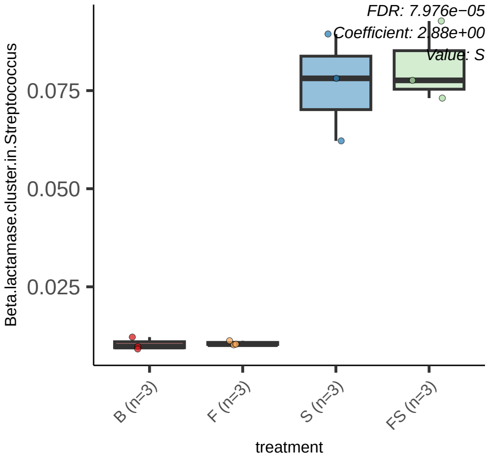
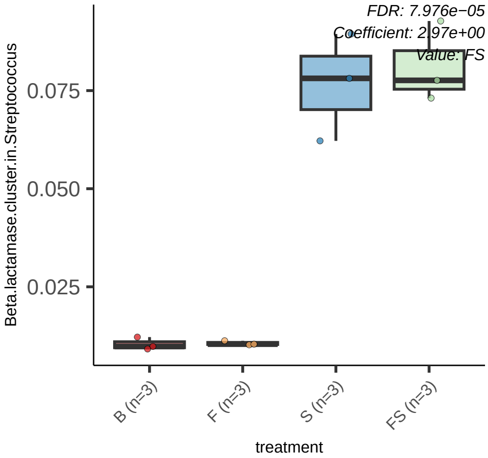
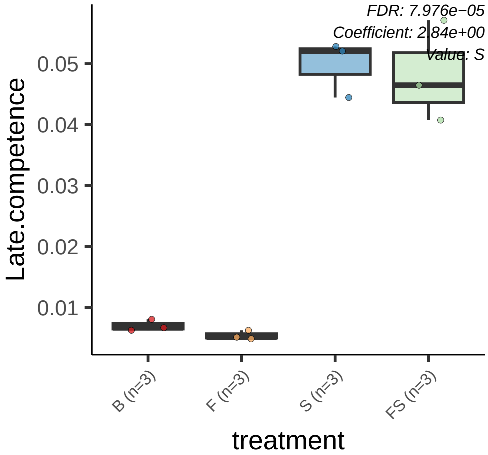
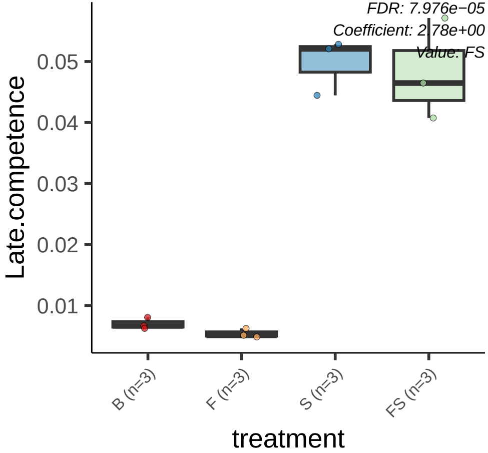
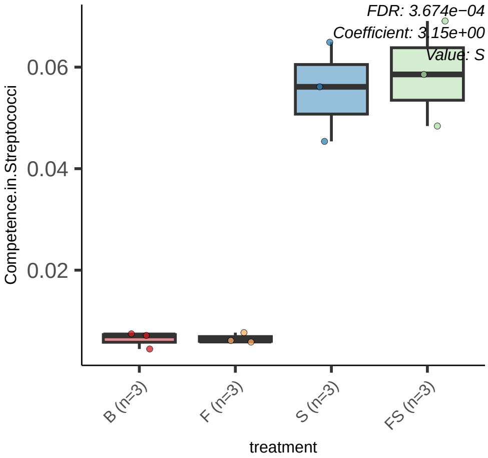
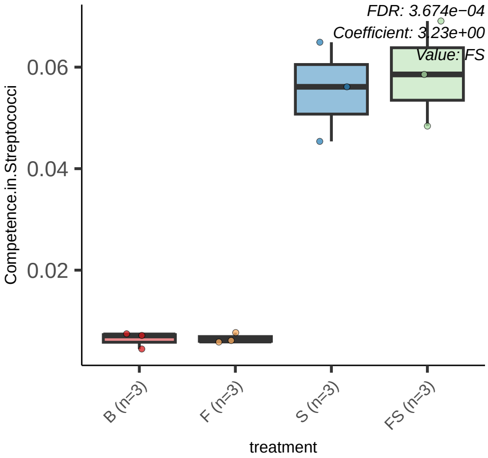

FDR: 7.976e−05
Coefficient: 2.88e+00
Value: S
Beta.lactamase.cluster.in.Streptococcus
0.075
0.050
0.025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

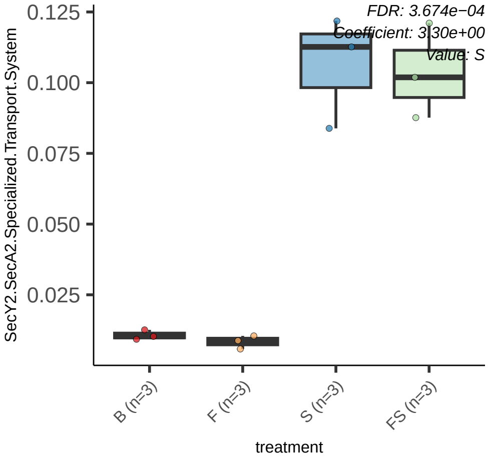

FDR: 7.976e−05
Coefficient: 2.97e+00
Value: FS
Beta.lactamase.cluster.in.Streptococcus
0.075
0.050
0.025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

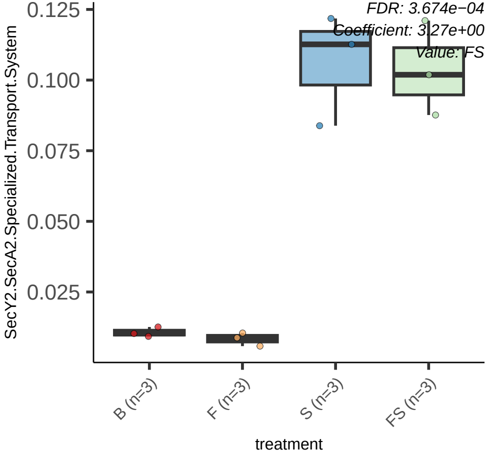

FDR: 7.976e−05
Coefficient: 2.84e+00
Value: S
Late.competence
0.05
0.04
0.03
0.02
0.01
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

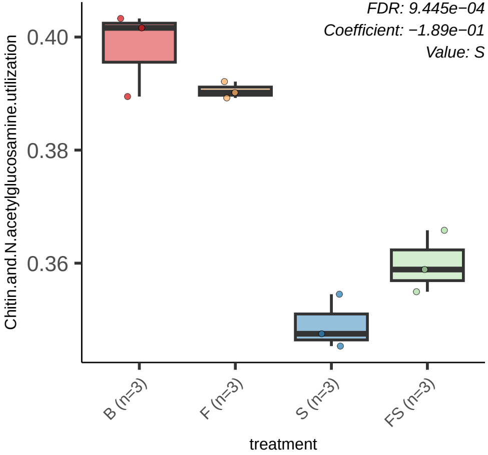

FDR: 7.976e−05
Coefficient: 2.78e+00
Value: FS
0.05
0.04
0.03
0.02
0.01
Late.competence
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

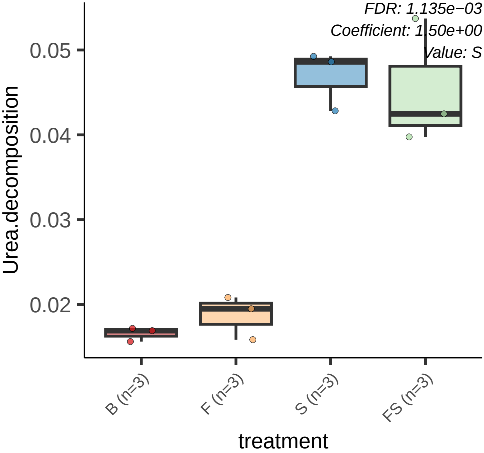

FDR: 3.674e−04
Coefficient: 3.15e+00
Value: S
0.06
0.04
0.02
Competence.in.Streptococci
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

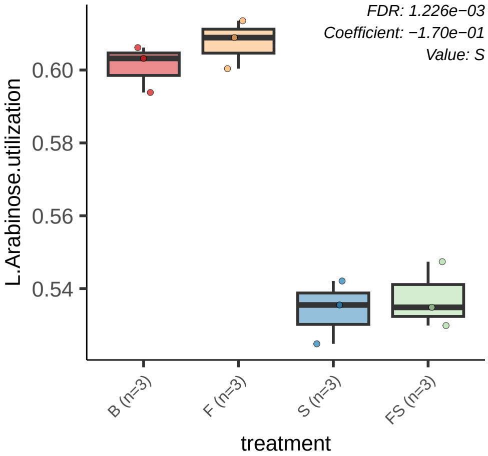

FDR: 3.674e−04
Coefficient: 3.23e+00
Value: FS
0.06
0.04
0.02
Competence.in.Streptococci
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

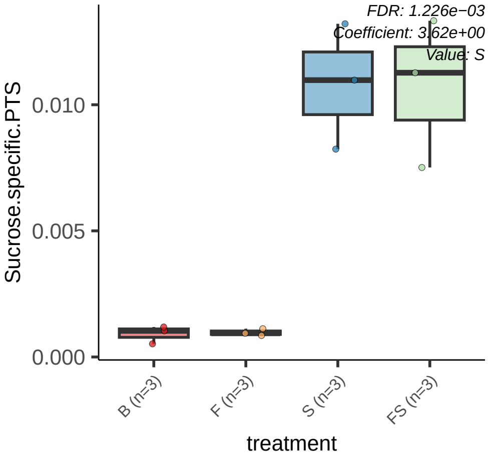

FDR: 3.674e−04
Coefficient: 3.30e+00
Value: S
SecY2.SecA2.Specialized.Transport.System
0.125
0.100
0.075
0.050
0.025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

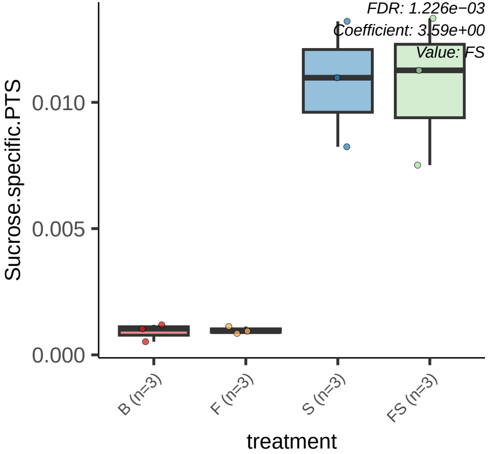

FDR: 3.674e−04
Coefficient: 3.27e+00
Value: FS
SecY2.SecA2.Specialized.Transport.System
0.125
0.100
0.075
0.050
0.025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

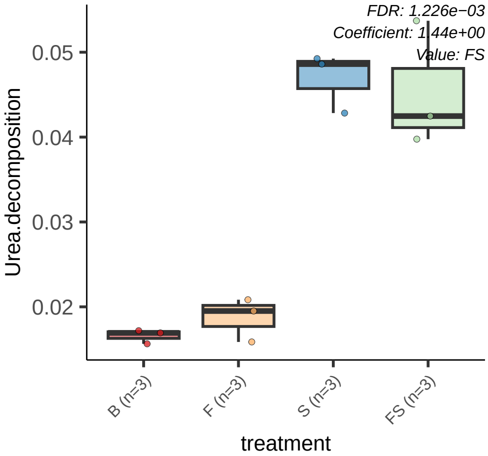

FDR: 9.445e−04
Coefficient: −1.89e−01
Value: S
Chitin.and.N.acetylglucosamine.utilization
0.40
0.38
0.36
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

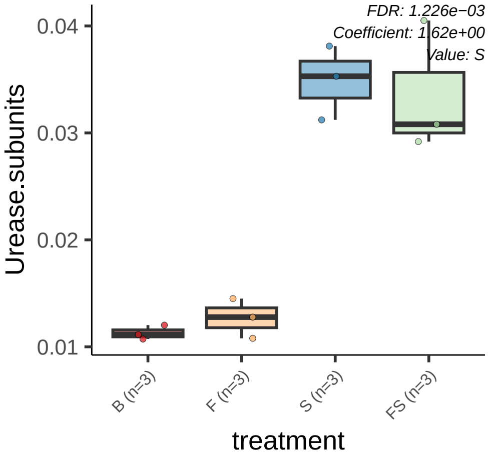

FDR: 1.135e−03
Coefficient: 1.50e+00
Value: S
Urea.decomposition
0.05
0.04
0.03
0.02
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

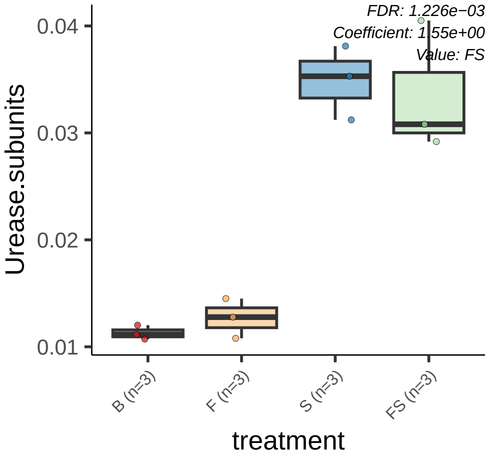

FDR: 1.226e−03
Coefficient: −1.70e−01
Value: S
L.Arabinose.utilization
0.60
0.58
0.56
0.54
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

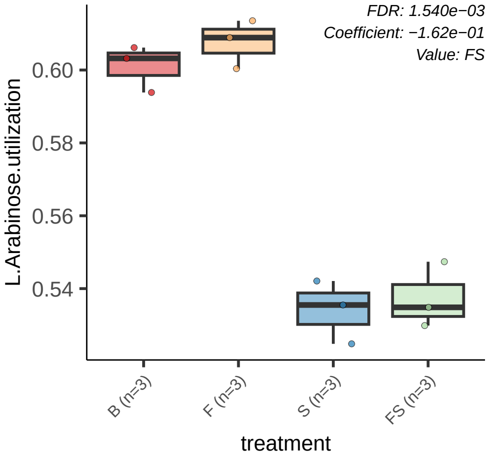

FDR: 1.226e−03
Coefficient: 3.62e+00
Value: S
Sucrose.specific.PTS
0.010
0.005
0.000
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

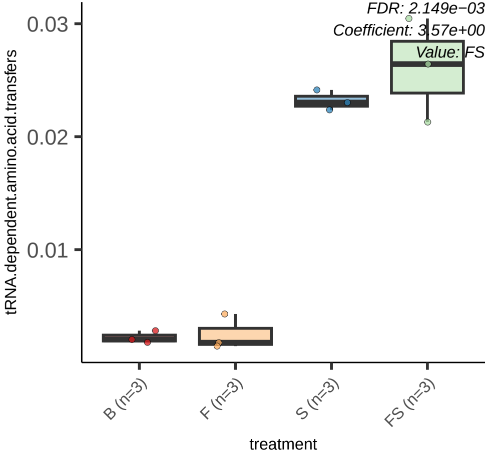

FDR: 1.226e−03
Coefficient: 3.59e+00
Value: FS
Sucrose.specific.PTS
0.010
0.005
0.000
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

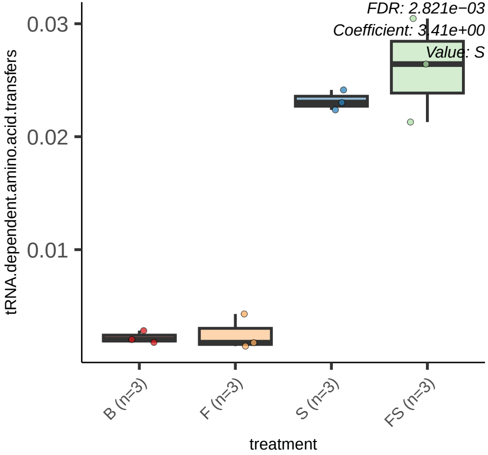

FDR: 1.226e−03
Coefficient: 1.44e+00
Value: FS
Urea.decomposition
0.05
0.04
0.03
0.02
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

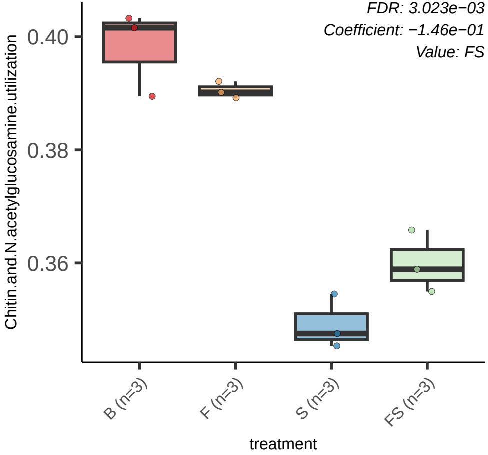

FDR: 1.226e−03
Coefficient: 1.62e+00
Value: S
Urease.subunits
0.04
0.03
0.02
0.01
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

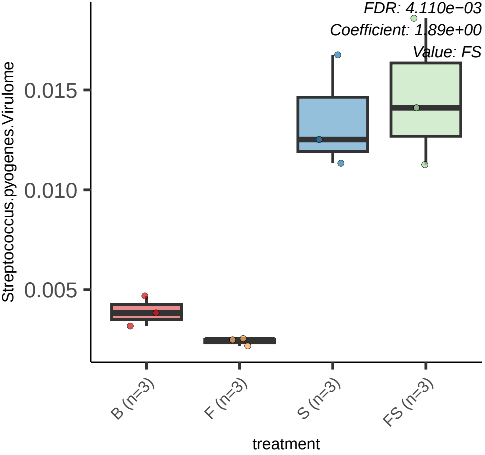

FDR: 1.226e−03
Coefficient: 1.55e+00
Value: FS
Urease.subunits
0.04
0.03
0.02
0.01
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

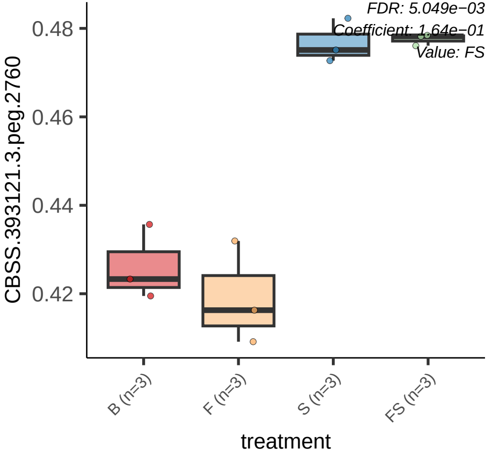

FDR: 1.540e−03
Coefficient: −1.62e−01
Value: FS
L.Arabinose.utilization
0.60
0.58
0.56
0.54
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

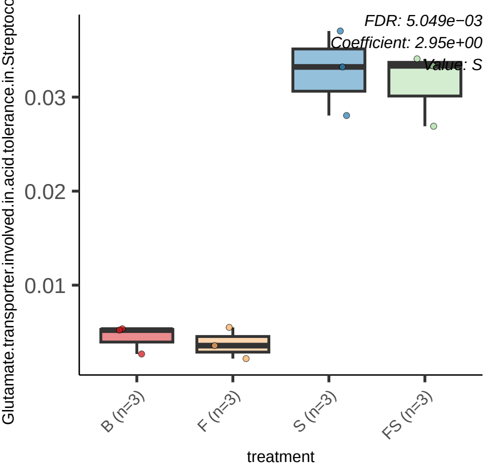

FDR: 2.149e−03
Coefficient: 3.57e+00
Value: FS
tRNA.dependent.amino.acid.transfers
0.03
0.02
0.01
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

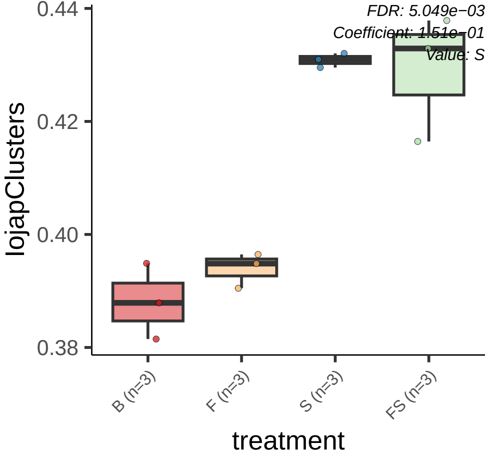

FDR: 2.821e−03
Coefficient: 3.41e+00
Value: S
tRNA.dependent.amino.acid.transfers
0.03
0.02
0.01
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

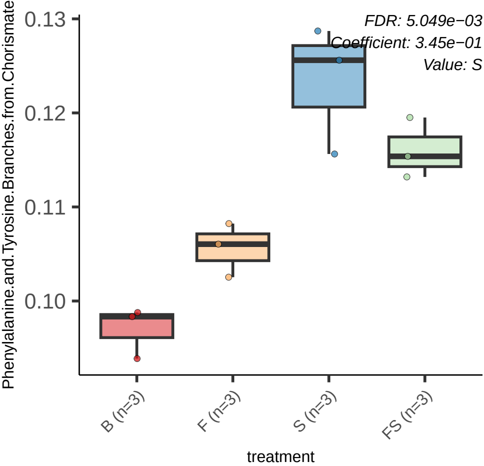

FDR: 3.023e−03
Coefficient: −1.46e−01
Value: FS
Chitin.and.N.acetylglucosamine.utilization
0.40
0.38
0.36
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

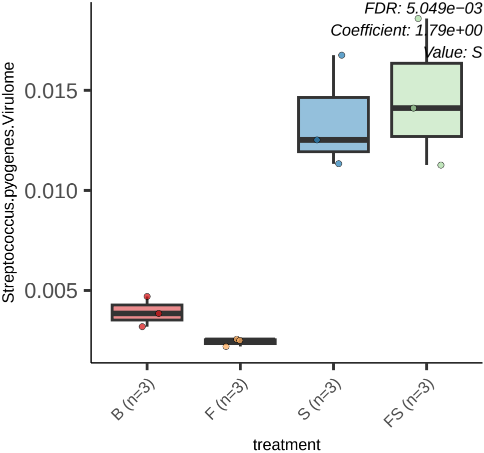

FDR: 4.110e−03
Coefficient: 1.89e+00
Value: FS
Streptococcus.pyogenes.Virulome
0.015
0.010
0.005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

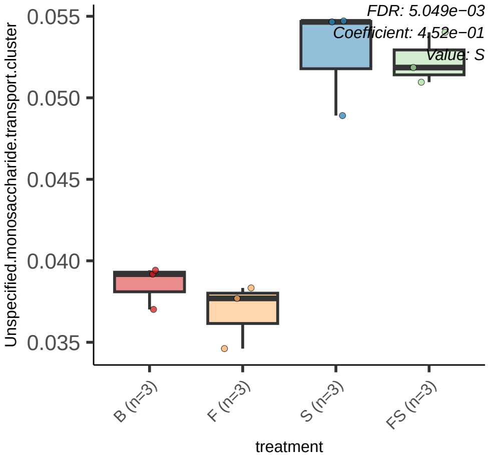

FDR: 5.049e−03
Coefficient: 1.64e−01
Value: FS
CBSS.393121.3.peg.2760
0.48
0.46
0.44
0.42
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

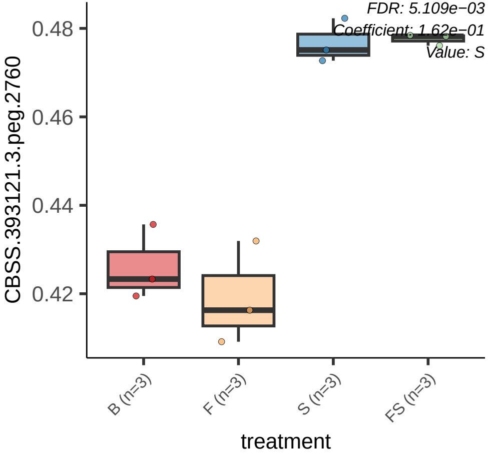

FDR: 5.049e−03
Coefficient: 2.95e+00
Value: S
Glutamate.transporter.involved.in.acid.tolerance.in.Streptocc
0.03
0.02
0.01
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

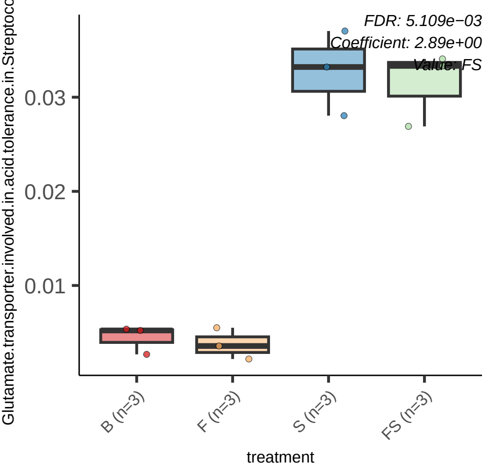

FDR: 5.049e−03
Coefficient: 1.51e−01
Value: S
0.44
0.42
0.40
0.38
lojapClusters
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

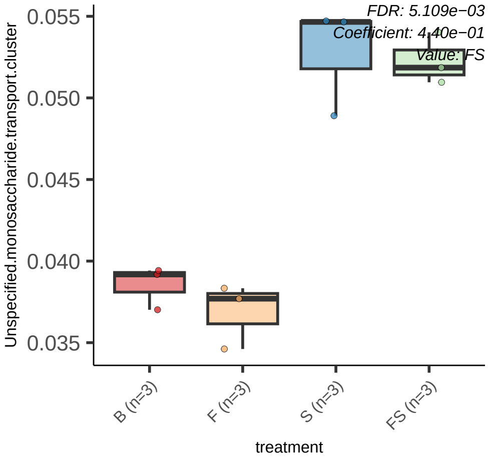

FDR: 5.049e−03
Coefficient: 3.45e−01
Value: S
Phenylalanine.and.Tyrosine.Branches.from.Chorismate
0.13
0.12
0.11
0.10
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

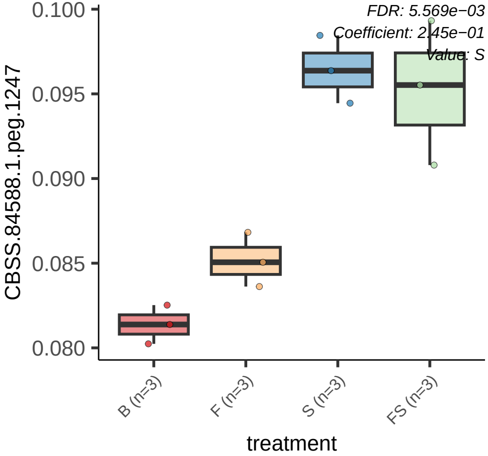

FDR: 5.049e−03
Coefficient: 1.79e+00
Value: S
Streptococcus.pyogenes.Virulome
0.015
0.010
0.005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

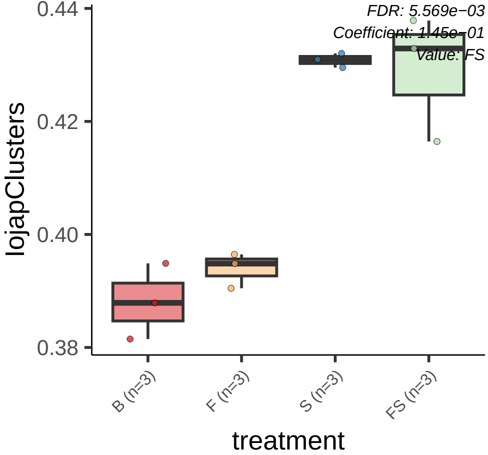

FDR: 5.049e−03
Coefficient: 4.52e−01
Value: S
Unspecified.monosaccharide.transport.cluster
0.055
0.050
0.045
0.040
0.035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

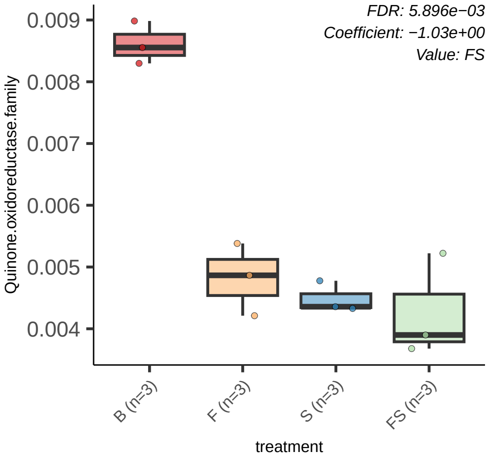

FDR: 5.109e−03
Coefficient: 1.62e−01
Value: S
CBSS.393121.3.peg.2760
0.48
0.46
0.44
0.42
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

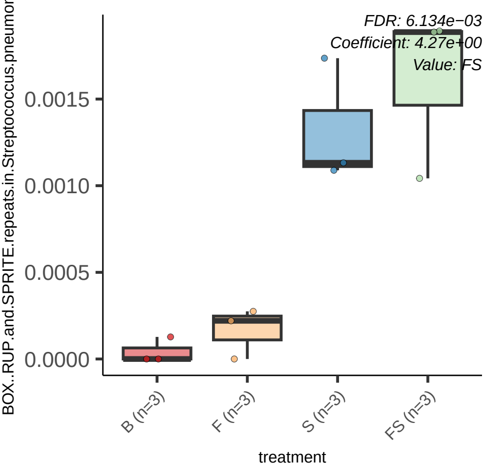

FDR: 5.109e−03
Coefficient: 2.89e+00
Value: FS
Glutamate.transporter.involved.in.acid.tolerance.in.Streptoco
0.03
0.02
0.01
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

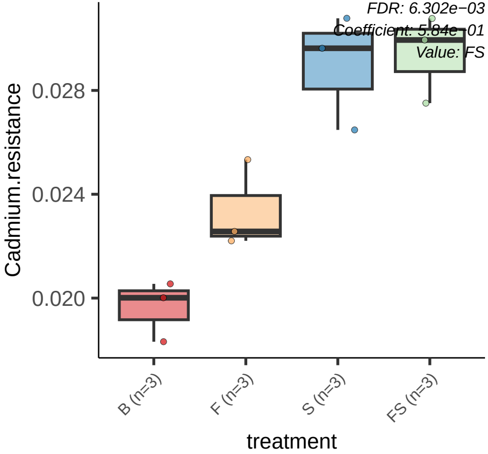

FDR: 5.109e−03
Coefficient: 4.40e−01
Value: FS
Unspecified.monosaccharide.transport.cluster
0.055
0.050
0.045
0.040
0.035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

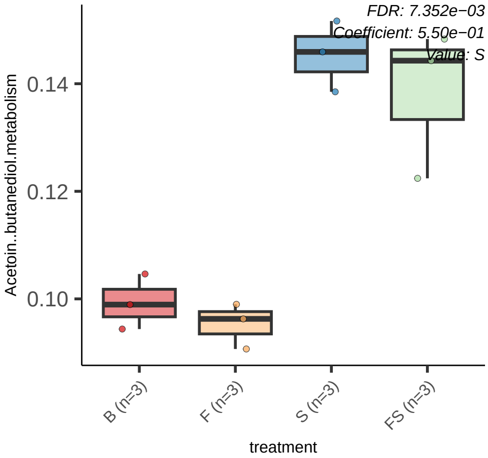

FDR: 5.569e−03
Coefficient: 2.45e−01
Value: S
CBSS.84588.1.peg.1247
0.100
0.095
0.090
0.085
0.080
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

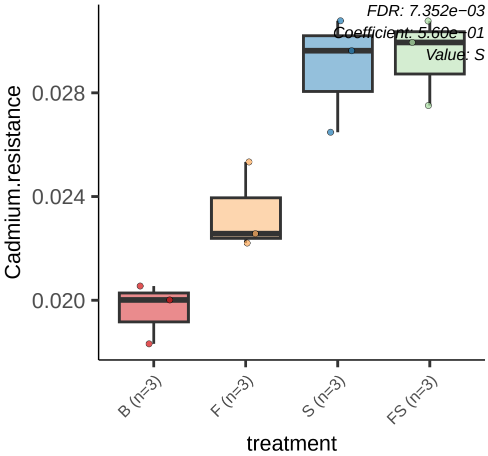

FDR: 5.569e−03
Coefficient: 1.45e−01
Value: FS
0.44
0.42
0.40
0.38
lojapClusters
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

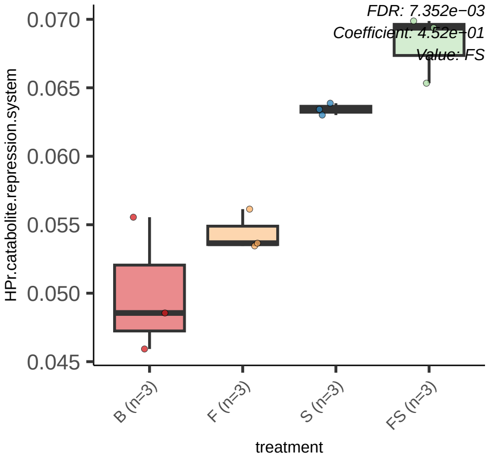

FDR: 5.896e−03
Coefficient: −1.03e+00
Value: FS
Quinone.oxidoreductase.family
0.009
0.008
0.007
0.006
0.005
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

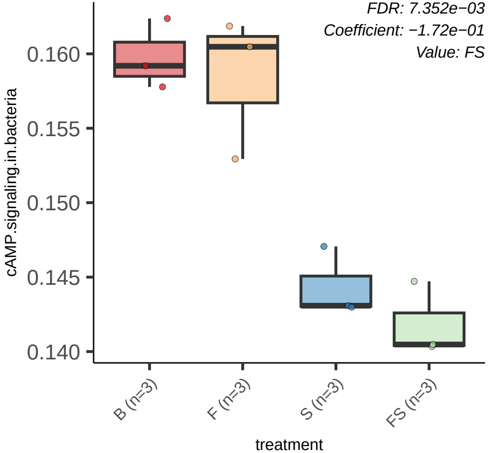

FDR: 6.134e−03
Coefficient: 4.27e+00
Value: FS
BOX..RUP.and.SPRITE.repeats.in.Streptococcus.pneumo
0.0015
0.0010
0.0005
0.0000
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

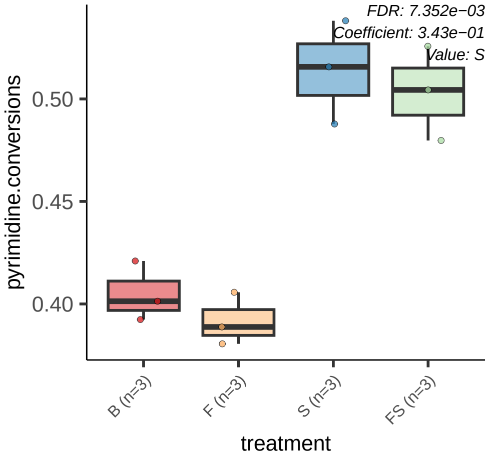

FDR: 6.302e−03
Coefficient: 5.84e−01
Value: FS
Cadmium.resistance
0.028
0.024
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

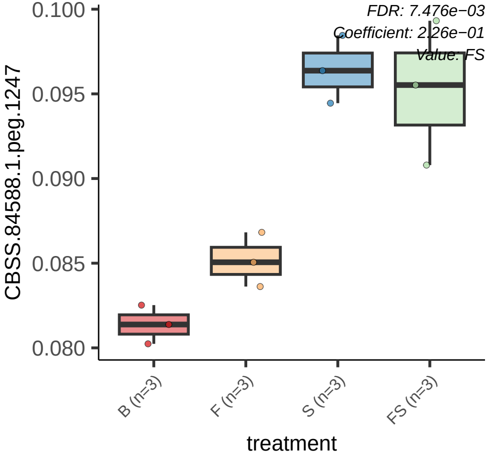

FDR: 7.352e−03
Coefficient: 5.50e−01
Value: S
Acetoin..butanediol.metabolism
0.14
0.12
0.10
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

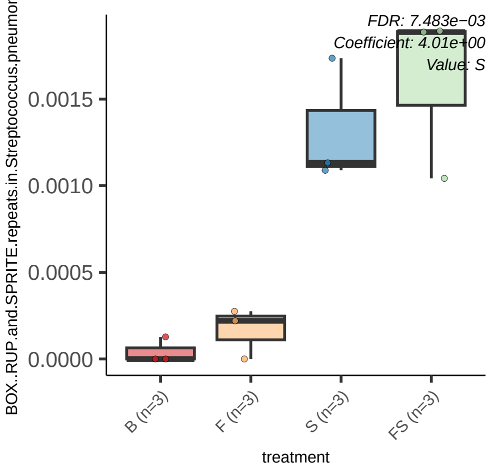

FDR: 7.352e−03
Coefficient: 5.60e−01
Value: S
Cadmium.resistance
0.028
0.024
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 7.352e−03
Coefficient: 4.52e−01
Value: FS
HPr.catabolite.repression.system
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

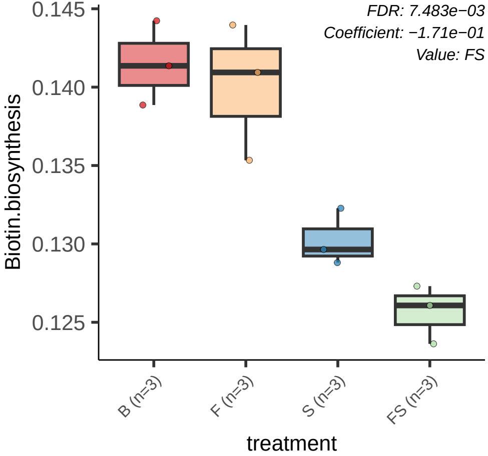

FDR: 7.352e−03
Coefficient: −1.72e−01
Value: FS
cAMP.signaling.in.bacteria
0.160
0.155
0.150
0.145
0.140
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

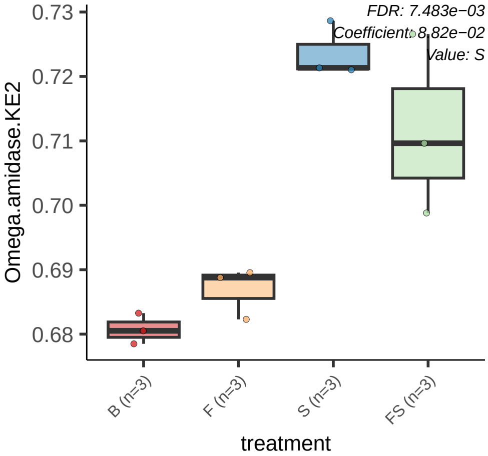

FDR: 7.352e−03
Coefficient: 3.43e−01
Value: S
pyrimidine.conversions
0.50
0.45
0.40
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

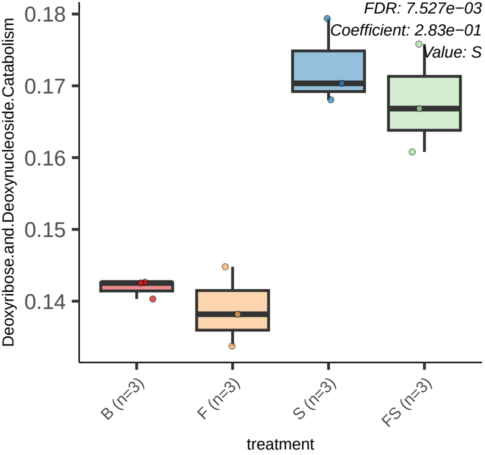

FDR: 7.476e−03
Coefficient: 2.26e−01
Value: FS
CBSS.84588.1.peg.1247
0.100
0.095
0.090
0.085
0.080
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

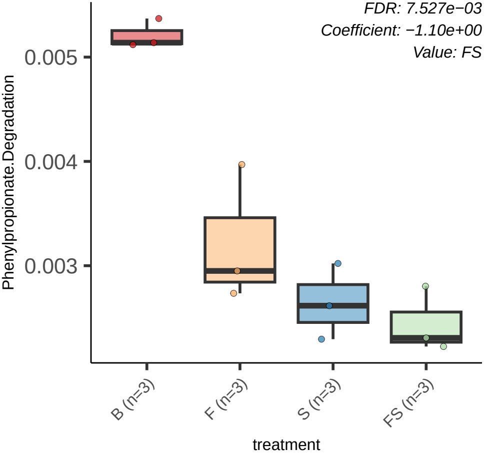


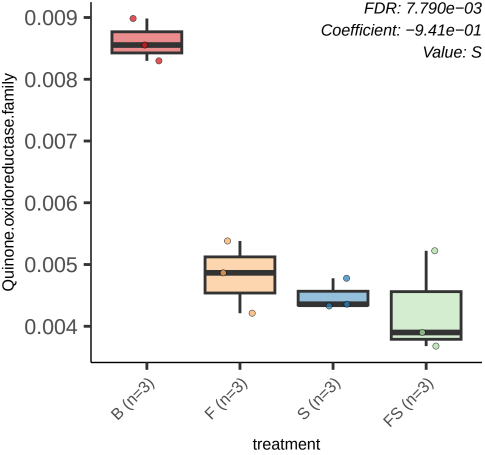
FDR: 7.483e−03
Coefficient: 4.01e+00
Value: S
BOX..RUP.and.SPRITE.repeats.in.Streptococcus.pneumor
0.0015
0.0010
0.0005
0.0000
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

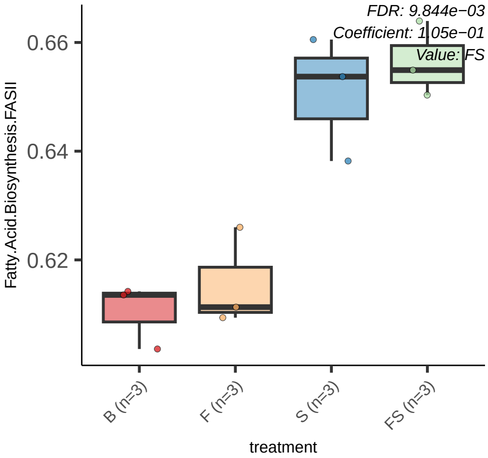

FDR: 7.483e−03
Coefficient: −1.71e−01
Value: FS
Biotin.biosynthesis
0.145
0.140
0.135
0.130
0.125
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

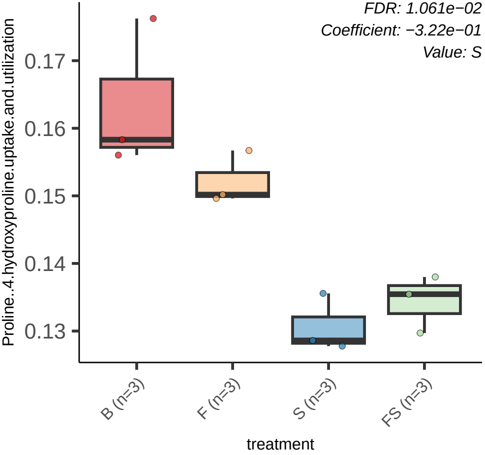

FDR: 7.483e−03
Coefficient: 8.82e−02
Value: S
Omega.amidase.KE2
0.73
0.72
0.71
0.70
0.69
0.68
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

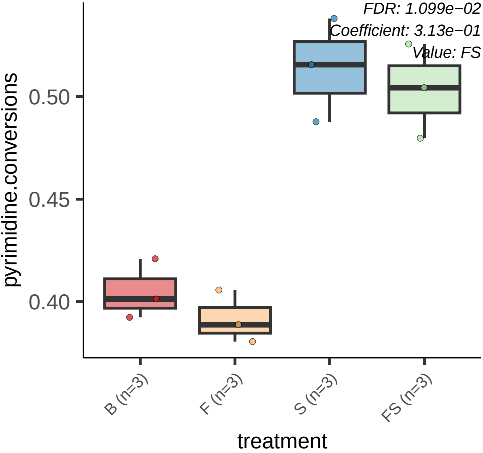

FDR: 7.527e−03
Coefficient: 2.83e−01
Value: S
Deoxyribose.and.Deoxynucleoside.Catabolism
0.18
0.17
0.16
0.15
0.14
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

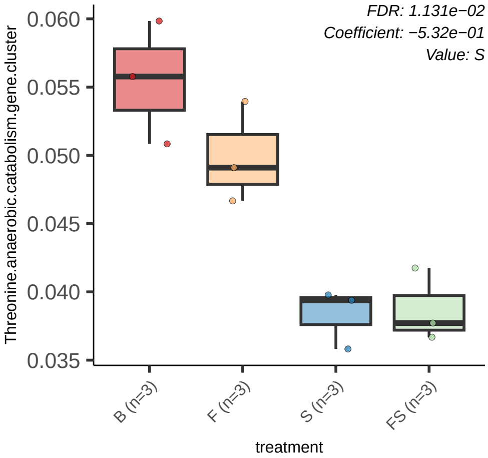

FDR: 7.527e−03
Coefficient: −1.10e+00
Value: FS
Phenylpropionate.Degradation
0.005
0.004
0.003
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

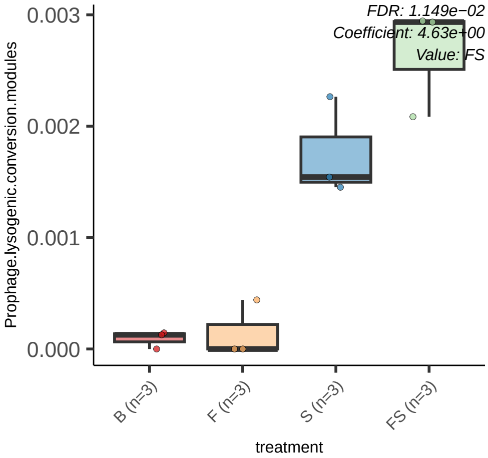

FDR: 7.790e−03
Coefficient: −9.41e−01
Value: S
Quinone.oxidoreductase.family
0.009
0.008
0.007
0.006
0.005
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

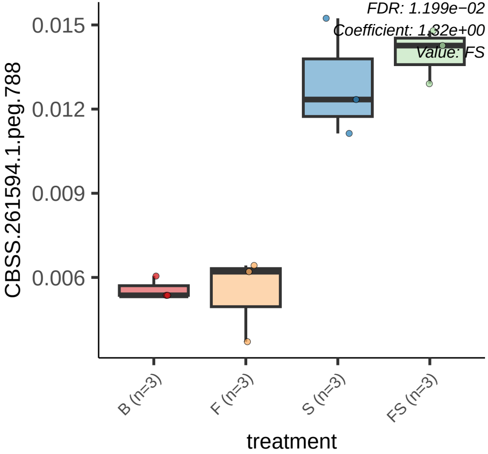

FDR: 9.844e−03
Coefficient: 1.05e−01
Value: FS
Fatty.Acid.Biosynthesis.FASII
0.66
0.64
0.62
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

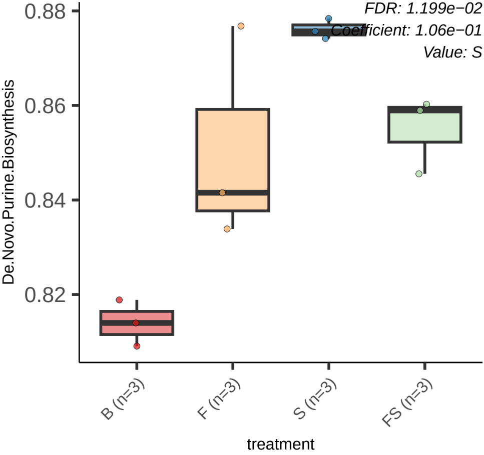

FDR: 1.061e−02
Coefficient: −3.22e−01
Value: S
Proline..4.hydroxyproline.uptake.and.utilization
0.17
0.16
0.15
0.14
0.13
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

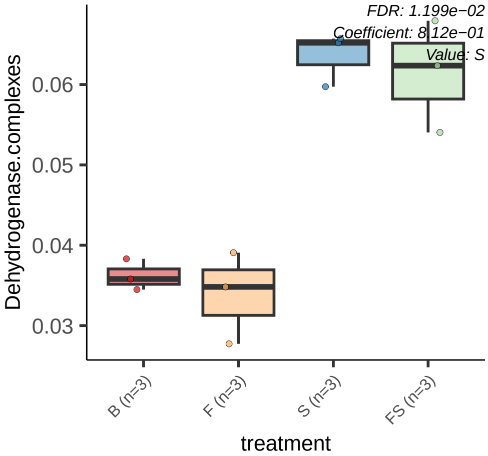

FDR: 1.099e−02
Coefficient: 3.13e−01
Value: FS
pyrimidine.conversions
0.50
0.45
0.40
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

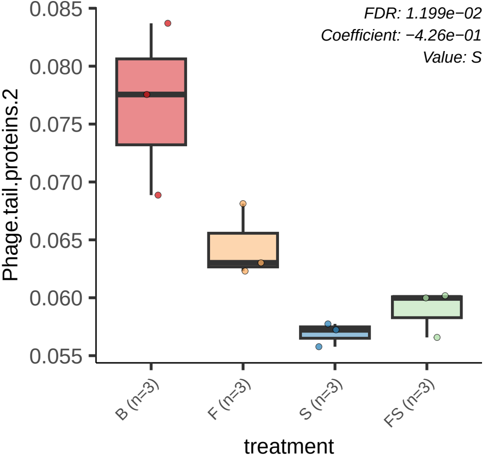

FDR: 1.131e−02
Coefficient: −5.32e−01
Value: S
Threonine.anaerobic.catabolism.gene.cluster
0.060
0.055
0.050
0.045
0.040
0.035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

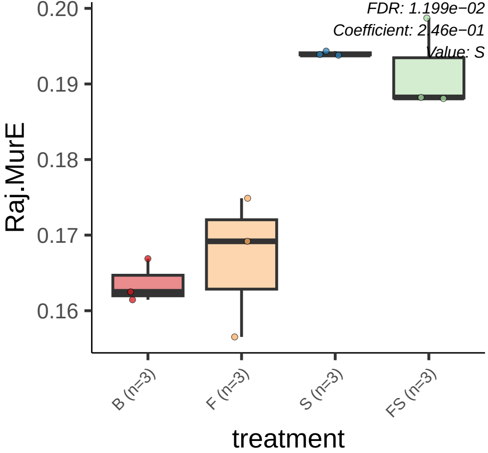

FDR: 1.149e−02
Coefficient: 4.63e+00
Value: FS
Prophage.lysogenic.conversion.modules
0.003
0.002
0.001
0.000
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

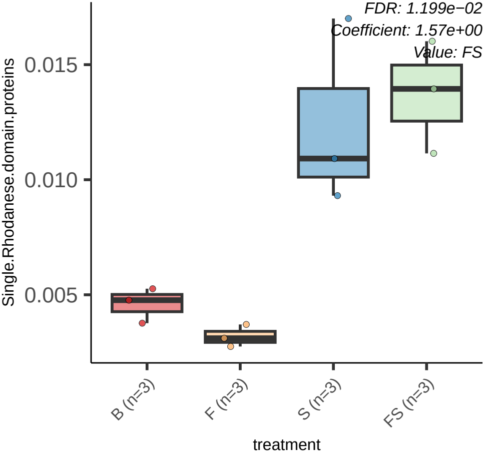

FDR: 1.199e−02
Coefficient: 1.32e+00
Value: FS
CBSS.261594.1.peg.788
0.015
0.012
0.009
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

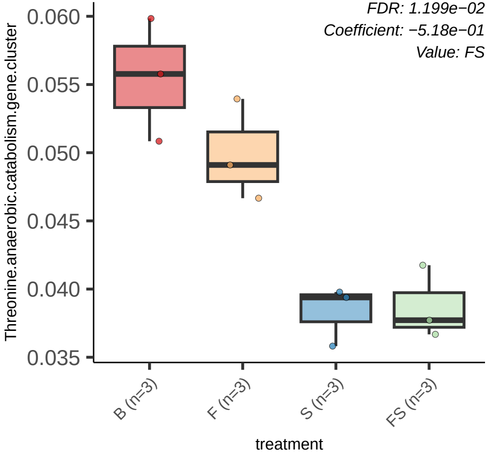

FDR: 1.199e−02
Coefficient: 1.06e−01
Value: S
De.Novo.Purine.Biosynthesis
0.88
0.86
0.84
0.82
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

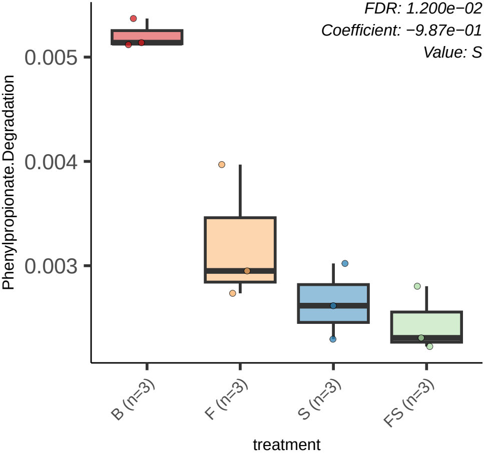

FDR: 1.199e−02
Coefficient: 8.12e−01
Value: S
Dehydrogenase.complexes
0.06
0.05
0.04
0.03
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

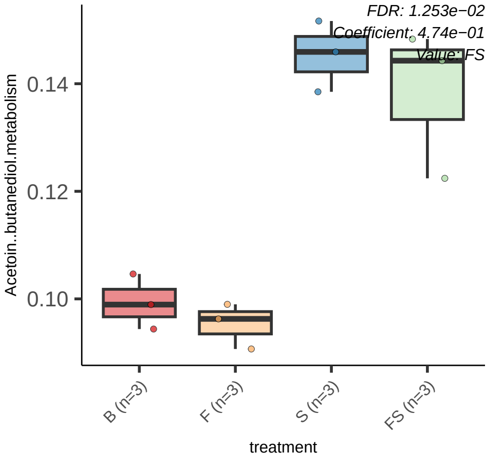

FDR: 1.199e−02
Coefficient: −4.26e−01
Value: S
Phage.tail.proteins.2
0.085
0.080
0.075
0.070
0.065
0.060
0.055
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

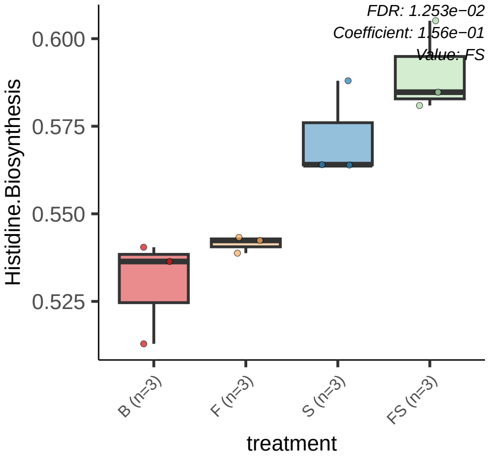

FDR: 1.199e−02
Coefficient: 2.46e−01
Value: S
Raj.MurE
0.20
0.19
0.18
0.17
0.16
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

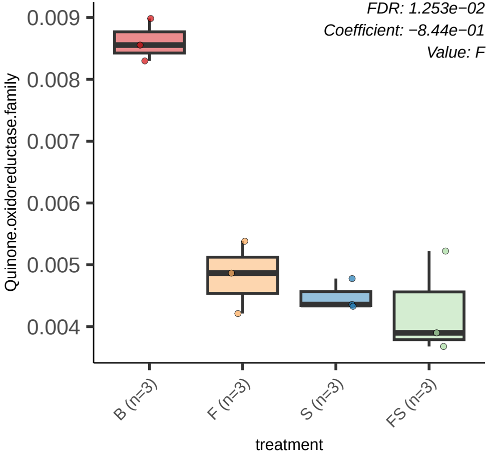

FDR: 1.199e−02
Coefficient: 1.57e+00
Value: FS
Single.Rhodanese.domain.proteins
0.015
0.010
0.005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

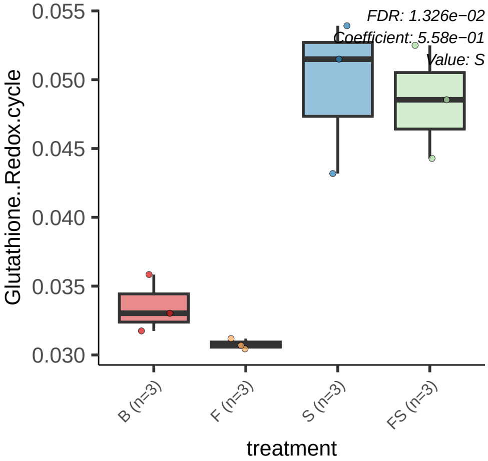

FDR: 1.199e−02
Coefficient: −5.18e−01
Value: FS
Threonine.anaerobic.catabolism.gene.cluster
0.060
0.055
0.050
0.045
0.040
0.035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

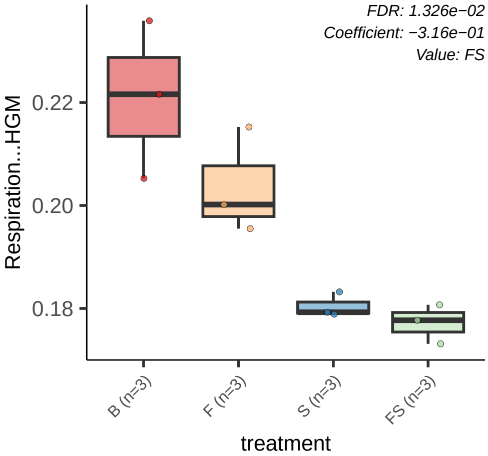

FDR: 1.200e−02
Coefficient: −9.87e−01
Value: S
Phenylpropionate.Degradation
0.005
0.004
0.003
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

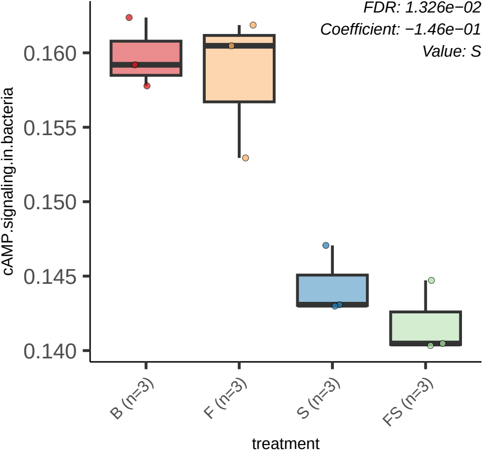

FDR: 1.253e−02
Coefficient: 4.74e−01
Value: FS
Acetoin..butanediol.metabolism
0.14
0.12
0.10
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

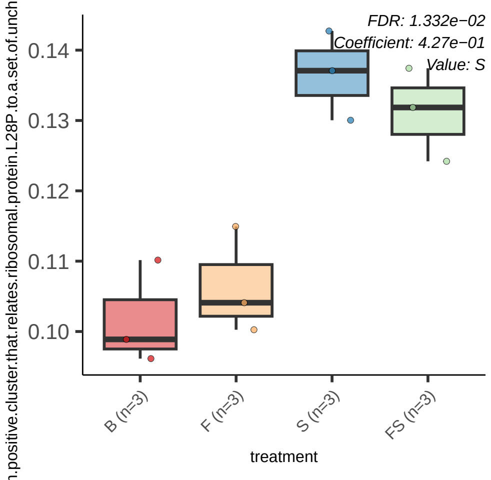

FDR: 1.253e−02
Coefficient: 1.56e−01
Value: FS
Histidine.Biosynthesis
0.600
0.575
0.550
0.525
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

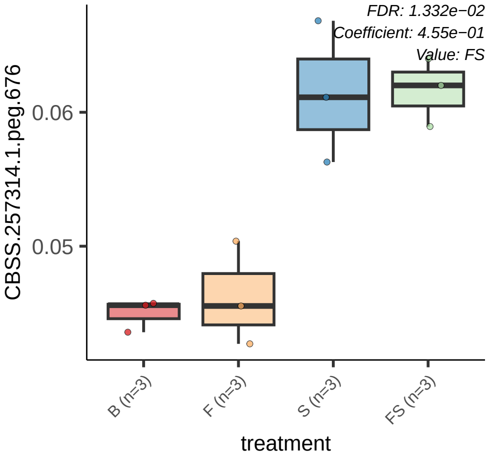

FDR: 1.253e−02
Coefficient: −8.44e−01
Value: F
Quinone.oxidoreductase.family
0.009
0.008
0.007
0.006
0.005
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

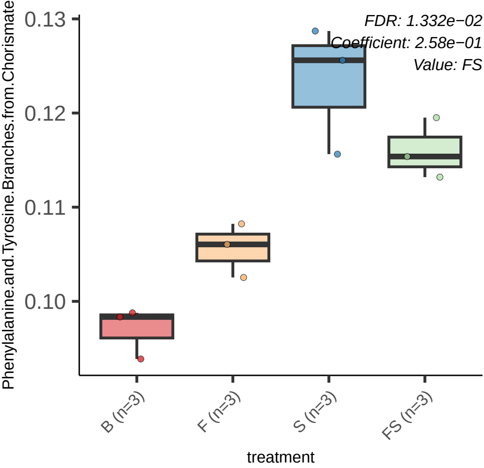

FDR: 1.326e−02
Coefficient: 5.58e−01
Value: S
Glutathione..Redox.cycle
0.055
0.050
0.045
0.040
0.035
0.030
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

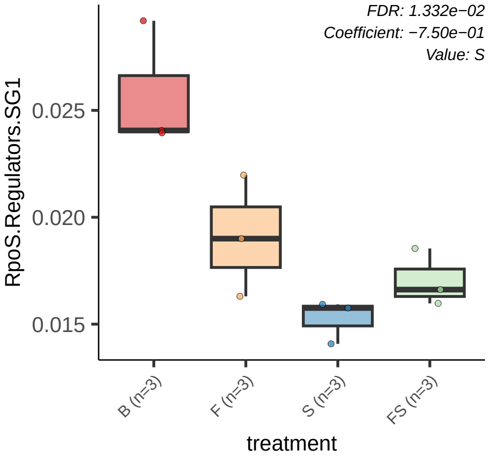

FDR: 1.326e−02
Coefficient: −3.16e−01
Value: FS
Respiration...HGM
0.22
0.20
0.18
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

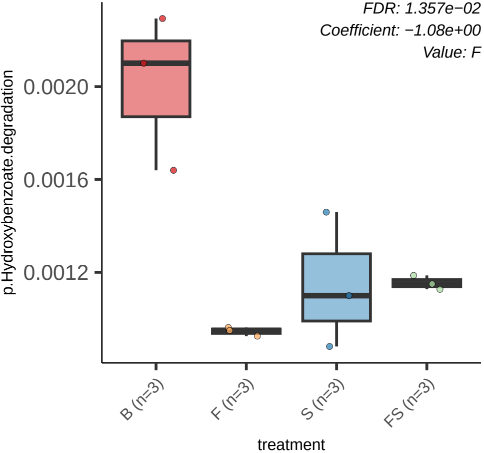

FDR: 1.326e−02
Coefficient: −1.46e−01
Value: S
cAMP.signaling.in.bacteria
0.160
0.155
0.150
0.145
0.140
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

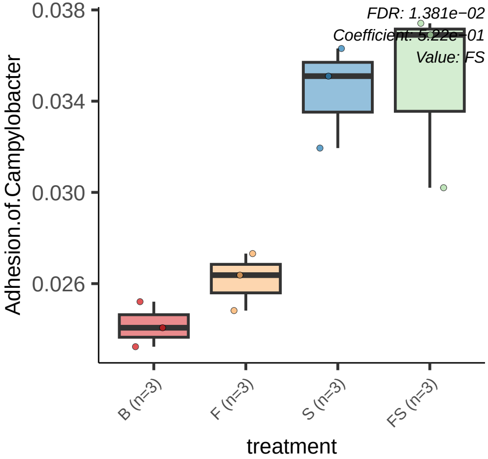

FDR: 1.332e−02
Coefficient: 4.27e−01
Value: S
n.positive.cluster.that.relates.ribosomal.protein.L28P.to.a.set.of.unch
0.14
0.13
0.12
0.11
0.10
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

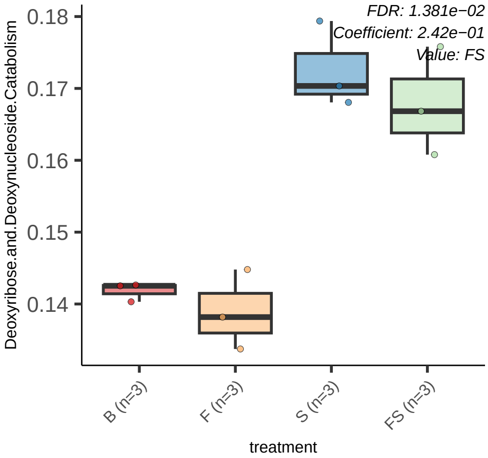

FDR: 1.332e−02
Coefficient: 4.55e−01
Value: FS
CBSS.257314.1.peg.676
0.06
0.05
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

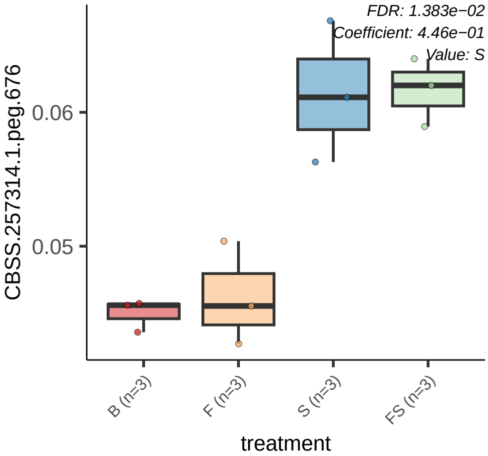

FDR: 1.332e−02
Coefficient: 2.58e−01
Value: FS
Phenylalanine.and.Tyrosine.Branches.from.Chorismate
0.13
0.12
0.11
0.10
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

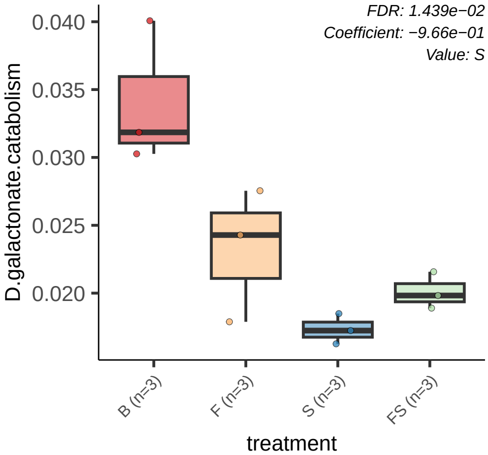

FDR: 1.332e−02
Coefficient: −7.50e−01
Value: S
RpoS.Regulators.SG1
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

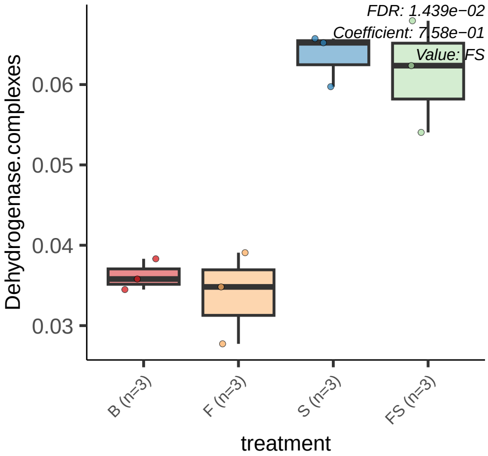

FDR: 1.357e−02
Coefficient: −1.08e+00
Value: F
p.Hydroxybenzoate.degradation
0.0020
0.0016
0.0012
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

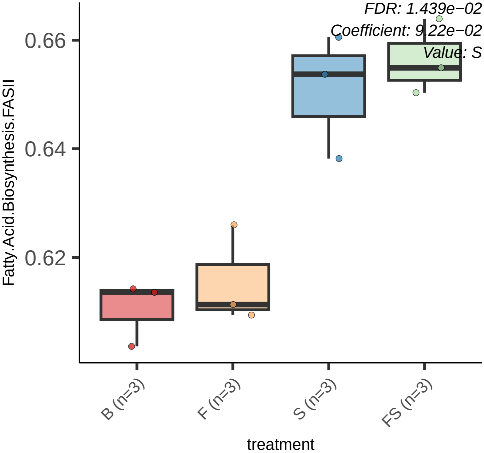

FDR: 1.381e−02
Coefficient: 5.22e−01
Value: FS
Adhesion.of.Campylobacter
0.038
0.034
0.030
0.026
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

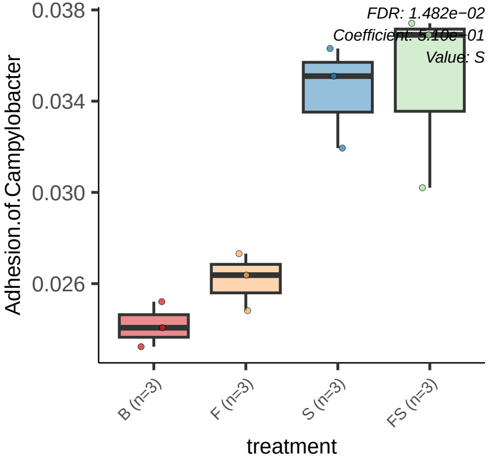

FDR: 1.381e−02
Coefficient: 2.42e−01
Value: FS
Deoxyribose.and.Deoxynucleoside.Catabolism
0.18
0.17
0.16
0.15
0.14
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

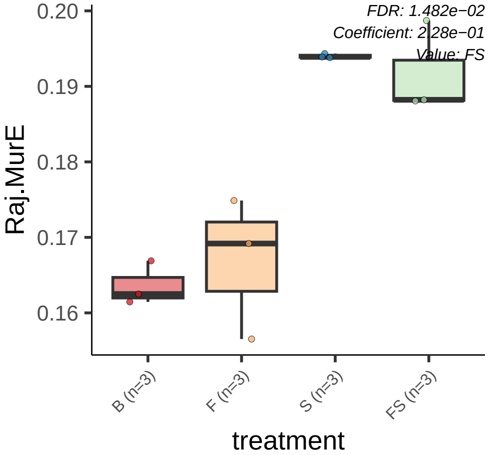

FDR: 1.383e−02
Coefficient: 4.46e−01
Value: S
CBSS.257314.1.peg.676
0.06
0.05
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

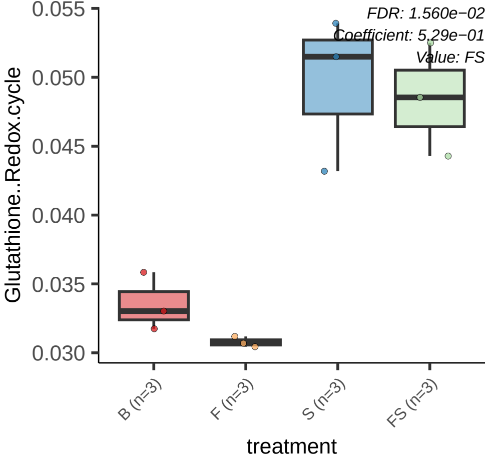

FDR: 1.439e−02
Coefficient: −9.66e−01
Value: S
D.galactonate.catabolism
0.040
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

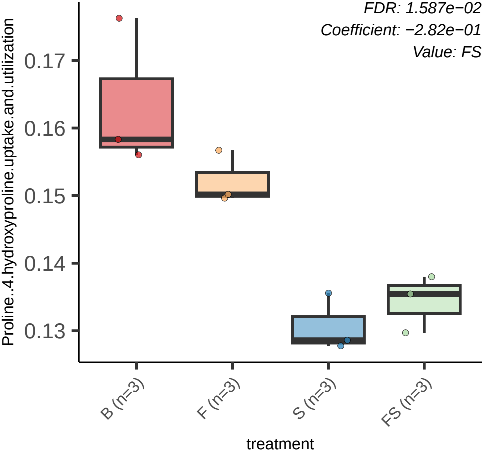

FDR: 1.439e−02
Coefficient: 7.58e−01
Value: FS
Dehydrogenase.complexes
0.06
0.05
0.04
0.03
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

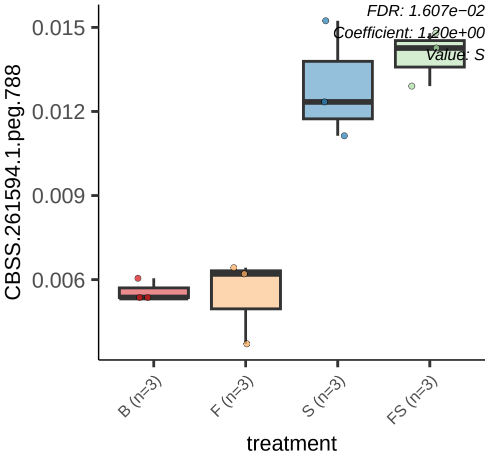

FDR: 1.439e−02
Coefficient: 9.22e−02
Value: S
Fatty.Acid.Biosynthesis.FASII
0.66
0.64
0.62
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

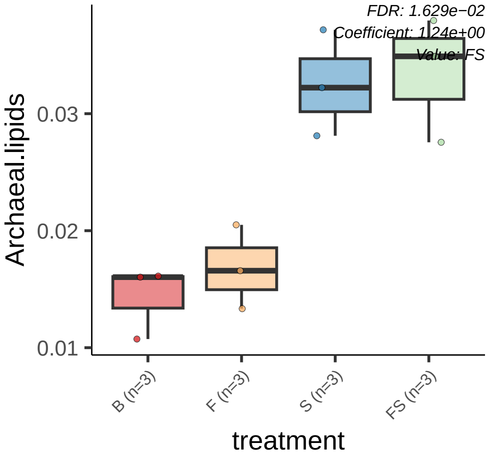

FDR: 1.482e−02
Coefficient: 5.10e−01
Value: S
Adhesion.of.Campylobacter
0.038
0.034
0.030
0.026
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

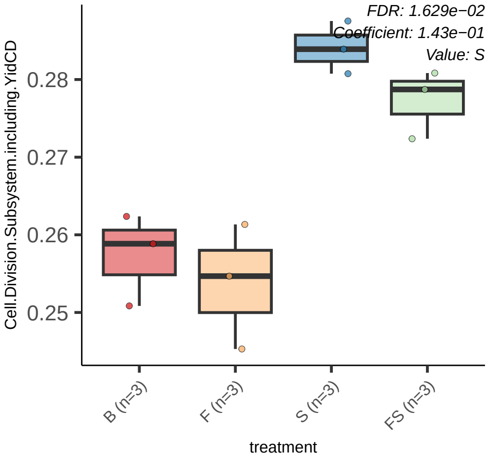

FDR: 1.482e−02
Coefficient: 2.28e−01
Value: FS
Raj.MurE
0.20
0.19
0.18
0.17
0.16
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

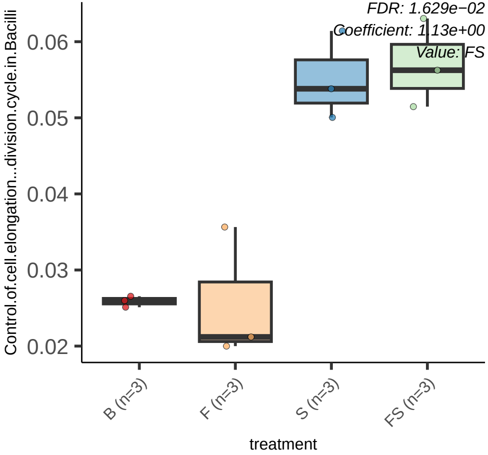

FDR: 1.560e−02
Coefficient: 5.29e−01
Value: FS
Glutathione..Redox.cycle
0.055
0.050
0.045
0.040
0.035
0.030
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

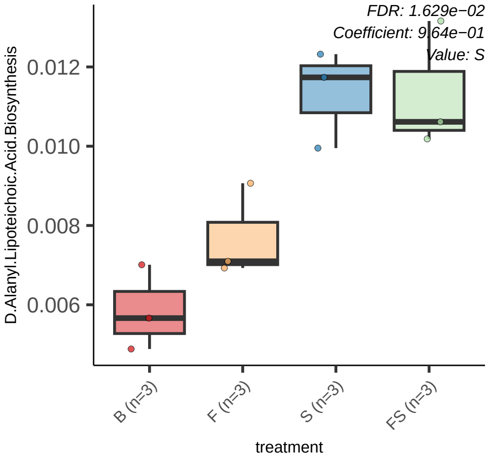

FDR: 1.587e−02
Coefficient: −2.82e−01
Value: FS
Proline..4.hydroxyproline.uptake.and.utilization
0.17
0.16
0.15
0.14
0.13
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

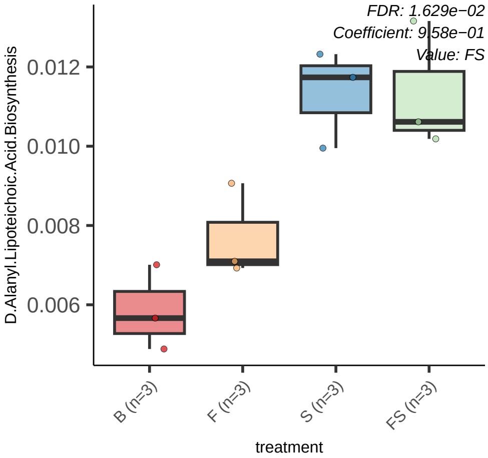

FDR: 1.607e−02
Coefficient: 1.20e+00
Value: S
CBSS.261594.1.peg.788
0.015
0.012
0.009
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

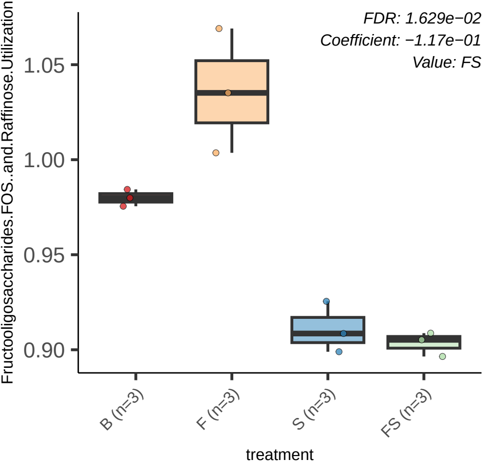

FDR: 1.629e−02
Coefficient: 1.24e+00
Value: FS
Archaeal.lipids
0.03
0.02
0.01
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

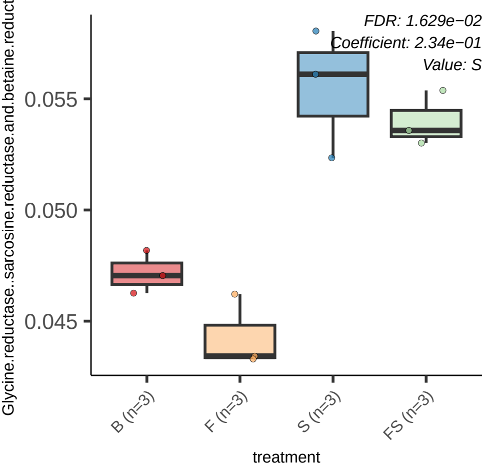

FDR: 1.629e−02
Coefficient: 1.43e−01
Value: S
Cell.Division.Subsystem.including.YidCD
0.28
0.27
0.26
0.25
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

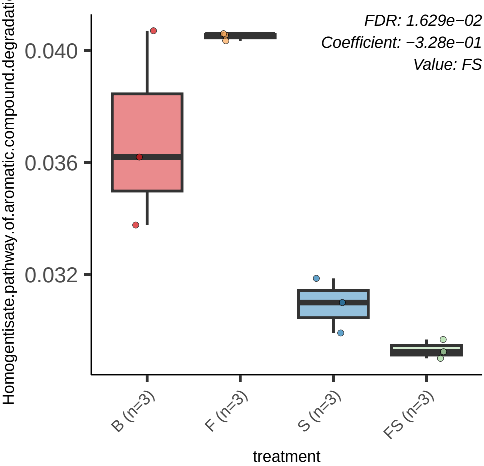

FDR: 1.629e−02
Coefficient: 1.13e+00
Value: FS
Control.of.cell.elongation...division.cycle.in.Bacilli
0.06
0.05
0.04
0.03
0.02
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

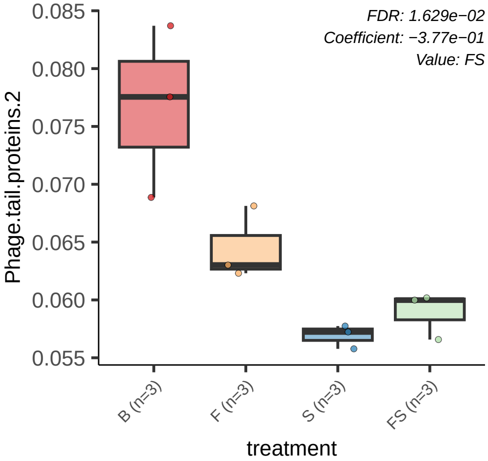

FDR: 1.629e−02
Coefficient: 9.64e−01
Value: S
D.Alanyl.Lipoteichoic.Acid.Biosynthesis
0.012
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

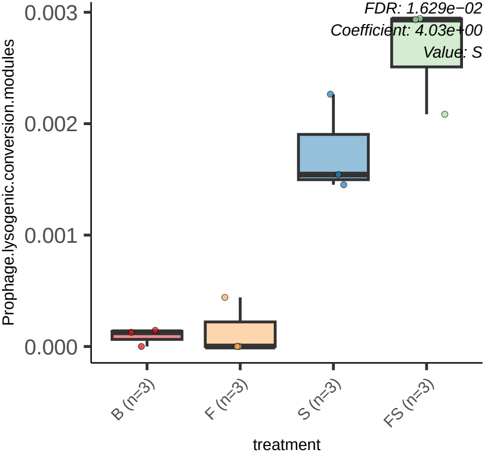

FDR: 1.629e−02
Coefficient: 9.58e−01
Value: FS
D.Alanyl.Lipoteichoic.Acid.Biosynthesis
0.012
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

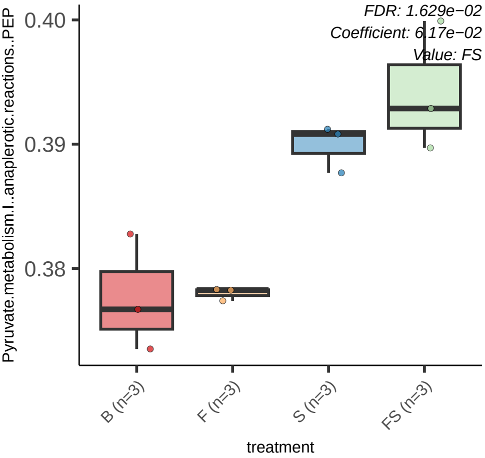

FDR: 1.629e−02
Coefficient: −1.17e−01
Value: FS
Fructooligosaccharides.FOS..and.Raffinose.Utilization
1.05
1.00
0.95
0.90
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

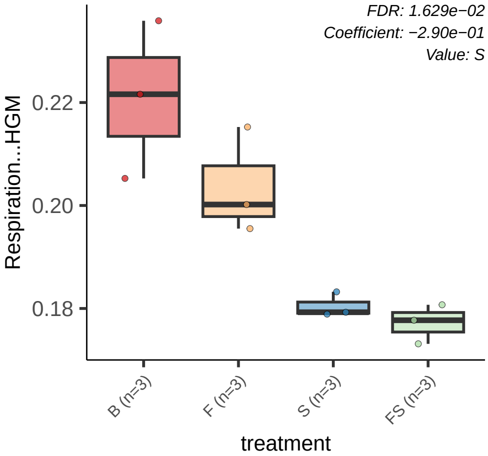

FDR: 1.629e−02
Coefficient: 2.34e−01
Value: S
Glycine.reductase..sarcosine.reductase.and.betaine.reduct
0.055
0.050
0.045
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

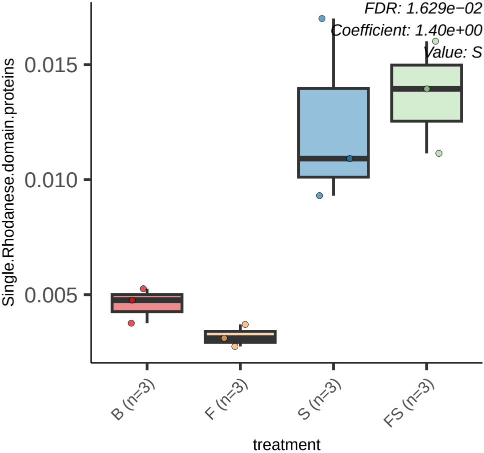

FDR: 1.629e−02
Coefficient: −3.28e−01
Value: FS
Homogentisate.pathway.of.aromatic.compound.degradati
0.040
0.036
0.032
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

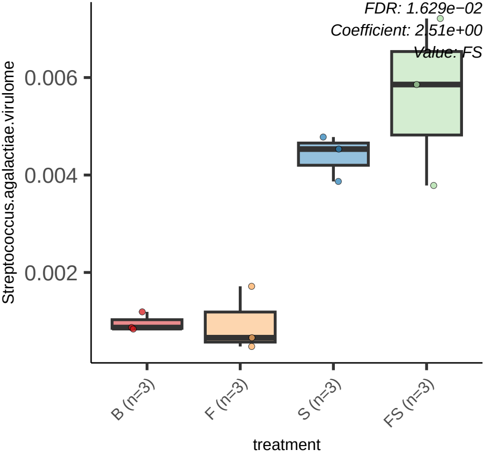

FDR: 1.629e−02
Coefficient: −3.77e−01
Value: FS
Phage.tail.proteins.2
0.085
0.080
0.075
0.070
0.065
0.060
0.055
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

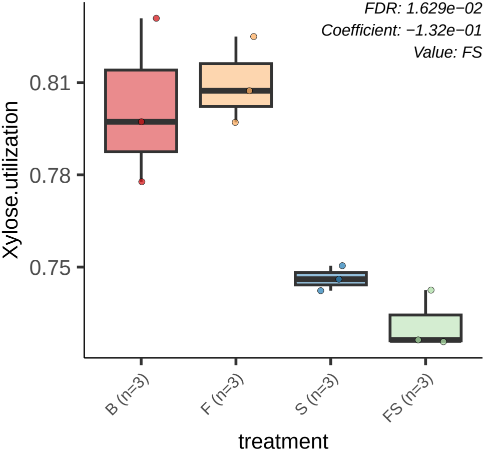

FDR: 1.629e−02
Coefficient: 4.03e+00
Value: S
Prophage.lysogenic.conversion.modules
0.003
0.002
0.001
0.000
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

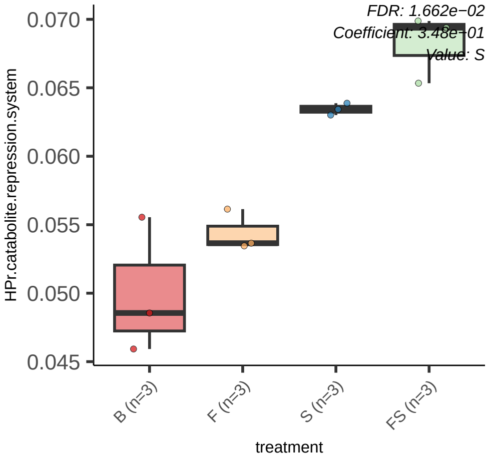

FDR: 1.629e−02
Coefficient: 6.17e−02
Value: FS
Pyruvate.metabolism.I..anaplerotic.reactions..PEP
0.40
0.39
0.38
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

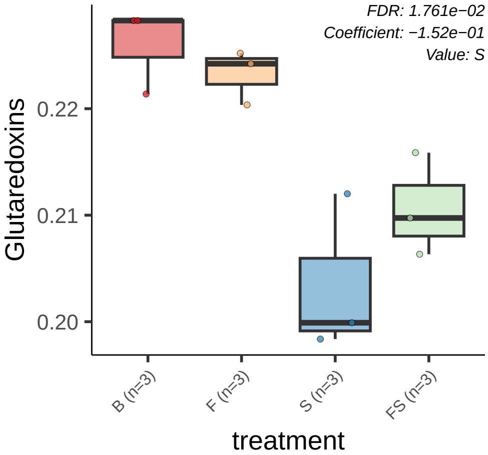

FDR: 1.629e−02
Coefficient: −2.90e−01
Value: S
Respiration...HGM
0.22
0.20
0.18
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

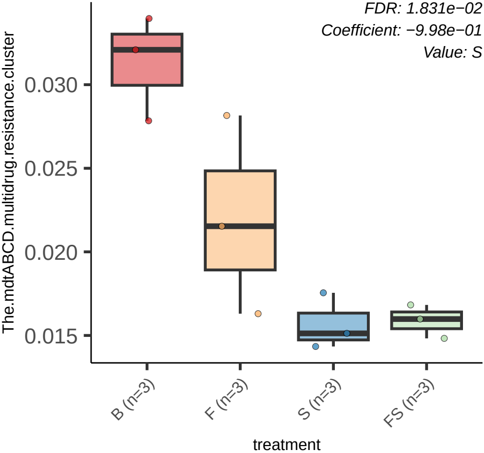

FDR: 1.629e−02
Coefficient: 1.40e+00
Value: S
Single.Rhodanese.domain.proteins
0.015
0.010
0.005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

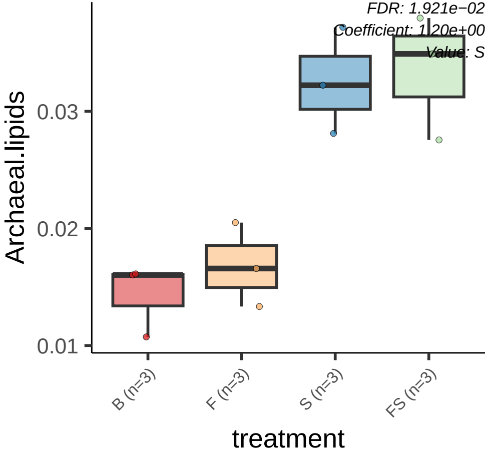

FDR: 1.629e−02
Coefficient: 2.51e+00
Value: FS
Streptococcus.agalactiae.virulome
0.006
0.004
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

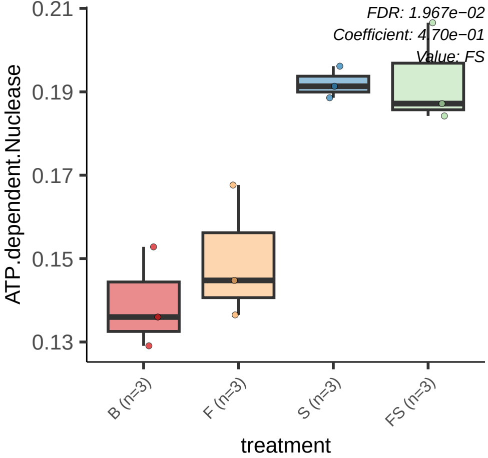

FDR: 1.629e−02
Coefficient: −1.32e−01
Value: FS
Xylose.utilization
0.81
0.78
0.75
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

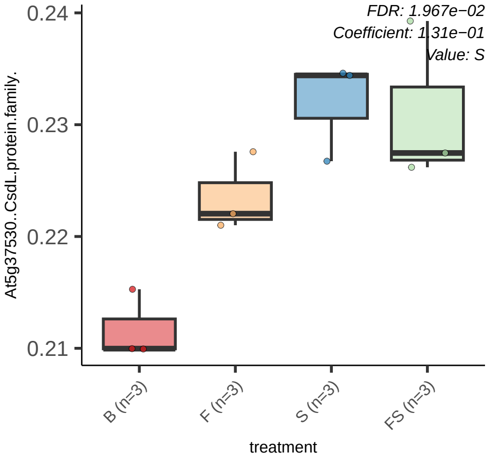

FDR: 1.662e−02
Coefficient: 3.48e−01
Value: S
HPr.catabolite.repression.system
0.070
0.065
0.060
0.055
0.050
0.045
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 1.761e−02
Coefficient: −1.52e−01
Value: S
Glutaredoxins
0.22
0.21
0.20
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

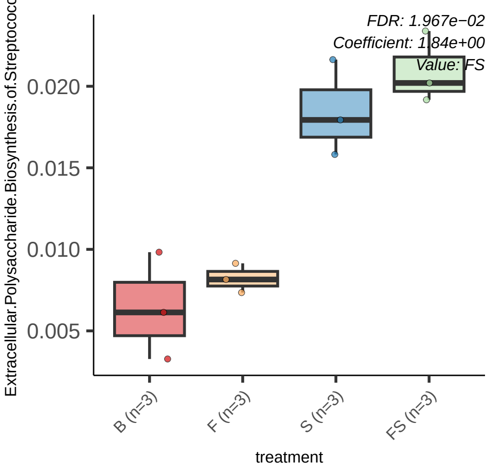

FDR: 1.831e−02
Coefficient: −9.98e−01
Value: S
The.mdtABCD.multidrug.resistance.cluster
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

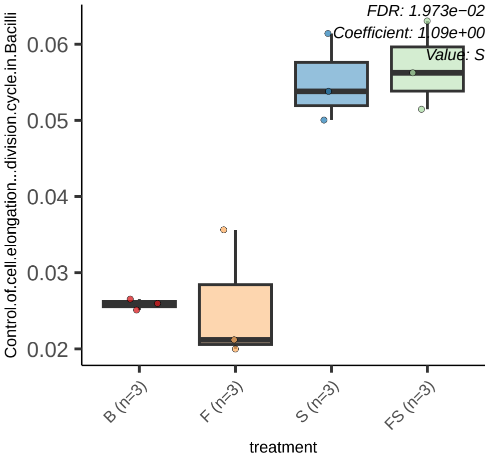

FDR: 1.921e−02
Coefficient: 1.20e+00
Value: S
Archaeal.lipids
0.03
0.02
0.01
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

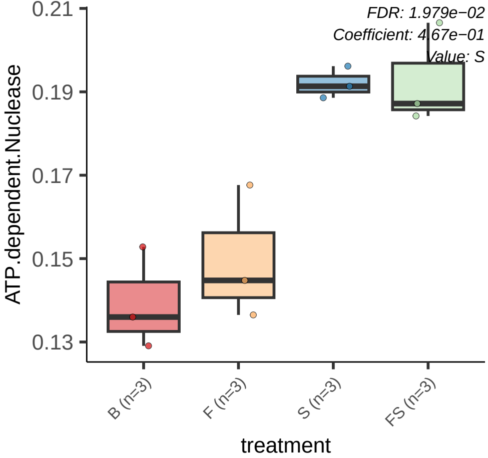

FDR: 1.967e−02
Coefficient: 4.70e−01
Value: FS
ATP.dependent.Nuclease
0.21
0.19
0.17
0.15
0.13
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

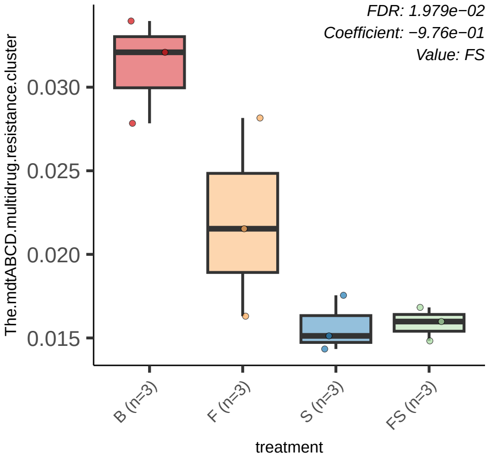


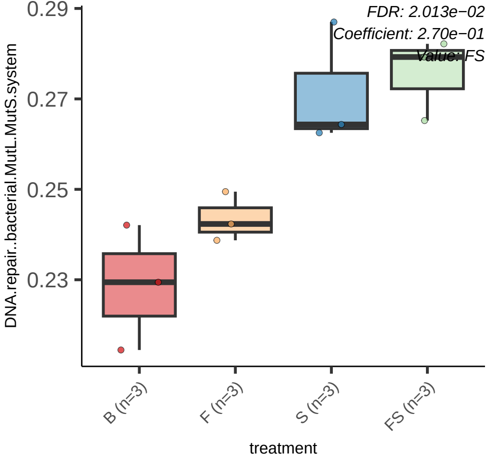
FDR: 1.967e−02
Coefficient: 1.31e−01
Value: S
0.24
0.23
0.22
0.21
At5g37530..CsdL.protein.family.
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

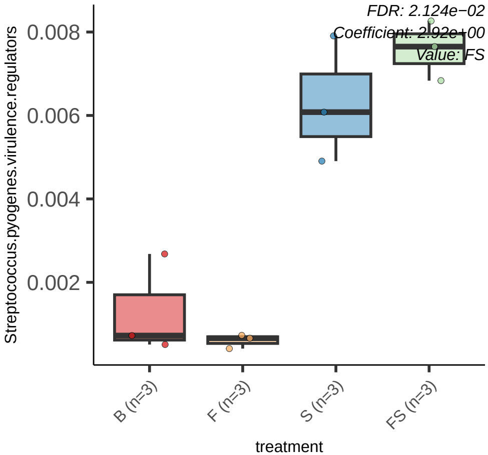

FDR: 1.967e−02
Coefficient: 1.84e+00
Value: FS
Extracellular.Polysaccharide.Biosynthesis.of.Streptococ
0.020
0.015
0.010
0.005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

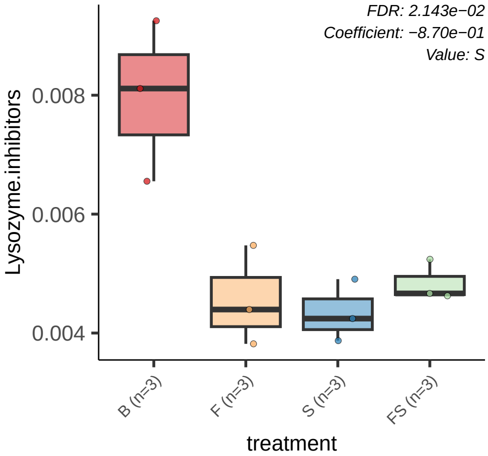

FDR: 1.973e−02
Coefficient: 1.09e+00
Value: S
Control.of.cell.elongation...division.cycle.in.Bacilli
0.06
0.05
0.04
0.03
0.02
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

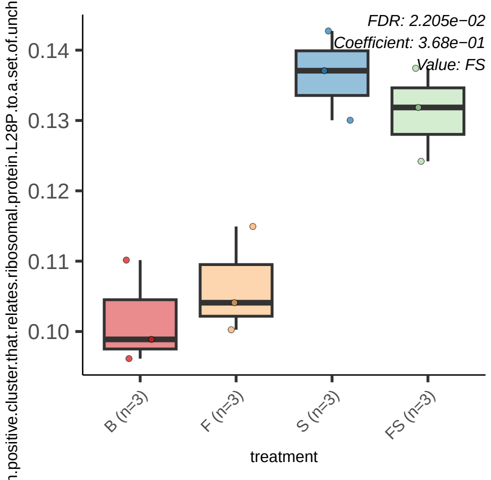

FDR: 1.979e−02
Coefficient: 4.67e−01
Value: S
0.21
0.19
0.17
0.15
0.13
ATP.dependent.Nuclease
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 1.979e−02
Coefficient: −9.76e−01
Value: FS
The.mdtABCD.multidrug.resistance.cluster
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

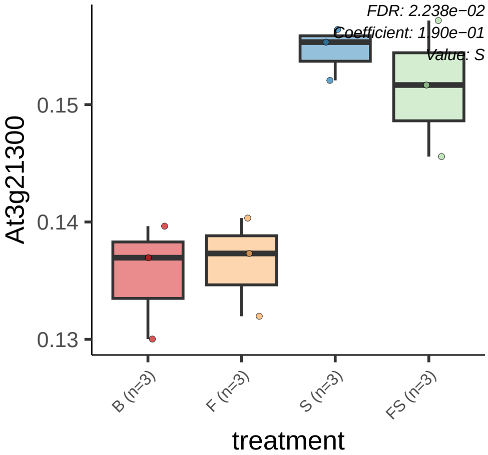

FDR: 2.013e−02
Coefficient: 2.70e−01
Value: FS
DNA.repair..bacterial.MutL.MutS.system
0.29
0.27
0.25
0.23
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

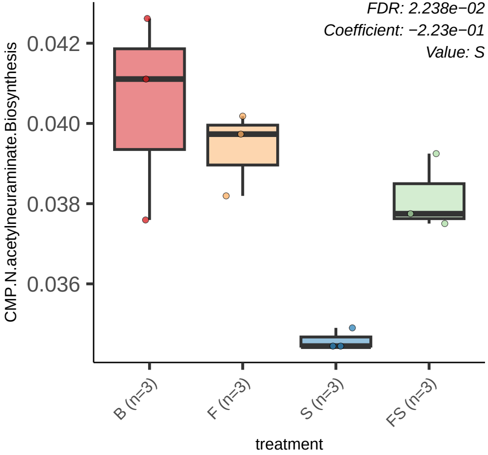

FDR: 2.124e−02
Coefficient: 2.92e+00
Value: FS
Streptococcus.pyogenes.virulence.regulators
0.008
0.006
0.004
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

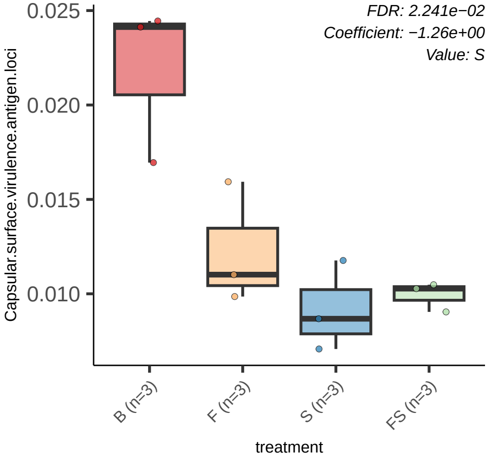

FDR: 2.143e−02
Coefficient: −8.70e−01
Value: S
Lysozyme.inhibitors
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

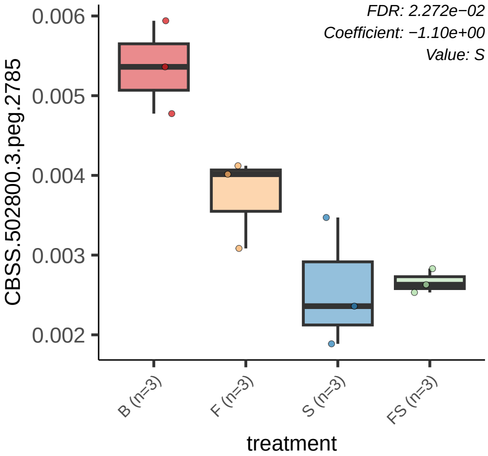


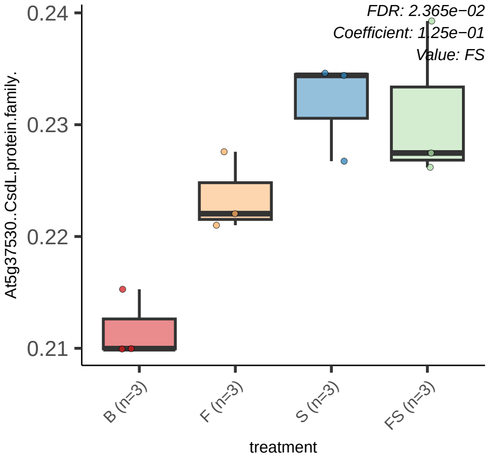
FDR: 2.205e−02
Coefficient: 3.68e−01
Value: FS
n.positive.cluster.that.relates.ribosomal.protein.L28P.to.a.set.of.unch
0.14
0.13
0.12
0.11
0.10
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 2.238e−02
Coefficient: 1.90e−01
Value: S
At3g21300
0.15
0.14
0.13
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

