0.0100
0.0075
0.0050



Cysteine.Biosynthesis..MCB.432

FDR: 2.341e-01
Coefficient: -5.11e-02
Value: S

0.205
0.200
0.195

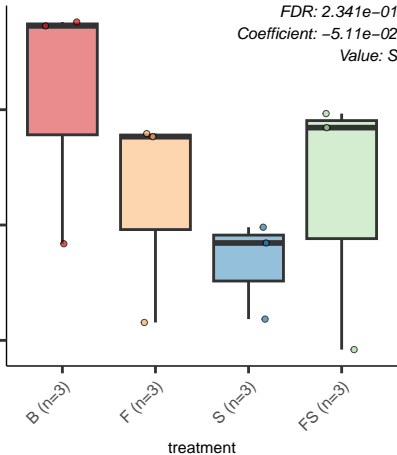
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



DNA.repair..bacterial.RecBCD.pathway

FDR: 2.341e-01
Coefficient: -7.75e-02
Value: FS

0.40
0.38
0.36

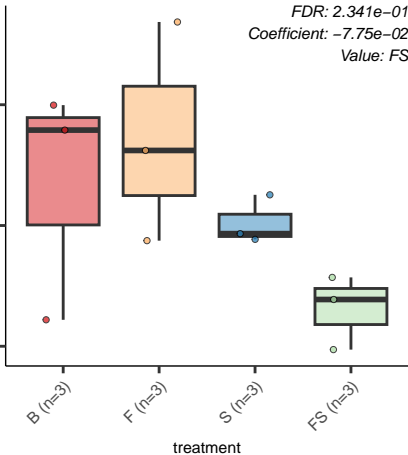
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



At3g21300

0.15
0.14
0.13
0.12

B (n=3)

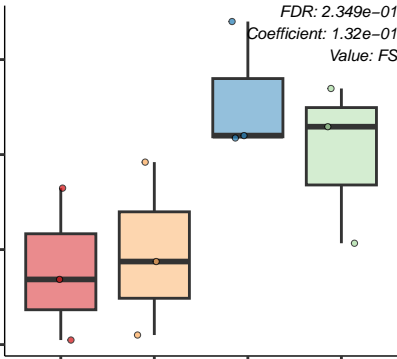
F (n=3)

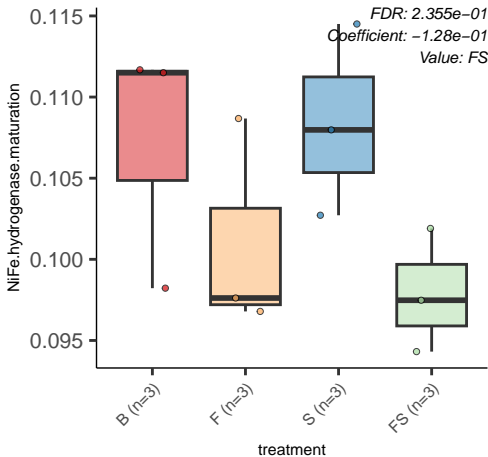
S (n=3)

FS (n=3)

treatment

FDR: 2.349e-01
Coefficient: 1.32e-01
Value: FS





Alkanesulfonate.assimilation

FDR: 2.359e-01
Coefficient: -2.07e-01
Value: S

0.09
0.08

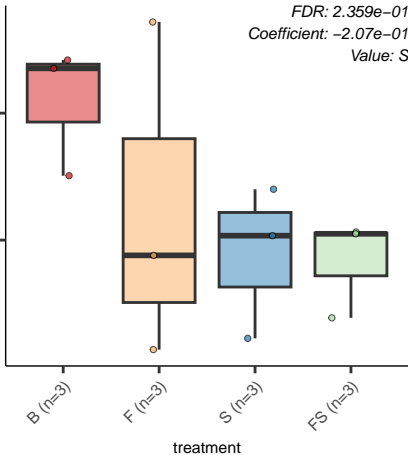
B (n=3)

F (n=3)

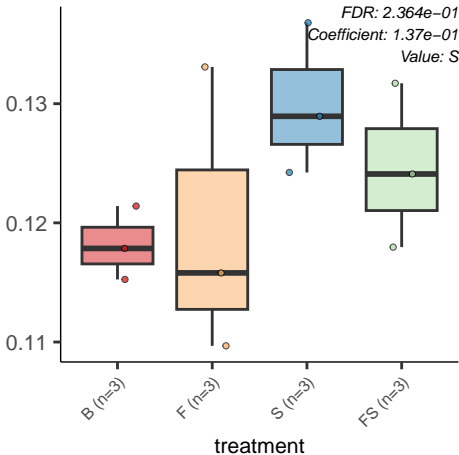
S (n=3)

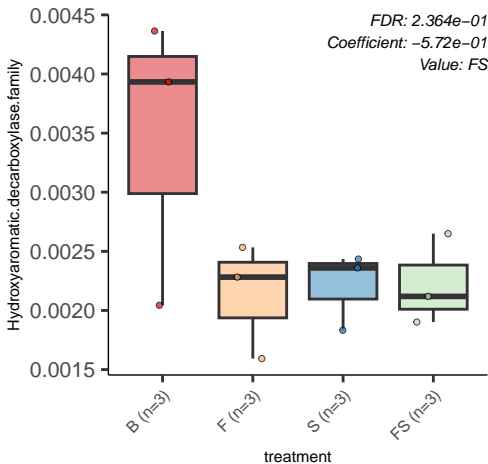
FS (n=3)

treatment



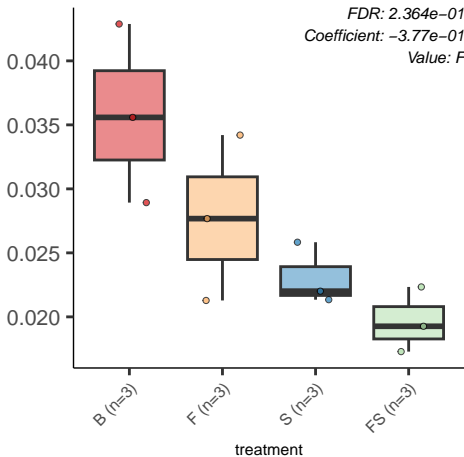
CBSS.281090.3.peg.464





Inner.membrane.protein.YhjD.and.conservd.cluster.involved.in.LPS

FDR: 2.364e-01
Coefficient: -3.77e-01
Value: F



Phage.DNA.methyltransferases

FDR: 2.364e-01
Coefficient: 1.65e-01
Value: FS

0.014
0.013
0.012
0.011

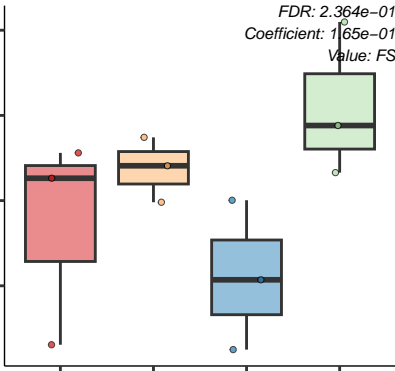
B (n=3)

F (n=3)

S (n=3)

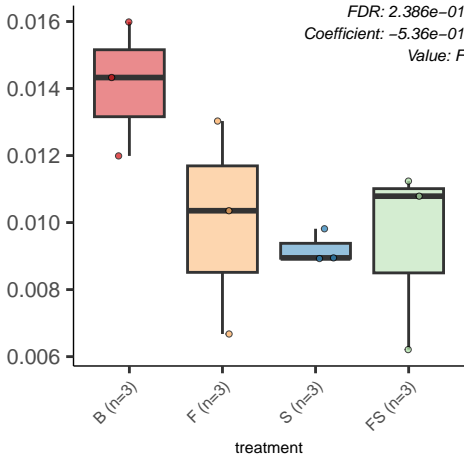
FS (n=3)