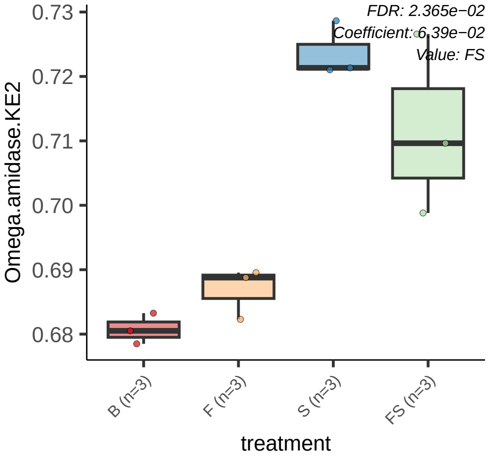

FDR: 2.238e−02
Coefficient: −2.23e−01
Value: S
CMP.N.acetylneuraminate.Biosynthesis
0.042
0.040
0.038
0.036
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

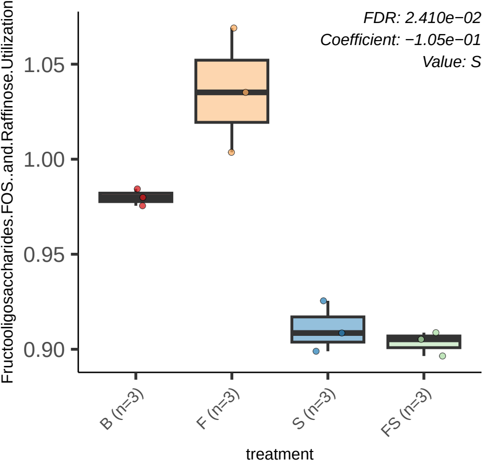

FDR: 2.241e−02
Coefficient: −1.26e+00
Value: S
Capsular.surface.virulence.antigen.loci
0.025
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

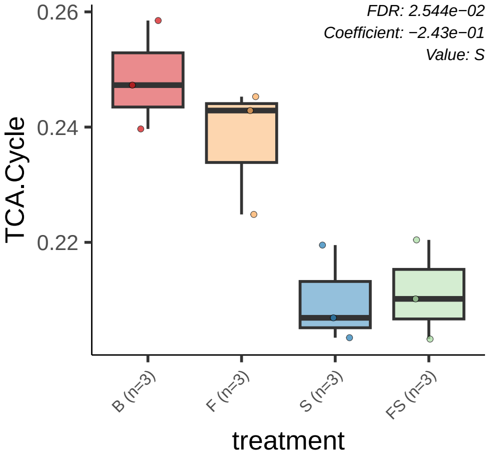

FDR: 2.272e−02
Coefficient: −1.10e+00
Value: S
CBSS.502800.3.peg.2785
0.006
0.005
0.004
0.003
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

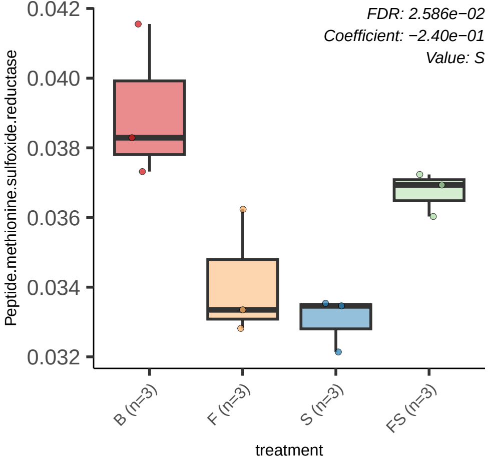


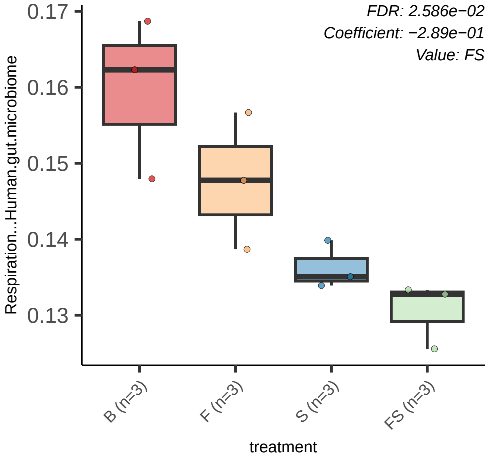
FDR: 2.365e−02
Coefficient: 1.25e−01
Value: FS
At5g37530..CsdL.protein.family.
0.24
0.23
0.22
0.21
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

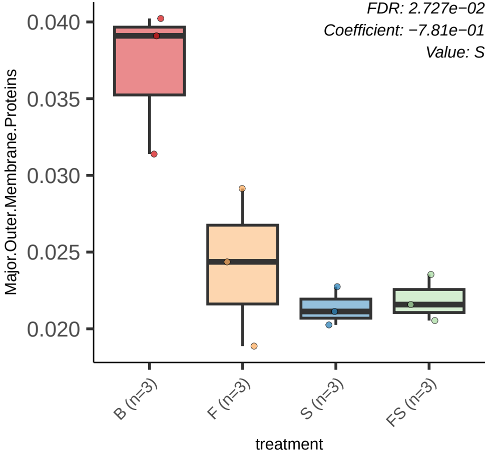

FDR: 2.365e−02
Coefficient: 6.39e−02
Value: FS
Omega.amidase.KE2
0.73
0.72
0.71
0.70
0.69
0.68
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

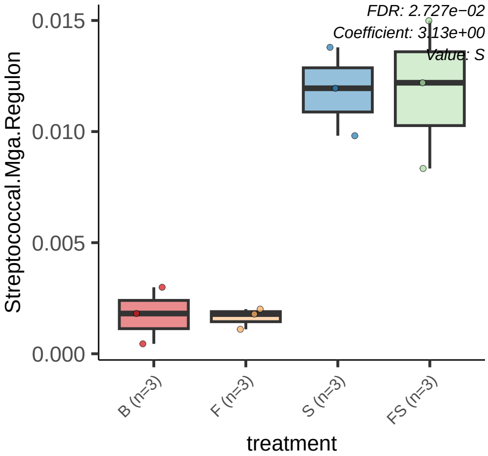

FDR: 2.410e−02
Coefficient: −1.05e−01
Value: S
Fructooligosaccharides.FOS..and.Raffinose.Utilization
1.05
1.00
0.95
0.90
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

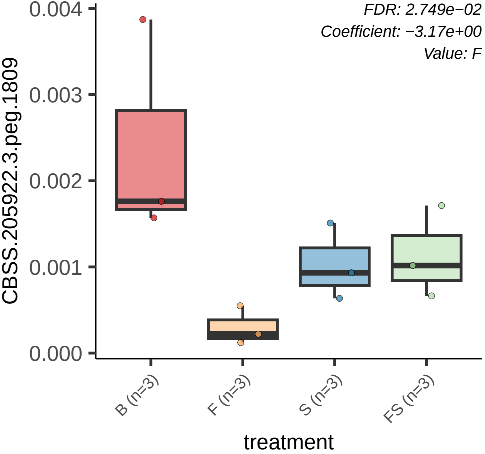

FDR: 2.544e−02
Coefficient: −2.43e−01
Value: S
TCA.Cycle
0.26
0.24
0.22
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

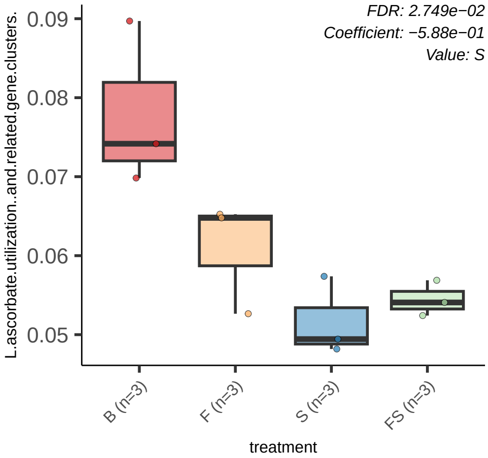

FDR: 2.586e−02
Coefficient: −2.40e−01
Value: S
Peptide.methionine.sulfoxide.reductase
0.042
0.040
0.038
0.036
0.034
0.032
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

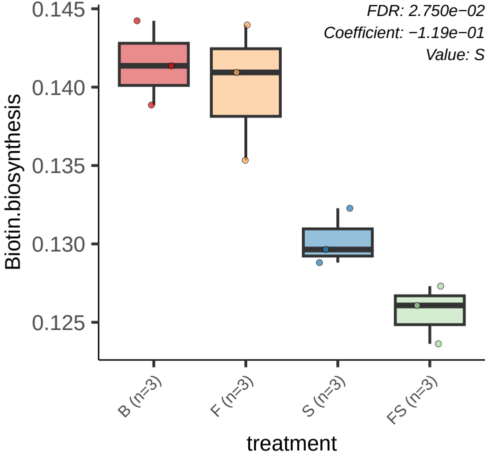

FDR: 2.586e−02
Coefficient: −2.89e−01
Value: FS
Respiration...Human.gut.microbiome
0.17
0.16
0.15
0.14
0.13
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

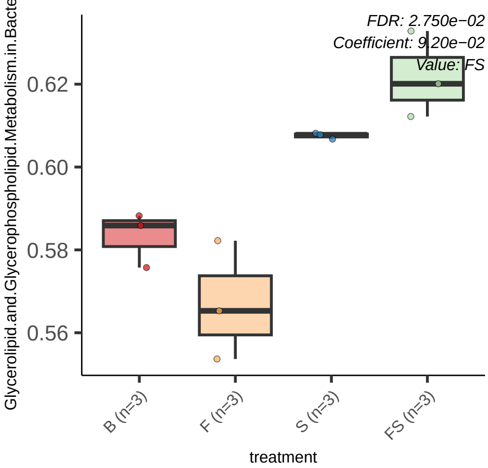

FDR: 2.727e−02
Coefficient: −7.81e−01
Value: S
Major.Outer.Membrane.Proteins
0.040
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 2.727e−02
Coefficient: 3.13e+00
Value: S
Streptococcal.Mga.Regulon
0.015
0.010
0.005
0.000
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

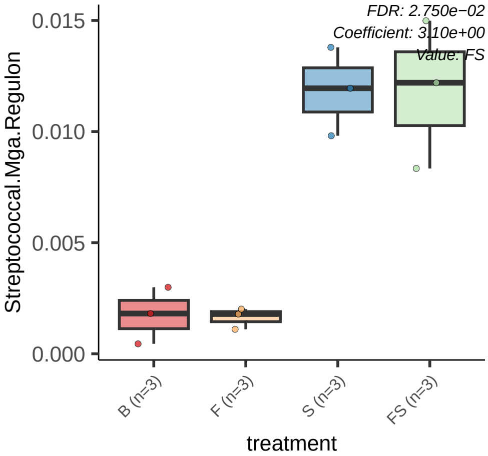

FDR: 2.749e−02
Coefficient: −3.17e+00
Value: F
CBSS.205922.3.peg.1809
0.004
0.003
0.002
0.001
0.000
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

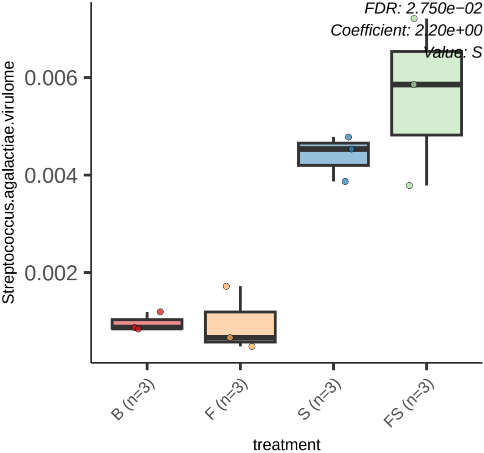

FDR: 2.749e−02
Coefficient: −5.88e−01
Value: S
L.ascorbate.utilization..and.related.gene.clusters.
0.09
0.08
0.07
0.06
0.05
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

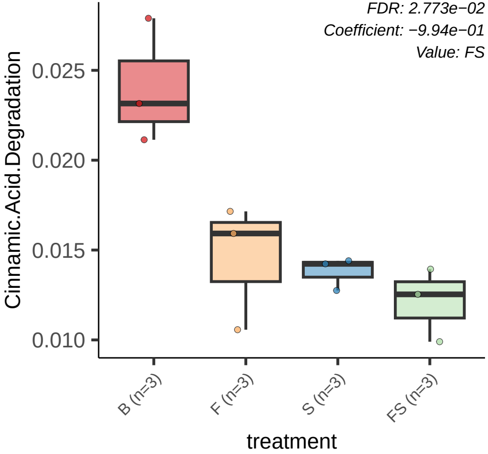

FDR: 2.750e−02
Coefficient: −1.19e−01
Value: S
Biotin.biosynthesis
0.145
0.140
0.135
0.130
0.125
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

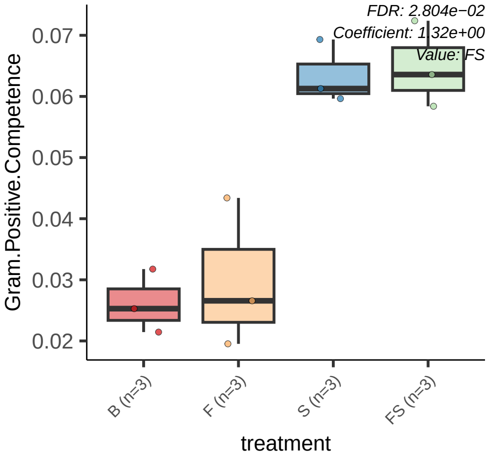


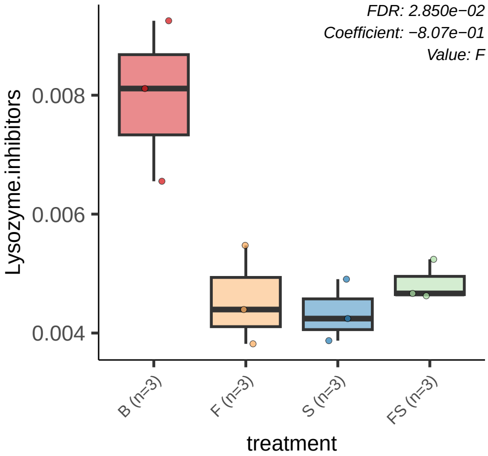
FDR: 2.750e−02
Coefficient: 9.20e−02
Value: FS
Glycerolipid.and.Glycerophospholipid.Metabolism.in.Bacte
0.62
0.60
0.58
0.56
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

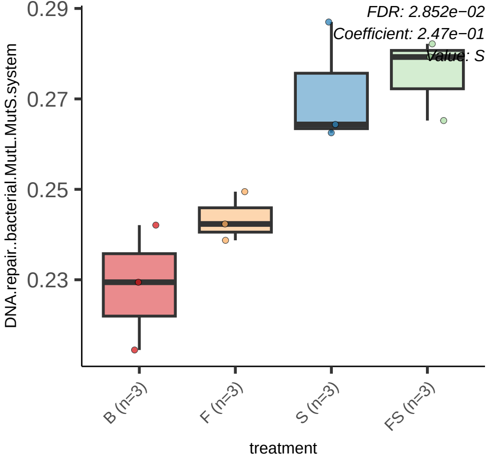

FDR: 2.750e−02
Coefficient: 3.10e+00
Value: FS
Streptococcal.Mga.Regulon
0.015
0.010
0.005
0.000
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

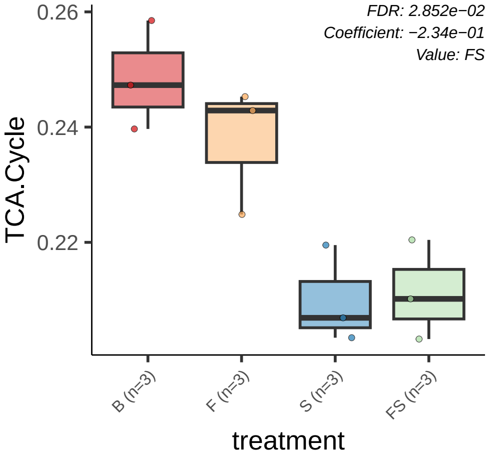

FDR: 2.750e−02
Coefficient: 2.20e+00
Value: S
Streptococcus.agalactiae.virulome
0.006
0.004
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

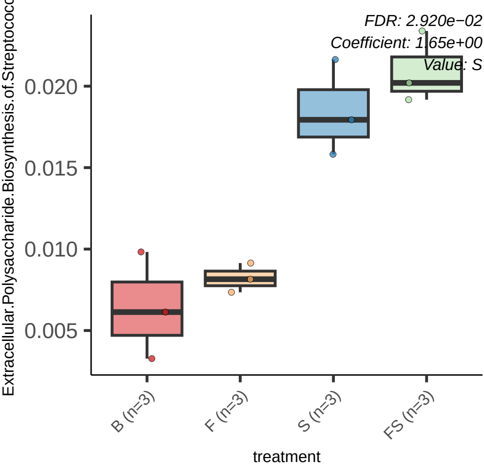

FDR: 2.773e−02
Coefficient: −9.94e−01
Value: FS
Cinnamic.Acid.Degradation
0.025
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

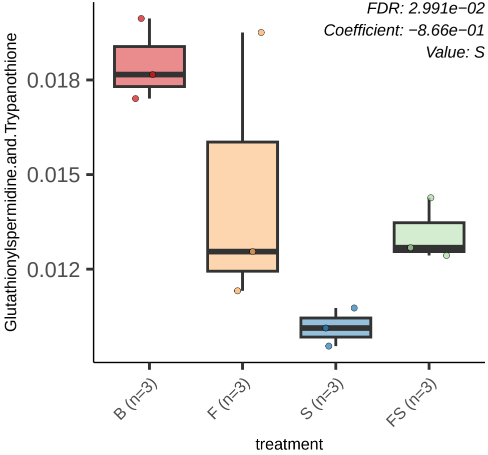

FDR: 2.804e−02
Coefficient: 1.32e+00
Value: FS
Gram.Positive.Competence
0.07
0.06
0.05
0.04
0.03
0.02
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

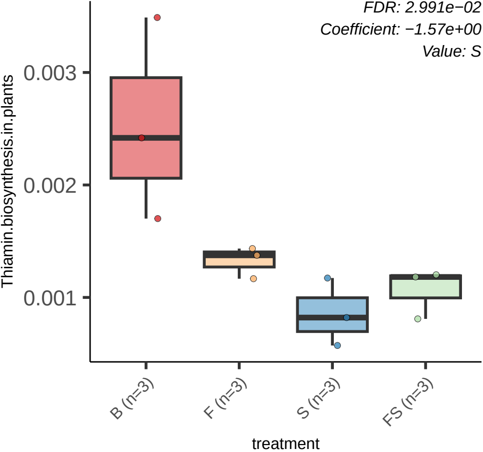

FDR: 2.850e−02
Coefficient: −8.07e−01
Value: F
Lysozyme.inhibitors
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

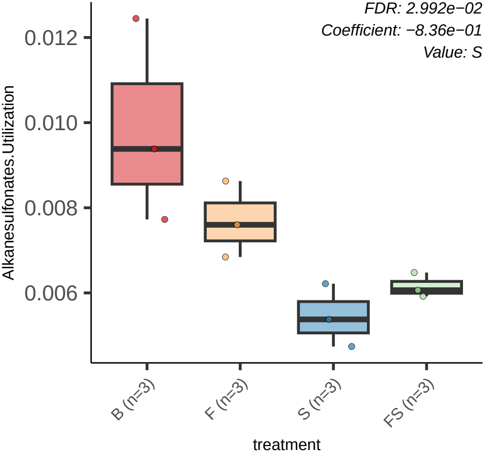

FDR: 2.852e−02
Coefficient: 2.47e−01
Value: S
DNA.repair..bacterial.MutL.MutS.system
0.29
0.27
0.25
0.23
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

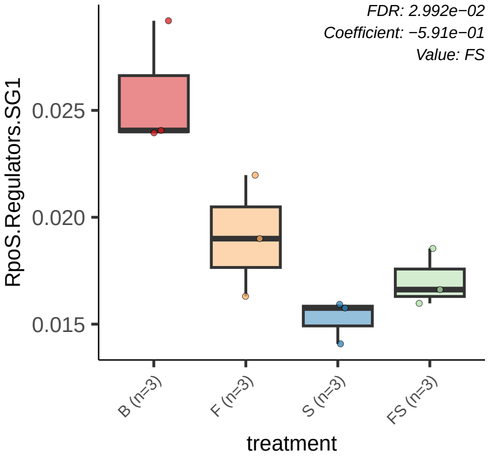

FDR: 2.852e−02
Coefficient: −2.34e−01
Value: FS
TCA.Cycle
0.26
0.24
0.22
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

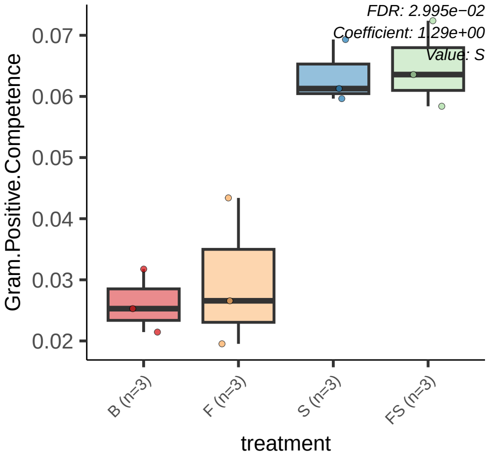

FDR: 2.920e−02
Coefficient: 1.65e+00
Value: S
Extracellular.Polysaccharide.Biosynthesis.of.Streptococc
0.020
0.015
0.010
0.005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

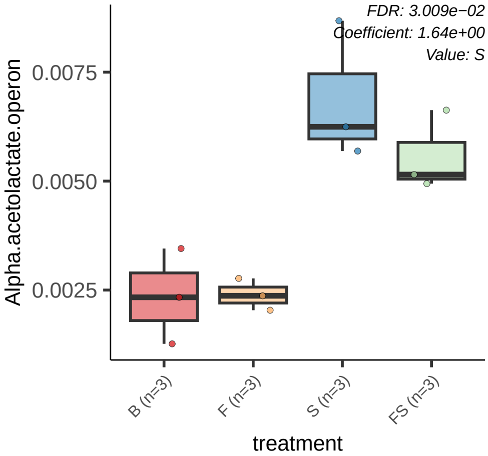

FDR: 2.991e−02
Coefficient: −8.66e−01
Value: S
Glutathionylspermidine.and.Trypanothione
0.018
0.015
0.012
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

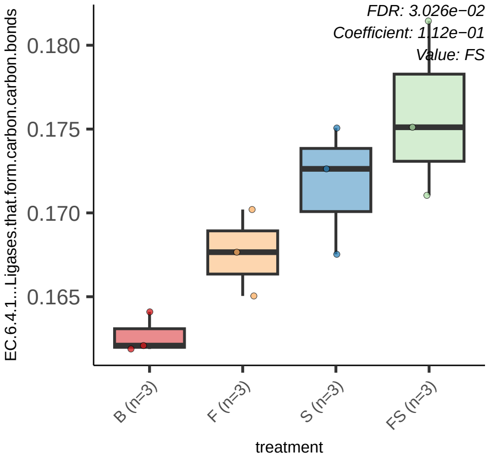

FDR: 2.991e−02
Coefficient: −1.57e+00
Value: S
Thiamin.biosynthesis.in.plants
0.003
0.002
0.001
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

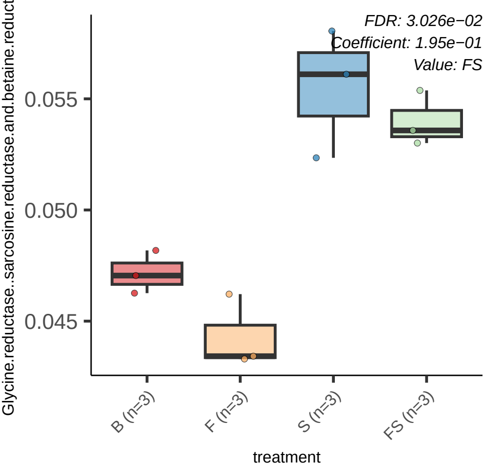

FDR: 2.992e−02
Coefficient: −8.36e−01
Value: S
Alkanesulfonates.Utilization
0.012
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

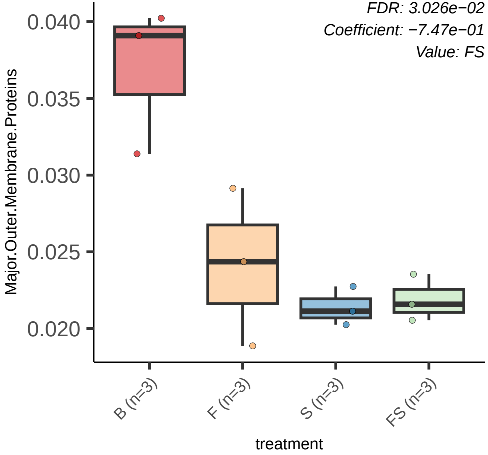

FDR: 2.992e−02
Coefficient: −5.91e−01
Value: FS
RpoS.Regulators.SG1
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

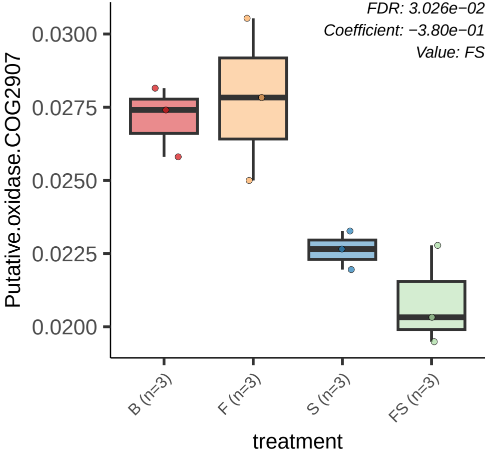

FDR: 2.995e−02
Coefficient: 1.29e+00
Value: S
Gram.Positive.Competence
0.07
0.06
0.05
0.04
0.03
0.02
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

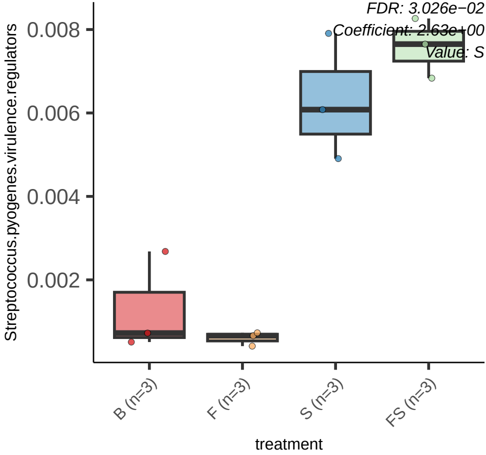

FDR: 3.009e−02
Coefficient: 1.64e+00
Value: S
Alpha.acetolactate.operon
0.0075
0.0050
0.0025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

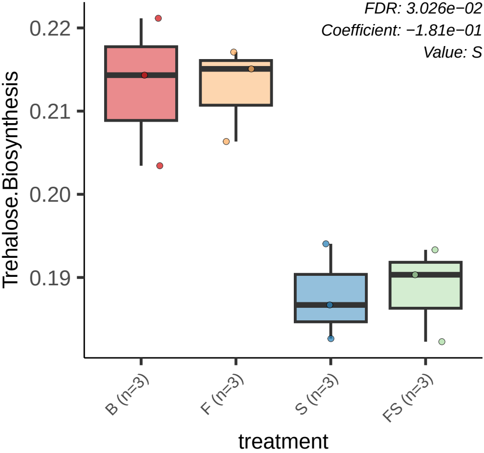

FDR: 3.026e−02
Coefficient: 1.12e−01
Value: FS
EC.6.4.1...Ligases.that.form.carbon.carbon.bonds
0.180
0.175
0.170
0.165
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

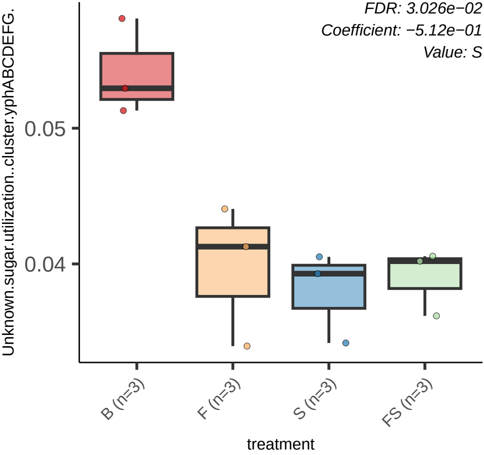

FDR: 3.026e−02
Coefficient: 1.95e−01
Value: FS
0.055
0.050
0.045
Glycine.reductase..sarcosine.reductase.and.betaine.reduct
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

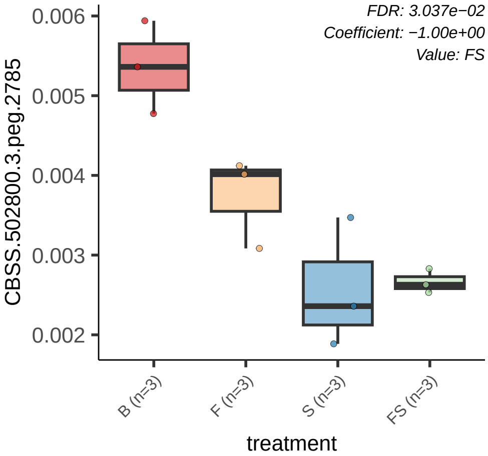

FDR: 3.026e−02
Coefficient: −7.47e−01
Value: FS
Major.Outer.Membrane.Proteins
0.040
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

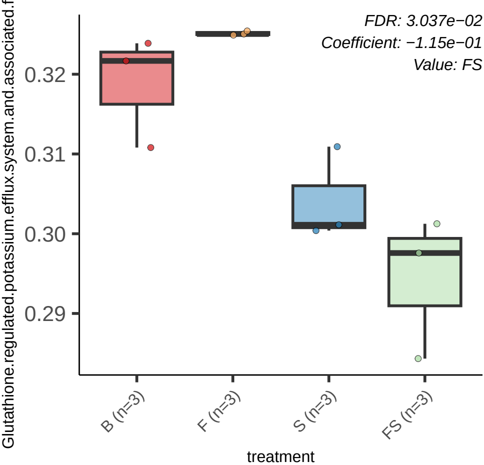

FDR: 3.026e−02
Coefficient: −3.80e−01
Value: FS
Putative.oxidase.COG2907
0.0300
0.0275
0.0250
0.0225
0.0200
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

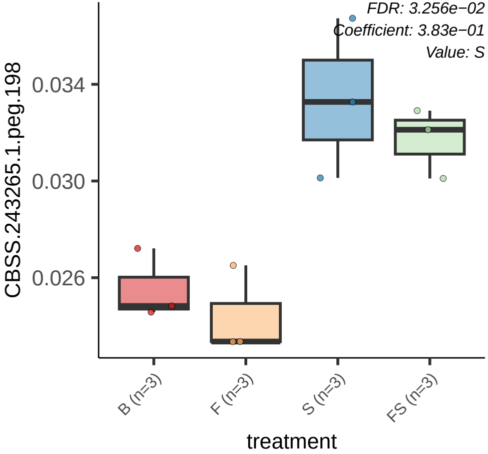

FDR: 3.026e−02
Coefficient: 2.63e+00
Value: S
Streptococcus.pyogenes.virulence.regulators
0.008
0.006
0.004
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

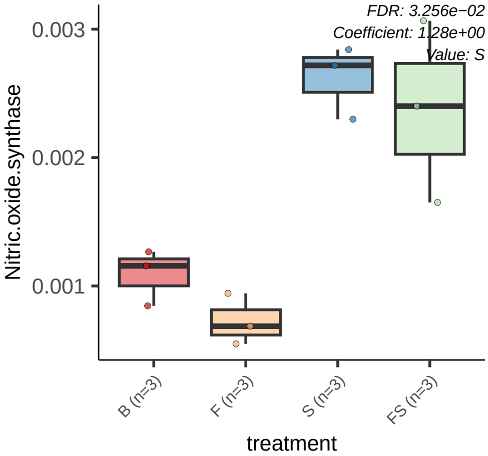

FDR: 3.026e−02
Coefficient: −1.81e−01
Value: S
0.22
0.21
0.20
0.19
Trehalose.Biosynthesis
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

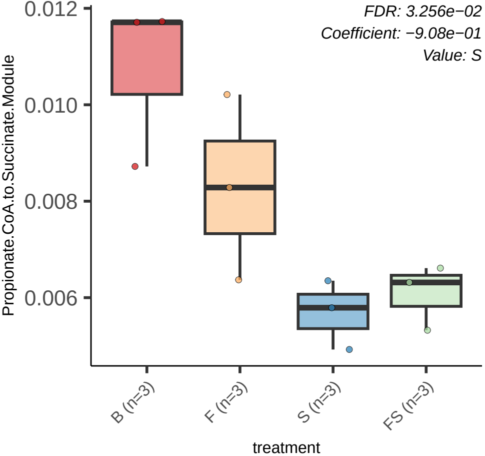

FDR: 3.026e−02
Coefficient: −5.12e−01
Value: S
Unknown.sugar.utilization..cluster.yphABCDEFG.
0.05
0.04
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

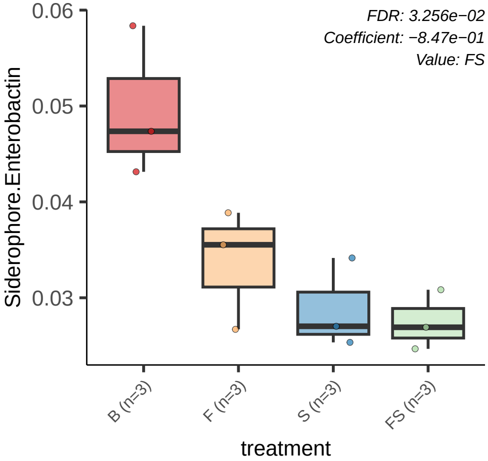

FDR: 3.037e−02
Coefficient: −1.00e+00
Value: FS
CBSS.502800.3.peg.2785
0.006
0.005
0.004
0.003
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

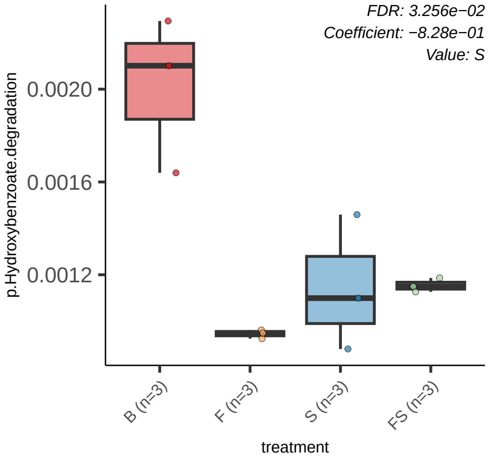

FDR: 3.037e−02
Coefficient: −1.15e−01
Value: FS
Glutathione.regulated.potassium.efflux.system.and.associated.f
0.32
0.31
0.30
0.29
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

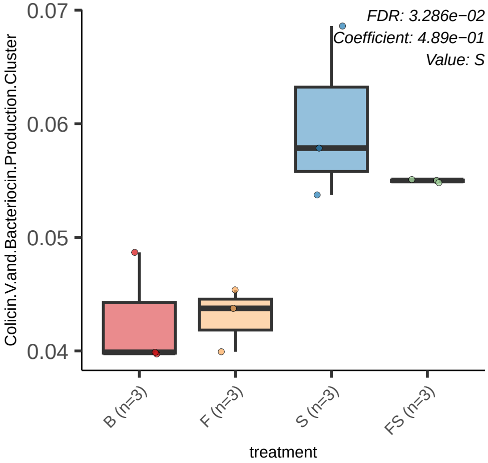

FDR: 3.256e−02
Coefficient: 3.83e−01
Value: S
CBSS.243265.1.peg.198
0.034
0.030
0.026
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 3.256e−02
Coefficient: 1.28e+00
Value: S
Nitric.oxide.synthase
0.003
0.002
0.001
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

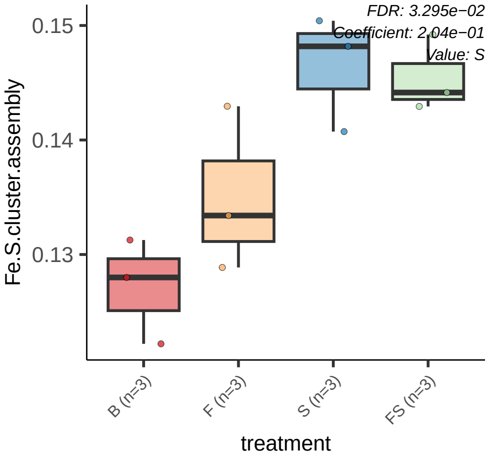

FDR: 3.256e−02
Coefficient: −9.08e−01
Value: S
Propionate.CoA.to.Succinate.Module
0.012
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

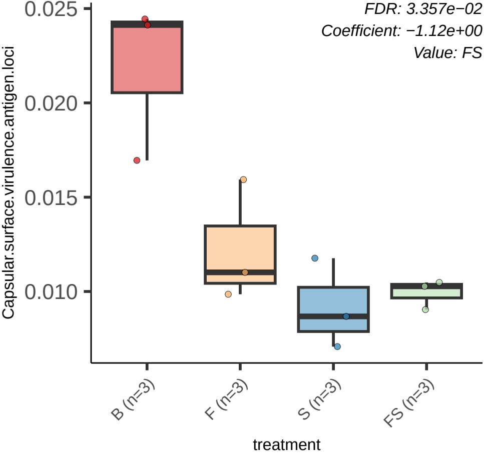

FDR: 3.256e−02
Coefficient: −8.47e−01
Value: FS
0.06
0.05
0.04
0.03
Siderophore.Enterobactin
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

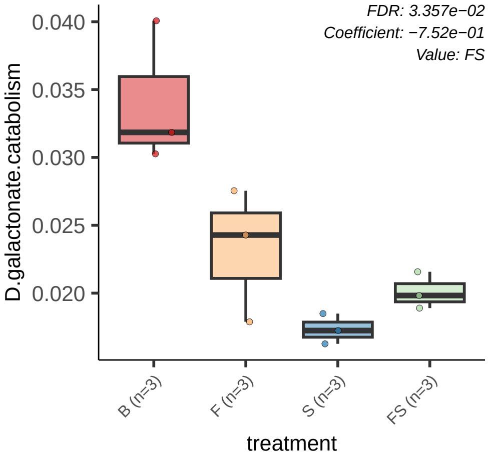

FDR: 3.256e−02
Coefficient: −8.28e−01
Value: S
p.Hydroxybenzoate.degradation
0.0020
0.0016
0.0012
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

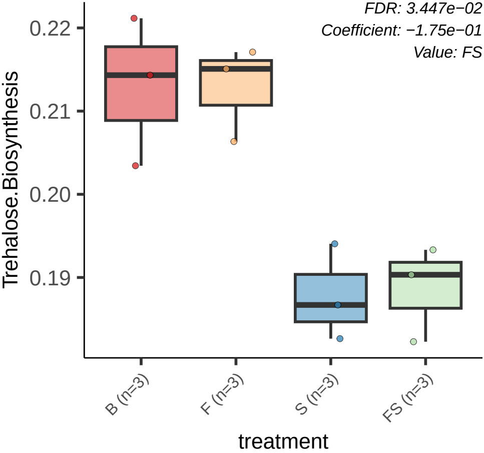


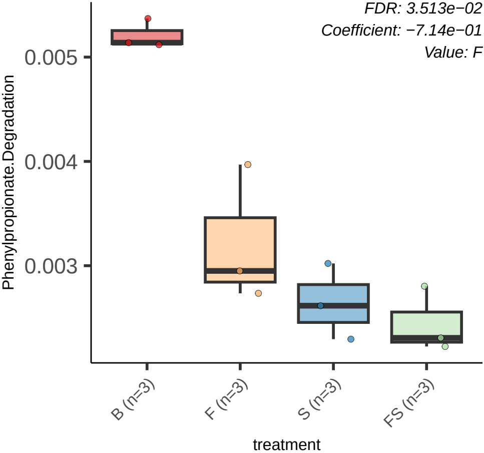
FDR: 3.286e−02
Coefficient: 4.89e−01
Value: S
0.07
0.06
0.05
0.04
Colicin.V.and.Bacteriocin.Production.Cluster
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

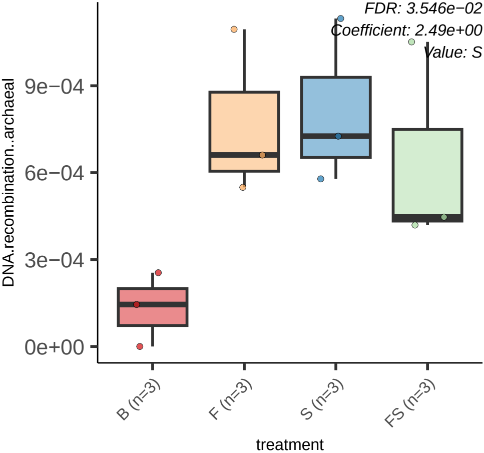

FDR: 3.295e−02
Coefficient: 2.04e−01
Value: S
Fe.S.cluster.assembly
0.15
0.14
0.13
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

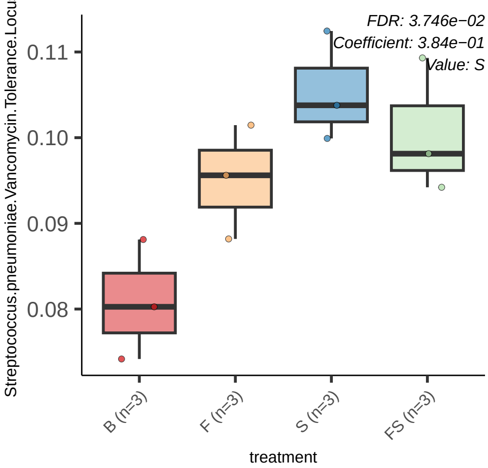

FDR: 3.357e−02
Coefficient: −1.12e+00
Value: FS
Capsular.surface.virulence.antigen.loci
0.025
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 3.357e−02
Coefficient: −7.52e−01
Value: FS
D.galactonate.catabolism
0.040
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

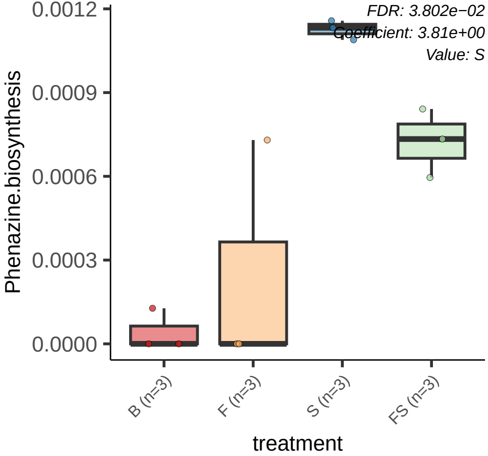

FDR: 3.447e−02
Coefficient: −1.75e−01
Value: FS
Trehalose.Biosynthesis
0.22
0.21
0.20
0.19
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

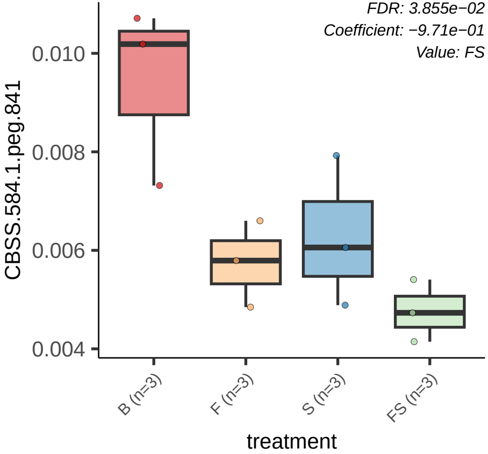

FDR: 3.513e−02
Coefficient: −7.14e−01
Value: F
Phenylpropionate.Degradation
0.005
0.004
0.003
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

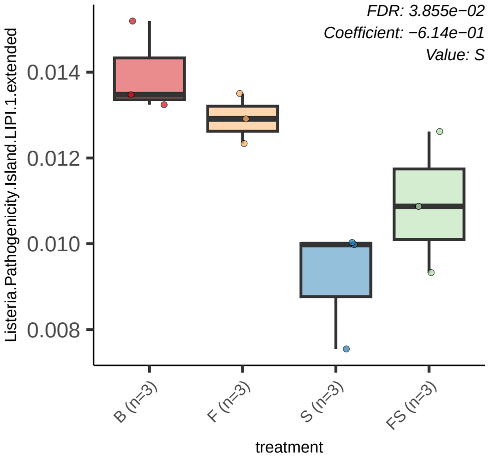

FDR: 3.546e−02
Coefficient: 2.49e+00
Value: S
DNA.recombination..archaeal
9e−04
6e−04
3e−04
0e+00
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

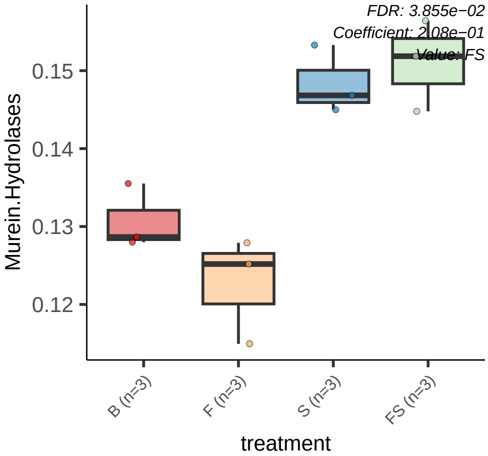


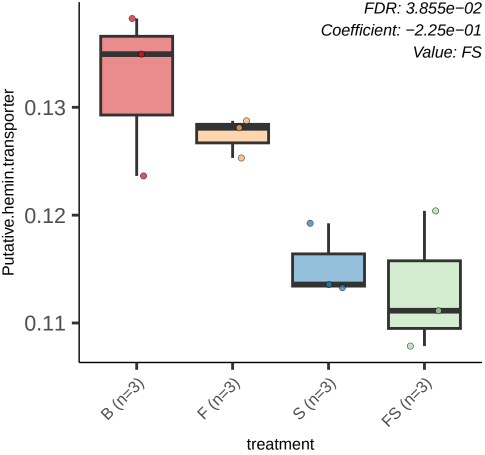
FDR: 3.746e−02
Coefficient: 3.84e−01
Value: S
Streptococcus.pneumoniae.Vancomycin.Tolerance.Locu
0.11
0.10
0.09
0.08
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

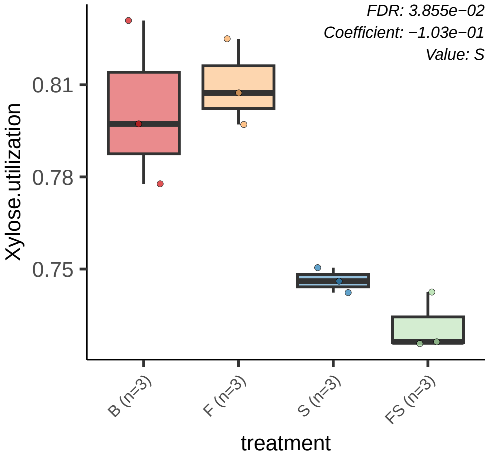

FDR: 3.802e−02
Coefficient: 3.81e+00
Value: S
Phenazine.biosynthesis
0.0012
0.0009
0.0006
0.0003
0.0000
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

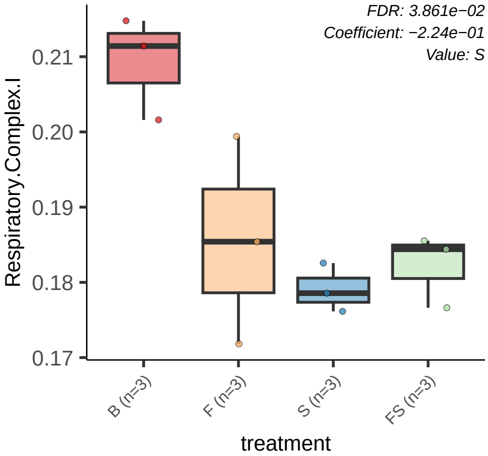

FDR: 3.855e−02
Coefficient: −9.71e−01
Value: FS
CBSS.584.1.peg.841
0.010
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

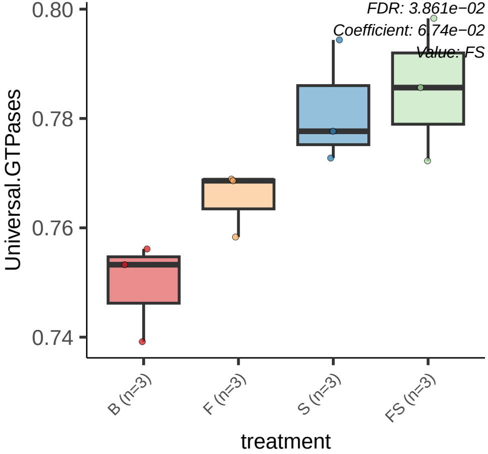

FDR: 3.855e−02
Coefficient: −6.14e−01
Value: S
Listeria.Pathogenicity.Island.LIPI.1.extended
0.014
0.012
0.010
0.008
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

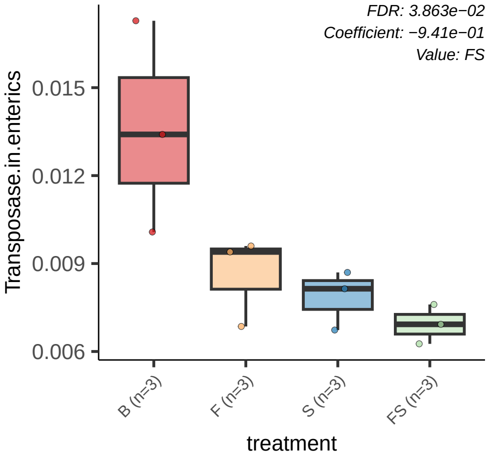

FDR: 3.855e−02
Coefficient: 2.08e−01
Value: FS
Murein.Hydrolases
0.15
0.14
0.13
0.12
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

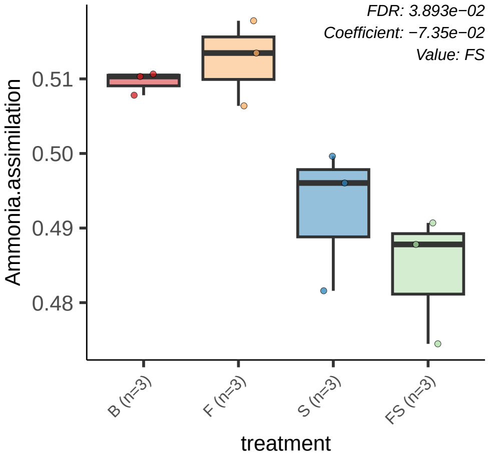

FDR: 3.855e−02
Coefficient: −2.25e−01
Value: FS
Putative.hemin.transporter
0.13
0.12
0.11
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

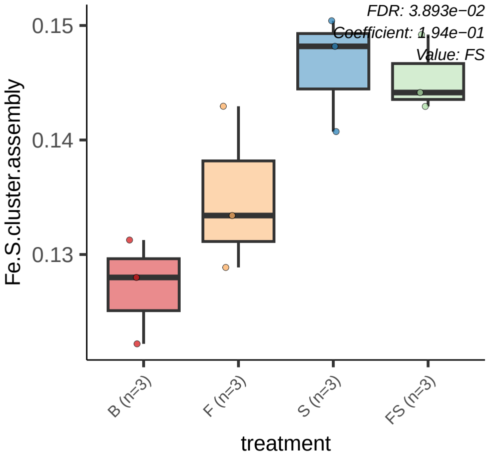

FDR: 3.855e−02
Coefficient: −1.03e−01
Value: S
Xylose.utilization
0.81
0.78
0.75
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

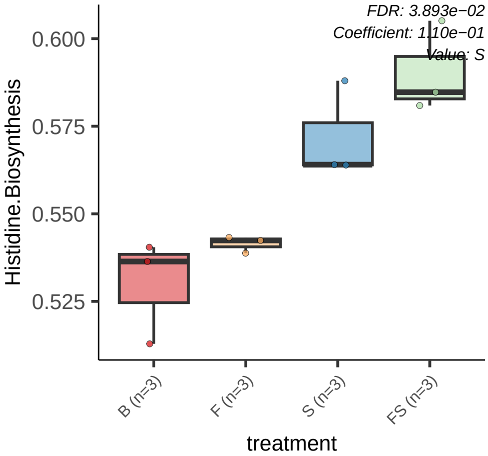

FDR: 3.861e−02
Coefficient: −2.24e−01
Value: S
Respiratory.Complex.I
0.21
0.20
0.19
0.18
0.17
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

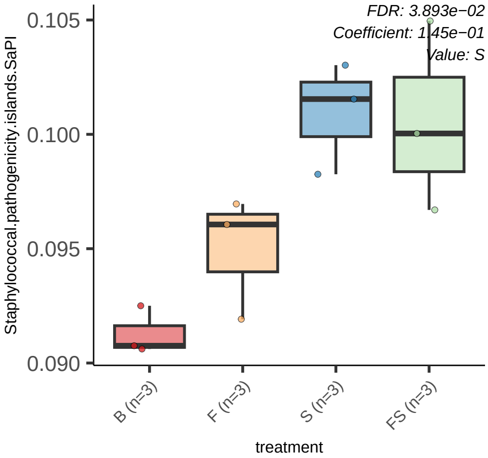

FDR: 3.861e−02
Coefficient: 6.74e−02
Value: FS
Universal.GTPases
0.80
0.78
0.76
0.74
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

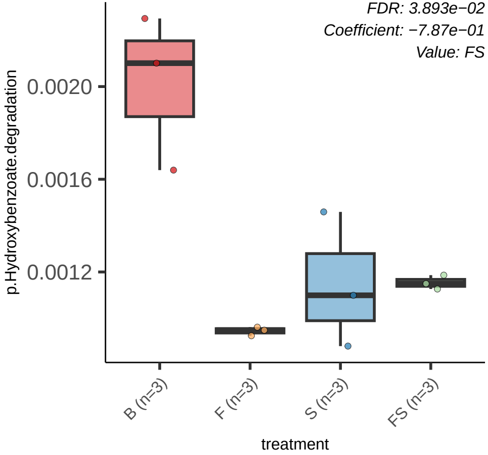

FDR: 3.863e−02
Coefficient: −9.41e−01
Value: FS
Transposase.in.enterics
0.015
0.012
0.009
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

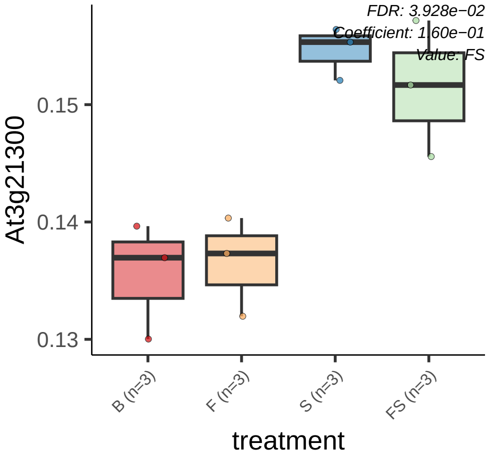

FDR: 3.893e−02
Coefficient: −7.35e−02
Value: FS
Ammonia.assimilation
0.51
0.50
0.49
0.48
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

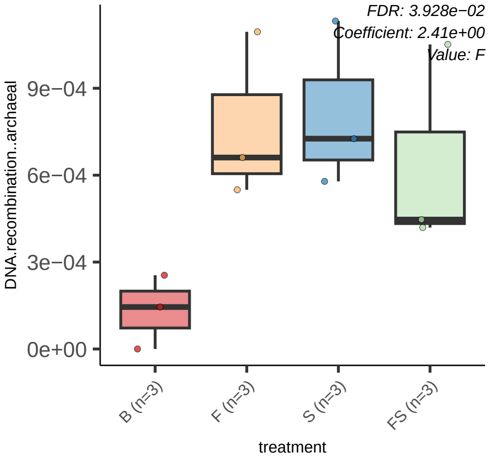

FDR: 3.893e−02
Coefficient: 1.94e−01
Value: FS
Fe.S.cluster.assembly
0.15
0.14
0.13
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

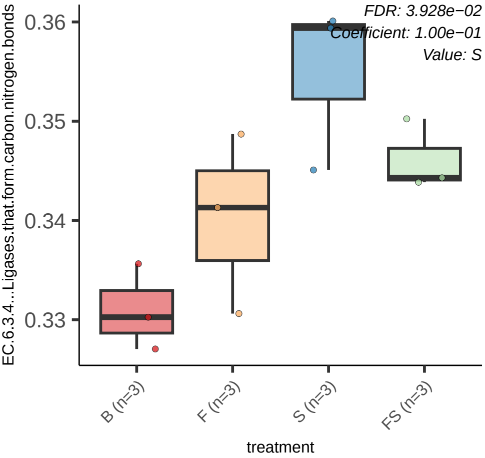

FDR: 3.893e−02
Coefficient: 1.10e−01
Value: S
Histidine.Biosynthesis
0.600
0.575
0.550
0.525
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

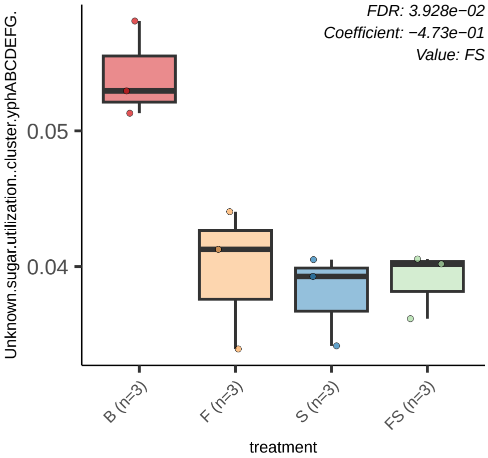

FDR: 3.893e−02
Coefficient: 1.45e−01
Value: S
Staphylococcal.pathogenicity.islands.SaPI
0.105
0.100
0.095
0.090
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

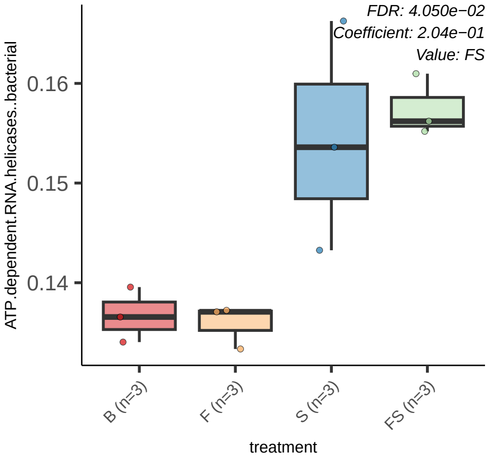

FDR: 3.893e−02
Coefficient: −7.87e−01
Value: FS
p.Hydroxybenzoate.degradation
0.0020
0.0016
0.0012
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

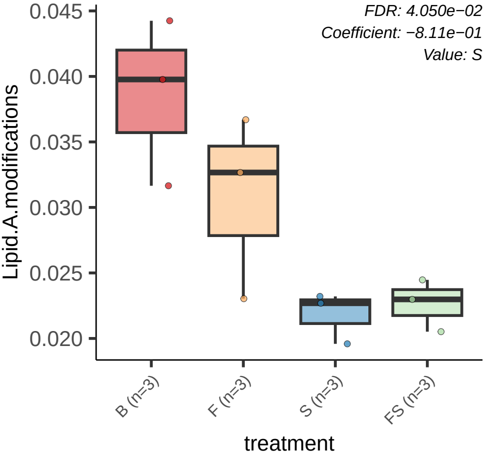

FDR: 3.928e−02
Coefficient: 1.60e−01
Value: FS
At3g21300
0.15
0.14
0.13
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

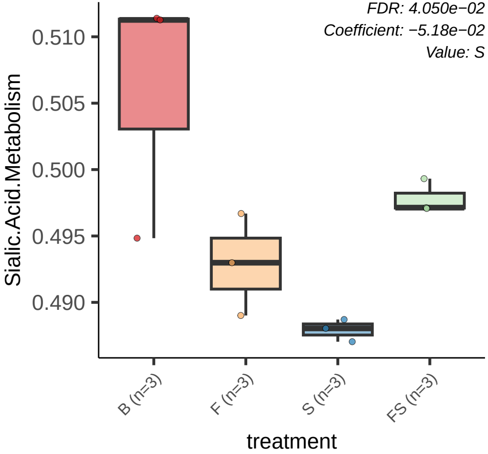

FDR: 3.928e−02
Coefficient: 2.41e+00
Value: F
DNA.recombination..archaeal
9e−04
6e−04
3e−04
0e+00
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

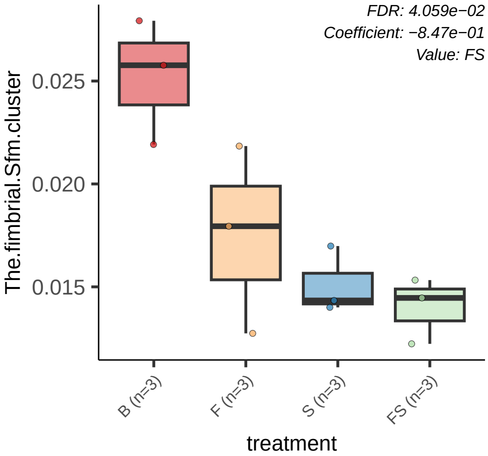

FDR: 3.928e−02
Coefficient: 1.00e−01
Value: S
EC.6.3.4...Ligases.that.form.carbon.nitrogen.bonds
0.36
0.35
0.34
0.33
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

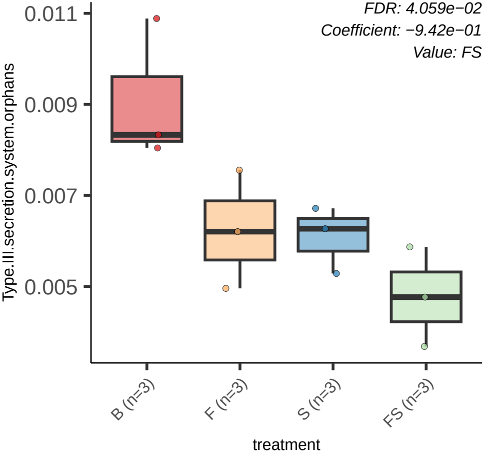

FDR: 3.928e−02
Coefficient: −4.73e−01
Value: FS
Unknown.sugar.utilization..cluster.yphABCDEFG.
0.05
0.04
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

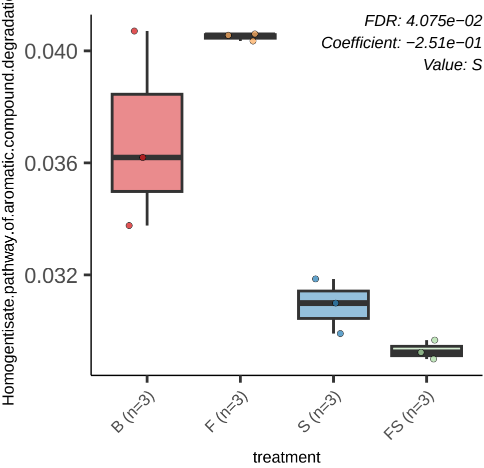

FDR: 4.050e−02
Coefficient: 2.04e−01
Value: FS
ATP.dependent.RNA.helicases..bacterial
0.16
0.15
0.14
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

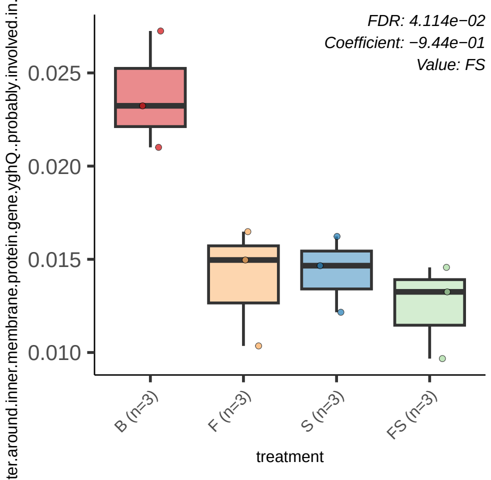

FDR: 4.050e−02
Coefficient: −8.11e−01
Value: S
Lipid.A.modifications
0.045
0.040
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

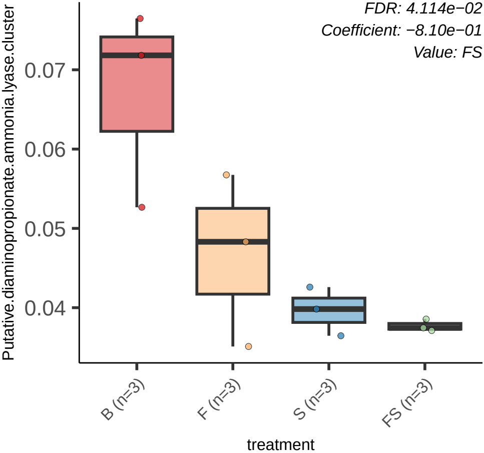

FDR: 4.050e−02
Coefficient: −5.18e−02
Value: S
Sialic.Acid.Metabolism
0.510
0.505
0.500
0.495
0.490
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

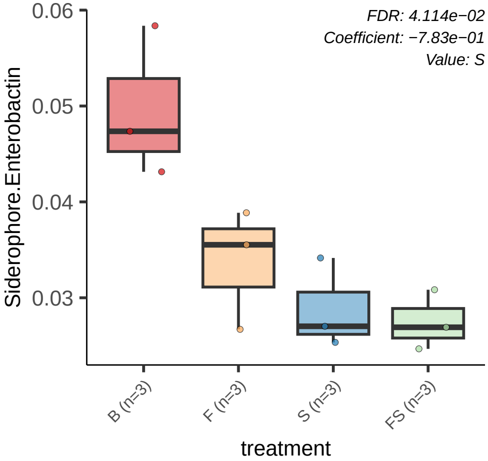

FDR: 4.059e−02
Coefficient: −8.47e−01
Value: FS
The.fimbrial.Sfm.cluster
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

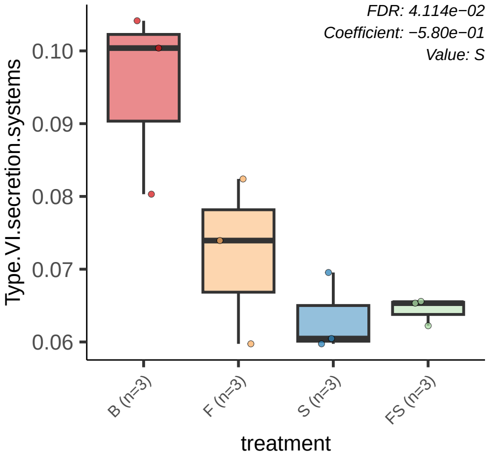

FDR: 4.059e−02
Coefficient: −9.42e−01
Value: FS
Type.III.secretion.system.orphans
0.011
0.009
0.007
0.005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

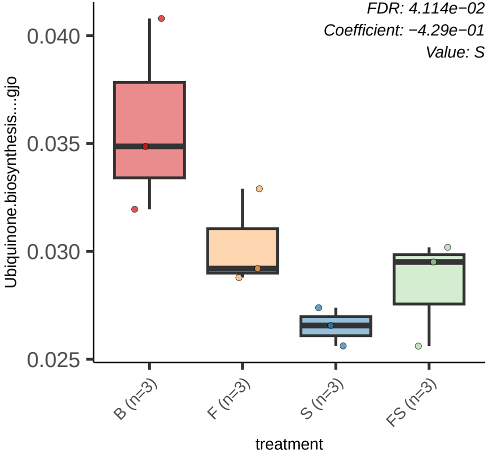

FDR: 4.075e−02
Coefficient: −2.51e−01
Value: S
Homogentisate.pathway.of.aromatic.compound.degradati
0.040
0.036
0.032
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

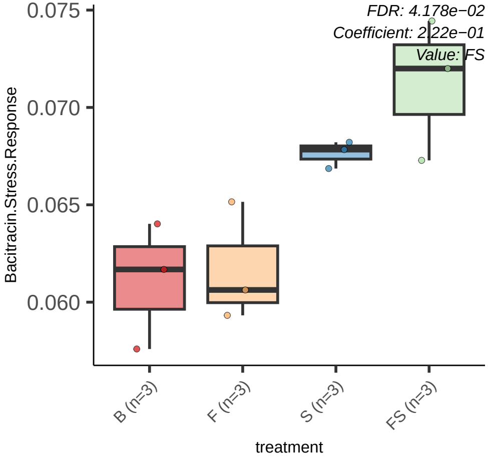

FDR: 4.114e−02
Coefficient: −9.44e−01
Value: FS
ter.around.inner.membrane.protein.gene.yghQ..probably.involved.in.
0.025
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

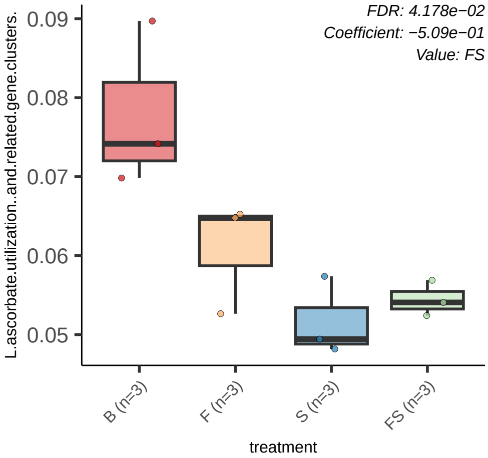

FDR: 4.114e−02
Coefficient: −8.10e−01
Value: FS
Putative.diaminopropionate.ammonia.lyase.cluster
0.07
0.06
0.05
0.04
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

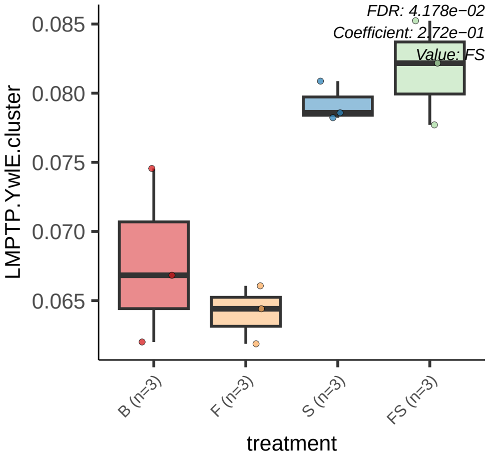

FDR: 4.114e−02
Coefficient: −7.83e−01
Value: S
Siderophore.Enterobactin
0.06
0.05
0.04
0.03
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 4.114e−02
Coefficient: −5.80e−01
Value: S
Type.VI.secretion.systems
0.10
0.09
0.08
0.07
0.06
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

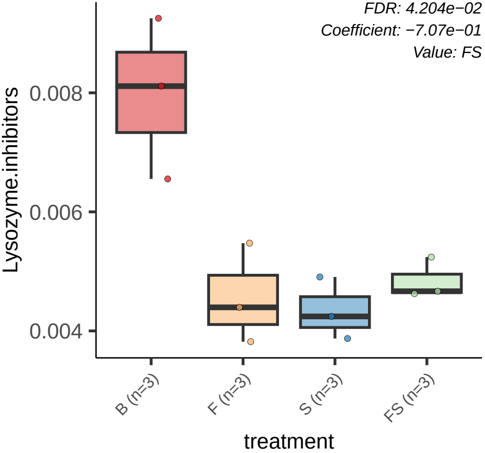

FDR: 4.114e−02
Coefficient: −4.29e−01
Value: S
Ubiquinone.biosynthesis...gjo
0.040
0.035
0.030
0.025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

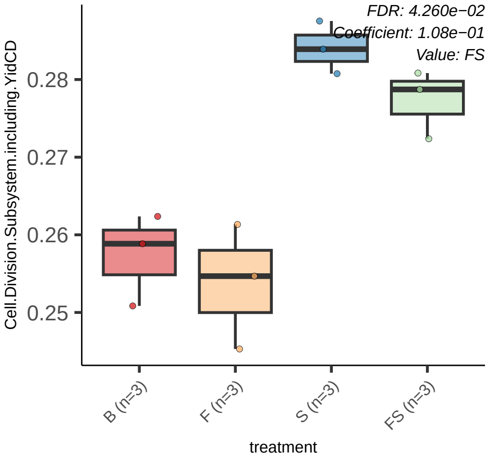

FDR: 4.178e−02
Coefficient: 2.22e−01
Value: FS
Bacitracin.Stress.Response
0.075
0.070
0.065
0.060
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

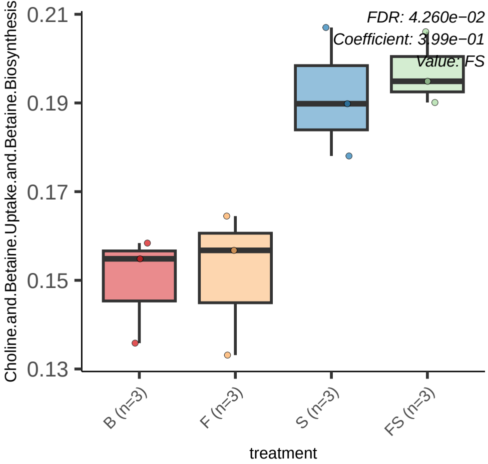

FDR: 4.178e−02
Coefficient: −5.09e−01
Value: FS
L.ascorbate.utilization..and.related.gene.clusters.
0.09
0.08
0.07
0.06
0.05
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

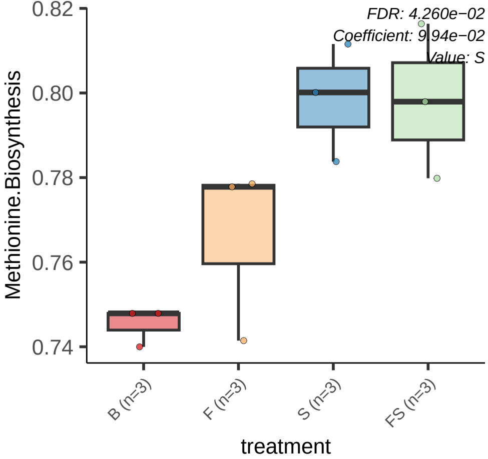


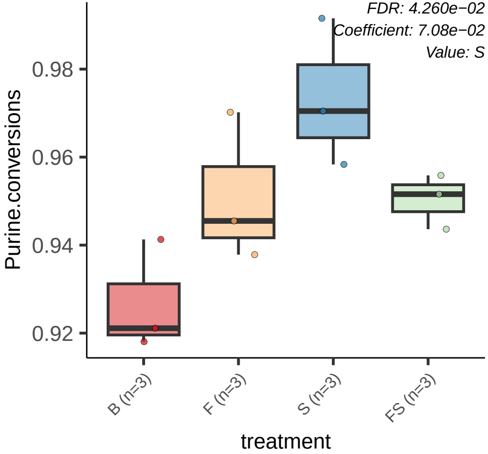
FDR: 4.178e−02
Coefficient: 2.72e−01
Value: FS
LMPTP.YwlE.cluster
0.085
0.080
0.075
0.070
0.065
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

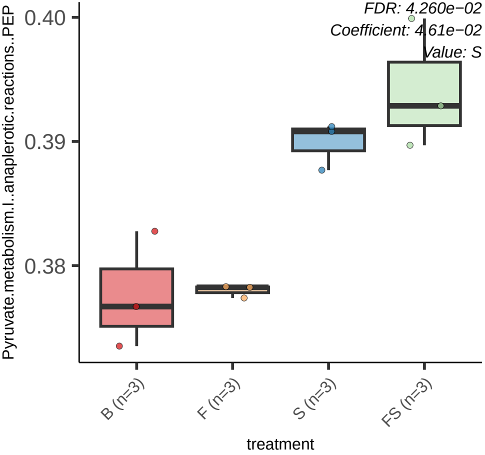

FDR: 4.204e−02
Coefficient: −7.07e−01
Value: FS
Lysozyme.inhibitors
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

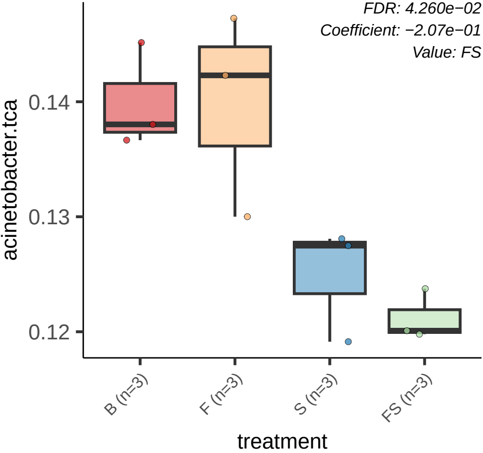

FDR: 4.260e−02
Coefficient: 1.08e−01
Value: FS
Cell.Division.Subsystem.including.YidCD
0.28
0.27
0.26
0.25
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

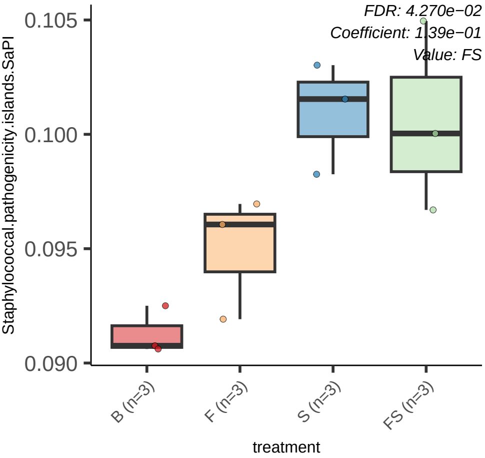

FDR: 4.260e−02
Coefficient: 3.99e−01
Value: FS
Choline.and.Betaine.Uptake.and.Betaine.Biosynthesis
0.21
0.19
0.17
0.15
0.13
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

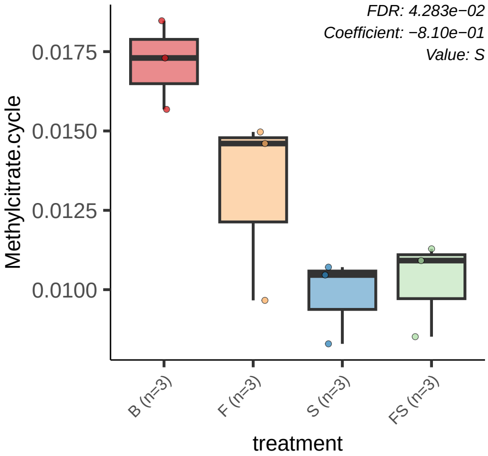

FDR: 4.260e−02
Coefficient: 9.94e−02
Value: S
Methionine.Biosynthesis
0.82
0.80
0.78
0.76
0.74
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

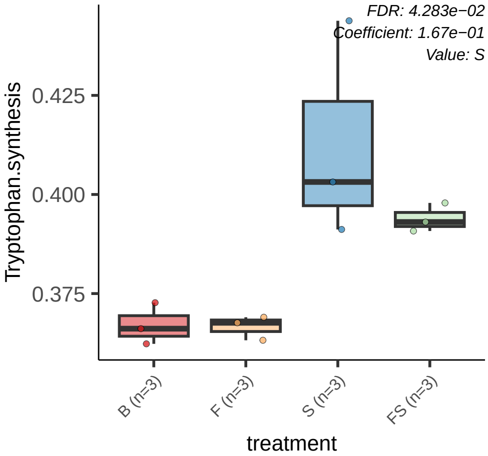

FDR: 4.260e−02
Coefficient: 7.08e−02
Value: S
Purine.conversions
0.98
0.96
0.94
0.92
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

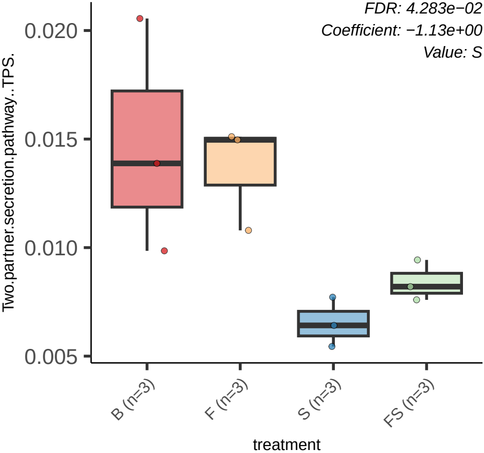

FDR: 4.260e−02
Coefficient: 4.61e−02
Value: S
Pyruvate.metabolism.I..anaplerotic.reactions..PEP
0.40
0.39
0.38
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

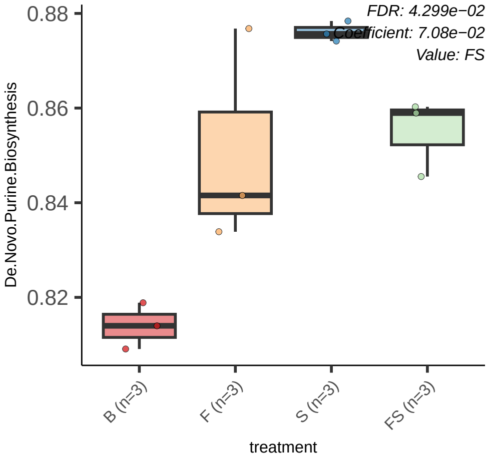

FDR: 4.260e−02
Coefficient: −2.07e−01
Value: FS
acinetobacter.tca
0.14
0.13
0.12
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

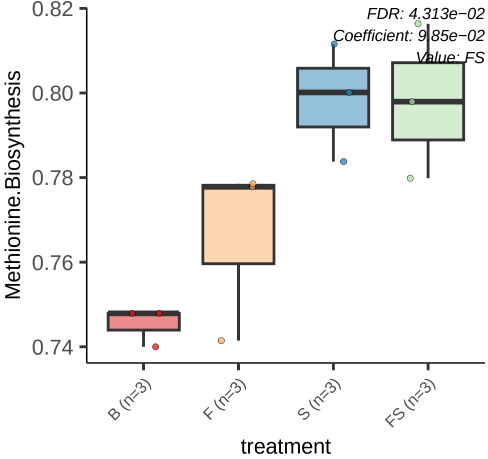

FDR: 4.270e−02
Coefficient: 1.39e−01
Value: FS
Staphylococcal.pathogenicity.islands.SaPI
0.105
0.100
0.095
0.090
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

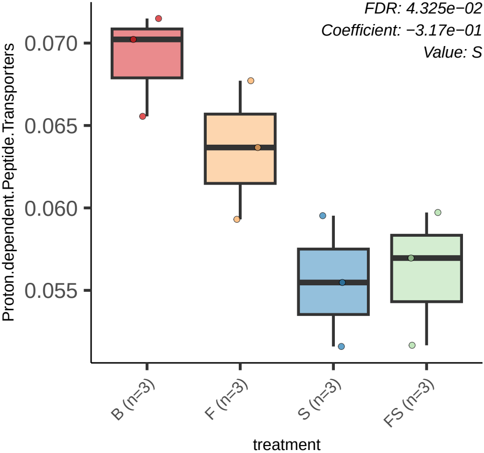

FDR: 4.283e−02
Coefficient: −8.10e−01
Value: S
Methylcitrate.cycle
0.0175
0.0150
0.0125
0.0100
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

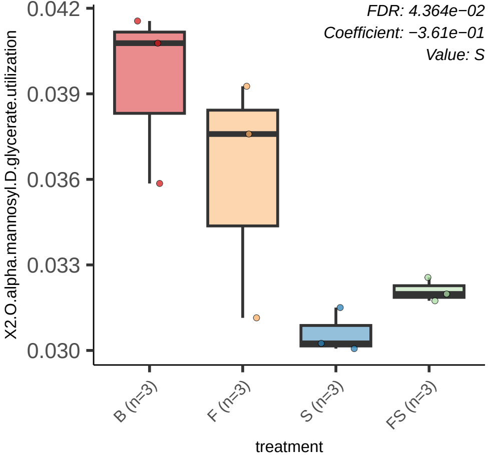

FDR: 4.283e−02
Coefficient: 1.67e−01
Value: S
Tryptophan.synthesis
0.425
0.400
0.375
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

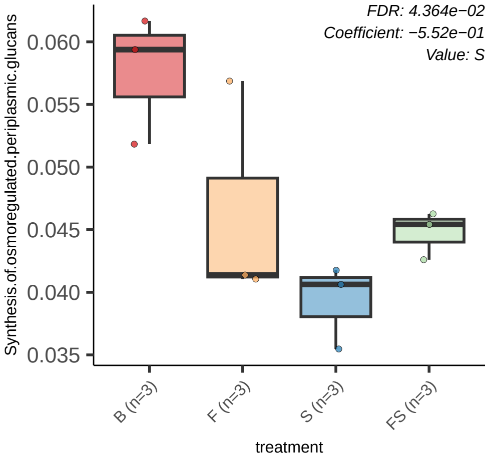

FDR: 4.283e−02
Coefficient: −1.13e+00
Value: S
Two.partner.secretion.pathway..TPS.
0.020
0.015
0.010
0.005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

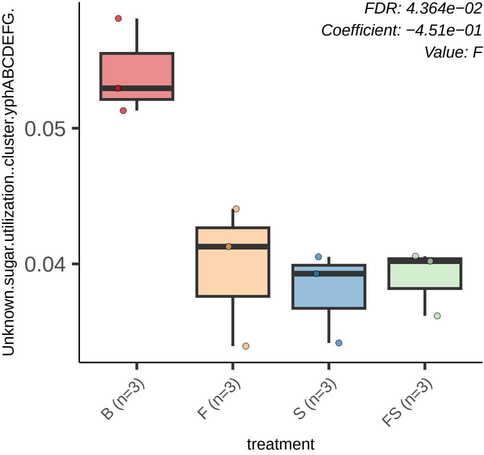

FDR: 4.299e−02
Coefficient: 7.08e−02
Value: FS
De.Novo.Purine.Biosynthesis
0.88
0.86
0.84
0.82
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

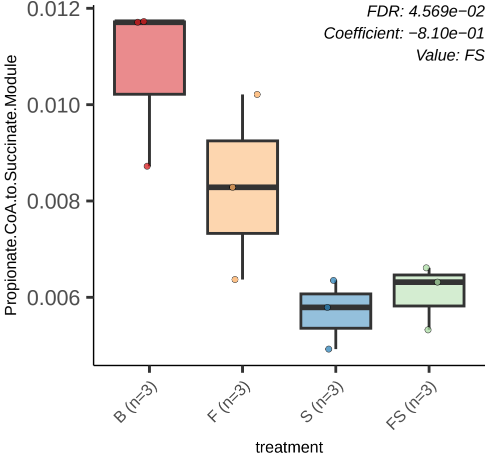

FDR: 4.313e−02
Coefficient: 9.85e−02
Value: FS
Methionine.Biosynthesis
0.82
0.80
0.78
0.76
0.74
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

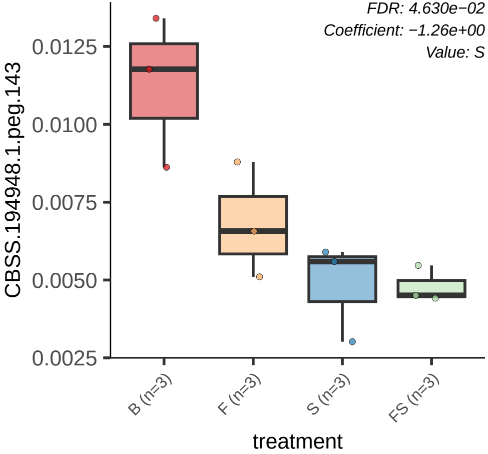

FDR: 4.325e−02
Coefficient: −3.17e−01
Value: S
Proton.dependent.Peptide.Transporters
0.070
0.065
0.060
0.055
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

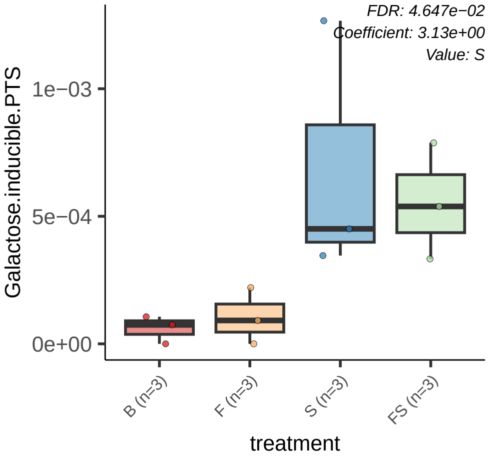

FDR: 4.364e−02
Coefficient: −3.61e−01
Value: S
X2.O.alpha.mannosyl.D.glycerate.utilization
0.042
0.039
0.036
0.033
0.030
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

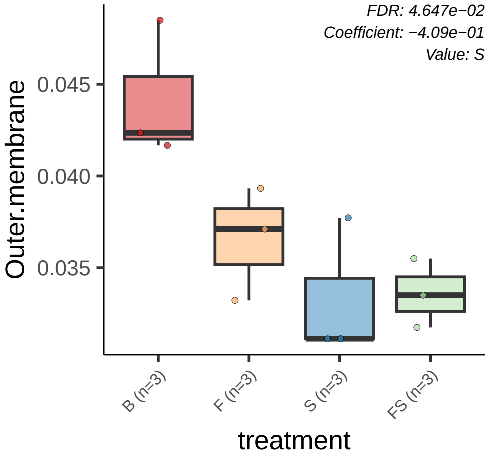

FDR: 4.364e−02
Coefficient: −5.52e−01
Value: S
Synthesis.of.osmoregulated.periplasmic.glucans
0.060
0.055
0.050
0.045
0.040
0.035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

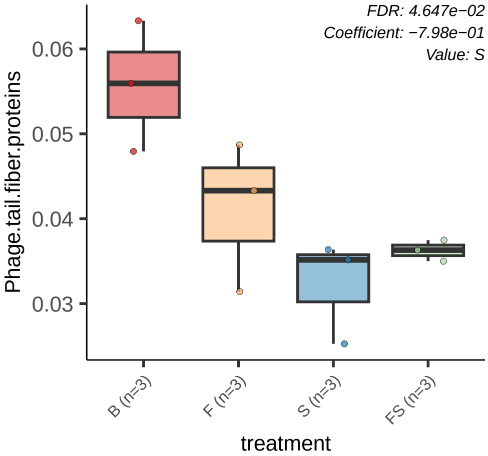

FDR: 4.364e−02
Coefficient: −4.51e−01
Value: F
Unknown.sugar.utilization..cluster.yphABCDEFG.
0.05
0.04
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

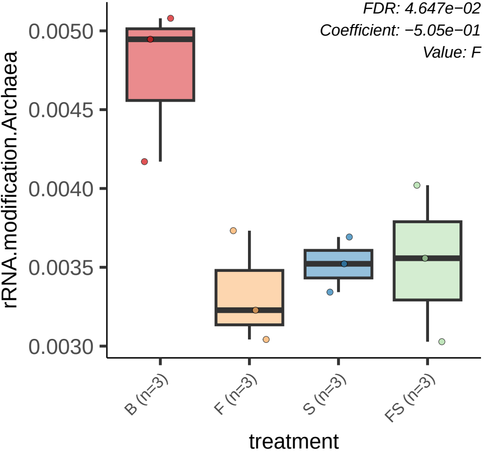

FDR: 4.569e−02
Coefficient: −8.10e−01
Value: FS
Propionate.CoA.to.Succinate.Module
0.012
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

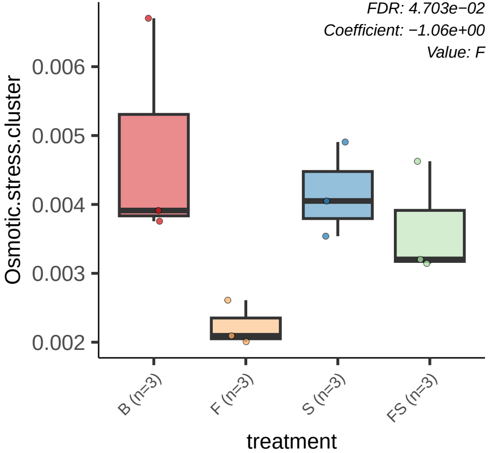

FDR: 4.630e−02
Coefficient: −1.26e+00
Value: S
CBSS.194948.1.peg.143
0.0125
0.0100
0.0075
0.0050
0.0025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

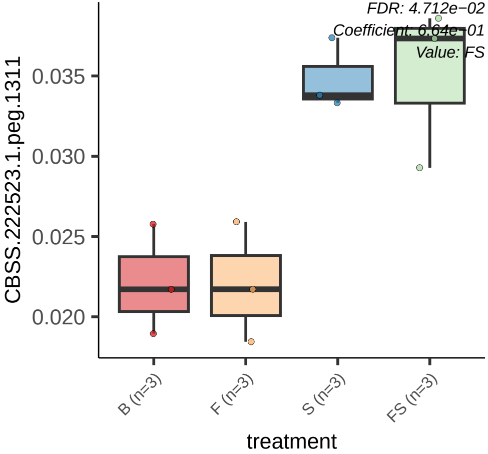

FDR: 4.647e−02
Coefficient: 3.13e+00
Value: S
Galactose.inducible.PTS
1e−03
5e−04
0e+00
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

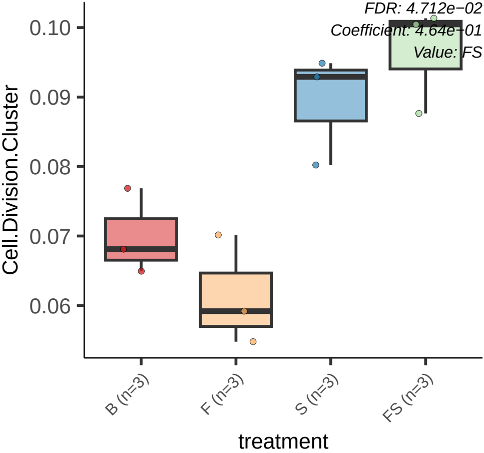

FDR: 4.647e−02
Coefficient: −4.09e−01
Value: S
Outer.membrane
0.045
0.040
0.035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

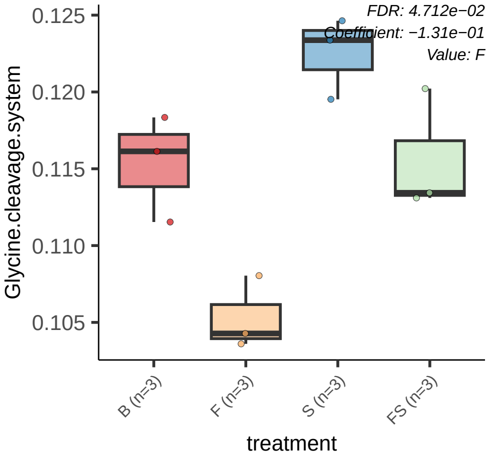

FDR: 4.647e−02
Coefficient: −7.98e−01
Value: S
Phage.tail.fiber.proteins
0.06
0.05
0.04
0.03
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

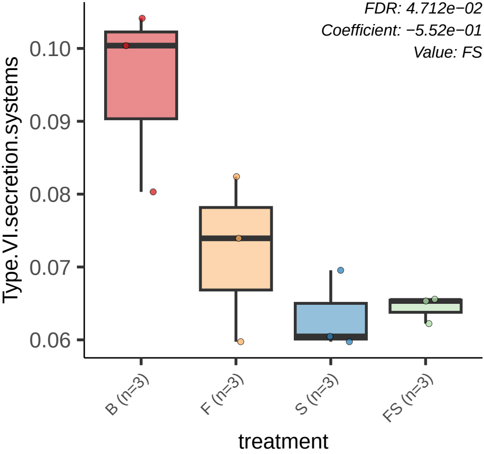

FDR: 4.647e−02
Coefficient: −5.05e−01
Value: F
rRNA.modification.Archaea
0.0050
0.0045
0.0040
0.0035
0.0030
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

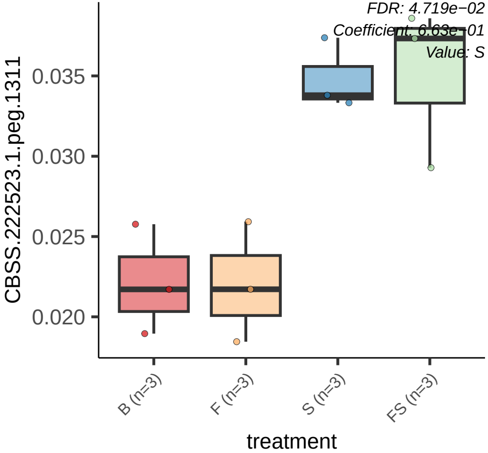

FDR: 4.703e−02
Coefficient: −1.06e+00
Value: F
Osmotic.stress.cluster
0.006
0.005
0.004
0.003
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

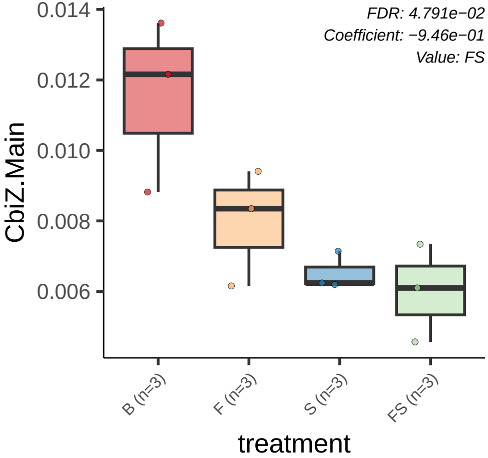

FDR: 4.712e−02
Coefficient: 6.64e−01
Value: FS
CBSS.222523.1.peg.1311
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 4.712e−02
Coefficient: 4.64e−01
Value: FS
0.10
0.09
0.08
0.07
0.06
Cell.Division.Cluster
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

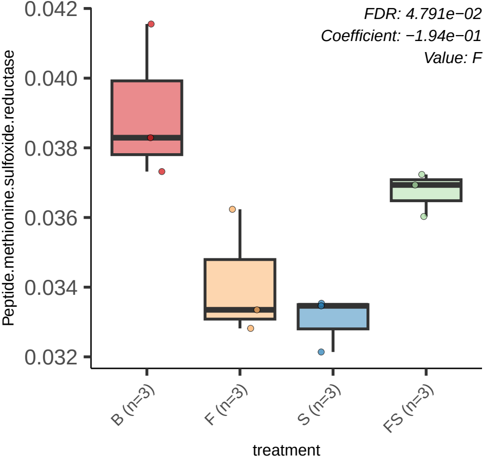

FDR: 4.712e−02
Coefficient: −1.31e−01
Value: F
Glycine.cleavage.system
0.125
0.120
0.115
0.110
0.105
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

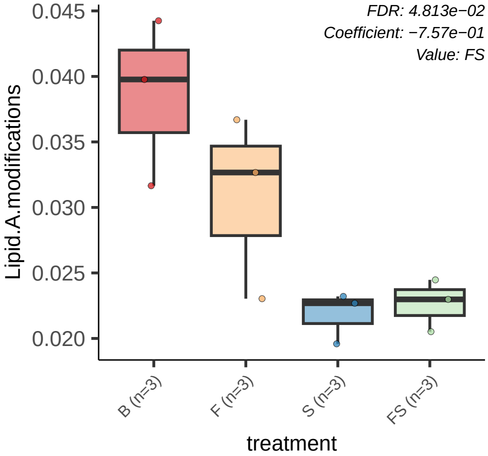

FDR: 4.712e−02
Coefficient: −5.52e−01
Value: FS
Type.VI.secretion.systems
0.10
0.09
0.08
0.07
0.06
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

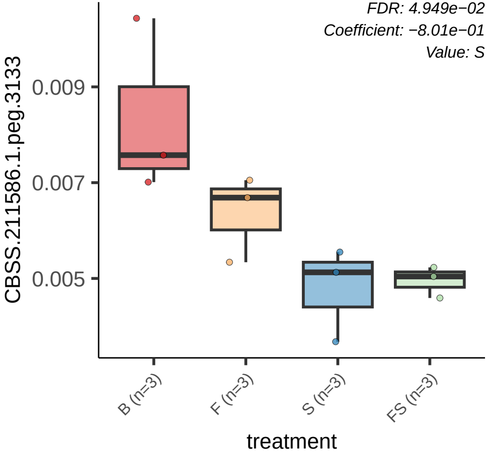

FDR: 4.719e−02
Coefficient: 6.63e−01
Value: S
CBSS.222523.1.peg.1311
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

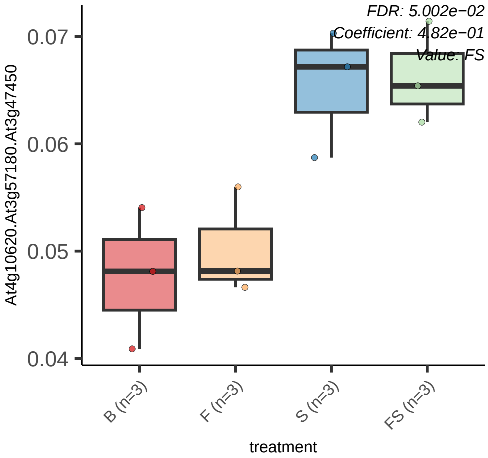


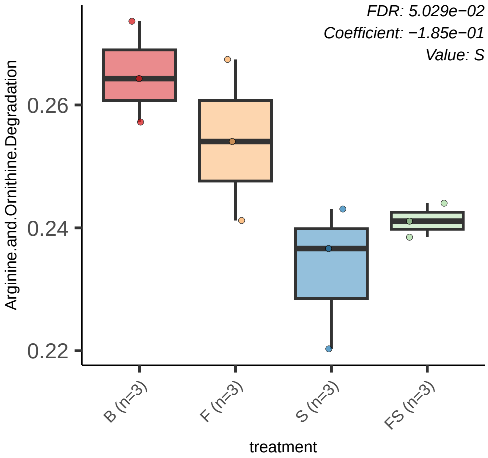
FDR: 4.791e−02
Coefficient: −9.46e−01
Value: FS
CbiZ.Main
0.014
0.012
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