treatment

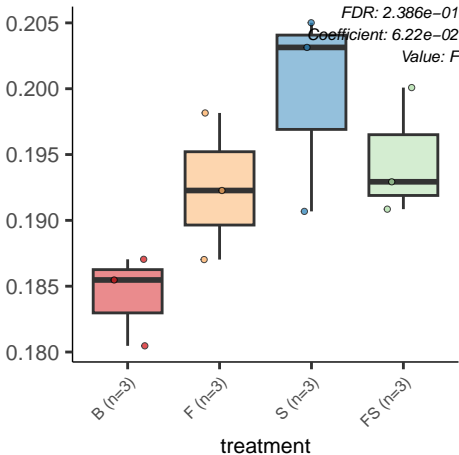


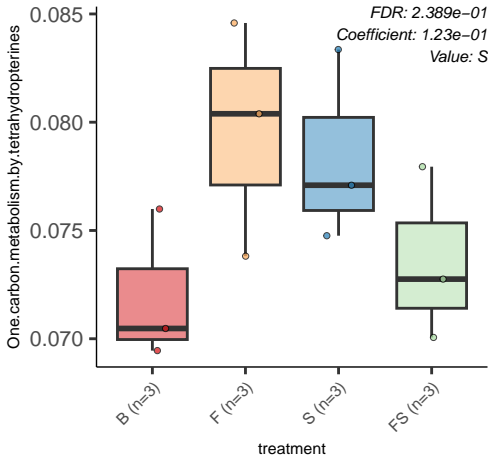
MukBEF:Chromosome.Condensation

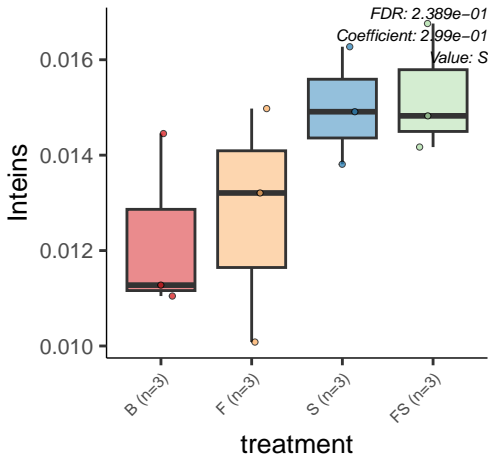
FDR: 2.386e-01
Coefficient: -5.36e-01
Value: F

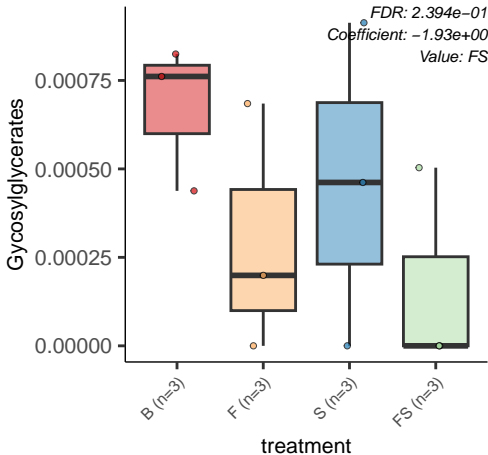


Test.Pyridoxin.B6



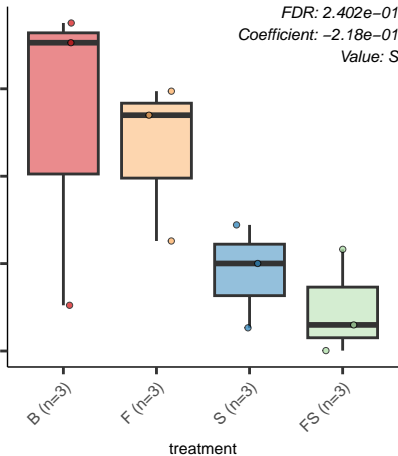


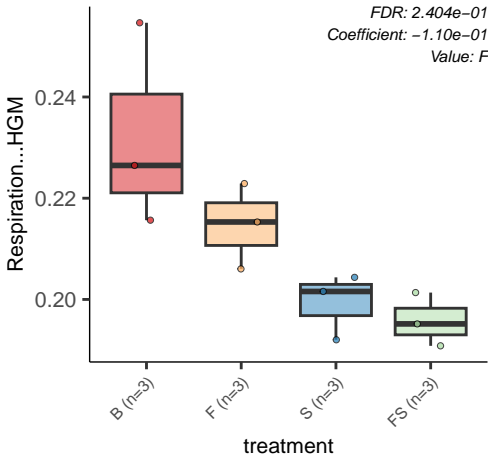




Homogenisate.pathway.of.aromatic.compound.degradati

FDR: 2.402e-01
Coefficient: -2.18e-01
Value: S





Fructose.utilization

0.29
0.28
0.27
0.26
0.25

B (n=3)

F (n=3)

S (n=3)

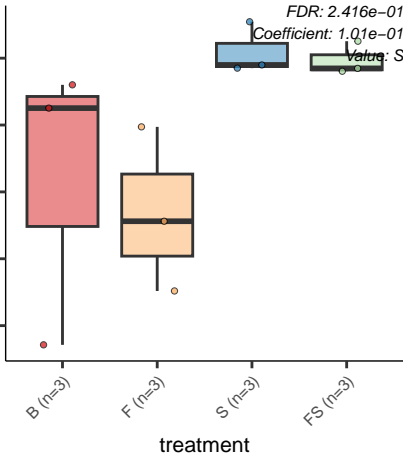
FS (n=3)

treatment

FDR: 2.416e-01

Coefficient: 1.01e-01

Value: S



Two.component.Response.Regulator.of.Virulence.ResD

FDR: 2.416e-01
Coefficient: 8.75e-01
Value: S

0.0015
0.0010
0.0005

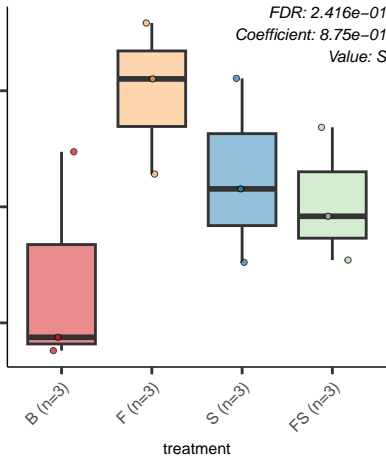
B (n=3)

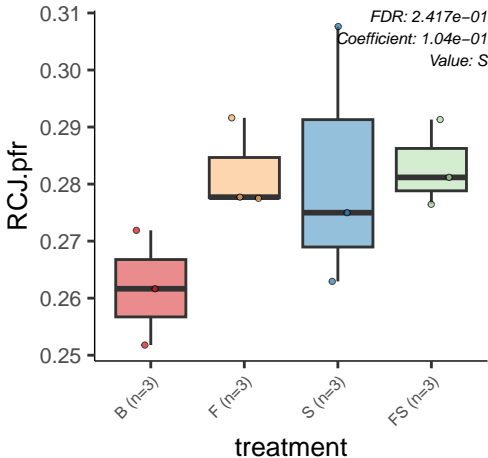
F (n=3)

S (n=3)

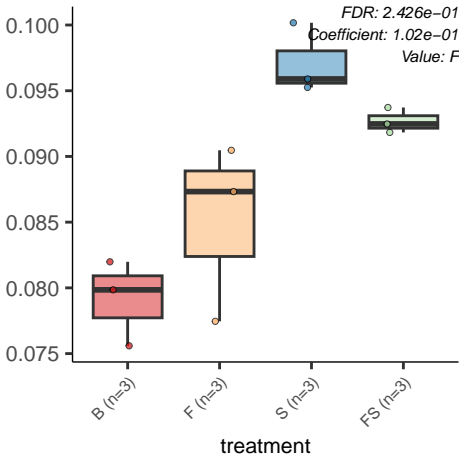
FS (n=3)