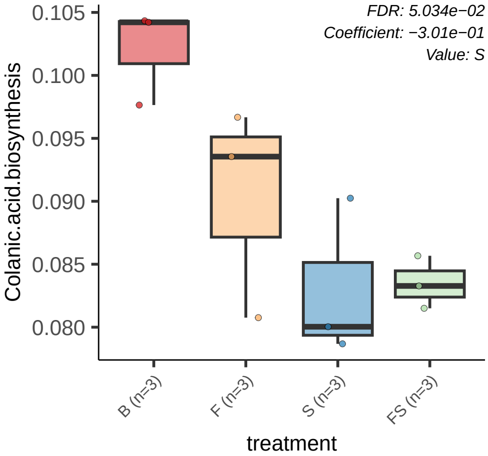

FDR: 4.791e−02
Coefficient: −1.94e−01
Value: F
Peptide.methionine.sulfoxide.reductase
0.042
0.040
0.038
0.036
0.034
0.032
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 4.813e−02
Coefficient: −7.57e−01
Value: FS
Lipid.A.modifications
0.045
0.040
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

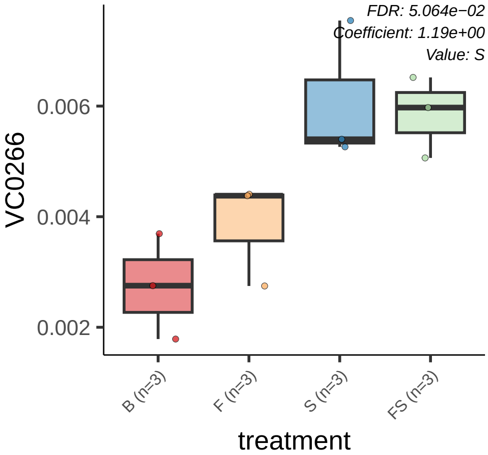

FDR: 4.949e−02
Coefficient: −8.01e−01
Value: S
CBSS.211586.1.peg.3133
0.009
0.007
0.005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

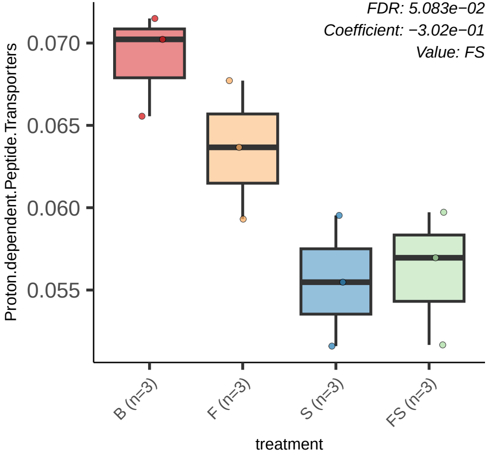

FDR: 5.002e−02
Coefficient: 4.82e−01
Value: FS
At4g10620.At3g57180.At3g47450
0.07
0.06
0.05
0.04
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

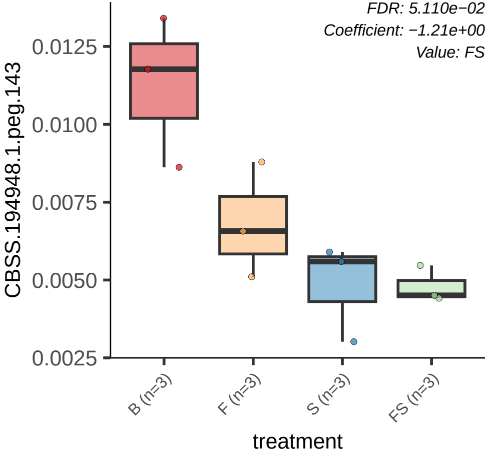

FDR: 5.029e−02
Coefficient: −1.85e−01
Value: S
Arginine.and.Ornithine.Degradation
0.26
0.24
0.22
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

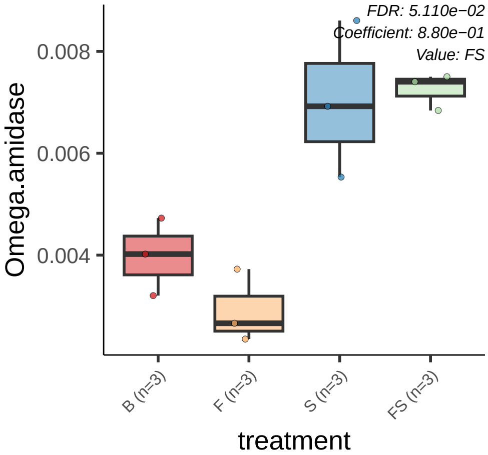


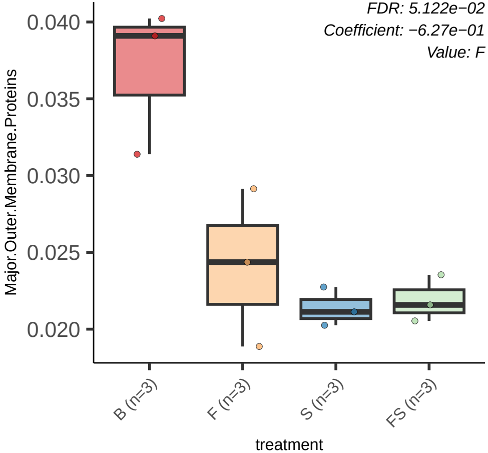
FDR: 5.034e−02
Coefficient: −3.01e−01
Value: S
Colanic.acid.biosynthesis
0.105
0.100
0.095
0.090
0.085
0.080
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

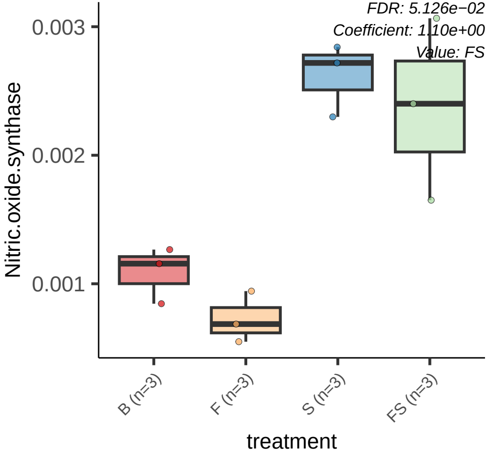

FDR: 5.064e−02
Coefficient: 1.19e+00
Value: S
VC0266
0.006
0.004
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

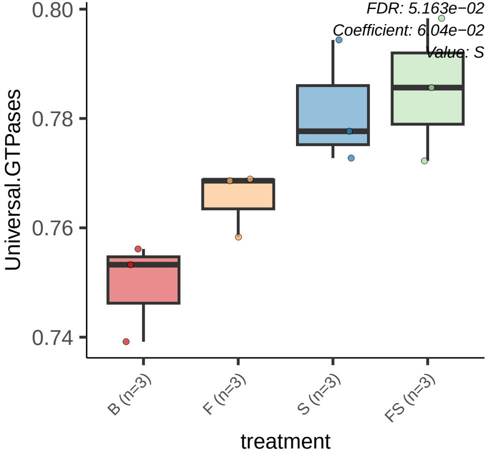

FDR: 5.083e−02
Coefficient: −3.02e−01
Value: FS
Proton.dependent.Peptide.Transporters
0.070
0.065
0.060
0.055
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

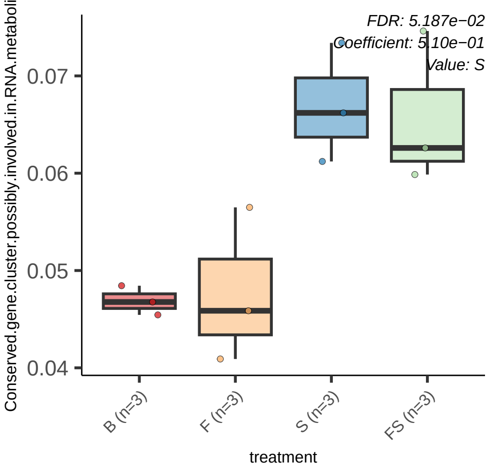

FDR: 5.110e−02
Coefficient: −1.21e+00
Value: FS
CBSS.194948.1.peg.143
0.0125
0.0100
0.0075
0.0050
0.0025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

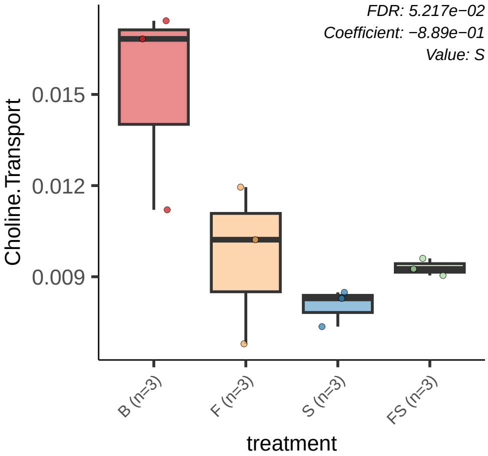

FDR: 5.110e−02
Coefficient: 8.80e−01
Value: FS
Omega.amidase
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 5.122e−02
Coefficient: −6.27e−01
Value: F
Major.Outer.Membrane.Proteins
0.040
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

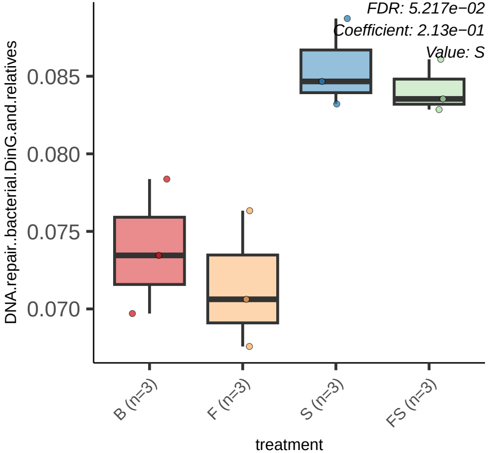

FDR: 5.126e−02
Coefficient: 1.10e+00
Value: FS
Nitric.oxide.synthase
0.003
0.002
0.001
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

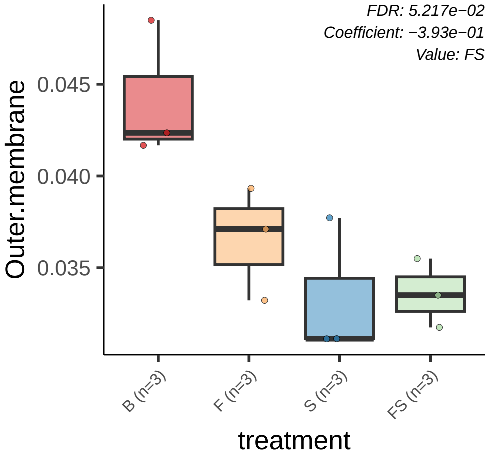

FDR: 5.163e−02
Coefficient: 6.04e−02
Value: S
Universal.GTPases
0.80
0.78
0.76
0.74
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

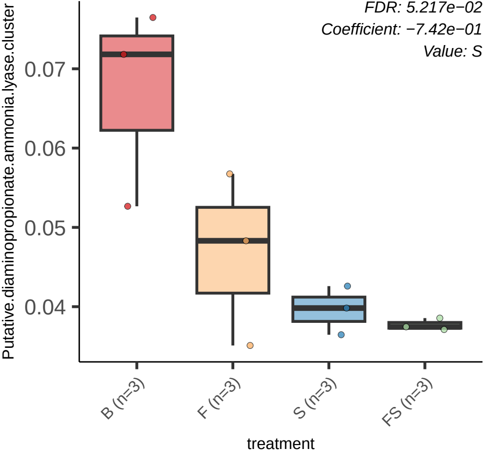

FDR: 5.187e−02
Coefficient: 5.10e−01
Value: S
Conserved.gene.cluster.possibly.involved.in.RNA.metaboli
0.07
0.06
0.05
0.04
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

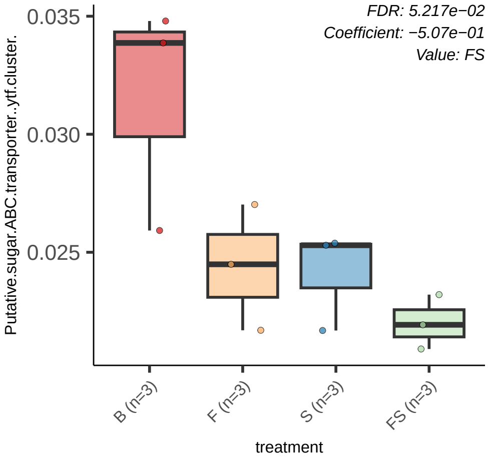


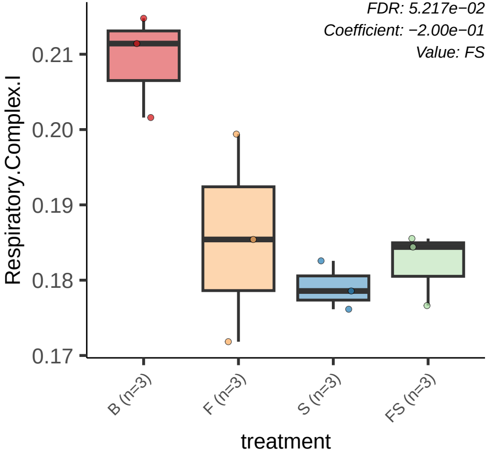
FDR: 5.217e−02
Coefficient: −8.89e−01
Value: S
Choline.Transport
0.015
0.012
0.009
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

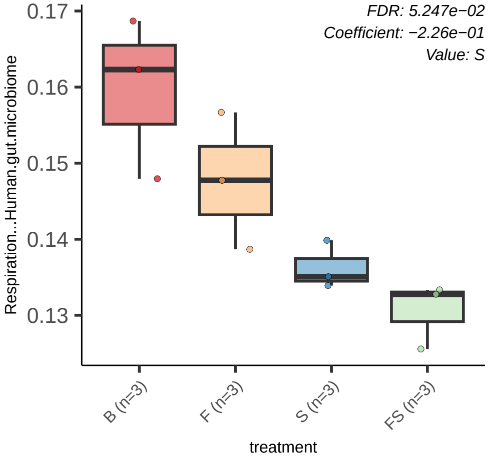

FDR: 5.217e−02
Coefficient: 2.13e−01
Value: S
DNA.repair..bacterial.DinG.and.relatives
0.085
0.080
0.075
0.070
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

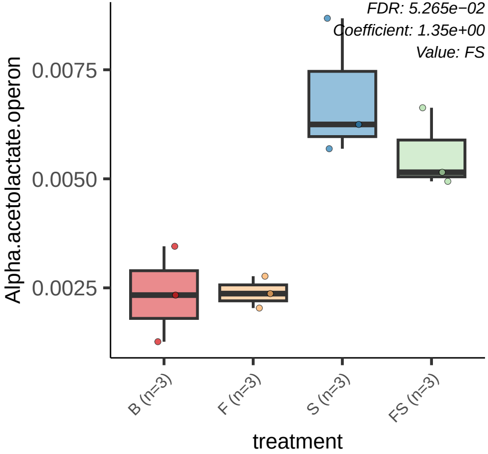

FDR: 5.217e−02
Coefficient: −3.93e−01
Value: FS
Outer.membrane
0.045
0.040
0.035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

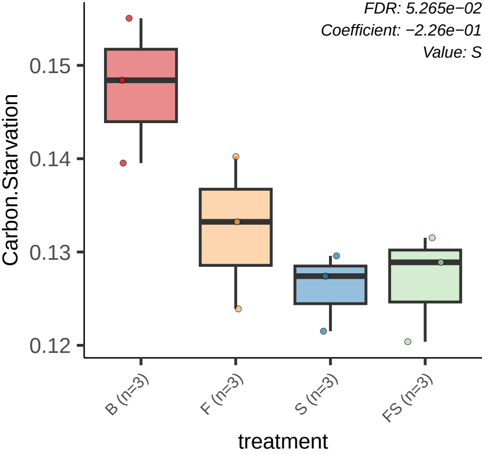

FDR: 5.217e−02
Coefficient: −7.42e−01
Value: S
Putative.diaminopropionate.ammonia.lyase.cluster
0.07
0.06
0.05
0.04
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

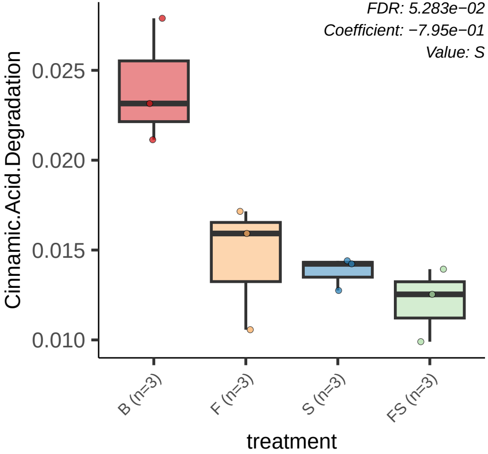

FDR: 5.217e−02
Coefficient: −5.07e−01
Value: FS
Putative.sugar.ABC.transporter..ytf.cluster.
0.035
0.030
0.025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

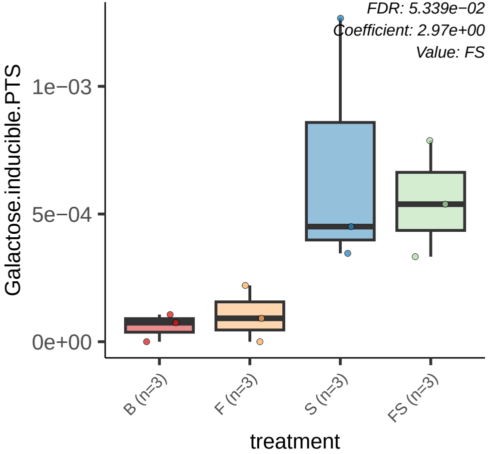

FDR: 5.217e−02
Coefficient: −2.00e−01
Value: FS
Respiratory.Complex.I
0.21
0.20
0.19
0.18
0.17
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

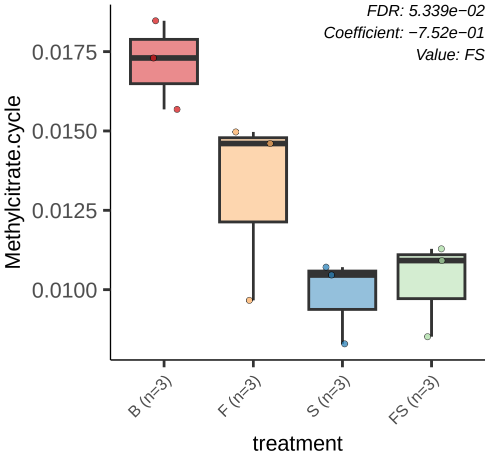

FDR: 5.247e−02
Coefficient: −2.26e−01
Value: S
Respiration...Human.gut.microbiome
0.17
0.16
0.15
0.14
0.13
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

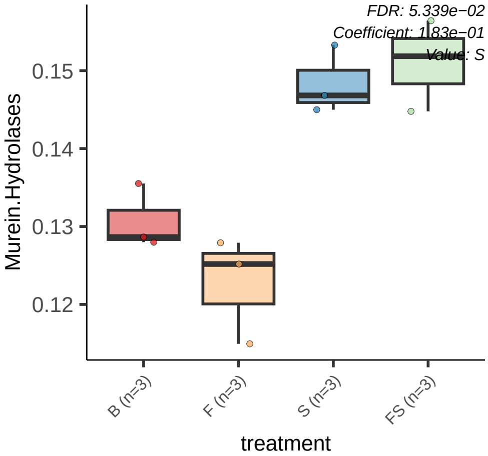

FDR: 5.265e−02
Coefficient: 1.35e+00
Value: FS
Alpha.acetolactate.operon
0.0075
0.0050
0.0025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

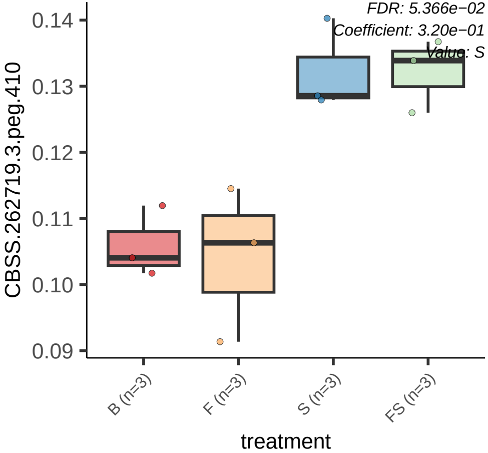

FDR: 5.265e−02
Coefficient: −2.26e−01
Value: S
Carbon.Starvation
0.15
0.14
0.13
0.12
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

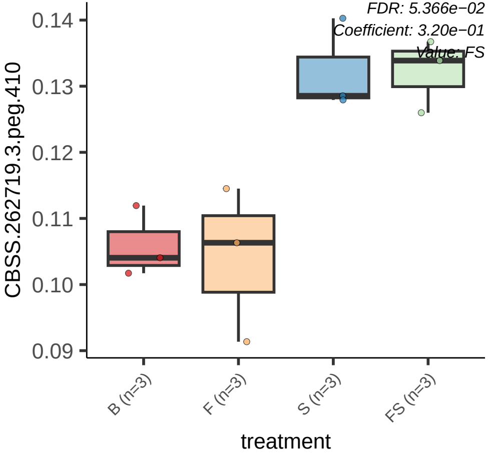

FDR: 5.283e−02
Coefficient: −7.95e−01
Value: S
Cinnamic.Acid.Degradation
0.025
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

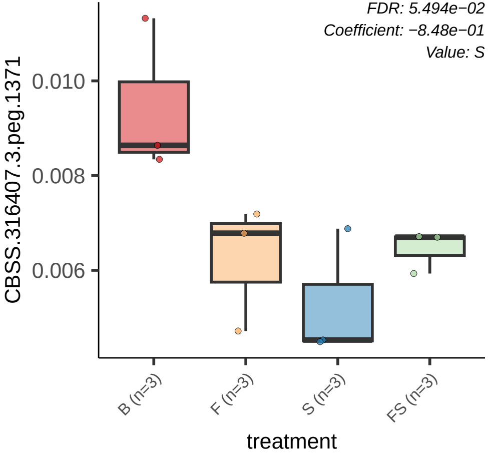

FDR: 5.339e−02
Coefficient: 2.97e+00
Value: FS
Galactose.inducible.PTS
1e−03
5e−04
0e+00
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 5.339e−02
Coefficient: −7.52e−01
Value: FS
Methylcitrate.cycle
0.0175
0.0150
0.0125
0.0100
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

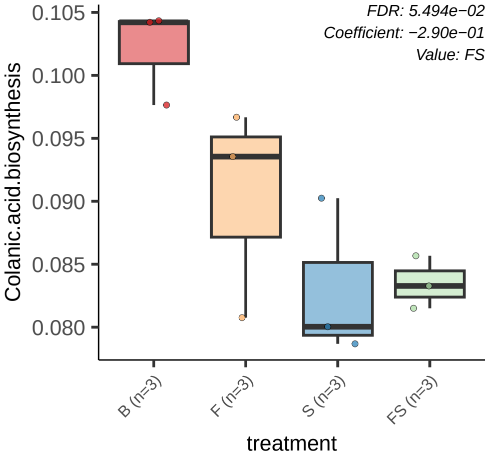

FDR: 5.339e−02
Coefficient: 1.83e−01
Value: S
Murein.Hydrolases
0.15
0.14
0.13
0.12
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

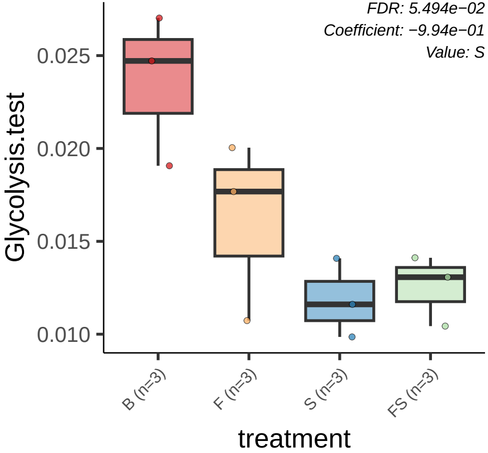

FDR: 5.366e−02
Coefficient: 3.20e−01
Value: S
CBSS.262719.3.peg.410
0.14
0.13
0.12
0.11
0.10
0.09
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

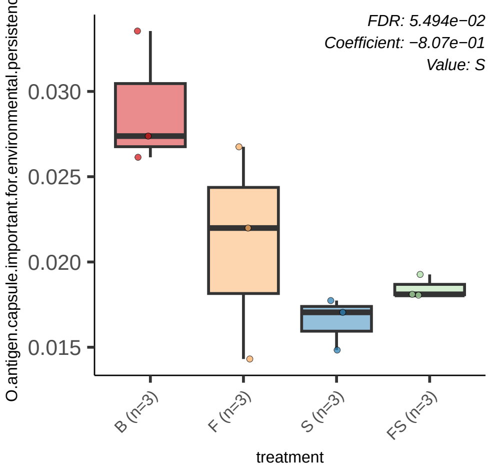

FDR: 5.366e−02
Coefficient: 3.20e−01
Value: FS
CBSS.262719.3.peg.410
0.14
0.13
0.12
0.11
0.10
0.09
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

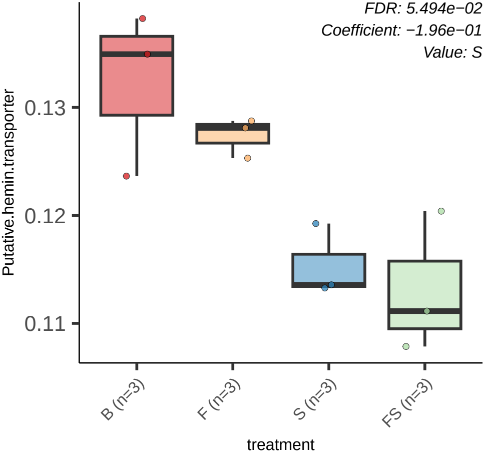


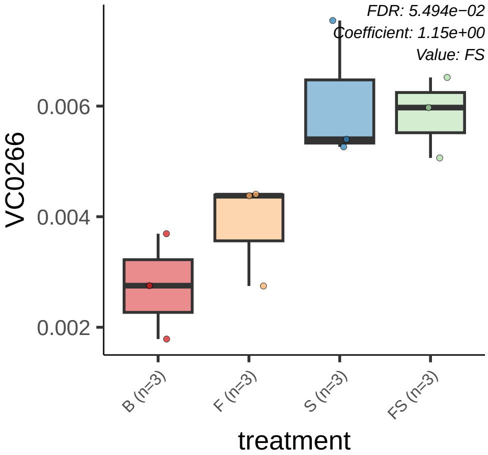
FDR: 5.494e−02
Coefficient: −8.48e−01
Value: S
CBSS.316407.3.peg.1371
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

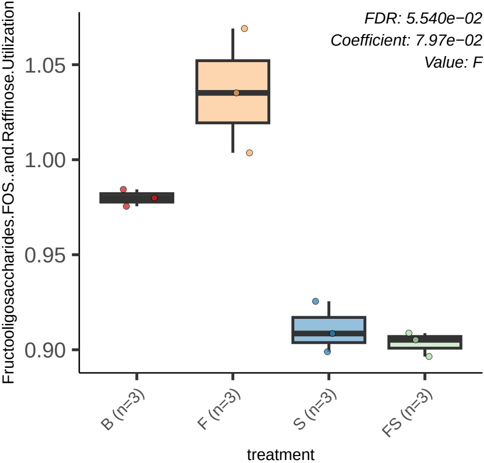

FDR: 5.494e−02
Coefficient: −2.90e−01
Value: FS
Colanic.acid.biosynthesis
0.105
0.100
0.095
0.090
0.085
0.080
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 5.494e−02
Coefficient: −9.94e−01
Value: S
Glycolysis.test
0.025
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

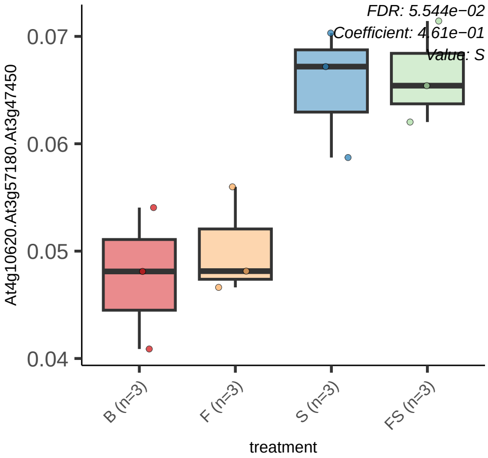

FDR: 5.494e−02
Coefficient: −8.07e−01
Value: S
O.antigen.capsule.important.for.environmental.persistenc
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

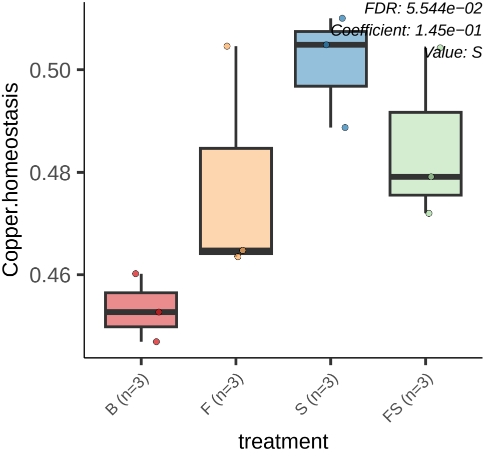

FDR: 5.494e−02
Coefficient: −1.96e−01
Value: S
Putative.hemin.transporter
0.13
0.12
0.11
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

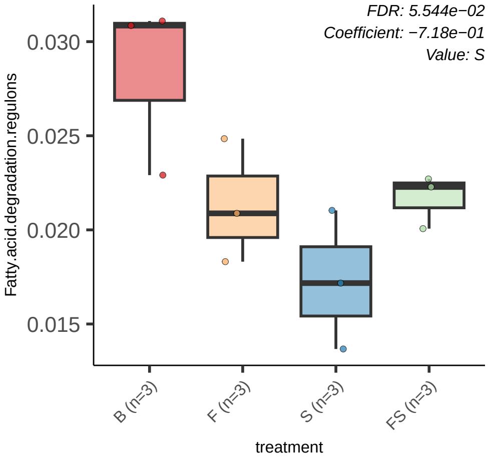

FDR: 5.494e−02
Coefficient: 1.15e+00
Value: FS
VC0266
0.006
0.004
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

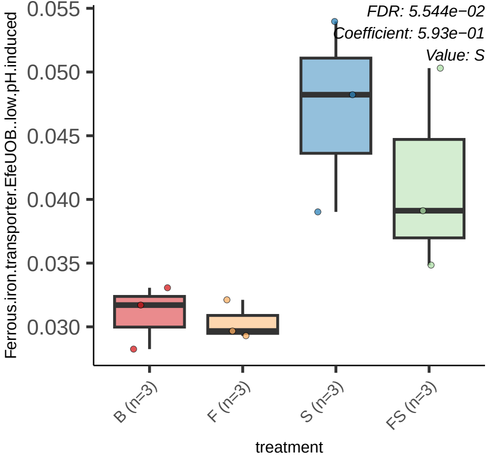


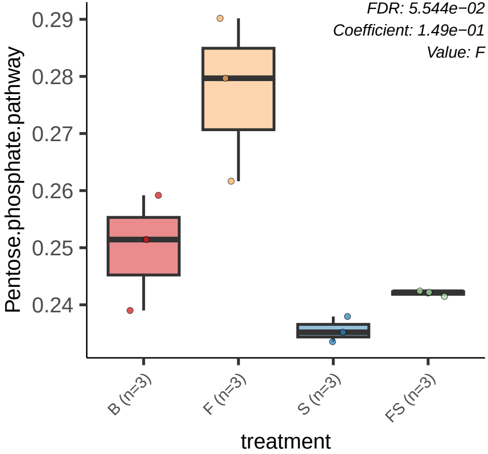
FDR: 5.540e−02
Coefficient: 7.97e−02
Value: F
Fructooligosaccharides.FOS..and.Raffinose.Utilization
1.05
1.00
0.95
0.90
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

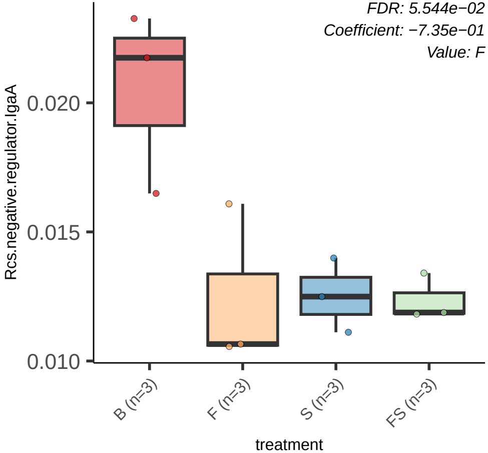

FDR: 5.544e−02
Coefficient: 4.61e−01
Value: S
0.07
0.06
0.05
0.04
At4g10620.At3g57180.At3g47450
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

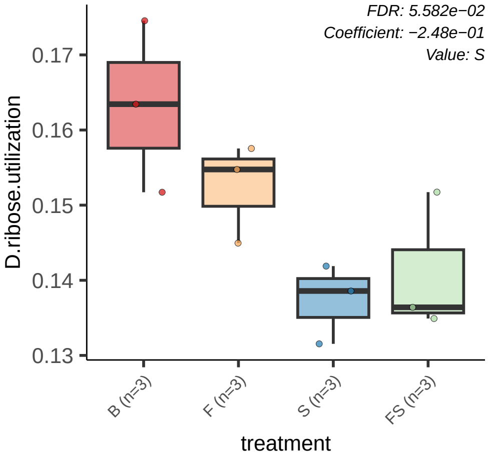

FDR: 5.544e−02
Coefficient: 1.45e−01
Value: S
Copper.homeostasis
0.50
0.48
0.46
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

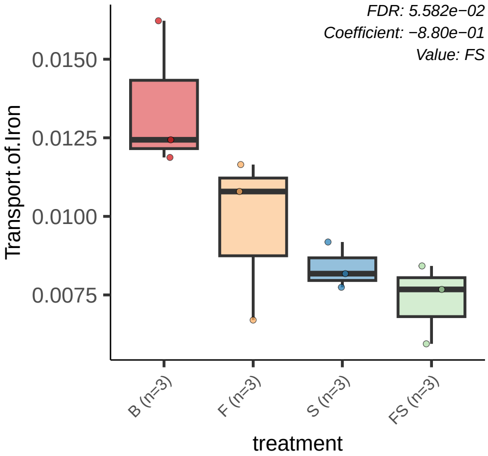

FDR: 5.544e−02
Coefficient: −7.18e−01
Value: S
Fatty.acid.degradation.regulons
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

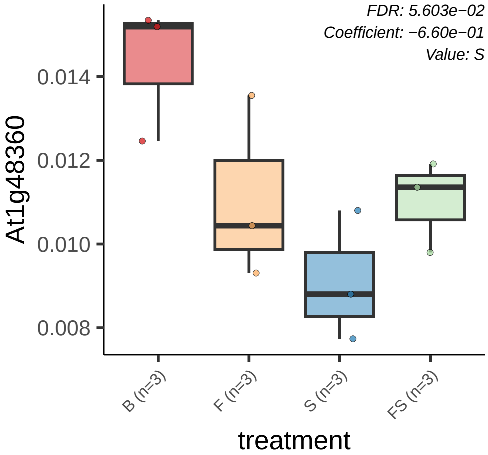

FDR: 5.544e−02
Coefficient: 5.93e−01
Value: S
Ferrous.iron.transporter.EfeUOB..low.pH.induced
0.055
0.050
0.045
0.040
0.035
0.030
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

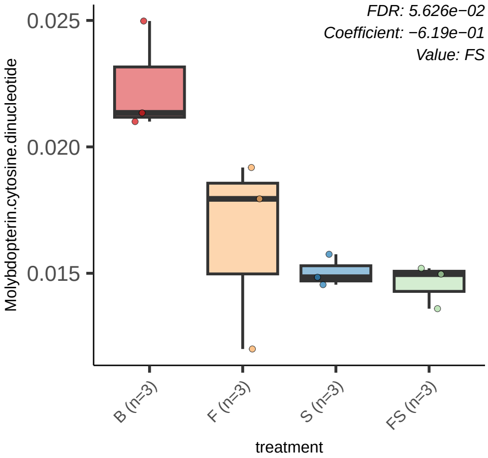

FDR: 5.544e−02
Coefficient: 1.49e−01
Value: F
Pentose.phosphate.pathway
0.29
0.28
0.27
0.26
0.25
0.24
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

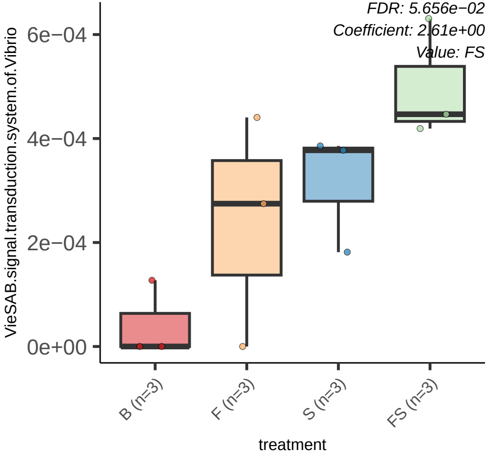

FDR: 5.544e−02
Coefficient: −7.35e−01
Value: F
Rcs.negative.regulator.IgaA
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

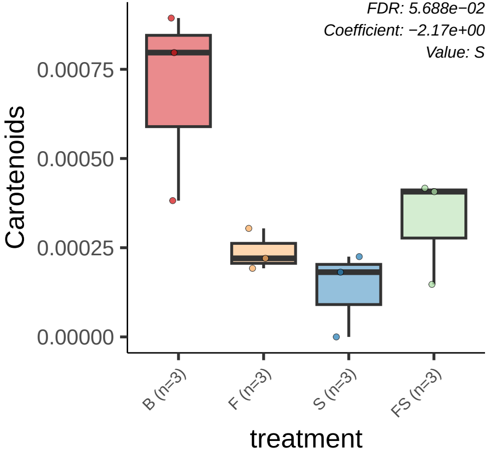

FDR: 5.582e−02
Coefficient: −2.48e−01
Value: S
D.ribose.utilization
0.17
0.16
0.15
0.14
0.13
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

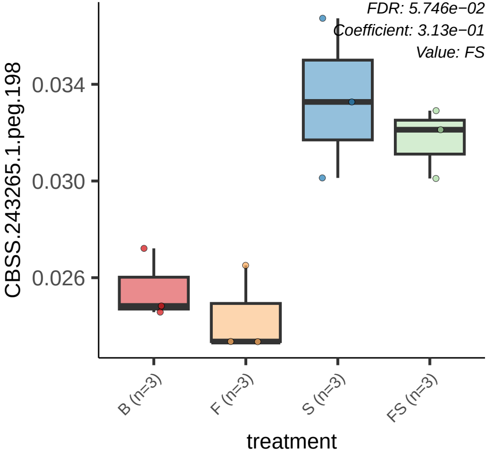

FDR: 5.582e−02
Coefficient: −8.80e−01
Value: FS
Transport.of.Iron
0.0150
0.0125
0.0100
0.0075
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

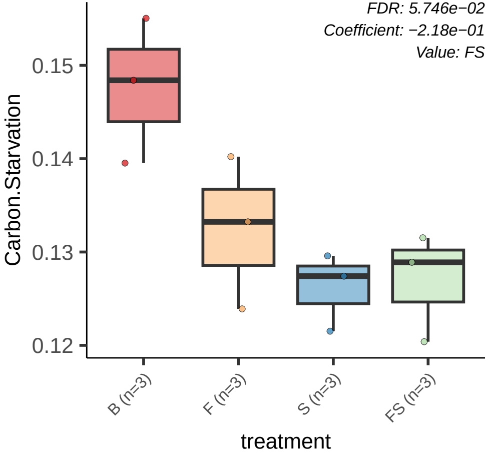

FDR: 5.603e−02
Coefficient: −6.60e−01
Value: S
At1g48360
0.014
0.012
0.010
0.008
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

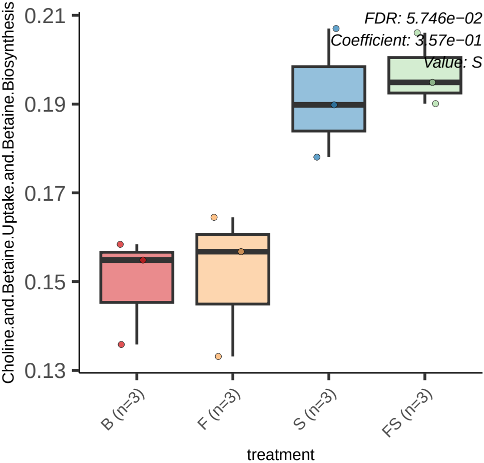

FDR: 5.626e−02
Coefficient: −6.19e−01
Value: FS
Molybdopterin.cytosine.dinucleotide
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

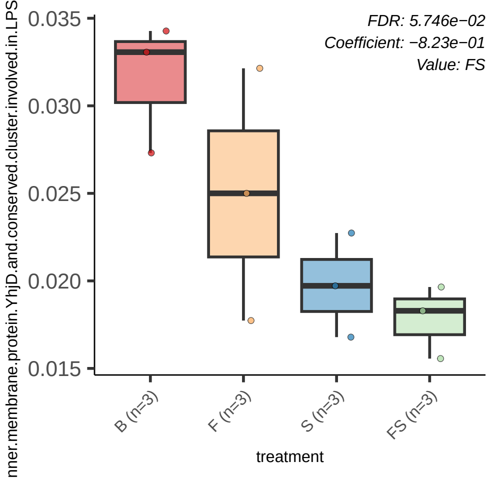

FDR: 5.656e−02
Coefficient: 2.61e+00
Value: FS
VieSAB.signal.transduction.system.of.Vibrio
6e−04
4e−04
2e−04
0e+00
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

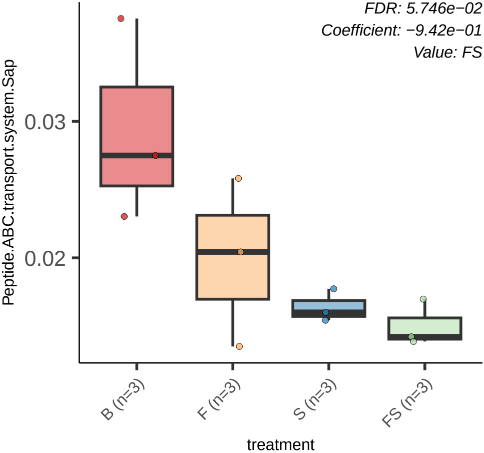

FDR: 5.688e−02
Coefficient: −2.17e+00
Value: S
Carotenoids
0.00075
0.00050
0.00025
0.00000
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

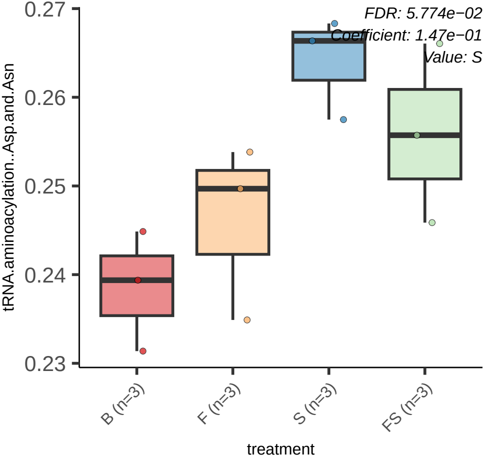

FDR: 5.746e−02
Coefficient: 3.13e−01
Value: FS
CBSS.243265.1.peg.198
0.034
0.030
0.026
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

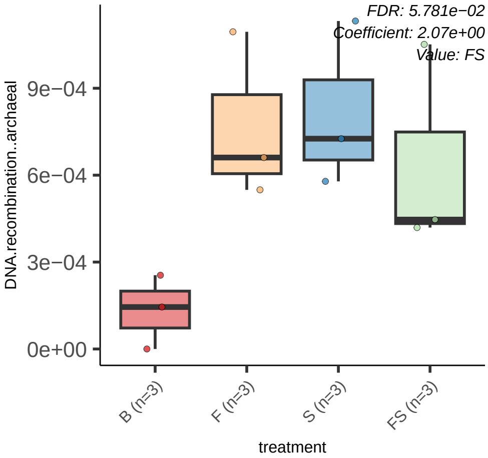

FDR: 5.746e−02
Coefficient: −2.18e−01
Value: FS
Carbon.Starvation
0.15
0.14
0.13
0.12
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

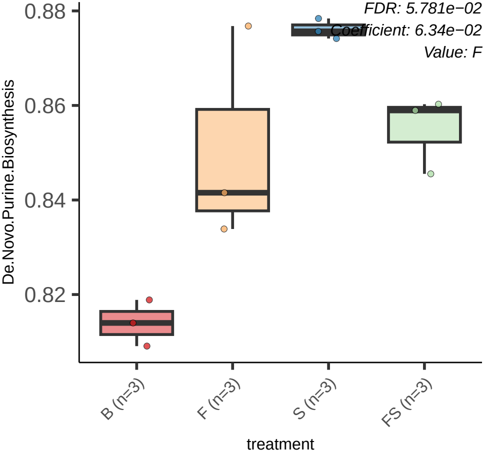

FDR: 5.746e−02
Coefficient: 3.57e−01
Value: S
Choline.and.Betaine.Uptake.and.Betaine.Biosynthesis
0.21
0.19
0.17
0.15
0.13
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

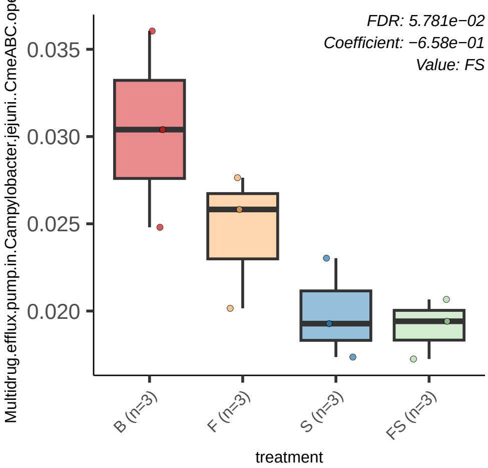

FDR: 5.746e−02
Coefficient: −8.23e−01
Value: FS
Inner.membrane.protein.YhjD.and.conserved.cluster.involved.in.LPS
0.035
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

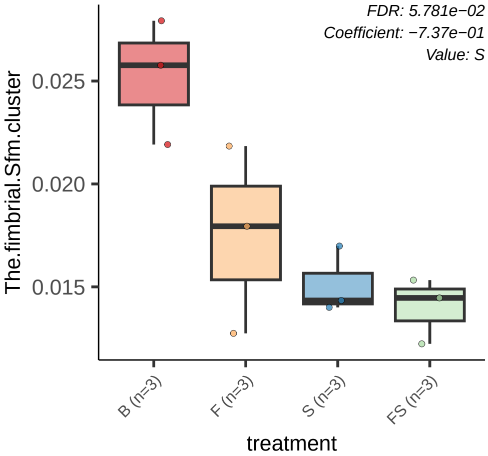

FDR: 5.746e−02
Coefficient: −9.42e−01
Value: FS
Peptide.ABC.transport.system.Sap
0.03
0.02
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

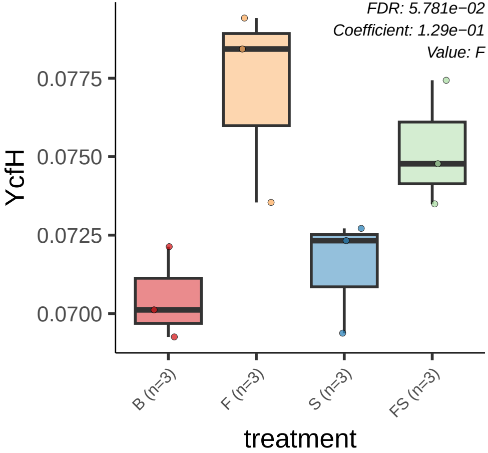

FDR: 5.774e−02
Coefficient: 1.47e−01
Value: S
0.27
0.26
0.25
0.24
0.23
tRNA.aminoacylation..Asp.and.Asn
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

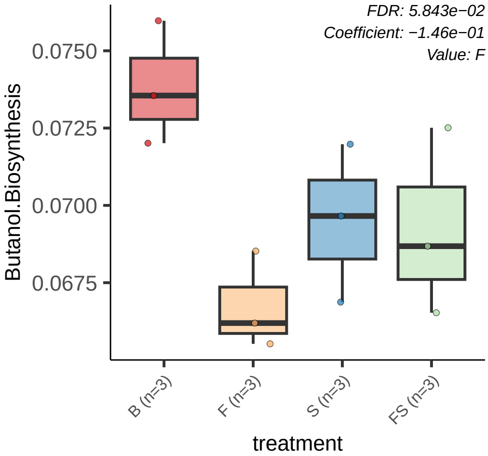

FDR: 5.781e−02
Coefficient: 2.07e+00
Value: FS
DNA.recombination..archaeal
9e−04
6e−04
3e−04
0e+00
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

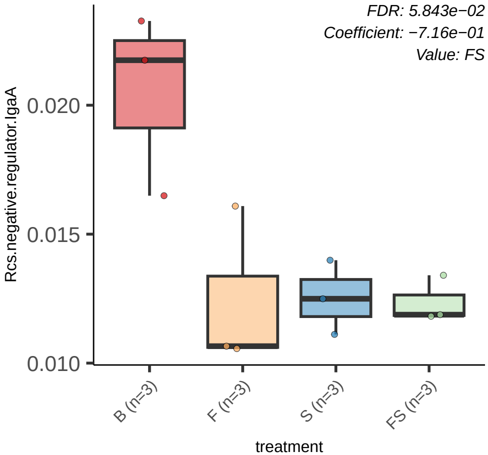

FDR: 5.781e−02
Coefficient: 6.34e−02
Value: F
De.Novo.Purine.Biosynthesis
0.88
0.86
0.84
0.82
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

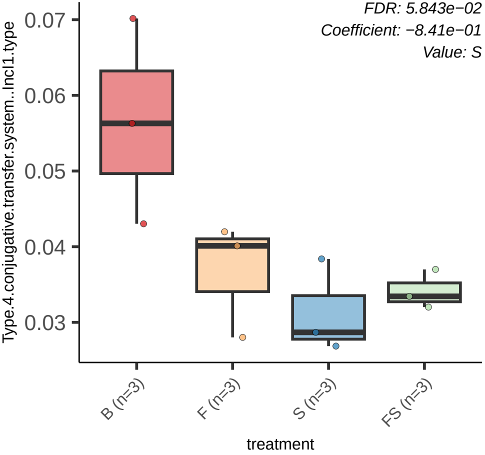

FDR: 5.781e−02
Coefficient: −6.58e−01
Value: FS
Multidrug.efflux.pump.in.Campylobacter.jejuni..CmeABC.ope
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

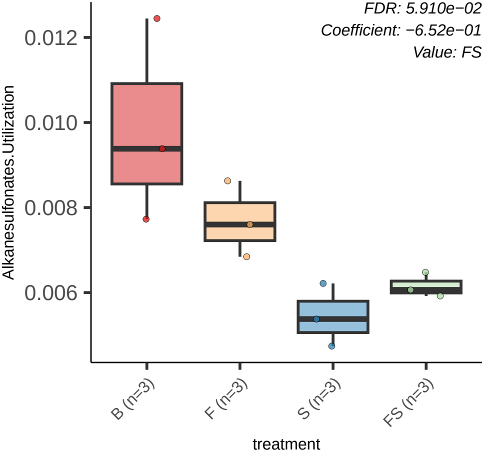

FDR: 5.781e−02
Coefficient: −7.37e−01
Value: S
The.fimbrial.Sfm.cluster
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

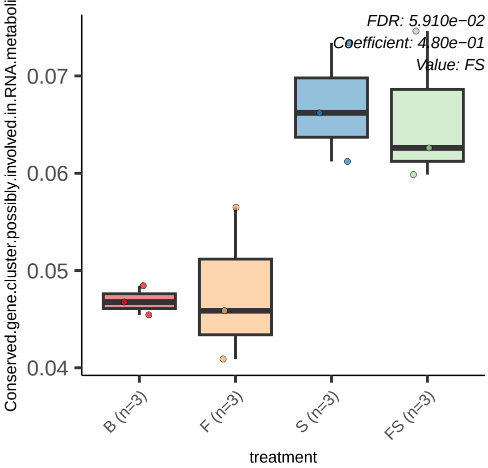

FDR: 5.781e−02
Coefficient: 1.29e−01
Value: F
YcfH
0.0775
0.0750
0.0725
0.0700
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

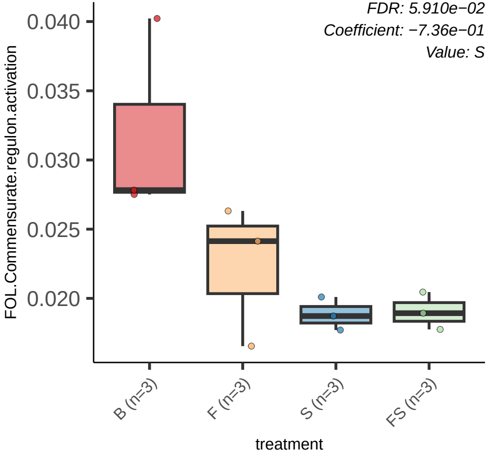

FDR: 5.843e−02
Coefficient: −1.46e−01
Value: F
Butanol.Biosynthesis
0.0750
0.0725
0.0700
0.0675
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

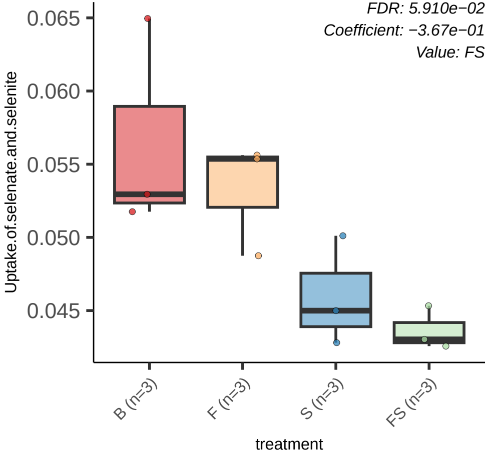

FDR: 5.843e−02
Coefficient: −7.16e−01
Value: FS
Rcs.negative.regulator.IgaA
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

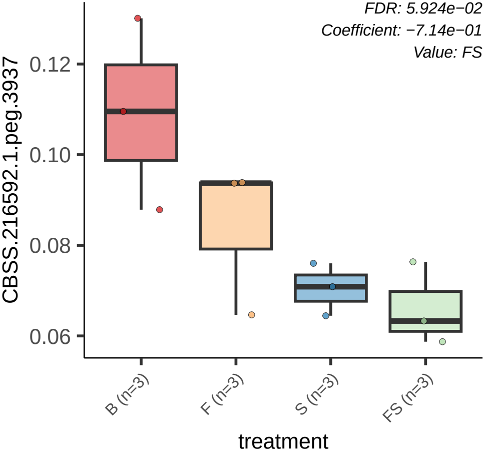

FDR: 5.843e−02
Coefficient: −8.41e−01
Value: S
Type.4.conjugative.transfer.system..IncI1.type
0.07
0.06
0.05
0.04
0.03
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

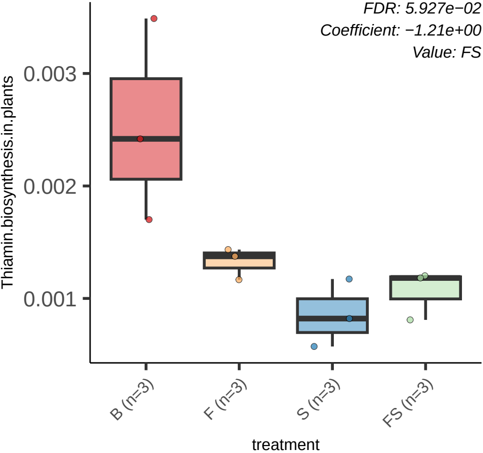

FDR: 5.910e−02
Coefficient: −6.52e−01
Value: FS
Alkanesulfonates.Utilization
0.012
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

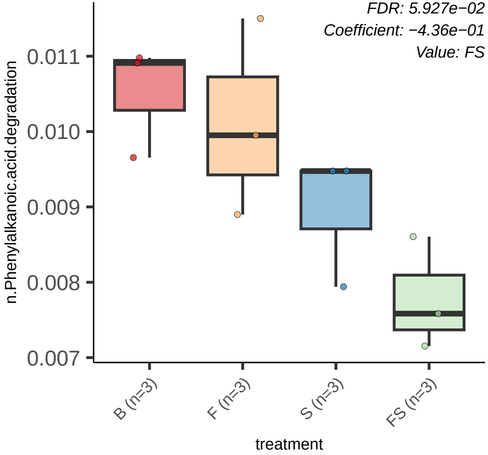

FDR: 5.910e−02
Coefficient: 4.80e−01
Value: FS
Conserved.gene.cluster.possibly.involved.in.RNA.metaboli
0.07
0.06
0.05
0.04
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

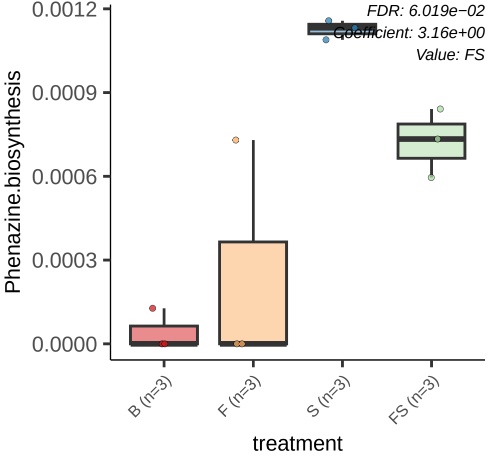

FDR: 5.910e−02
Coefficient: −7.36e−01
Value: S
FOL.Commensurate.regulon.activation
0.040
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

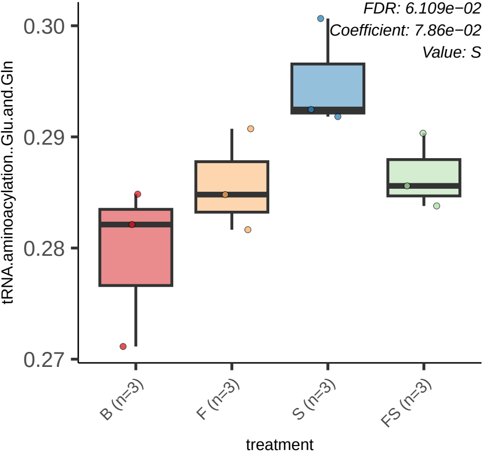

FDR: 5.910e−02
Coefficient: −3.67e−01
Value: FS
Uptake.of.selenate.and.selenite
0.065
0.060
0.055
0.050
0.045
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 5.924e−02
Coefficient: −7.14e−01
Value: FS
CBSS.216592.1.peg.3937
0.12
0.10
0.08
0.06
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

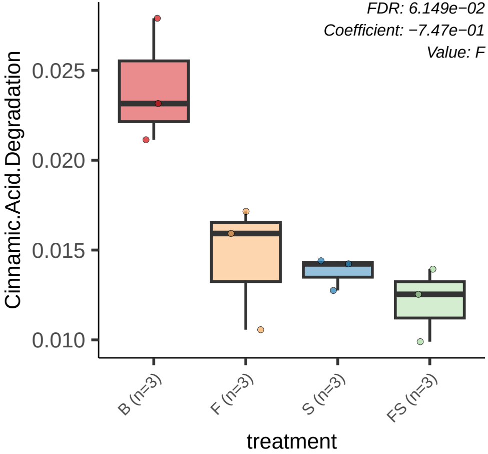

FDR: 5.927e−02
Coefficient: −1.21e+00
Value: FS
Thiamin.biosynthesis.in.plants
0.003
0.002
0.001
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 5.927e−02
Coefficient: −4.36e−01
Value: FS
n.Phenylalkanoic.acid.degradation
0.011
0.010
0.009
0.008
0.007
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

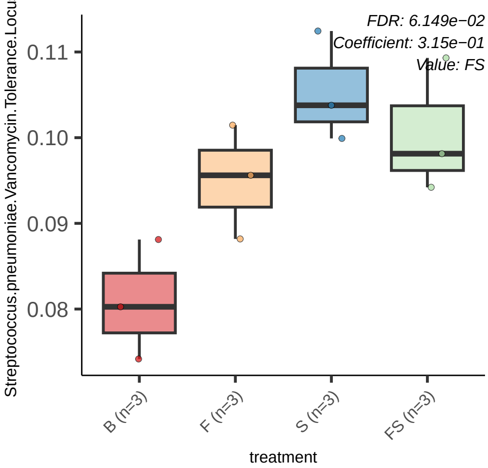

FDR: 6.019e−02
Coefficient: 3.16e+00
Value: FS
Phenazine.biosynthesis
0.0012
0.0009
0.0006
0.0003
0.0000
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

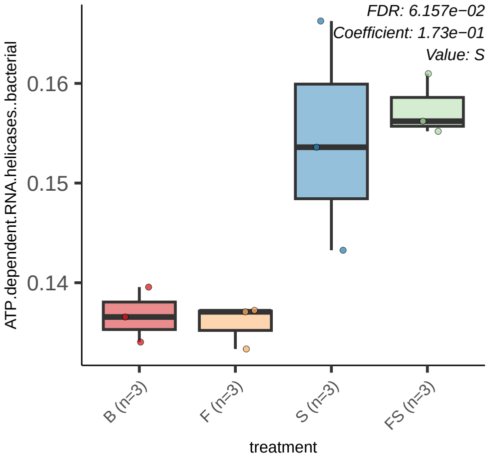


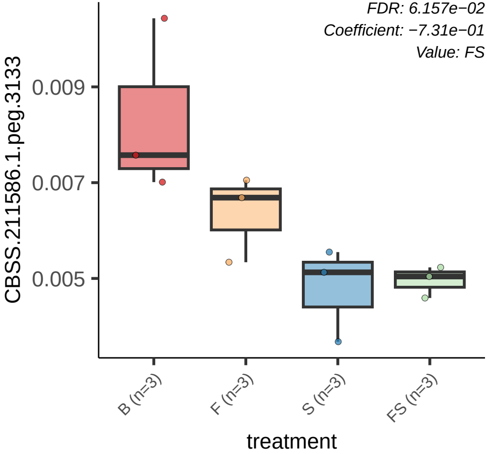
FDR: 6.109e−02
Coefficient: 7.86e−02
Value: S
tRNA.aminoacylation..Glu.and.Gln
0.30
0.29
0.28
0.27
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

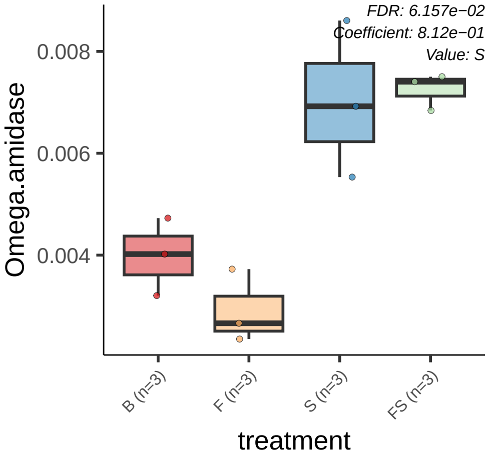


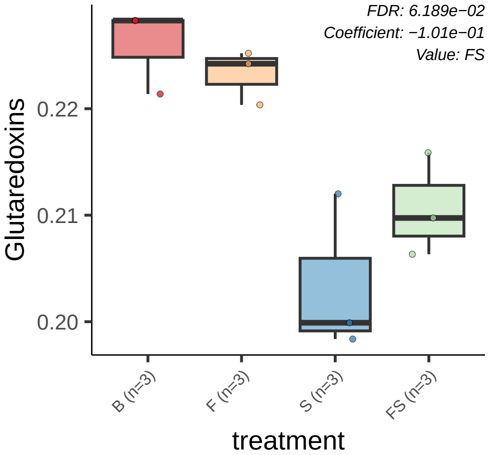
FDR: 6.149e−02
Coefficient: −7.47e−01
Value: F
Cinnamic.Acid.Degradation
0.025
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

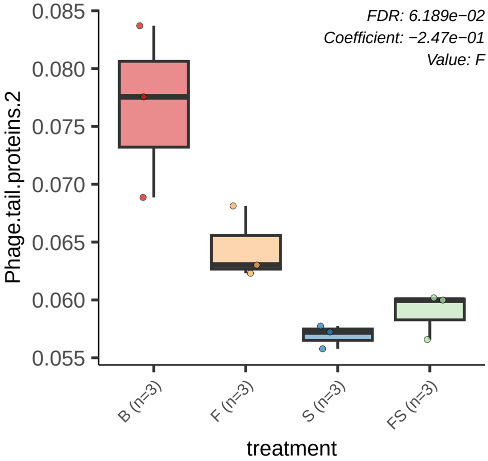

Streptococcus.pneumoniae.Vancomycin.Tolerance.Locu
FDR: 6.149e−02
Coefficient: 3.15e−01
Value: FS
0.11
0.10
0.09
0.08
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

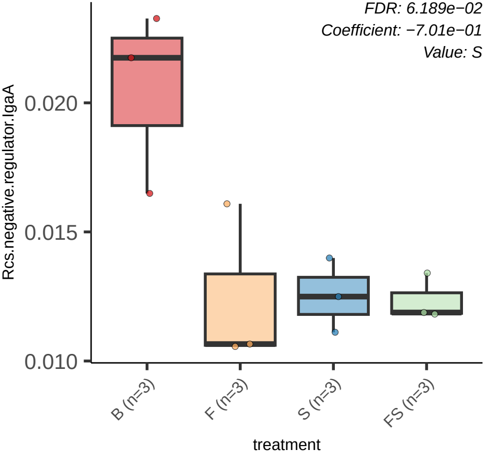

FDR: 6.157e−02
Coefficient: 1.73e−01
Value: S
ATP.dependent.RNA.helicases..bacterial
0.16
0.15
0.14
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

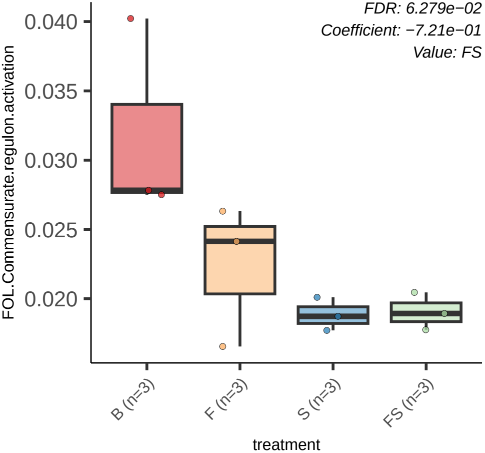

FDR: 6.157e−02
Coefficient: −7.31e−01
Value: FS
CBSS.211586.1.peg.3133
0.009
0.007
0.005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

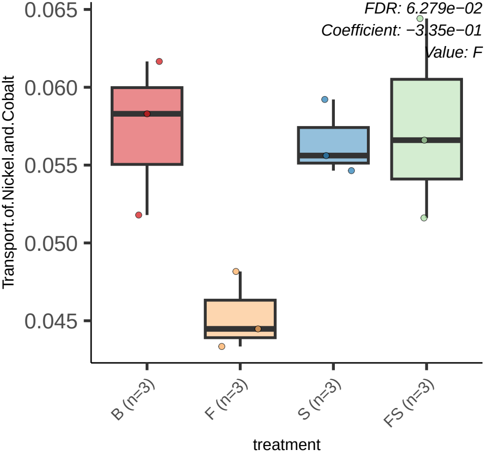

FDR: 6.157e−02
Coefficient: 8.12e−01
Value: S
Omega.amidase
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 6.189e−02
Coefficient: −1.01e−01
Value: FS
Glutaredoxins
0.22
0.21
0.20
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

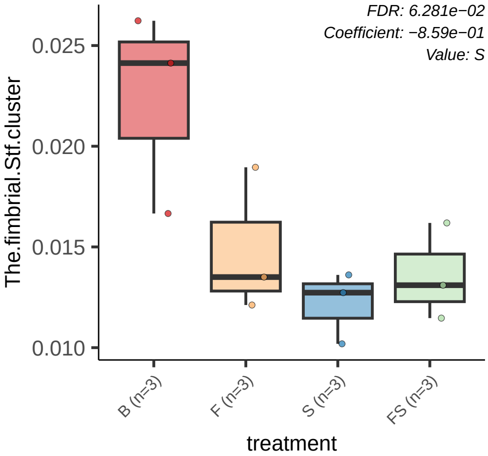

FDR: 6.189e−02
Coefficient: −2.47e−01
Value: F
Phage.tail.proteins.2
0.085
0.080
0.075
0.070
0.065
0.060
0.055
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

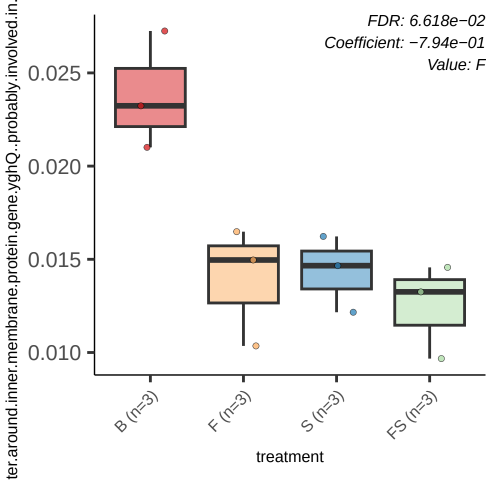

FDR: 6.189e−02
Coefficient: −7.01e−01
Value: S
Rcs.negative.regulator.IgaA
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

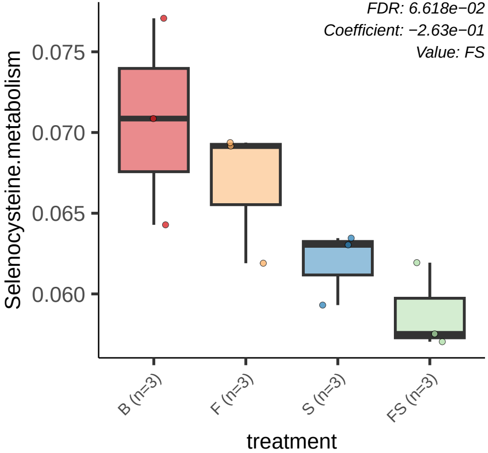

FDR: 6.279e−02
Coefficient: −7.21e−01
Value: FS
FOL.Commensurate.regulon.activation
0.040
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

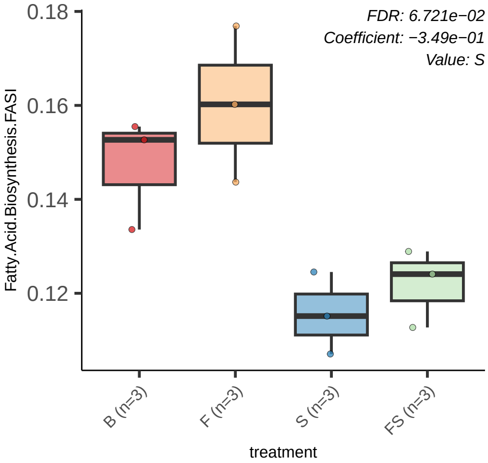


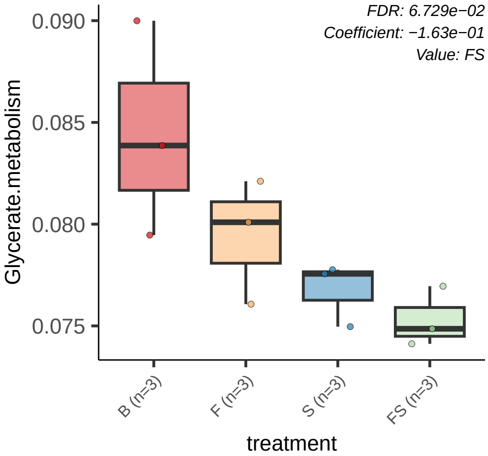
FDR: 6.279e−02
Coefficient: −3.35e−01
Value: F
0.065
0.060
0.055
0.050
0.045
Transport.of.Nickel.and.Cobalt
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

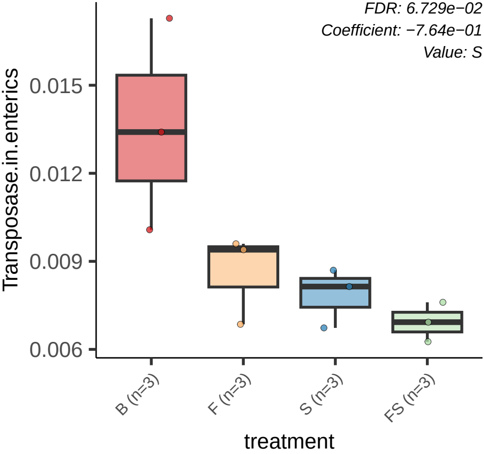

FDR: 6.281e−02
Coefficient: −8.59e−01
Value: S
The.fimbrial.Stf.cluster
0.025
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

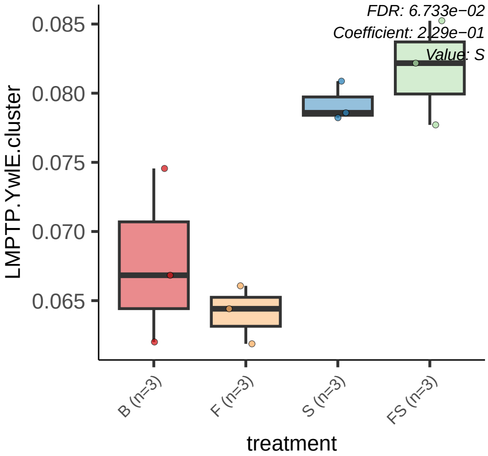

FDR: 6.618e−02
Coefficient: −7.94e−01
Value: F
ter.around.inner.membrane.protein.gene.yghQ..probably.involved.in.
0.025
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

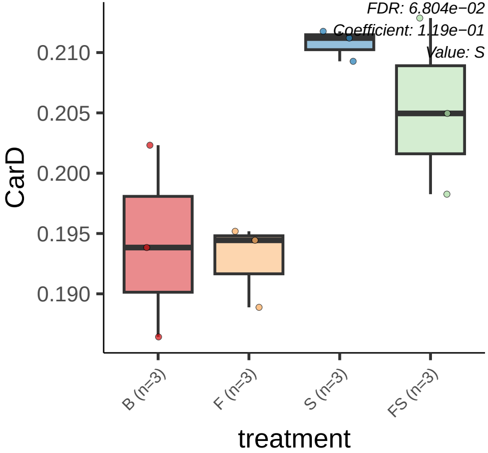

FDR: 6.618e−02
Coefficient: −2.63e−01
Value: FS
Selenocysteine.metabolism
0.075
0.070
0.065
0.060
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

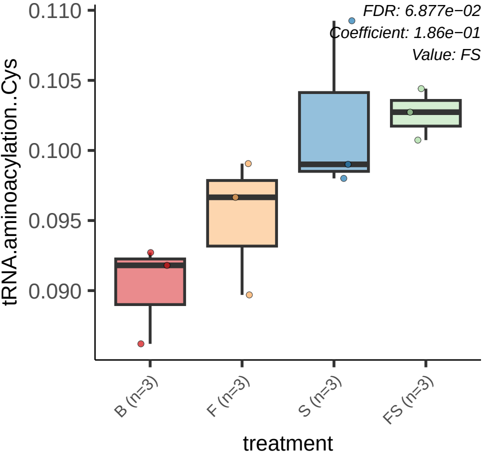

FDR: 6.721e−02
Coefficient: −3.49e−01
Value: S
Fatty.Acid.Biosynthesis.FASI
0.18
0.16
0.14
0.12
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

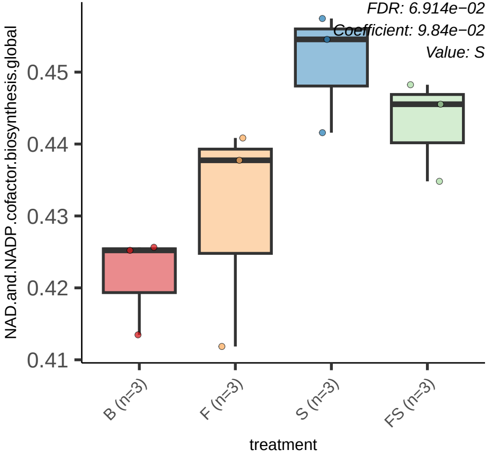

FDR: 6.729e−02
Coefficient: −1.63e−01
Value: FS
Glycerate.metabolism
0.090
0.085
0.080
0.075
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

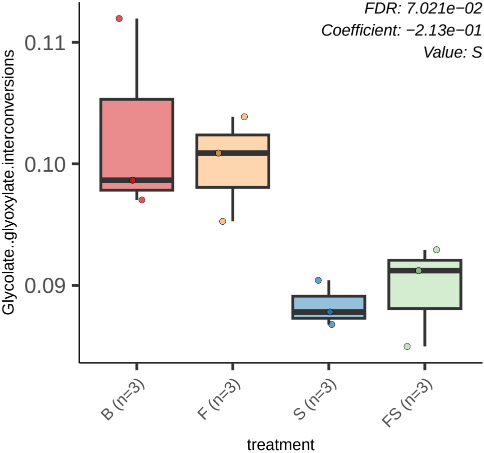

FDR: 6.729e−02
Coefficient: −7.64e−01
Value: S
Transposase.in.enterics
0.015
0.012
0.009
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

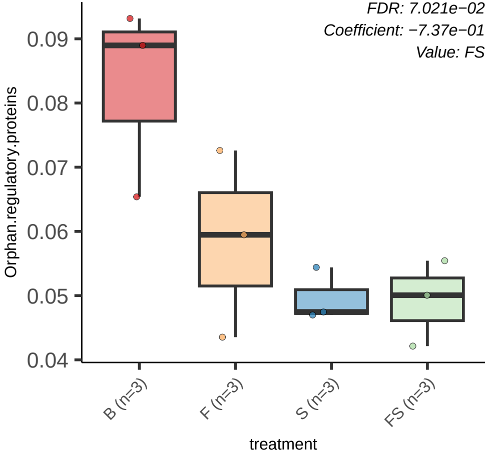

FDR: 6.733e−02
Coefficient: 2.29e−01
Value: S
LMPTP.YwlE.cluster
0.085
0.080
0.075
0.070
0.065
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

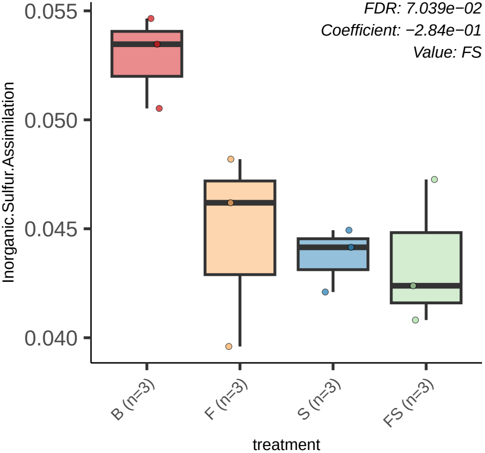

FDR: 6.804e−02
Coefficient: 1.19e−01
Value: S
CarD
0.210
0.205
0.200
0.195
0.190
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

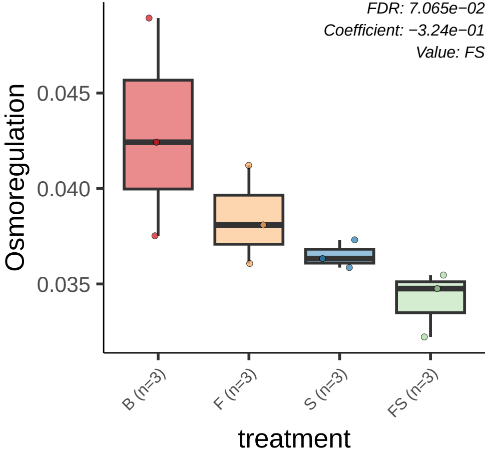

FDR: 6.877e−02
Coefficient: 1.86e−01
Value: FS
tRNA.aminoacylation..Cys
0.110
0.105
0.100
0.095
0.090
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

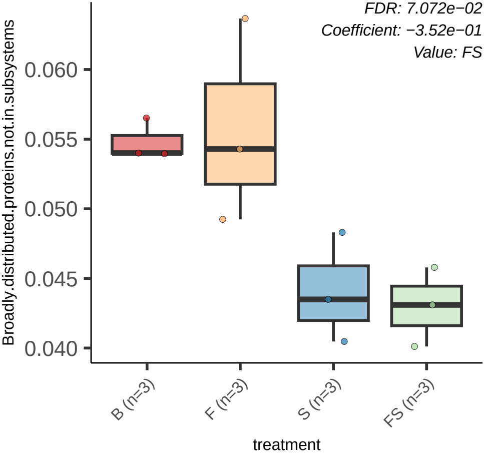

FDR: 6.914e−02
Coefficient: 9.84e−02
Value: S
NAD.and.NADP.cofactor.biosynthesis.global
0.45
0.44
0.43
0.42
0.41
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

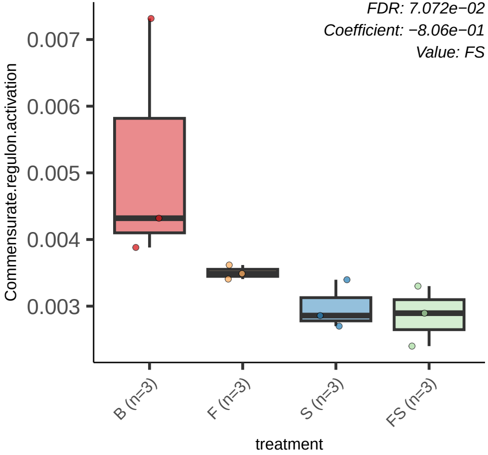

FDR: 7.021e−02
Coefficient: −2.13e−01
Value: S
Glycolate..glyoxylate.interconversions
0.11
0.10
0.09
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

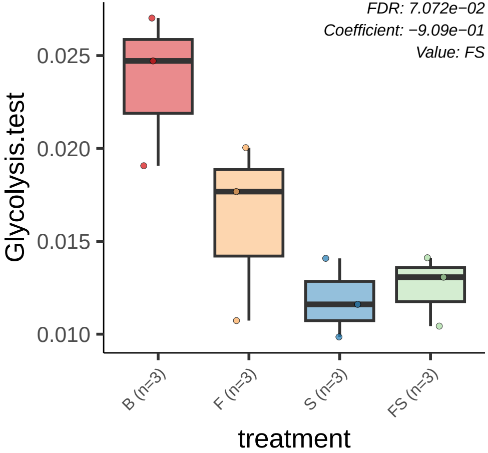

FDR: 7.021e−02
Coefficient: −7.37e−01
Value: FS
Orphan.regulatory.proteins
0.09
0.08
0.07
0.06
0.05
0.04
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

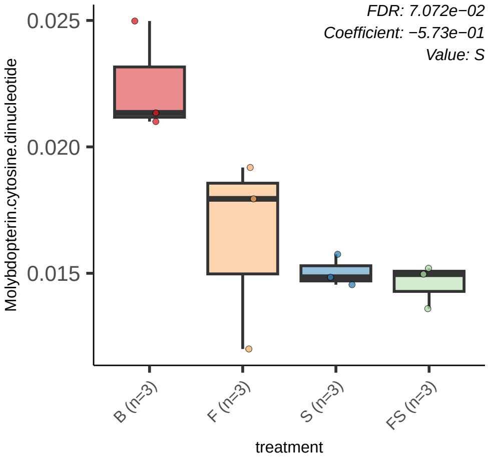

FDR: 7.039e−02
Coefficient: −2.84e−01
Value: FS
Inorganic.Sulfur.Assimilation
0.055
0.050
0.045
0.040
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

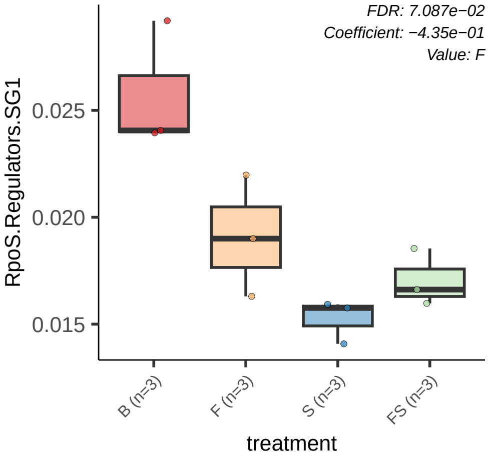

FDR: 7.065e−02
Coefficient: −3.24e−01
Value: FS
Osmoregulation
0.045
0.040
0.035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

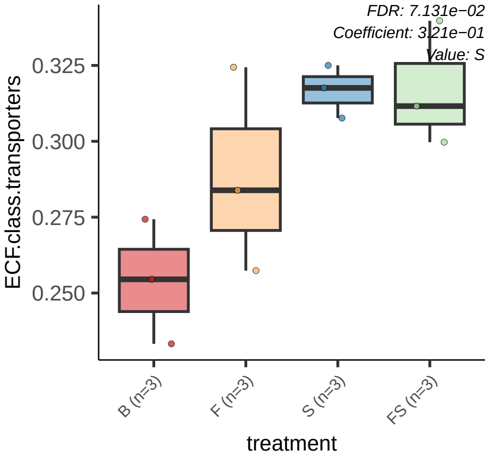

FDR: 7.072e−02
Coefficient: −3.52e−01
Value: FS
Broadly.distributed.proteins.not.in.subsystems
0.060
0.055
0.050
0.045
0.040
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

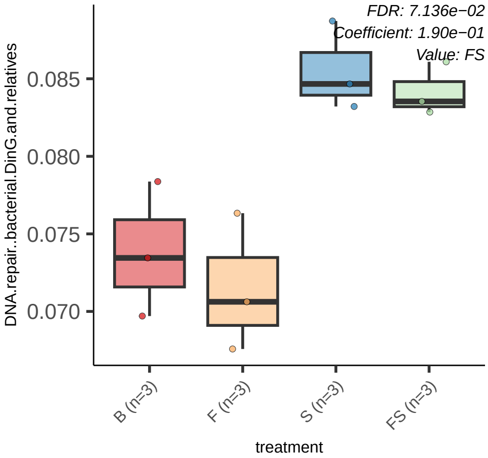

FDR: 7.072e−02
Coefficient: −8.06e−01
Value: FS
Commensurate.regulon.activation
0.007
0.006
0.005
0.004
0.003
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

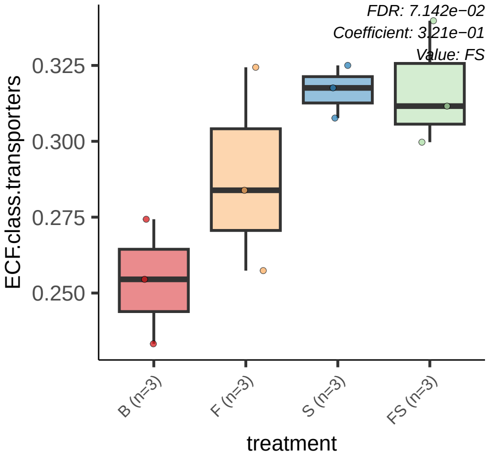

FDR: 7.072e−02
Coefficient: −9.09e−01
Value: FS
Glycolysis.test
0.025
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

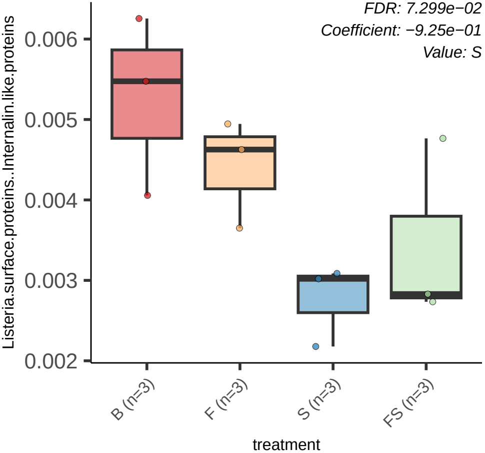

FDR: 7.072e−02
Coefficient: −5.73e−01
Value: S
Molybdopterin.cytosine.dinucleotide
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

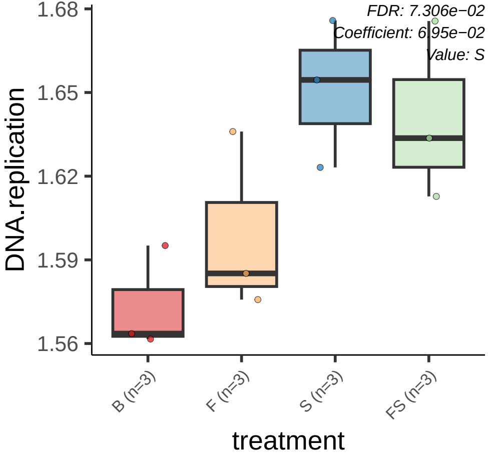

FDR: 7.087e−02
Coefficient: −4.35e−01
Value: F
RpoS.Regulators.SG1
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

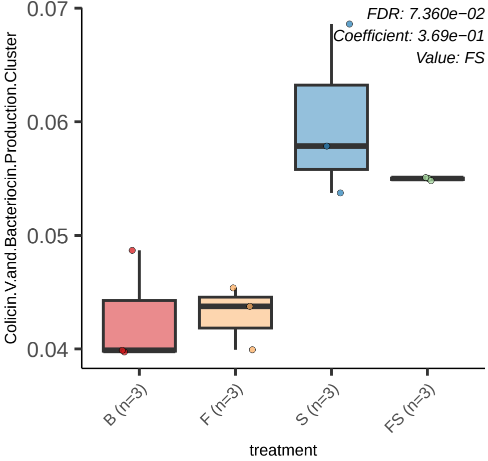

FDR: 7.131e−02
Coefficient: 3.21e−01
Value: S
ECF.class.transporters
0.325
0.300
0.275
0.250
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

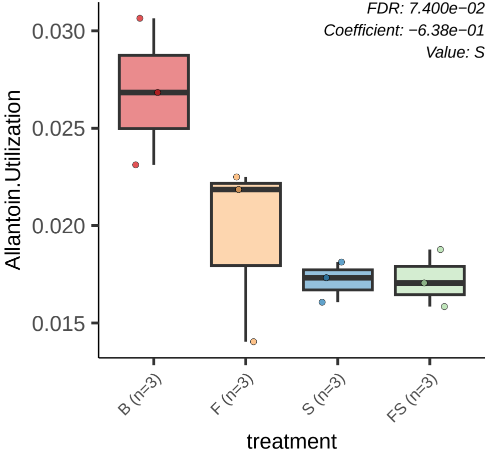

FDR: 7.136e−02
Coefficient: 1.90e−01
Value: FS
DNA.repair..bacterial.DinG.and.relatives
0.085
0.080
0.075
0.070
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

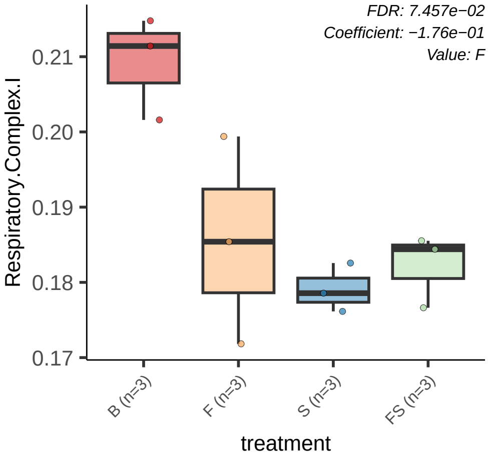

FDR: 7.142e−02
Coefficient: 3.21e−01
Value: FS
ECF.class.transporters
0.325
0.300
0.275
0.250
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

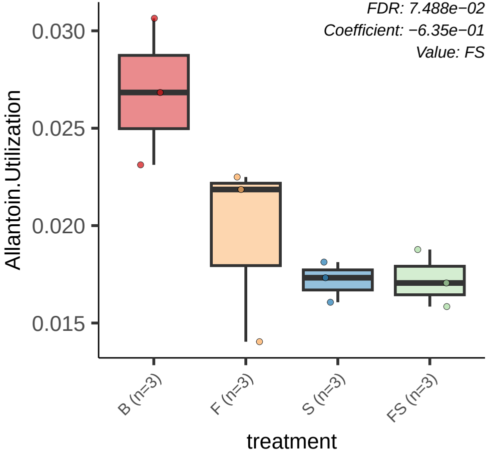

FDR: 7.299e−02
Coefficient: −9.25e−01
Value: S
Listeria.surface.proteins..Internalin.like.proteins
0.006
0.005
0.004
0.003
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 7.306e−02
Coefficient: 6.95e−02
Value: S
DNA.replication
1.68
1.65
1.62
1.59
1.56
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

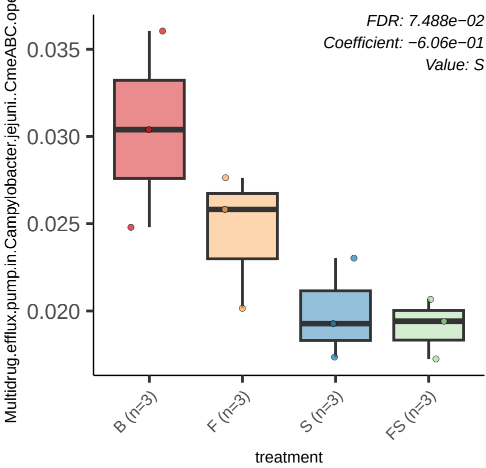

FDR: 7.360e−02
Coefficient: 3.69e−01
Value: FS
Colicin.V.and.Bacteriocin.Production.Cluster
0.07
0.06
0.05
0.04
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

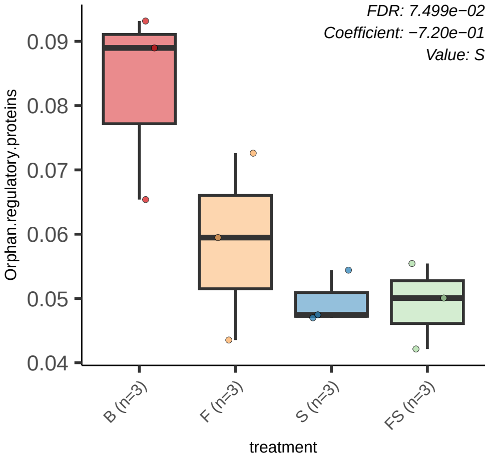

FDR: 7.400e−02
Coefficient: −6.38e−01
Value: S
Allantoin.Utilization
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

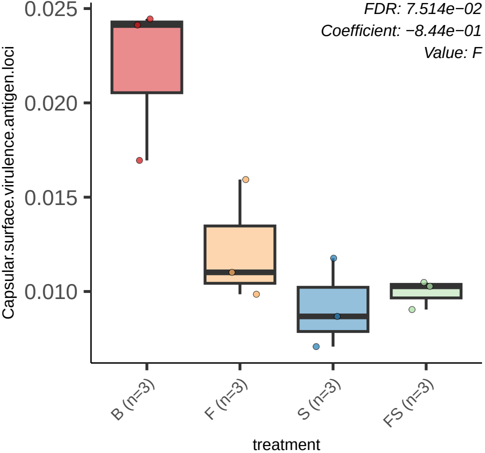

FDR: 7.457e−02
Coefficient: −1.76e−01
Value: F
Respiratory.Complex.I
0.21
0.20
0.19
0.18
0.17
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

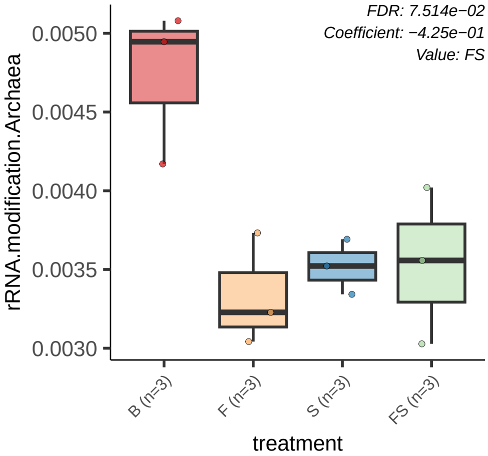


FDR: 7.488e−02
Coefficient: −6.35e−01
Value: FS
Allantoin.Utilization
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

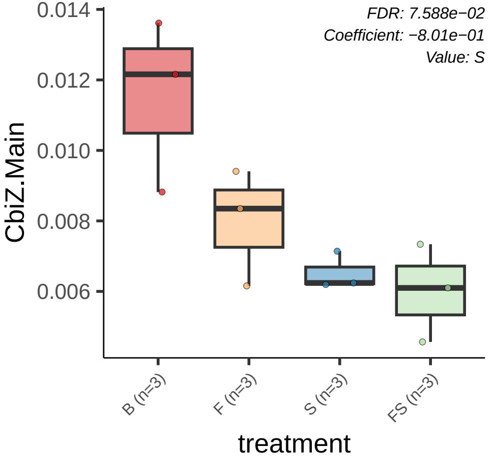

FDR: 7.488e−02
Coefficient: −6.06e−01
Value: S
Multidrug.efflux.pump.in.Campylobacter.jejuni..CmeABC.ope
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

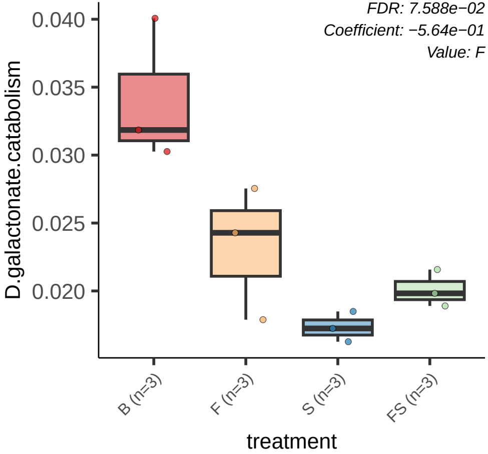

FDR: 7.499e−02
Coefficient: −7.20e−01
Value: S
Orphan.regulatory.proteins
0.09
0.08
0.07
0.06
0.05
0.04
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

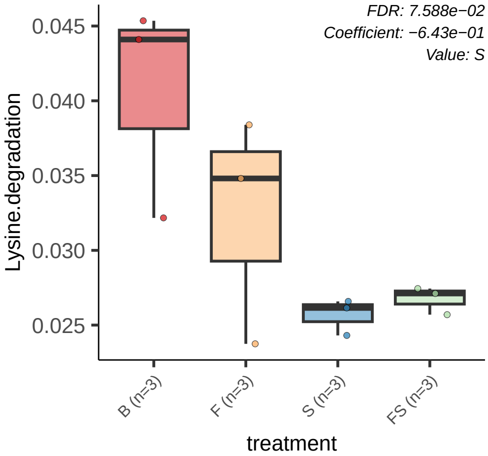

FDR: 7.514e−02
Coefficient: −8.44e−01
Value: F
Capsular.surface.virulence.antigen.loci
0.025
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment



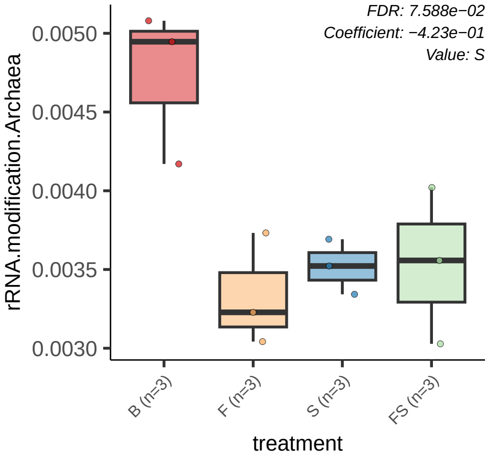
FDR: 7.514e−02
Coefficient: −4.25e−01
Value: FS
rRNA.modification.Archaea
0.0050
0.0045
0.0040
0.0035
0.0030
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

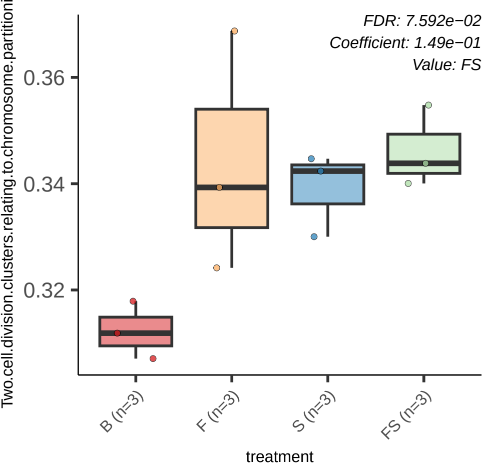

FDR: 7.588e−02
Coefficient: −8.01e−01
Value: S
CbiZ.Main
0.014
0.012
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

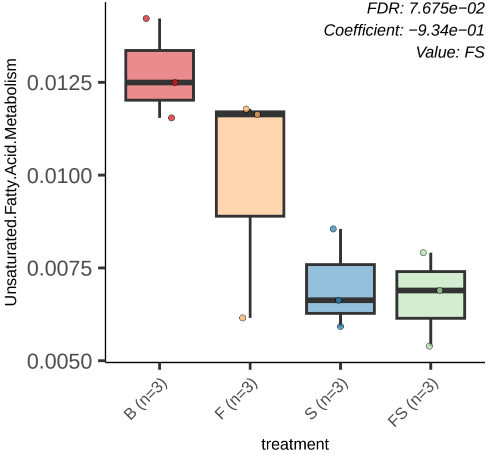

FDR: 7.588e−02
Coefficient: −5.64e−01
Value: F
D.galactonate.catabolism
0.040
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

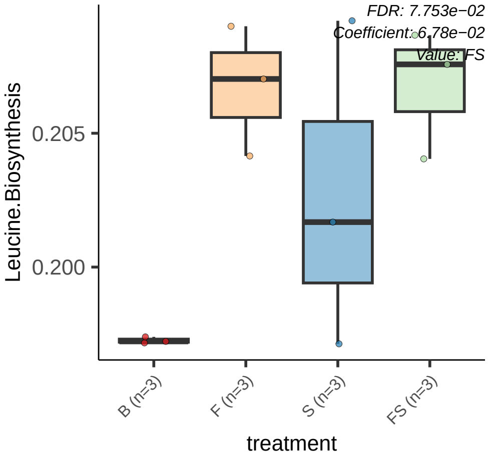


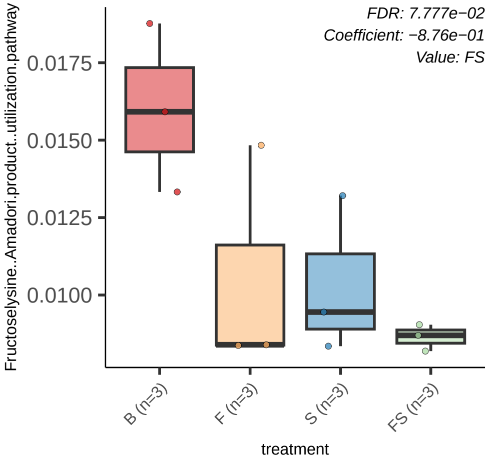
FDR: 7.588e−02
Coefficient: −6.43e−01
Value: S
Lysine.degradation
0.045
0.040
0.035
0.030
0.025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

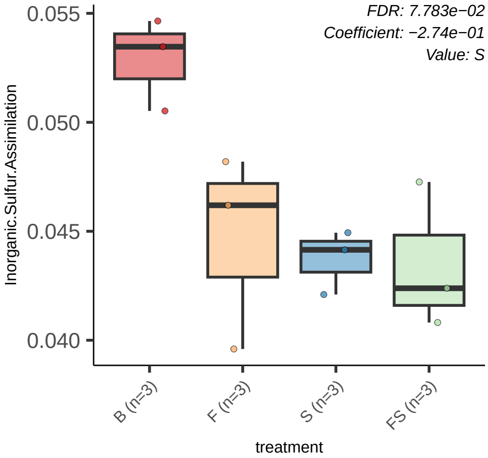

FDR: 7.588e−02
Coefficient: −4.23e−01
Value: S
rRNA.modification.Archaea
0.0050
0.0045
0.0040
0.0035
0.0030
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

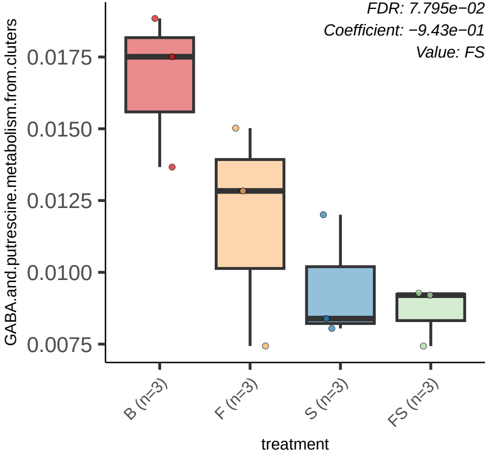

FDR: 7.592e−02
Coefficient: 1.49e−01
Value: FS
Two.cell.division.clusters.relating.to.chromosome.partitioni
0.36
0.34
0.32
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

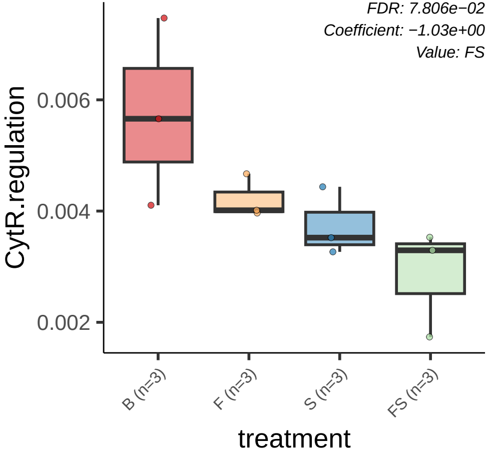

FDR: 7.675e−02
Coefficient: −9.34e−01
Value: FS
Unsaturated.Fatty.Acid.Metabolism
0.0125
0.0100
0.0075
0.0050
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

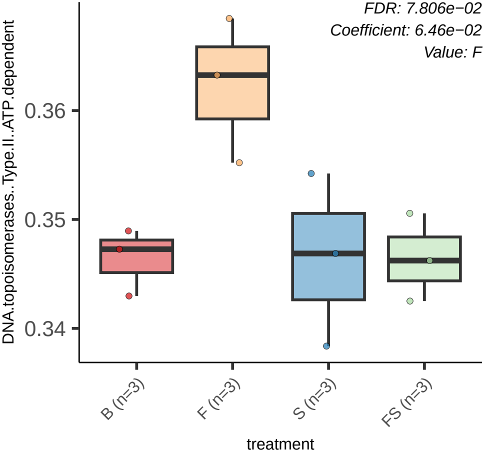

FDR: 7.753e−02
Coefficient: 6.78e−02
Value: FS
Leucine.Biosynthesis
0.205
0.200
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

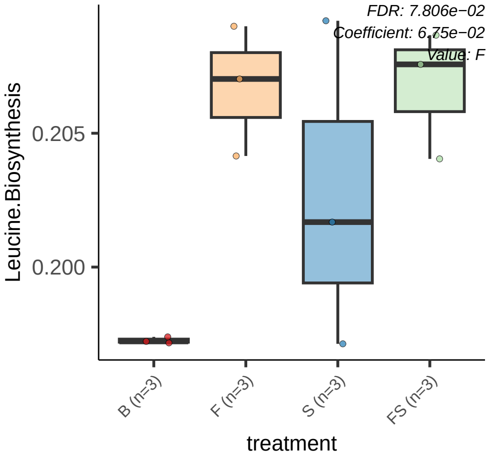

FDR: 7.777e−02
Coefficient: −8.76e−01
Value: FS
Fructoselysine..Amadori.product..utilization.pathway
0.0175
0.0150
0.0125
0.0100
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

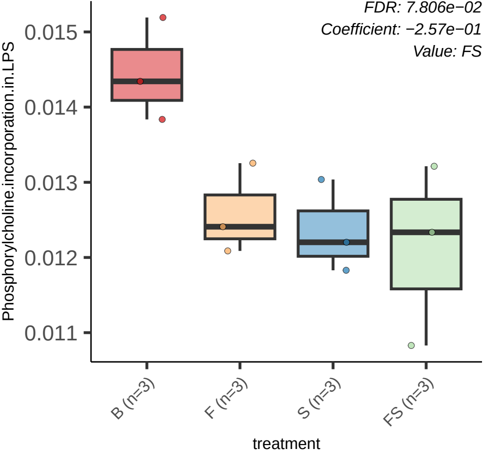

FDR: 7.783e−02
Coefficient: −2.74e−01
Value: S
Inorganic.Sulfur.Assimilation
0.055
0.050
0.045
0.040
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

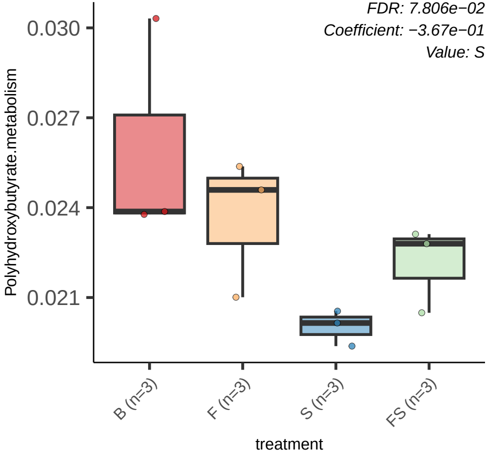

FDR: 7.795e−02
Coefficient: −9.43e−01
Value: FS
GABA.and.putrescine.metabolism.from.cluters
0.0175
0.0150
0.0125
0.0100
0.0075
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

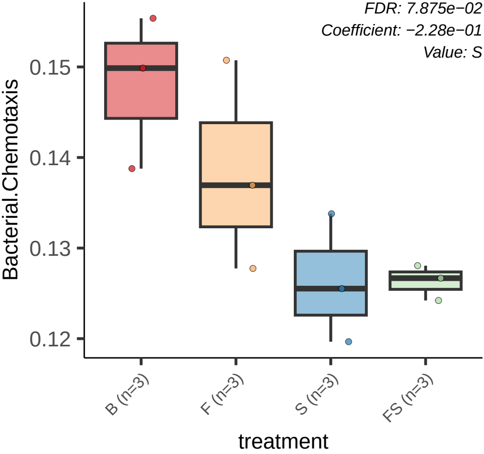

FDR: 7.806e−02
Coefficient: −1.03e+00
Value: FS
CytR.regulation
0.006
0.004
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

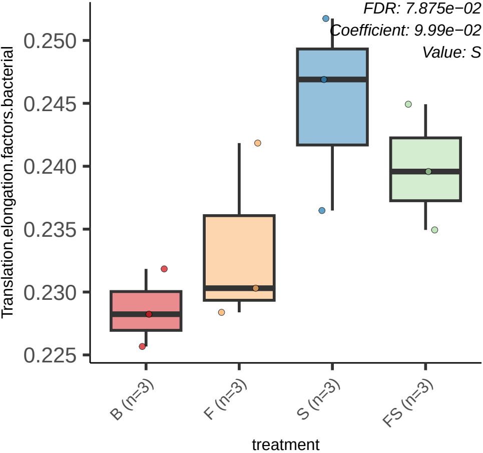

FDR: 7.806e−02
Coefficient: 6.46e−02
Value: F
DNA.topoisomerases..Type.II..ATP.dependent
0.36
0.35
0.34
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

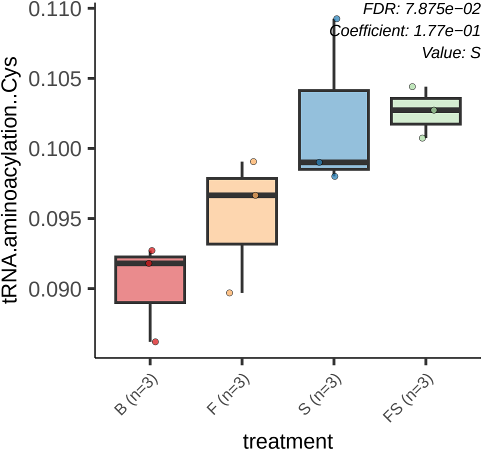

FDR: 7.806e−02
Coefficient: 6.75e−02
Value: F
Leucine.Biosynthesis
0.205
0.200
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

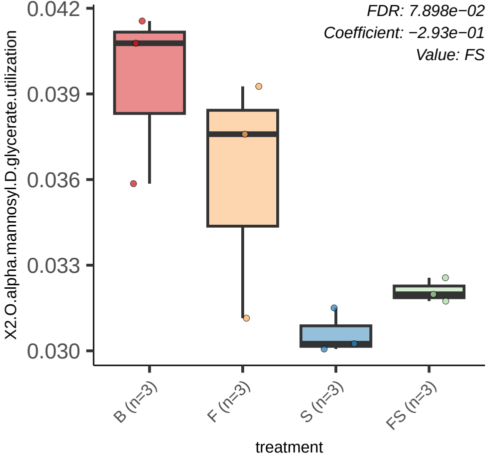

FDR: 7.806e−02
Coefficient: −2.57e−01
Value: FS
Phosphorylcholine.incorporation.in.LPS
0.015
0.014
0.013
0.012
0.011
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

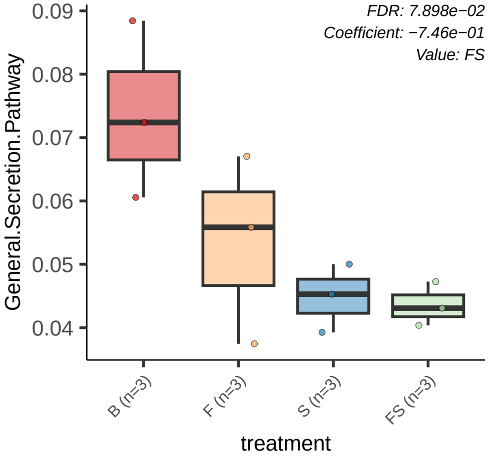

FDR: 7.806e−02
Coefficient: −3.67e−01
Value: S
Polyhydroxybutyrate.metabolism
0.030
0.027
0.024
0.021
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

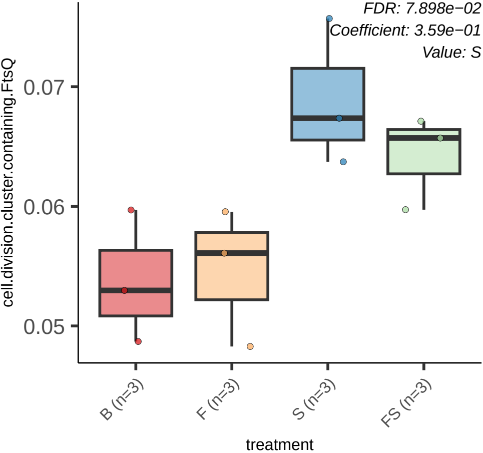

FDR: 7.875e−02
Coefficient: −2.28e−01
Value: S
Bacterial.Chemotaxis
0.15
0.14
0.13
0.12
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

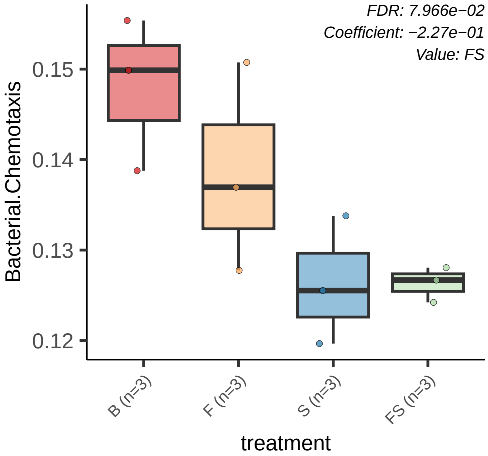

FDR: 7.875e−02
Coefficient: 9.99e−02
Value: S
Translation.elongation.factors.bacterial
0.250
0.245
0.240
0.235
0.230
0.225
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 7.875e−02
Coefficient: 1.77e−01
Value: S
tRNA.aminoacylation..Cys
0.110
0.105
0.100
0.095
0.090
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

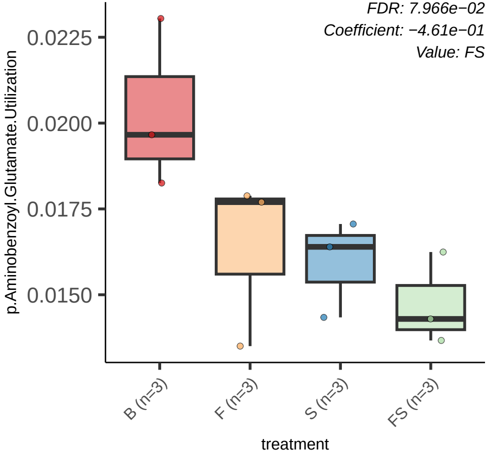

FDR: 7.898e−02
Coefficient: −2.93e−01
Value: FS
X2.O.alpha.mannosyl.D.glycerate.utilization
0.042
0.039
0.036
0.033
0.030
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

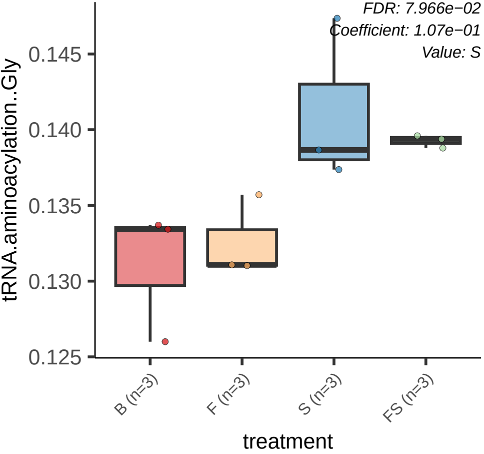

FDR: 7.898e−02
Coefficient: −7.46e−01
Value: FS
General.Secretion.Pathway
0.09
0.08
0.07
0.06
0.05
0.04
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

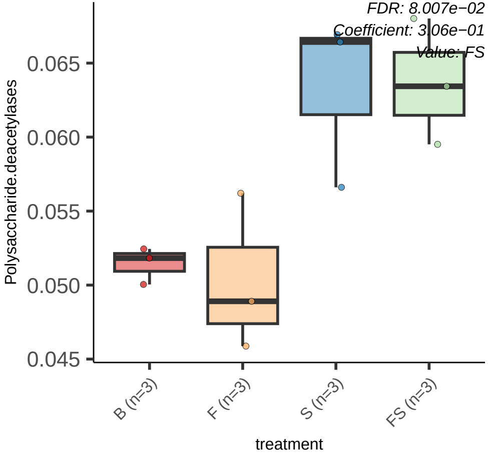

FDR: 7.898e−02
Coefficient: 3.59e−01
Value: S
cell.division.cluster.containing.FtsQ
0.07
0.06
0.05
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

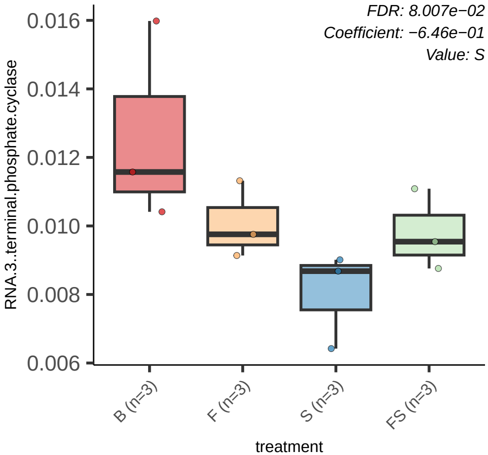


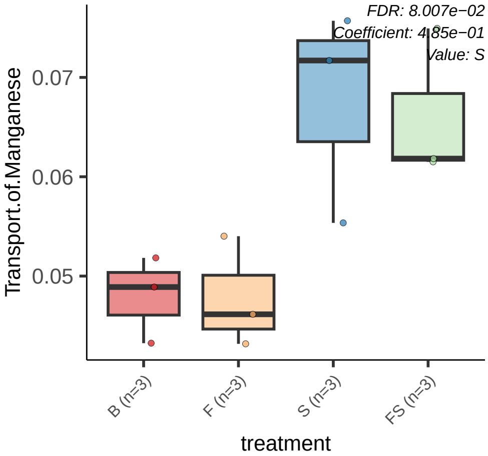
FDR: 7.966e−02
Coefficient: −2.27e−01
Value: FS
Bacterial.Chemotaxis
0.15
0.14
0.13
0.12
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

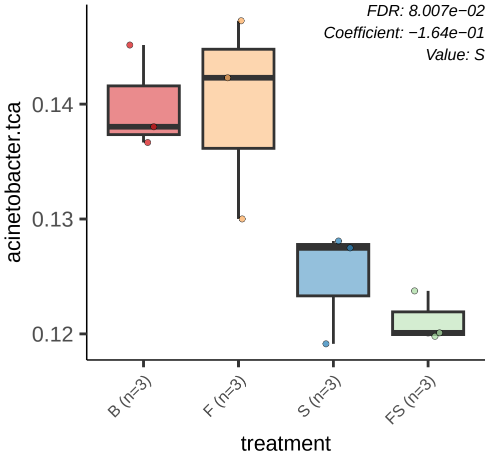

FDR: 7.966e−02
Coefficient: −4.61e−01
Value: FS
p.Aminobenzoyl.Glutamate.Utilization
0.0225
0.0200
0.0175
0.0150
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

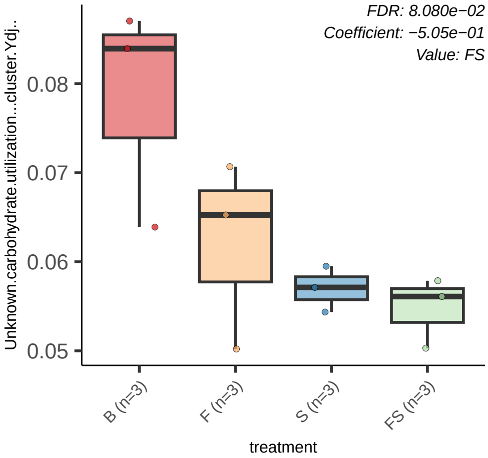

FDR: 7.966e−02
Coefficient: 1.07e−01
Value: S
tRNA.aminoacylation..Gly
0.145
0.140
0.135
0.130
0.125
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

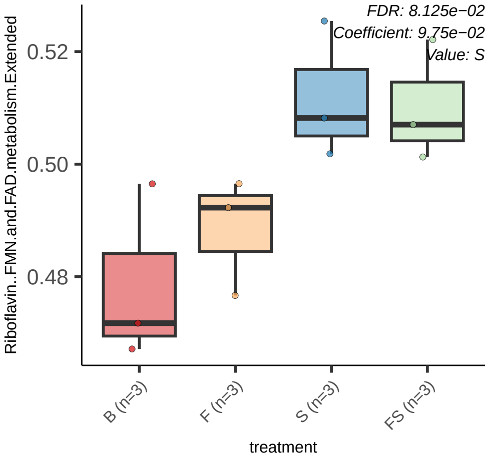

FDR: 8.007e−02
Coefficient: 3.06e−01
Value: FS
Polysaccharide.deacetylases
0.065
0.060
0.055
0.050
0.045
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

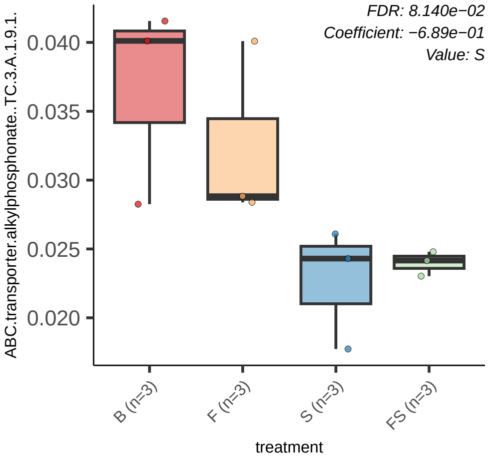

FDR: 8.007e−02
Coefficient: −6.46e−01
Value: S
RNA.3..terminal.phosphate.cyclase
0.016
0.014
0.012
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

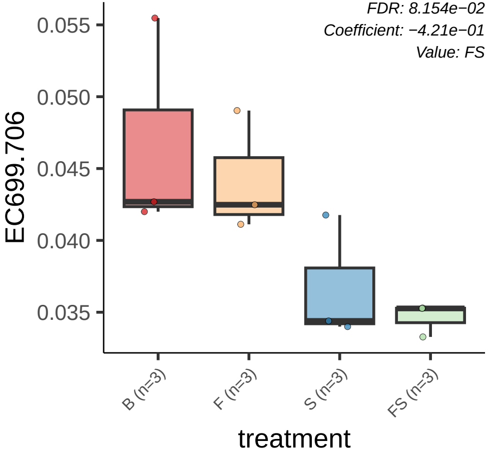

FDR: 8.007e−02
Coefficient: 4.85e−01
Value: S
Transport.of.Manganese
0.07
0.06
0.05
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

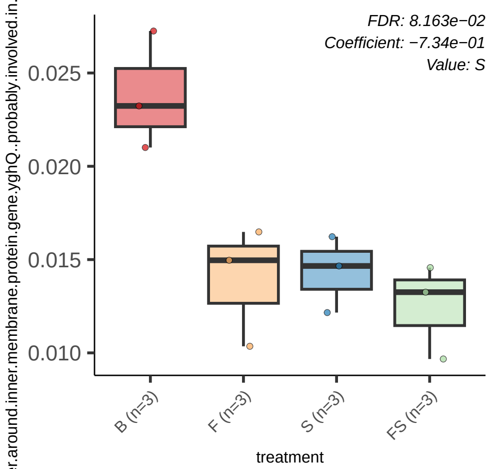

FDR: 8.007e−02
Coefficient: −1.64e−01
Value: S
acinetobacter.tca
0.14
0.13
0.12
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

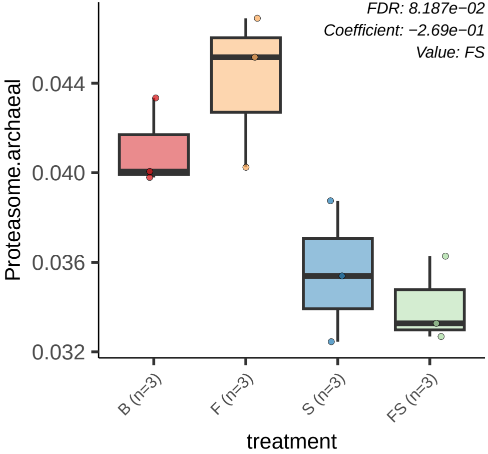

FDR: 8.080e−02
Coefficient: −5.05e−01
Value: FS
Unknown.carbohydrate.utilization..cluster.Ydj..
0.08
0.07
0.06
0.05
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

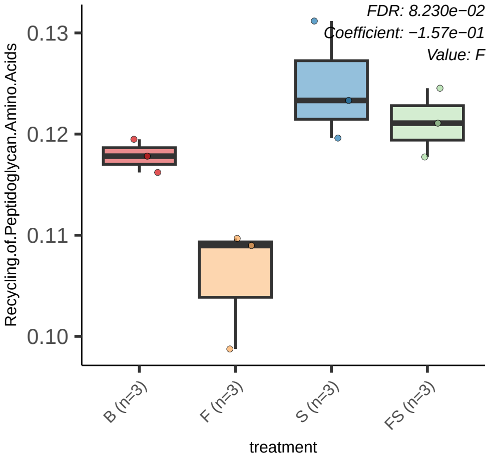

FDR: 8.125e−02
Coefficient: 9.75e−02
Value: S
Riboflavin..FMN.and.FAD.metabolism.Extended
0.52
0.50
0.48
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

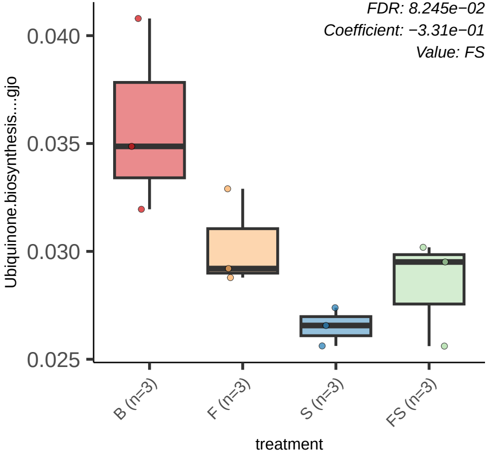

FDR: 8.140e−02
Coefficient: −6.89e−01
Value: S
ABC.transporter.alkylphosphonate..TC.3.A.1.9.1.
0.040
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

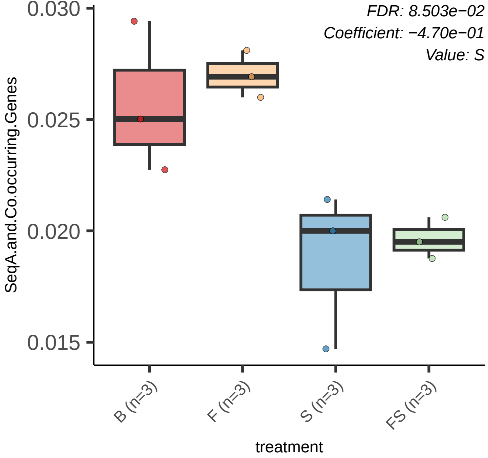

FDR: 8.154e−02
Coefficient: −4.21e−01
Value: FS
EC699.706
0.055
0.050
0.045
0.040
0.035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

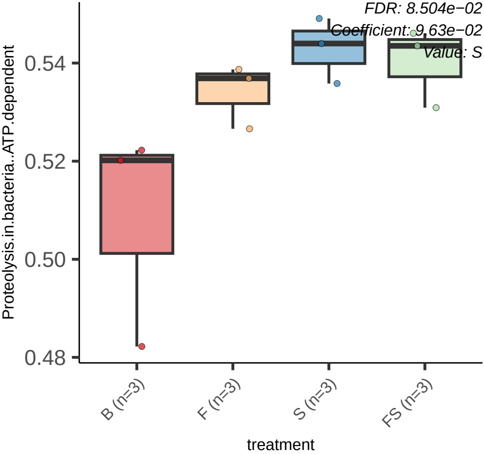

FDR: 8.163e−02
Coefficient: −7.34e−01
Value: S
ter.around.inner.membrane.protein.gene.yghQ..probably.involved.in.
0.025
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

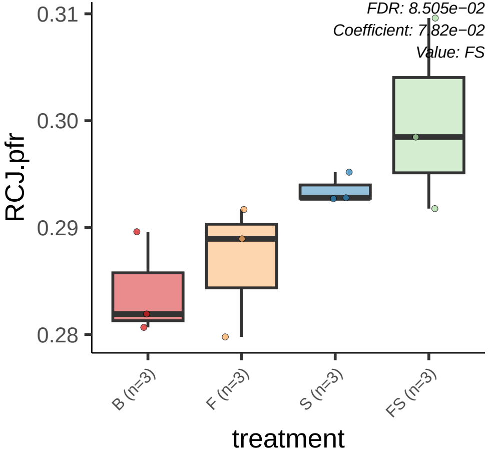

FDR: 8.187e−02
Coefficient: −2.69e−01
Value: FS
Proteasome.archaeal
0.044
0.040
0.036
0.032
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

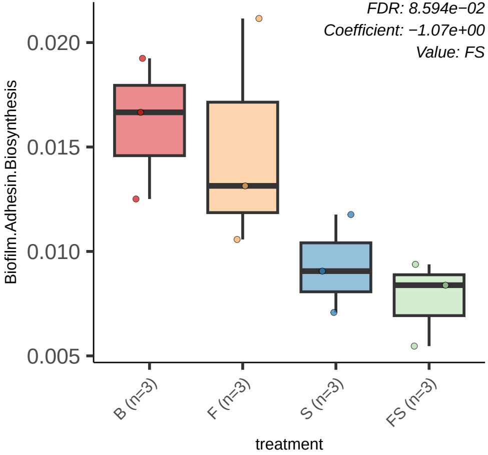

FDR: 8.230e−02
Coefficient: −1.57e−01
Value: F
Recycling.of.Peptidoglycan.Amino.Acids
0.13
0.12
0.11
0.10
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

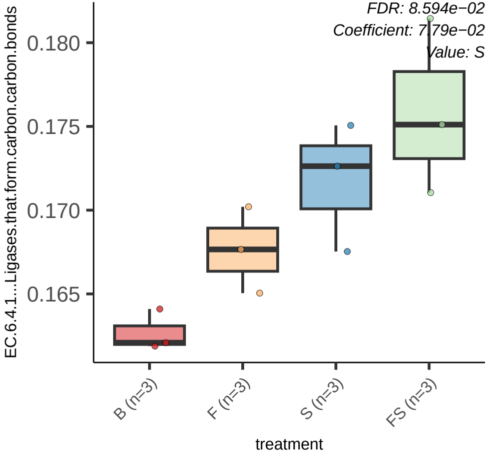

FDR: 8.245e−02
Coefficient: −3.31e−01
Value: FS
Ubiquinone.biosynthesis...gjo
0.040
0.035
0.030
0.025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

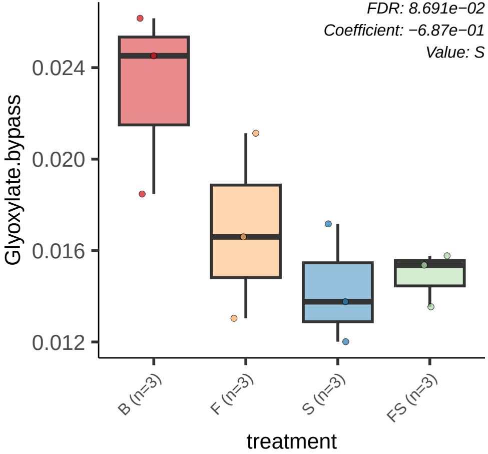

FDR: 8.503e−02
Coefficient: −4.70e−01
Value: S
0.030
0.025
0.020
0.015
SeqA.and.Co.occurring.Genes
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

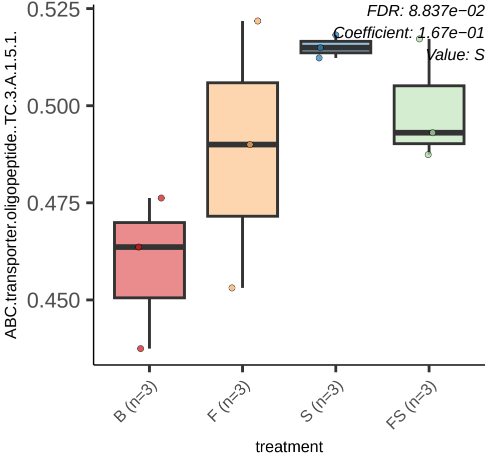

FDR: 8.504e−02
Coefficient: 9.63e−02
Value: S
Proteolysis.in.bacteria..ATP.dependent
0.54
0.52
0.50
0.48
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

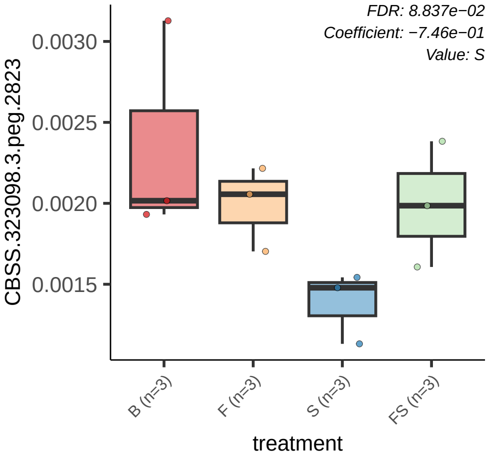

FDR: 8.505e−02
Coefficient: 7.82e−02
Value: FS
RCJ.pfr
0.31
0.30
0.29
0.28
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

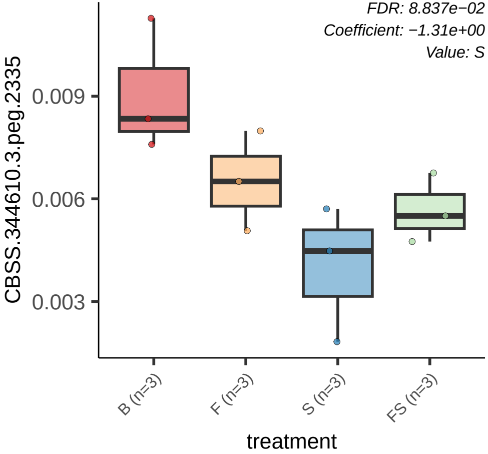

FDR: 8.594e−02
Coefficient: −1.07e+00
Value: FS
Biofilm.Adhesin.Biosynthesis
0.020
0.015
0.010
0.005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

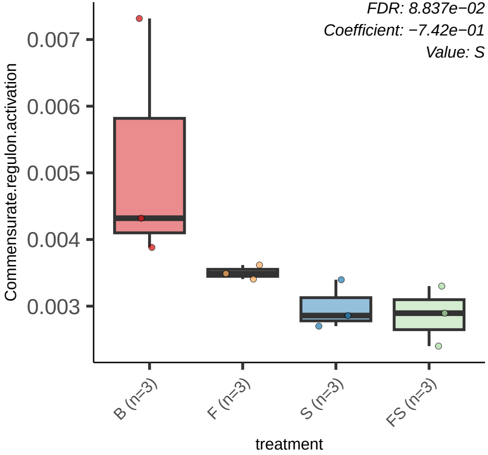

FDR: 8.594e−02
Coefficient: 7.79e−02
Value: S
EC.6.4.1...Ligases.that.form.carbon.carbon.bonds
0.180
0.175
0.170
0.165
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

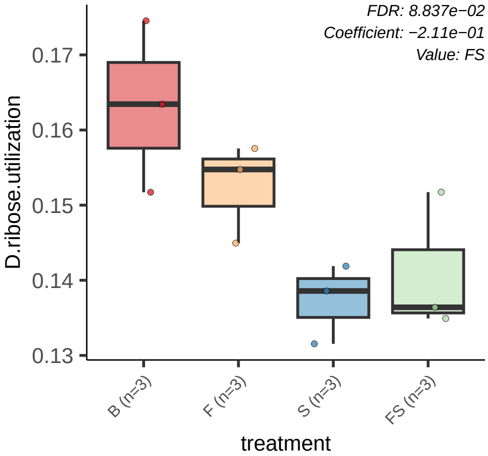

FDR: 8.691e−02
Coefficient: −6.87e−01
Value: S
Glyoxylate.bypass
0.024
0.020
0.016
0.012
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

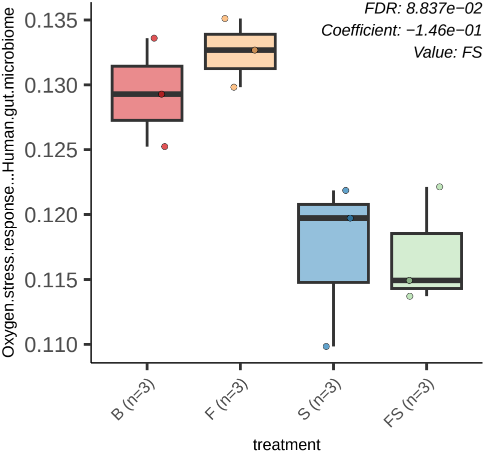

FDR: 8.837e−02
Coefficient: 1.67e−01
Value: S
ABC.transporter.oligopeptide..TC.3.A.1.5.1.
0.525
0.500
0.475
0.450
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

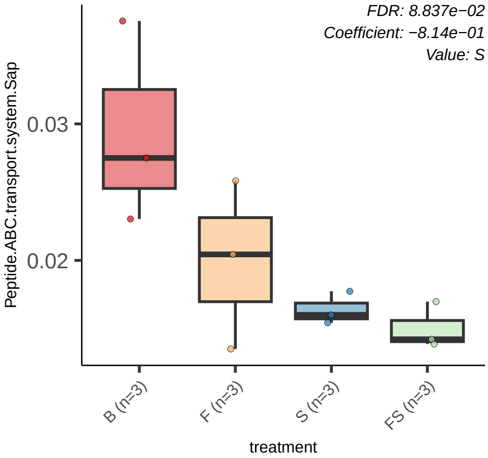

FDR: 8.837e−02
Coefficient: −7.46e−01
Value: S
CBSS.323098.3.peg.2823
0.0030
0.0025
0.0020
0.0015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 8.837e−02
Coefficient: −1.31e+00
Value: S
CBSS.344610.3.peg.2335
0.009
0.006
0.003
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

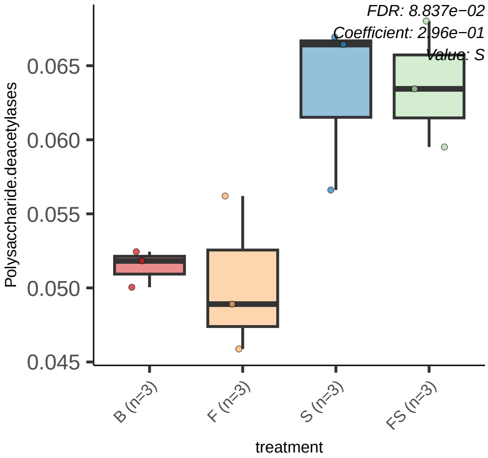

FDR: 8.837e−02
Coefficient: −7.42e−01
Value: S
Commensurate.regulon.activation
0.007
0.006
0.005
0.004
0.003
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

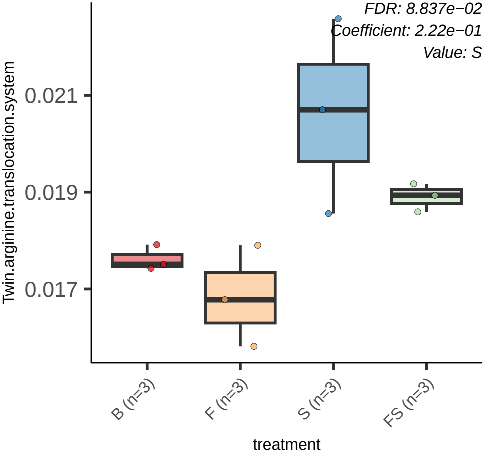

FDR: 8.837e−02
Coefficient: −2.11e−01
Value: FS
D.ribose.utilization
0.17
0.16
0.15
0.14
0.13
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

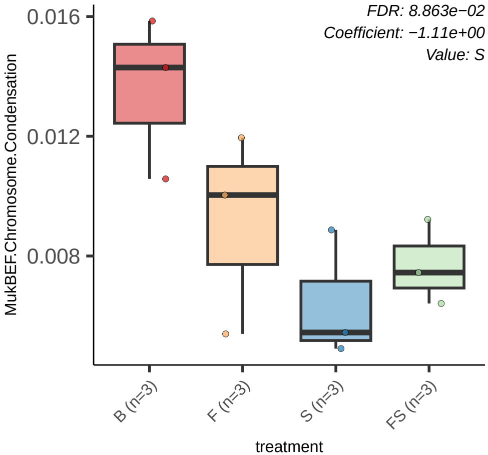

FDR: 8.837e−02
Coefficient: −1.46e−01
Value: FS
Oxygen.stress.response...Human.gut.microbiome
0.135
0.130
0.125
0.120
0.115
0.110
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

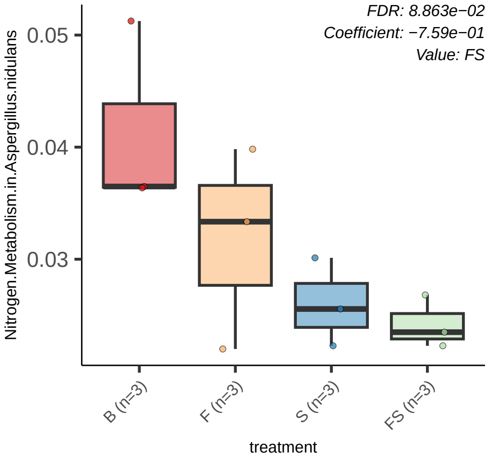


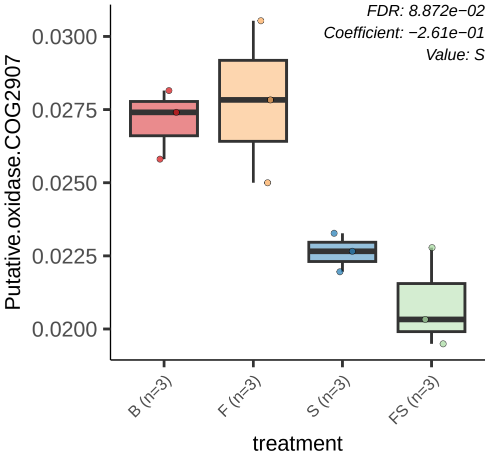
FDR: 8.837e−02
Coefficient: −8.14e−01
Value: S
Peptide.ABC.transport.system.Sap
0.03
0.02
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

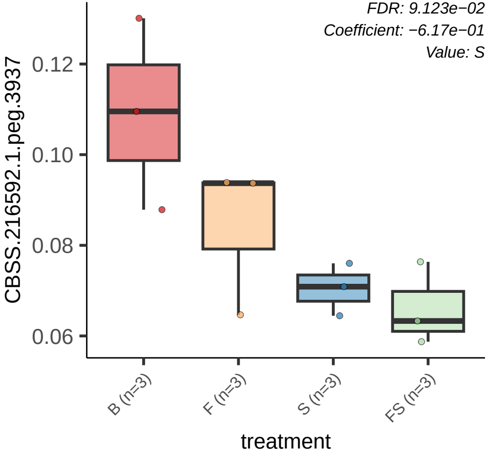

FDR: 8.837e−02
Coefficient: 2.96e−01
Value: S
Polysaccharide.deacetylases
0.065
0.060
0.055
0.050
0.045
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

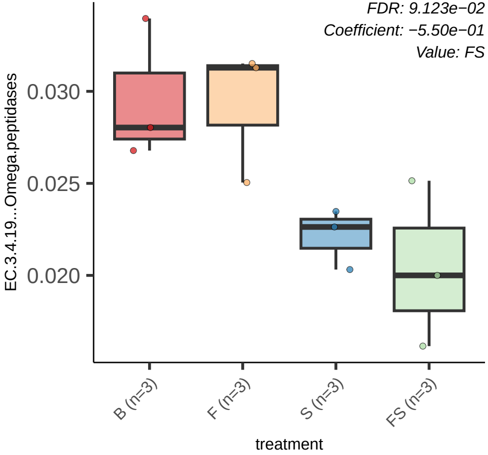

FDR: 8.837e−02
Coefficient: 2.22e−01
Value: S
Twin.arginine.translocation.system
0.021
0.019
0.017
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

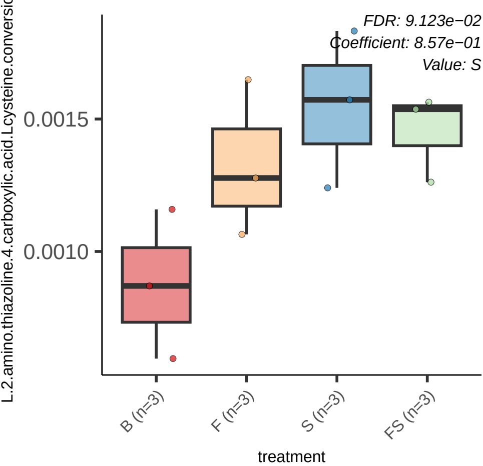

FDR: 8.863e−02
Coefficient: −1.11e+00
Value: S
MukBEF.Chromosome.Condensation
0.016
0.012
0.008
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

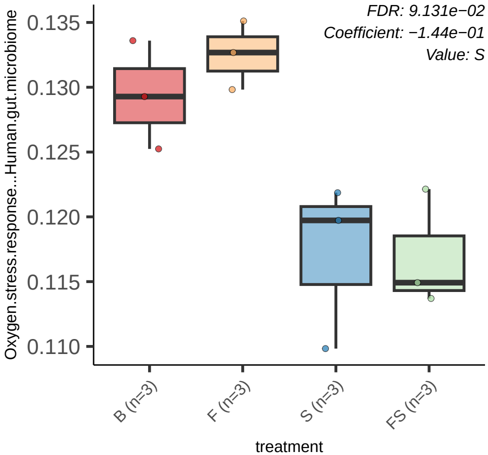

FDR: 8.863e−02
Coefficient: −7.59e−01
Value: FS
Nitrogen.Metabolism.in.Aspergillus.nidulans
0.05
0.04
0.03
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

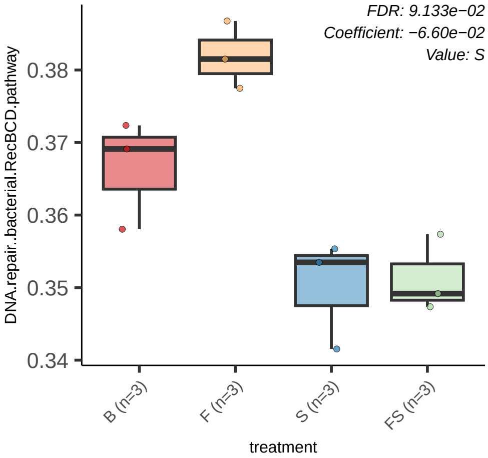

FDR: 8.872e−02
Coefficient: −2.61e−01
Value: S
Putative.oxidase.COG2907
0.0300
0.0275
0.0250
0.0225
0.0200
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

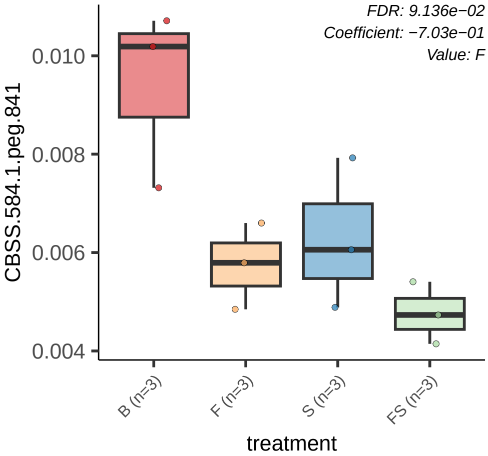

FDR: 9.123e−02
Coefficient: −6.17e−01
Value: S
CBSS.216592.1.peg.3937
0.12
0.10
0.08
0.06
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

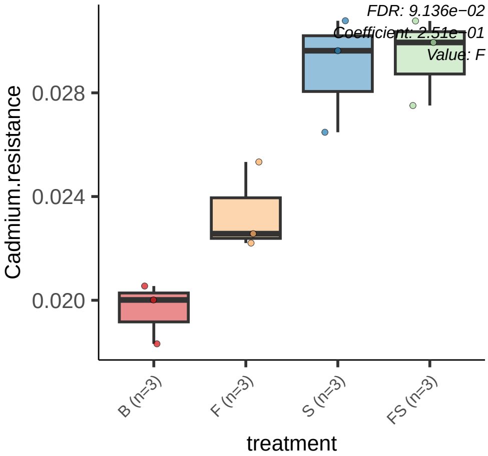

FDR: 9.123e−02
Coefficient: −5.50e−01
Value: FS
EC.3.4.19...Omega.peptidases
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

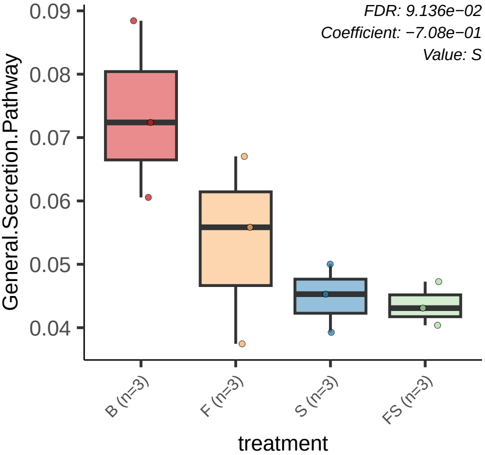

FDR: 9.123e−02
Coefficient: 8.57e−01
Value: S
L.2.amino.thiazoline.4.carboxylic.acid.Lcysteine.conversio
0.0015
0.0010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

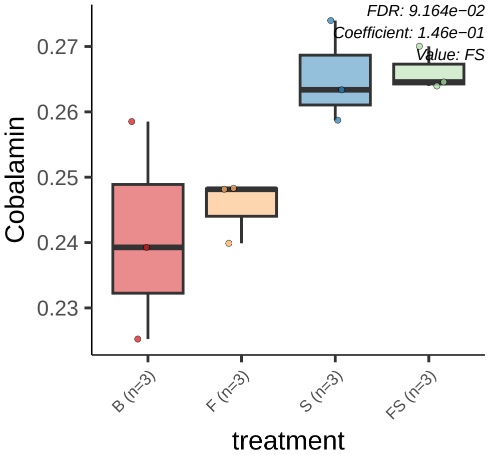

FDR: 9.131e−02
Coefficient: −1.44e−01
Value: S
Oxygen.stress.response...Human.gut.microbiome
0.135
0.130
0.125
0.120
0.115
0.110
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

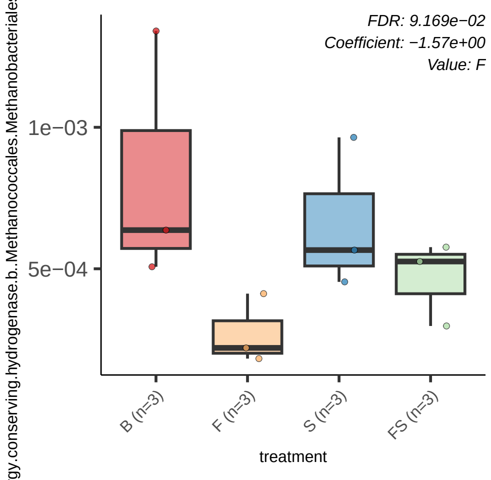

FDR: 9.133e−02
Coefficient: −6.60e−02
Value: S
DNA.repair..bacterial.RecBCD.pathway
0.38
0.37
0.36
0.35
0.34
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

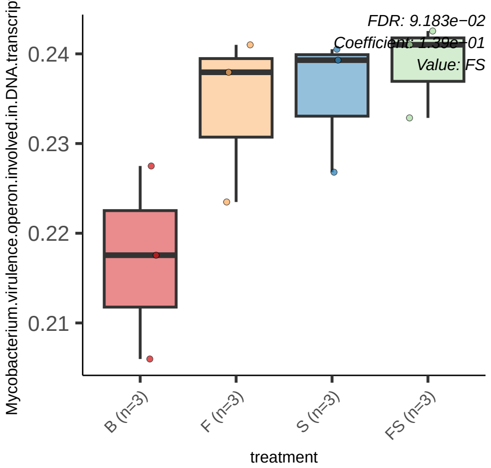

FDR: 9.136e−02
Coefficient: −7.03e−01
Value: F
CBSS.584.1.peg.841
0.010
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

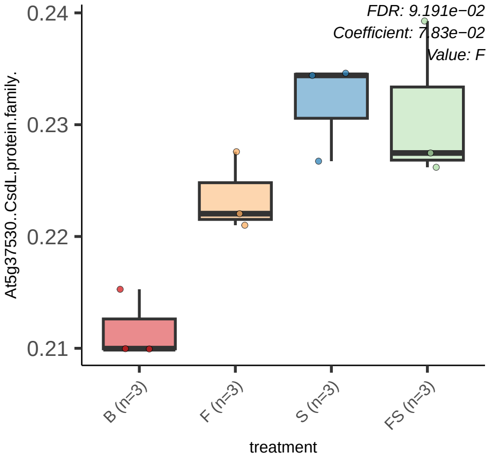

FDR: 9.136e−02
Coefficient: 2.51e−01
Value: F
Cadmium.resistance
0.028
0.024
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

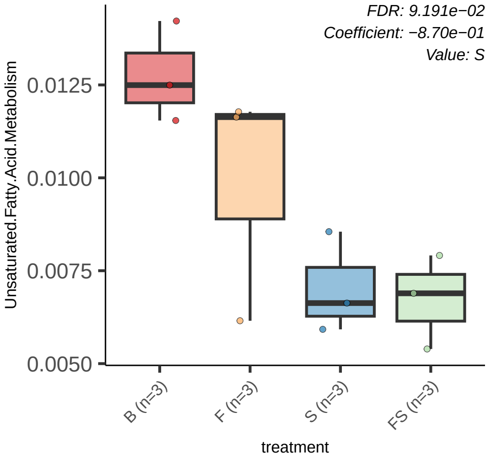

FDR: 9.136e−02
Coefficient: −7.08e−01
Value: S
General.Secretion.Pathway
0.09
0.08
0.07
0.06
0.05
0.04
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

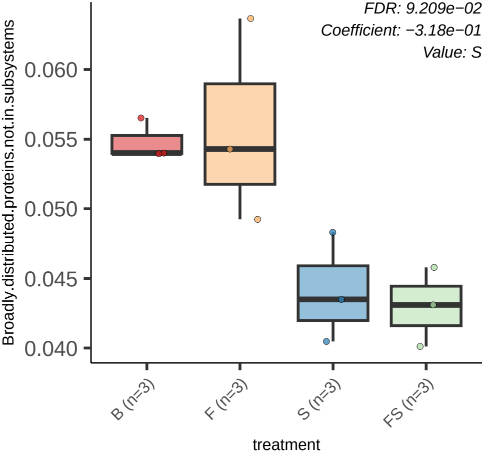

FDR: 9.164e−02
Coefficient: 1.46e−01
Value: FS
Cobalamin
0.27
0.26
0.25
0.24
0.23
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

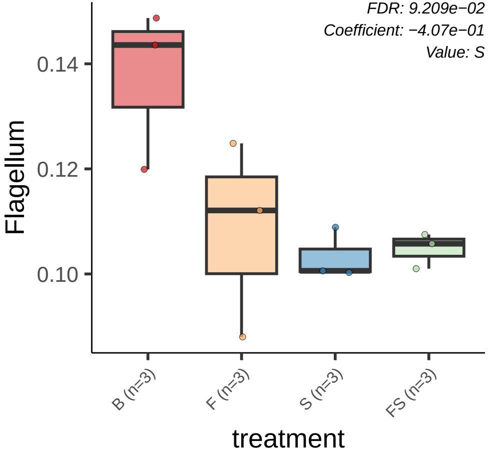

FDR: 9.169e−02
Coefficient: −1.57e+00
Value: F
gy.conserving.hydrogenase.b..Methanococcales.Methanobacteriales
1e−03
5e−04
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

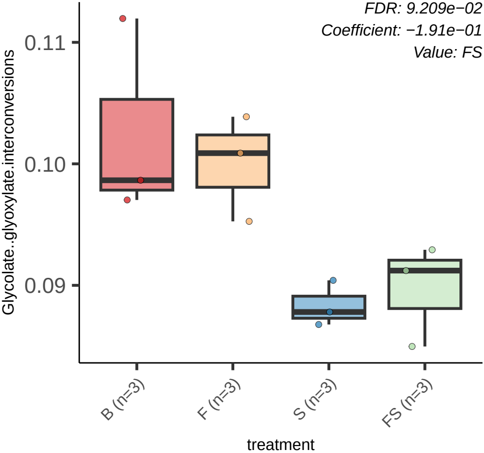

FDR: 9.183e−02
Coefficient: 1.39e−01
Value: FS
Mycobacterium.virulence.operon.involved.in.DNA.transcrip
0.24
0.23
0.22
0.21
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

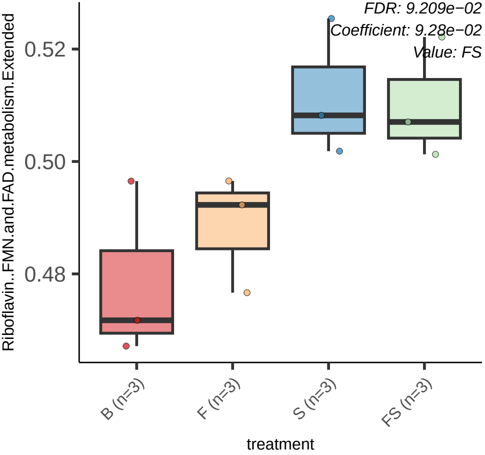

FDR: 9.191e−02
Coefficient: 7.83e−02
Value: F
At5g37530..CsdL.protein.family.
0.24
0.23
0.22
0.21
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

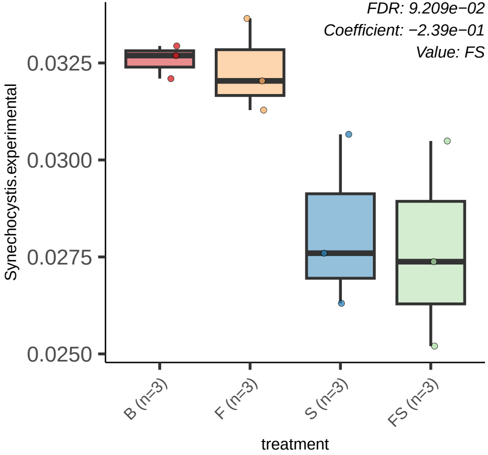

FDR: 9.191e−02
Coefficient: −8.70e−01
Value: S
Unsaturated.Fatty.Acid.Metabolism
0.0125
0.0100
0.0075
0.0050
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

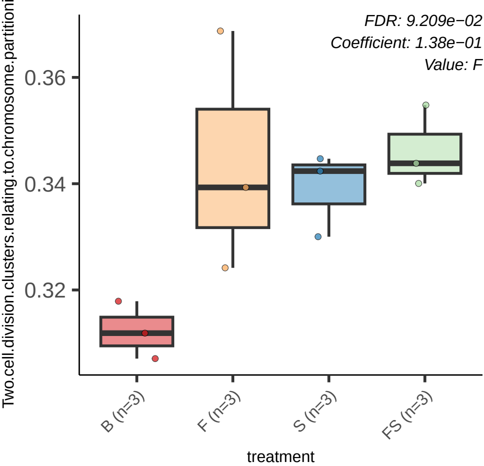

FDR: 9.209e−02
Coefficient: −3.18e−01
Value: S
Broadly.distributed.proteins.not.in.subsystems
0.060
0.055
0.050
0.045
0.040
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

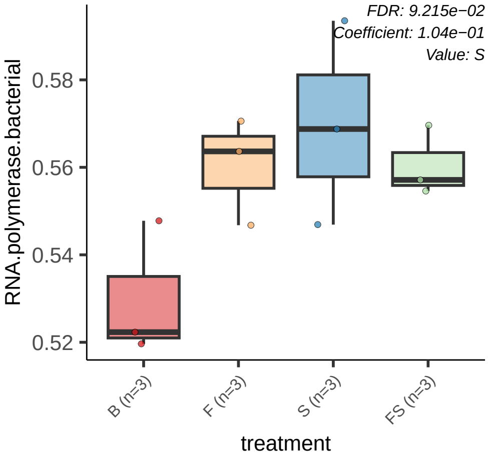

FDR: 9.209e−02
Coefficient: −4.07e−01
Value: S
Flagellum
0.14
0.12
0.10
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

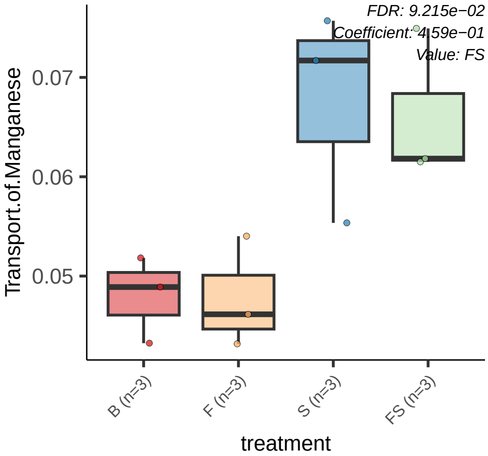

FDR: 9.209e−02
Coefficient: −1.91e−01
Value: FS
Glycolate..glyoxylate.interconversions
0.11
0.10
0.09
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

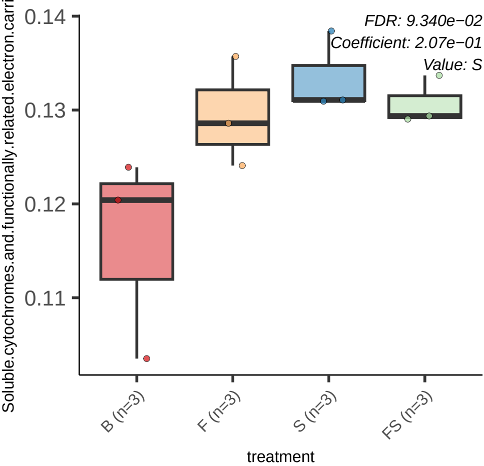

FDR: 9.209e−02
Coefficient: 9.28e−02
Value: FS
Riboflavin..FMN.and.FAD.metabolism.Extended
0.52
0.50
0.48
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

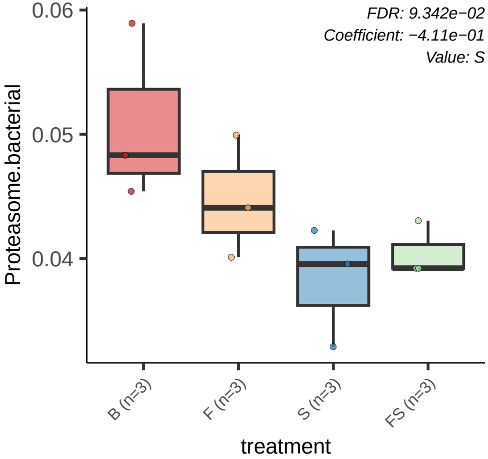

FDR: 9.209e−02
Coefficient: −2.39e−01
Value: FS
Synechocystis.experimental
0.0325
0.0300
0.0275
0.0250
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

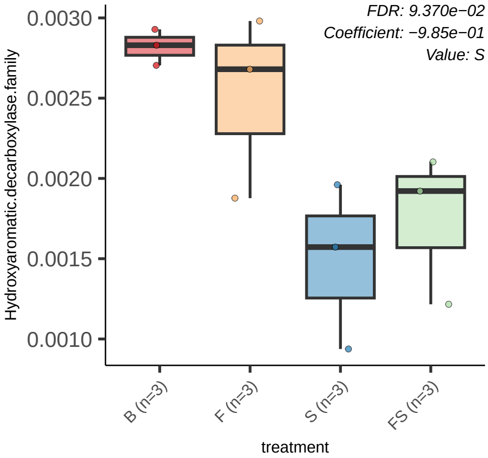

FDR: 9.209e−02
Coefficient: 1.38e−01
Value: F
Two.cell.division.clusters.relating.to.chromosome.partitioni
0.36
0.34
0.32
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

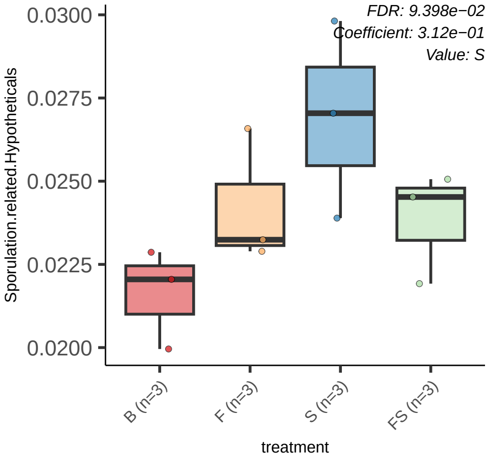

FDR: 9.215e−02
Coefficient: 1.04e−01
Value: S
RNA.polymerase.bacterial
0.58
0.56
0.54
0.52
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

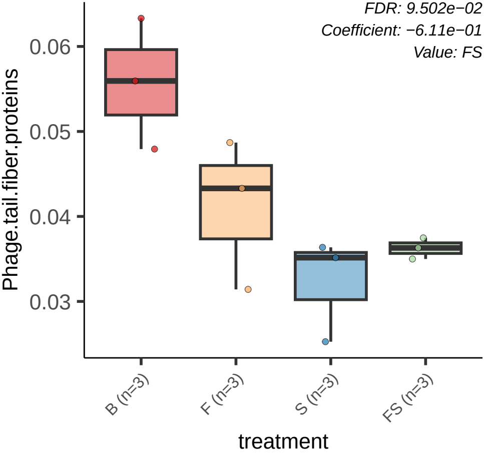

FDR: 9.215e−02
Coefficient: 4.59e−01
Value: FS
Transport.of.Manganese
0.07
0.06
0.05
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

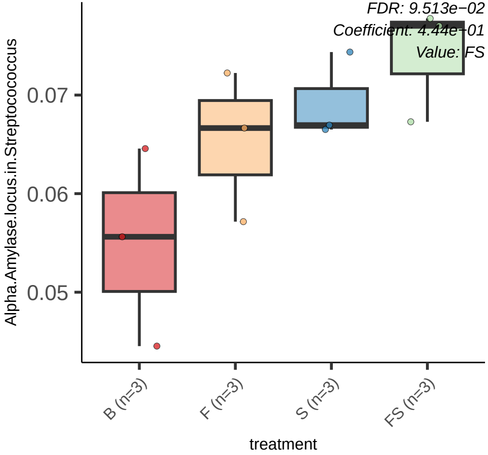

Soluble.cytochromes.and.functionally.related.electron.carri
0.14
0.13
0.12
0.11
FDR: 9.340e−02
Coefficient: 2.07e−01
Value: S
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

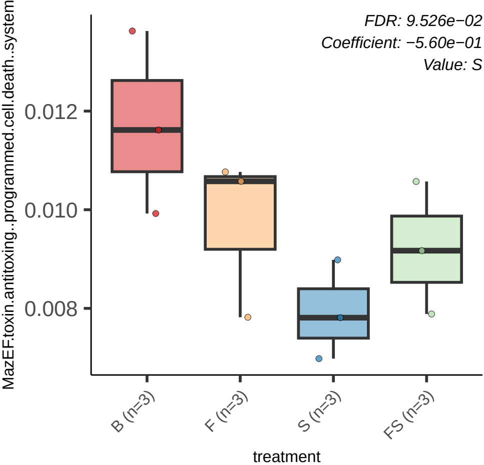

FDR: 9.342e−02
Coefficient: −4.11e−01
Value: S
0.06
0.05
0.04
Proteasome.bacterial
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

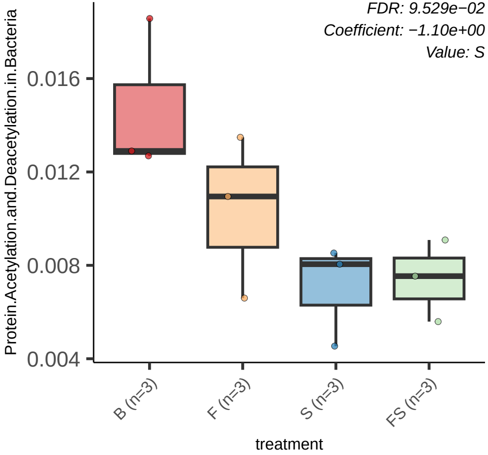

FDR: 9.370e−02
Coefficient: −9.85e−01
Value: S
Hydroxyaromatic.decarboxylase.family
0.0030
0.0025
0.0020
0.0015
0.0010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

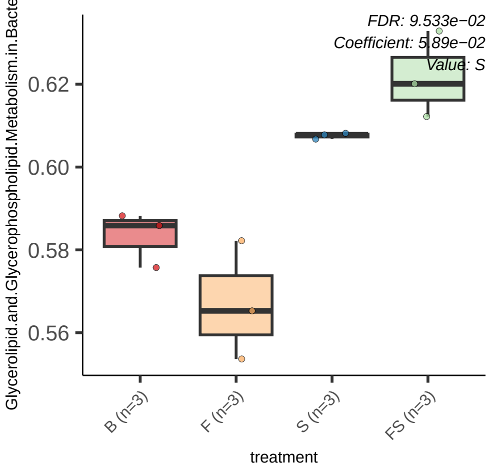

FDR: 9.398e−02
Coefficient: 3.12e−01
Value: S
Sporulation.related.Hypotheticals
0.0300
0.0275
0.0250
0.0225
0.0200
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

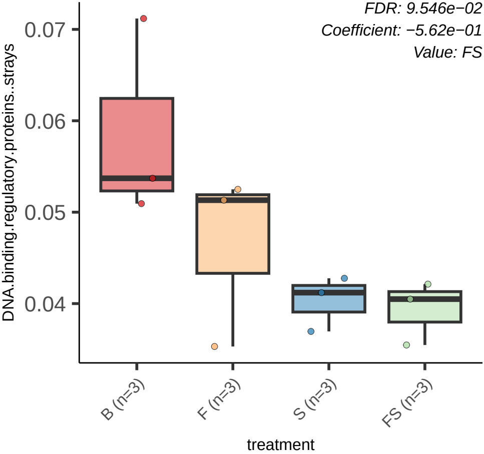

FDR: 9.502e−02
Coefficient: −6.11e−01
Value: FS
Phage.tail.fiber.proteins
0.06
0.05
0.04
0.03
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

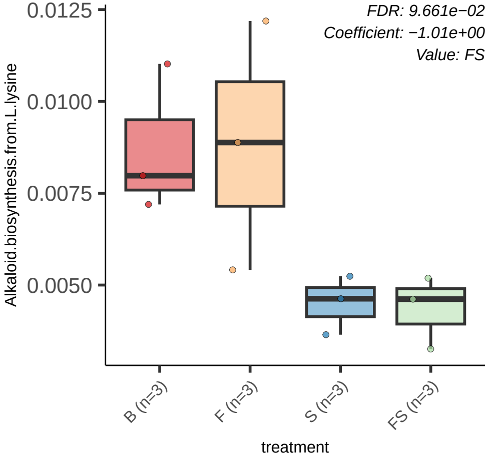

FDR: 9.513e−02
Coefficient: 4.44e−01
Value: FS
Alpha.Amylase.locus.in.Streptococcus
0.07
0.06
0.05
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

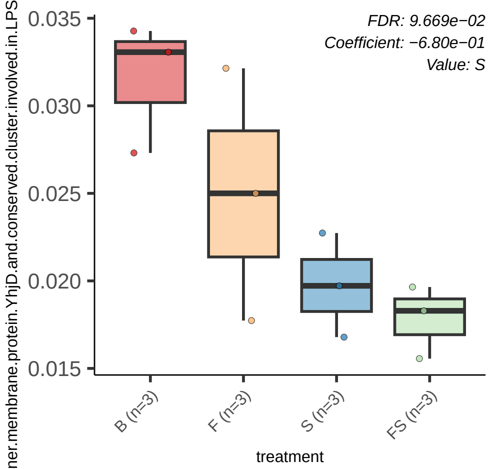

FDR: 9.526e−02
Coefficient: −5.60e−01
Value: S
MazEF.toxin.antitoxing..programmed.cell.death..system
0.012
0.010
0.008
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

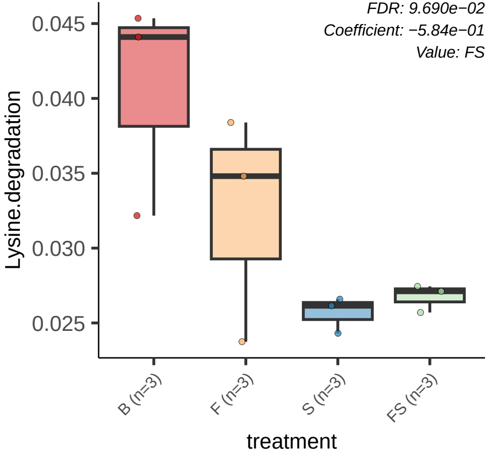

FDR: 9.529e−02
Coefficient: −1.10e+00
Value: S
Protein.Acetylation.and.Deacetylation.in.Bacteria
0.016
0.012
0.008
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

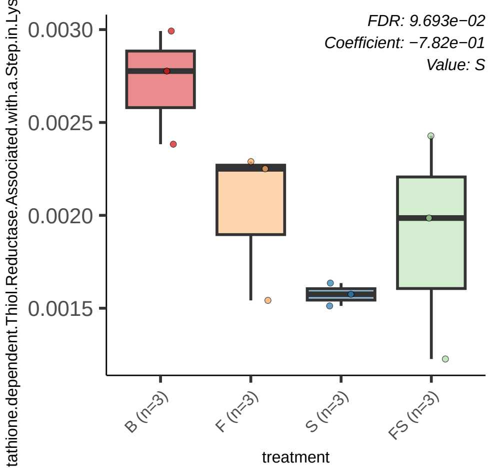

FDR: 9.533e−02
Coefficient: 5.89e−02
Value: S
Glycerolipid.and.Glycerophospholipid.Metabolism.in.Bacte
0.62
0.60
0.58
0.56
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

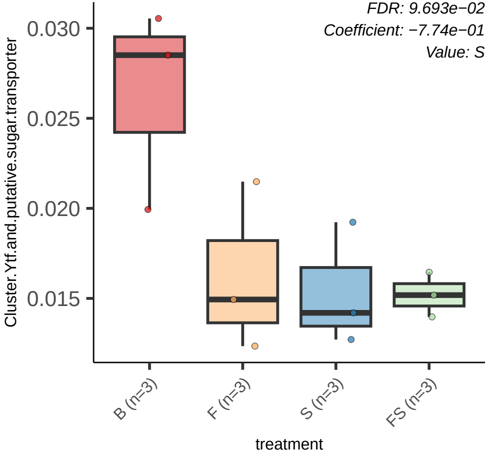

FDR: 9.546e−02
Coefficient: −5.62e−01
Value: FS
DNA.binding.regulatory.proteins..strays
0.07
0.06
0.05
0.04
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

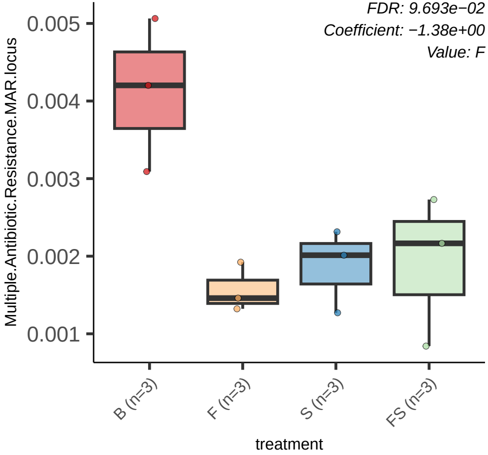

FDR: 9.661e−02
Coefficient: −1.01e+00
Value: FS
Alkaloid.biosynthesis.from.L.lysine
0.0125
0.0100
0.0075
0.0050
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

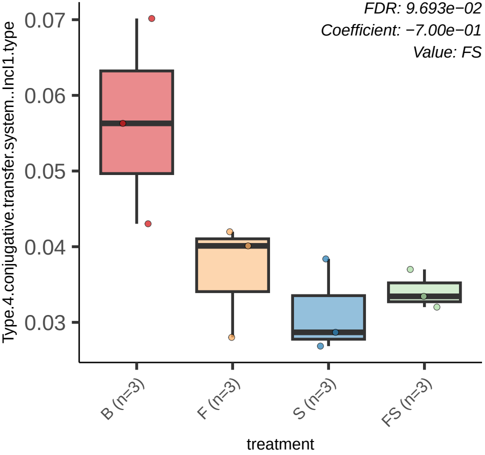

Inner.membrane.protein.YhjD.and.conserved.cluster.involved.in.LPS
0.035
0.030
0.025
0.020
0.015
FDR: 9.669e−02
Coefficient: −6.80e−01
Value: S
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

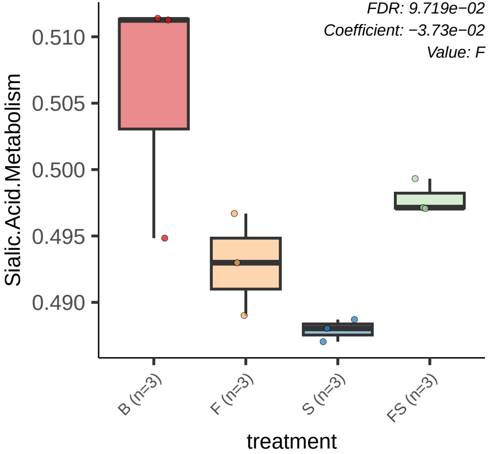

FDR: 9.690e−02
Coefficient: −5.84e−01
Value: FS
Lysine.degradation
0.045
0.040
0.035
0.030
0.025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

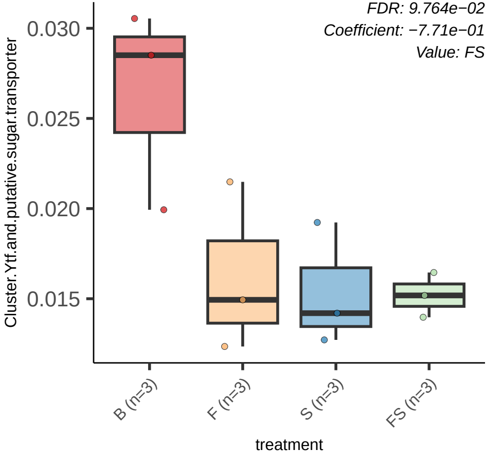

FDR: 9.693e−02
Coefficient: −7.82e−01
Value: S
lutathione.dependent.Thiol.Reductase.Associated.with.a.Step.in.Lys
0.0030
0.0025
0.0020
0.0015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

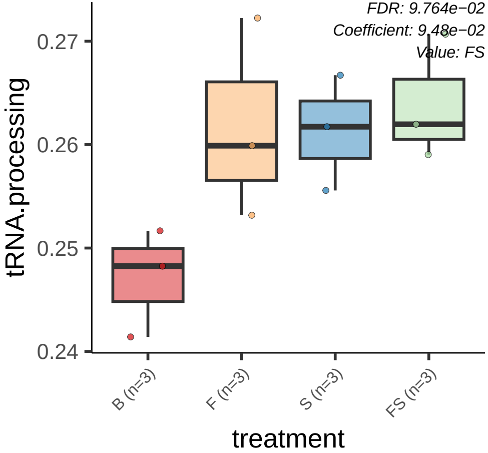

FDR: 9.693e−02
Coefficient: −7.74e−01
Value: S
Cluster.Ytf.and.putative.sugar.transporter
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

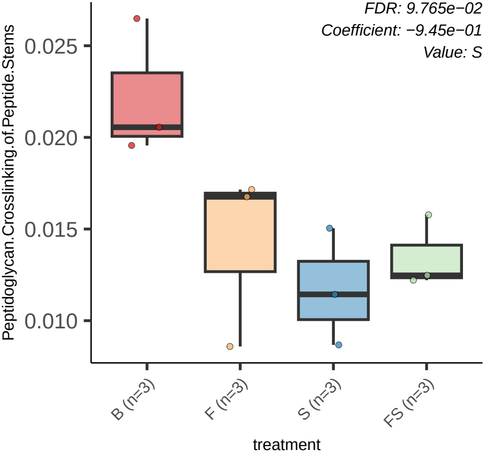

FDR: 9.693e−02
Coefficient: −1.38e+00
Value: F
Multiple.Antibiotic.Resistance.MAR.locus
0.005
0.004
0.003
0.002
0.001
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

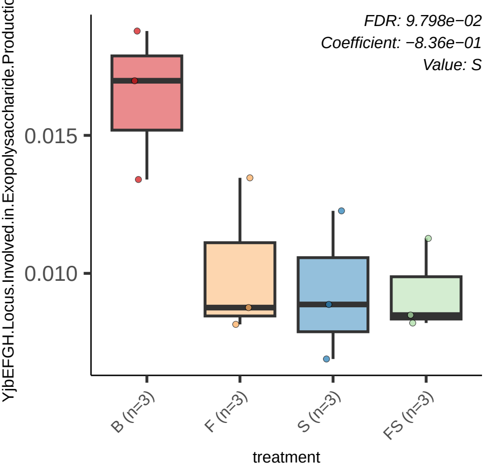

FDR: 9.693e−02
Coefficient: −7.00e−01
Value: FS
Type.4.conjugative.transfer.system..IncI1.type
0.07
0.06
0.05
0.04
0.03
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

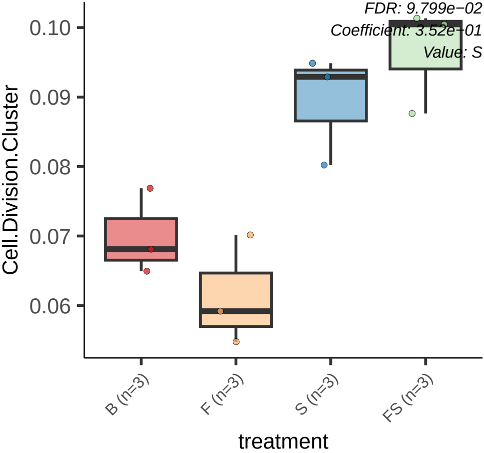

FDR: 9.719e−02
Coefficient: −3.73e−02
Value: F
Sialic.Acid.Metabolism
0.510
0.505
0.500
0.495
0.490
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

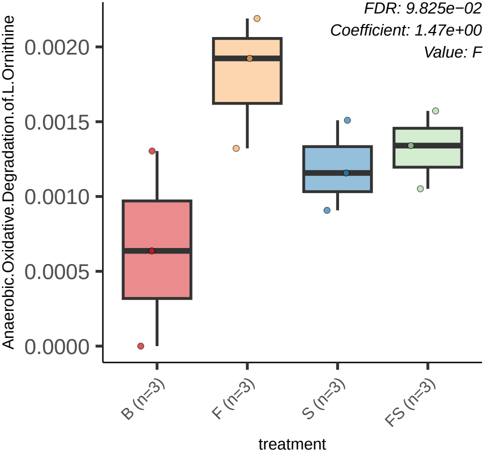

FDR: 9.764e−02
Coefficient: −7.71e−01
Value: FS
Cluster.Ytf.and.putative.sugar.transporter
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

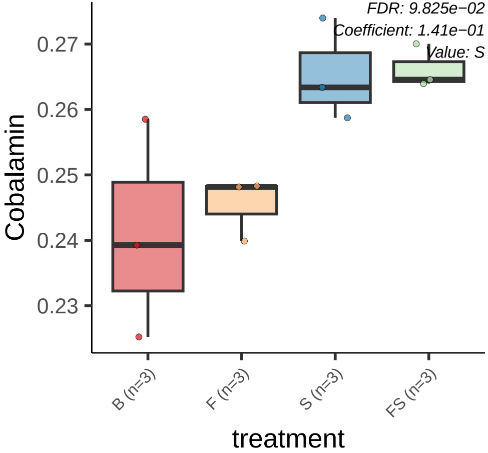

FDR: 9.764e−02
Coefficient: 9.48e−02
Value: FS
tRNA.processing
0.27
0.26
0.25
0.24
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

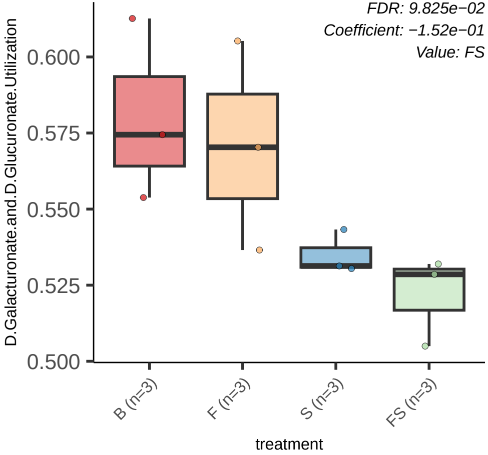

FDR: 9.765e−02
Coefficient: −9.45e−01
Value: S
Peptidoglycan.Crosslinking.of.Peptide.Stems
0.025
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

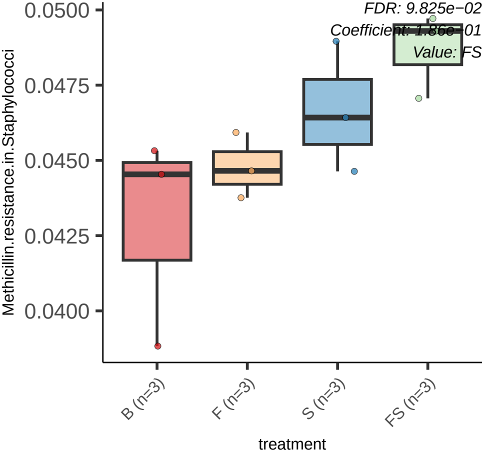

FDR: 9.798e−02
Coefficient: −8.36e−01
Value: S
YjbEFGH.Locus.Involved.in.Exopolysaccharide.Productio
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

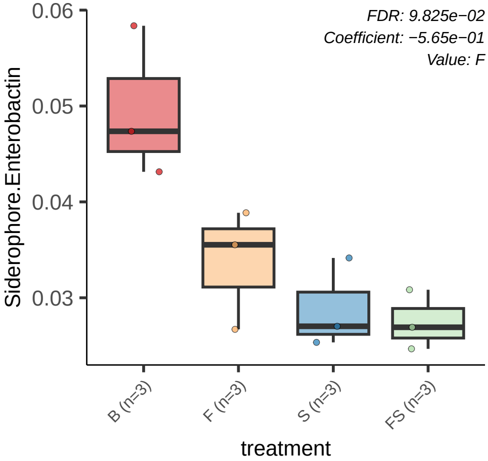

FDR: 9.799e−02
Coefficient: 3.52e−01
Value: S
Cell.Division.Cluster
0.10
0.09
0.08
0.07
0.06
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

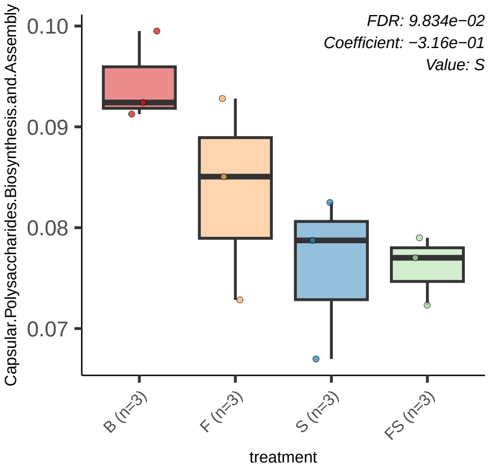

FDR: 9.825e−02
Coefficient: 1.47e+00
Value: F
Anaerobic.Oxidative.Degradation.of.L.Ornithine
0.0020
0.0015
0.0010
0.0005
0.0000
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

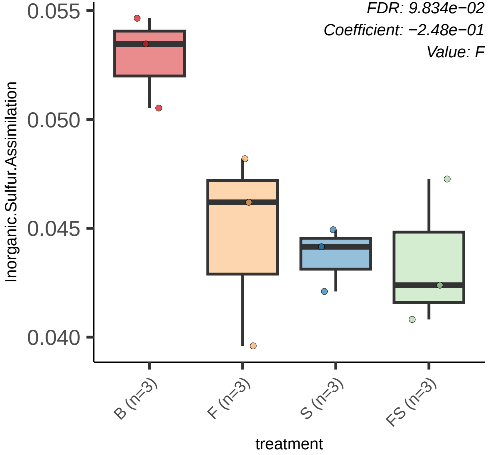

FDR: 9.825e−02
Coefficient: 1.41e−01
Value: S
Cobalamin
0.27
0.26
0.25
0.24
0.23
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

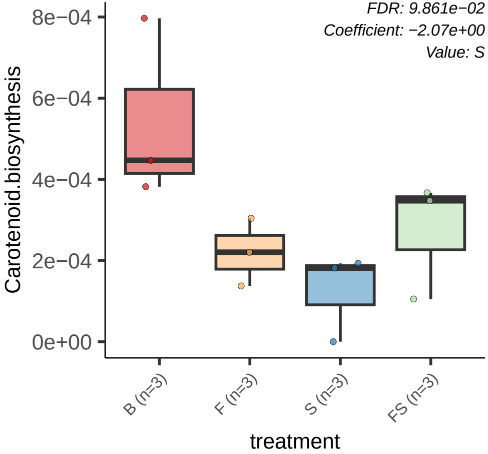

FDR: 9.825e−02
Coefficient: −1.52e−01
Value: FS
D.Galacturonate.and.D.Glucuronate.Utilization
0.600
0.575
0.550
0.525
0.500
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

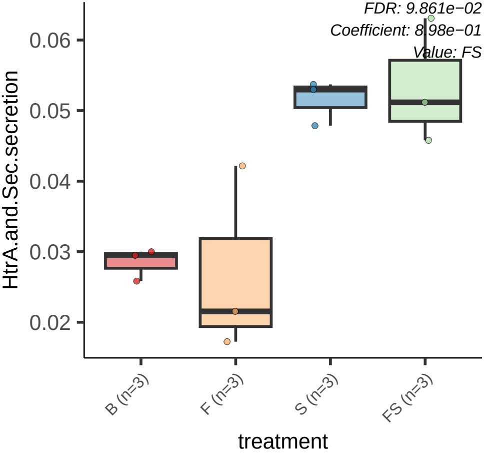

FDR: 9.825e−02
Coefficient: 1.86e−01
Value: FS
Methicillin.resistance.in.Staphylococci
0.0500
0.0475
0.0450
0.0425
0.0400
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

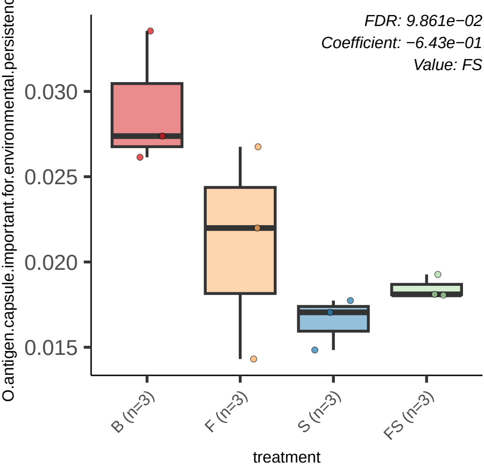

FDR: 9.825e−02
Coefficient: −5.65e−01
Value: F
Siderophore.Enterobactin
0.06
0.05
0.04
0.03
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

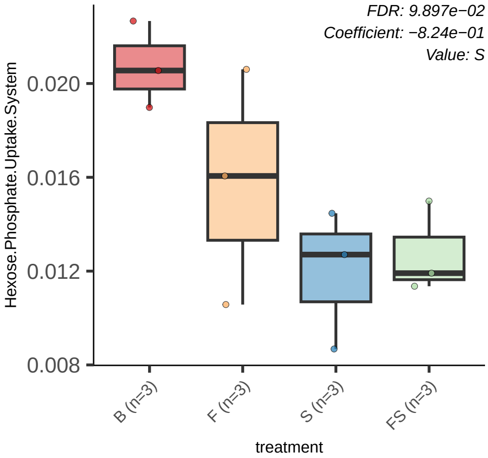

FDR: 9.834e−02
Coefficient: −3.16e−01
Value: S
Capsular.Polysaccharides.Biosynthesis.and.Assembly
0.10
0.09
0.08
0.07
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

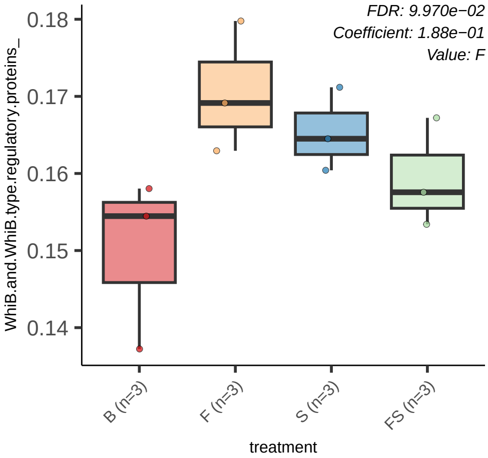

FDR: 9.834e−02
Coefficient: −2.48e−01
Value: F
Inorganic.Sulfur.Assimilation
0.055
0.050
0.045
0.040
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

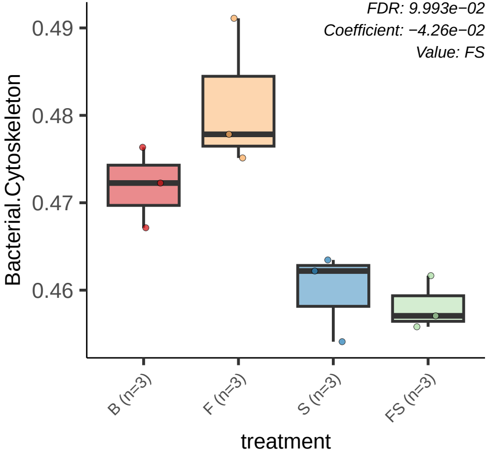

FDR: 9.861e−02
Coefficient: −2.07e+00
Value: S
Carotenoid.biosynthesis
8e−04
6e−04
4e−04
2e−04
0e+00
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

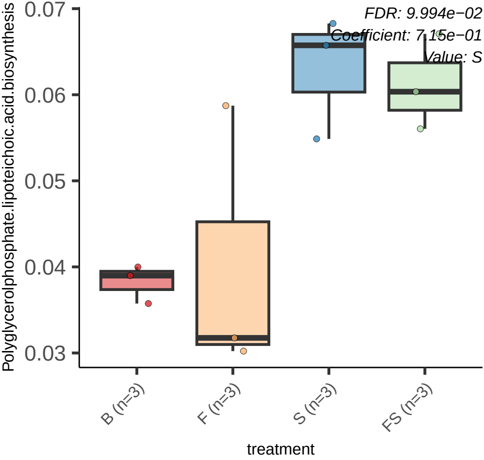

FDR: 9.861e−02
Coefficient: 8.98e−01
Value: FS
HtrA.and.Sec.secretion
0.06
0.05
0.04
0.03
0.02
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

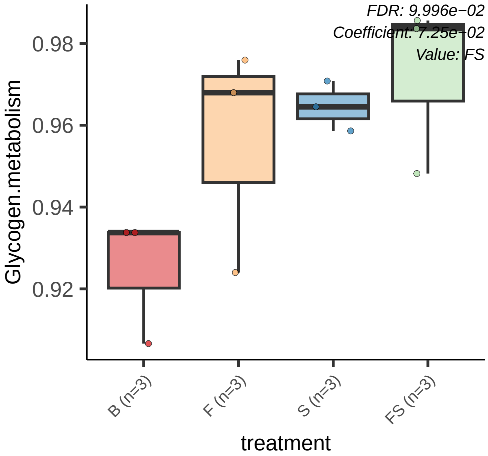

FDR: 9.861e−02
Coefficient: −6.43e−01
Value: FS
O.antigen.capsule.important.for.environmental.persistenc
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

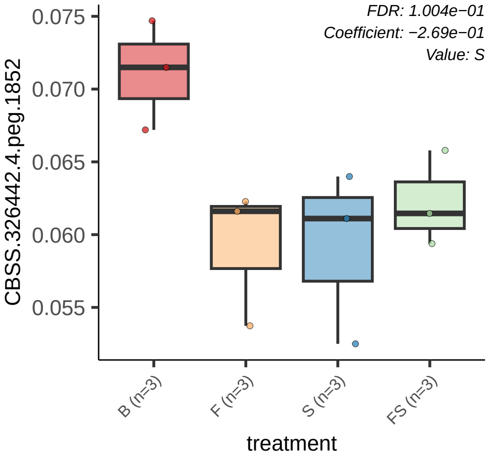

FDR: 9.897e−02
Coefficient: −8.24e−01
Value: S
Hexose.Phosphate.Uptake.System
0.020
0.016
0.012
0.008
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

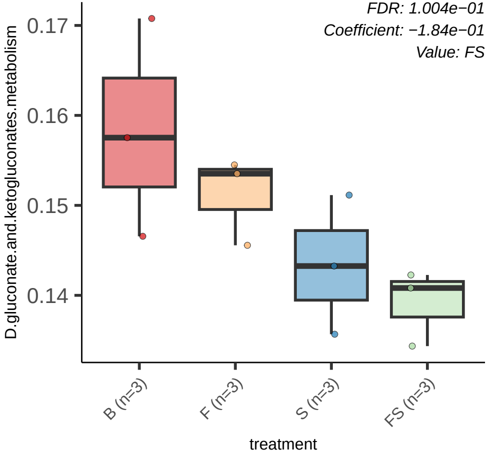

FDR: 9.970e−02
Coefficient: 1.88e−01
Value: F
WhiB.and.WhiB.type.regulatory.proteins_
0.18
0.17
0.16
0.15
0.14
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

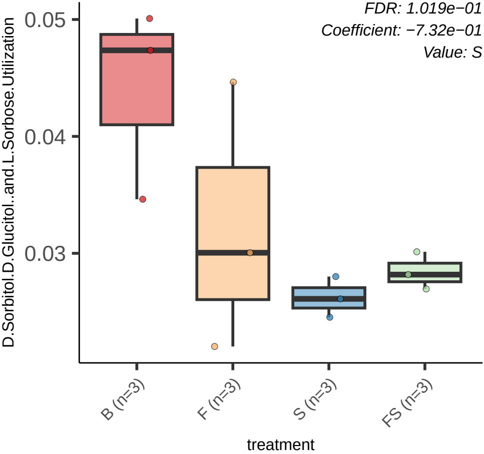

FDR: 9.993e−02
Coefficient: −4.26e−02
Value: FS
Bacterial.Cytoskeleton
0.49
0.48
0.47
0.46
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

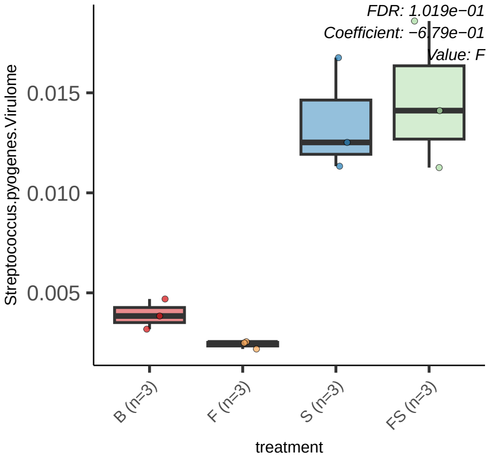

FDR: 9.994e−02
Coefficient: 7.15e−01
Value: S
Polyglycerolphosphate.lipoteichoic.acid.biosynthesis
0.07
0.06
0.05
0.04
0.03
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

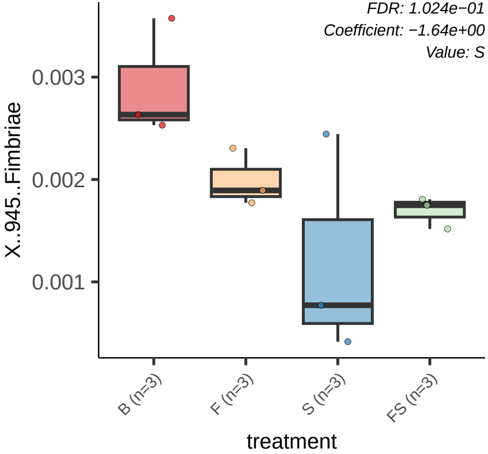

FDR: 9.996e−02
Coefficient: 7.25e−02
Value: FS
Glycogen.metabolism
0.98
0.96
0.94
0.92
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

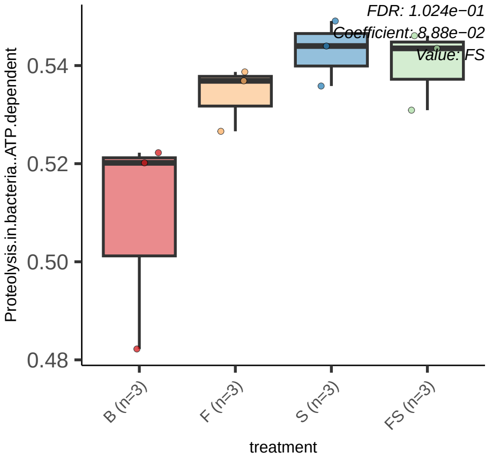

FDR: 1.004e−01
Coefficient: −2.69e−01
Value: S
CBSS.326442.4.peg.1852
0.075
0.070
0.065
0.060
0.055
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

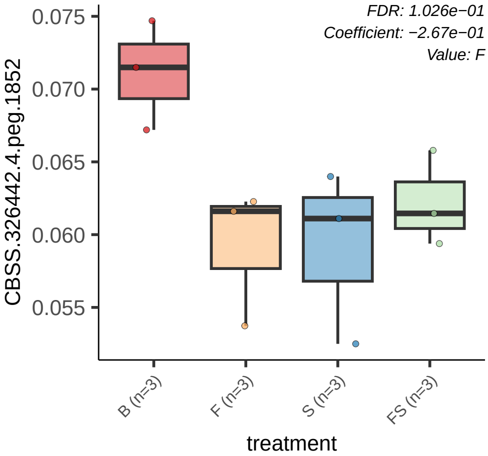

FDR: 1.004e−01
Coefficient: −1.84e−01
Value: FS
D.gluconate.and.ketogluconates.metabolism
0.17
0.16
0.15
0.14
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

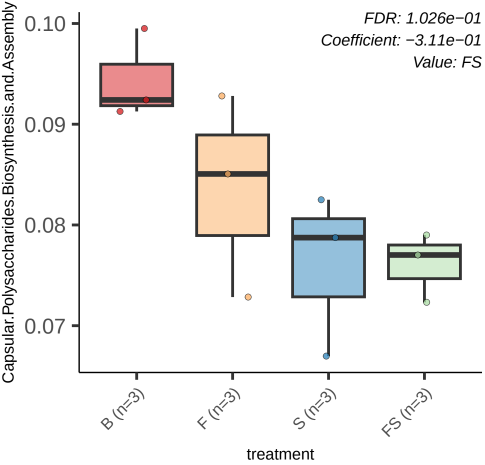

FDR: 1.019e−01
Coefficient: −7.32e−01
Value: S
D.Sorbitol.D.Glucitol..and.L.Sorbose.Utilization
0.05
0.04
0.03
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

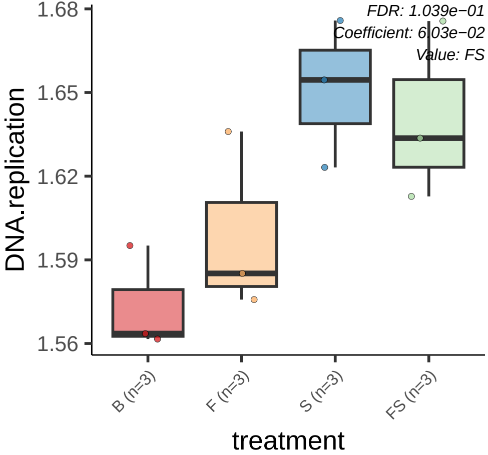

FDR: 1.019e−01
Coefficient: −6.79e−01
Value: F
Streptococcus.pyogenes.Virulome
0.015
0.010
0.005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