treatment



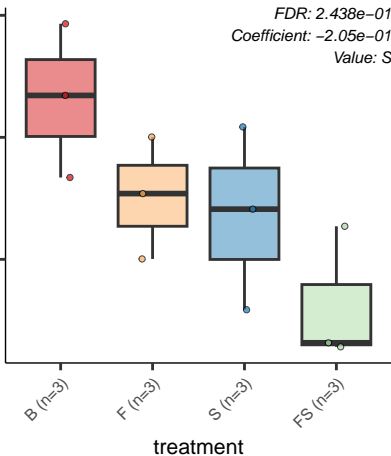


CBSS.84588.1.pcg.1247



Propanediol.utilization

FDR: 2.438e-01
Coefficient: -2.05e-01
Value: S



Ribosome.LSU.bacterial

FDR: 2.441e-01

Coefficient: 6.01e-02

Value: S

0.53

0.52

0.51

0.50

0.49

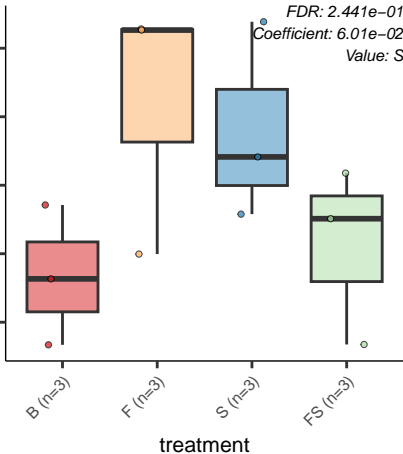
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



At1g14345

FDR: 2.442e-01
Coefficient: -2.23e-01
Value: FS

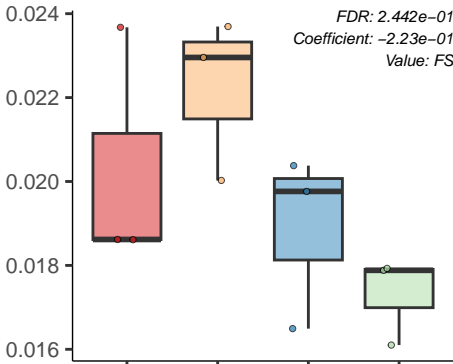
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



Cold.shock..CspA.family.of.proteins

FDR: 2.442e-01
Coefficient: -2.27e-01
Value: S

0.0275
0.0250
0.0225
0.0200

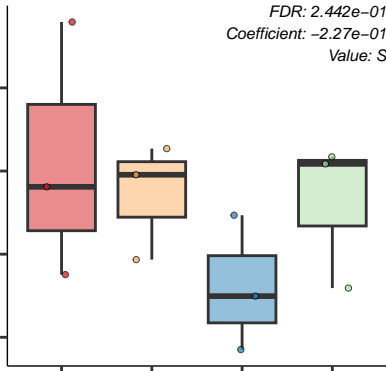
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

treatment



DNA.Repair.Base.Excision

FDR: 2.444e-01

Coefficient: 5.25e-02

Value: S

0.44

0.43

0.42

0.41

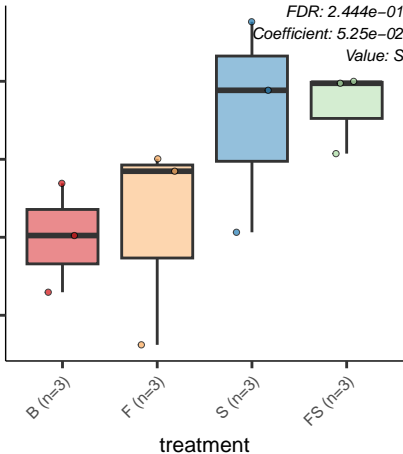
B (n=3)

F (n=3)

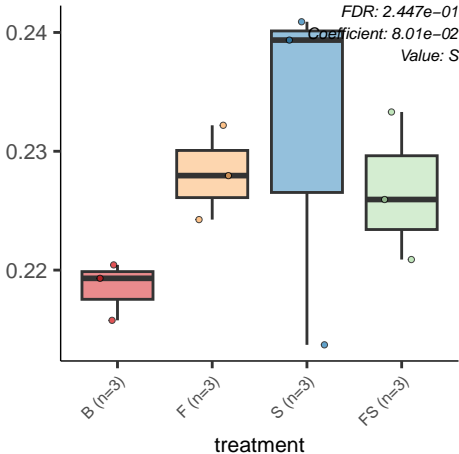
S (n=3)