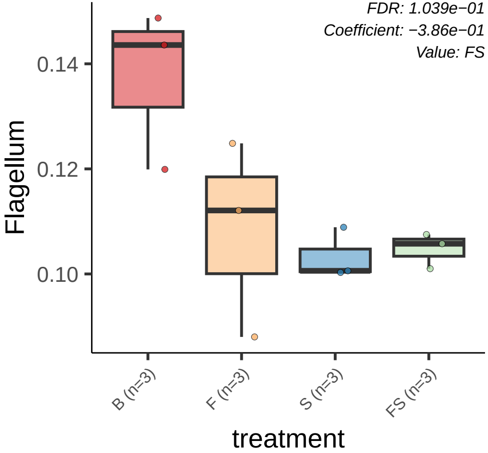

FDR: 1.024e−01
Coefficient: −1.64e+00
Value: S
X..945..Fimbriae
0.003
0.002
0.001
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

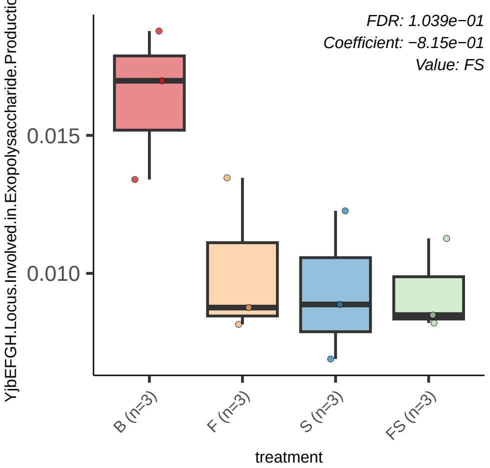

FDR: 1.024e−01
Coefficient: 8.88e−02
Value: FS
Proteolysis.in.bacteria..ATP.dependent
0.54
0.52
0.50
0.48
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

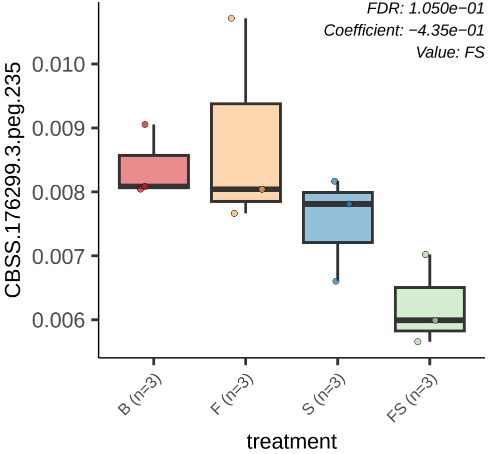

FDR: 1.026e−01
Coefficient: −2.67e−01
Value: F
CBSS.326442.4.peg.1852
0.075
0.070
0.065
0.060
0.055
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

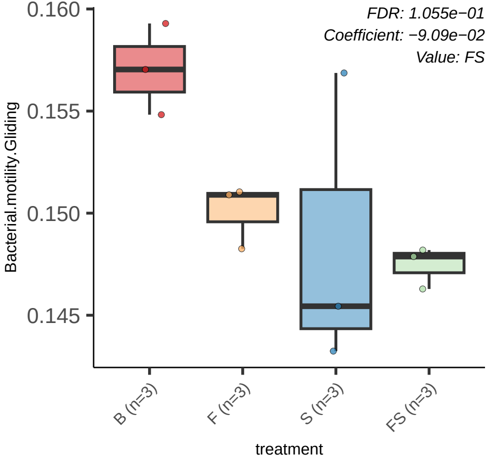

FDR: 1.026e−01
Coefficient: −3.11e−01
Value: FS
Capsular.Polysaccharides.Biosynthesis.and.Assembly
0.10
0.09
0.08
0.07
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

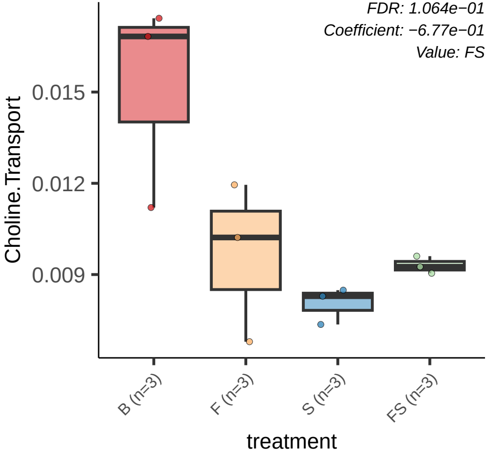

FDR: 1.039e−01
Coefficient: 6.03e−02
Value: FS
DNA.replication
1.68
1.65
1.62
1.59
1.56
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

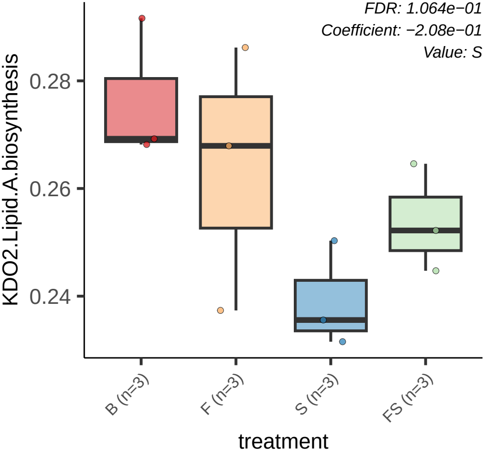

FDR: 1.039e−01
Coefficient: −3.86e−01
Value: FS
Flagellum
0.14
0.12
0.10
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

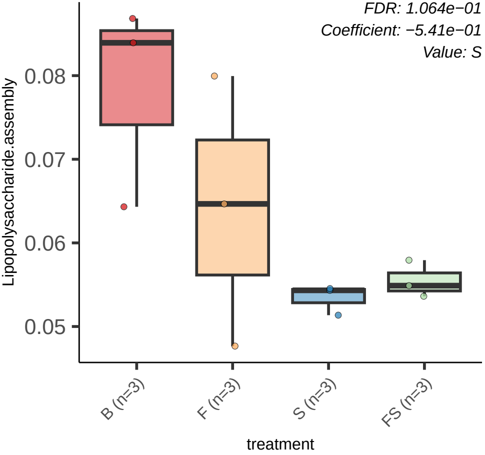

FDR: 1.039e−01
Coefficient: −8.15e−01
Value: FS
YjbEFGH.Locus.Involved.in.Exopolysaccharide.Productio
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

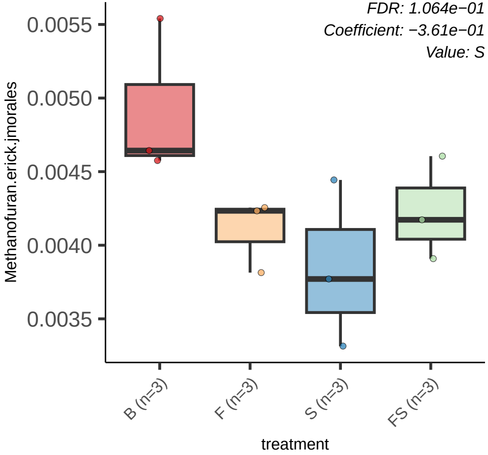

FDR: 1.050e−01
Coefficient: −4.35e−01
Value: FS
CBSS.176299.3.peg.235
0.010
0.009
0.008
0.007
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

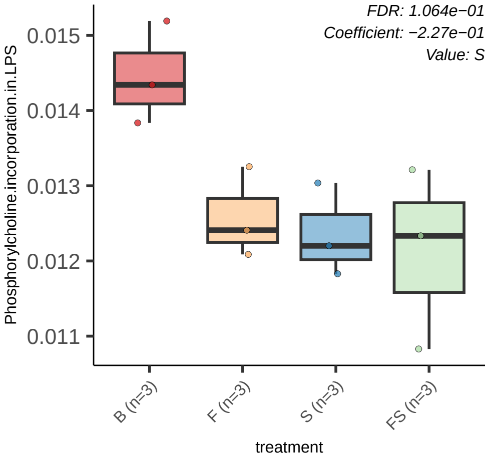

FDR: 1.055e−01
Coefficient: −9.09e−02
Value: FS
Bacterial.motility.Gliding
0.160
0.155
0.150
0.145
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

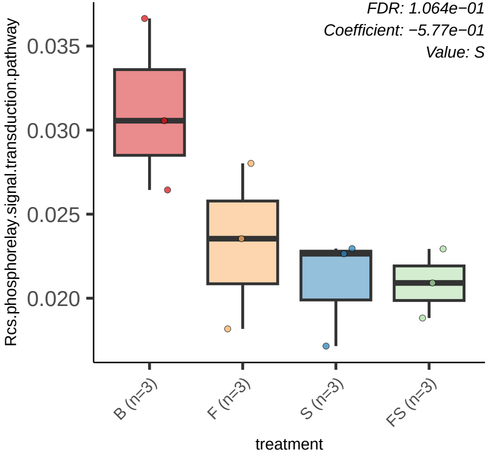

FDR: 1.064e−01
Coefficient: −6.77e−01
Value: FS
Choline.Transport
0.015
0.012
0.009
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

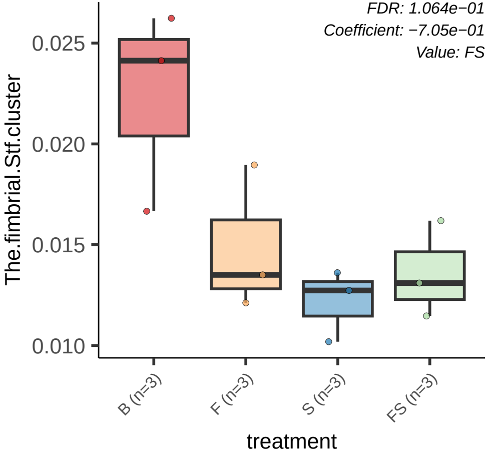

FDR: 1.064e−01
Coefficient: −2.08e−01
Value: S
KDO2.Lipid.A.biosynthesis
0.28
0.26
0.24
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

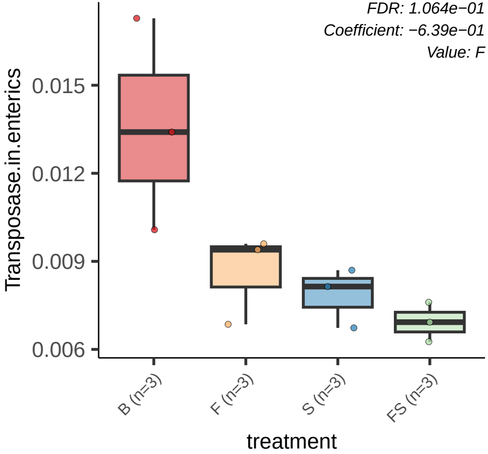

FDR: 1.064e−01
Coefficient: −5.41e−01
Value: S
Lipopolysaccharide.assembly
0.08
0.07
0.06
0.05
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

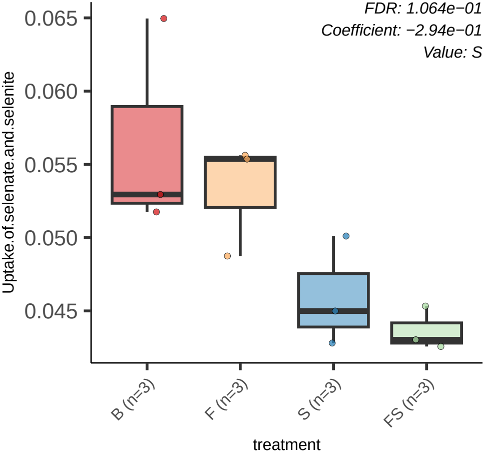

FDR: 1.064e−01
Coefficient: −3.61e−01
Value: S
Methanofuran.erick.jmorales
0.0055
0.0050
0.0045
0.0040
0.0035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

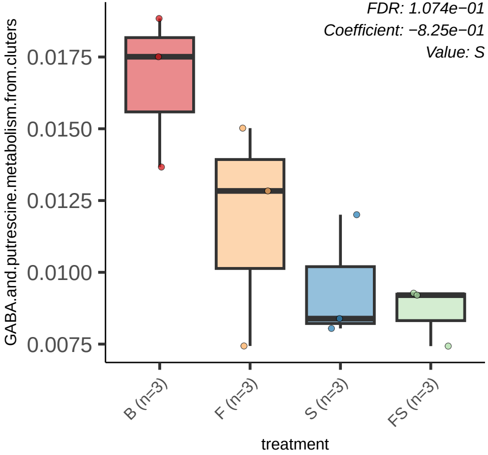

FDR: 1.064e−01
Coefficient: −2.27e−01
Value: S
Phosphorylcholine.incorporation.in.LPS
0.015
0.014
0.013
0.012
0.011
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

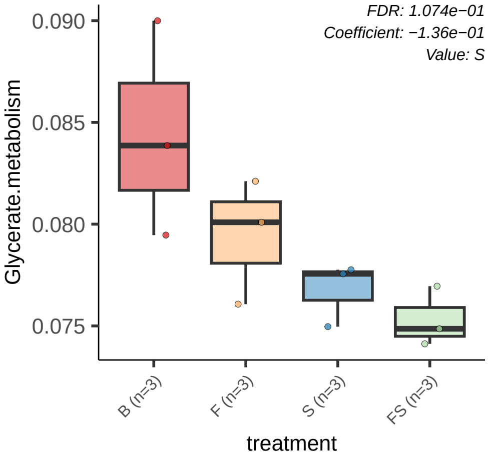

FDR: 1.064e−01
Coefficient: −5.77e−01
Value: S
Rcs.phosphorelay.signal.transduction.pathway
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

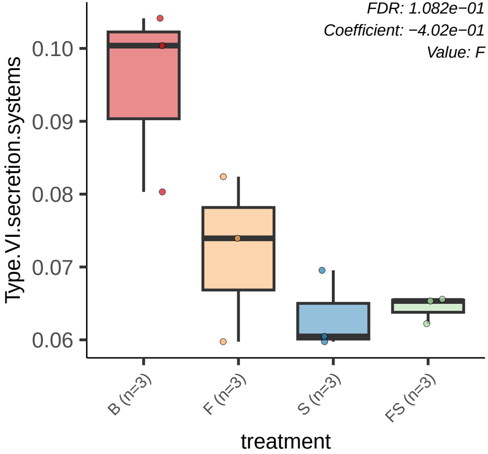

FDR: 1.064e−01
Coefficient: −7.05e−01
Value: FS
The.fimbrial.Stf.cluster
0.025
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

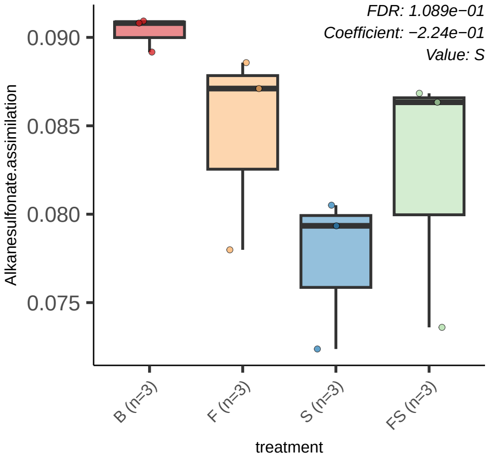

FDR: 1.064e−01
Coefficient: −6.39e−01
Value: F
Transposase.in.enterics
0.015
0.012
0.009
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

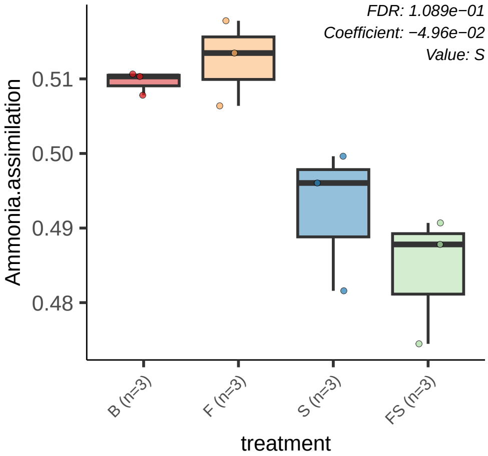

FDR: 1.064e−01
Coefficient: −2.94e−01
Value: S
Uptake.of.selenate.and.selenite
0.065
0.060
0.055
0.050
0.045
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

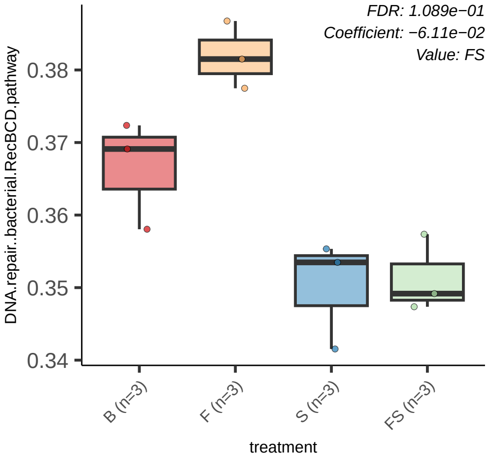

FDR: 1.074e−01
Coefficient: −8.25e−01
Value: S
GABA.and.putrescine.metabolism.from.cluters
0.0175
0.0150
0.0125
0.0100
0.0075
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

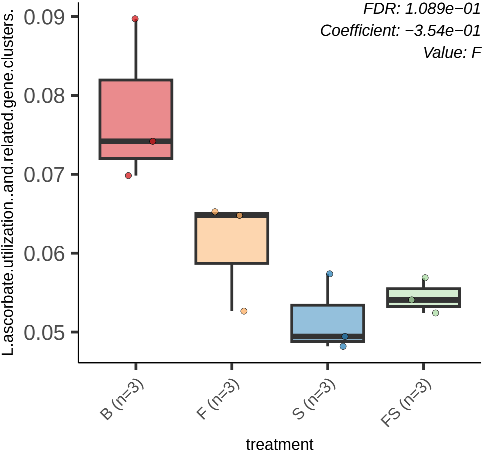

FDR: 1.074e−01
Coefficient: −1.36e−01
Value: S
Glycerate.metabolism
0.090
0.085
0.080
0.075
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

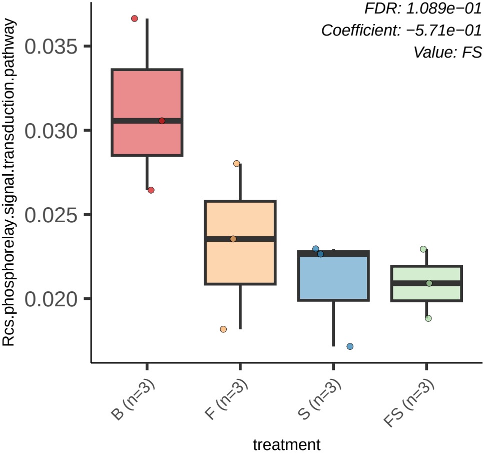

FDR: 1.082e−01
Coefficient: −4.02e−01
Value: F
Type.VI.secretion.systems
0.10
0.09
0.08
0.07
0.06
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

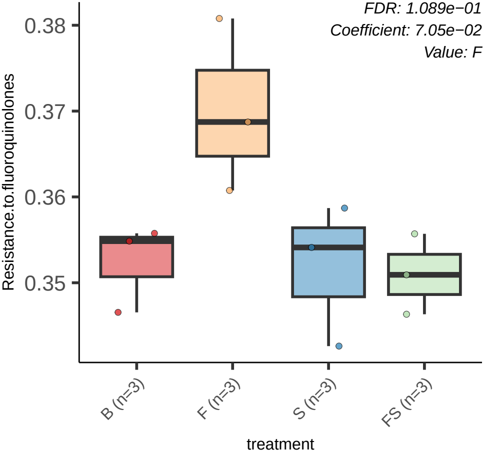

FDR: 1.089e−01
Coefficient: −2.24e−01
Value: S
Alkanesulfonate.assimilation
0.090
0.085
0.080
0.075
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

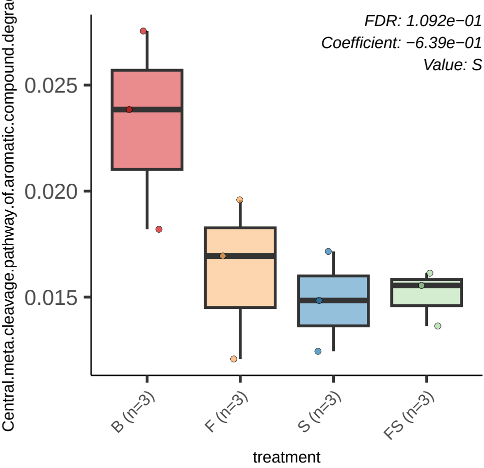

FDR: 1.089e−01
Coefficient: −4.96e−02
Value: S
Ammonia.assimilation
0.51
0.50
0.49
0.48
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

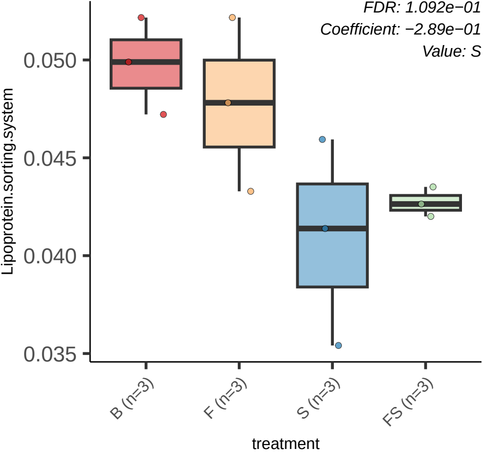

FDR: 1.089e−01
Coefficient: −6.11e−02
Value: FS
DNA.repair..bacterial.RecBCD.pathway
0.38
0.37
0.36
0.35
0.34
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

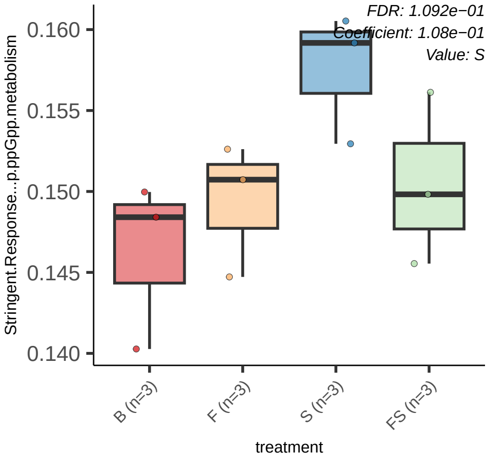

FDR: 1.089e−01
Coefficient: −3.54e−01
Value: F
L.ascorbate.utilization..and.related.gene.clusters.
0.09
0.08
0.07
0.06
0.05
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

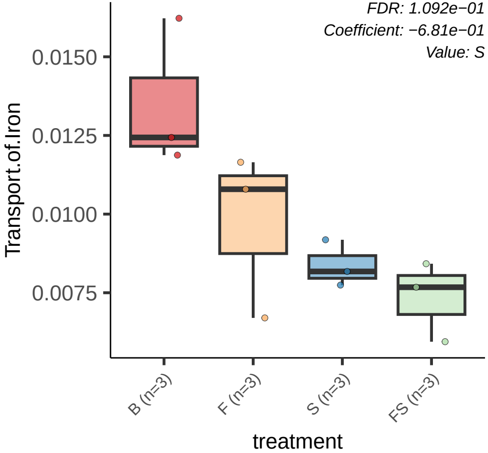

FDR: 1.089e−01
Coefficient: −5.71e−01
Value: FS
Rcs.phosphorelay.signal.transduction.pathway
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

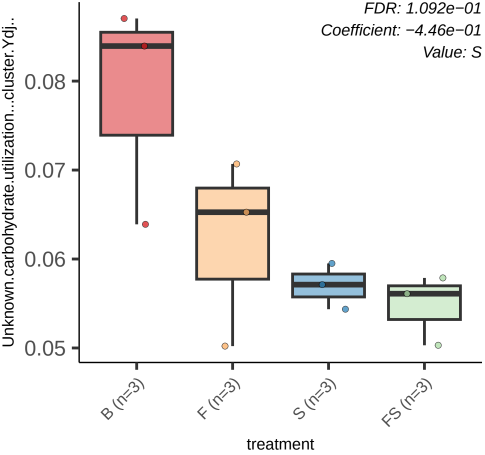

FDR: 1.089e−01
Coefficient: 7.05e−02
Value: F
Resistance.to.fluoroquinolones
0.38
0.37
0.36
0.35
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 1.092e−01
Coefficient: −6.39e−01
Value: S
Central.meta.cleavage.pathway.of.aromatic.compound.degra
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

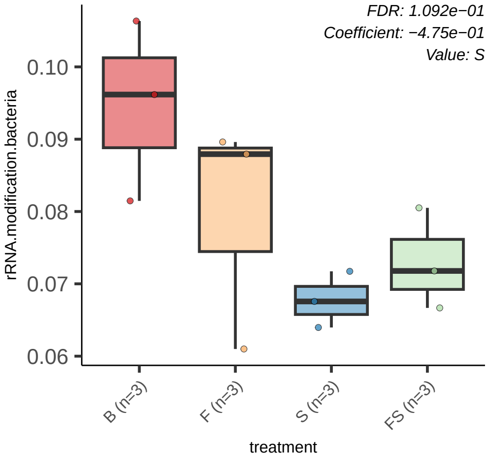

FDR: 1.092e−01
Coefficient: −2.89e−01
Value: S
Lipoprotein.sorting.system
0.050
0.045
0.040
0.035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

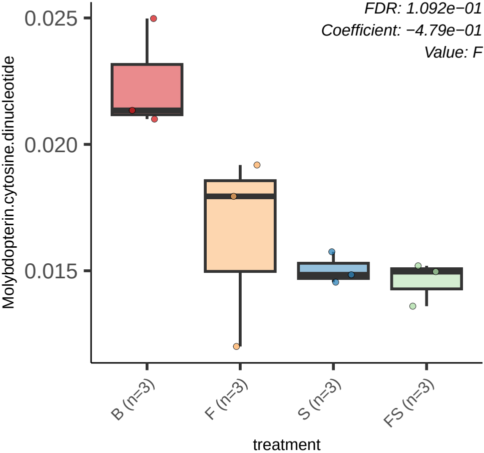

FDR: 1.092e−01
Coefficient: 1.08e−01
Value: S
Stringent.Response...p.ppGpp.metabolism
0.160
0.155
0.150
0.145
0.140
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

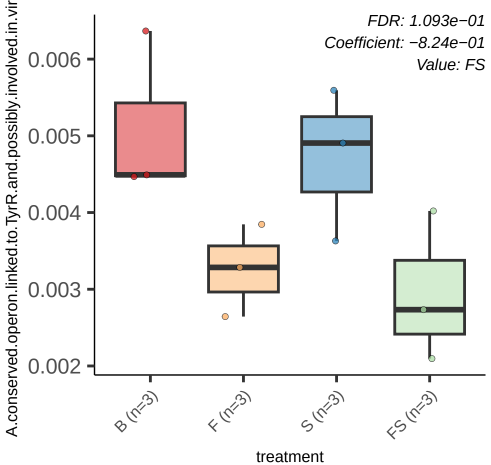

FDR: 1.092e−01
Coefficient: −6.81e−01
Value: S
Transport.of.Iron
0.0150
0.0125
0.0100
0.0075
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

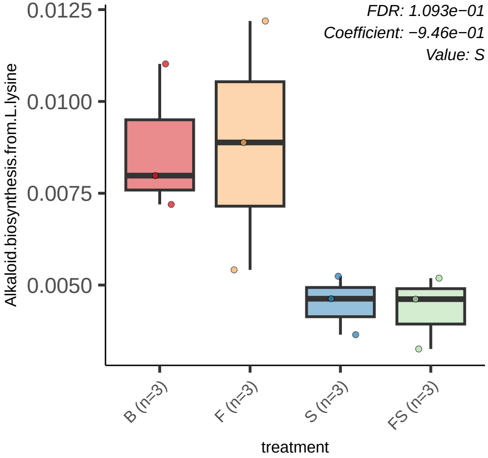


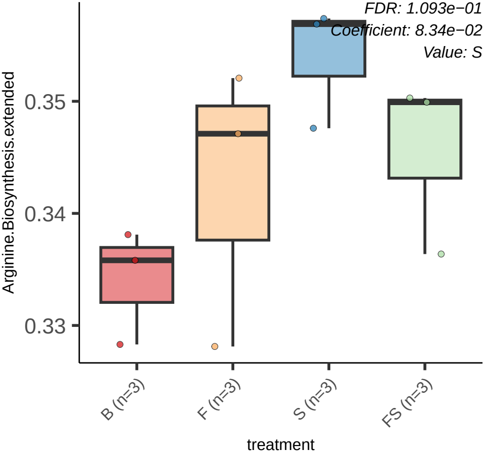
FDR: 1.092e−01
Coefficient: −4.46e−01
Value: S
Unknown.carbohydrate.utilization..cluster.Ydj..
0.08
0.07
0.06
0.05
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

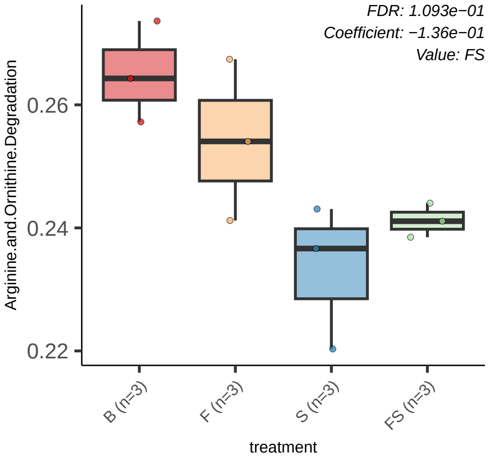

FDR: 1.092e−01
Coefficient: −4.75e−01
Value: S
rRNA.modification.bacteria
0.10
0.09
0.08
0.07
0.06
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

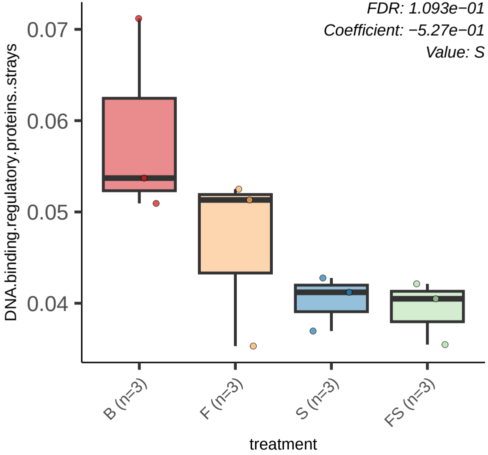

FDR: 1.092e−01
Coefficient: −4.79e−01
Value: F
Molybdopterin.cytosine.dinucleotide
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

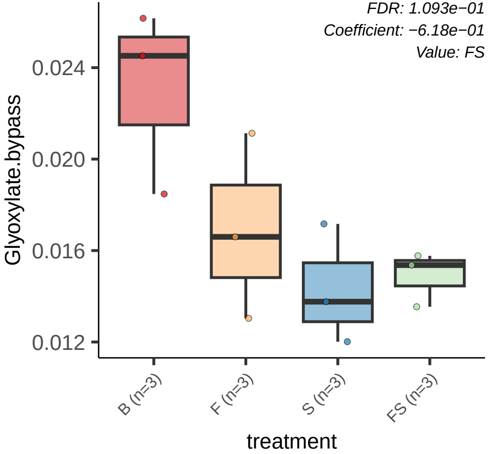

FDR: 1.093e−01
Coefficient: −8.24e−01
Value: FS
A.conserved.operon.linked.to.TyrR.and.possibly.involved.in.vir
0.006
0.005
0.004
0.003
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

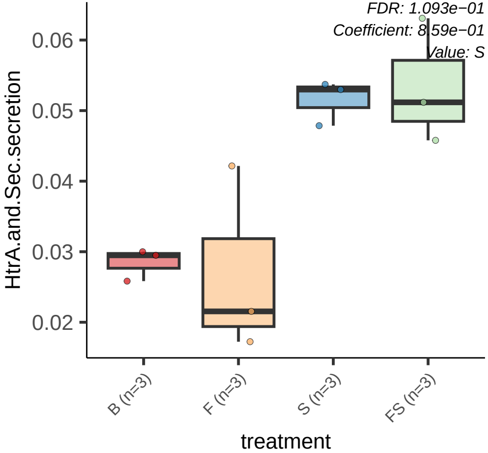

FDR: 1.093e−01
Coefficient: −9.46e−01
Value: S
Alkaloid.biosynthesis.from.L.lysine
0.0125
0.0100
0.0075
0.0050
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

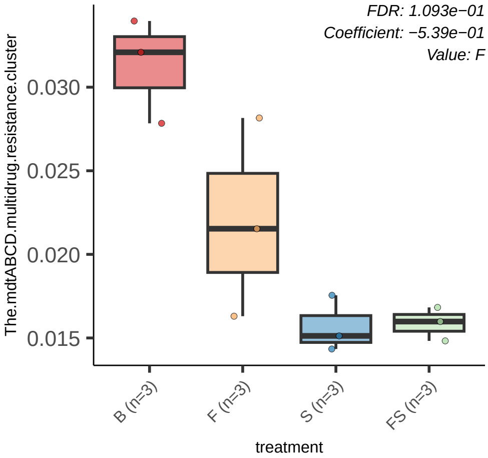

FDR: 1.093e−01
Coefficient: 8.34e−02
Value: S
Arginine.Biosynthesis.extended
0.35
0.34
0.33
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

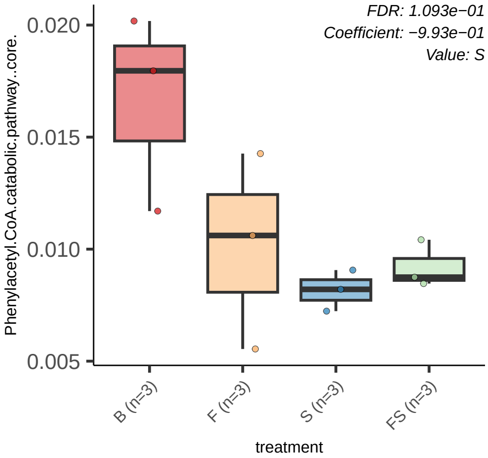

FDR: 1.093e−01
Coefficient: −1.36e−01
Value: FS
Arginine.and.Ornithine.Degradation
0.26
0.24
0.22
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

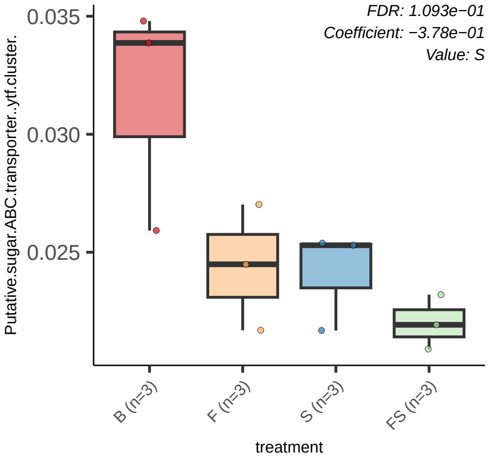

FDR: 1.093e−01
Coefficient: −5.27e−01
Value: S
DNA.binding.regulatory.proteins..strays
0.07
0.06
0.05
0.04
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

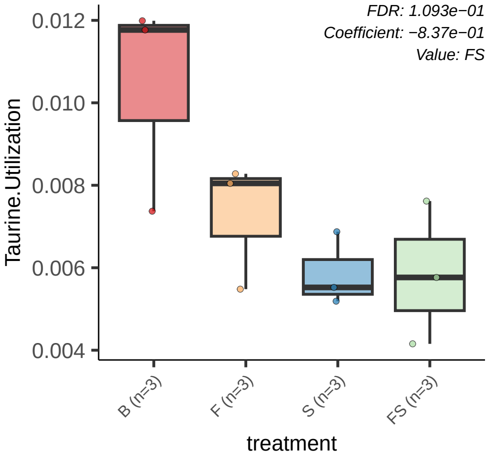

FDR: 1.093e−01
Coefficient: −6.18e−01
Value: FS
Glyoxylate.bypass
0.024
0.020
0.016
0.012
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

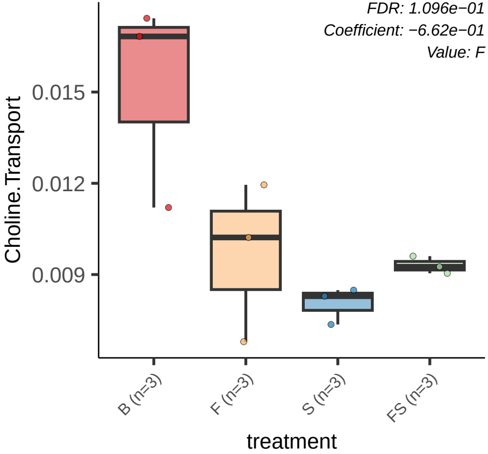

FDR: 1.093e−01
Coefficient: 8.59e−01
Value: S
HtrA.and.Sec.secretion
0.06
0.05
0.04
0.03
0.02
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

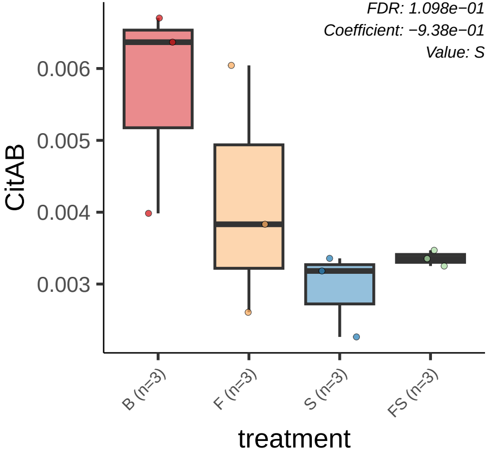

FDR: 1.093e−01
Coefficient: −5.39e−01
Value: F
The.mdtABCD.multidrug.resistance.cluster
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

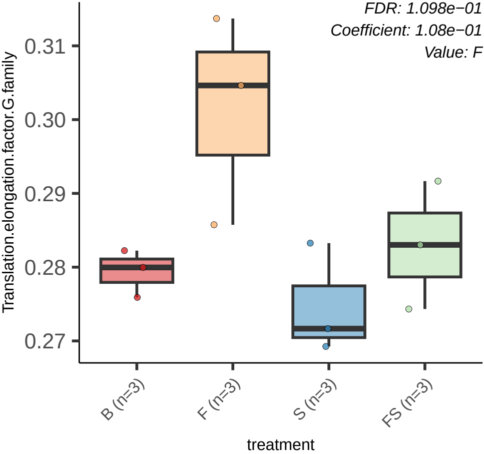

FDR: 1.093e−01
Coefficient: −9.93e−01
Value: S
Phenylacetyl.CoA.catabolic.pathway..core.
0.020
0.015
0.010
0.005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

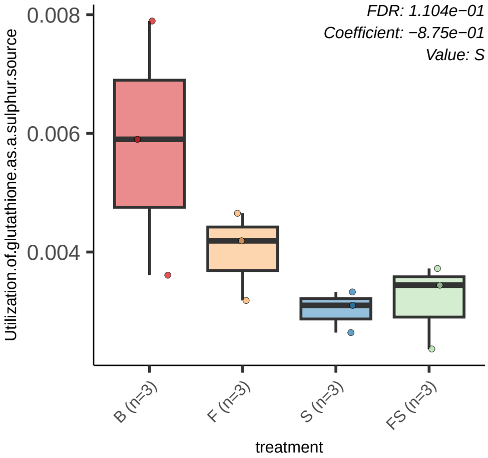

FDR: 1.093e−01
Coefficient: −3.78e−01
Value: S
Putative.sugar.ABC.transporter..ytf.cluster.
0.035
0.030
0.025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

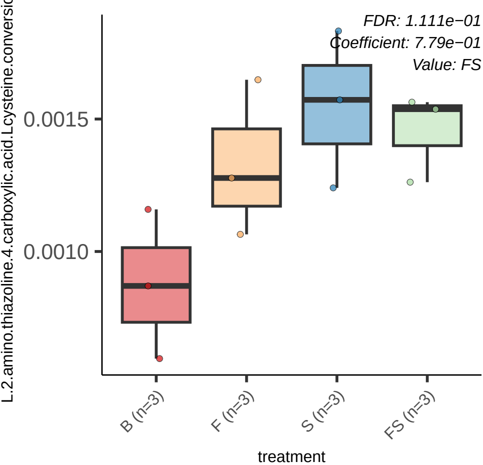

FDR: 1.093e−01
Coefficient: −8.37e−01
Value: FS
Taurine.Utilization
0.012
0.010
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

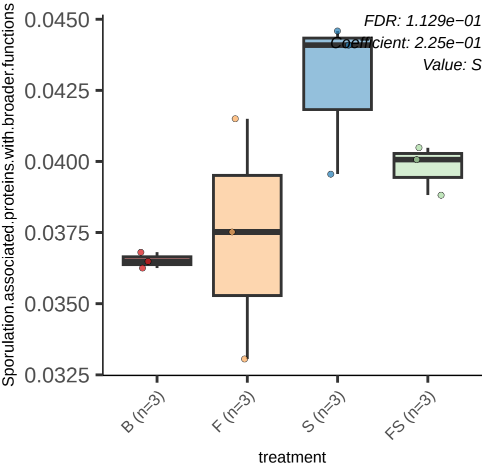

FDR: 1.096e−01
Coefficient: −6.62e−01
Value: F
Choline.Transport
0.015
0.012
0.009
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

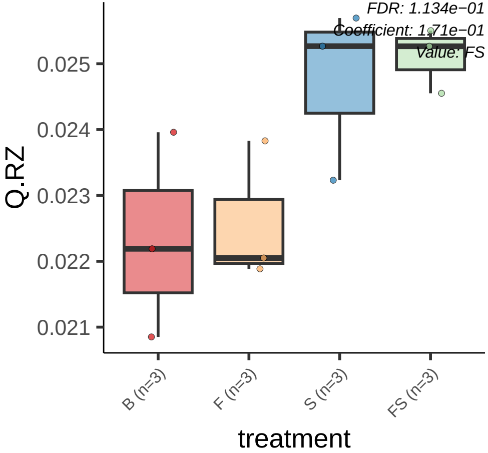

FDR: 1.098e−01
Coefficient: −9.38e−01
Value: S
CitAB
0.006
0.005
0.004
0.003
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

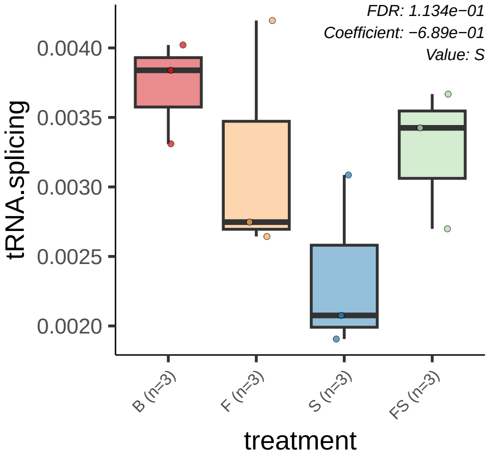

FDR: 1.098e−01
Coefficient: 1.08e−01
Value: F
Translation.elongation.factor.G.family
0.31
0.30
0.29
0.28
0.27
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

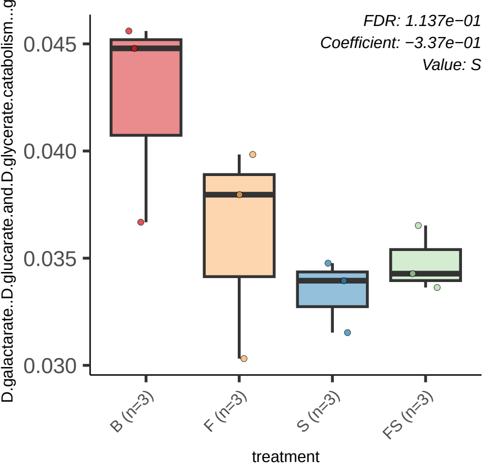

FDR: 1.104e−01
Coefficient: −8.75e−01
Value: S
Utilization.of.glutathione.as.a.sulphur.source
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

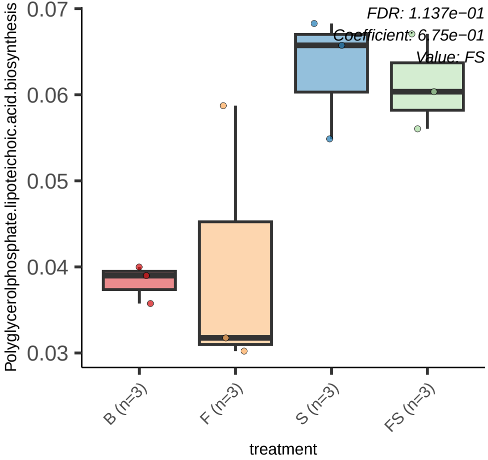

FDR: 1.111e−01
Coefficient: 7.79e−01
Value: FS
L.2.amino.thiazoline.4.carboxylic.acid.Lcysteine.conversio
0.0015
0.0010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

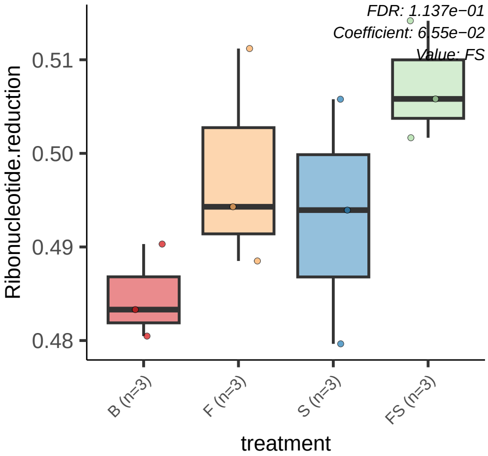

FDR: 1.129e−01
Coefficient: 2.25e−01
Value: S
Sporulation.associated.proteins.with.broader.functions
0.0450
0.0425
0.0400
0.0375
0.0350
0.0325
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

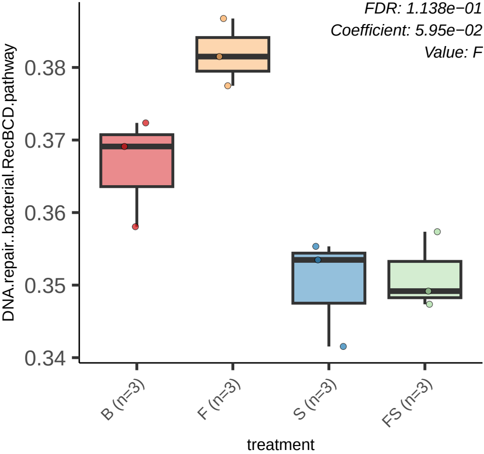

FDR: 1.134e−01
Coefficient: 1.71e−01
Value: FS
Q.RZ
0.025
0.024
0.023
0.022
0.021
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

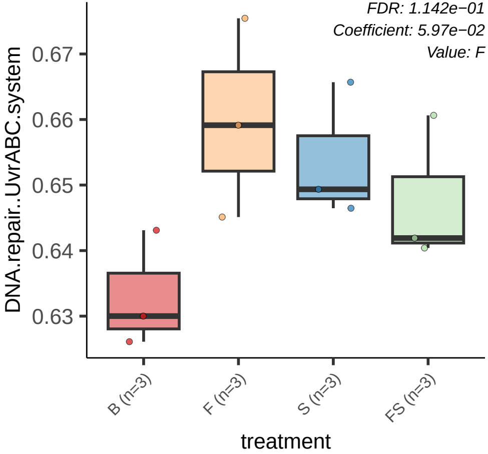

FDR: 1.134e−01
Coefficient: −6.89e−01
Value: S
tRNA.splicing
0.0040
0.0035
0.0030
0.0025
0.0020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

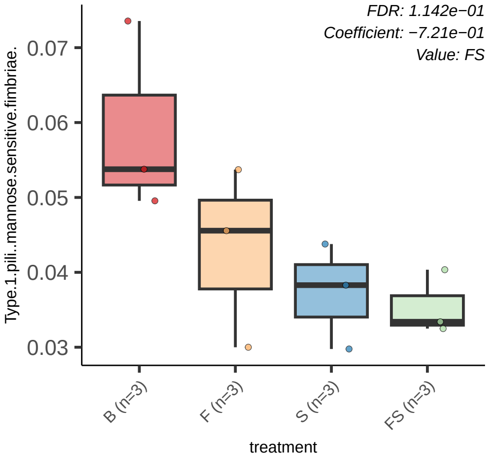

FDR: 1.137e−01
Coefficient: −3.37e−01
Value: S
D.galactarate..D.glucarate.and.D.glycerate.catabolism..g
0.045
0.040
0.035
0.030
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

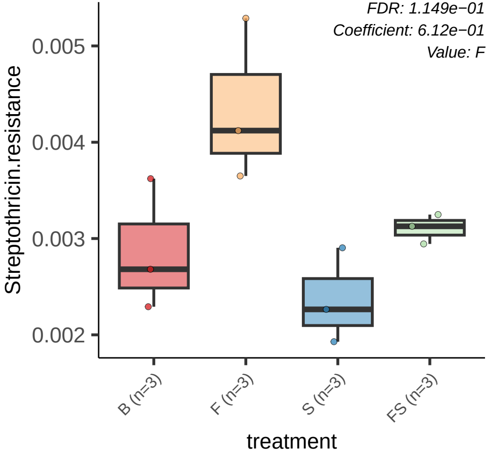

FDR: 1.137e−01
Coefficient: 6.75e−01
Value: FS
Polyglycerolphosphate.lipoteichoic.acid.biosynthesis
0.07
0.06
0.05
0.04
0.03
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

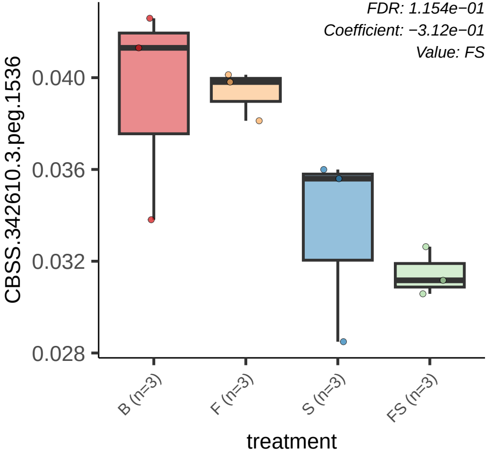

FDR: 1.137e−01
Coefficient: 6.55e−02
Value: FS
Ribonucleotide.reduction
0.51
0.50
0.49
0.48
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

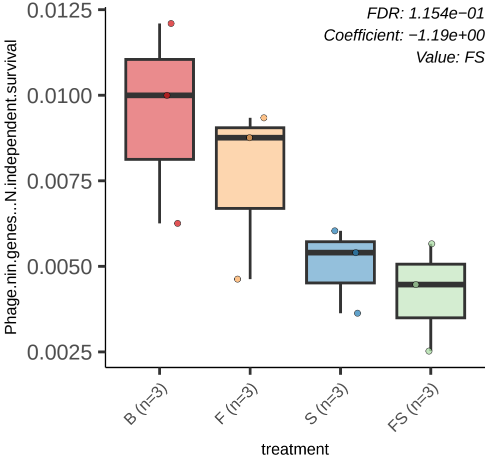

FDR: 1.138e−01
Coefficient: 5.95e−02
Value: F
DNA.repair..bacterial.RecBCD.pathway
0.38
0.37
0.36
0.35
0.34
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

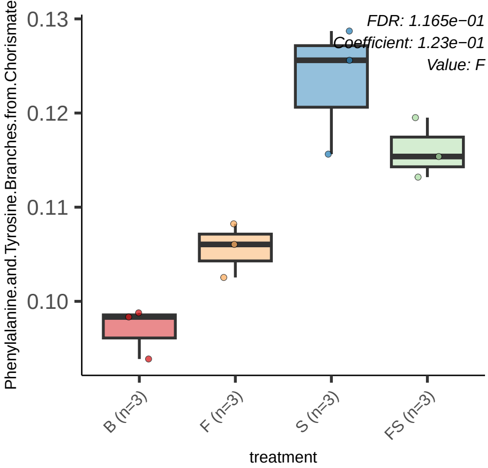

FDR: 1.142e−01
Coefficient: 5.97e−02
Value: F
DNA.repair..UvrABC.system
0.67
0.66
0.65
0.64
0.63
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

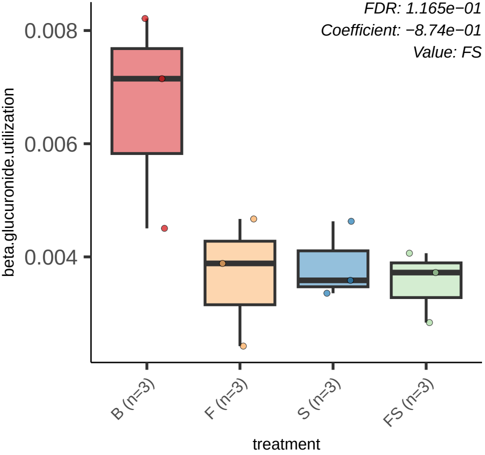

FDR: 1.142e−01
Coefficient: −7.21e−01
Value: FS
Type.1.pili..mannose.sensitive.fimbriae.
0.07
0.06
0.05
0.04
0.03
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

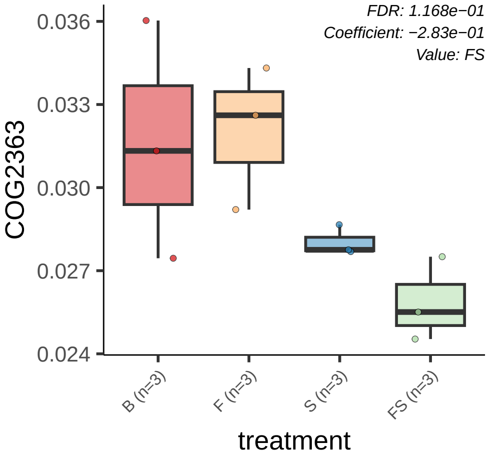

FDR: 1.149e−01
Coefficient: 6.12e−01
Value: F
Streptothricin.resistance
0.005
0.004
0.003
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

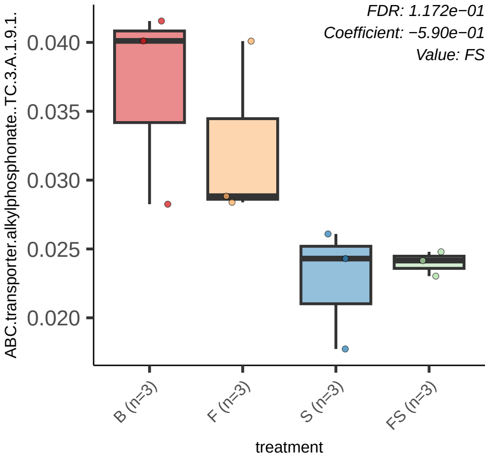

FDR: 1.154e−01
Coefficient: −3.12e−01
Value: FS
CBSS.342610.3.peg.1536
0.040
0.036
0.032
0.028
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

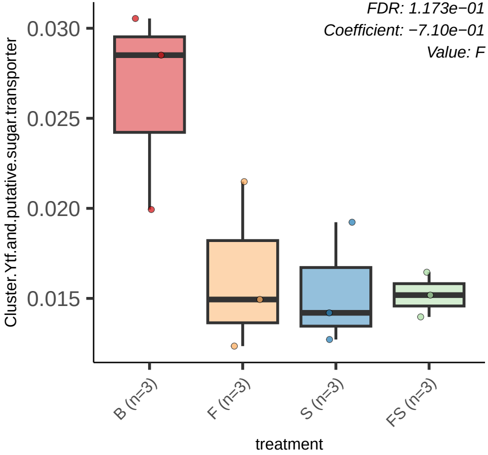

FDR: 1.154e−01
Coefficient: −1.19e+00
Value: FS
Phage.nin.genes...N.independent.survival
0.0125
0.0100
0.0075
0.0050
0.0025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

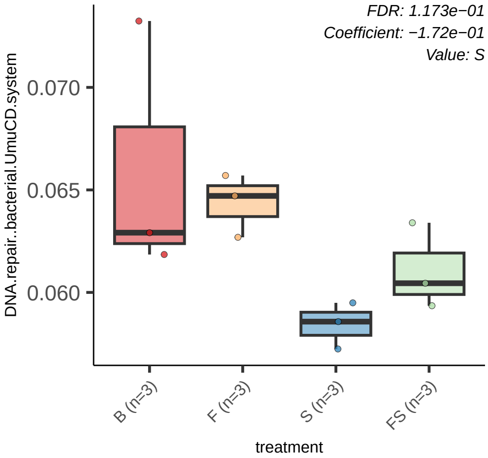

FDR: 1.165e−01
Coefficient: 1.23e−01
Value: F
Phenylalanine.and.Tyrosine.Branches.from.Chorismate
0.13
0.12
0.11
0.10
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

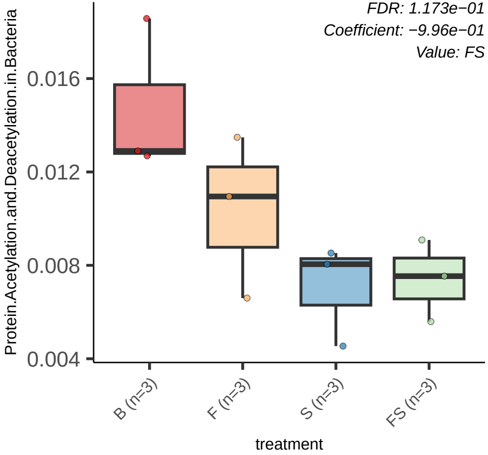

FDR: 1.165e−01
Coefficient: −8.74e−01
Value: FS
beta.glucuronide.utilization
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

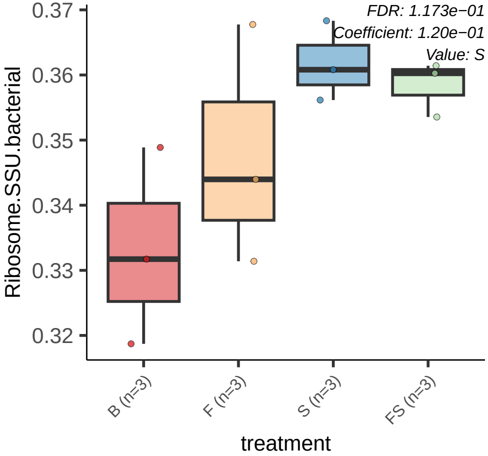

FDR: 1.168e−01
Coefficient: −2.83e−01
Value: FS
COG2363
0.036
0.033
0.030
0.027
0.024
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

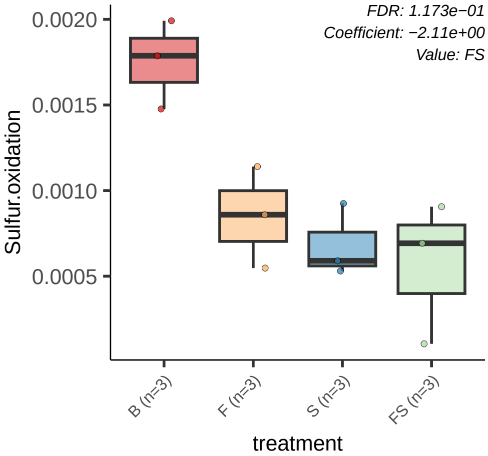

FDR: 1.172e−01
Coefficient: −5.90e−01
Value: FS
ABC.transporter.alkylphosphonate..TC.3.A.1.9.1.
0.040
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

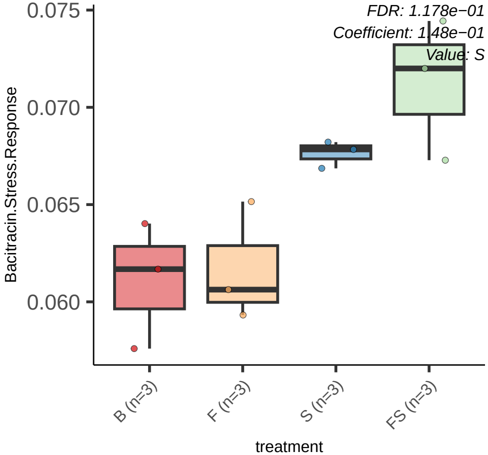

FDR: 1.173e−01
Coefficient: −7.10e−01
Value: F
Cluster.Ytf.and.putative.sugar.transporter
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

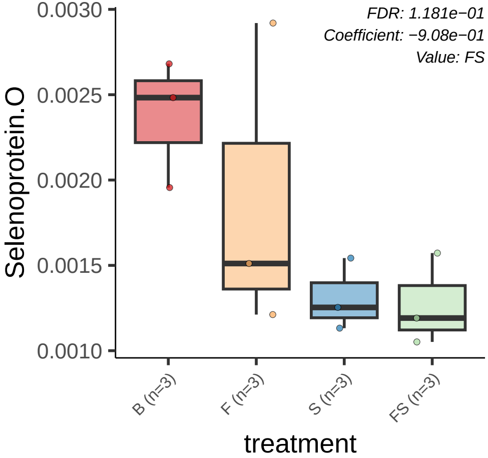

FDR: 1.173e−01
Coefficient: −1.72e−01
Value: S
DNA.repair..bacterial.UmuCD.system
0.070
0.065
0.060
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

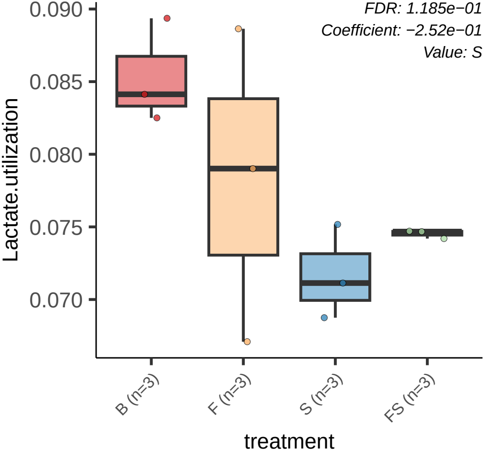

FDR: 1.173e−01
Coefficient: −9.96e−01
Value: FS
Protein.Acetylation.and.Deacetylation.in.Bacteria
0.016
0.012
0.008
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

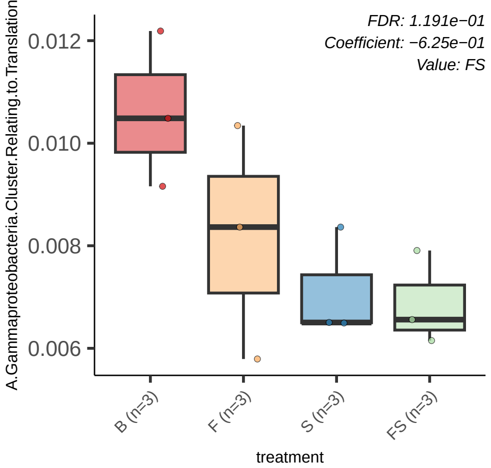

FDR: 1.173e−01
Coefficient: 1.20e−01
Value: S
Ribosome.SSU.bacterial
0.37
0.36
0.35
0.34
0.33
0.32
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

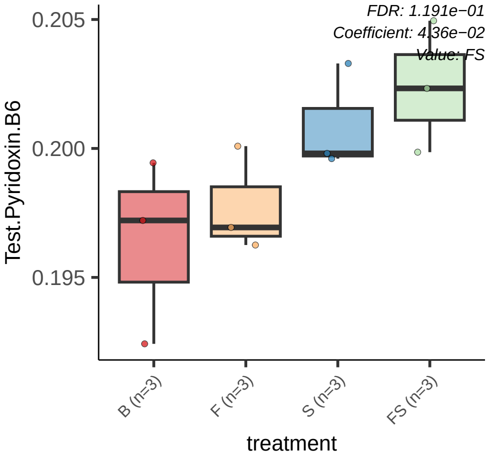

FDR: 1.173e−01
Coefficient: −2.11e+00
Value: FS
Sulfur.oxidation
0.0020
0.0015
0.0010
0.0005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

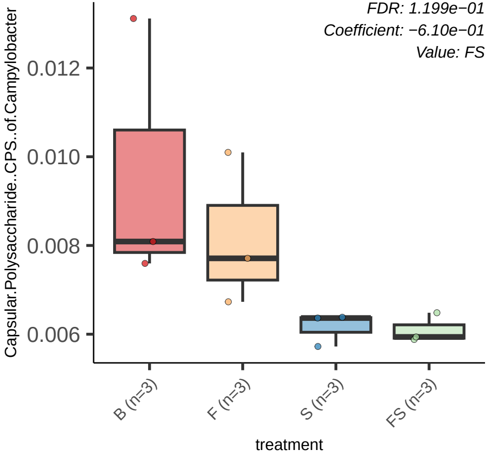

FDR: 1.178e−01
Coefficient: 1.48e−01
Value: S
Bacitracin.Stress.Response
0.075
0.070
0.065
0.060
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

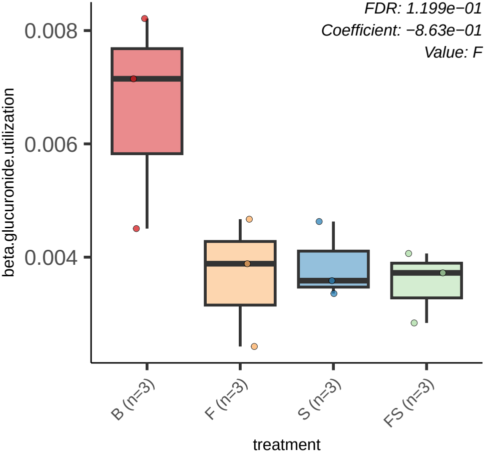

FDR: 1.181e−01
Coefficient: −9.08e−01
Value: FS
Selenoprotein.O
0.0030
0.0025
0.0020
0.0015
0.0010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

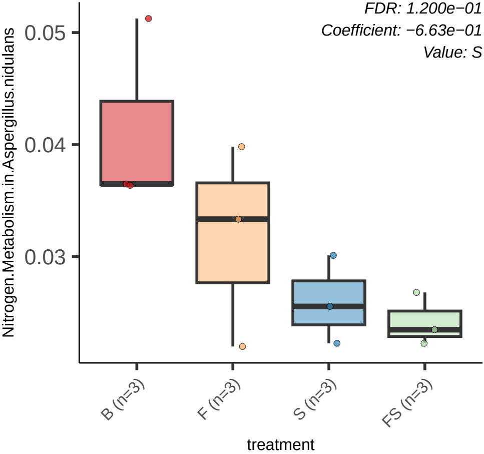

FDR: 1.185e−01
Coefficient: −2.52e−01
Value: S
Lactate.utilization
0.090
0.085
0.080
0.075
0.070
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

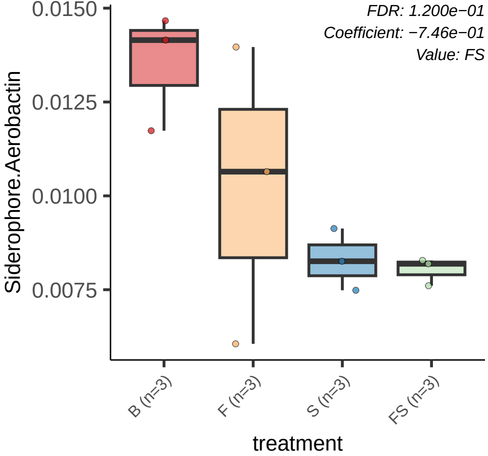

FDR: 1.191e−01
Coefficient: −6.25e−01
Value: FS
A.Gammaproteobacteria.Cluster.Relating.to.Translation
0.012
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

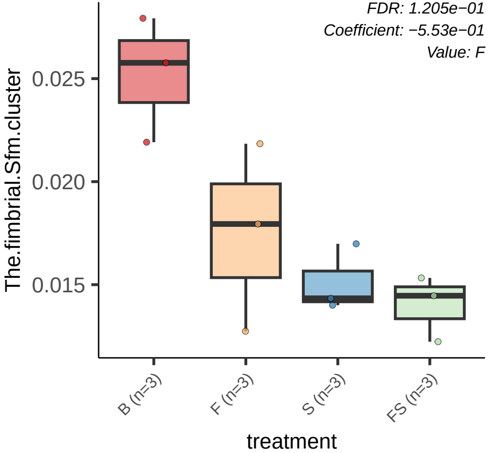

FDR: 1.191e−01
Coefficient: 4.36e−02
Value: FS
Test.Pyridoxin.B6
0.205
0.200
0.195
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

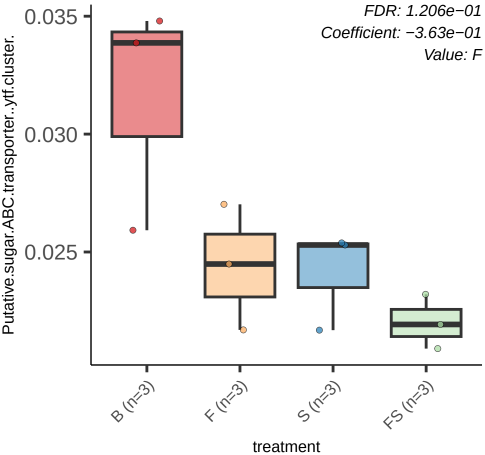

FDR: 1.199e−01
Coefficient: −6.10e−01
Value: FS
Capsular.Polysaccharide..CPS..of.Campylobacter
0.012
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

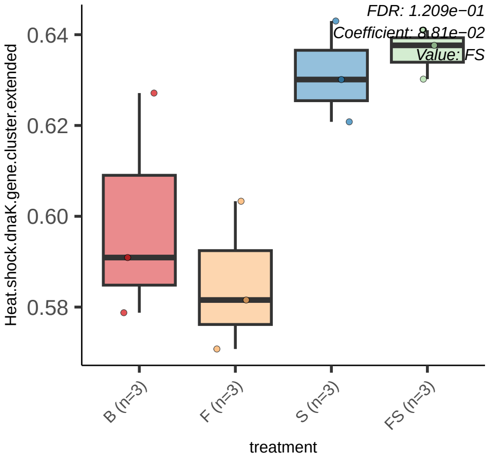

FDR: 1.199e−01
Coefficient: −8.63e−01
Value: F
beta.glucuronide.utilization
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

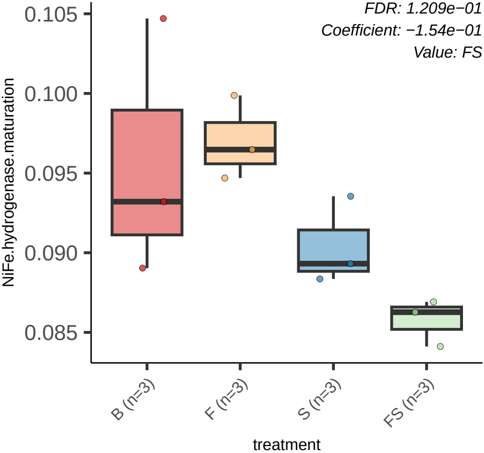

FDR: 1.200e−01
Coefficient: −6.63e−01
Value: S
Nitrogen.Metabolism.in.Aspergillus.nidulans
0.05
0.04
0.03
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

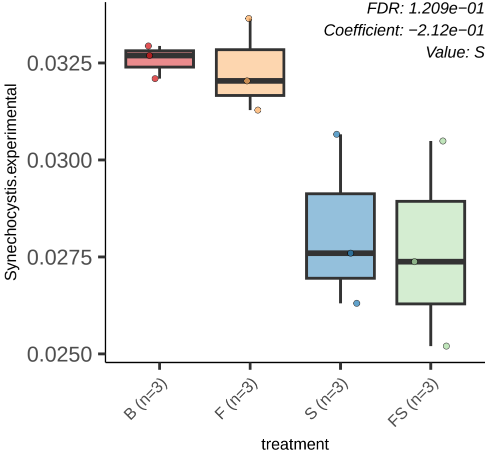

FDR: 1.200e−01
Coefficient: −7.46e−01
Value: FS
Siderophore.Aerobactin
0.0150
0.0125
0.0100
0.0075
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

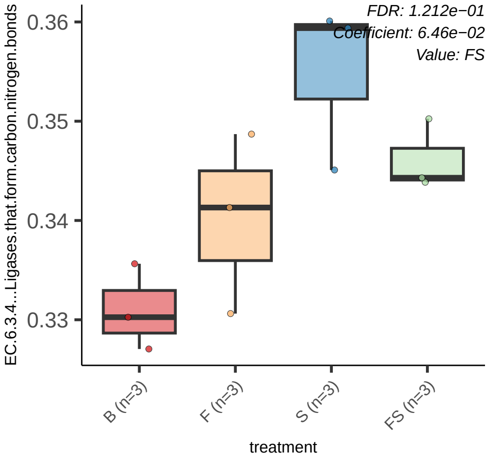

FDR: 1.205e−01
Coefficient: −5.53e−01
Value: F
The.fimbrial.Sfm.cluster
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

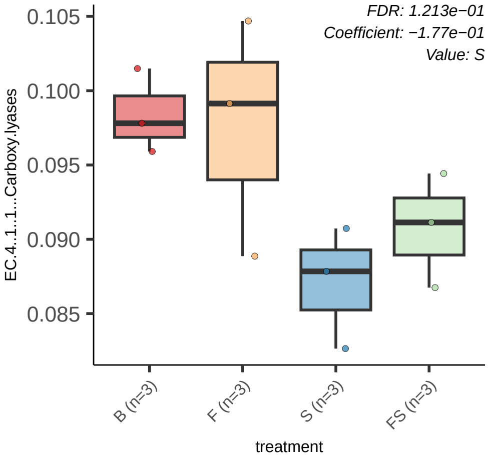

FDR: 1.206e−01
Coefficient: −3.63e−01
Value: F
Putative.sugar.ABC.transporter..ytf.cluster.
0.035
0.030
0.025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

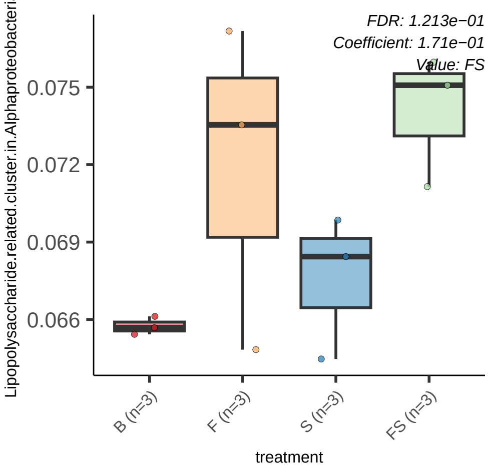

FDR: 1.209e−01
Coefficient: 8.81e−02
Value: FS
Heat.shock.dnaK.gene.cluster.extended
0.64
0.62
0.60
0.58
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

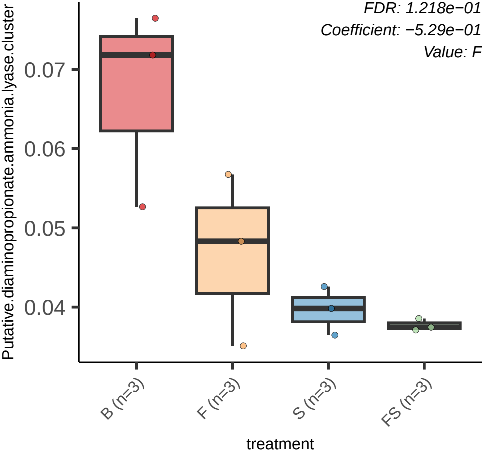

FDR: 1.209e−01
Coefficient: −1.54e−01
Value: FS
NiFe.hydrogenase.maturation
0.105
0.100
0.095
0.090
0.085
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

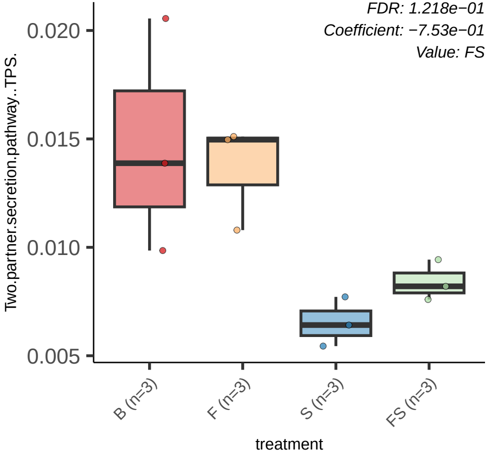

FDR: 1.209e−01
Coefficient: −2.12e−01
Value: S
Synechocystis.experimental
0.0325
0.0300
0.0275
0.0250
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

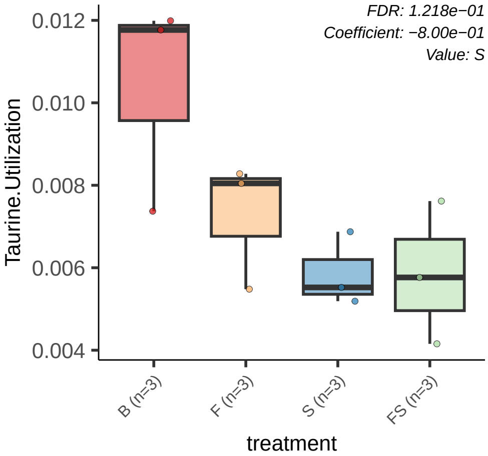

FDR: 1.212e−01
Coefficient: 6.46e−02
Value: FS
EC.6.3.4...Ligases.that.form.carbon.nitrogen.bonds
0.36
0.35
0.34
0.33
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

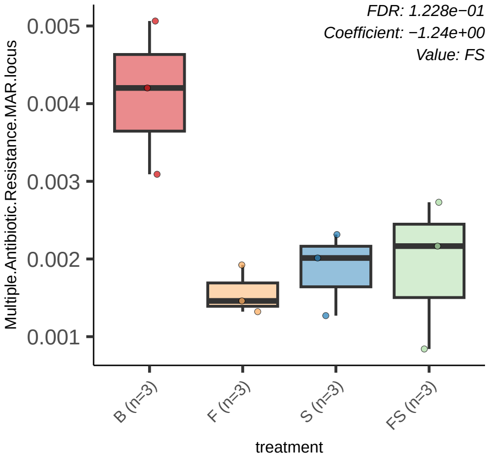

FDR: 1.213e−01
Coefficient: −1.77e−01
Value: S
EC.4..1..1...Carboxy.lyases
0.105
0.100
0.095
0.090
0.085
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

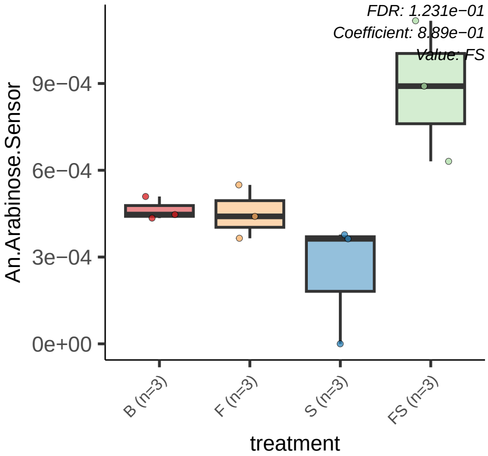

FDR: 1.213e−01
Coefficient: 1.71e−01
Value: FS
Lipopolysaccharide.related.cluster.in.Alphaproteobacteri
0.075
0.072
0.069
0.066
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

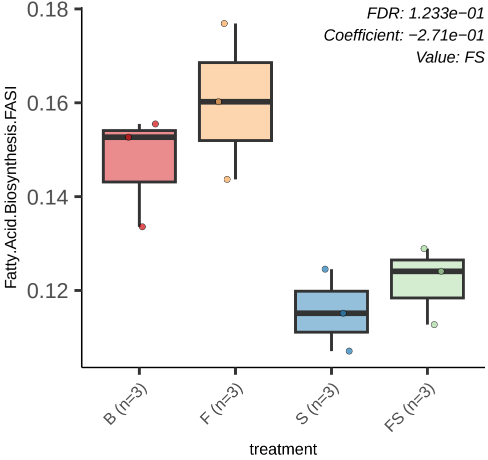

FDR: 1.218e−01
Coefficient: −5.29e−01
Value: F
Putative.diaminopropionate.ammonia.lyase.cluster
0.07
0.06
0.05
0.04
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

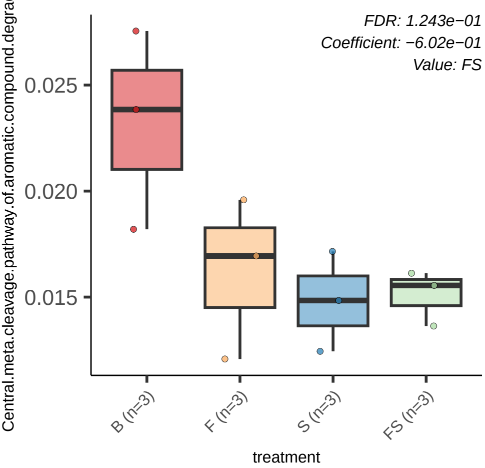

FDR: 1.218e−01
Coefficient: −7.53e−01
Value: FS
Two.partner.secretion.pathway..TPS.
0.020
0.015
0.010
0.005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

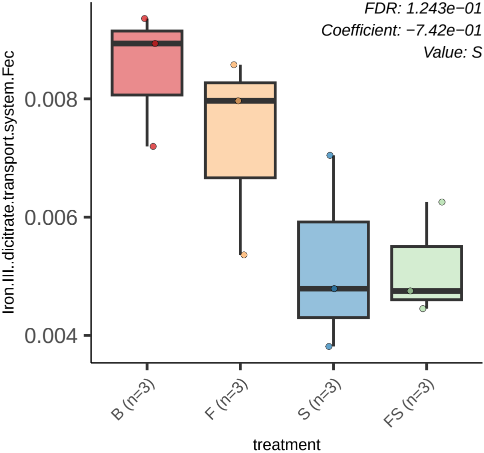

FDR: 1.218e−01
Coefficient: −8.00e−01
Value: S
Taurine.Utilization
0.012
0.010
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

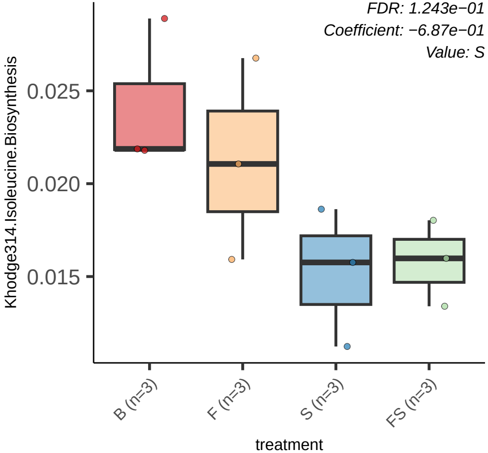

FDR: 1.228e−01
Coefficient: −1.24e+00
Value: FS
Multiple.Antibiotic.Resistance.MAR.locus
0.005
0.004
0.003
0.002
0.001
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

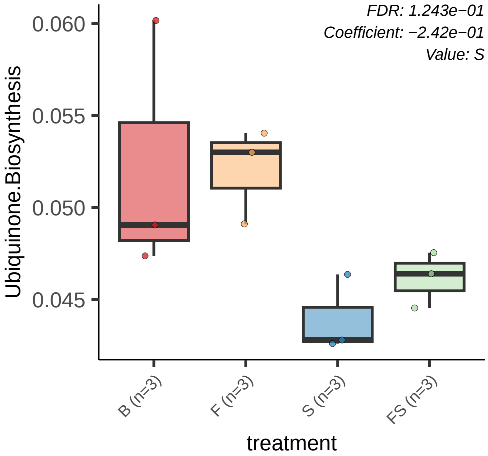

FDR: 1.231e−01
Coefficient: 8.89e−01
Value: FS
An.Arabinose.Sensor
9e−04
6e−04
3e−04
0e+00
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

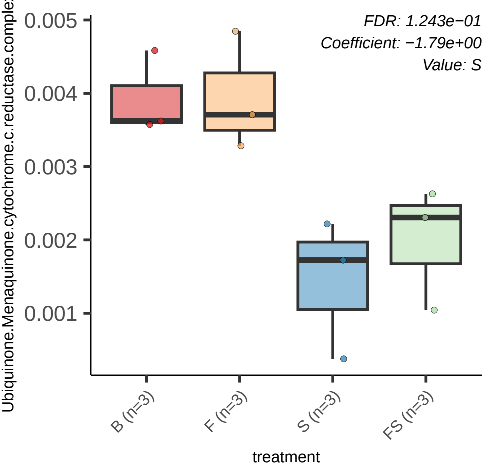

FDR: 1.233e−01
Coefficient: −2.71e−01
Value: FS
Fatty.Acid.Biosynthesis.FASI
0.18
0.16
0.14
0.12
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

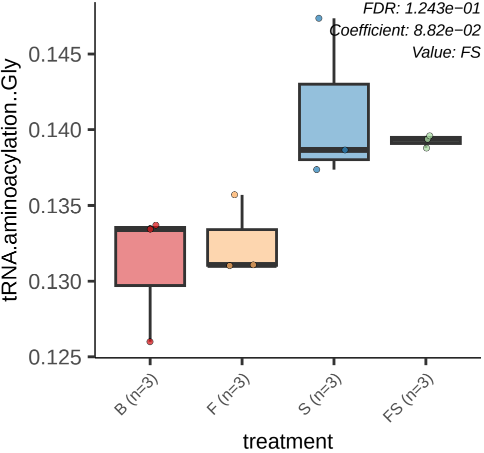

FDR: 1.243e−01
Coefficient: −6.02e−01
Value: FS
Central.meta.cleavage.pathway.of.aromatic.compound.degrad
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

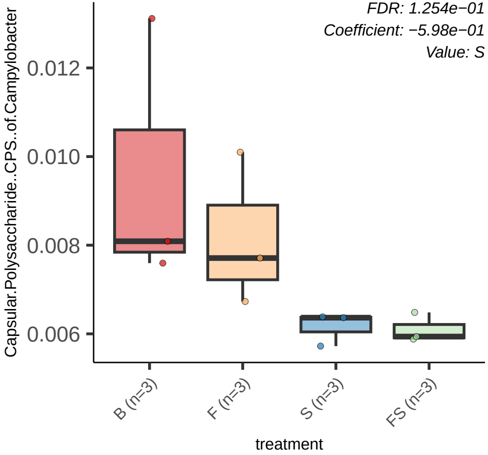

FDR: 1.243e−01
Coefficient: −7.42e−01
Value: S
Iron.III..dicitrate.transport.system.Fec
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

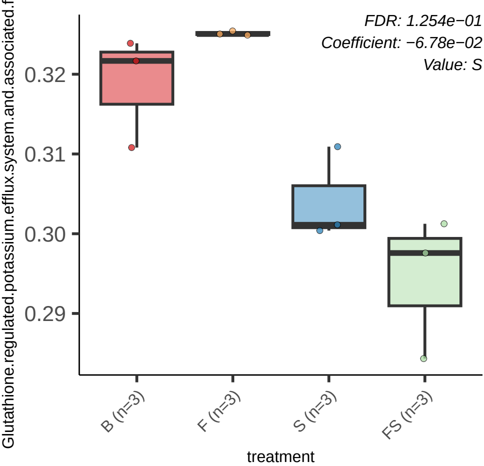

FDR: 1.243e−01
Coefficient: −6.87e−01
Value: S
Khodge314.Isoleucine.Biosynthesis
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

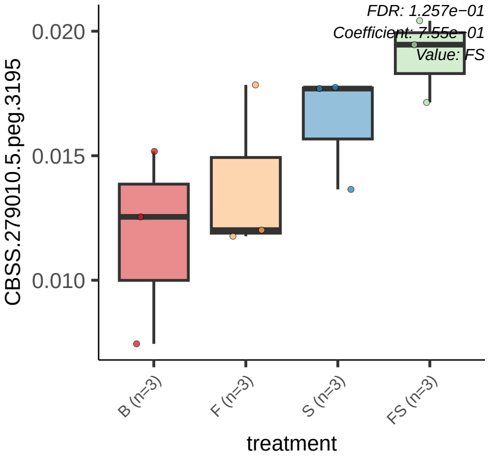

FDR: 1.243e−01
Coefficient: −2.42e−01
Value: S
Ubiquinone.Biosynthesis
0.060
0.055
0.050
0.045
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

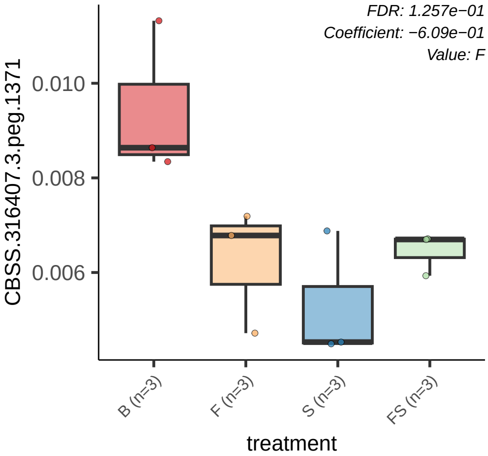

FDR: 1.243e−01
Coefficient: −1.79e+00
Value: S
Ubiquinone.Menaquinone.cytochrome.c.reductase.comple
0.005
0.004
0.003
0.002
0.001
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

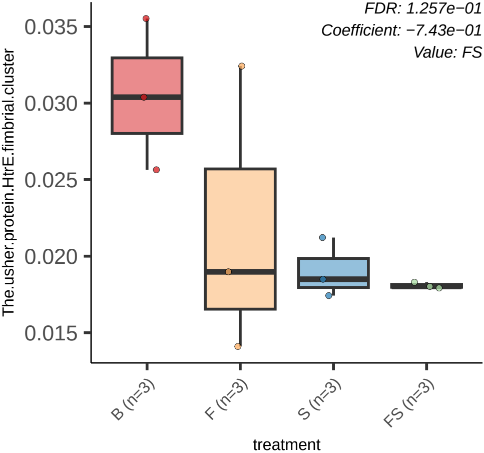

FDR: 1.243e−01
Coefficient: 8.82e−02
Value: FS
tRNA.aminoacylation..Gly
0.145
0.140
0.135
0.130
0.125
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

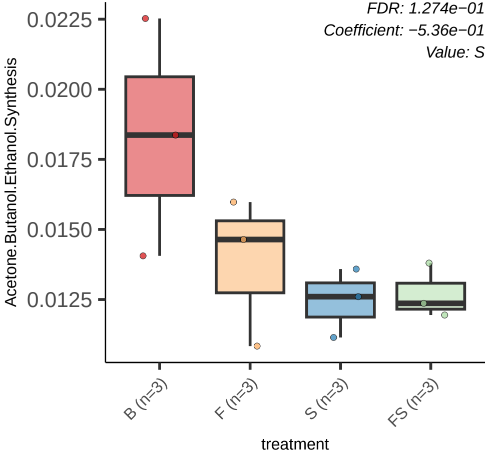

FDR: 1.254e−01
Coefficient: −5.98e−01
Value: S
Capsular.Polysaccharide..CPS..of.Campylobacter
0.012
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

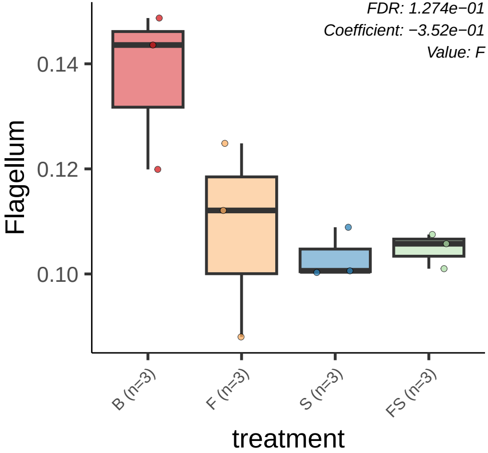

FDR: 1.254e−01
Coefficient: −6.78e−02
Value: S
Glutathione.regulated.potassium.efflux.system.and.associated.f
0.32
0.31
0.30
0.29
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

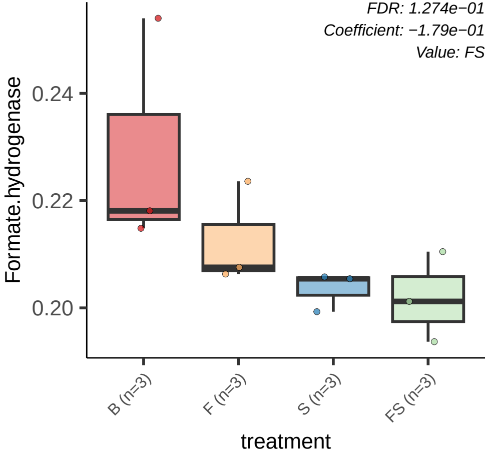

FDR: 1.257e−01
Coefficient: 7.55e−01
Value: FS
CBSS.279010.5.peg.3195
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

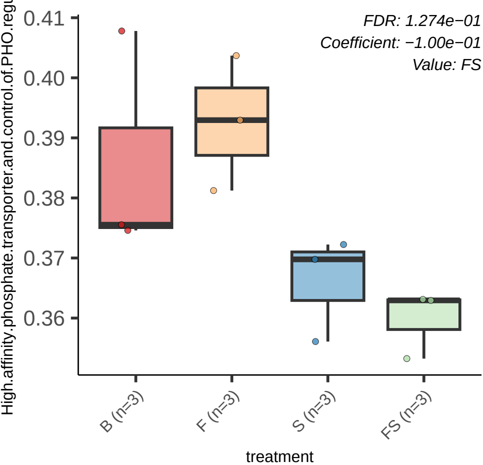

FDR: 1.257e−01
Coefficient: −6.09e−01
Value: F
CBSS.316407.3.peg.1371
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

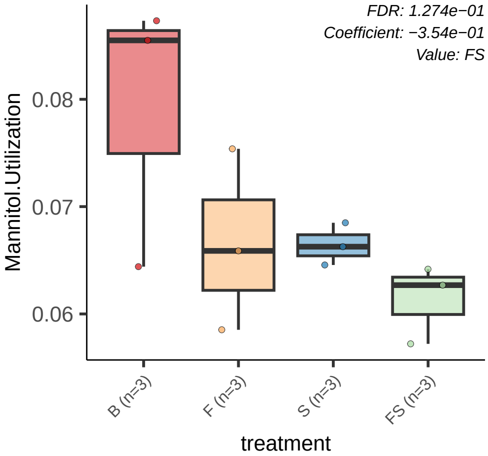

FDR: 1.257e−01
Coefficient: −7.43e−01
Value: FS
The.usher.protein.HtrE.fimbrial.cluster
0.035
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

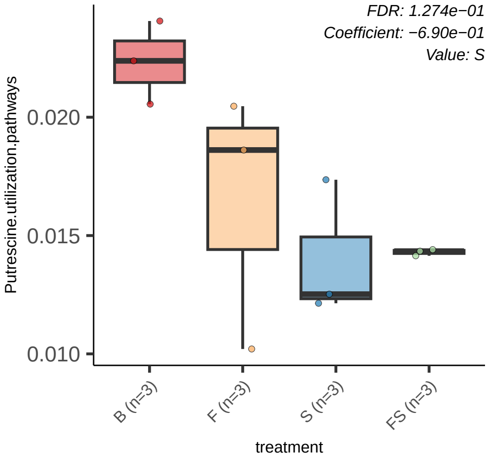

FDR: 1.274e−01
Coefficient: −5.36e−01
Value: S
Acetone.Butanol.Ethanol.Synthesis
0.0225
0.0200
0.0175
0.0150
0.0125
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

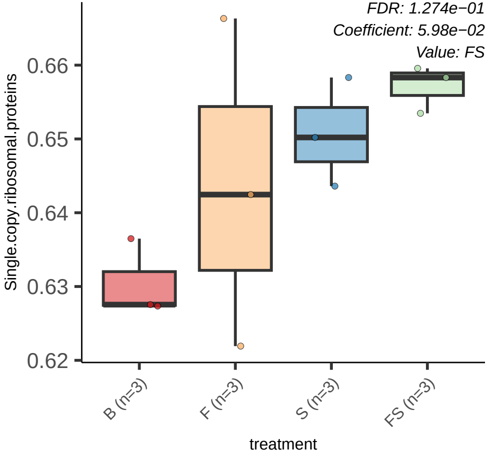

FDR: 1.274e−01
Coefficient: −3.52e−01
Value: F
Flagellum
0.14
0.12
0.10
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

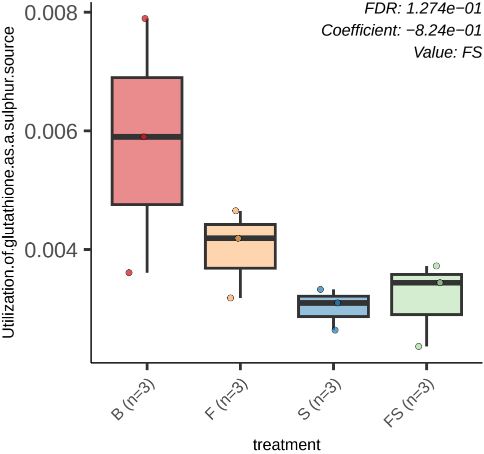

FDR: 1.274e−01
Coefficient: −1.79e−01
Value: FS
Formate.hydrogenase
0.24
0.22
0.20
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

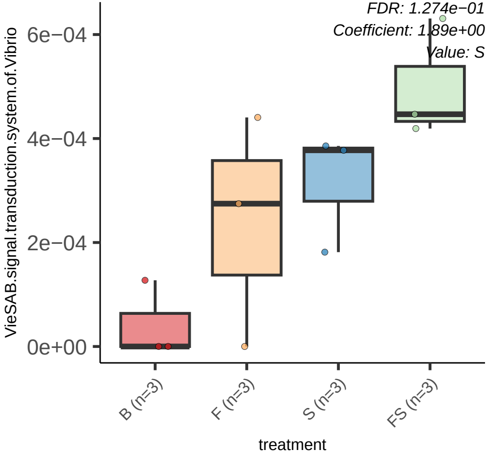

FDR: 1.274e−01
Coefficient: −1.00e−01
Value: FS
High.affinity.phosphate.transporter.and.control.of.PHO.regu
0.41
0.40
0.39
0.38
0.37
0.36
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

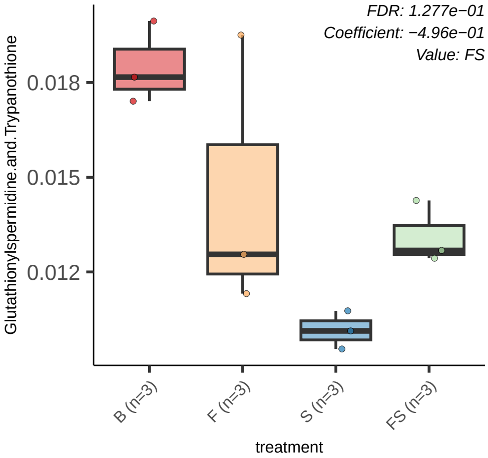

FDR: 1.274e−01
Coefficient: −3.54e−01
Value: FS
Mannitol.Utilization
0.08
0.07
0.06
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

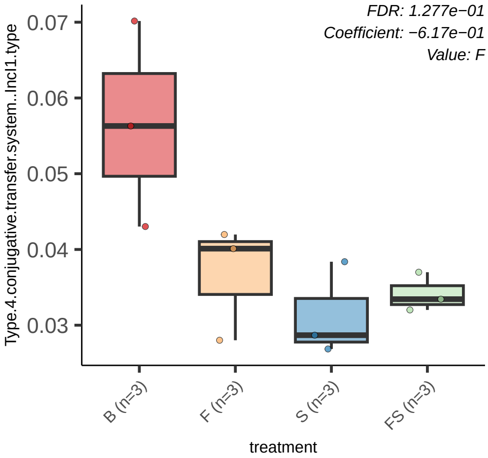

FDR: 1.274e−01
Coefficient: −6.90e−01
Value: S
Putrescine.utilization.pathways
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

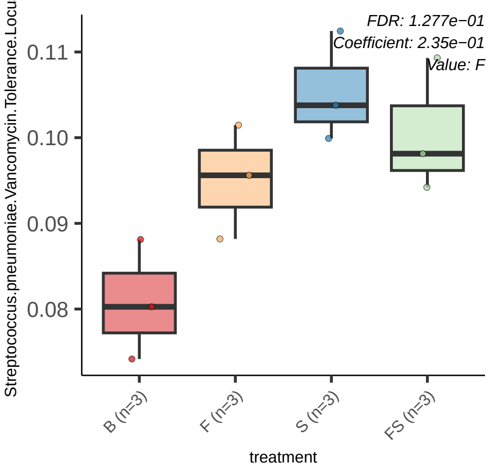

FDR: 1.274e−01
Coefficient: 5.98e−02
Value: FS
0.66
0.65
0.64
0.63
0.62
Single.copy.ribosomal.proteins
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

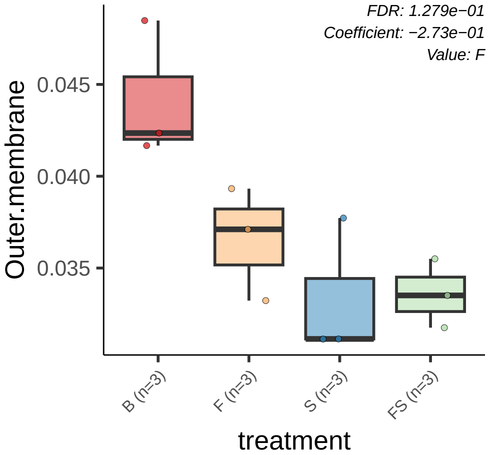

FDR: 1.274e−01
Coefficient: −8.24e−01
Value: FS
Utilization.of.glutathione.as.a.sulphur.source
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

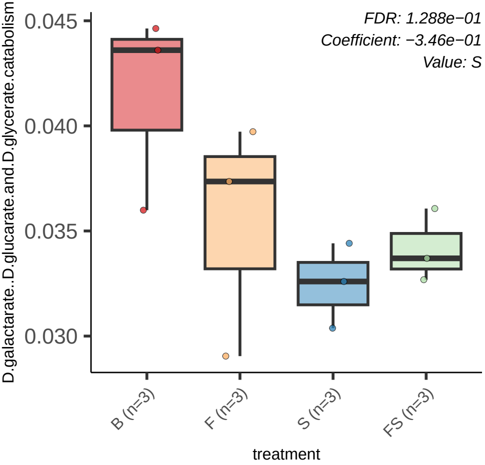

FDR: 1.274e−01
Coefficient: 1.89e+00
Value: S
VieSAB.signal.transduction.system.of.Vibrio
6e−04
4e−04
2e−04
0e+00
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 1.277e−01
Coefficient: −4.96e−01
Value: FS
Glutathionylspermidine.and.Trypanothione
0.018
0.015
0.012
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

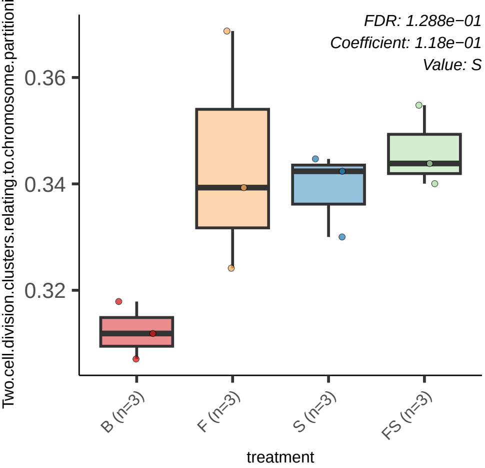

FDR: 1.277e−01
Coefficient: −6.17e−01
Value: F
Type.4.conjugative.transfer.system..IncI1.type
0.07
0.06
0.05
0.04
0.03
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

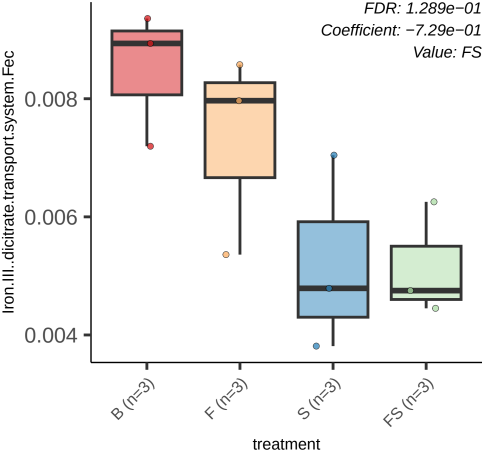

FDR: 1.277e−01
Coefficient: 2.35e−01
Value: F
Streptococcus.pneumoniae.Vancomycin.Tolerance.Locu
0.11
0.10
0.09
0.08
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

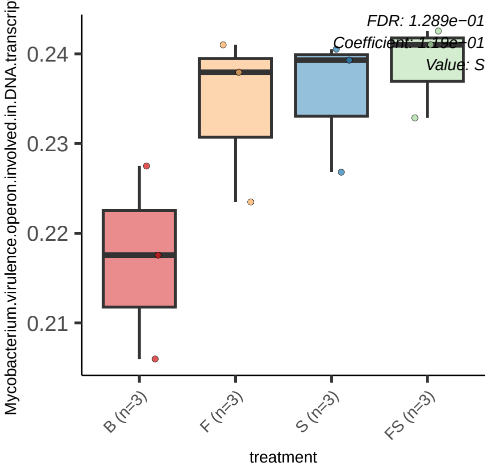

FDR: 1.279e−01
Coefficient: −2.73e−01
Value: F
Outer.membrane
0.045
0.040
0.035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

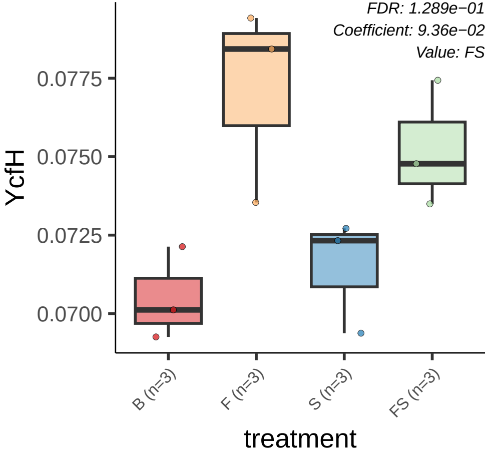


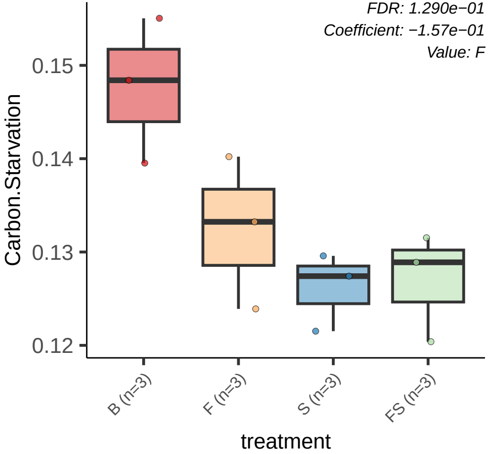
FDR: 1.288e−01
Coefficient: −3.46e−01
Value: S
D.galactarate..D.glucarate.and.D.glycerate.catabolism
0.045
0.040
0.035
0.030
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

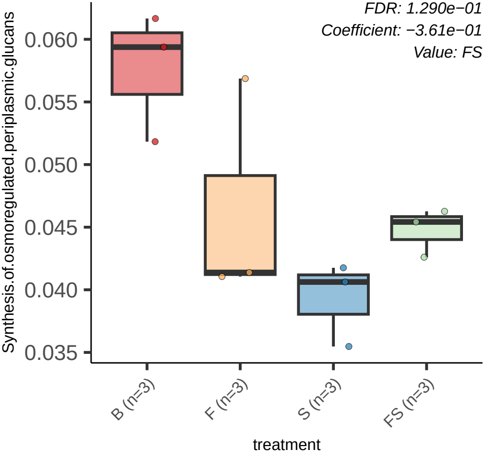

FDR: 1.288e−01
Coefficient: 1.18e−01
Value: S
Two.cell.division.clusters.relating.to.chromosome.partitioni
0.36
0.34
0.32
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

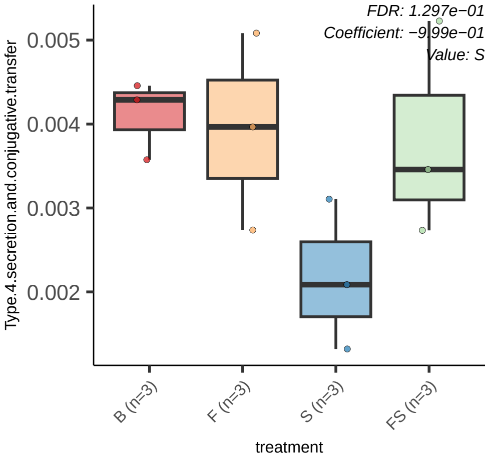

FDR: 1.289e−01
Coefficient: −7.29e−01
Value: FS
Iron.III..dicitrate.transport.system.Fec
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

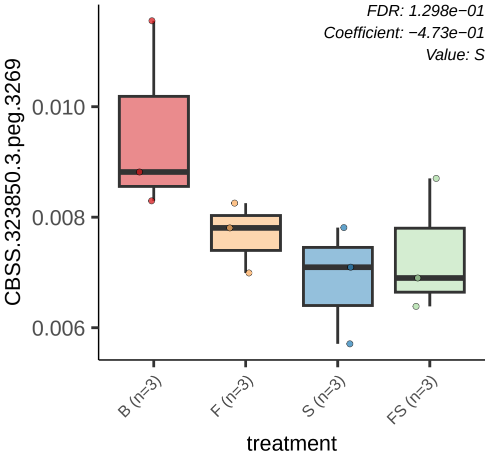

FDR: 1.289e−01
Coefficient: 1.19e−01
Value: S
Mycobacterium.virulence.operon.involved.in.DNA.transcrip
0.24
0.23
0.22
0.21
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

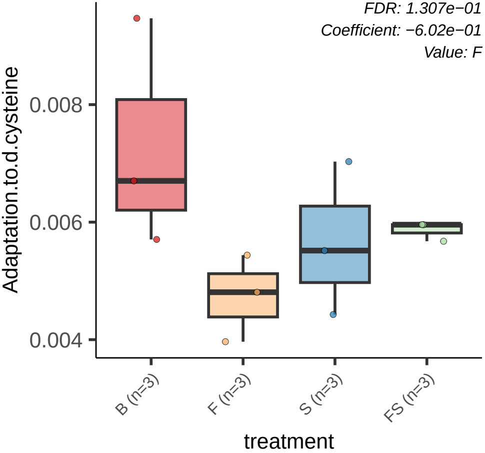

FDR: 1.289e−01
Coefficient: 9.36e−02
Value: FS
YcfH
0.0775
0.0750
0.0725
0.0700
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

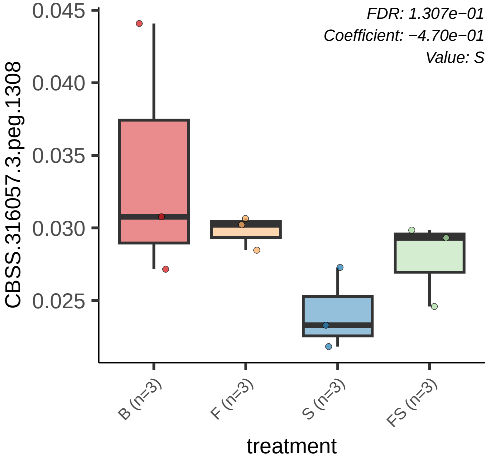

FDR: 1.290e−01
Coefficient: −1.57e−01
Value: F
Carbon.Starvation
0.15
0.14
0.13
0.12
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

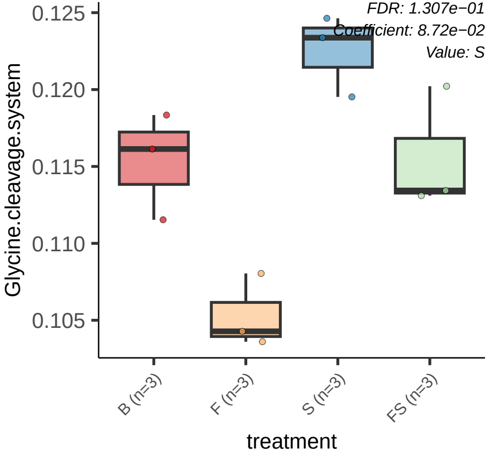

FDR: 1.290e−01
Coefficient: −3.61e−01
Value: FS
Synthesis.of.osmoregulated.periplasmic.glucans
0.060
0.055
0.050
0.045
0.040
0.035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

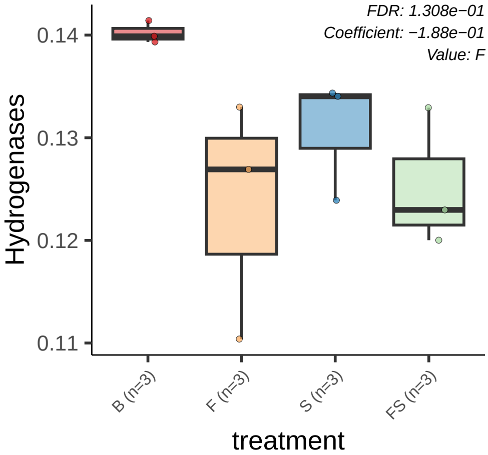

FDR: 1.297e−01
Coefficient: −9.99e−01
Value: S
Type.4.secretion.and.conjugative.transfer
0.005
0.004
0.003
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

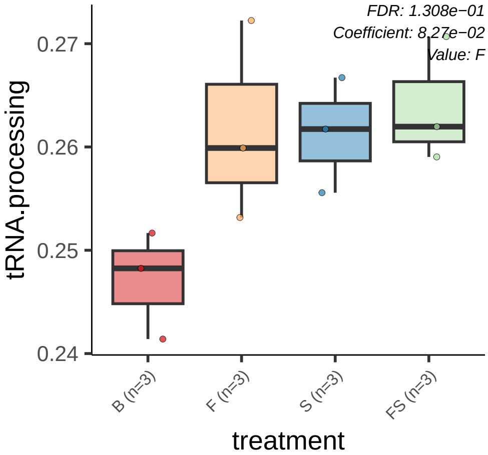

FDR: 1.298e−01
Coefficient: −4.73e−01
Value: S
CBSS.323850.3.peg.3269
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

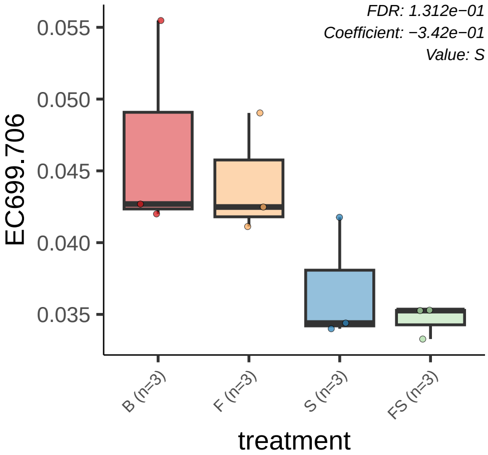

FDR: 1.307e−01
Coefficient: −6.02e−01
Value: F
Adaptation.to.d.cysteine
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

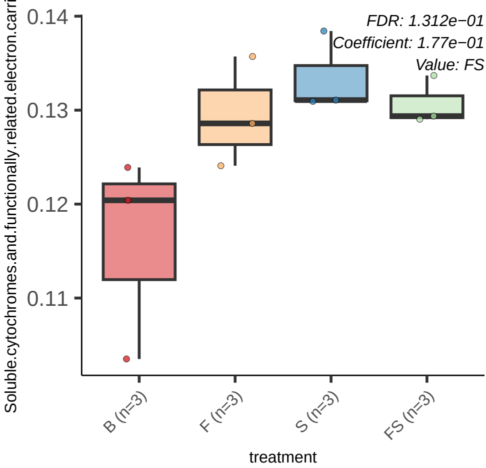

FDR: 1.307e−01
Coefficient: −4.70e−01
Value: S
CBSS.316057.3.peg.1308
0.045
0.040
0.035
0.030
0.025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

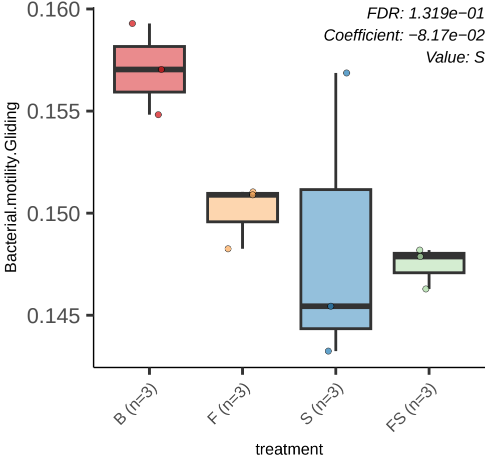

FDR: 1.307e−01
Coefficient: 8.72e−02
Value: S
Glycine.cleavage.system
0.125
0.120
0.115
0.110
0.105
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

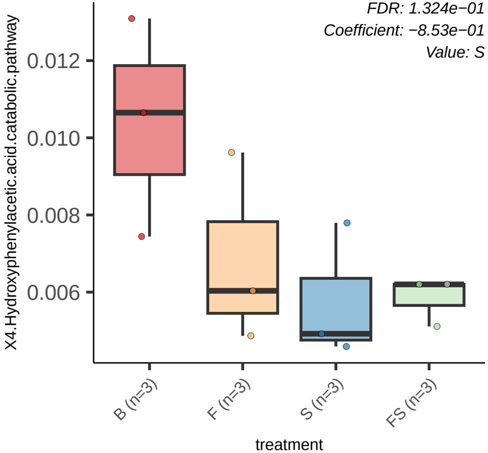

FDR: 1.308e−01
Coefficient: −1.88e−01
Value: F
Hydrogenases
0.14
0.13
0.12
0.11
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

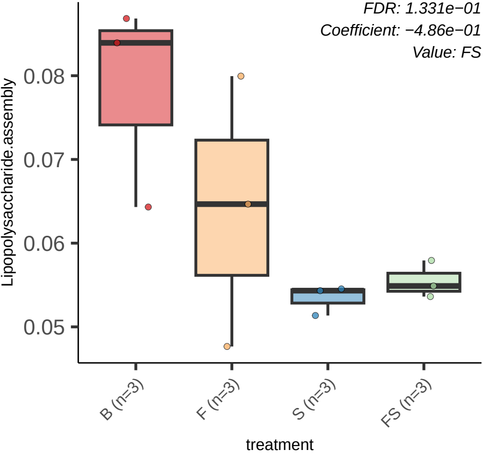

FDR: 1.308e−01
Coefficient: 8.27e−02
Value: F
tRNA.processing
0.27
0.26
0.25
0.24
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

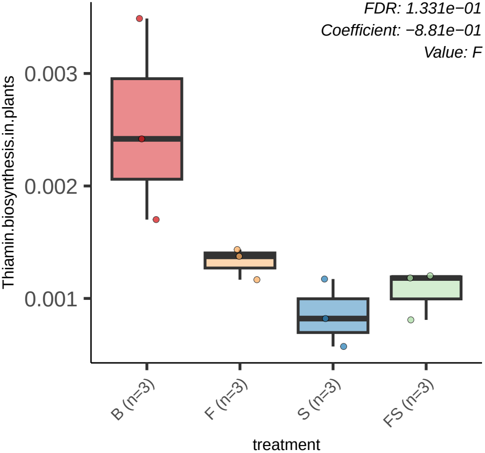

FDR: 1.312e−01
Coefficient: −3.42e−01
Value: S
EC699.706
0.055
0.050
0.045
0.040
0.035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

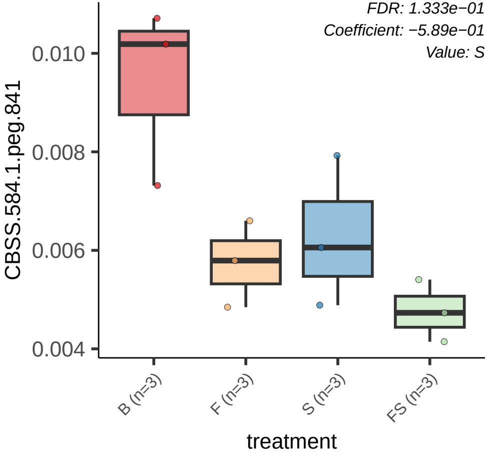

FDR: 1.312e−01
Coefficient: 1.77e−01
Value: FS
Soluble.cytochromes.and.functionally.related.electron.carri
0.14
0.13
0.12
0.11
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

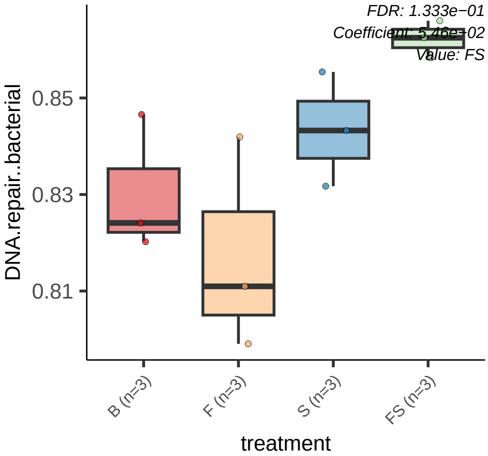

FDR: 1.319e−01
Coefficient: −8.17e−02
Value: S
Bacterial.motility.Gliding
0.160
0.155
0.150
0.145
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

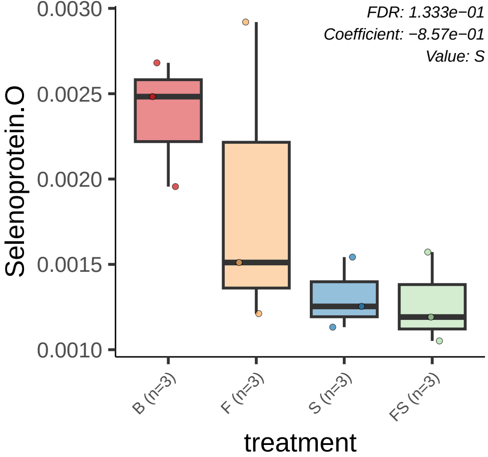

FDR: 1.324e−01
Coefficient: −8.53e−01
Value: S
X4.Hydroxyphenylacetic.acid.catabolic.pathway
0.012
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

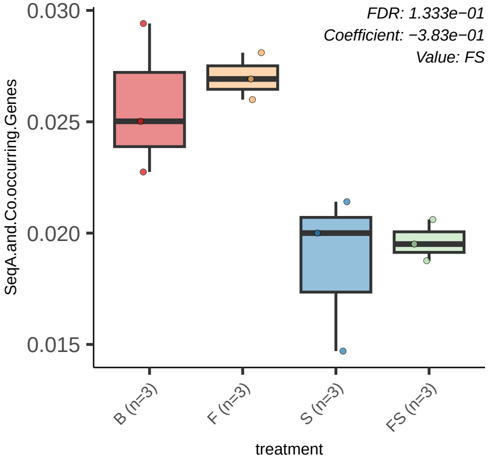

FDR: 1.331e−01
Coefficient: −4.86e−01
Value: FS
Lipopolysaccharide.assembly
0.08
0.07
0.06
0.05
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

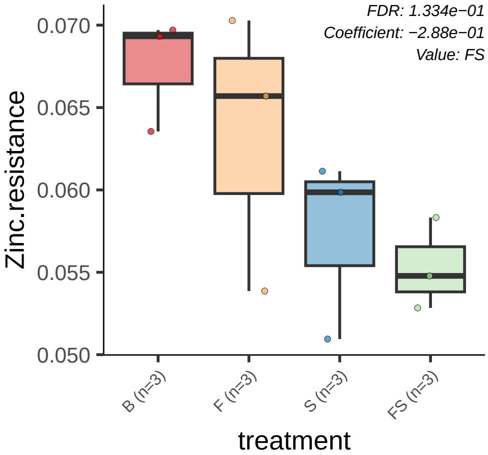

FDR: 1.331e−01
Coefficient: −8.81e−01
Value: F
Thiamin.biosynthesis.in.plants
0.003
0.002
0.001
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

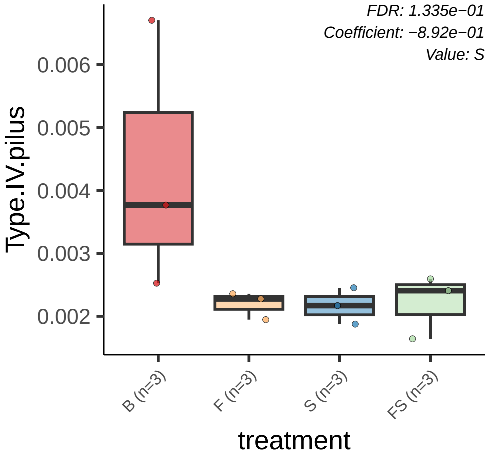

FDR: 1.333e−01
Coefficient: −5.89e−01
Value: S
CBSS.584.1.peg.841
0.010
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

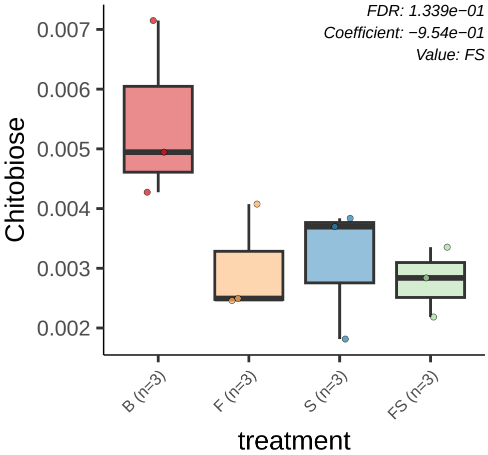

FDR: 1.333e−01
Coefficient: 5.46e−02
Value: FS
DNA.repair..bacterial
0.85
0.83
0.81
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

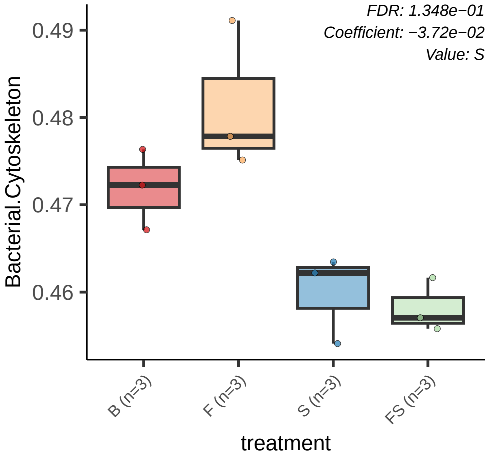

FDR: 1.333e−01
Coefficient: −8.57e−01
Value: S
Selenoprotein.O
0.0030
0.0025
0.0020
0.0015
0.0010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

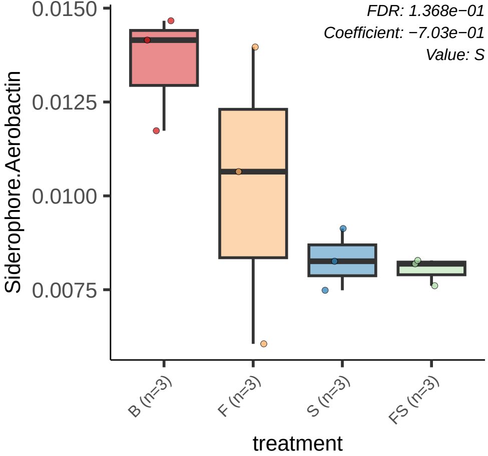

FDR: 1.333e−01
Coefficient: −3.83e−01
Value: FS
SeqA.and.Co.occurring.Genes
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

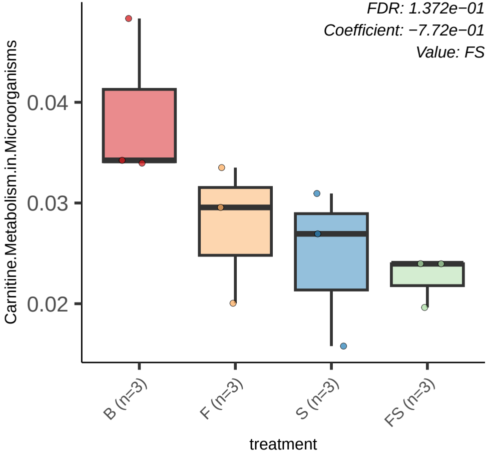

FDR: 1.334e−01
Coefficient: −2.88e−01
Value: FS
Zinc.resistance
0.070
0.065
0.060
0.055
0.050
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

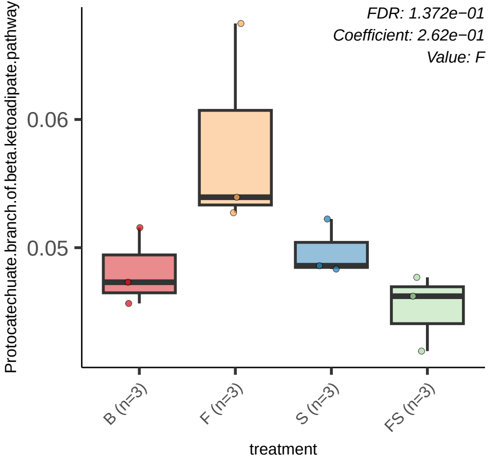

FDR: 1.335e−01
Coefficient: −8.92e−01
Value: S
Type.IV.pilus
0.006
0.005
0.004
0.003
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

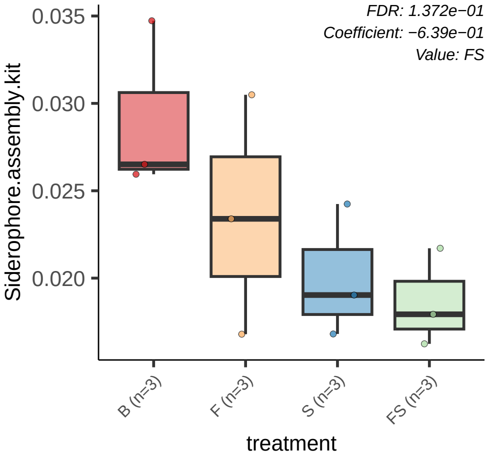

FDR: 1.339e−01
Coefficient: −9.54e−01
Value: FS
Chitobiose
0.007
0.006
0.005
0.004
0.003
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 1.348e−01
Coefficient: −3.72e−02
Value: S
Bacterial.Cytoskeleton
0.49
0.48
0.47
0.46
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

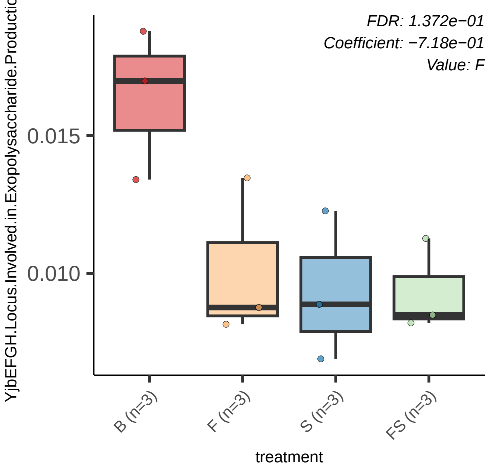

FDR: 1.368e−01
Coefficient: −7.03e−01
Value: S
Siderophore.Aerobactin
0.0150
0.0125
0.0100
0.0075
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

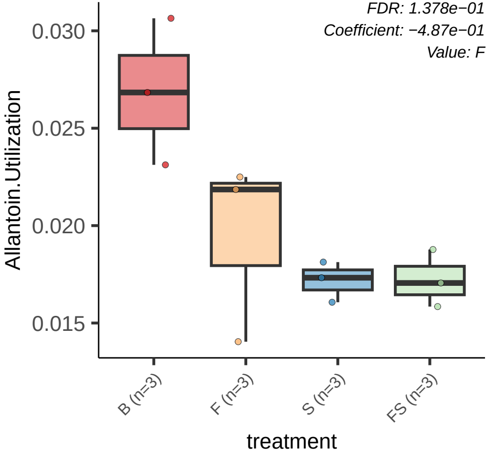

FDR: 1.372e−01
Coefficient: −7.72e−01
Value: FS
Carnitine.Metabolism.in.Microorganisms
0.04
0.03
0.02
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

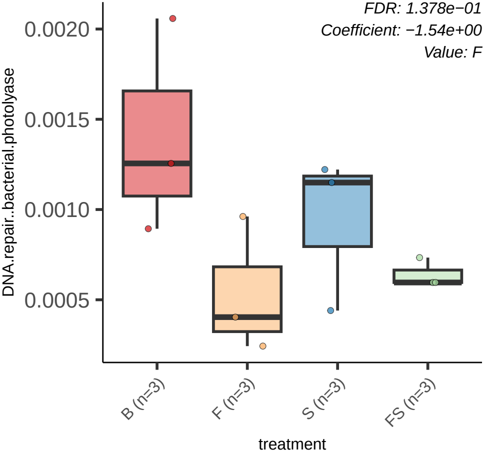

FDR: 1.372e−01
Coefficient: 2.62e−01
Value: F
Protocatechuate.branch.of.beta.ketoadipate.pathway
0.06
0.05
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

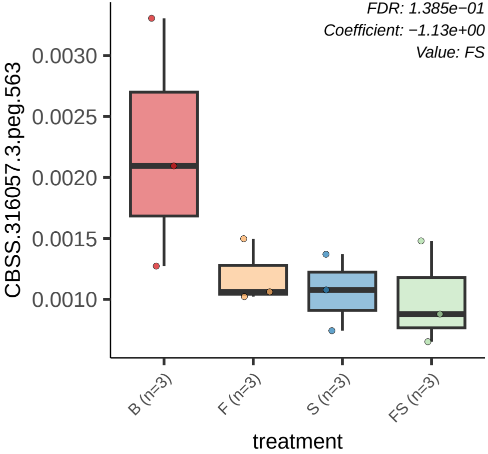


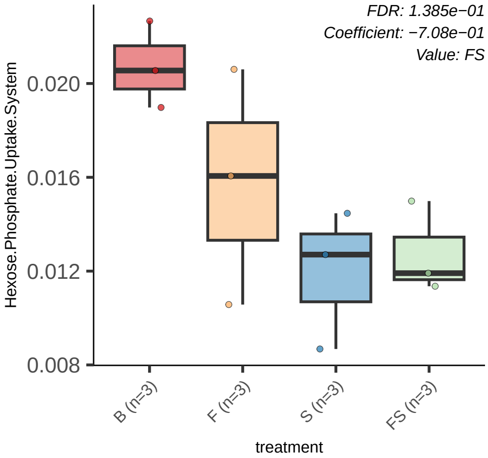
FDR: 1.372e−01
Coefficient: −6.39e−01
Value: FS
Siderophore.assembly.kit
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

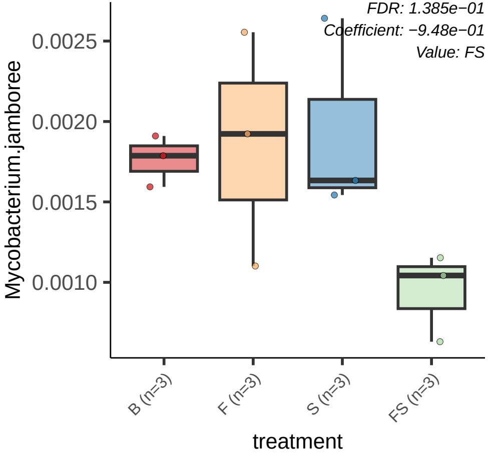

FDR: 1.372e−01
Coefficient: −7.18e−01
Value: F
YjbEFGH.Locus.Involved.in.Exopolysaccharide.Productio
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

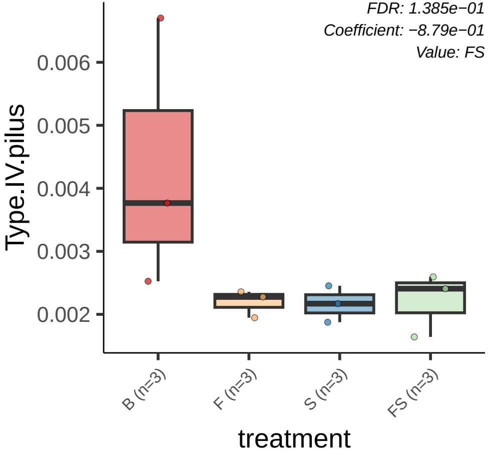

FDR: 1.378e−01
Coefficient: −4.87e−01
Value: F
Allantoin.Utilization
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

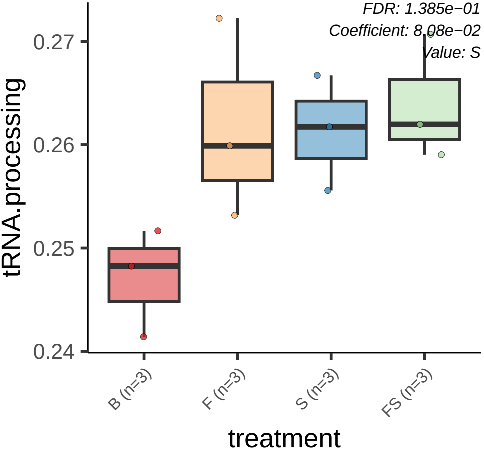

FDR: 1.378e−01
Coefficient: −1.54e+00
Value: F
DNA.repair..bacterial.photolyase
0.0020
0.0015
0.0010
0.0005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

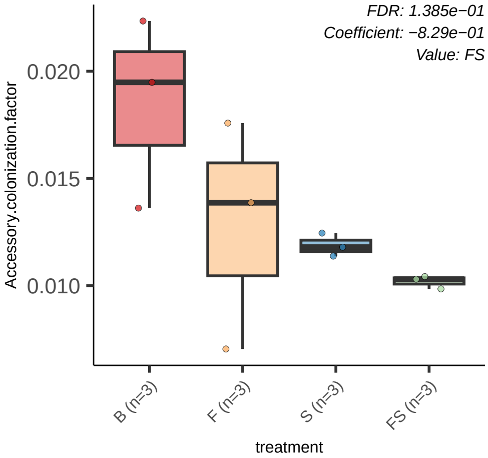

FDR: 1.385e−01
Coefficient: −1.13e+00
Value: FS
CBSS.316057.3.peg.563
0.0030
0.0025
0.0020
0.0015
0.0010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

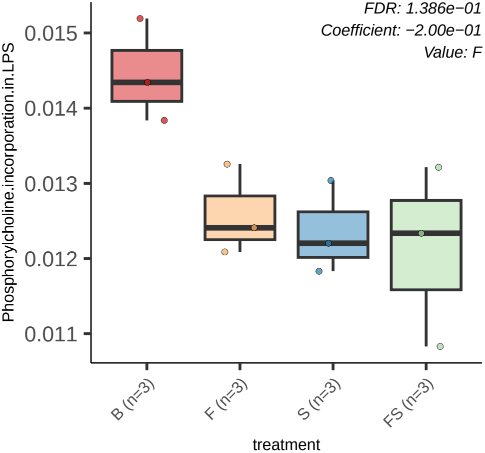

FDR: 1.385e−01
Coefficient: −7.08e−01
Value: FS
Hexose.Phosphate.Uptake.System
0.020
0.016
0.012
0.008
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

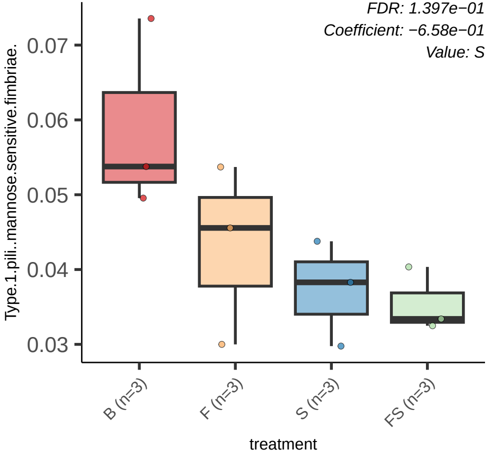

FDR: 1.385e−01
Coefficient: −9.48e−01
Value: FS
Mycobacterium.jamboree
0.0025
0.0020
0.0015
0.0010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

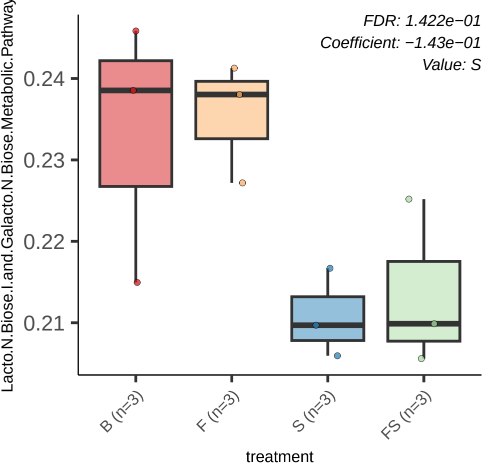

FDR: 1.385e−01
Coefficient: −8.79e−01
Value: FS
Type.IV.pilus
0.006
0.005
0.004
0.003
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

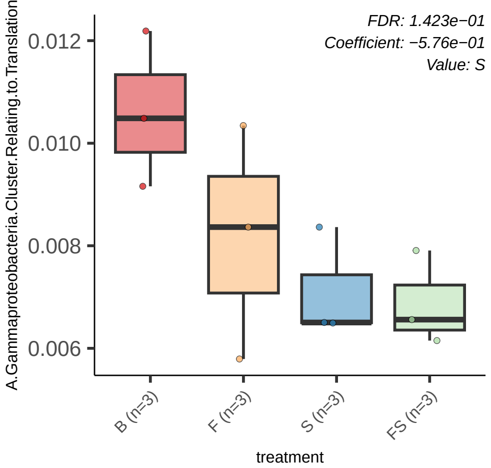

FDR: 1.385e−01
Coefficient: 8.08e−02
Value: S
tRNA.processing
0.27
0.26
0.25
0.24
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

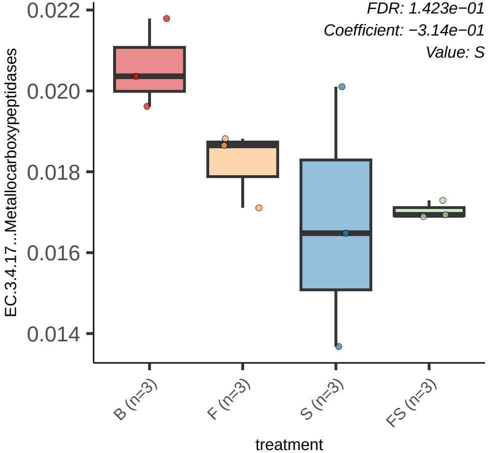

FDR: 1.385e−01
Coefficient: −8.29e−01
Value: FS
Accessory.colonization.factor
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

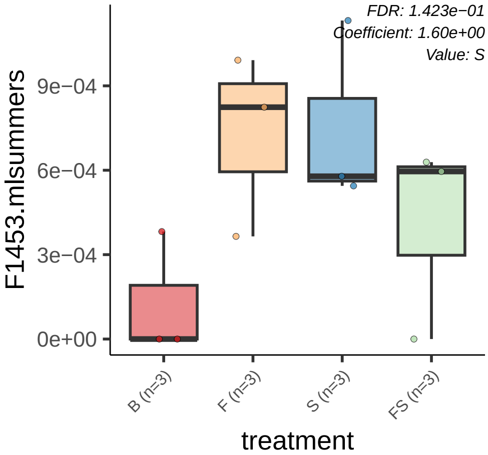

FDR: 1.386e−01
Coefficient: −2.00e−01
Value: F
Phosphorylcholine.incorporation.in.LPS
0.015
0.014
0.013
0.012
0.011
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

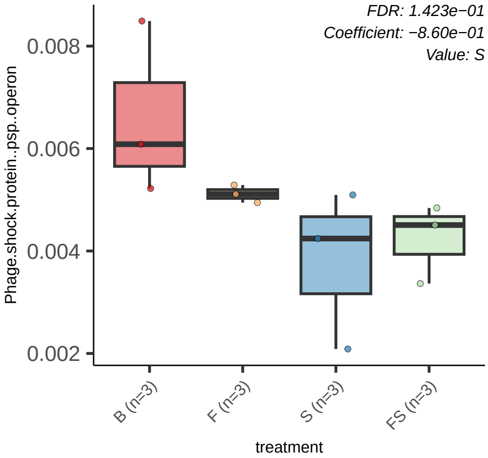

FDR: 1.397e−01
Coefficient: −6.58e−01
Value: S
Type.1.pili..mannose.sensitive.fimbriae.
0.07
0.06
0.05
0.04
0.03
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

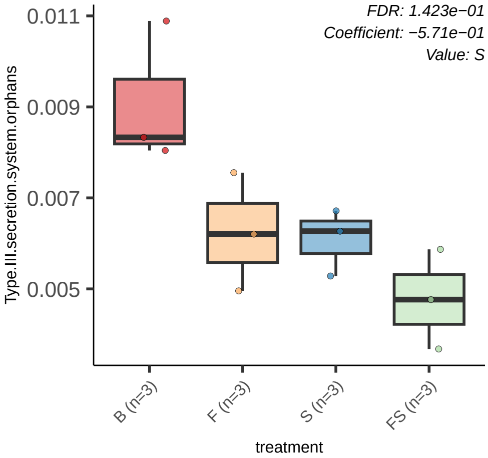

FDR: 1.422e−01
Coefficient: −1.43e−01
Value: S
Lacto.N.Biose.I.and.Galacto.N.Biose.Metabolic.Pathway
0.24
0.23
0.22
0.21
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

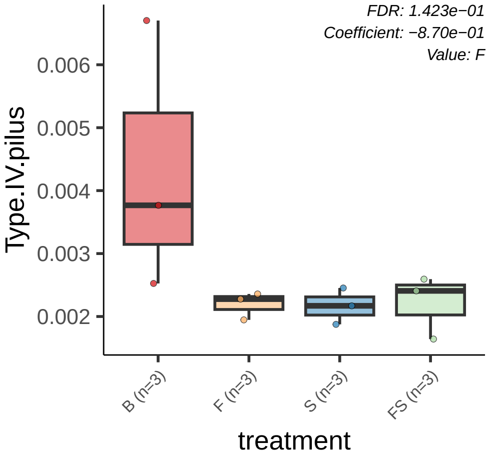

FDR: 1.423e−01
Coefficient: −5.76e−01
Value: S
A.Gammaproteobacteria.Cluster.Relating.to.Translation
0.012
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

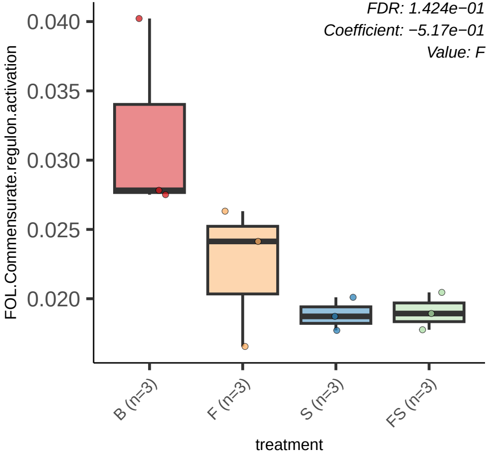

FDR: 1.423e−01
Coefficient: −3.14e−01
Value: S
EC.3.4.17...Metallocarboxypeptidases
0.022
0.020
0.018
0.016
0.014
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

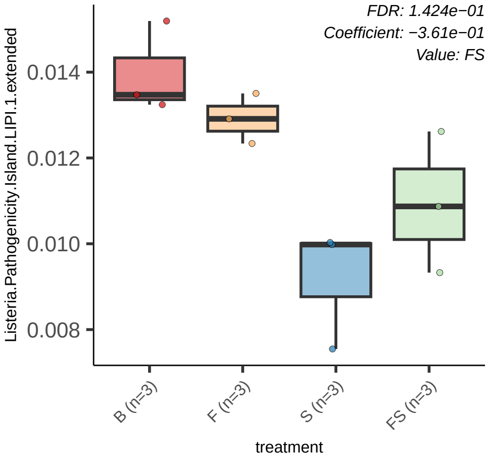

FDR: 1.423e−01
Coefficient: 1.60e+00
Value: S
F1453.mlsummers
9e−04
6e−04
3e−04
0e+00
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

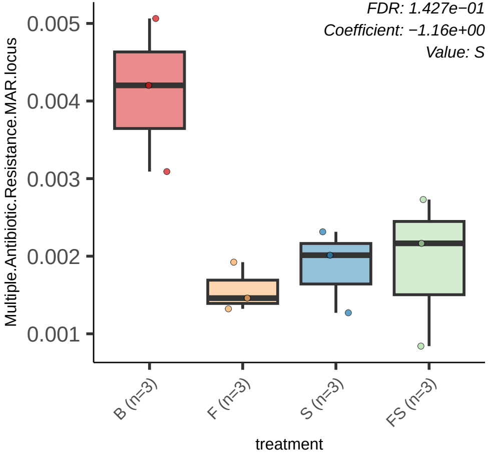

FDR: 1.423e−01
Coefficient: −8.60e−01
Value: S
Phage.shock.protein..psp.operon
0.008
0.006
0.004
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

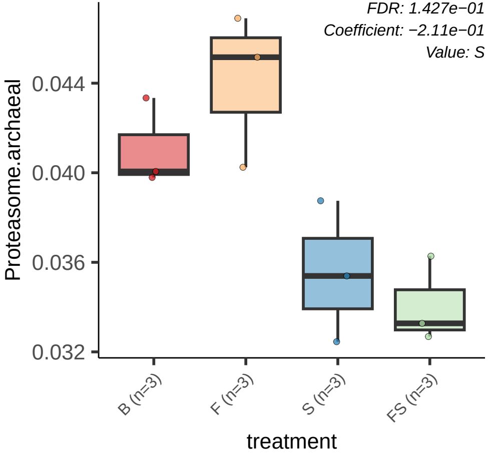

FDR: 1.423e−01
Coefficient: −5.71e−01
Value: S
Type.III.secretion.system.orphans
0.011
0.009
0.007
0.005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

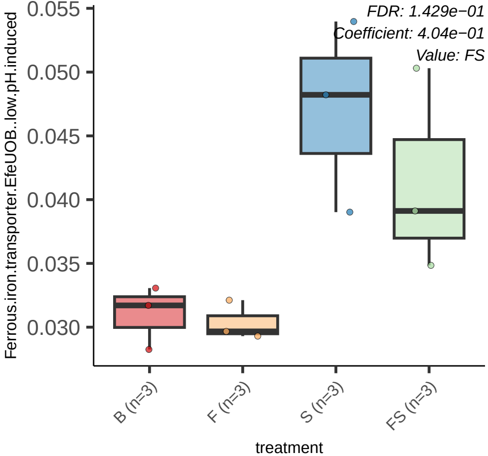

FDR: 1.423e−01
Coefficient: −8.70e−01
Value: F
Type.IV.pilus
0.006
0.005
0.004
0.003
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 1.424e−01
Coefficient: −5.17e−01
Value: F
FOL.Commensurate.regulon.activation
0.040
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

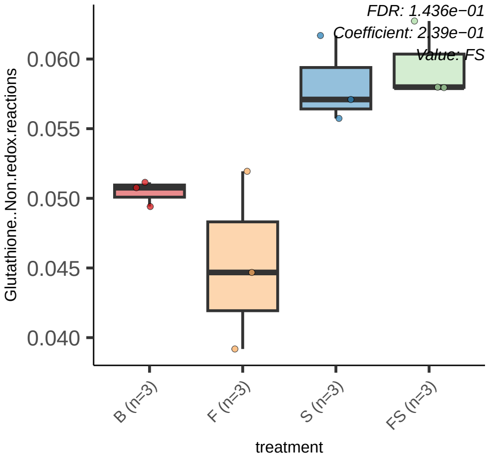

FDR: 1.424e−01
Coefficient: −3.61e−01
Value: FS
Listeria.Pathogenicity.Island.LIPI.1.extended
0.014
0.012
0.010
0.008
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

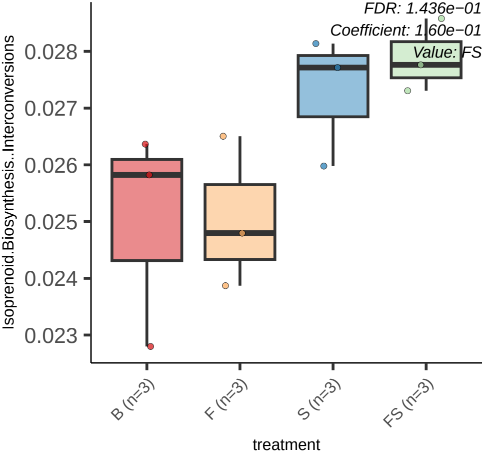

FDR: 1.427e−01
Coefficient: −1.16e+00
Value: S
Multiple.Antibiotic.Resistance.MAR.locus
0.005
0.004
0.003
0.002
0.001
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

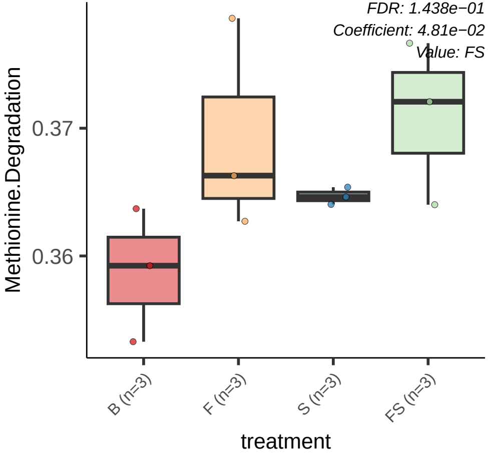

FDR: 1.427e−01
Coefficient: −2.11e−01
Value: S
Proteasome.archaeal
0.044
0.040
0.036
0.032
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

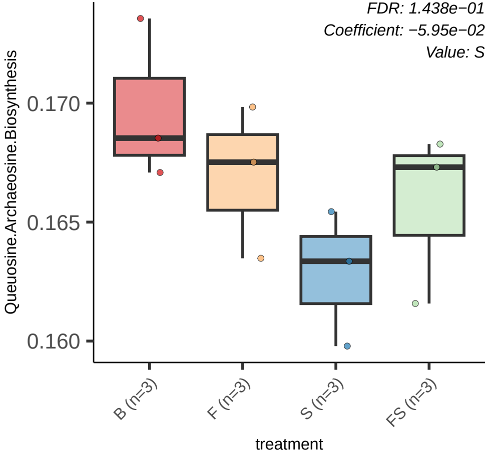


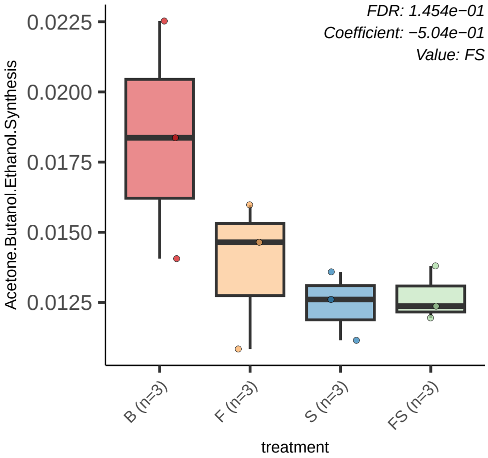
FDR: 1.429e−01
Coefficient: 4.04e−01
Value: FS
Ferrous.iron.transporter.EfeUOB..low.pH.induced
0.055
0.050
0.045
0.040
0.035
0.030
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

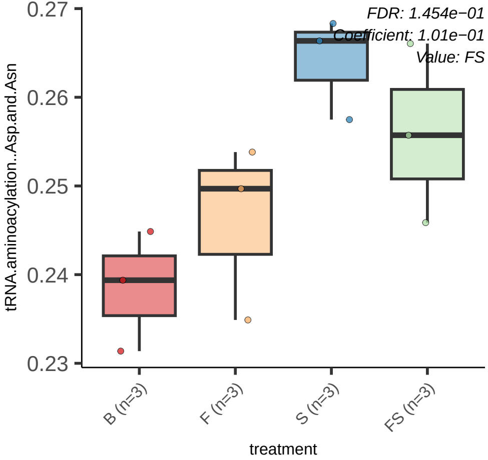

FDR: 1.436e−01
Coefficient: 2.39e−01
Value: FS
Glutathione..Non.redox.reactions
0.060
0.055
0.050
0.045
0.040
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 1.436e−01
Coefficient: 1.60e−01
Value: FS
Isoprenoid.Biosynthesis..Interconversions
0.028
0.027
0.026
0.025
0.024
0.023
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

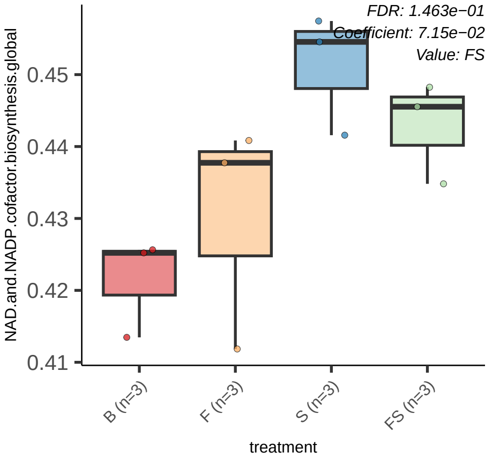

FDR: 1.438e−01
Coefficient: 4.81e−02
Value: FS
Methionine.Degradation
0.37
0.36
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 1.438e−01
Coefficient: −5.95e−02
Value: S
Queuosine.Archaeosine.Biosynthesis
0.170
0.165
0.160
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

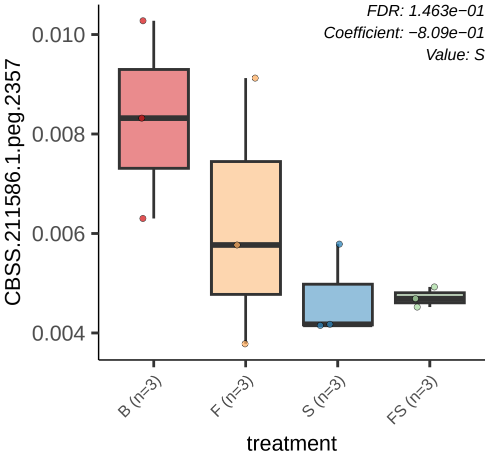

FDR: 1.454e−01
Coefficient: −5.04e−01
Value: FS
Acetone.Butanol.Ethanol.Synthesis
0.0225
0.0200
0.0175
0.0150
0.0125
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

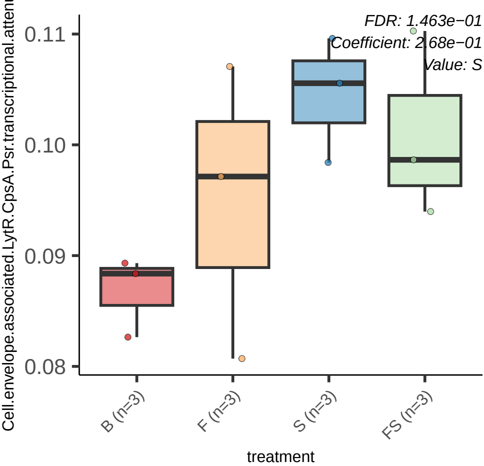


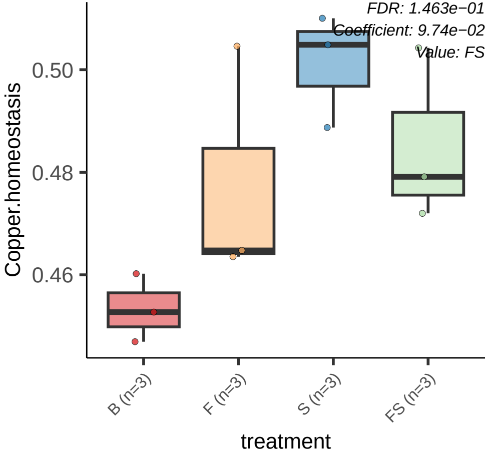
FDR: 1.454e−01
Coefficient: 1.01e−01
Value: FS
0.27
0.26
0.25
0.24
0.23
tRNA.aminoacylation..Asp.and.Asn
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

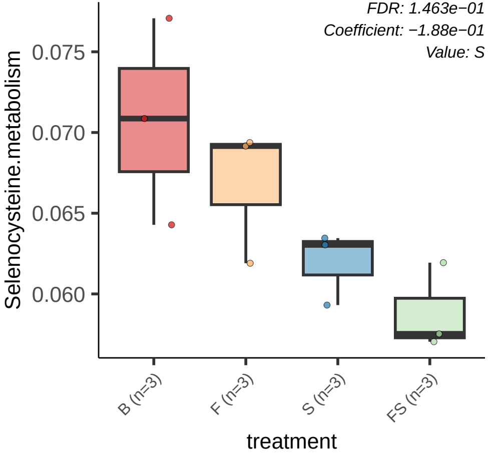


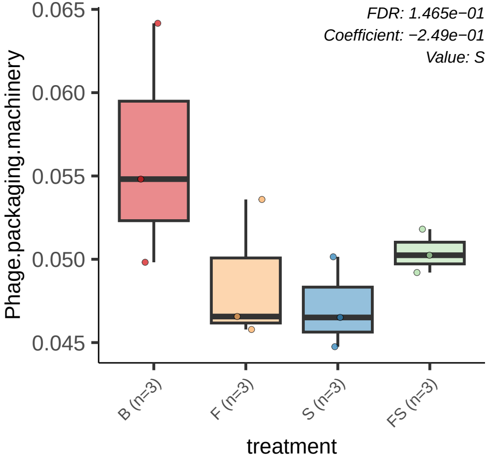
FDR: 1.463e−01
Coefficient: 7.15e−02
Value: FS
NAD.and.NADP.cofactor.biosynthesis.global
0.45
0.44
0.43
0.42
0.41
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

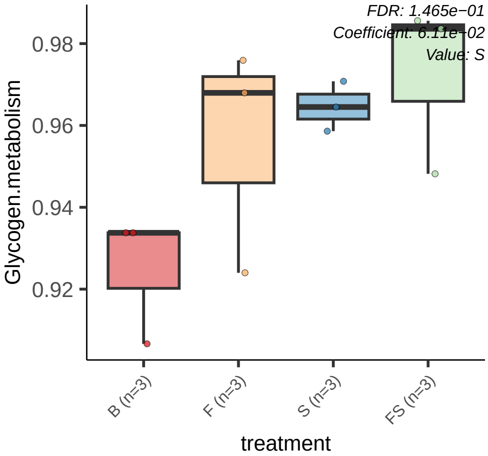

FDR: 1.463e−01
Coefficient: −8.09e−01
Value: S
CBSS.211586.1.peg.2357
0.010
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

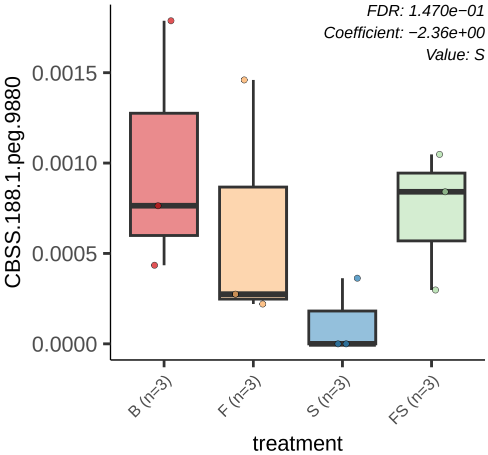

FDR: 1.463e−01
Coefficient: 2.68e−01
Value: S
Cell.envelope.associated.LytR.CpsA.Psr.transcriptional.atten
0.11
0.10
0.09
0.08
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

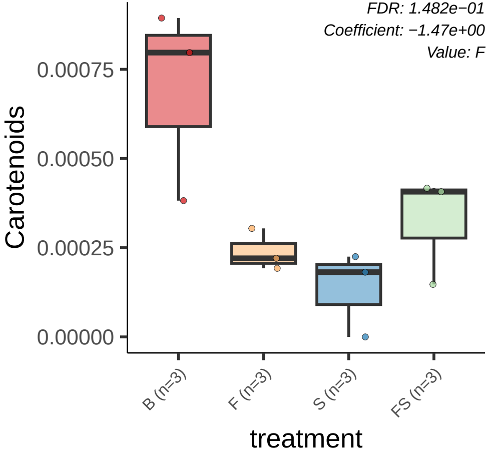

FDR: 1.463e−01
Coefficient: 9.74e−02
Value: FS
Copper.homeostasis
0.50
0.48
0.46
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

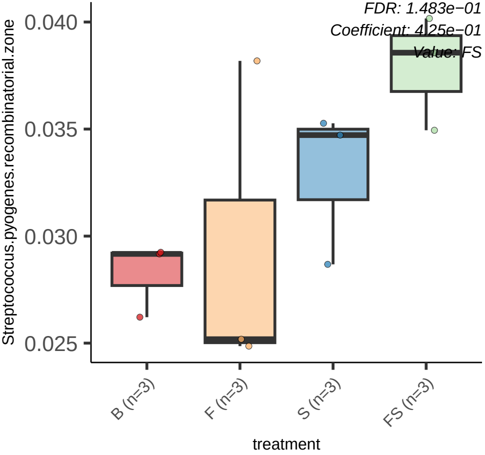

FDR: 1.463e−01
Coefficient: −1.88e−01
Value: S
Selenocysteine.metabolism
0.075
0.070
0.065
0.060
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

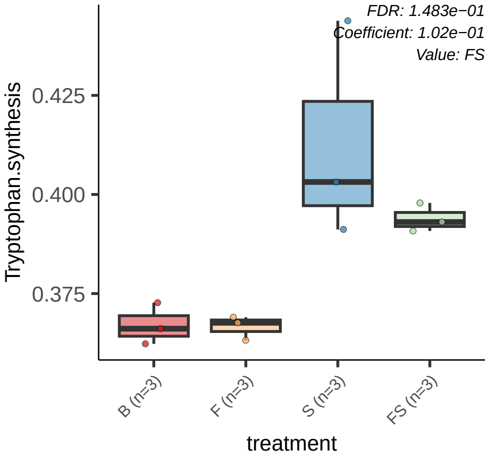

FDR: 1.465e−01
Coefficient: −2.49e−01
Value: S
Phage.packaging.machinery
0.065
0.060
0.055
0.050
0.045
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

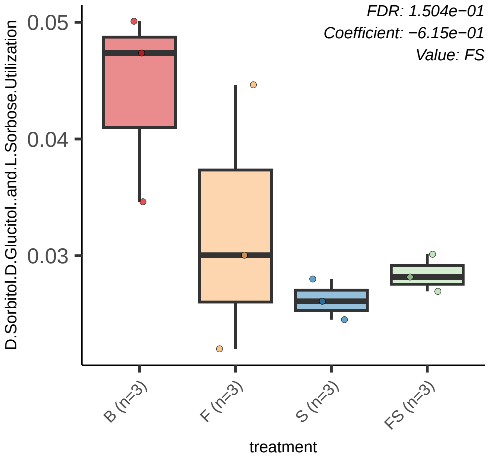

FDR: 1.465e−01
Coefficient: 6.11e−02
Value: S
Glycogen.metabolism
0.98
0.96
0.94
0.92
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

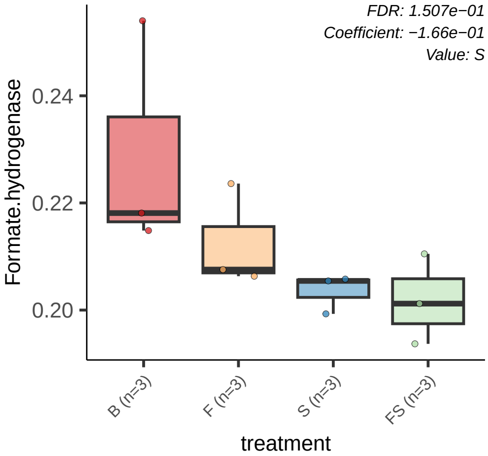

FDR: 1.470e−01
Coefficient: −2.36e+00
Value: S
CBSS.188.1.peg.9880
0.0015
0.0010
0.0005
0.0000
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

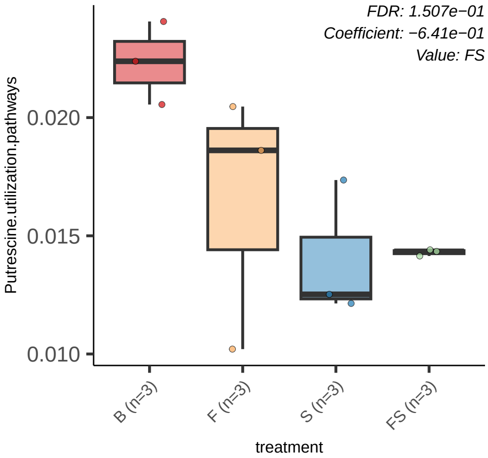

FDR: 1.482e−01
Coefficient: −1.47e+00
Value: F
Carotenoids
0.00075
0.00050
0.00025
0.00000
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

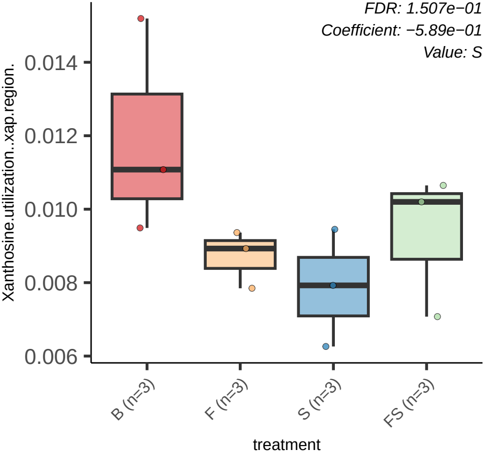

FDR: 1.483e−01
Coefficient: 4.25e−01
Value: FS
Streptococcus.pyogenes.recombinatorial.zone
0.040
0.035
0.030
0.025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

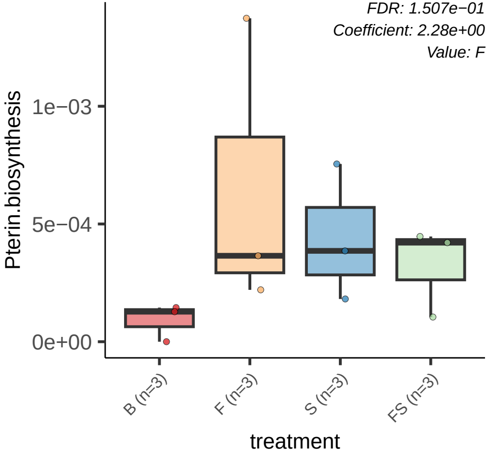

FDR: 1.483e−01
Coefficient: 1.02e−01
Value: FS
Tryptophan.synthesis
0.425
0.400
0.375
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

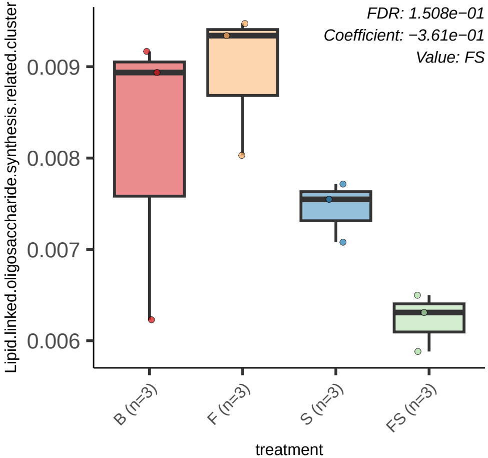

FDR: 1.504e−01
Coefficient: −6.15e−01
Value: FS
D.Sorbitol.D.Glucitol..and.L.Sorbose.Utilization
0.05
0.04
0.03
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

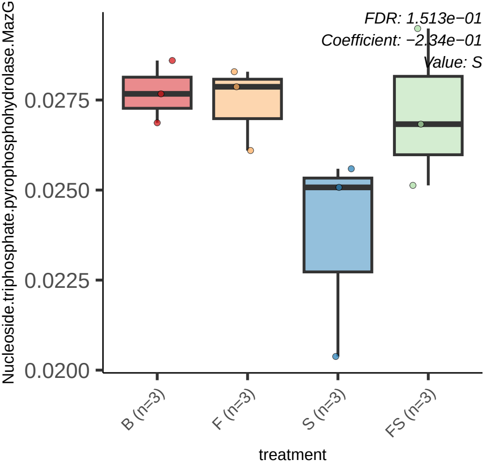

FDR: 1.507e−01
Coefficient: −1.66e−01
Value: S
Formate.hydrogenase
0.24
0.22
0.20
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

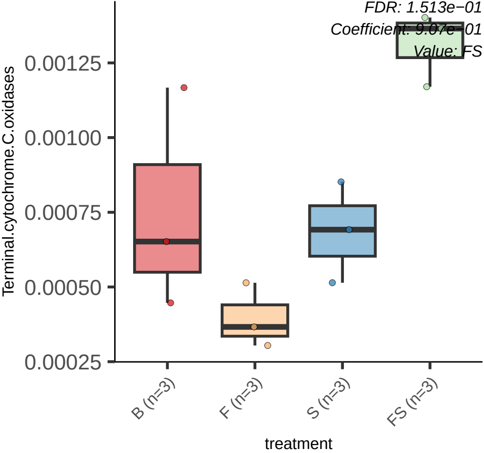

FDR: 1.507e−01
Coefficient: −6.41e−01
Value: FS
Putrescine.utilization.pathways
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

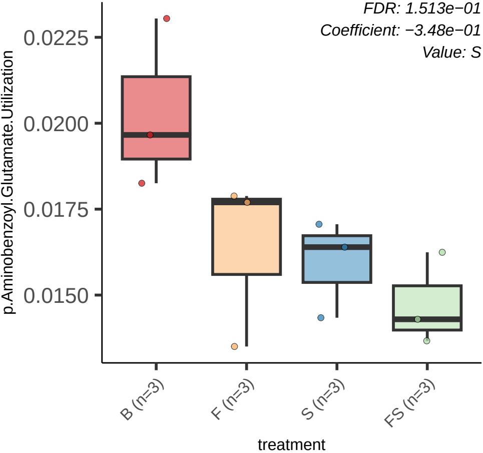

FDR: 1.507e−01
Coefficient: −5.89e−01
Value: S
Xanthosine.utilization..xap.region.
0.014
0.012
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

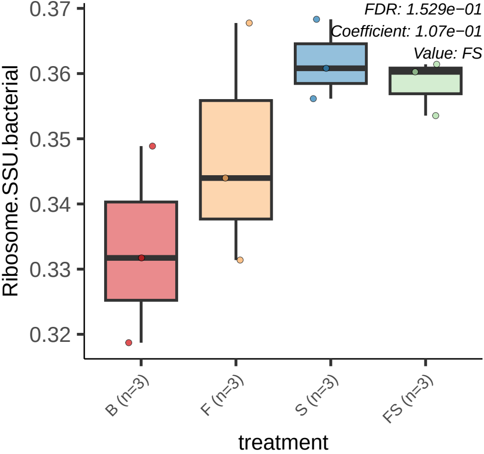

FDR: 1.507e−01
Coefficient: 2.28e+00
Value: F
Pterin.biosynthesis
1e−03
5e−04
0e+00
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

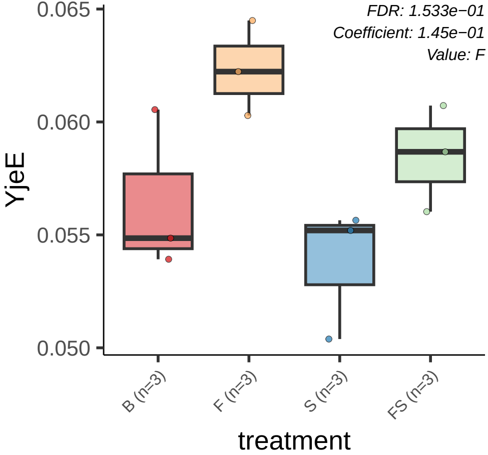

FDR: 1.508e−01
Coefficient: −3.61e−01
Value: FS
Lipid.linked.oligosaccharide.synthesis.related.cluster
0.009
0.008
0.007
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

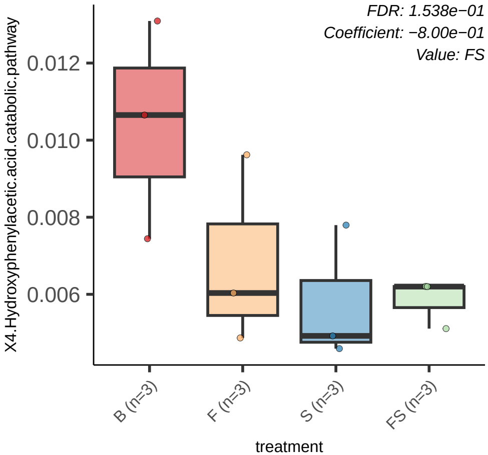

FDR: 1.513e−01
Coefficient: −2.34e−01
Value: S
Nucleoside.triphosphate.pyrophosphohydrolase.MazG
0.0275
0.0250
0.0225
0.0200
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

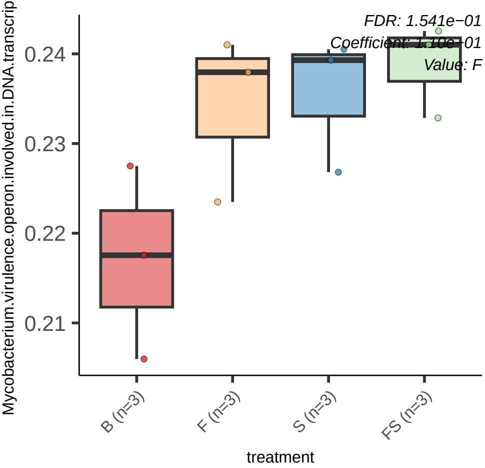

FDR: 1.513e−01
Coefficient: 9.07e−01
Value: FS
Terminal.cytochrome.C.oxidases
0.00125
0.00100
0.00075
0.00050
0.00025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

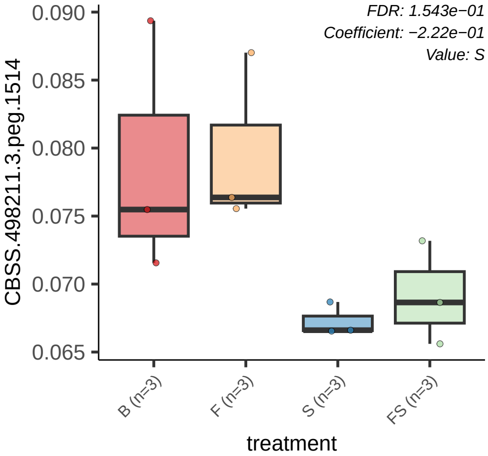

FDR: 1.513e−01
Coefficient: −3.48e−01
Value: S
p.Aminobenzoyl.Glutamate.Utilization
0.0225
0.0200
0.0175
0.0150
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

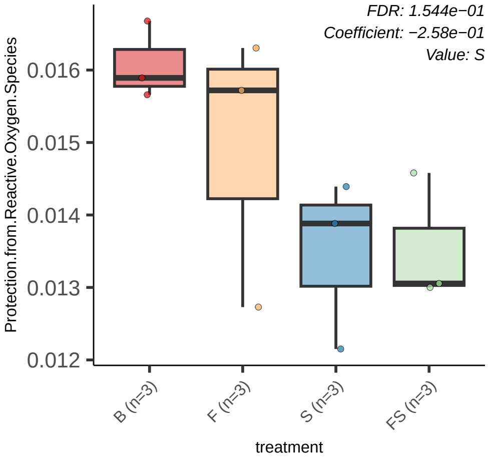

FDR: 1.529e−01
Coefficient: 1.07e−01
Value: FS
Ribosome.SSU.bacterial
0.37
0.36
0.35
0.34
0.33
0.32
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

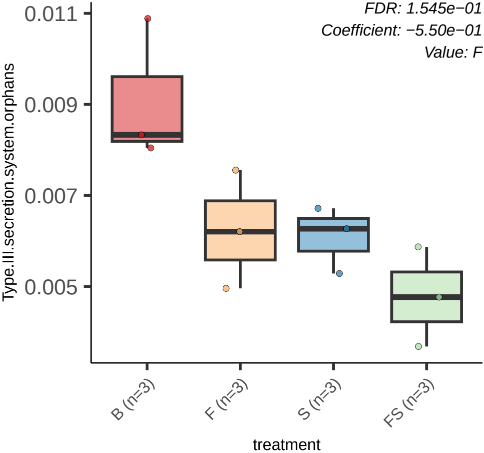

FDR: 1.533e−01
Coefficient: 1.45e−01
Value: F
YjeE
0.065
0.060
0.055
0.050
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

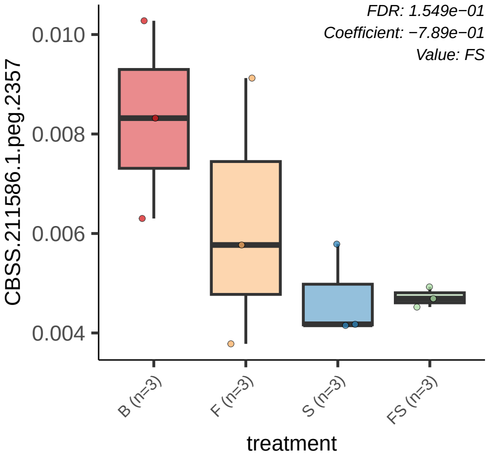

FDR: 1.538e−01
Coefficient: −8.00e−01
Value: FS
X4.Hydroxyphenylacetic.acid.catabolic.pathway
0.012
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

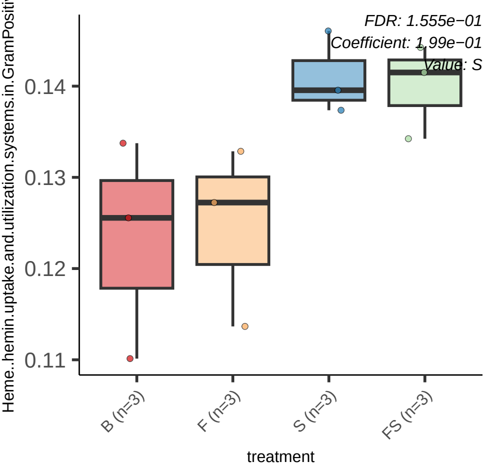

FDR: 1.541e−01
Coefficient: 1.10e−01
Value: F
Mycobacterium.virulence.operon.involved.in.DNA.transcrip
0.24
0.23
0.22
0.21
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

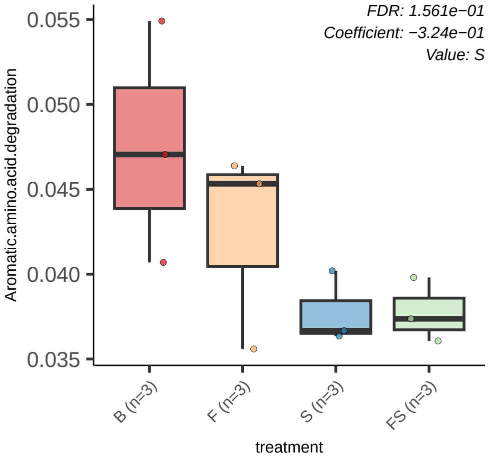

FDR: 1.543e−01
Coefficient: −2.22e−01
Value: S
CBSS.498211.3.peg.1514
0.090
0.085
0.080
0.075
0.070
0.065
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

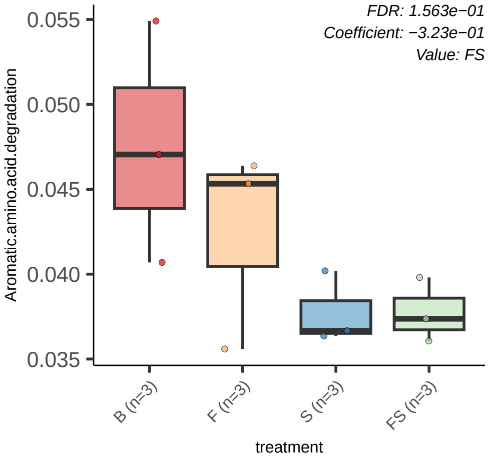

FDR: 1.544e−01
Coefficient: −2.58e−01
Value: S
Protection.from.Reactive.Oxygen.Species
0.016
0.015
0.014
0.013
0.012
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

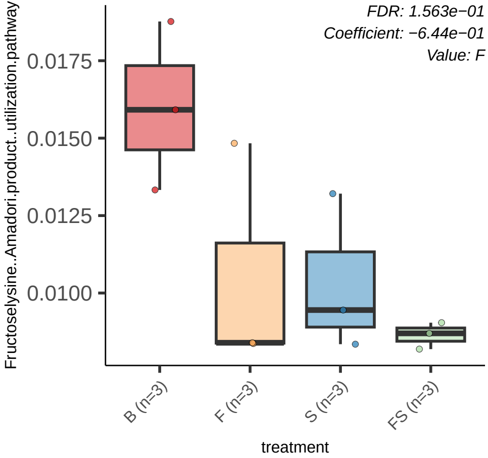

FDR: 1.545e−01
Coefficient: −5.50e−01
Value: F
Type.III.secretion.system.orphans
0.011
0.009
0.007
0.005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

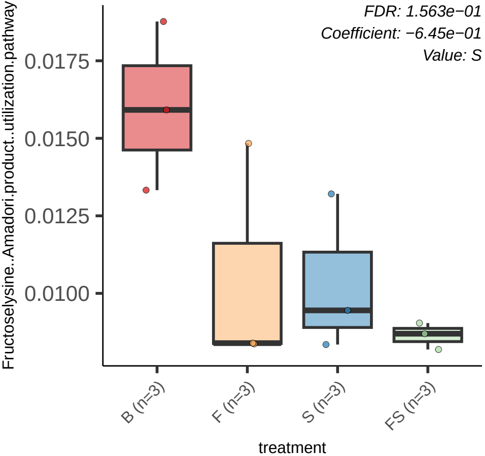

FDR: 1.549e−01
Coefficient: −7.89e−01
Value: FS
CBSS.211586.1.peg.2357
0.010
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

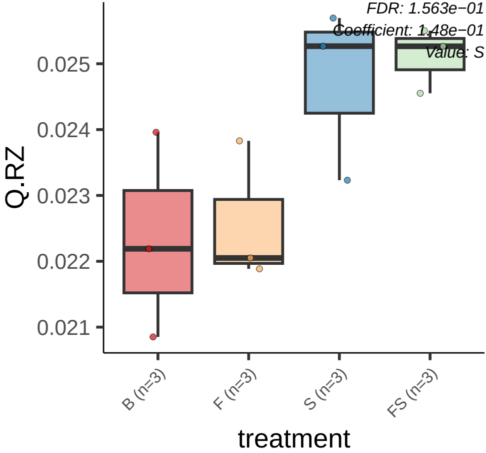

FDR: 1.555e−01
Coefficient: 1.99e−01
Value: S
Heme..hemin.uptake.and.utilization.systems.in.GramPositi
0.14
0.13
0.12
0.11
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

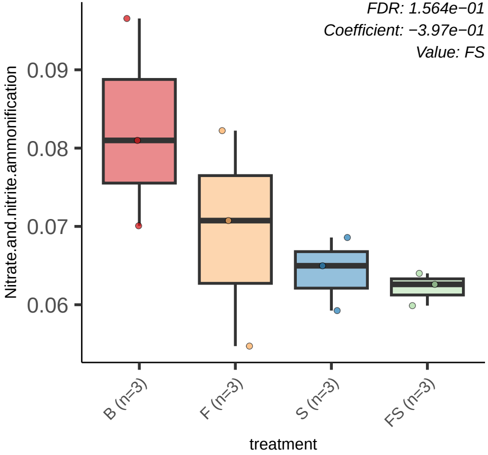

FDR: 1.561e−01
Coefficient: −3.24e−01
Value: S
Aromatic.amino.acid.degradation
0.055
0.050
0.045
0.040
0.035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

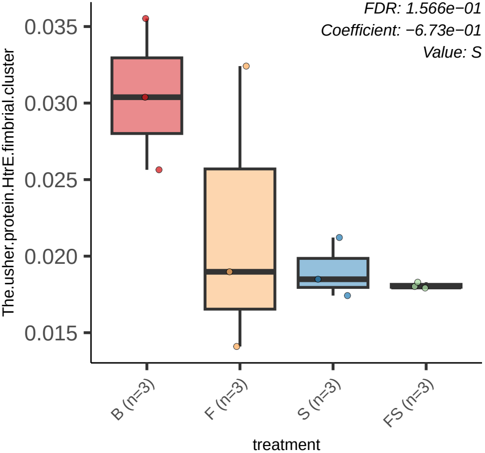

FDR: 1.563e−01
Coefficient: −3.23e−01
Value: FS
Aromatic.amino.acid.degradation
0.055
0.050
0.045
0.040
0.035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

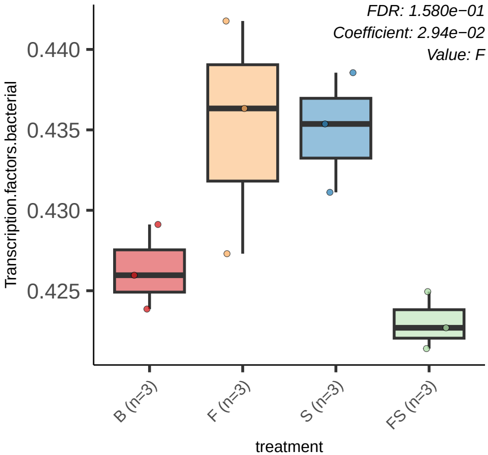

FDR: 1.563e−01
Coefficient: −6.44e−01
Value: F
Fructoselysine..Amadori.product..utilization.pathway
0.0175
0.0150
0.0125
0.0100
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

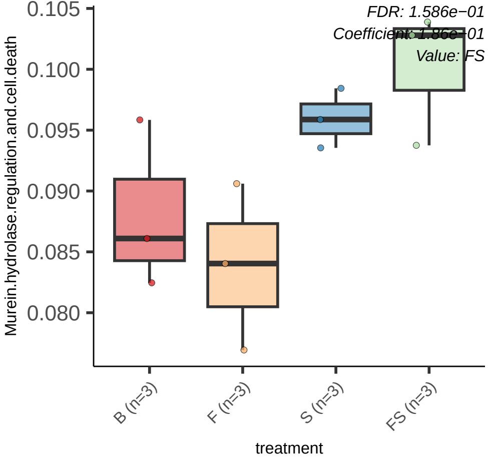

FDR: 1.563e−01
Coefficient: −6.45e−01
Value: S
Fructoselysine..Amadori.product..utilization.pathway
0.0175
0.0150
0.0125
0.0100
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

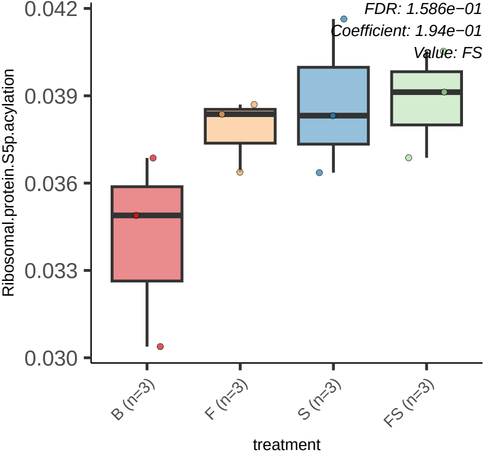

FDR: 1.563e−01
Coefficient: 1.48e−01
Value: S
Q.RZ
0.025
0.024
0.023
0.022
0.021
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

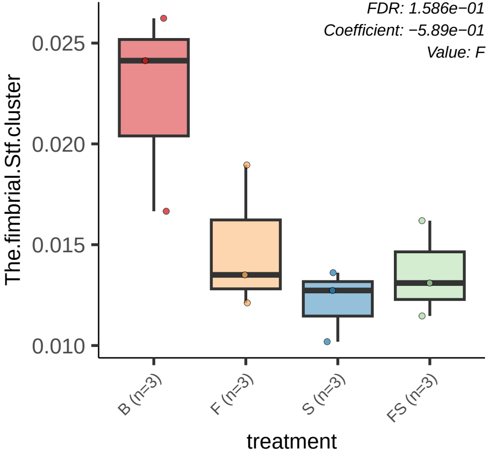

FDR: 1.564e−01
Coefficient: −3.97e−01
Value: FS
Nitrate.and.nitrite.ammonification
0.09
0.08
0.07
0.06
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

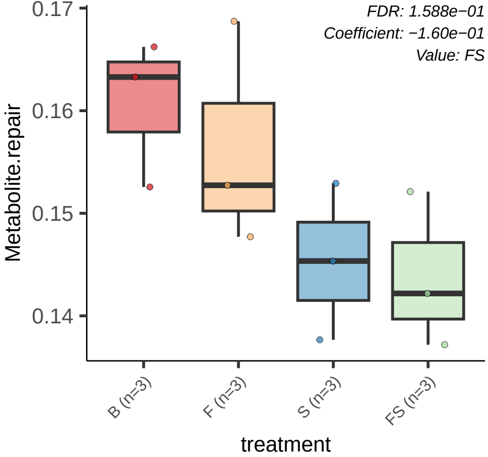

FDR: 1.566e−01
Coefficient: −6.73e−01
Value: S
The.usher.protein.HtrE.fimbrial.cluster
0.035
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

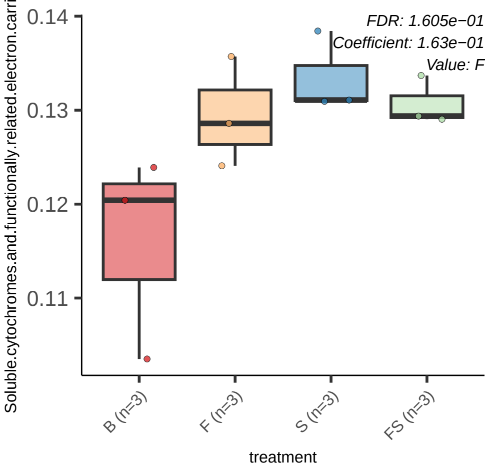

FDR: 1.580e−01
Coefficient: 2.94e−02
Value: F
Transcription.factors.bacterial
0.440
0.435
0.430
0.425
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

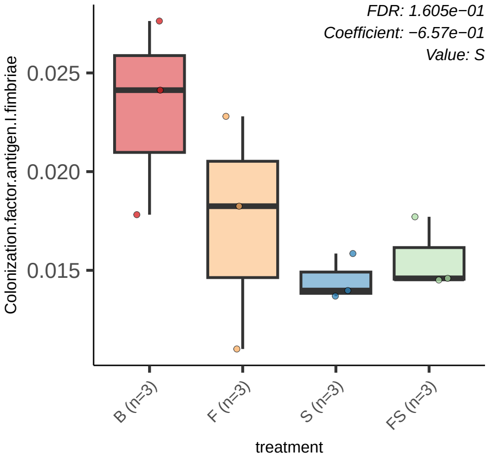

FDR: 1.586e−01
Coefficient: 1.86e−01
Value: FS
Murein.hydrolase.regulation.and.cell.death
0.105
0.100
0.095
0.090
0.085
0.080
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

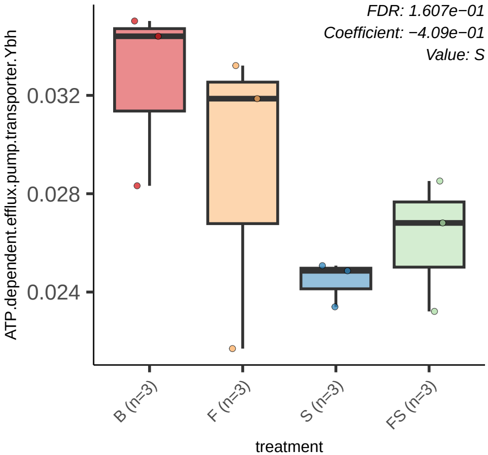

FDR: 1.586e−01
Coefficient: 1.94e−01
Value: FS
Ribosomal.protein.S5p.acylation
0.042
0.039
0.036
0.033
0.030
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

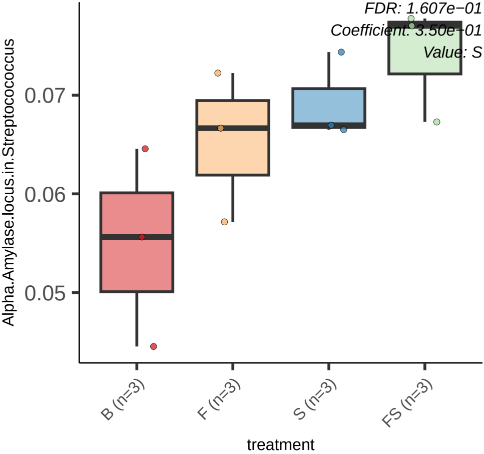

FDR: 1.586e−01
Coefficient: −5.89e−01
Value: F
The.fimbrial.Stf.cluster
0.025
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

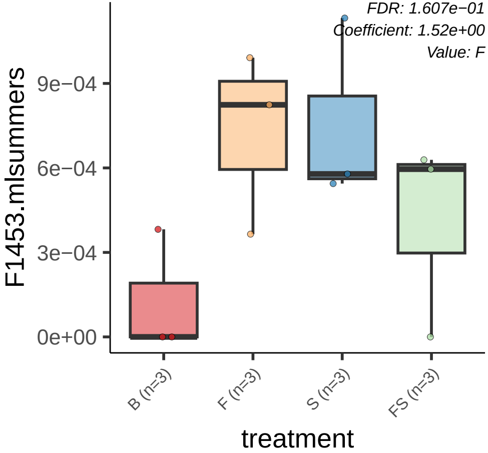

FDR: 1.588e−01
Coefficient: −1.60e−01
Value: FS
Metabolite.repair
0.17
0.16
0.15
0.14
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

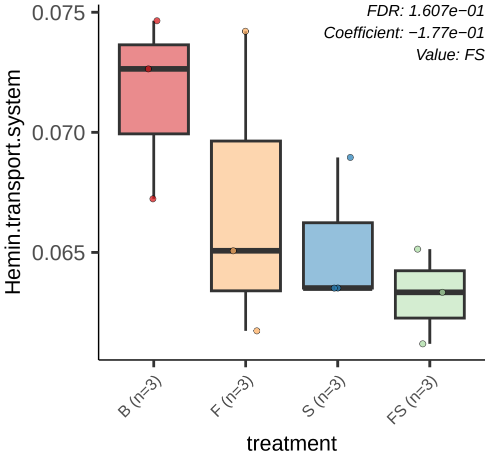

FDR: 1.605e−01
Coefficient: 1.63e−01
Value: F
Soluble.cytochromes.and.functionally.related.electron.carri
0.14
0.13
0.12
0.11
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

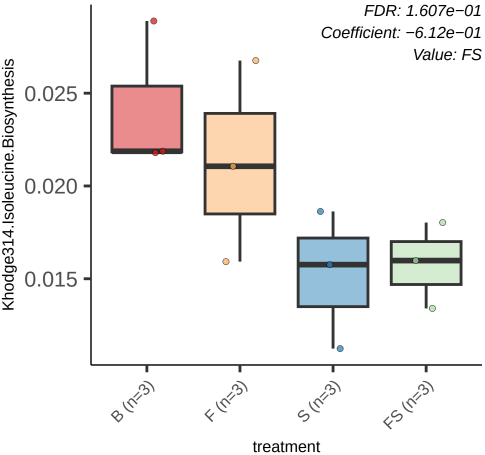

FDR: 1.605e−01
Coefficient: −6.57e−01
Value: S
Colonization.factor.antigen.I.fimbriae
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

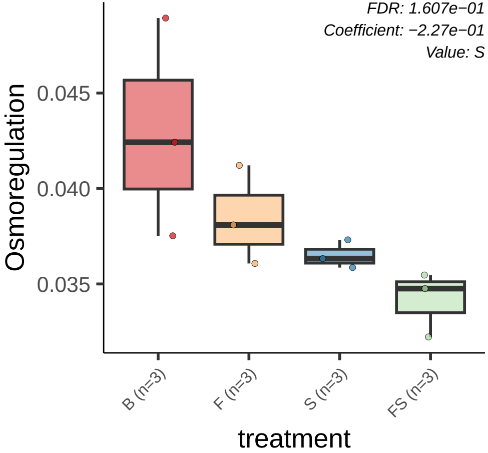

FDR: 1.607e−01
Coefficient: −4.09e−01
Value: S
ATP.dependent.efflux.pump.transporter.Ybh
0.032
0.028
0.024
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

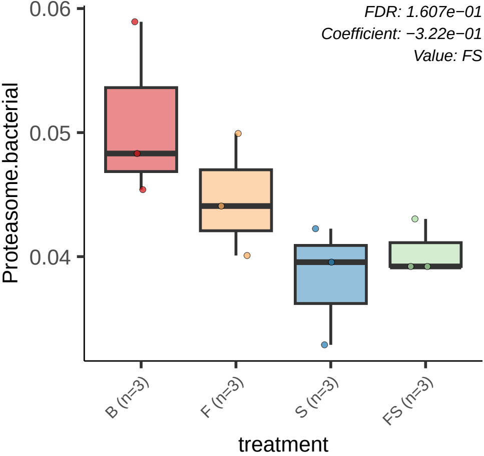

FDR: 1.607e−01
Coefficient: 3.50e−01
Value: S
Alpha.Amylase.locus.in.Streptococcus
0.07
0.06
0.05
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

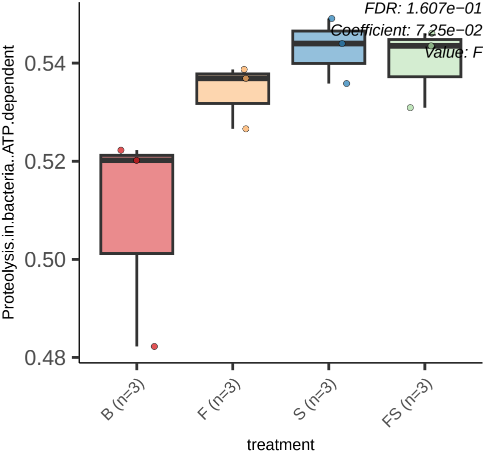

FDR: 1.607e−01
Coefficient: 1.52e+00
Value: F
F1453.mlsummers
9e−04
6e−04
3e−04
0e+00
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 1.607e−01
Coefficient: −1.77e−01
Value: FS
Hemin.transport.system
0.075
0.070
0.065
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

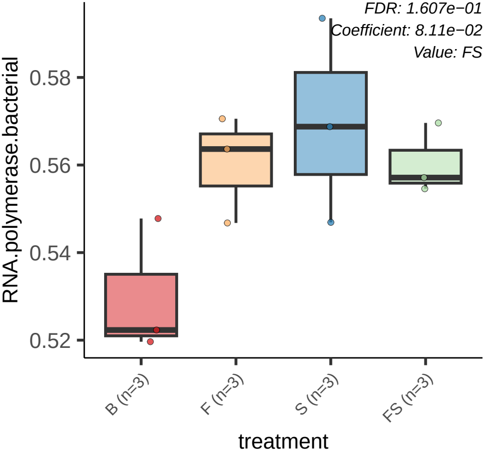

FDR: 1.607e−01
Coefficient: −6.12e−01
Value: FS
Khodge314.Isoleucine.Biosynthesis
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

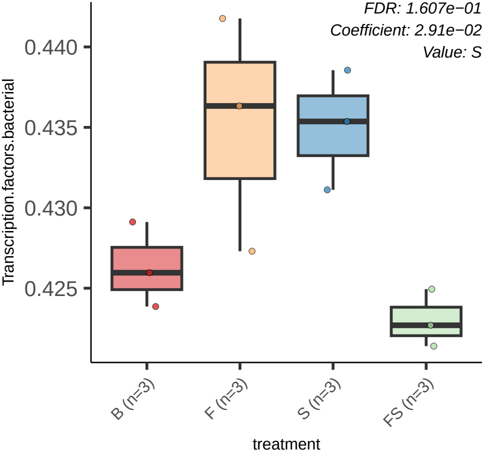

FDR: 1.607e−01
Coefficient: −2.27e−01
Value: S
Osmoregulation
0.045
0.040
0.035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

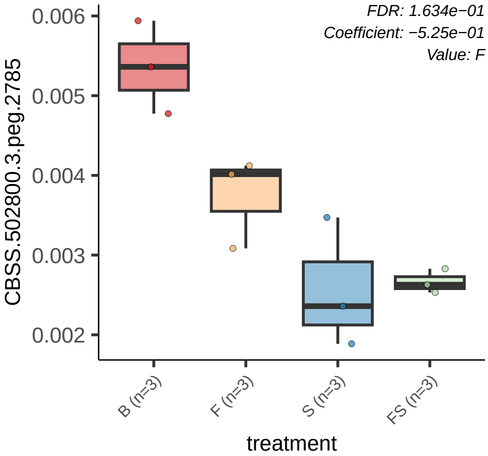

FDR: 1.607e−01
Coefficient: −3.22e−01
Value: FS
Proteasome.bacterial
0.06
0.05
0.04
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