FS (n=3)

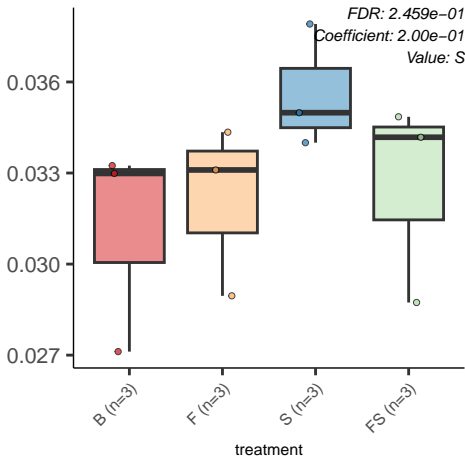
treatment



Fermentations..Lactate



A. Hypothetical.Protein.Related.to.Proline.Metabolism



Cyanate.hydrolysis

0.040

0.035

0.030

B (n=3)

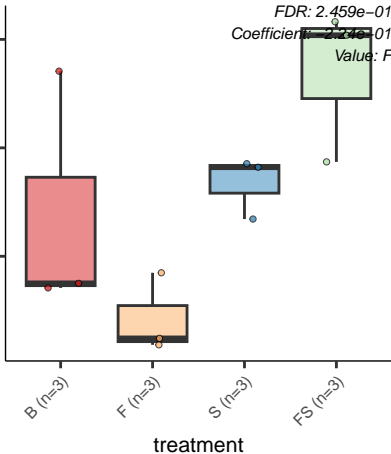
F (n=3)

S (n=3)

FS (n=3)

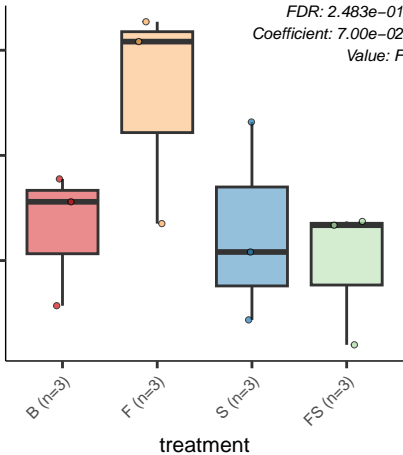
treatment

FDR: 2.459e-01
Coefficient: 2.24e-01
Value: F



Ammonia.assimilation

FDR: 2.483e-01
Coefficient: 7.00e-02
Value: F



Melibiose.Utilization

0.145
0.140
0.135
0.130

B (n=3)

F (n=3)

S (n=3)

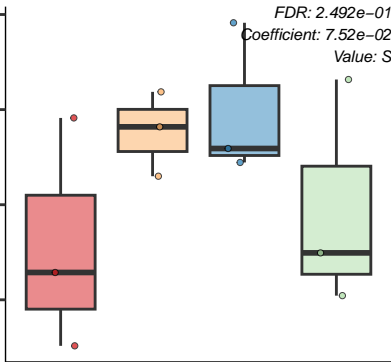
FS (n=3)

treatment

FDR: 2.492e-01

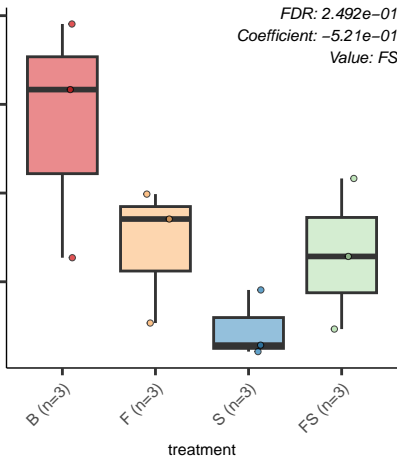
Coefficient: 7.52e-02

Value: S



Quinone.oxidoreductase.family

FDR: 2.492e-01
Coefficient: -5.21e-01
Value: FS



Glycolysis.and.Gluconeogenesis..including.Archaeal.enzym

FDR: 2.493e-01
Coefficient: -6.16e-02
Value: F