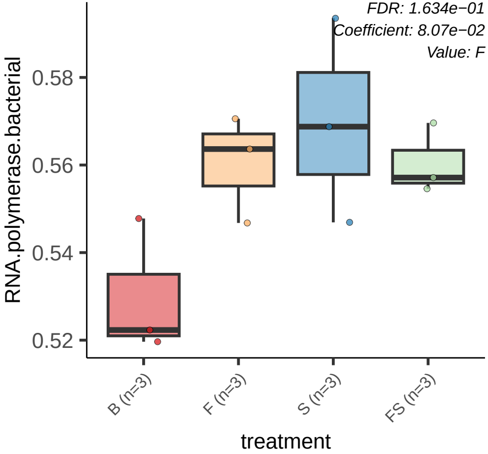


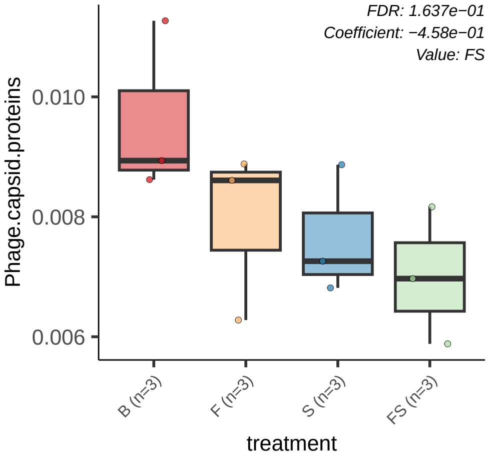
FDR: 1.607e−01
Coefficient: 7.25e−02
Value: F
Proteolysis.in.bacteria..ATP.dependent
0.54
0.52
0.50
0.48
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

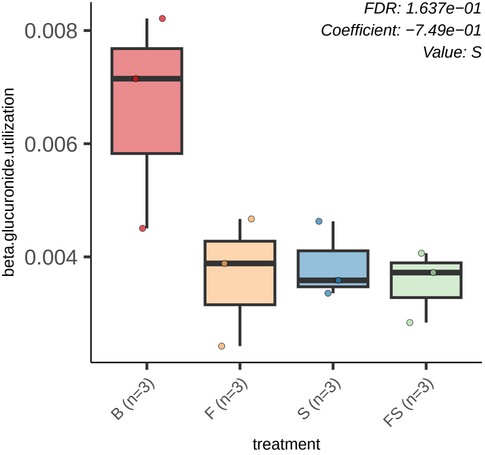

FDR: 1.607e−01
Coefficient: 8.11e−02
Value: FS
RNA.polymerase.bacterial
0.58
0.56
0.54
0.52
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

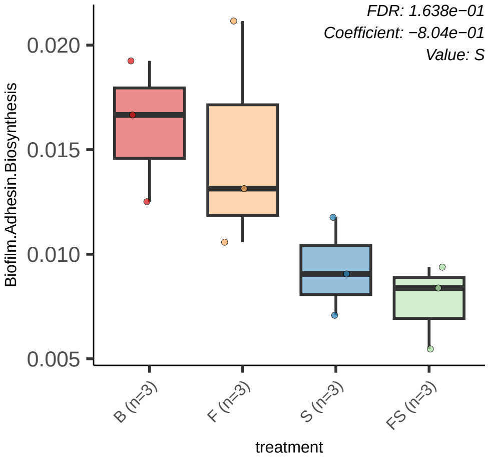

FDR: 1.607e−01
Coefficient: 2.91e−02
Value: S
Transcription.factors.bacterial
0.440
0.435
0.430
0.425
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

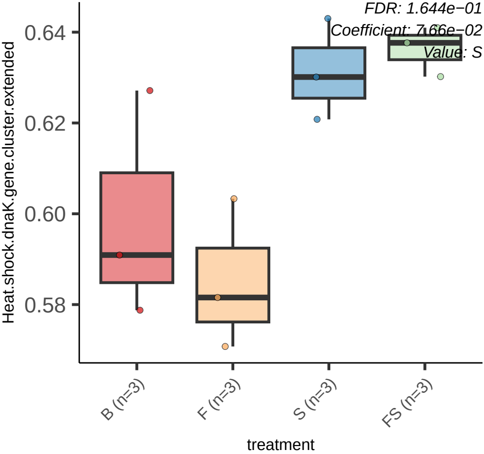

FDR: 1.634e−01
Coefficient: −5.25e−01
Value: F
CBSS.502800.3.peg.2785
0.006
0.005
0.004
0.003
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

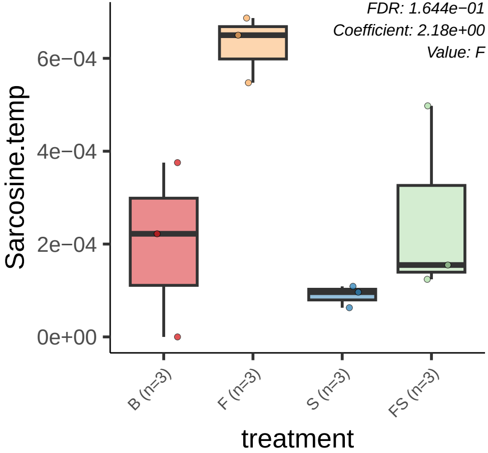

FDR: 1.634e−01
Coefficient: 8.07e−02
Value: F
RNA.polymerase.bacterial
0.58
0.56
0.54
0.52
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

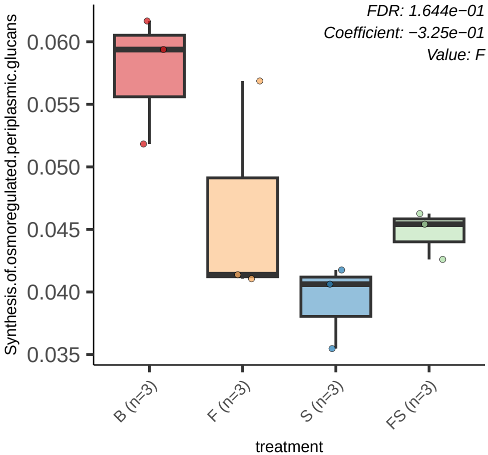

FDR: 1.637e−01
Coefficient: −4.58e−01
Value: FS
Phage.capsid.proteins
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

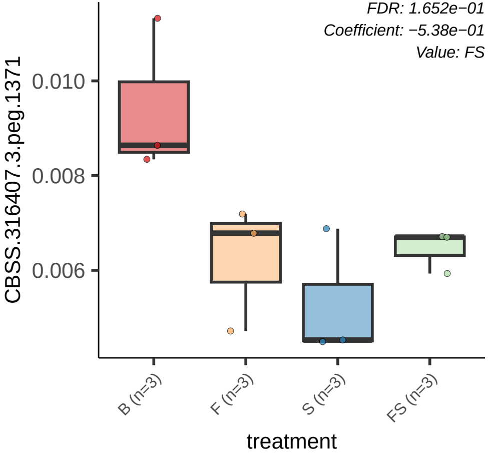

FDR: 1.637e−01
Coefficient: −7.49e−01
Value: S
beta.glucuronide.utilization
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

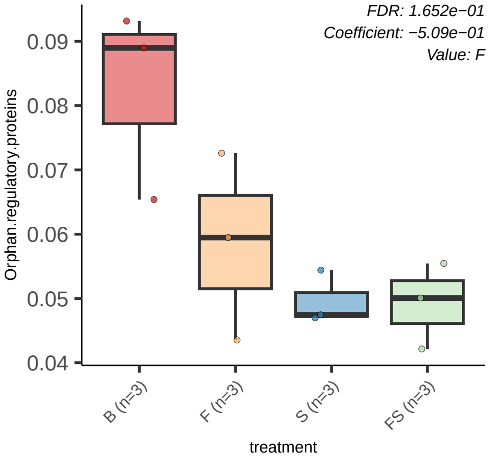

FDR: 1.638e−01
Coefficient: −8.04e−01
Value: S
Biofilm.Adhesin.Biosynthesis
0.020
0.015
0.010
0.005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

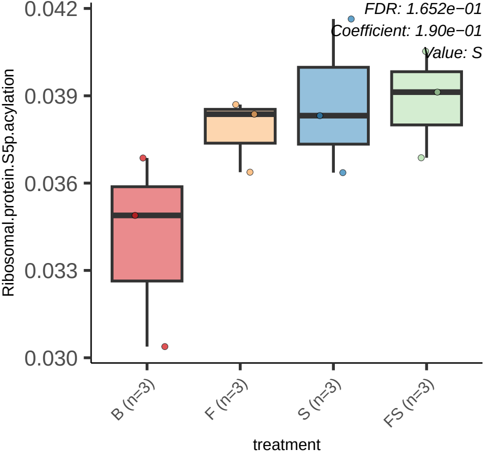

FDR: 1.644e−01
Coefficient: 7.66e−02
Value: S
Heat.shock.dnaK.gene.cluster.extended
0.64
0.62
0.60
0.58
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

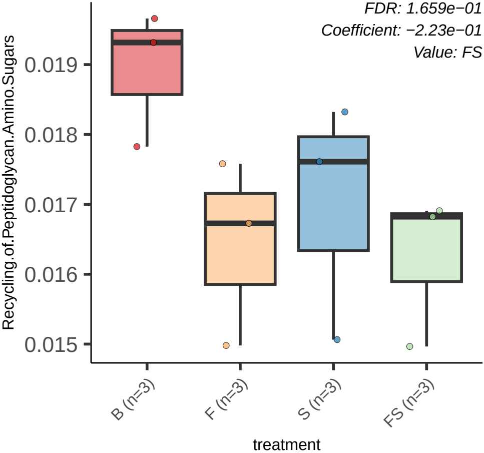

FDR: 1.644e−01
Coefficient: 2.18e+00
Value: F
Sarcosine.temp
6e−04
4e−04
2e−04
0e+00
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

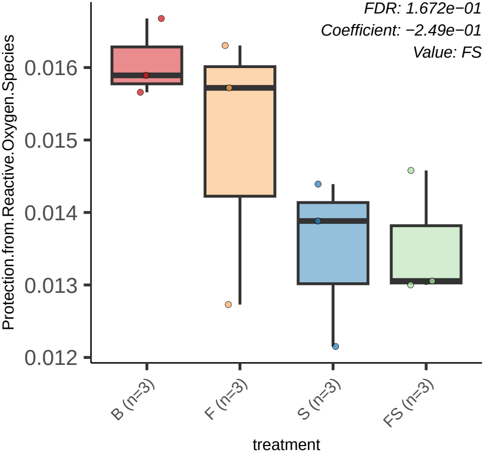

FDR: 1.644e−01
Coefficient: −3.25e−01
Value: F
Synthesis.of.osmoregulated.periplasmic.glucans
0.060
0.055
0.050
0.045
0.040
0.035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

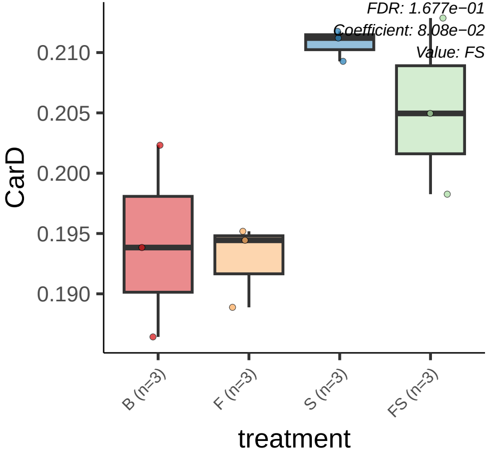

FDR: 1.652e−01
Coefficient: −5.38e−01
Value: FS
CBSS.316407.3.peg.1371
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

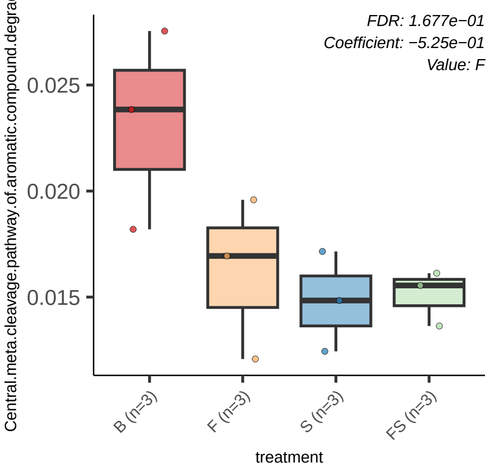

FDR: 1.652e−01
Coefficient: −5.09e−01
Value: F
Orphan.regulatory.proteins
0.09
0.08
0.07
0.06
0.05
0.04
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

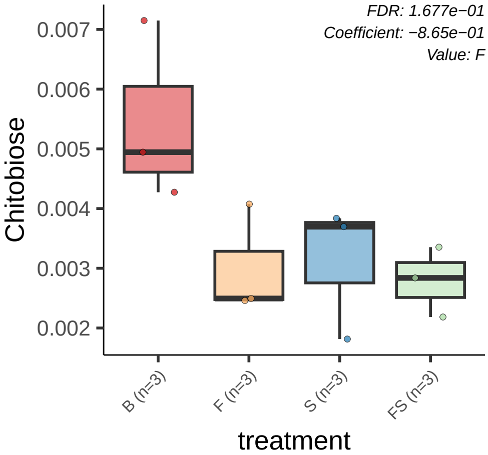

FDR: 1.652e−01
Coefficient: 1.90e−01
Value: S
Ribosomal.protein.S5p.acylation
0.042
0.039
0.036
0.033
0.030
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

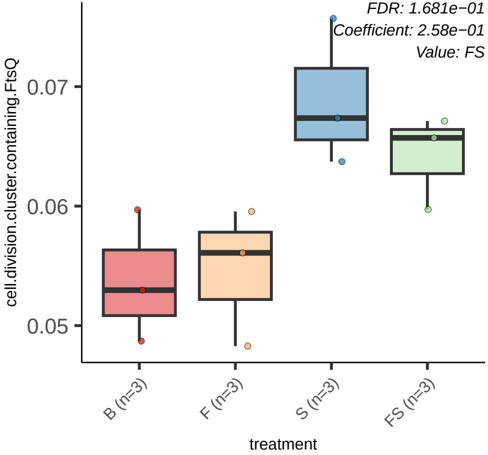

FDR: 1.659e−01
Coefficient: −2.23e−01
Value: FS
Recycling.of.Peptidoglycan.Amino.Sugars
0.019
0.018
0.017
0.016
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

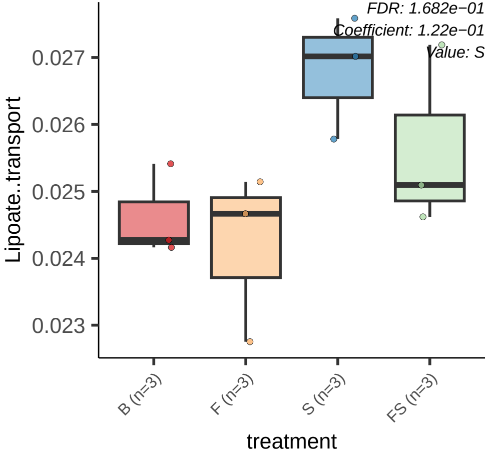

FDR: 1.672e−01
Coefficient: −2.49e−01
Value: FS
Protection.from.Reactive.Oxygen.Species
0.016
0.015
0.014
0.013
0.012
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

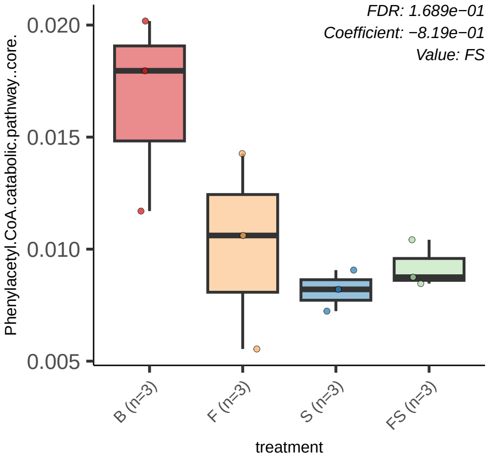

FDR: 1.677e−01
Coefficient: 8.08e−02
Value: FS
CarD
0.210
0.205
0.200
0.195
0.190
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

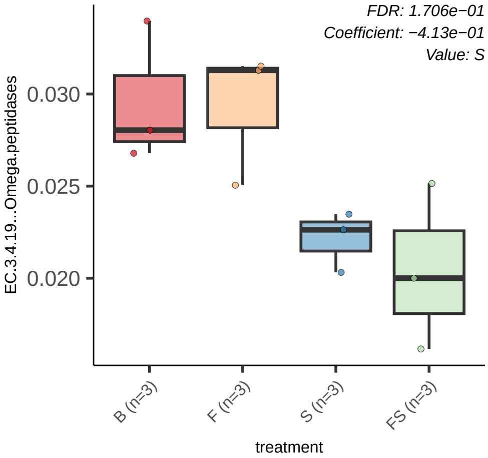

FDR: 1.677e−01
Coefficient: −5.25e−01
Value: F
Central.meta.cleavage.pathway.of.aromatic.compound.degrad
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

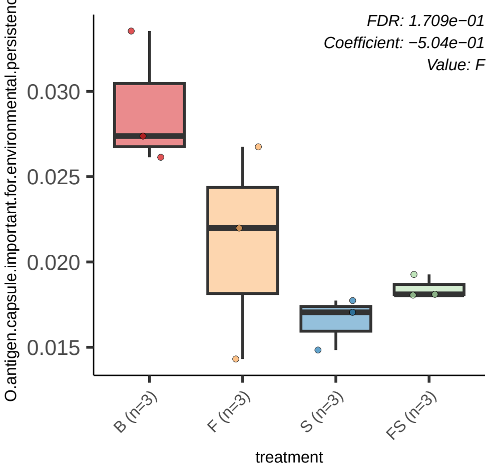

FDR: 1.677e−01
Coefficient: −8.65e−01
Value: F
Chitobiose
0.007
0.006
0.005
0.004
0.003
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

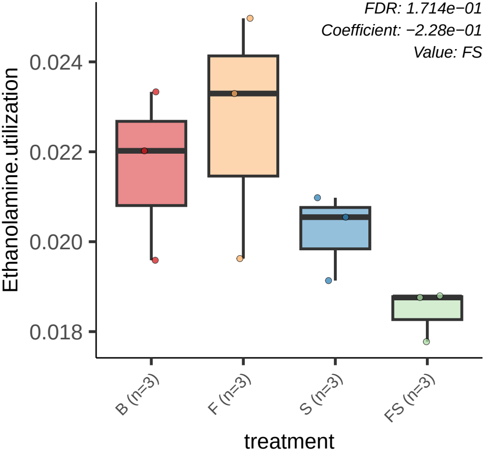

FDR: 1.681e−01
Coefficient: 2.58e−01
Value: FS
cell.division.cluster.containing.FtsQ
0.07
0.06
0.05
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

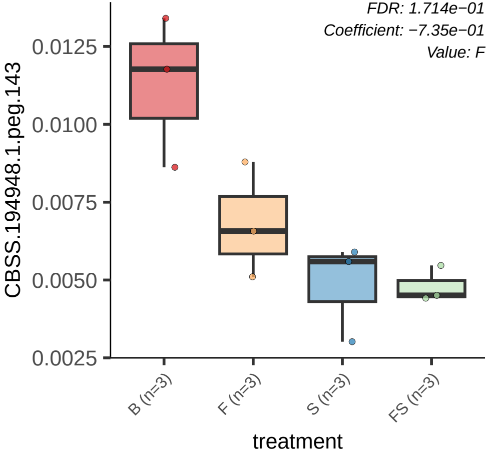

FDR: 1.682e−01
Coefficient: 1.22e−01
Value: S
Lipoate..transport
0.027
0.026
0.025
0.024
0.023
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

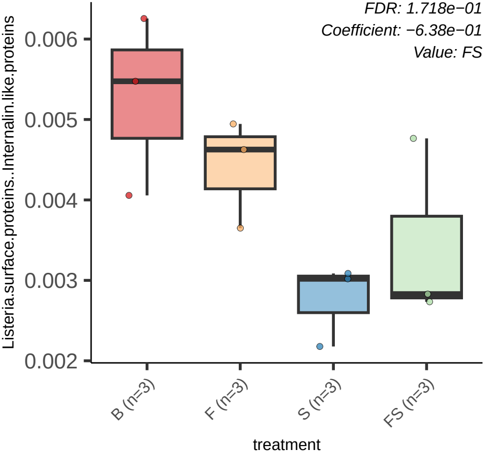

FDR: 1.689e−01
Coefficient: −8.19e−01
Value: FS
Phenylacetyl.CoA.catabolic.pathway..core.
0.020
0.015
0.010
0.005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

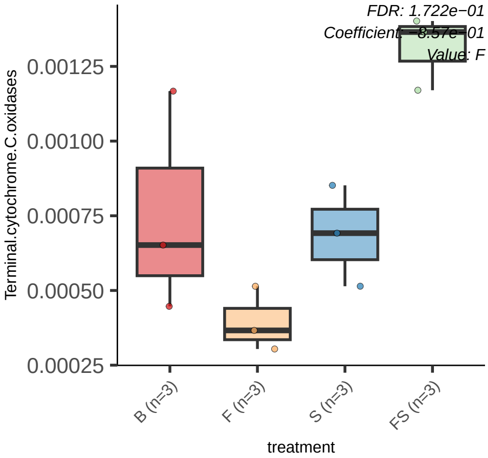

FDR: 1.706e−01
Coefficient: −4.13e−01
Value: S
EC.3.4.19...Omega.peptidases
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

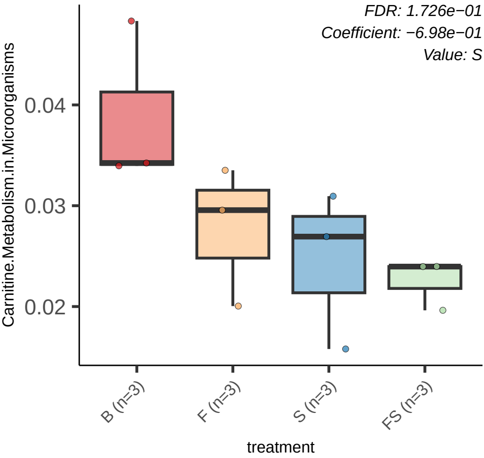

FDR: 1.709e−01
Coefficient: −5.04e−01
Value: F
O.antigen.capsule.important.for.environmental.persistenc
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

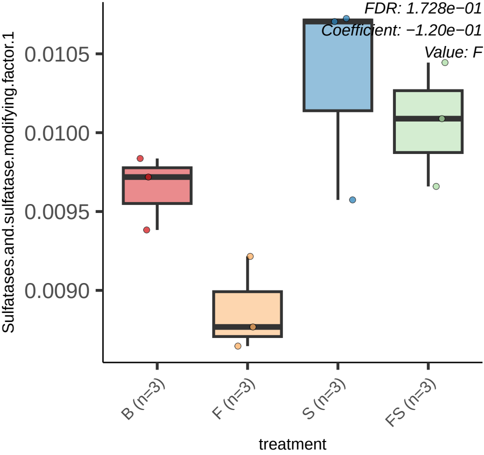

FDR: 1.714e−01
Coefficient: −2.28e−01
Value: FS
0.024
0.022
0.020
0.018
Ethanolamine.utilization
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

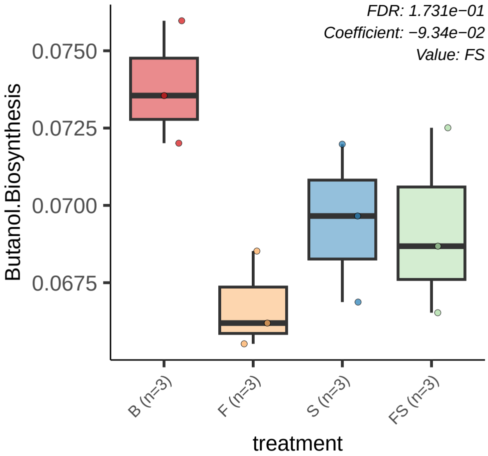

FDR: 1.714e−01
Coefficient: −7.35e−01
Value: F
CBSS.194948.1.peg.143
0.0125
0.0100
0.0075
0.0050
0.0025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

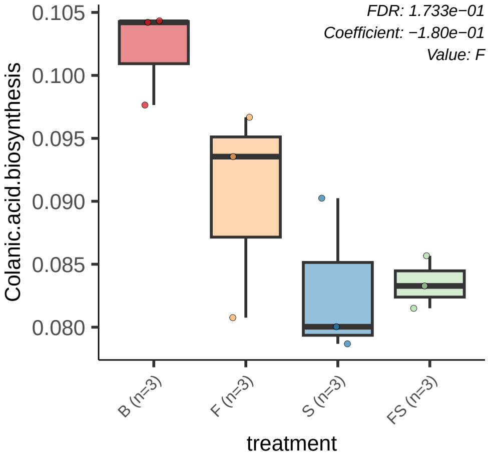

FDR: 1.718e−01
Coefficient: −6.38e−01
Value: FS
Listeria.surface.proteins..Internalin.like.proteins
0.006
0.005
0.004
0.003
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

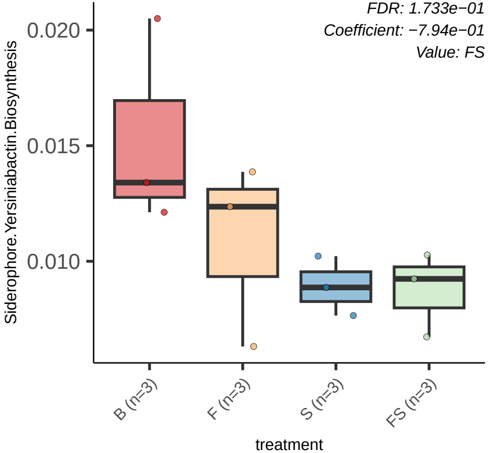

FDR: 1.722e−01
Coefficient: −8.57e−01
Value: F
Terminal.cytochrome.C.oxidases
0.00125
0.00100
0.00075
0.00050
0.00025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

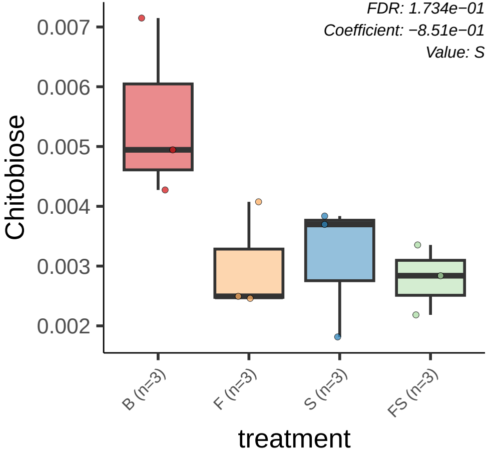

FDR: 1.726e−01
Coefficient: −6.98e−01
Value: S
Carnitine.Metabolism.in.Microorganisms
0.04
0.03
0.02
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

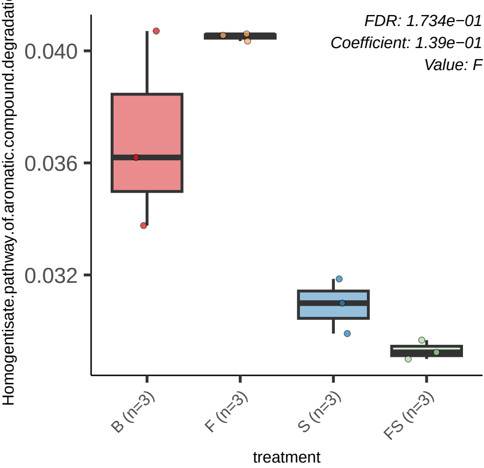

FDR: 1.728e−01
Coefficient: −1.20e−01
Value: F
Sulfatases.and.sulfatase.modifying.factor.1
0.0105
0.0100
0.0095
0.0090
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 1.731e−01
Coefficient: −9.34e−02
Value: FS
Butanol.Biosynthesis
0.0750
0.0725
0.0700
0.0675
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

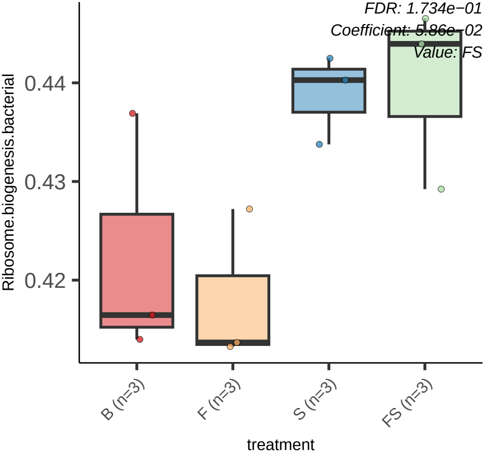

FDR: 1.733e−01
Coefficient: −1.80e−01
Value: F
Colanic.acid.biosynthesis
0.105
0.100
0.095
0.090
0.085
0.080
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

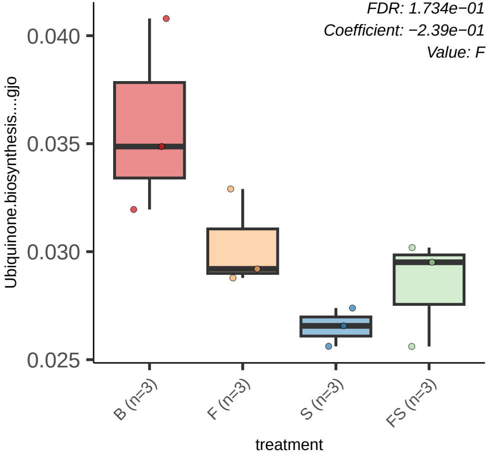

FDR: 1.733e−01
Coefficient: −7.94e−01
Value: FS
Siderophore.Yersiniabactin.Biosynthesis
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

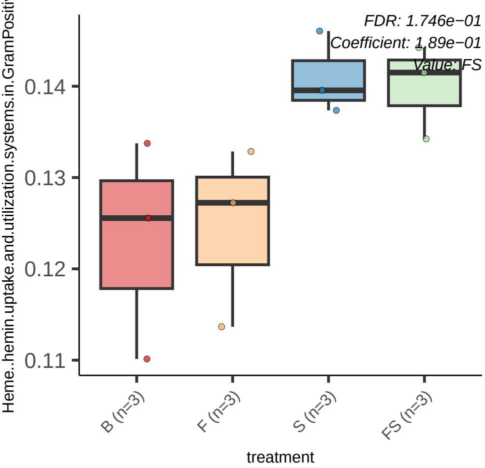

FDR: 1.734e−01
Coefficient: −8.51e−01
Value: S
Chitobiose
0.007
0.006
0.005
0.004
0.003
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

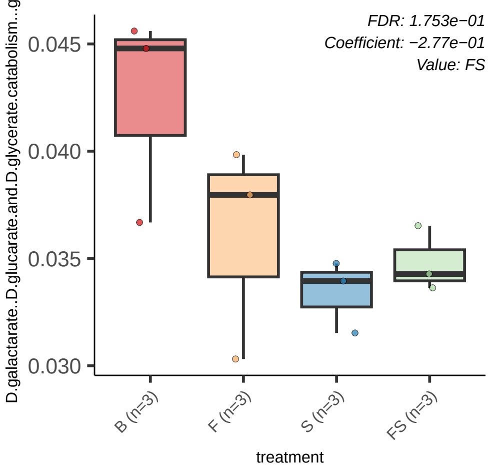


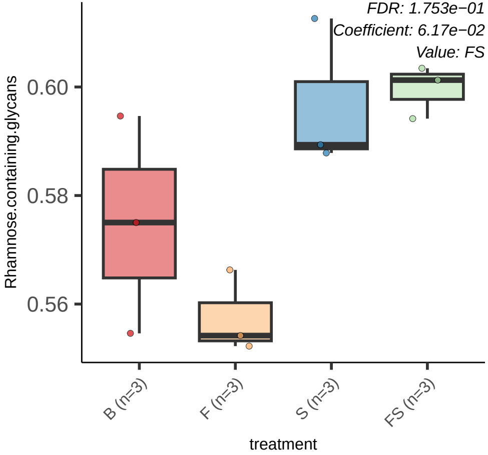
FDR: 1.734e−01
Coefficient: 1.39e−01
Value: F
Homogentisate.pathway.of.aromatic.compound.degradati
0.040
0.036
0.032
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

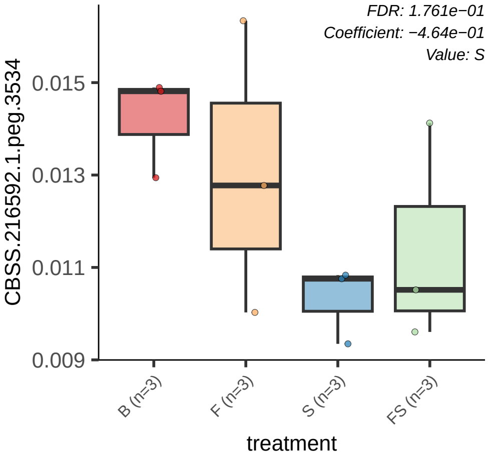

FDR: 1.734e−01
Coefficient: 5.86e−02
Value: FS
Ribosome.biogenesis.bacterial
0.44
0.43
0.42
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

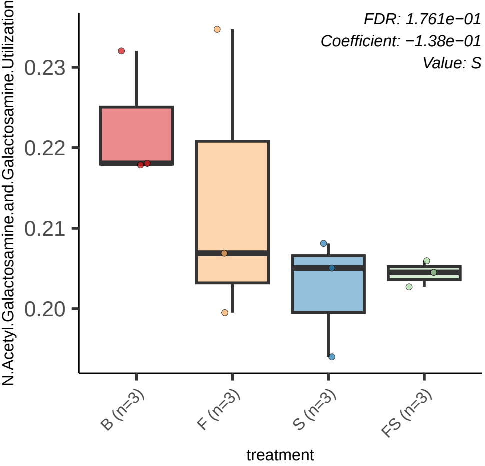

FDR: 1.734e−01
Coefficient: −2.39e−01
Value: F
Ubiquinone.biosynthesis...gjo
0.040
0.035
0.030
0.025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

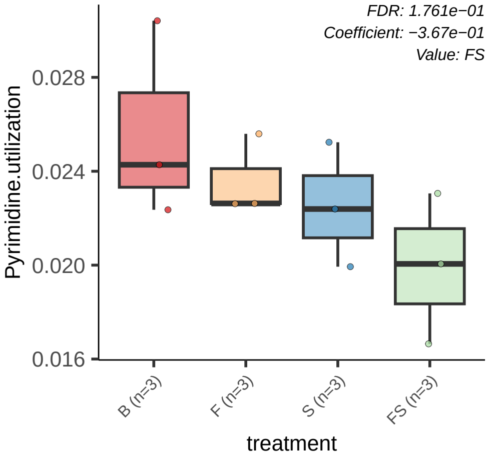

FDR: 1.746e−01
Coefficient: 1.89e−01
Value: FS
Heme..hemin.uptake.and.utilization.systems.in.GramPositi
0.14
0.13
0.12
0.11
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

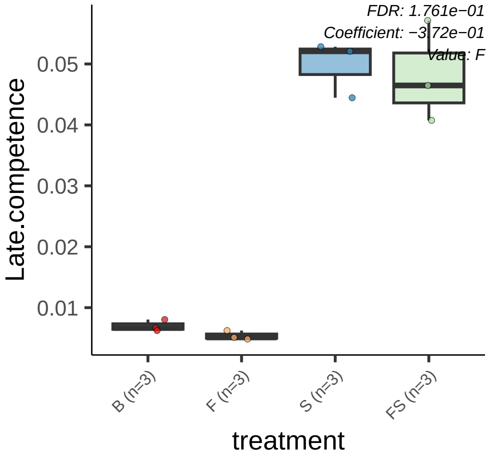

FDR: 1.753e−01
Coefficient: −2.77e−01
Value: FS
D.galactarate..D.glucarate.and.D.glycerate.catabolism...g
0.045
0.040
0.035
0.030
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

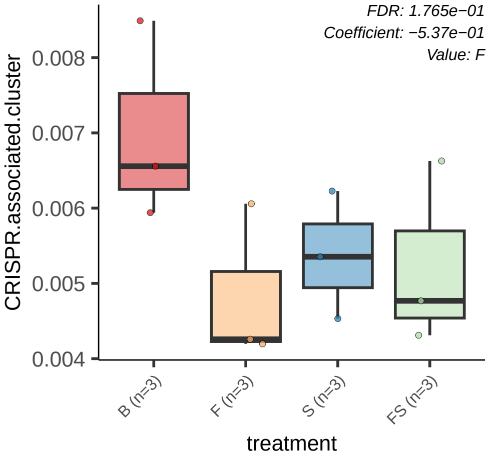

FDR: 1.753e−01
Coefficient: 6.17e−02
Value: FS
Rhamnose.containing.glycans
0.60
0.58
0.56
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

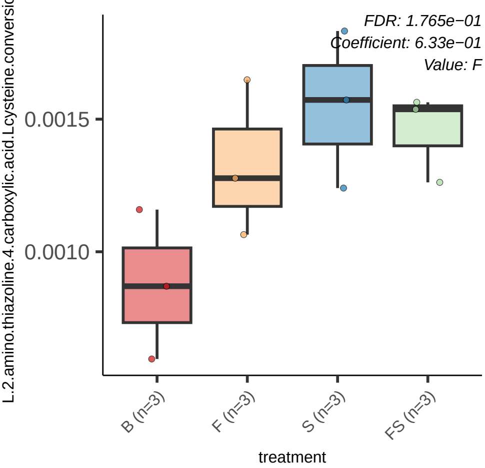

FDR: 1.761e−01
Coefficient: −4.64e−01
Value: S
CBSS.216592.1.peg.3534
0.015
0.013
0.011
0.009
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

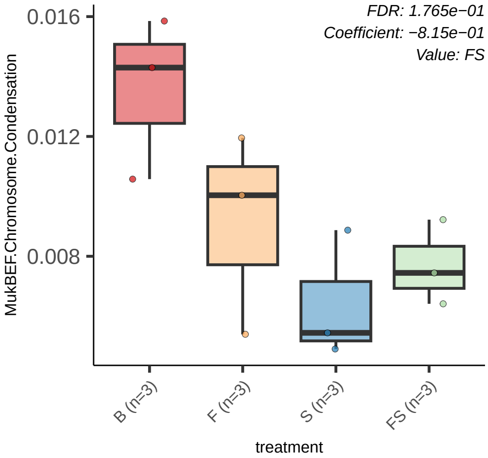

FDR: 1.761e−01
Coefficient: −1.38e−01
Value: S
N.Acetyl.Galactosamine.and.Galactosamine.Utilization
0.23
0.22
0.21
0.20
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

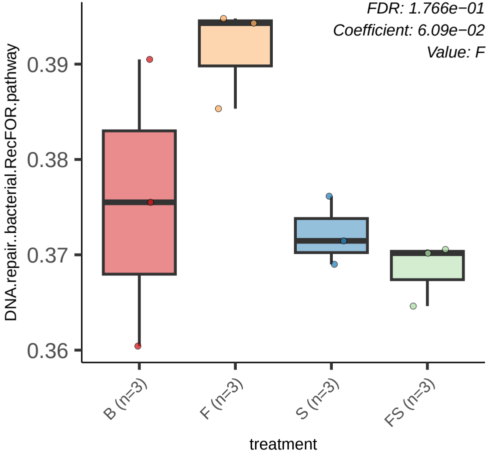

FDR: 1.761e−01
Coefficient: −3.67e−01
Value: FS
Pyrimidine.utilization
0.028
0.024
0.020
0.016
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

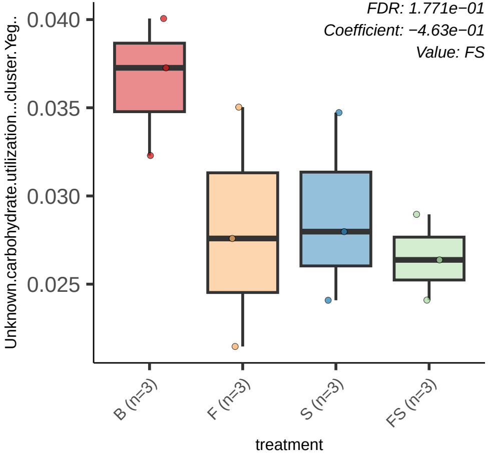

FDR: 1.761e−01
Coefficient: −3.72e−01
Value: F
Late.competence
0.05
0.04
0.03
0.02
0.01
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

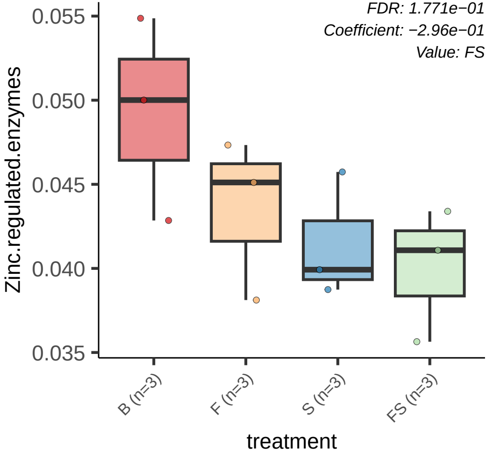

FDR: 1.765e−01
Coefficient: −5.37e−01
Value: F
CRISPR.associated.cluster
0.008
0.007
0.006
0.005
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

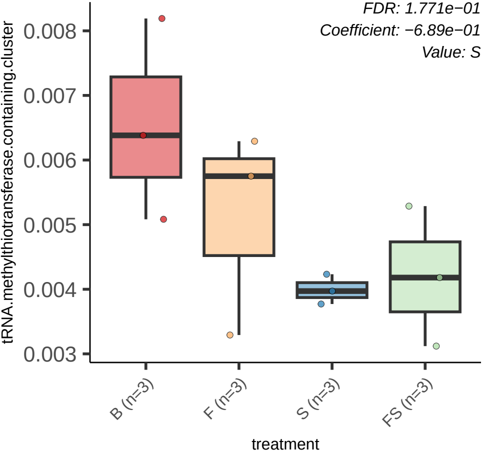

FDR: 1.765e−01
Coefficient: 6.33e−01
Value: F
L.2.amino.thiazoline.4.carboxylic.acid.Lcysteine.conversio
0.0015
0.0010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

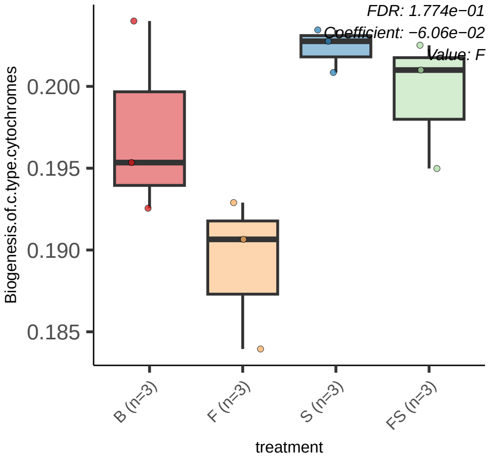

FDR: 1.765e−01
Coefficient: −8.15e−01
Value: FS
MukBEF.Chromosome.Condensation
0.016
0.012
0.008
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

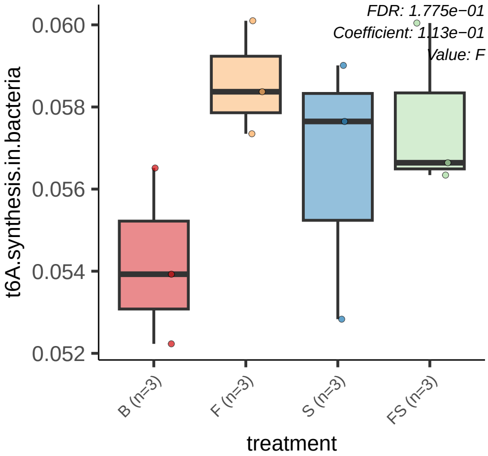

FDR: 1.766e−01
Coefficient: 6.09e−02
Value: F
DNA.repair..bacterial.RecFOR.pathway
0.39
0.38
0.37
0.36
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

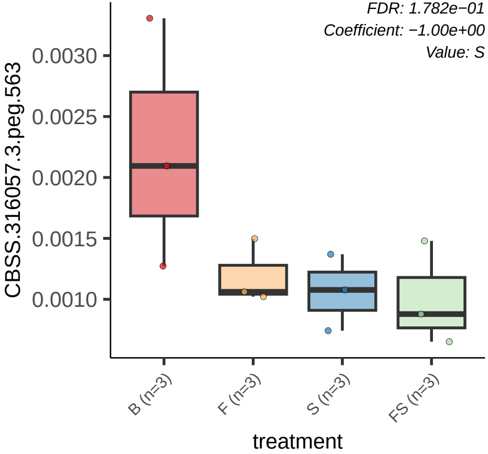

FDR: 1.771e−01
Coefficient: −4.63e−01
Value: FS
Unknown.carbohydrate.utilization...cluster.Yeg..
0.040
0.035
0.030
0.025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

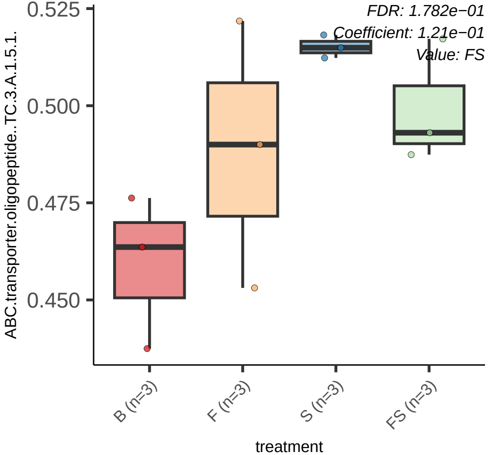

FDR: 1.771e−01
Coefficient: −2.96e−01
Value: FS
Zinc.regulated.enzymes
0.055
0.050
0.045
0.040
0.035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

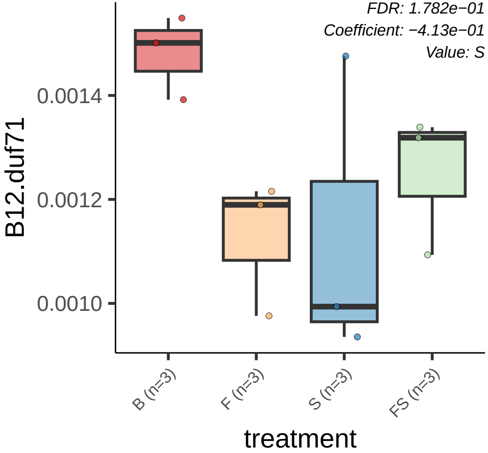

FDR: 1.771e−01
Coefficient: −6.89e−01
Value: S
tRNA.methylthiotransferase.containing.cluster
0.008
0.007
0.006
0.005
0.004
0.003
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

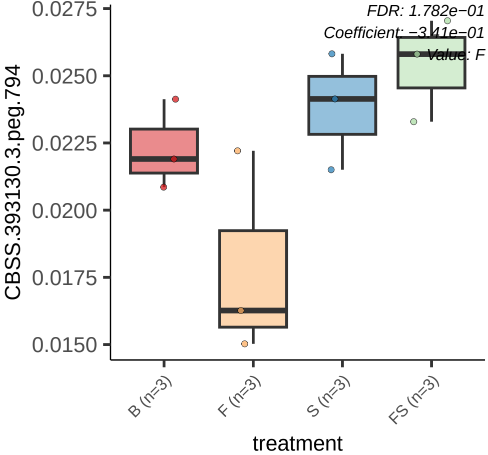

FDR: 1.774e−01
Coefficient: −6.06e−02
Value: F
Biogenesis.of.c.type.cytochromes
0.200
0.195
0.190
0.185
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

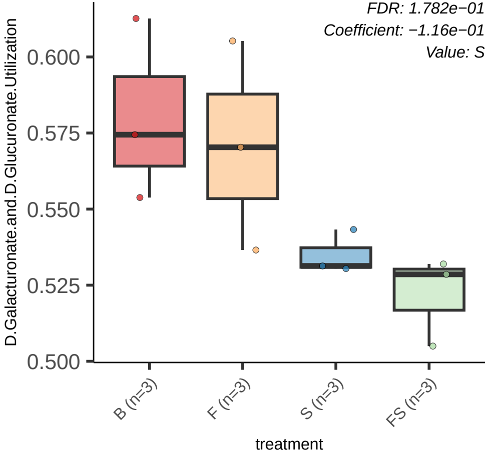

FDR: 1.775e−01
Coefficient: 1.13e−01
Value: F
t6A.synthesis.in.bacteria
0.060
0.058
0.056
0.054
0.052
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

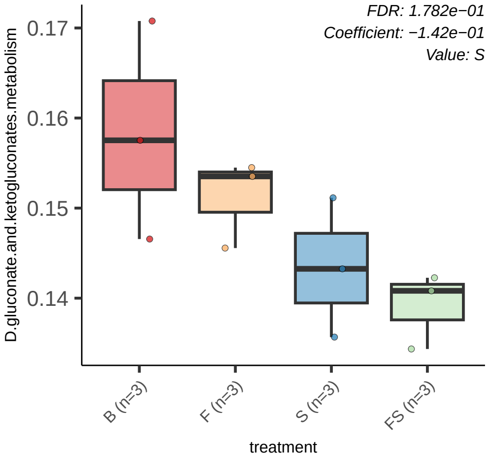

FDR: 1.782e−01
Coefficient: −1.00e+00
Value: S
CBSS.316057.3.peg.563
0.0030
0.0025
0.0020
0.0015
0.0010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

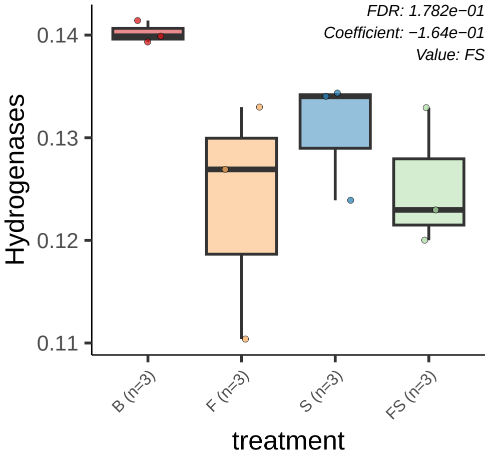

FDR: 1.782e−01
Coefficient: 1.21e−01
Value: FS
ABC.transporter.oligopeptide..TC.3.A.1.5.1.
0.525
0.500
0.475
0.450
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

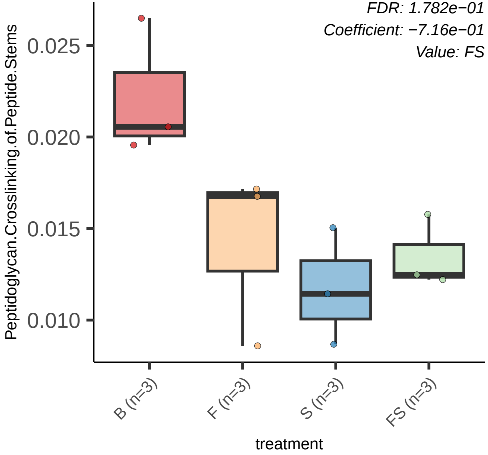

FDR: 1.782e−01
Coefficient: −4.13e−01
Value: S
B12.duf71
0.0014
0.0012
0.0010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

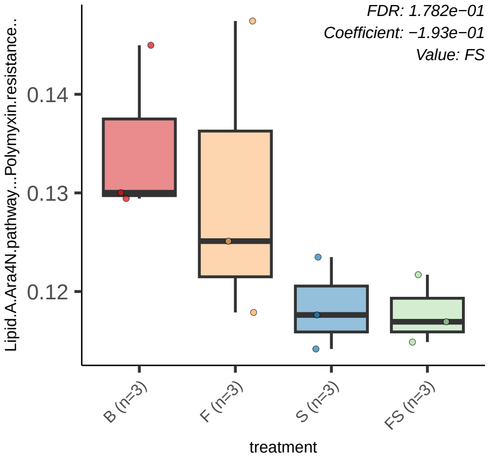

FDR: 1.782e−01
Coefficient: −3.41e−01
Value: F
CBSS.393130.3.peg.794
0.0275
0.0250
0.0225
0.0200
0.0175
0.0150
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

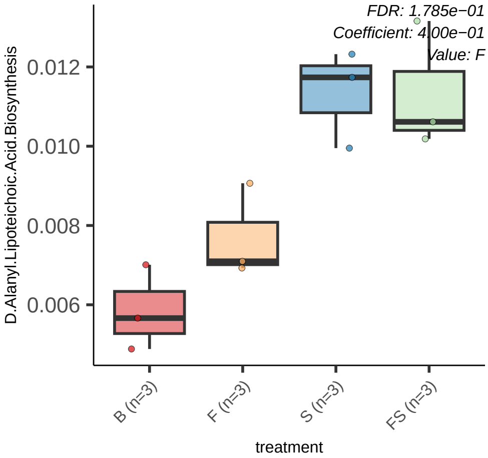

FDR: 1.782e−01
Coefficient: −1.16e−01
Value: S
D.Galacturonate.and.D.Glucuronate.Utilization
0.600
0.575
0.550
0.525
0.500
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

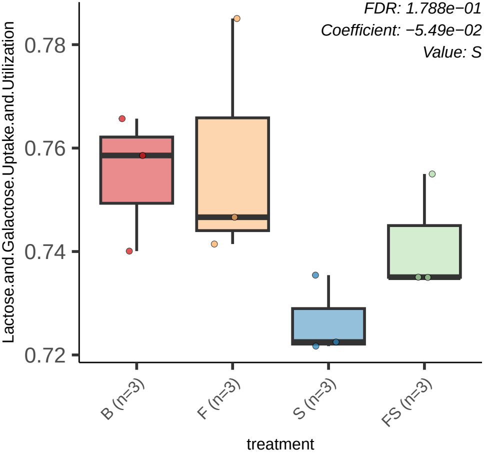

FDR: 1.782e−01
Coefficient: −1.42e−01
Value: S
D.gluconate.and.ketogluconates.metabolism
0.17
0.16
0.15
0.14
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

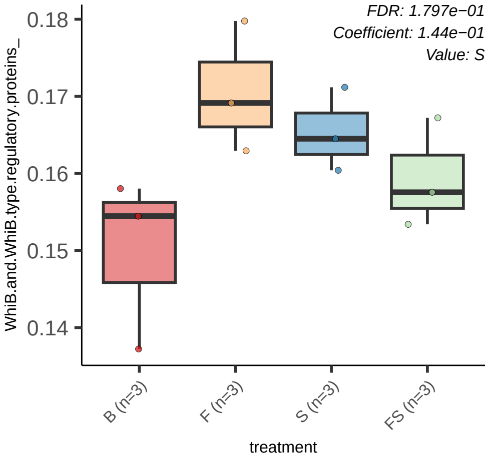

FDR: 1.782e−01
Coefficient: −1.64e−01
Value: FS
Hydrogenases
0.14
0.13
0.12
0.11
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

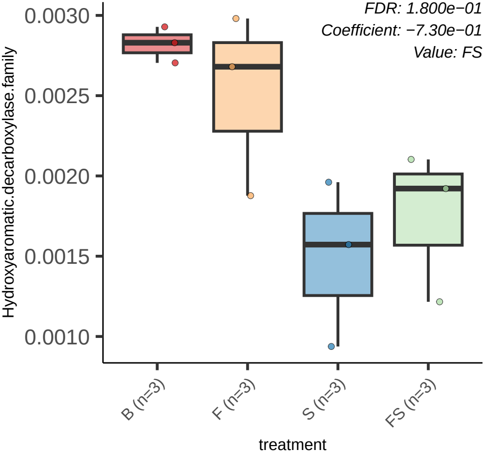

FDR: 1.782e−01
Coefficient: −7.16e−01
Value: FS
Peptidoglycan.Crosslinking.of.Peptide.Stems
0.025
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

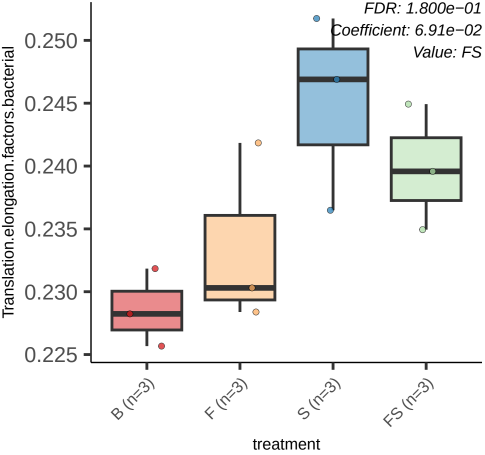

FDR: 1.782e−01
Coefficient: −1.93e−01
Value: FS
Lipid.A.Ara4N.pathway...Polymyxin.resistance..
0.14
0.13
0.12
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

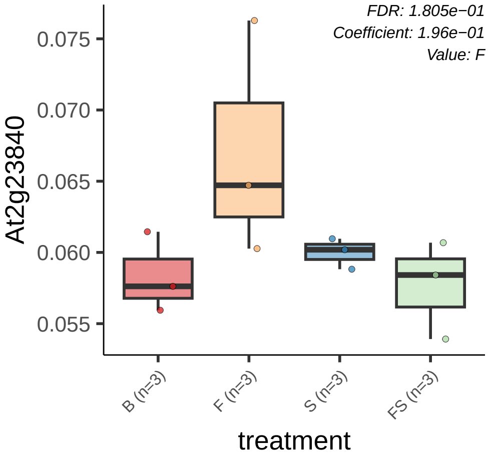

FDR: 1.785e−01
Coefficient: 4.00e−01
Value: F
D.Alanyl.Lipoteichoic.Acid.Biosynthesis
0.012
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

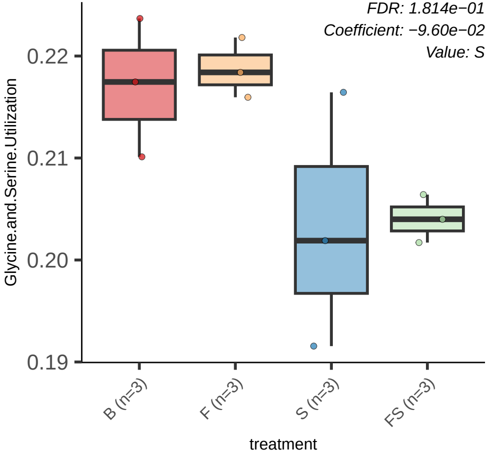

FDR: 1.788e−01
Coefficient: −5.49e−02
Value: S
Lactose.and.Galactose.Uptake.and.Utilization
0.78
0.76
0.74
0.72
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

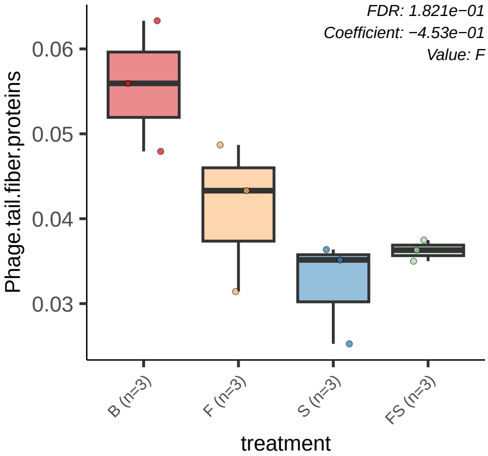

FDR: 1.797e−01
Coefficient: 1.44e−01
Value: S
WhiB.and.WhiB.type.regulatory.proteins_
0.18
0.17
0.16
0.15
0.14
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

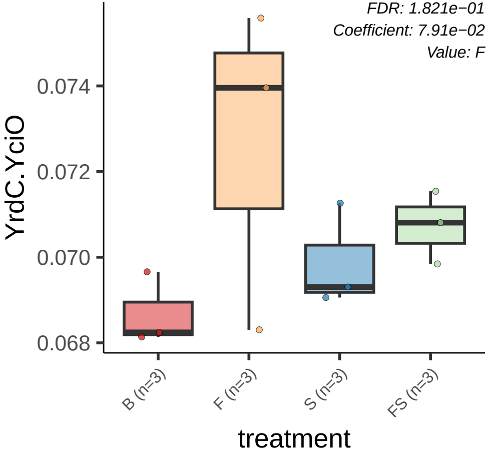

FDR: 1.800e−01
Coefficient: −7.30e−01
Value: FS
Hydroxyaromatic.decarboxylase.family
0.0030
0.0025
0.0020
0.0015
0.0010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

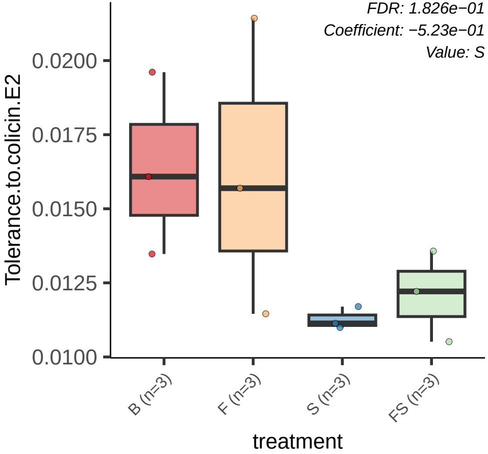

FDR: 1.800e−01
Coefficient: 6.91e−02
Value: FS
Translation.elongation.factors.bacterial
0.250
0.245
0.240
0.235
0.230
0.225
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

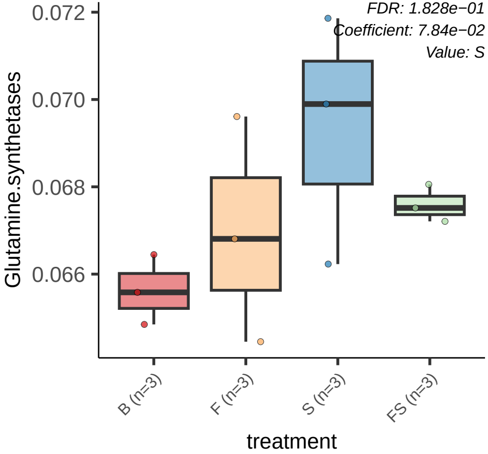

FDR: 1.805e−01
Coefficient: 1.96e−01
Value: F
At2g23840
0.075
0.070
0.065
0.060
0.055
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

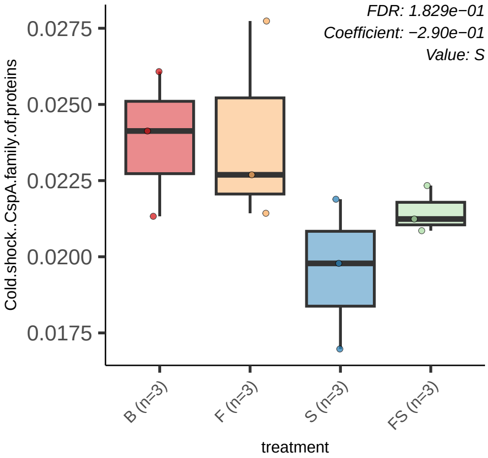

FDR: 1.814e−01
Coefficient: −9.60e−02
Value: S
Glycine.and.Serine.Utilization
0.22
0.21
0.20
0.19
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

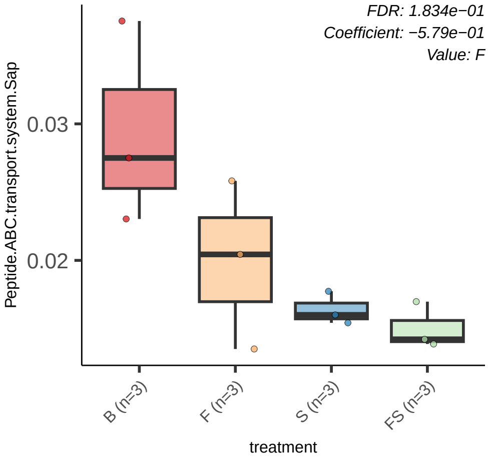

FDR: 1.821e−01
Coefficient: −4.53e−01
Value: F
Phage.tail.fiber.proteins
0.06
0.05
0.04
0.03
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

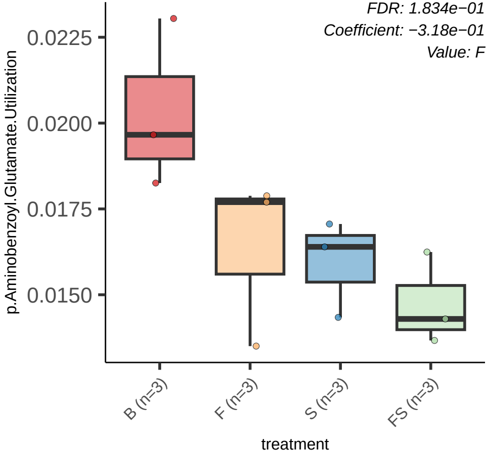

FDR: 1.821e−01
Coefficient: 7.91e−02
Value: F
YrdC.YciO
0.074
0.072
0.070
0.068
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

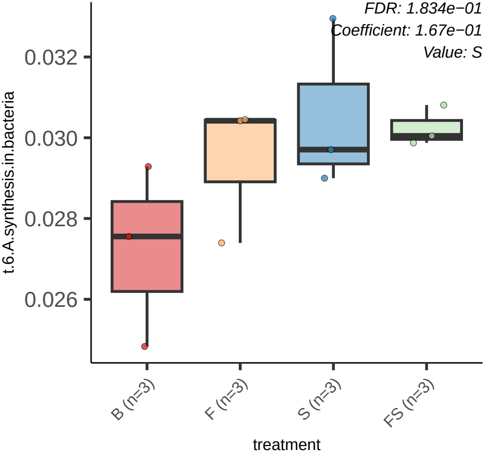

FDR: 1.826e−01
Coefficient: −5.23e−01
Value: S
Tolerance.to.colicin.E2
0.0200
0.0175
0.0150
0.0125
0.0100
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

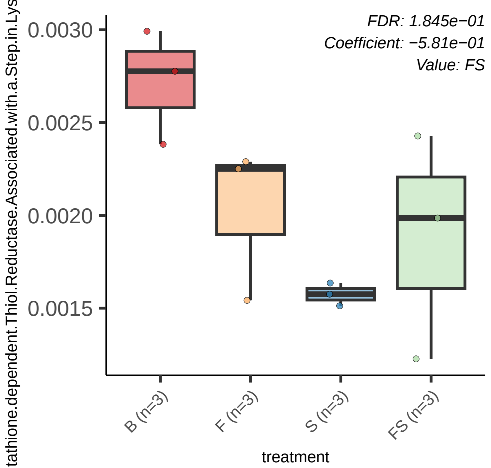

FDR: 1.828e−01
Coefficient: 7.84e−02
Value: S
Glutamine.synthetases
0.072
0.070
0.068
0.066
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

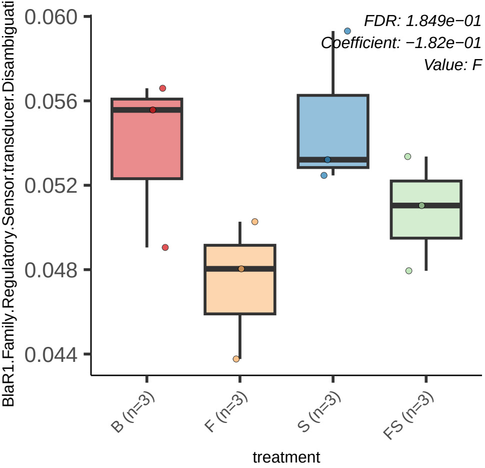

FDR: 1.829e−01
Coefficient: −2.90e−01
Value: S
Cold.shock..CspA.family.of.proteins
0.0275
0.0250
0.0225
0.0200
0.0175
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

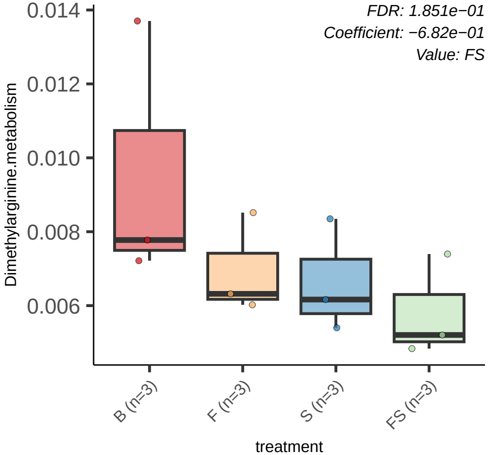

FDR: 1.834e−01
Coefficient: −5.79e−01
Value: F
Peptide.ABC.transport.system.Sap
0.03
0.02
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

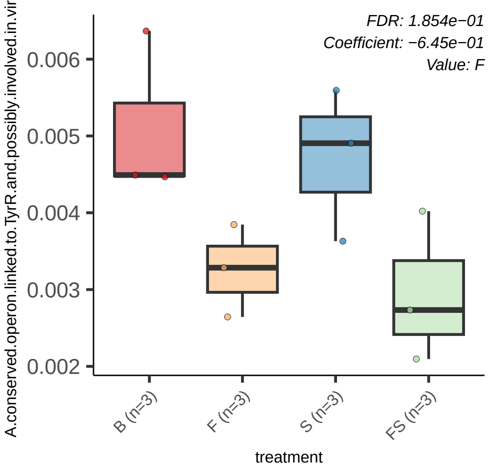

FDR: 1.834e−01
Coefficient: −3.18e−01
Value: F
p.Aminobenzoyl.Glutamate.Utilization
0.0225
0.0200
0.0175
0.0150
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

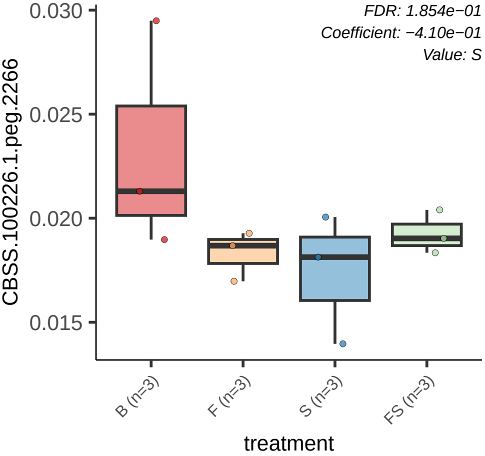

FDR: 1.834e−01
Coefficient: 1.67e−01
Value: S
0.032
0.030
0.028
0.026
t.6.A.synthesis.in.bacteria
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

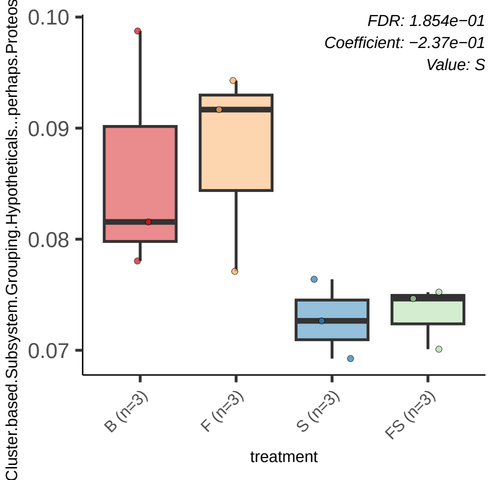

FDR: 1.845e−01
Coefficient: −5.81e−01
Value: FS
lutathione.dependent.Thiol.Reductase.Associated.with.a.Step.in.Lys
0.0030
0.0025
0.0020
0.0015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

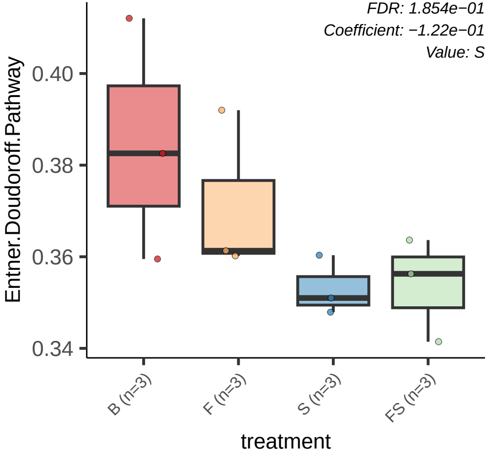

FDR: 1.849e−01
Coefficient: −1.82e−01
Value: F
BlaR1.Family.Regulatory.Sensor.transducer.Disambiguati
0.060
0.056
0.052
0.048
0.044
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

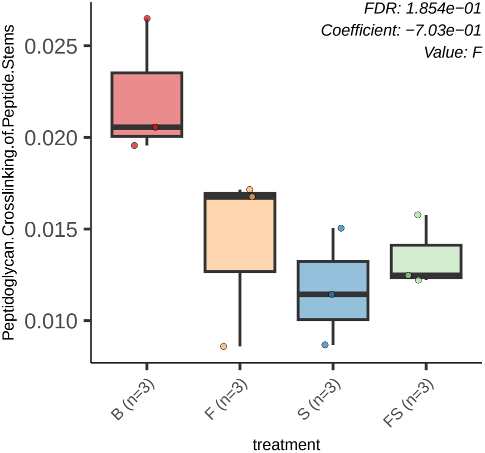

FDR: 1.851e−01
Coefficient: −6.82e−01
Value: FS
Dimethylarginine.metabolism
0.014
0.012
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

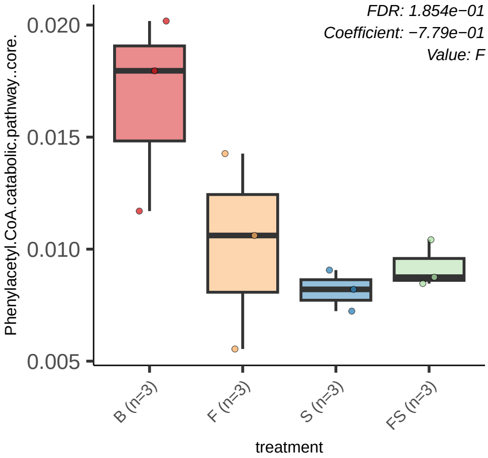

FDR: 1.854e−01
Coefficient: −6.45e−01
Value: F
A.conserved.operon.linked.to.TyrR.and.possibly.involved.in.vir
0.006
0.005
0.004
0.003
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

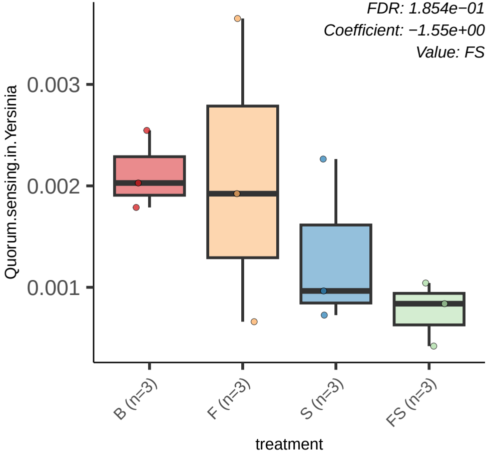

FDR: 1.854e−01
Coefficient: −4.10e−01
Value: S
CBSS.100226.1.peg.2266
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

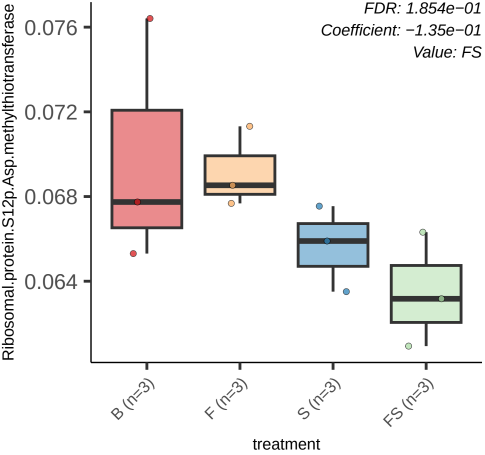

FDR: 1.854e−01
Coefficient: −2.37e−01
Value: S
Cluster.based.Subsystem.Grouping.Hypotheticals...perhaps.Proteos
0.10
0.09
0.08
0.07
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

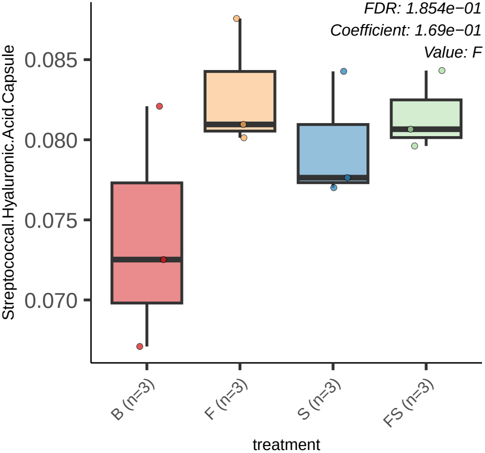

FDR: 1.854e−01
Coefficient: −1.22e−01
Value: S
Entner.Doudoroff.Pathway
0.40
0.38
0.36
0.34
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 1.854e−01
Coefficient: −7.03e−01
Value: F
Peptidoglycan.Crosslinking.of.Peptide.Stems
0.025
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

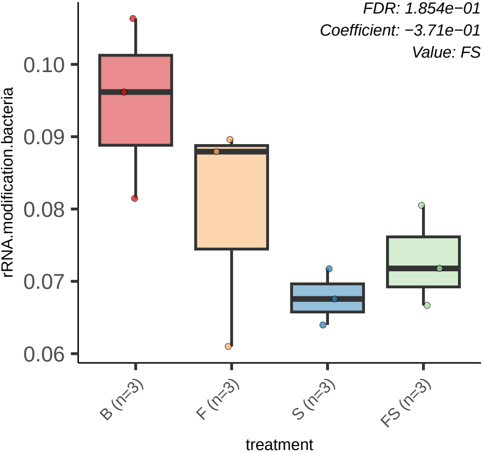

FDR: 1.854e−01
Coefficient: −7.79e−01
Value: F
Phenylacetyl.CoA.catabolic.pathway..core.
0.020
0.015
0.010
0.005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

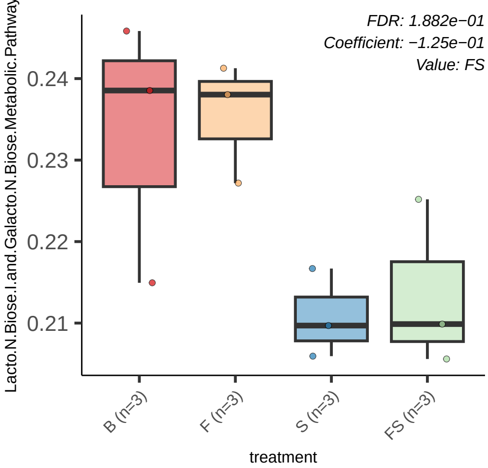

FDR: 1.854e−01
Coefficient: −1.55e+00
Value: FS
Quorum.sensing.in.Yersinia
0.003
0.002
0.001
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

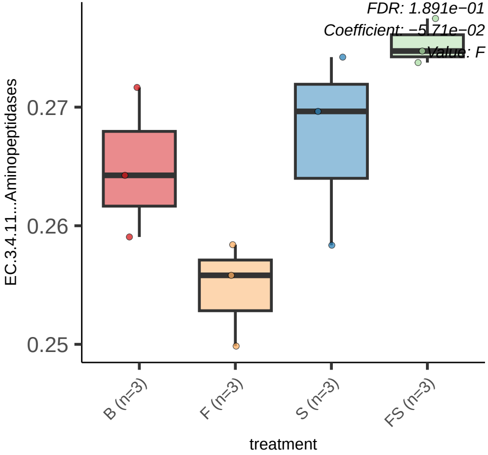

FDR: 1.854e−01
Coefficient: −1.35e−01
Value: FS
Ribosomal.protein.S12p.Asp.methylthiotransferase
0.076
0.072
0.068
0.064
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

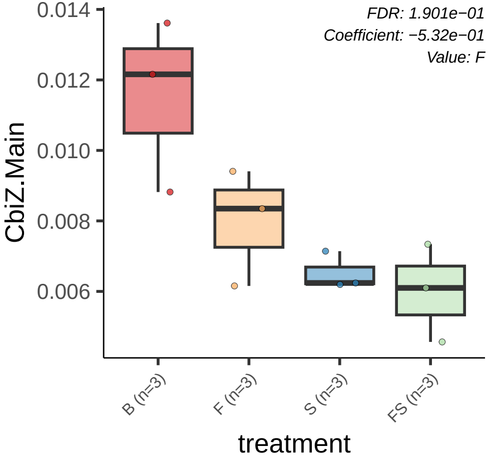


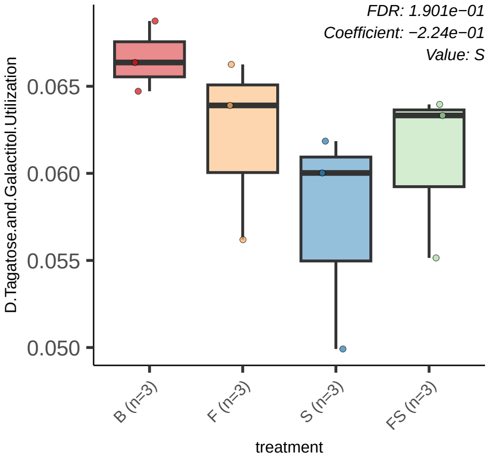
FDR: 1.854e−01
Coefficient: 1.69e−01
Value: F
Streptococcal.Hyaluronic.Acid.Capsule
0.085
0.080
0.075
0.070
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

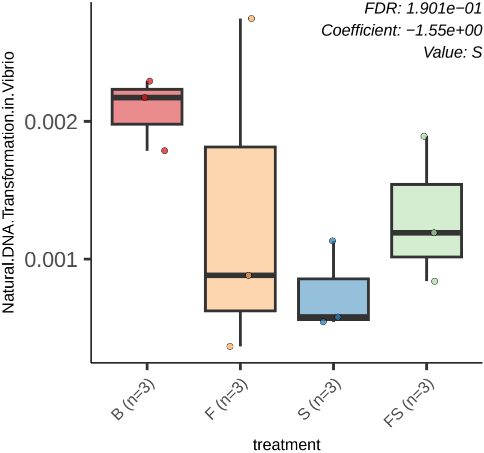

FDR: 1.854e−01
Coefficient: −3.71e−01
Value: FS
rRNA.modification.bacteria
0.10
0.09
0.08
0.07
0.06
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

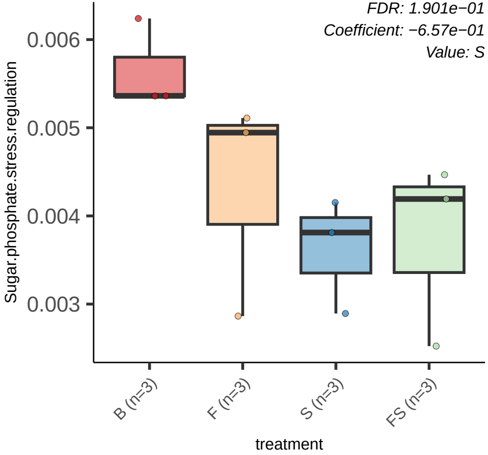

FDR: 1.882e−01
Coefficient: −1.25e−01
Value: FS
Lacto.N.Biose.I.and.Galacto.N.Biose.Metabolic.Pathway
0.24
0.23
0.22
0.21
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

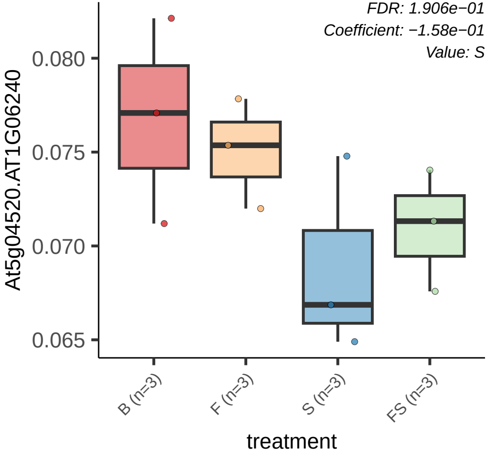

FDR: 1.891e−01
Coefficient: −5.71e−02
Value: F
EC.3.4.11...Aminopeptidases
0.27
0.26
0.25
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

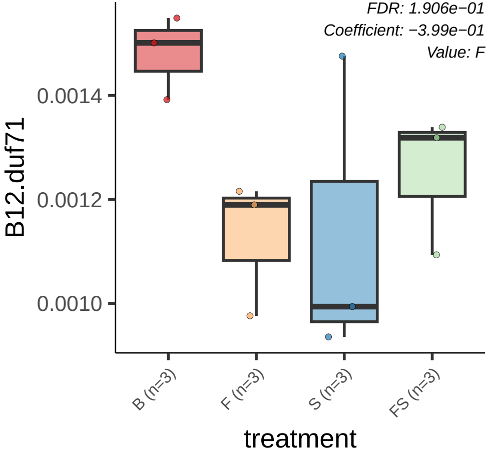

FDR: 1.901e−01
Coefficient: −5.32e−01
Value: F
CbiZ.Main
0.014
0.012
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

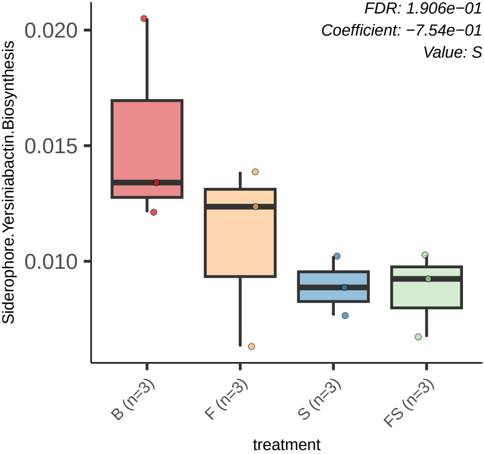

FDR: 1.901e−01
Coefficient: −2.24e−01
Value: S
D.Tagatose.and.Galactitol.Utilization
0.065
0.060
0.055
0.050
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

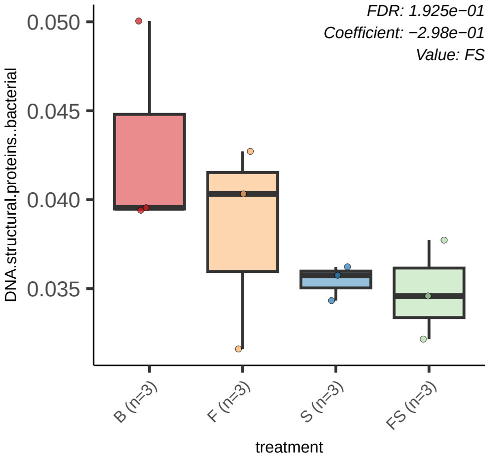

FDR: 1.901e−01
Coefficient: −1.55e+00
Value: S
Natural.DNA.Transformation.in.Vibrio
0.002
0.001
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

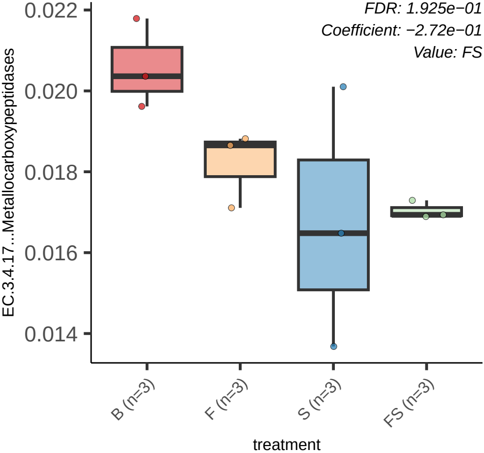

FDR: 1.901e−01
Coefficient: −6.57e−01
Value: S
Sugar.phosphate.stress.regulation
0.006
0.005
0.004
0.003
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

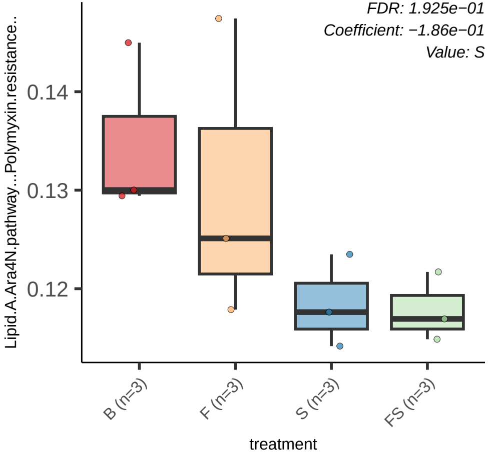

FDR: 1.906e−01
Coefficient: −1.58e−01
Value: S
At5g04520.AT1G06240
0.080
0.075
0.070
0.065
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

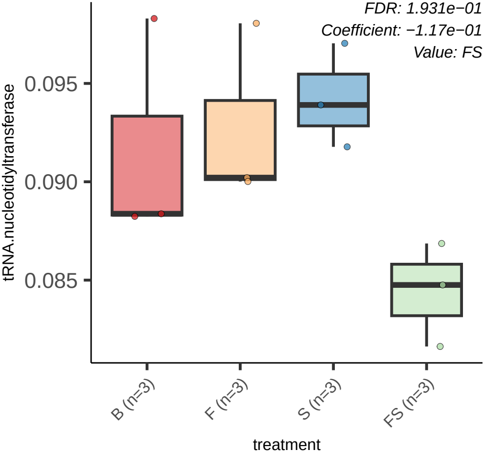

FDR: 1.906e−01
Coefficient: −3.99e−01
Value: F
B12.duf71
0.0014
0.0012
0.0010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

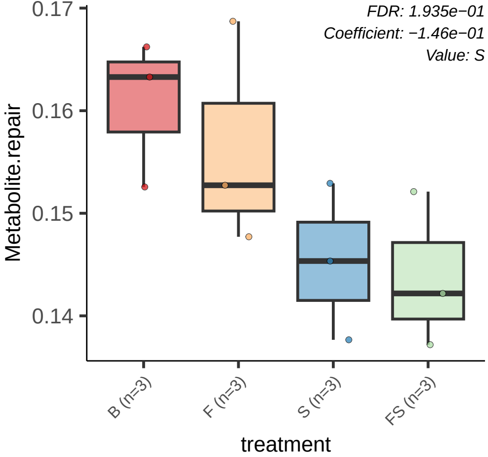

FDR: 1.906e−01
Coefficient: −7.54e−01
Value: S
Siderophore.Yersiniabactin.Biosynthesis
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

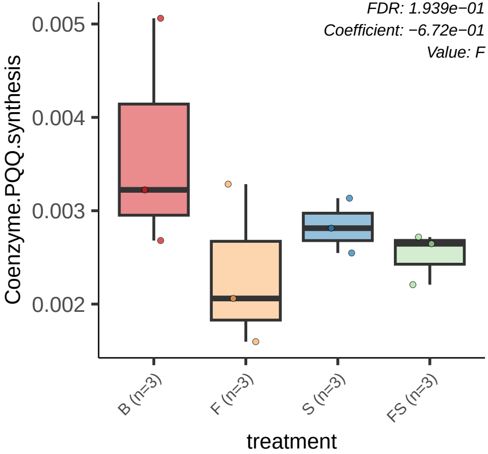

FDR: 1.925e−01
Coefficient: −2.98e−01
Value: FS
DNA.structural.proteins..bacterial
0.050
0.045
0.040
0.035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

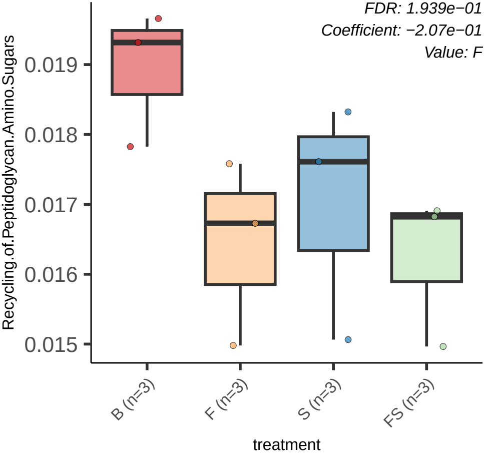

FDR: 1.925e−01
Coefficient: −2.72e−01
Value: FS
EC.3.4.17...Metallocarboxypeptidases
0.022
0.020
0.018
0.016
0.014
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

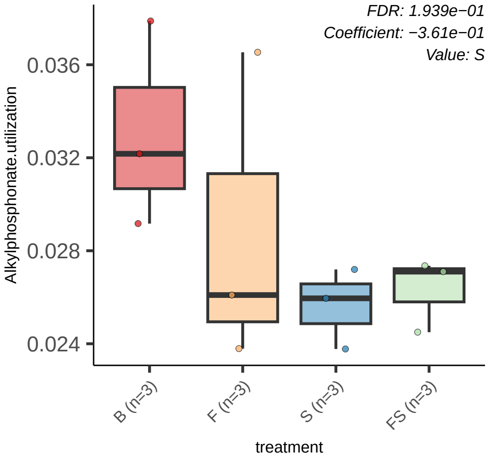

FDR: 1.925e−01
Coefficient: −1.86e−01
Value: S
Lipid.A.Ara4N.pathway...Polymyxin.resistance..
0.14
0.13
0.12
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

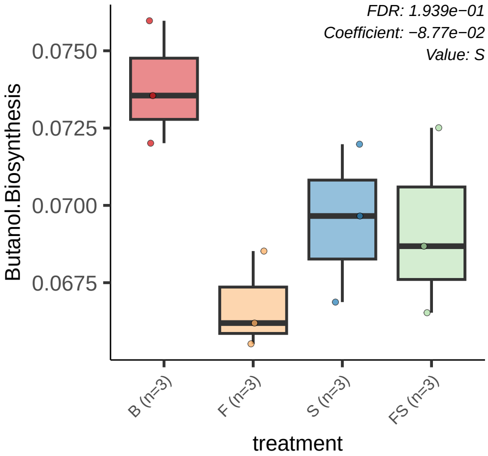

FDR: 1.931e−01
Coefficient: −1.17e−01
Value: FS
0.095
0.090
0.085
tRNA.nucleotidyltransferase
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

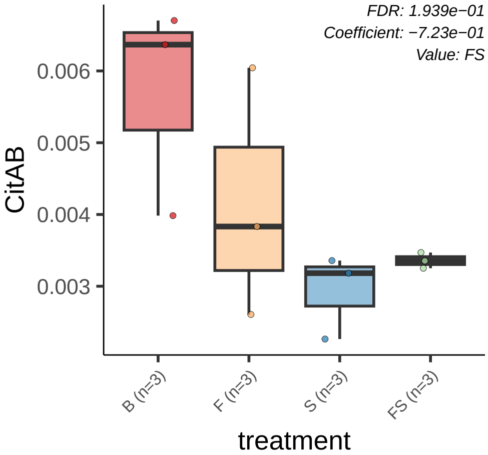

FDR: 1.935e−01
Coefficient: −1.46e−01
Value: S
Metabolite.repair
0.17
0.16
0.15
0.14
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

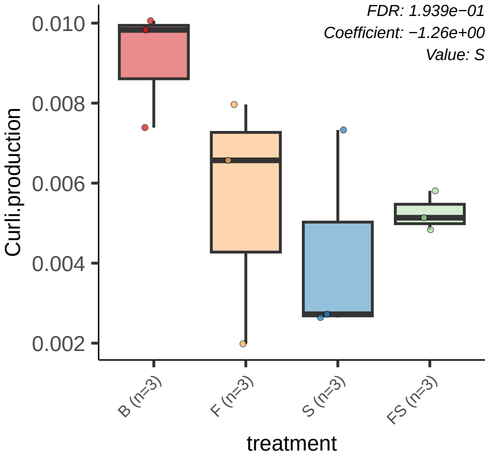

FDR: 1.939e−01
Coefficient: −6.72e−01
Value: F
Coenzyme.PQQ.synthesis
0.005
0.004
0.003
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

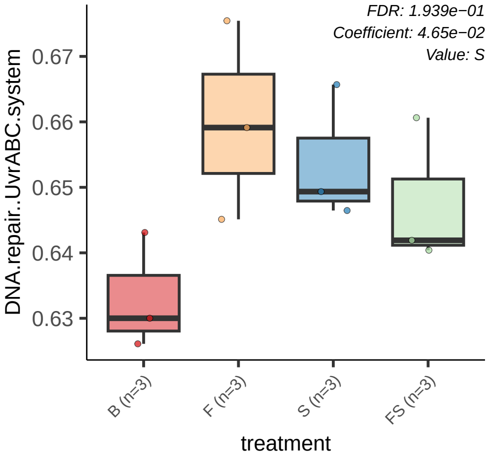

FDR: 1.939e−01
Coefficient: −2.07e−01
Value: F
Recycling.of.Peptidoglycan.Amino.Sugars
0.019
0.018
0.017
0.016
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

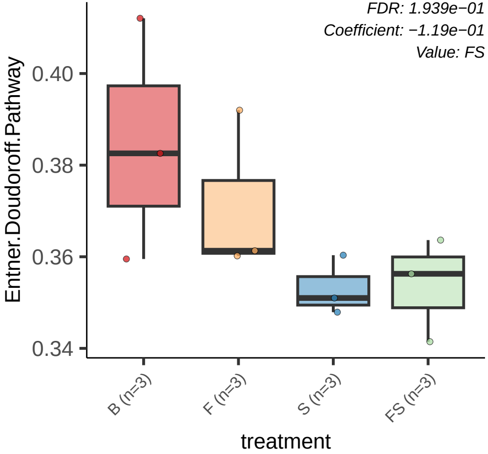

FDR: 1.939e−01
Coefficient: −3.61e−01
Value: S
Alkylphosphonate.utilization
0.036
0.032
0.028
0.024
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

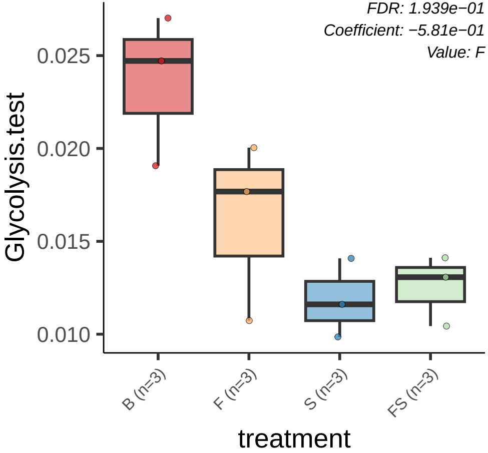

FDR: 1.939e−01
Coefficient: −8.77e−02
Value: S
Butanol.Biosynthesis
0.0750
0.0725
0.0700
0.0675
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

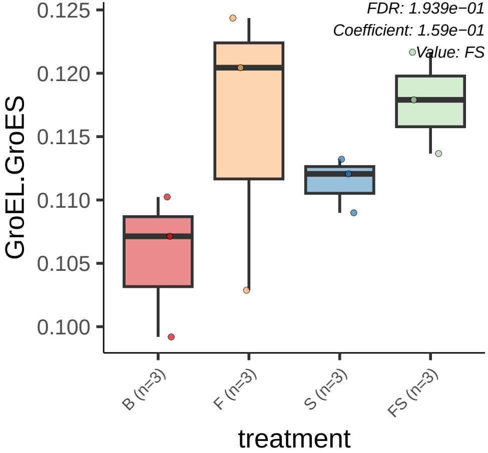

FDR: 1.939e−01
Coefficient: −7.23e−01
Value: FS
CitAB
0.006
0.005
0.004
0.003
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

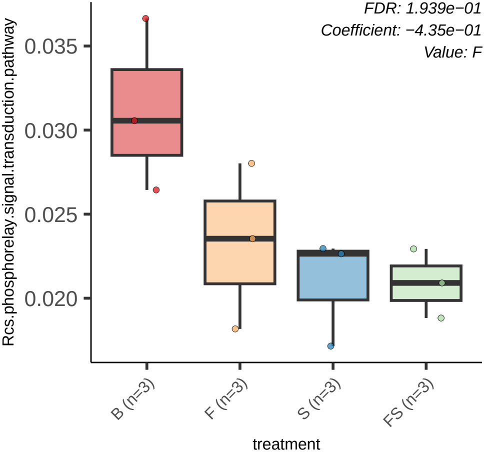

FDR: 1.939e−01
Coefficient: −1.26e+00
Value: S
Curli.production
0.010
0.008
0.006
0.004
0.002
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

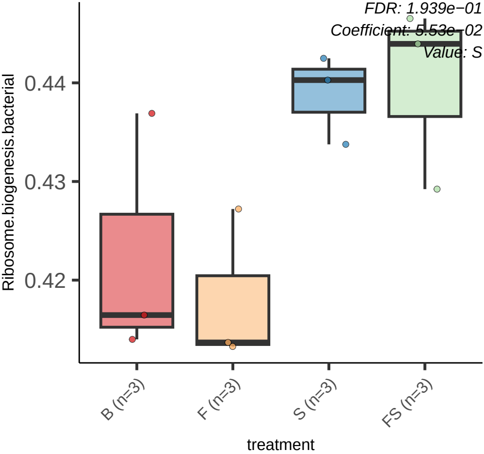

FDR: 1.939e−01
Coefficient: 4.65e−02
Value: S
DNA.repair..UvrABC.system
0.67
0.66
0.65
0.64
0.63
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

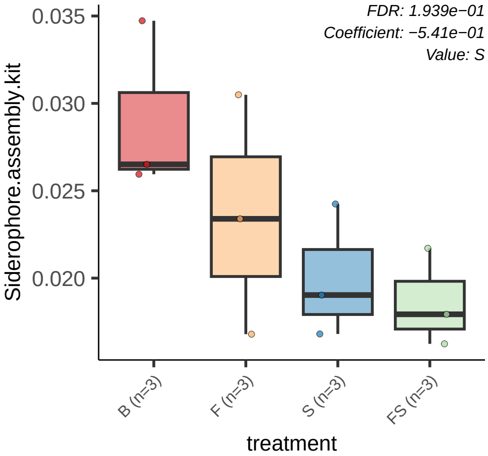

FDR: 1.939e−01
Coefficient: −1.19e−01
Value: FS
Entner.Doudoroff.Pathway
0.40
0.38
0.36
0.34
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

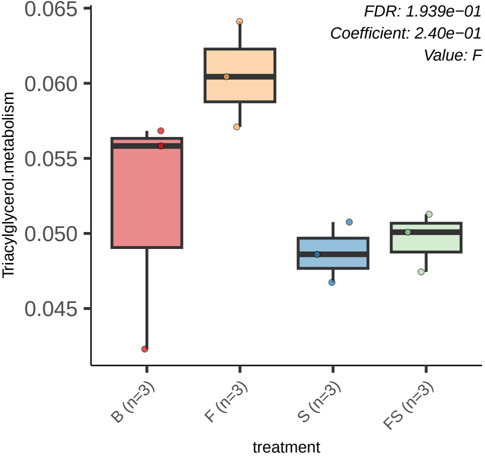

FDR: 1.939e−01
Coefficient: −5.81e−01
Value: F
Glycolysis.test
0.025
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

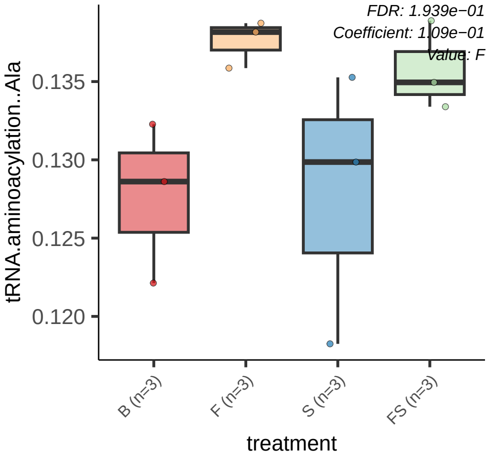

FDR: 1.939e−01
Coefficient: 1.59e−01
Value: FS
GroEL.GroES
0.125
0.120
0.115
0.110
0.105
0.100
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

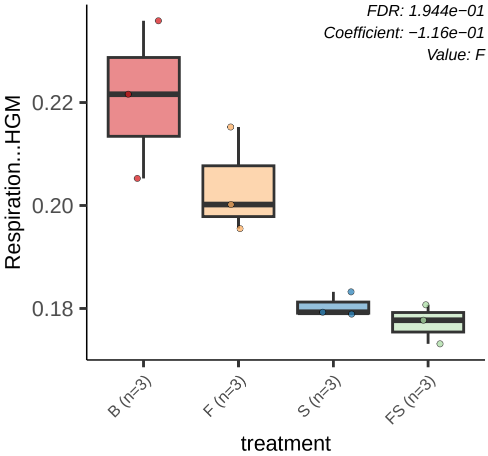

FDR: 1.939e−01
Coefficient: −4.35e−01
Value: F
Rcs.phosphorelay.signal.transduction.pathway
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

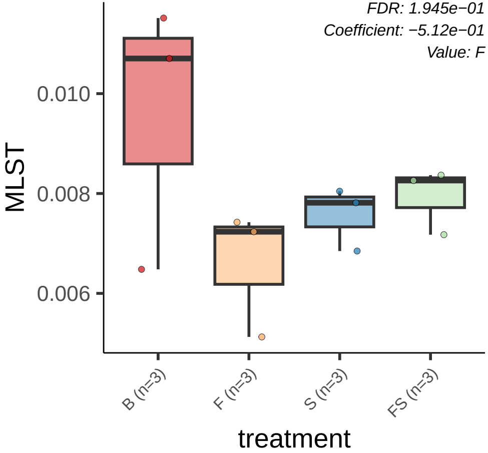

FDR: 1.939e−01
Coefficient: 5.53e−02
Value: S
Ribosome.biogenesis.bacterial
0.44
0.43
0.42
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

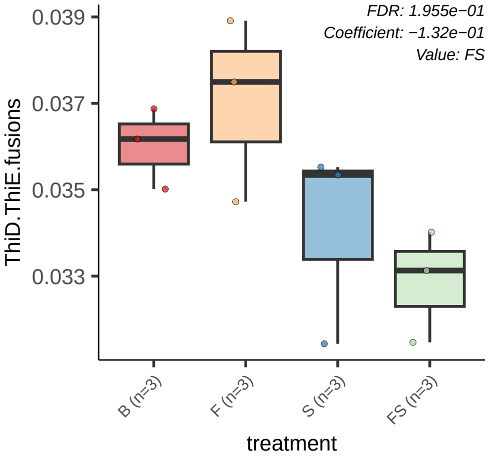

FDR: 1.939e−01
Coefficient: −5.41e−01
Value: S
Siderophore.assembly.kit
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

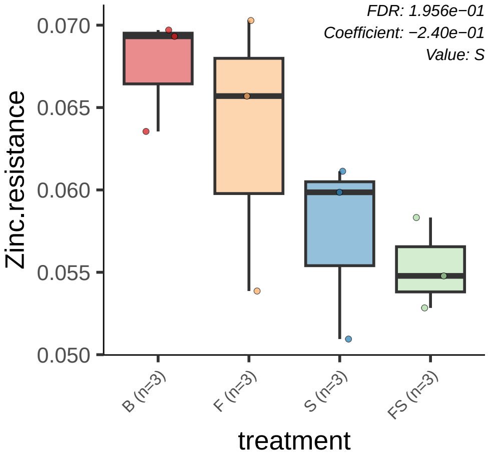

FDR: 1.939e−01
Coefficient: 2.40e−01
Value: F
Triacylglycerol.metabolism
0.065
0.060
0.055
0.050
0.045
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

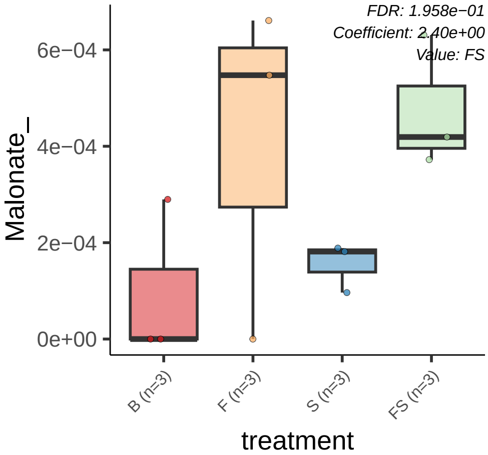

FDR: 1.939e−01
Coefficient: 1.09e−01
Value: F
tRNA.aminoacylation..Ala
0.135
0.130
0.125
0.120
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

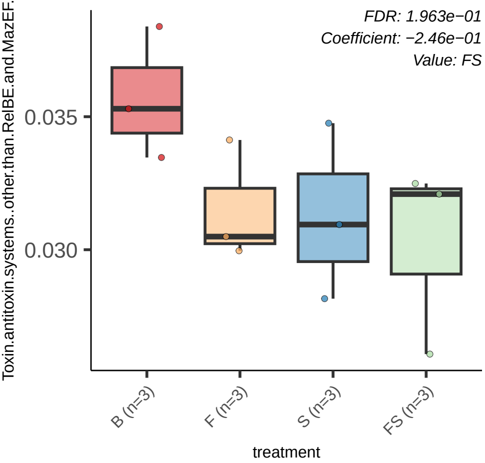

FDR: 1.944e−01
Coefficient: −1.16e−01
Value: F
Respiration...HGM
0.22
0.20
0.18
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

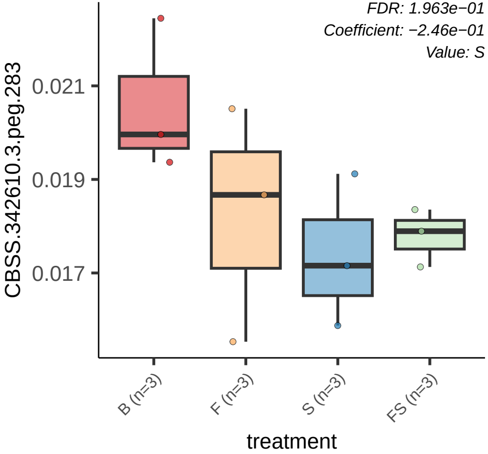

FDR: 1.945e−01
Coefficient: −5.12e−01
Value: F
MLST
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

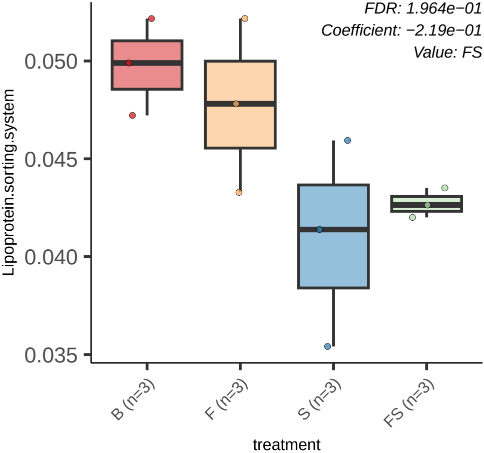

FDR: 1.955e−01
Coefficient: −1.32e−01
Value: FS
ThiD.ThiE.fusions
0.039
0.037
0.035
0.033
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

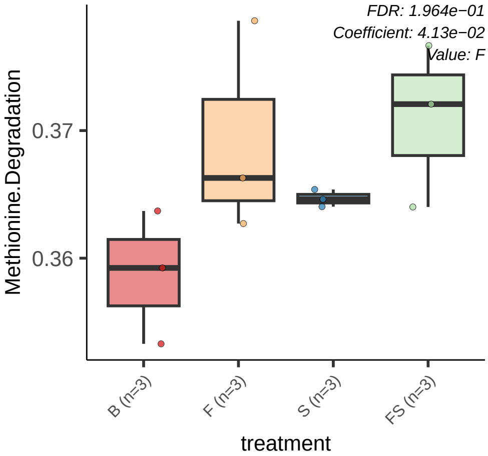

FDR: 1.956e−01
Coefficient: −2.40e−01
Value: S
Zinc.resistance
0.070
0.065
0.060
0.055
0.050
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

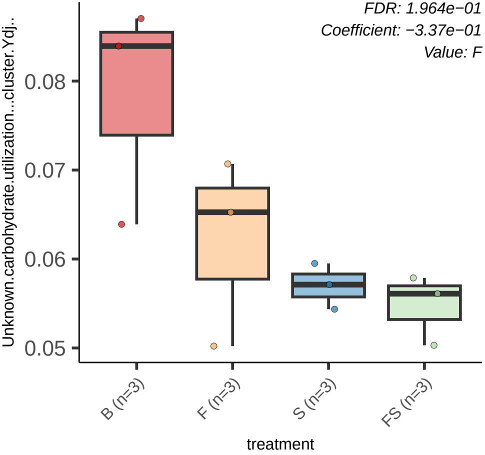

FDR: 1.958e−01
Coefficient: 2.40e+00
Value: FS
Malonate_
6e−04
4e−04
2e−04
0e+00
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

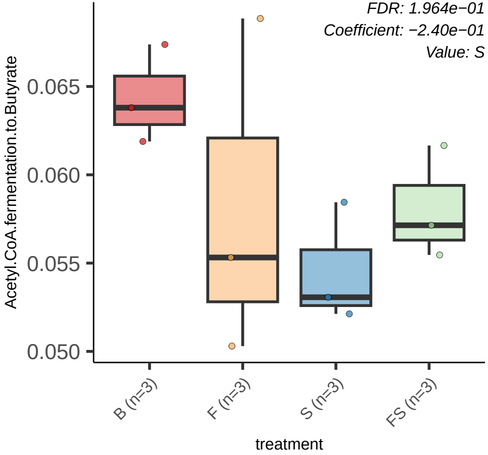

FDR: 1.963e−01
Coefficient: −2.46e−01
Value: FS
Toxin.antitoxin.systems..other.than.RelBE.and.MazEF.
0.035
0.030
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

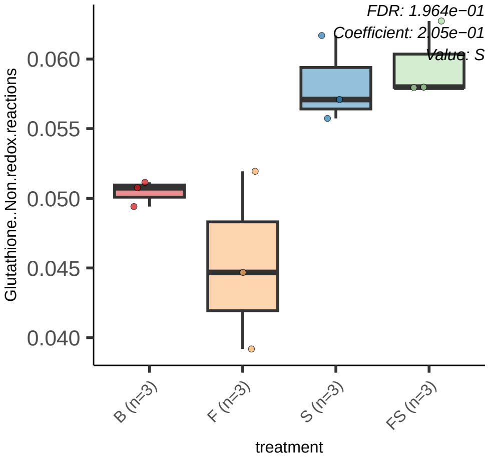

FDR: 1.963e−01
Coefficient: −2.46e−01
Value: S
CBSS.342610.3.peg.283
0.021
0.019
0.017
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

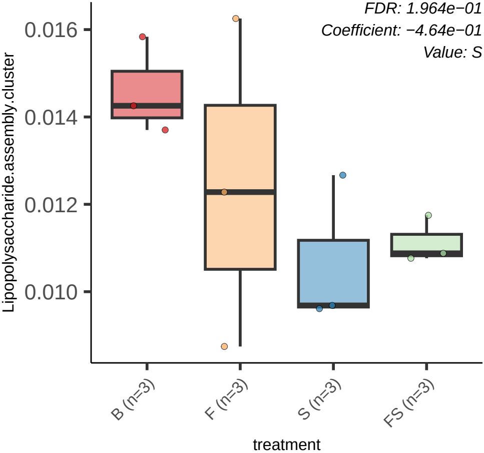

FDR: 1.964e−01
Coefficient: −2.19e−01
Value: FS
Lipoprotein.sorting.system
0.050
0.045
0.040
0.035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

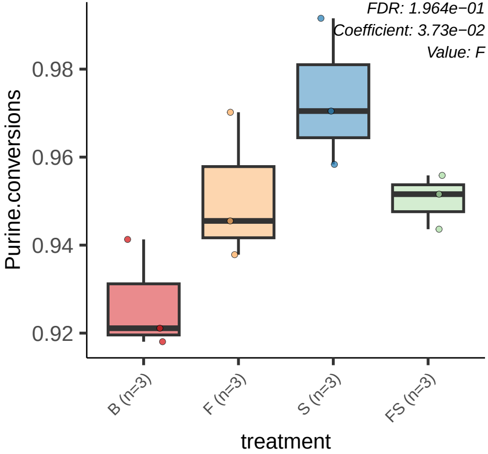

FDR: 1.964e−01
Coefficient: 4.13e−02
Value: F
Methionine.Degradation
0.37
0.36
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

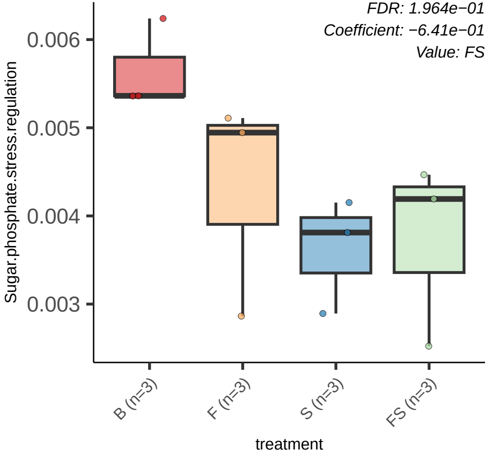

FDR: 1.964e−01
Coefficient: −3.37e−01
Value: F
Unknown.carbohydrate.utilization..cluster.Ydj..
0.08
0.07
0.06
0.05
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

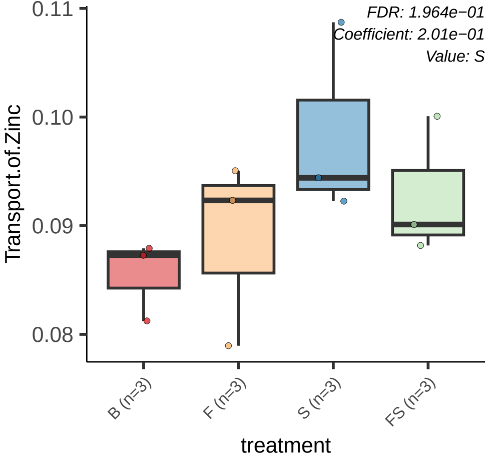

FDR: 1.964e−01
Coefficient: −2.40e−01
Value: S
Acetyl.CoA.fermentation.to.Butyrate
0.065
0.060
0.055
0.050
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

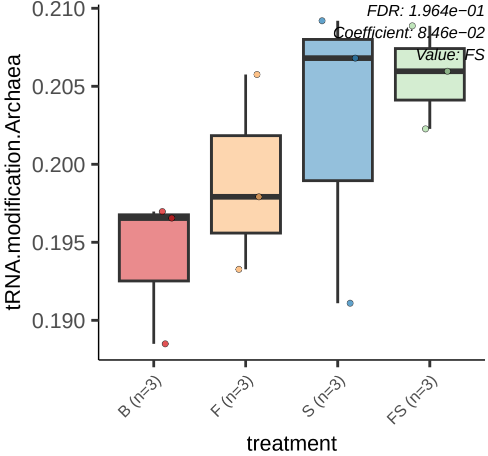

FDR: 1.964e−01
Coefficient: 2.05e−01
Value: S
Glutathione..Non.redox.reactions
0.060
0.055
0.050
0.045
0.040
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

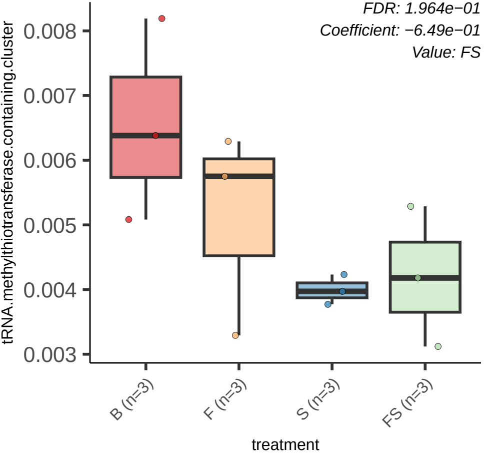

FDR: 1.964e−01
Coefficient: −4.64e−01
Value: S
Lipopolysaccharide.assembly.cluster
0.016
0.014
0.012
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

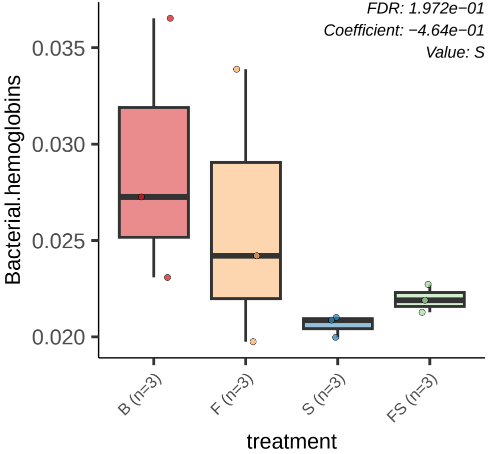

FDR: 1.964e−01
Coefficient: 3.73e−02
Value: F
0.98
0.96
0.94
0.92
Purine.conversions
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

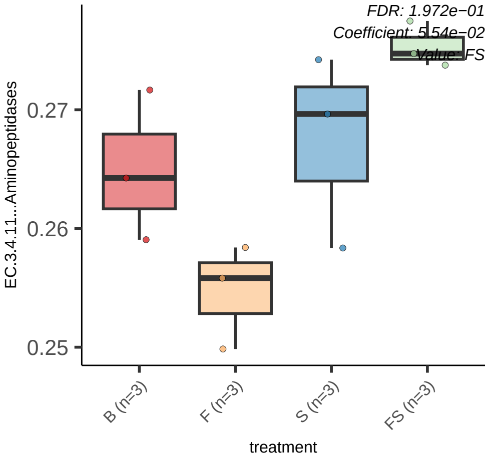

FDR: 1.964e−01
Coefficient: −6.41e−01
Value: FS
Sugar.phosphate.stress.regulation
0.006
0.005
0.004
0.003
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

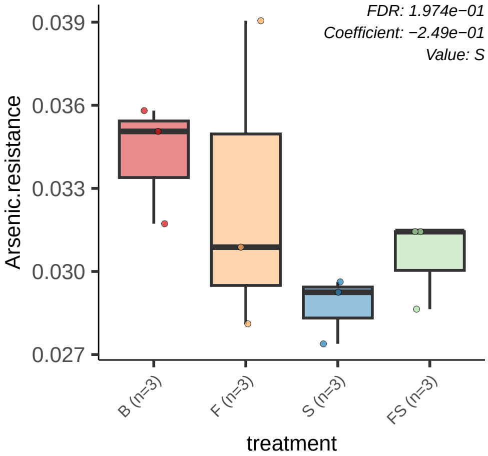

FDR: 1.964e−01
Coefficient: 2.01e−01
Value: S
Transport.of.Zinc
0.11
0.10
0.09
0.08
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

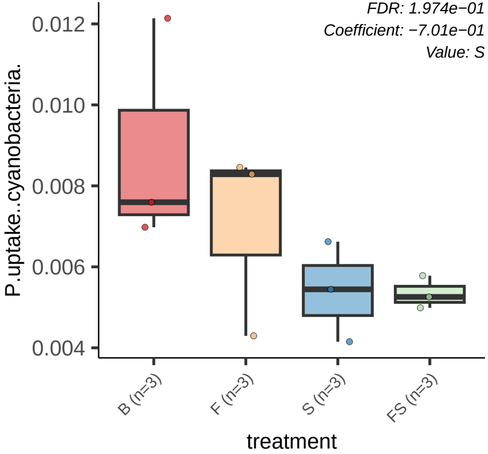

FDR: 1.964e−01
Coefficient: 8.46e−02
Value: FS
tRNA.modification.Archaea
0.210
0.205
0.200
0.195
0.190
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

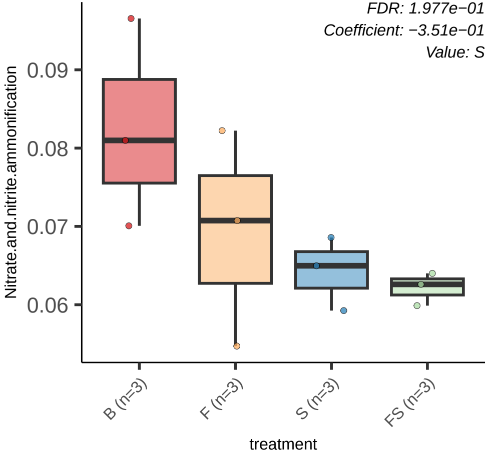

FDR: 1.964e−01
Coefficient: −6.49e−01
Value: FS
tRNA.methylthiotransferase.containing.cluster
0.008
0.007
0.006
0.005
0.004
0.003
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

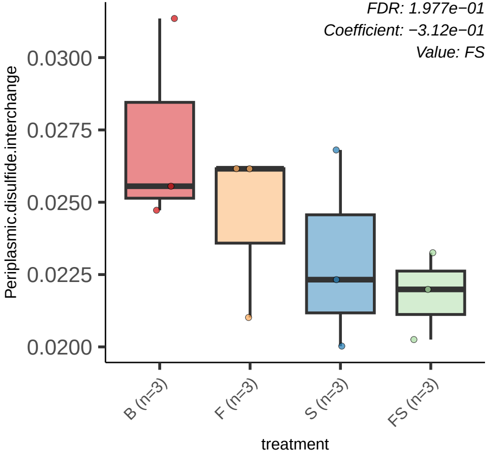

FDR: 1.972e−01
Coefficient: −4.64e−01
Value: S
Bacterial.hemoglobins
0.035
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

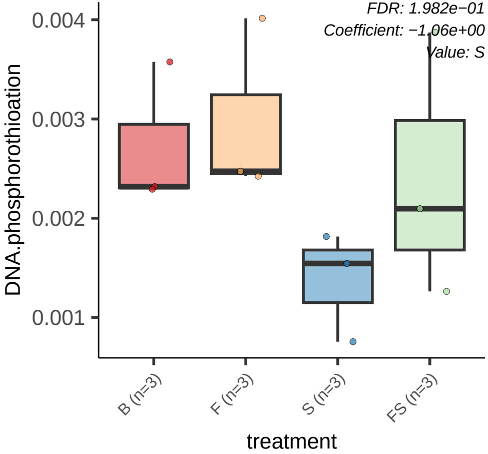

FDR: 1.972e−01
Coefficient: 5.54e−02
Value: FS
EC.3.4.11...Aminopeptidases
0.27
0.26
0.25
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 1.974e−01
Coefficient: −2.49e−01
Value: S
Arsenic.resistance
0.039
0.036
0.033
0.030
0.027
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

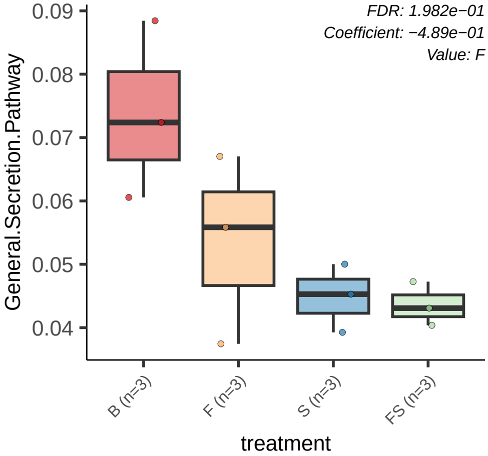

FDR: 1.974e−01
Coefficient: −7.01e−01
Value: S
P.uptake..cyanobacteria.
0.012
0.010
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

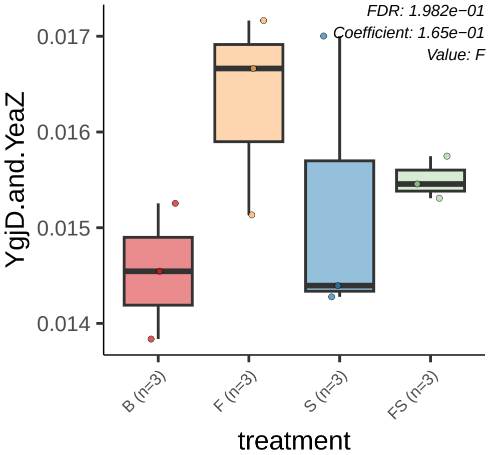

FDR: 1.977e−01
Coefficient: −3.51e−01
Value: S
Nitrate.and.nitrite.ammonification
0.09
0.08
0.07
0.06
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

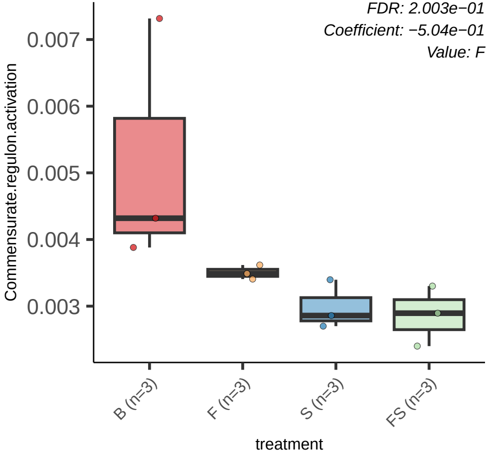

FDR: 1.977e−01
Coefficient: −3.12e−01
Value: FS
Periplasmic.disulfide.interchange
0.0300
0.0275
0.0250
0.0225
0.0200
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

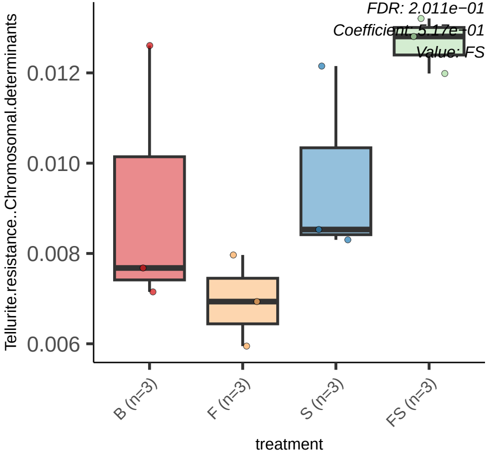


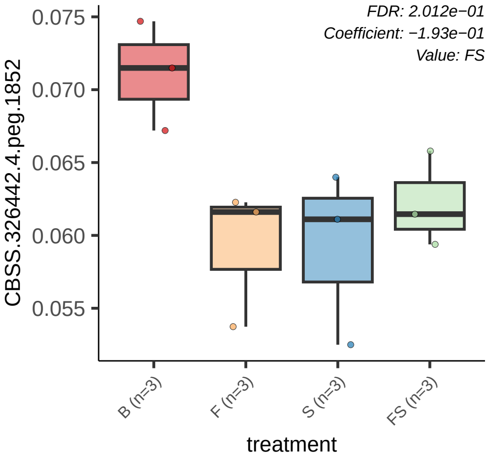
FDR: 1.982e−01
Coefficient: −1.06e+00
Value: S
DNA.phosphorothioation
0.004
0.003
0.002
0.001
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

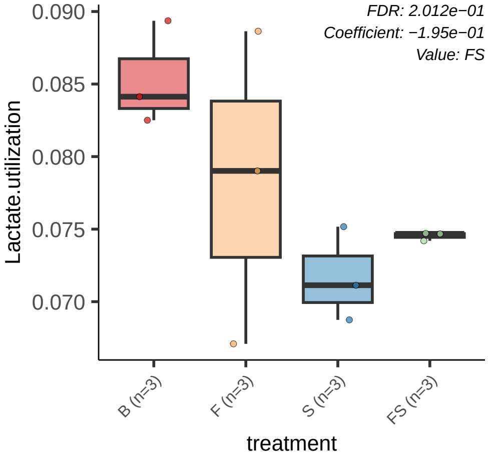

FDR: 1.982e−01
Coefficient: −4.89e−01
Value: F
General.Secretion.Pathway
0.09
0.08
0.07
0.06
0.05
0.04
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

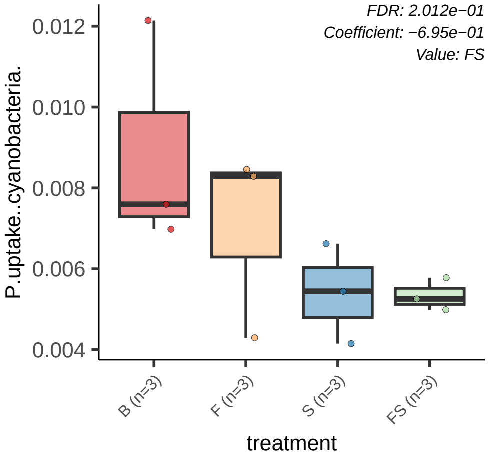

FDR: 1.982e−01
Coefficient: 1.65e−01
Value: F
YgjD.and.YeaZ
0.017
0.016
0.015
0.014
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

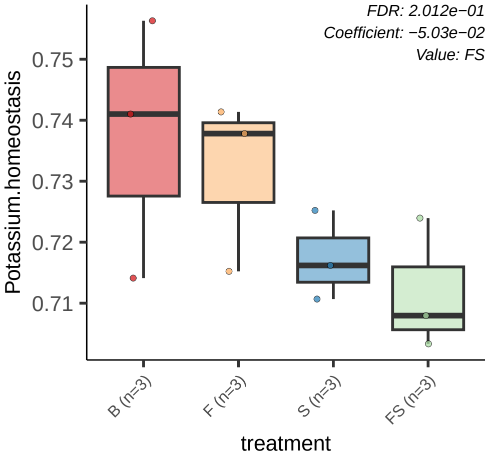

FDR: 2.003e−01
Coefficient: −5.04e−01
Value: F
Commensurate.regulon.activation
0.007
0.006
0.005
0.004
0.003
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

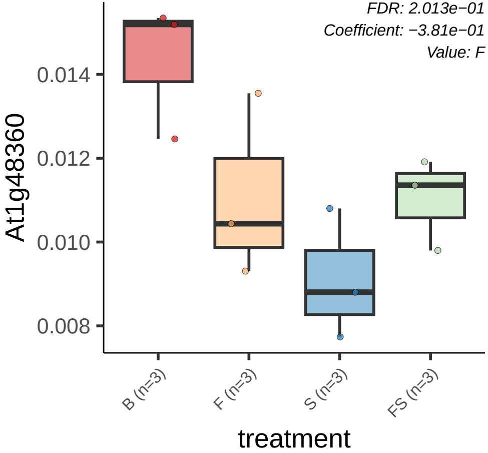

FDR: 2.011e−01
Coefficient: 5.17e−01
Value: FS
Tellurite.resistance..Chromosomal.determinants
0.012
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

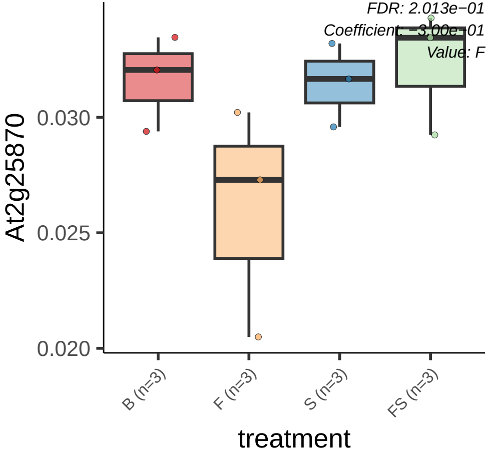

FDR: 2.012e−01
Coefficient: −1.93e−01
Value: FS
CBSS.326442.4.peg.1852
0.075
0.070
0.065
0.060
0.055
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

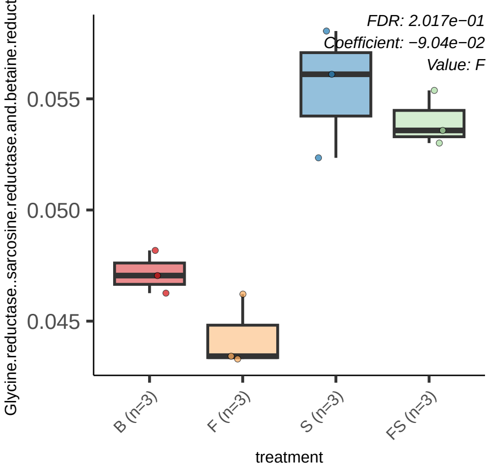

FDR: 2.012e−01
Coefficient: −1.95e−01
Value: FS
Lactate.utilization
0.090
0.085
0.080
0.075
0.070
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

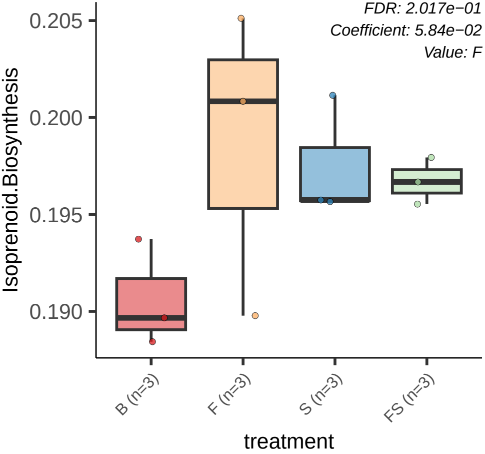

FDR: 2.012e−01
Coefficient: −6.95e−01
Value: FS
P.uptake..cyanobacteria.
0.012
0.010
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

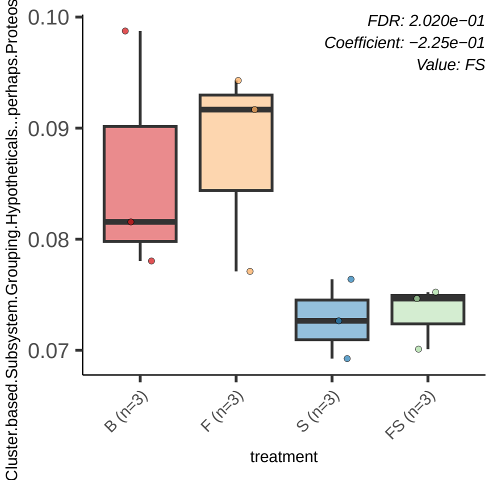

FDR: 2.012e−01
Coefficient: −5.03e−02
Value: FS
Potassium.homeostasis
0.75
0.74
0.73
0.72
0.71
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

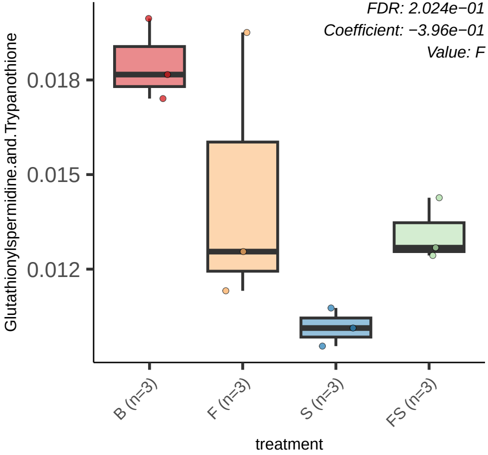

FDR: 2.013e−01
Coefficient: −3.81e−01
Value: F
At1g48360
0.014
0.012
0.010
0.008
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

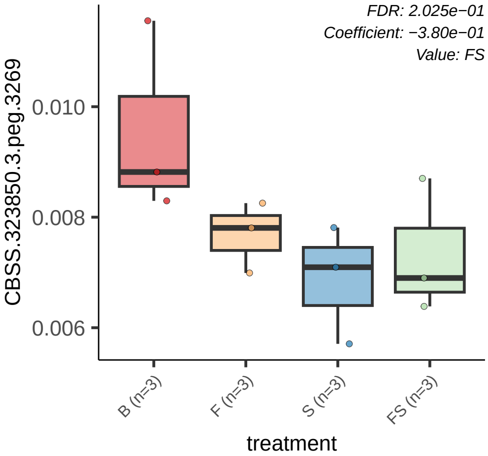

FDR: 2.013e−01
Coefficient: −3.00e−01
Value: F
At2g25870
0.030
0.025
0.020
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

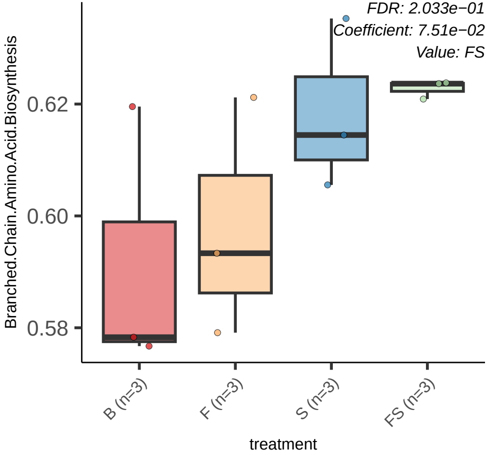

FDR: 2.017e−01
Coefficient: −9.04e−02
Value: F
Glycine.reductase..sarcosine.reductase.and.betaine.reduct
0.055
0.050
0.045
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

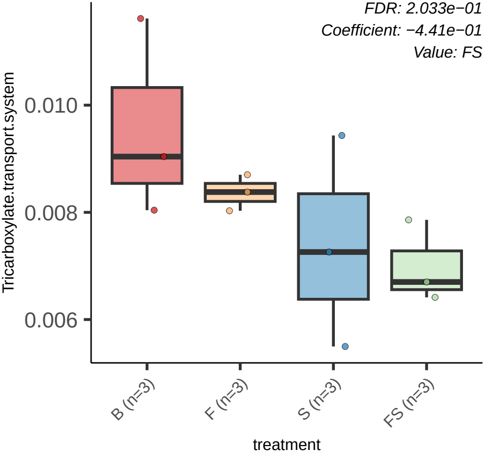

FDR: 2.017e−01
Coefficient: 5.84e−02
Value: F
Isoprenoid.Biosynthesis
0.205
0.200
0.195
0.190
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

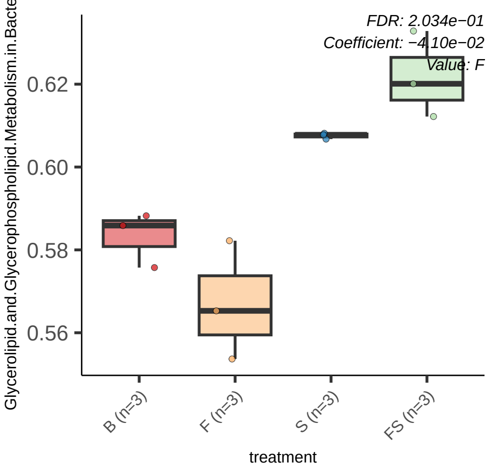

FDR: 2.020e−01
Coefficient: −2.25e−01
Value: FS
Cluster.based.Subsystem.Grouping.Hypotheticals...perhaps.Proteos
0.10
0.09
0.08
0.07
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

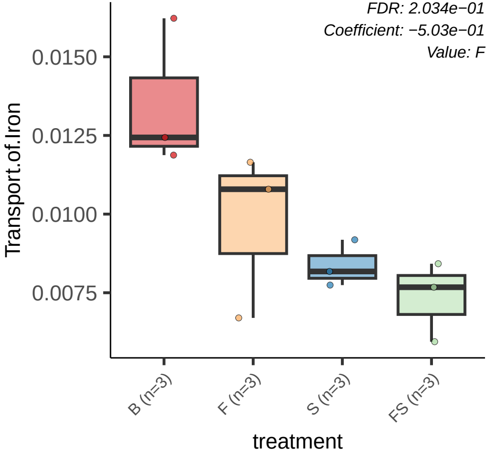

FDR: 2.024e−01
Coefficient: −3.96e−01
Value: F
Glutathionylspermidine.and.Trypanothione
0.018
0.015
0.012
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

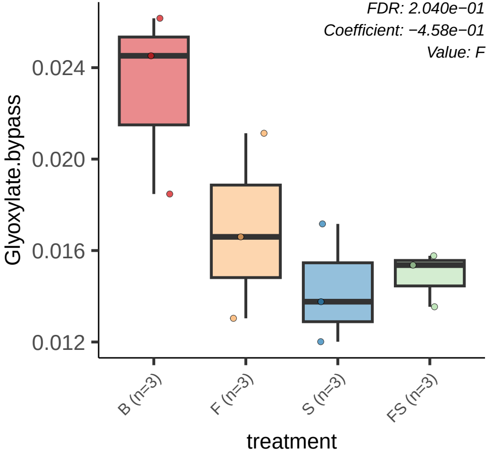

FDR: 2.025e−01
Coefficient: −3.80e−01
Value: FS
CBSS.323850.3.peg.3269
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

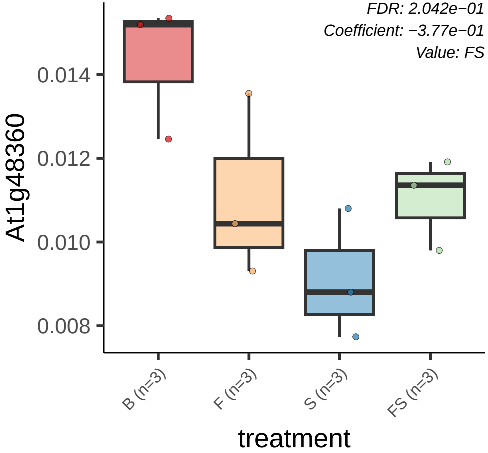

FDR: 2.033e−01
Coefficient: 7.51e−02
Value: FS
Branched.Chain.Amino.Acid.Biosynthesis
0.62
0.60
0.58
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

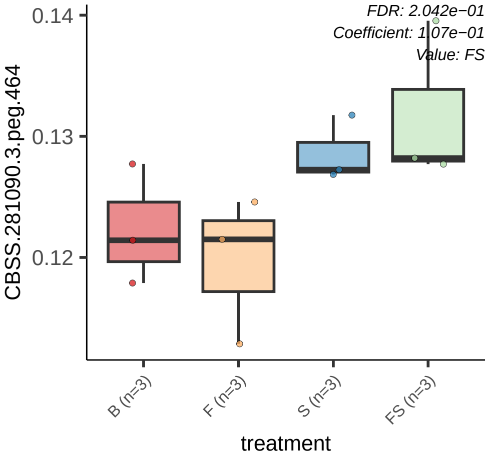

FDR: 2.033e−01
Coefficient: −4.41e−01
Value: FS
Tricarboxylate.transport.system
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

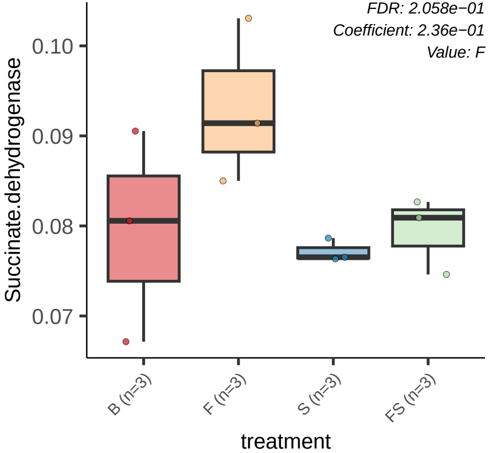

FDR: 2.034e−01
Coefficient: −4.10e−02
Value: F
Glycerolipid.and.Glycerophospholipid.Metabolism.in.Bacte
0.62
0.60
0.58
0.56
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

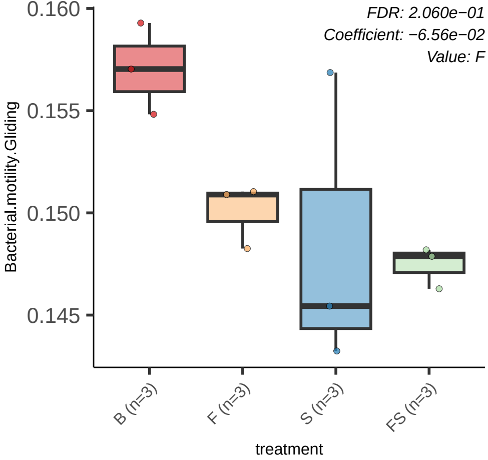

FDR: 2.034e−01
Coefficient: −5.03e−01
Value: F
Transport.of.Iron
0.0150
0.0125
0.0100
0.0075
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

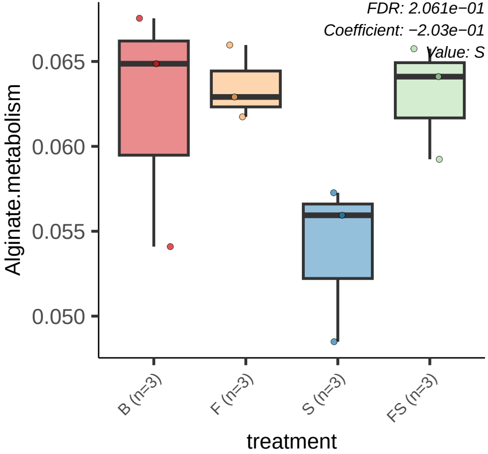

FDR: 2.040e−01
Coefficient: −4.58e−01
Value: F
Glyoxylate.bypass
0.024
0.020
0.016
0.012
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

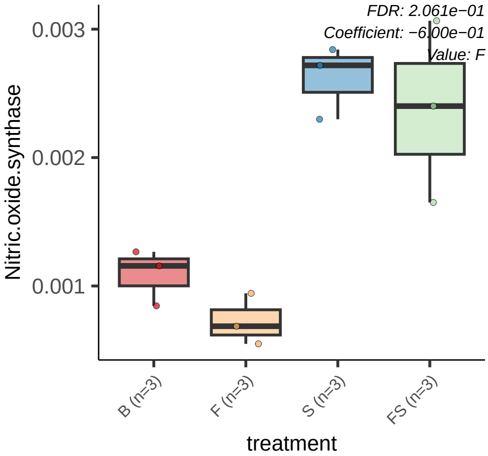

FDR: 2.042e−01
Coefficient: −3.77e−01
Value: FS
At1g48360
0.014
0.012
0.010
0.008
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

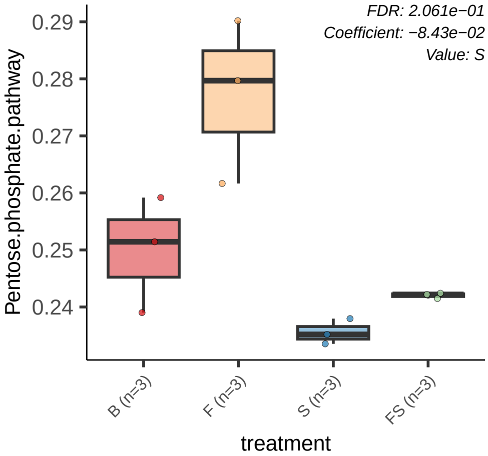

FDR: 2.042e−01
Coefficient: 1.07e−01
Value: FS
CBSS.281090.3.peg.464
0.14
0.13
0.12
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

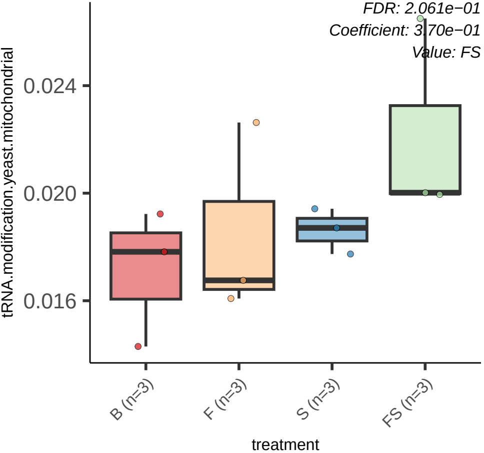

FDR: 2.058e−01
Coefficient: 2.36e−01
Value: F
Succinate.dehydrogenase
0.10
0.09
0.08
0.07
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

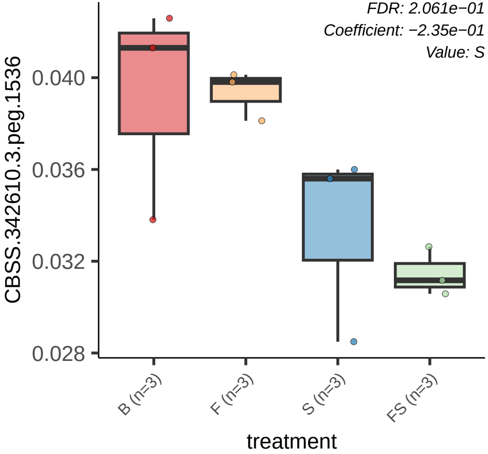

FDR: 2.060e−01
Coefficient: −6.56e−02
Value: F
Bacterial.motility.Gliding
0.160
0.155
0.150
0.145
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

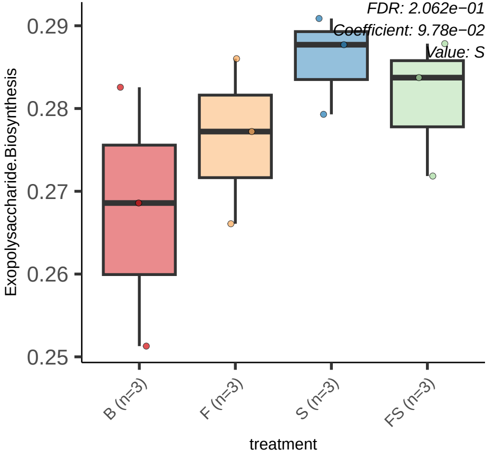

FDR: 2.061e−01
Coefficient: −2.03e−01
Value: S
Alginate.metabolism
0.065
0.060
0.055
0.050
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

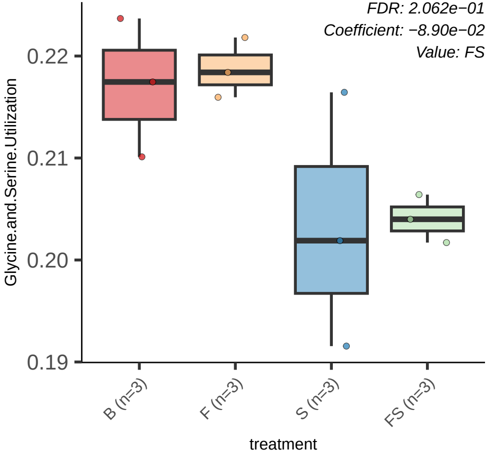

FDR: 2.061e−01
Coefficient: −6.00e−01
Value: F
Nitric.oxide.synthase
0.003
0.002
0.001
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

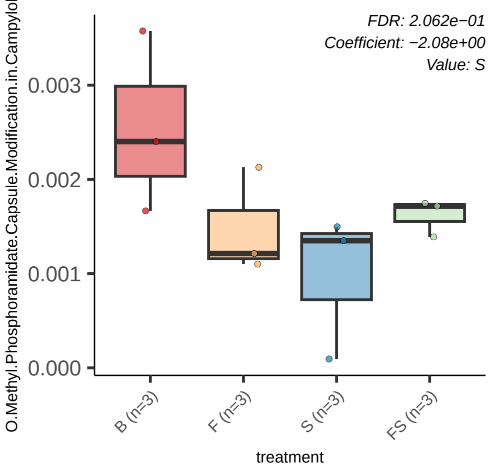

FDR: 2.061e−01
Coefficient: −8.43e−02
Value: S
Pentose.phosphate.pathway
0.29
0.28
0.27
0.26
0.25
0.24
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

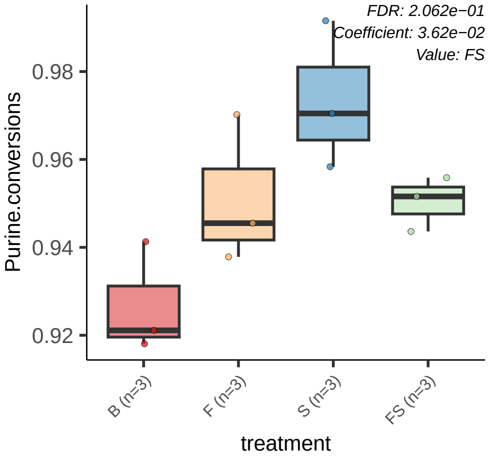

FDR: 2.061e−01
Coefficient: 3.70e−01
Value: FS
tRNA.modification.yeast.mitochondrial
0.024
0.020
0.016
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

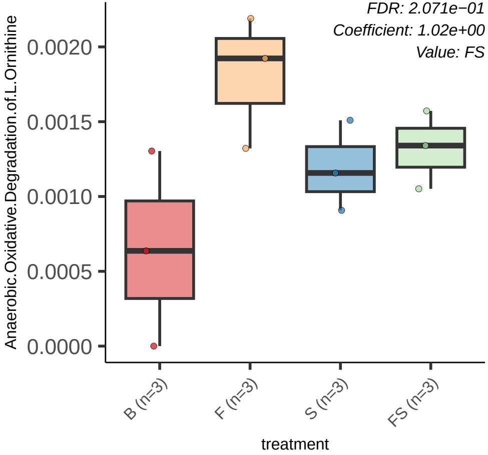

FDR: 2.061e−01
Coefficient: −2.35e−01
Value: S
CBSS.342610.3.peg.1536
0.040
0.036
0.032
0.028
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

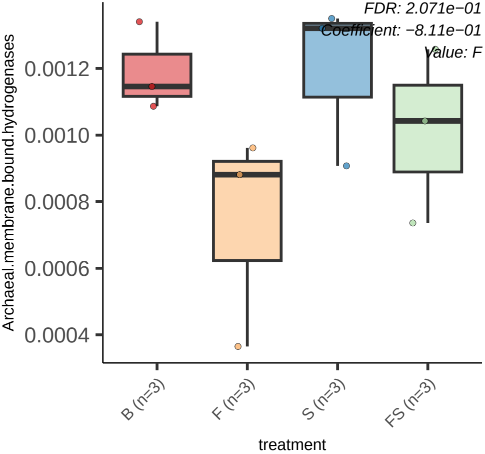

FDR: 2.062e−01
Coefficient: 9.78e−02
Value: S
Exopolysaccharide.Biosynthesis
0.29
0.28
0.27
0.26
0.25
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

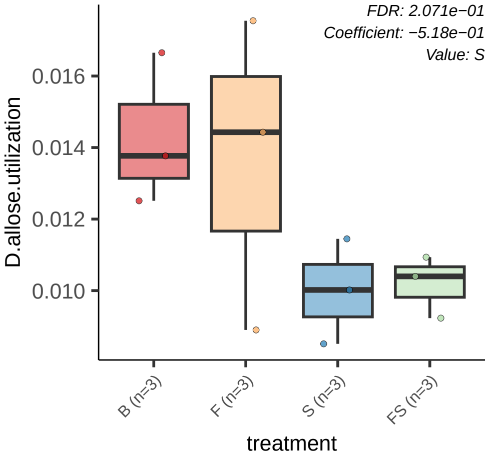

FDR: 2.062e−01
Coefficient: −8.90e−02
Value: FS
Glycine.and.Serine.Utilization
0.22
0.21
0.20
0.19
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

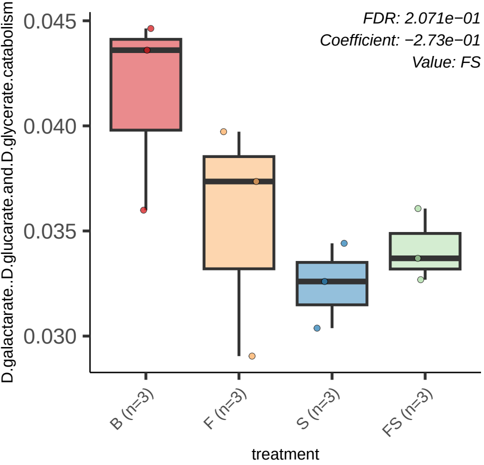

FDR: 2.062e−01
Coefficient: −2.08e+00
Value: S
O.Methyl.Phosphoramidate.Capsule.Modification.in.Campylo
0.003
0.002
0.001
0.000
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

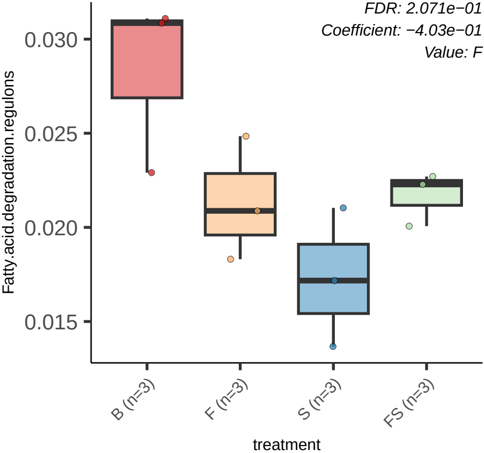

FDR: 2.062e−01
Coefficient: 3.62e−02
Value: FS
Purine.conversions
0.98
0.96
0.94
0.92
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

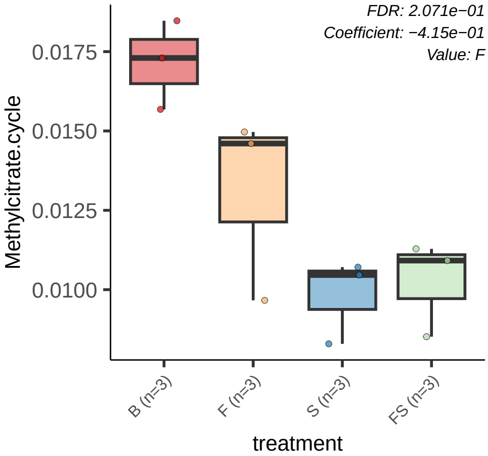

FDR: 2.071e−01
Coefficient: 1.02e+00
Value: FS
Anaerobic.Oxidative.Degradation.of.L.Ornithine
0.0020
0.0015
0.0010
0.0005
0.0000
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

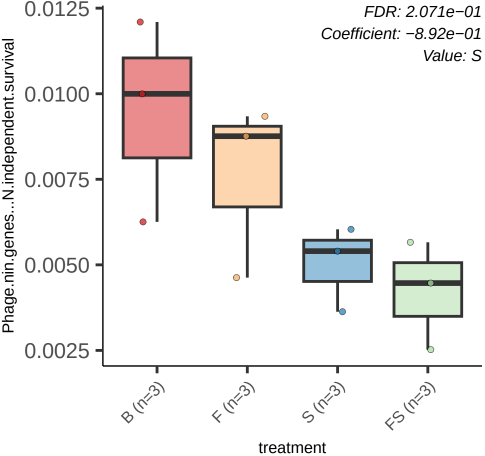

FDR: 2.071e−01
Coefficient: −8.11e−01
Value: F
Archaeal.membrane.bound.hydrogenases
0.0012
0.0010
0.0008
0.0006
0.0004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

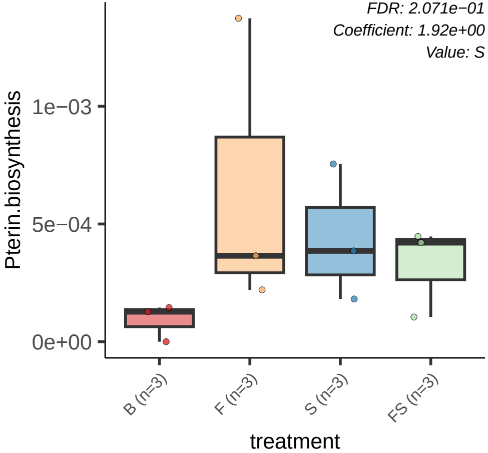

FDR: 2.071e−01
Coefficient: −5.18e−01
Value: S
D.allose.utilization
0.016
0.014
0.012
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

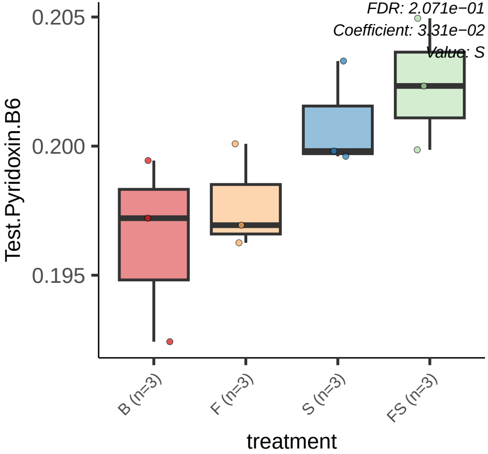

FDR: 2.071e−01
Coefficient: −2.73e−01
Value: FS
D.galactarate..D.glucarate.and.D.glycerate.catabolism
0.045
0.040
0.035
0.030
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

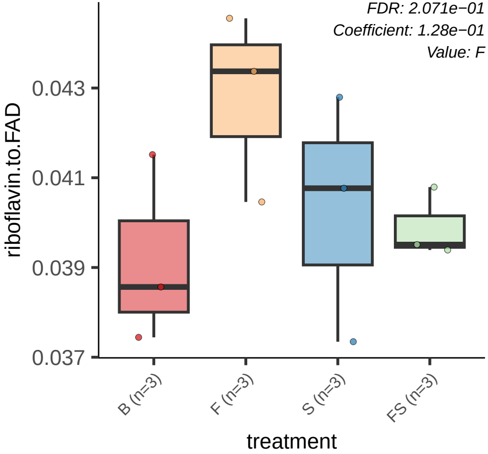

FDR: 2.071e−01
Coefficient: −4.03e−01
Value: F
Fatty.acid.degradation.regulons
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

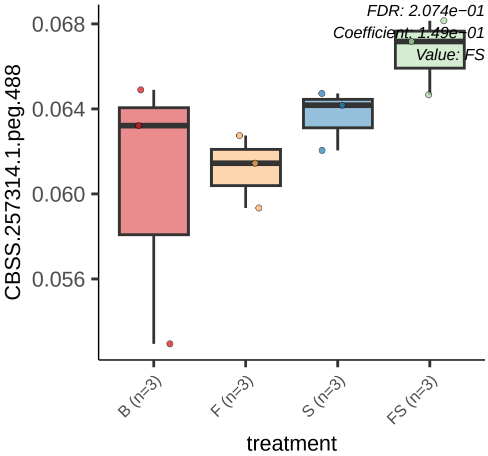

FDR: 2.071e−01
Coefficient: −4.15e−01
Value: F
Methylcitrate.cycle
0.0175
0.0150
0.0125
0.0100
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

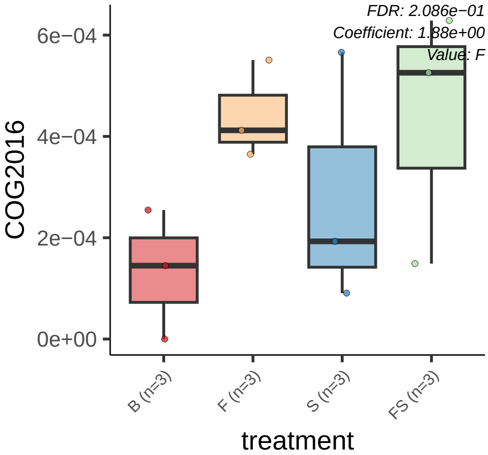

FDR: 2.071e−01
Coefficient: −8.92e−01
Value: S
Phage.nin.genes...N.independent.survival
0.0125
0.0100
0.0075
0.0050
0.0025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 2.071e−01
Coefficient: 1.92e+00
Value: S
Pterin.biosynthesis
1e−03
5e−04
0e+00
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

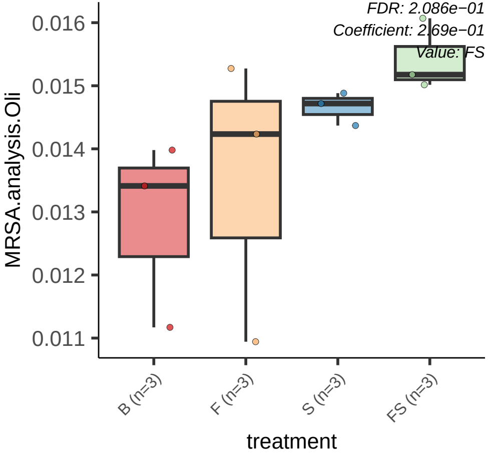

FDR: 2.071e−01
Coefficient: 3.31e−02
Value: S
Test.Pyridoxin.B6
0.205
0.200
0.195
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

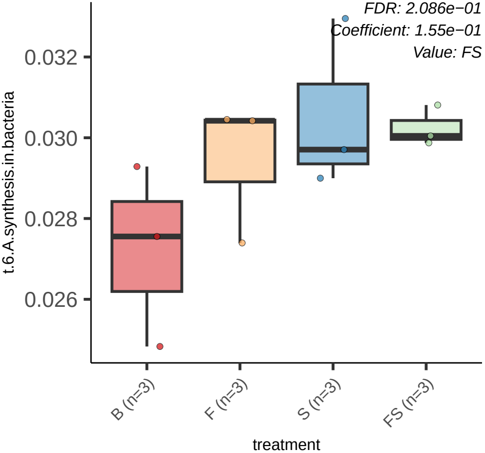

FDR: 2.071e−01
Coefficient: 1.28e−01
Value: F
0.043
0.041
0.039
0.037
riboflavin.to.FAD
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

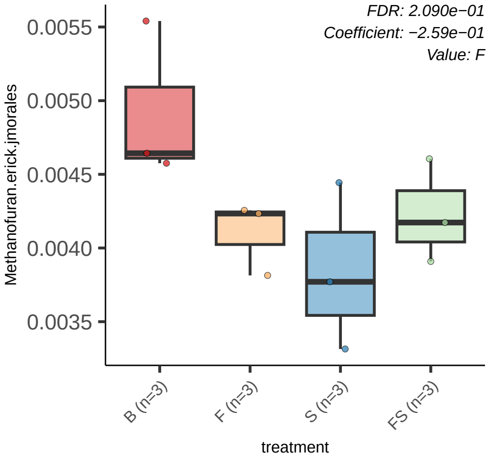

FDR: 2.074e−01
Coefficient: 1.49e−01
Value: FS
CBSS.257314.1.peg.488
0.068
0.064
0.060
0.056
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment



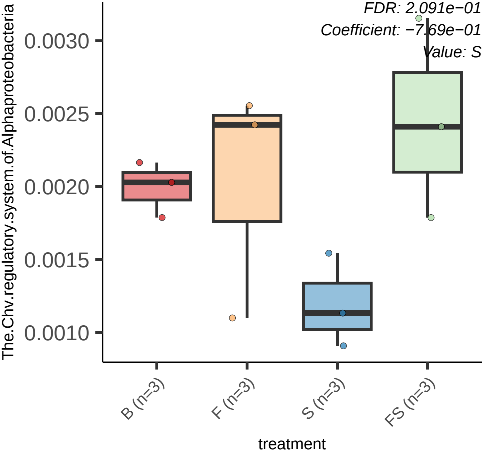
FDR: 2.086e−01
Coefficient: 1.88e+00
Value: F
COG2016
6e−04
4e−04
2e−04
0e+00
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

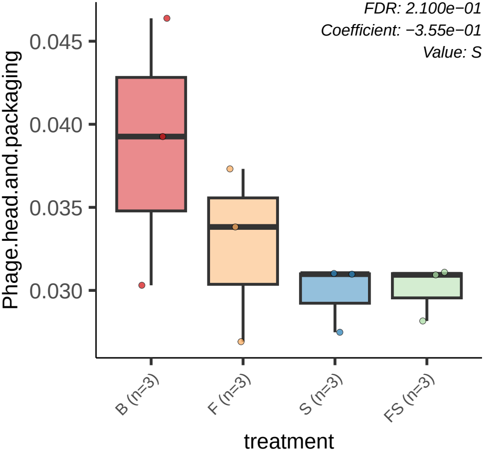

FDR: 2.086e−01
Coefficient: 2.69e−01
Value: FS
MRSA.analysis.Oli
0.016
0.015
0.014
0.013
0.012
0.011
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

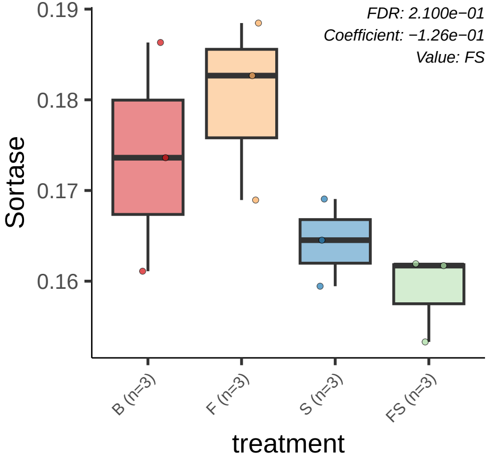

FDR: 2.086e−01
Coefficient: 1.55e−01
Value: FS
t.6.A.synthesis.in.bacteria
0.032
0.030
0.028
0.026
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

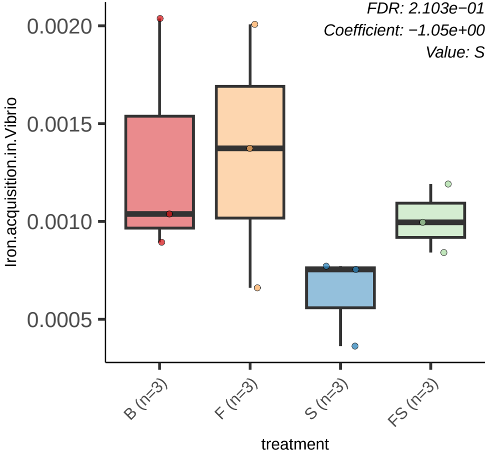


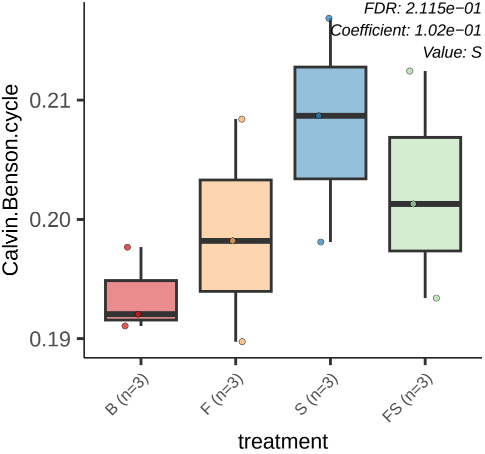
FDR: 2.090e−01
Coefficient: −2.59e−01
Value: F
Methanofuran.erick.jmorales
0.0055
0.0050
0.0045
0.0040
0.0035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

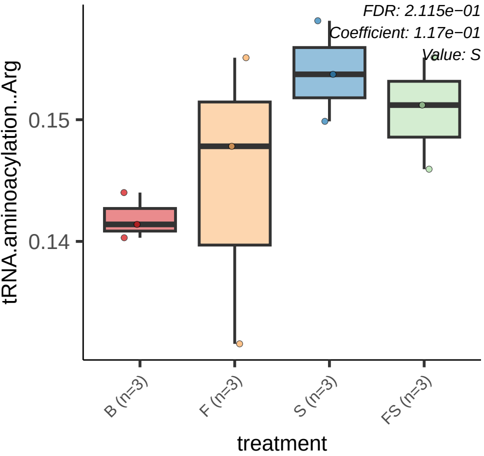

FDR: 2.091e−01
Coefficient: −7.69e−01
Value: S
The.Chv.regulatory.system.of.Alphaproteobacteria
0.0030
0.0025
0.0020
0.0015
0.0010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

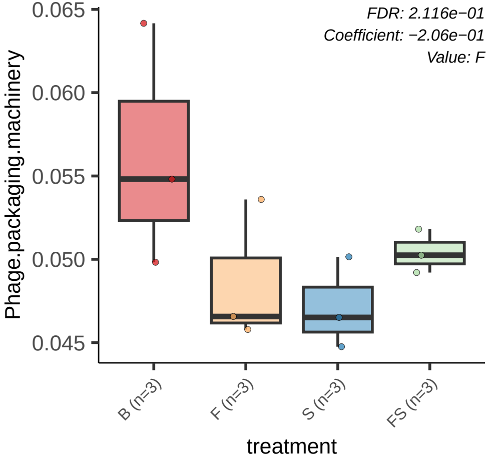

FDR: 2.100e−01
Coefficient: −3.55e−01
Value: S
Phage.head.and.packaging
0.045
0.040
0.035
0.030
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

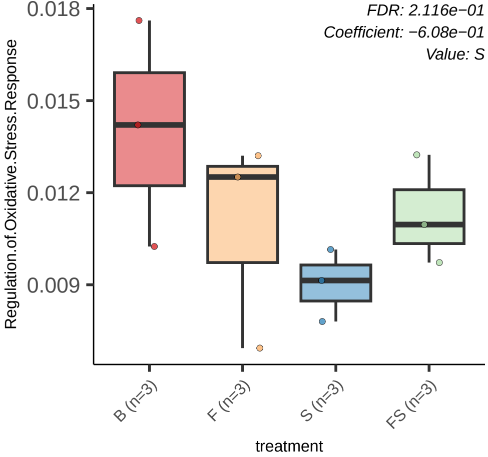

FDR: 2.100e−01
Coefficient: −1.26e−01
Value: FS
Sortase
0.19
0.18
0.17
0.16
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

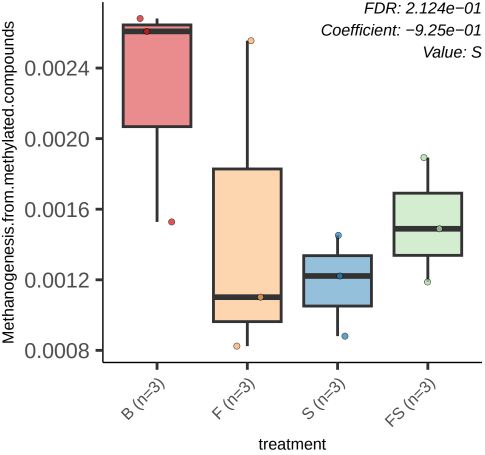

FDR: 2.103e−01
Coefficient: −1.05e+00
Value: S
0.0020
0.0015
0.0010
0.0005
Iron.acquisition.in.Vibrio
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

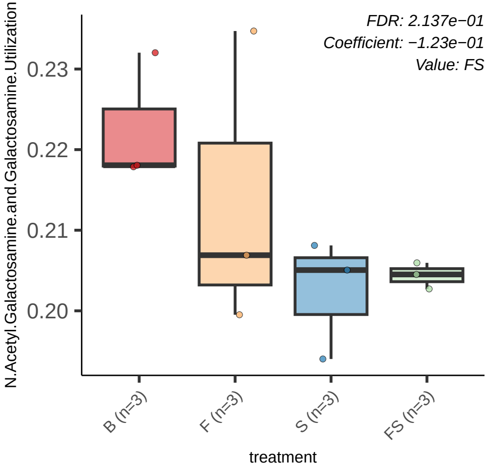

FDR: 2.115e−01
Coefficient: 1.02e−01
Value: S
Calvin.Benson.cycle
0.21
0.20
0.19
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

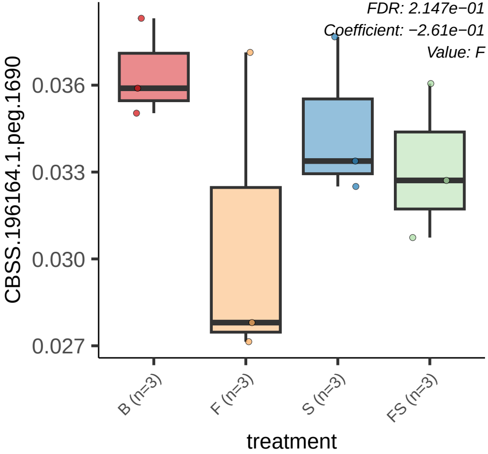

FDR: 2.115e−01
Coefficient: 1.17e−01
Value: S
tRNA.aminoacylation..Arg
0.15
0.14
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

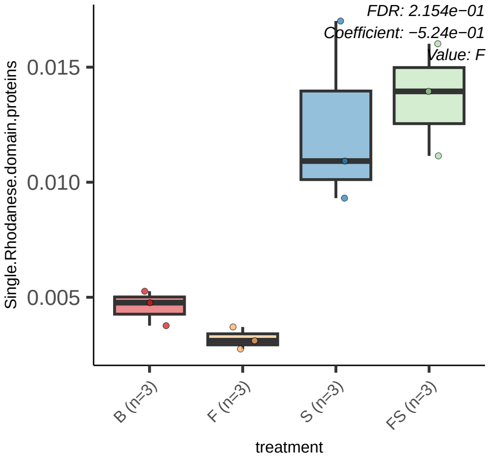

FDR: 2.116e−01
Coefficient: −2.06e−01
Value: F
Phage.packaging.machinery
0.065
0.060
0.055
0.050
0.045
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

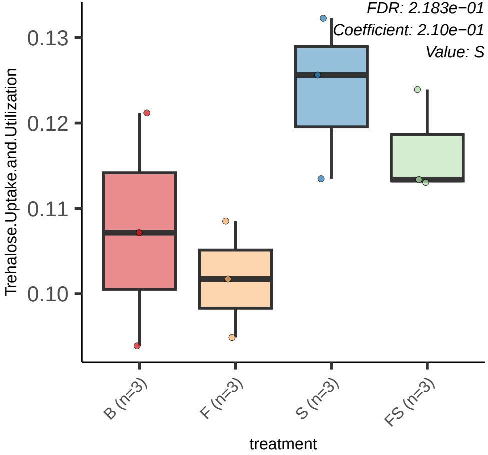

FDR: 2.116e−01
Coefficient: −6.08e−01
Value: S
Regulation.of.Oxidative.Stress.Response
0.018
0.015
0.012
0.009
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

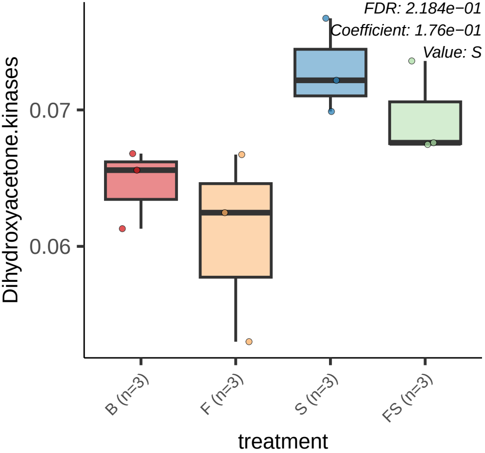

FDR: 2.124e−01
Coefficient: −9.25e−01
Value: S
Methanogenesis.from.methylated.compounds
0.0024
0.0020
0.0016
0.0012
0.0008
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

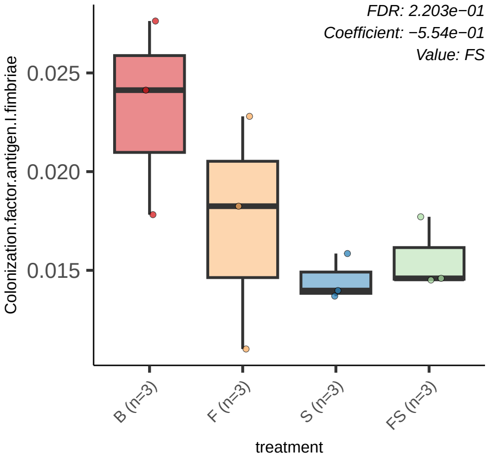

FDR: 2.137e−01
Coefficient: −1.23e−01
Value: FS
N.Acetyl.Galactosamine.and.Galactosamine.Utilization
0.23
0.22
0.21
0.20
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

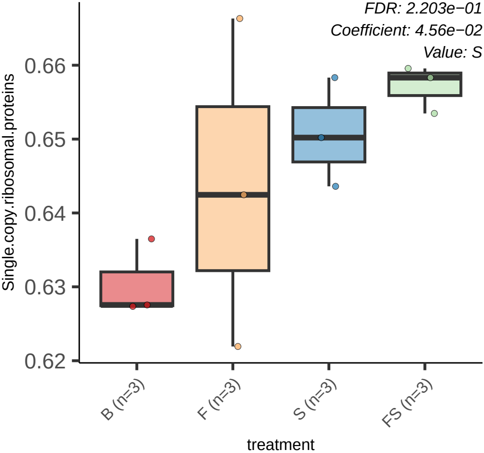

FDR: 2.147e−01
Coefficient: −2.61e−01
Value: F
CBSS.196164.1.peg.1690
0.036
0.033
0.030
0.027
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

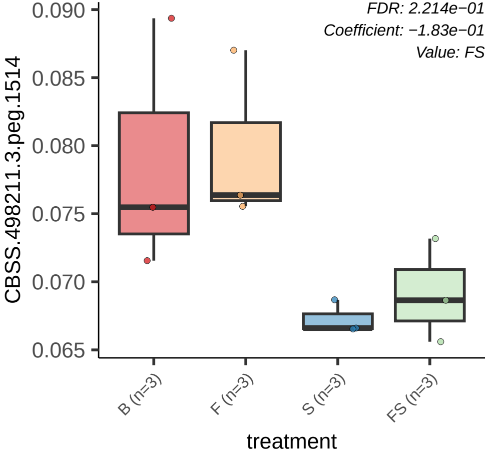

FDR: 2.154e−01
Coefficient: −5.24e−01
Value: F
Single.Rhodanese.domain.proteins
0.015
0.010
0.005
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

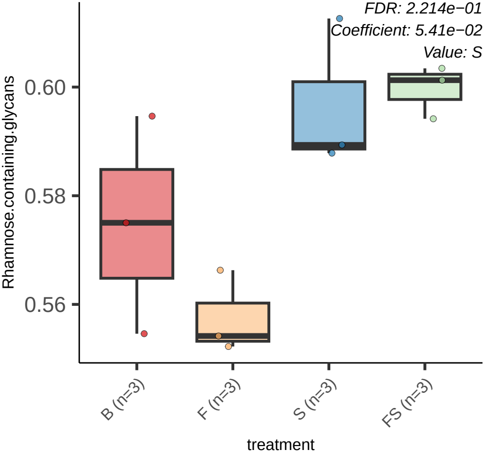

FDR: 2.183e−01
Coefficient: 2.10e−01
Value: S
Trehalose.Uptake.and.Utilization
0.13
0.12
0.11
0.10
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

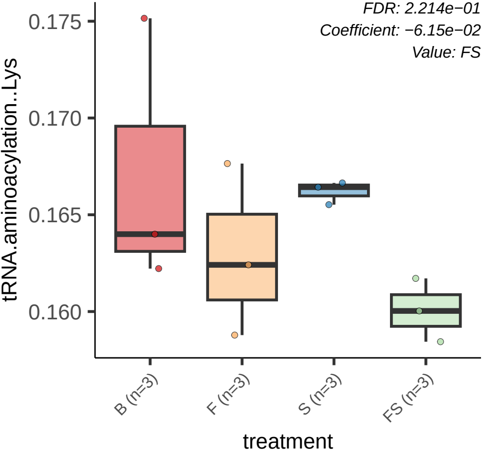

FDR: 2.184e−01
Coefficient: 1.76e−01
Value: S
Dihydroxyacetone.kinases
0.07
0.06
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

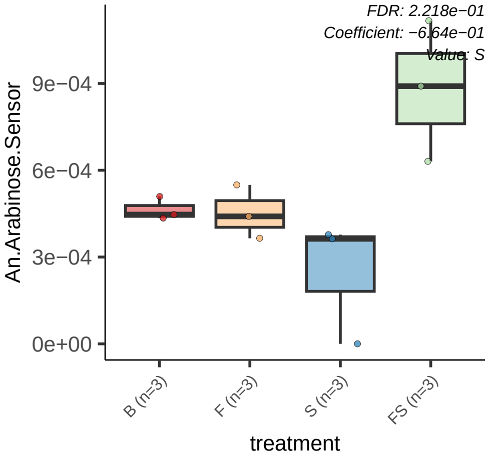

FDR: 2.203e−01
Coefficient: −5.54e−01
Value: FS
Colonization.factor.antigen.I.fimbriae
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

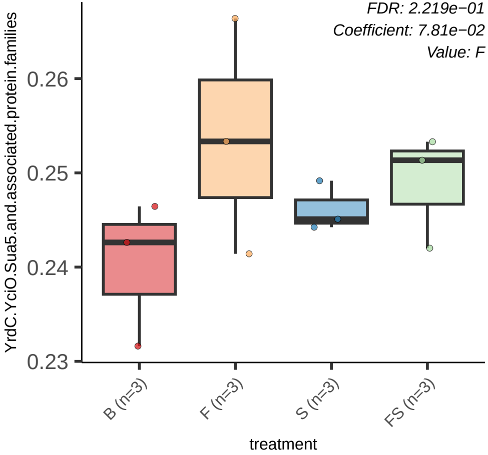

FDR: 2.203e−01
Coefficient: 4.56e−02
Value: S
Single.copy.ribosomal.proteins
0.66
0.65
0.64
0.63
0.62
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

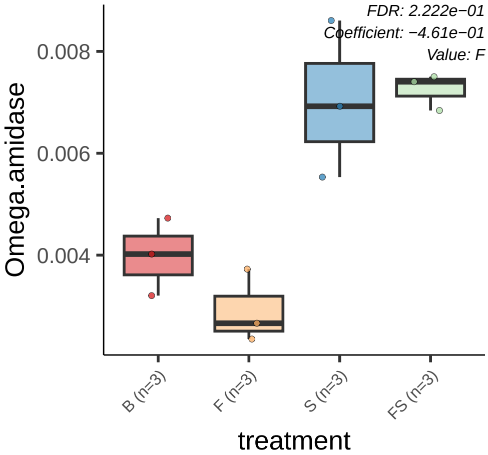

FDR: 2.214e−01
Coefficient: −1.83e−01
Value: FS
CBSS.498211.3.peg.1514
0.090
0.085
0.080
0.075
0.070
0.065
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

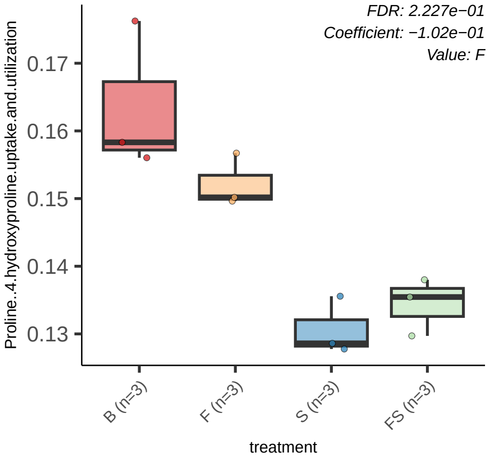

FDR: 2.214e−01
Coefficient: 5.41e−02
Value: S
Rhamnose.containing.glycans
0.60
0.58
0.56
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

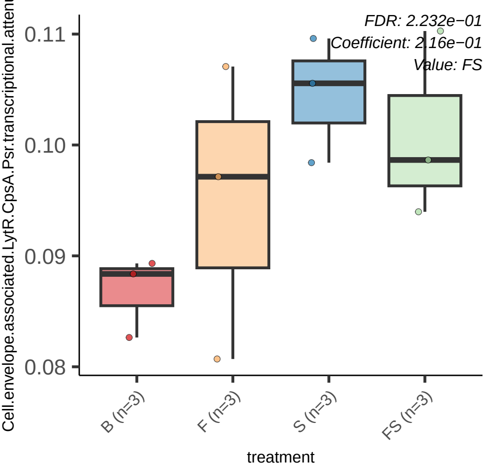

FDR: 2.214e−01
Coefficient: −6.15e−02
Value: FS
tRNA.aminoacylation..Lys
0.175
0.170
0.165
0.160
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

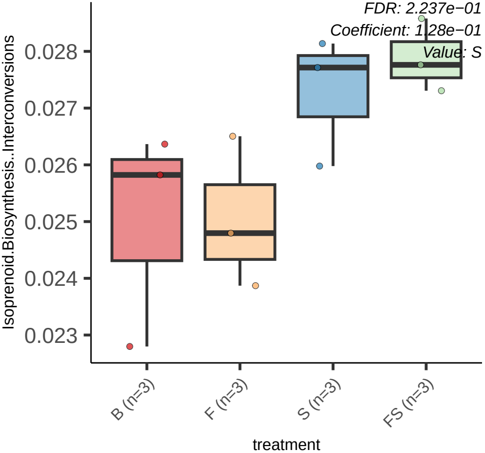

FDR: 2.218e−01
Coefficient: −6.64e−01
Value: S
An.Arabinose.Sensor
9e−04
6e−04
3e−04
0e+00
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

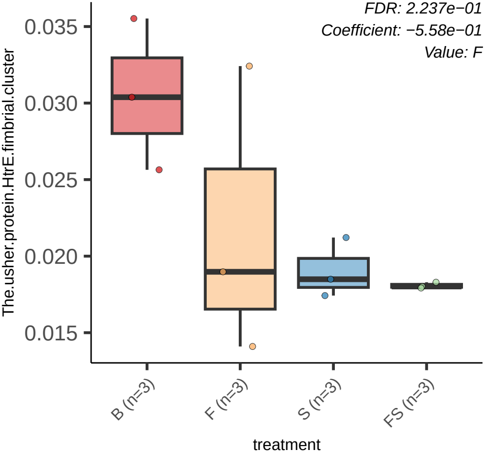

FDR: 2.219e−01
Coefficient: 7.81e−02
Value: F
YrdC.YciO.Sua5.and.associated.protein.families
0.26
0.25
0.24
0.23
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

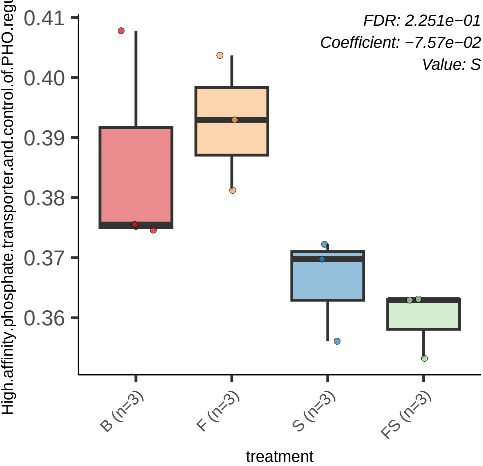

FDR: 2.222e−01
Coefficient: −4.61e−01
Value: F
Omega.amidase
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

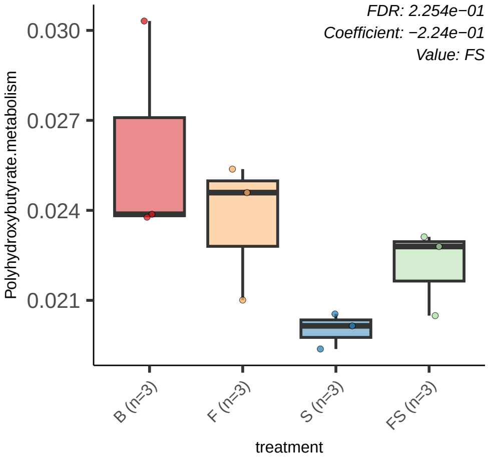

FDR: 2.227e−01
Coefficient: −1.02e−01
Value: F
Proline..4.hydroxyproline.uptake.and.utilization
0.17
0.16
0.15
0.14
0.13
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

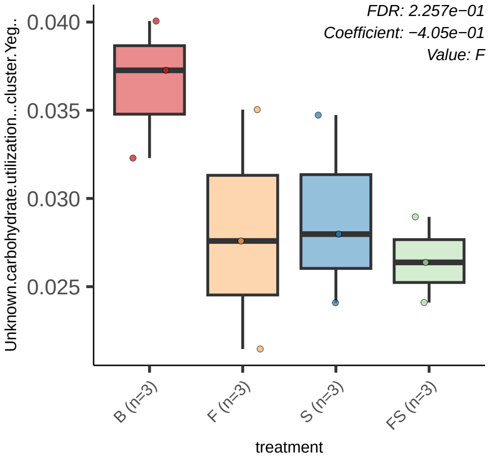

FDR: 2.232e−01
Coefficient: 2.16e−01
Value: FS
Cell.envelope.associated.LytR.CpsA.Psr.transcriptional.atten
0.11
0.10
0.09
0.08
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

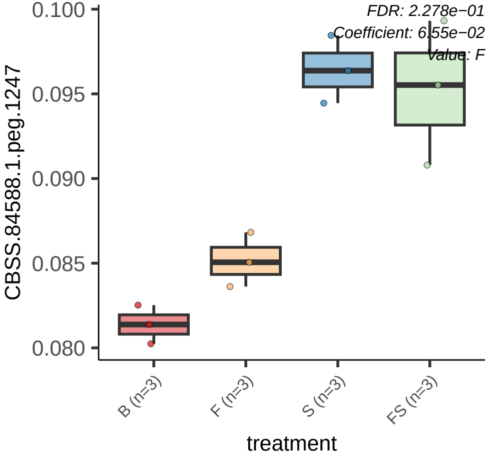

FDR: 2.237e−01
Coefficient: 1.28e−01
Value: S
Isoprenoid.Biosynthesis..Interconversions
0.028
0.027
0.026
0.025
0.024
0.023
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

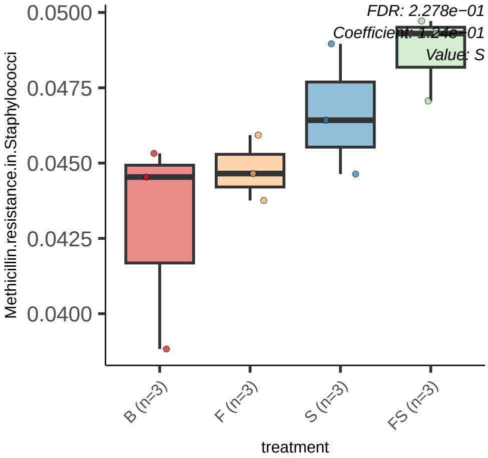

FDR: 2.237e−01
Coefficient: −5.58e−01
Value: F
The.usher.protein.HtrE.fimbrial.cluster
0.035
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

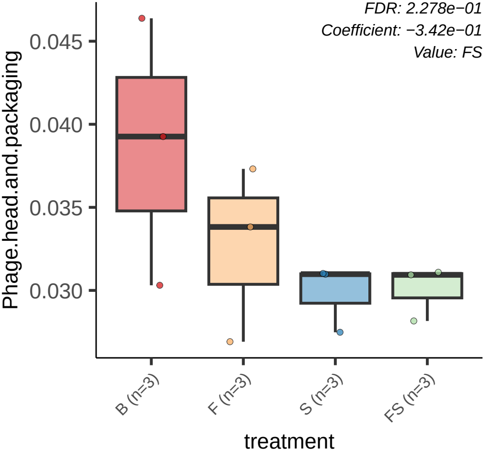

FDR: 2.251e−01
Coefficient: −7.57e−02
Value: S
High.affinity.phosphate.transporter.and.control.of.PHO.regu
0.41
0.40
0.39
0.38
0.37
0.36
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

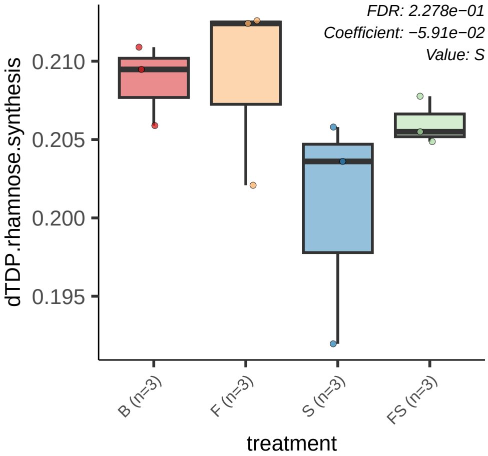

FDR: 2.254e−01
Coefficient: −2.24e−01
Value: FS
Polyhydroxybutyrate.metabolism
0.030
0.027
0.024
0.021
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

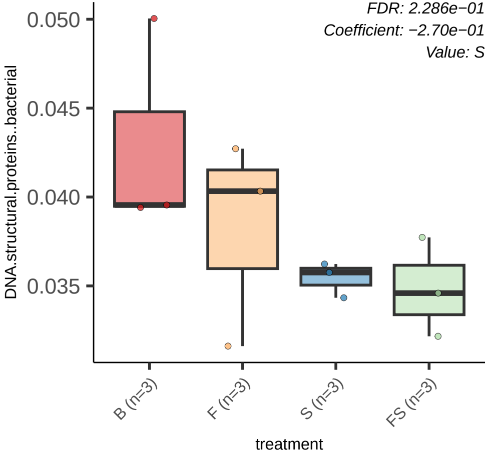

FDR: 2.257e−01
Coefficient: −4.05e−01
Value: F
Unknown.carbohydrate.utilization...cluster.Yeg..
0.040
0.035
0.030
0.025
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

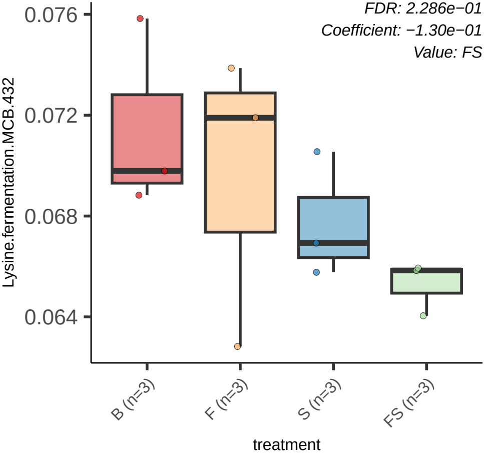

FDR: 2.278e−01
Coefficient: 6.55e−02
Value: F
CBSS.84588.1.peg.1247
0.100
0.095
0.090
0.085
0.080
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

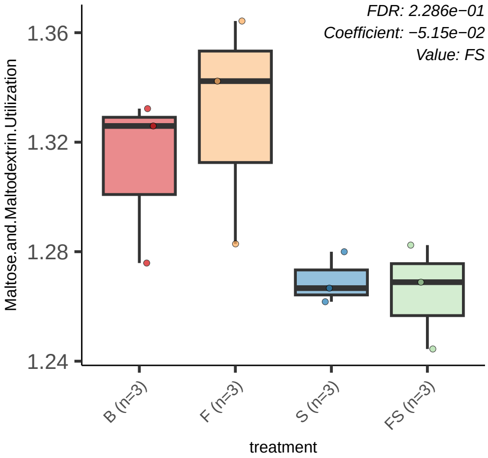

FDR: 2.278e−01
Coefficient: 1.24e−01
Value: S
Methicillin.resistance.in.Staphylococci
0.0500
0.0475
0.0450
0.0425
0.0400
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

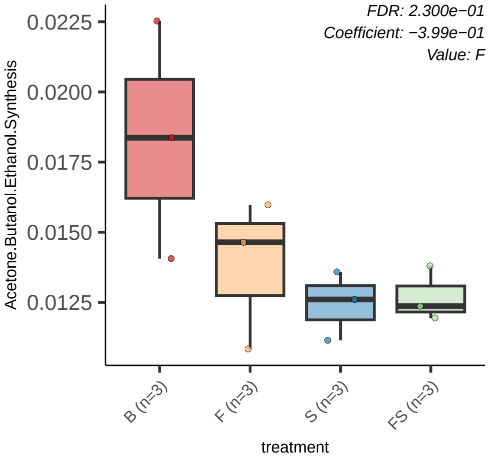

FDR: 2.278e−01
Coefficient: −3.42e−01
Value: FS
Phage.head.and.packaging
0.045
0.040
0.035
0.030
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

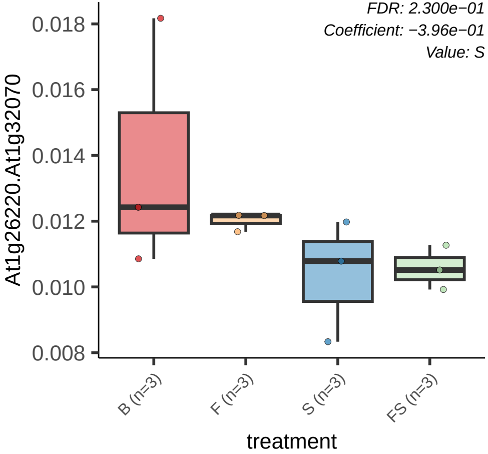

FDR: 2.278e−01
Coefficient: −5.91e−02
Value: S
dTDP.rhamnose.synthesis
0.210
0.205
0.200
0.195
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

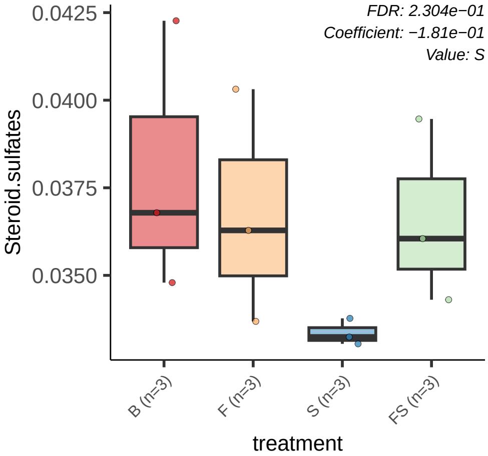

FDR: 2.286e−01
Coefficient: −2.70e−01
Value: S
DNA.structural.proteins..bacterial
0.050
0.045
0.040
0.035
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

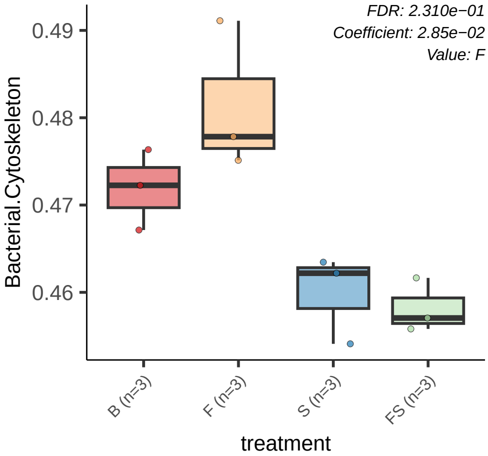

FDR: 2.286e−01
Coefficient: −1.30e−01
Value: FS
Lysine.fermentation.MCB.432
0.076
0.072
0.068
0.064
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

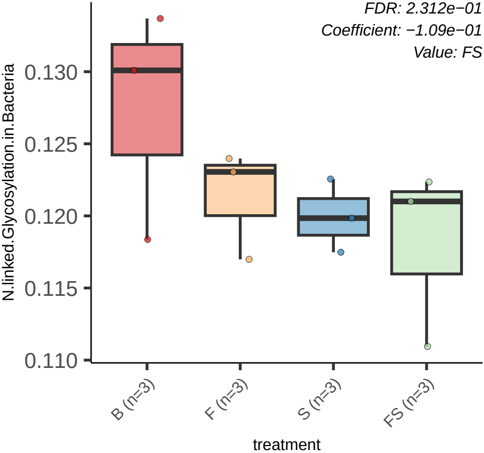

FDR: 2.286e−01
Coefficient: −5.15e−02
Value: FS
Maltose.and.Maltodextrin.Utilization
1.36
1.32
1.28
1.24
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

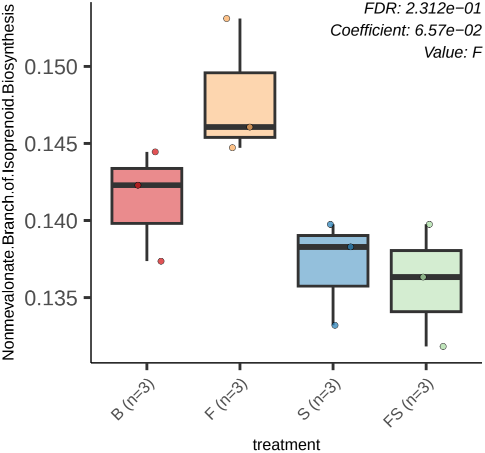

FDR: 2.300e−01
Coefficient: −3.99e−01
Value: F
Acetone.Butanol.Ethanol.Synthesis
0.0225
0.0200
0.0175
0.0150
0.0125
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

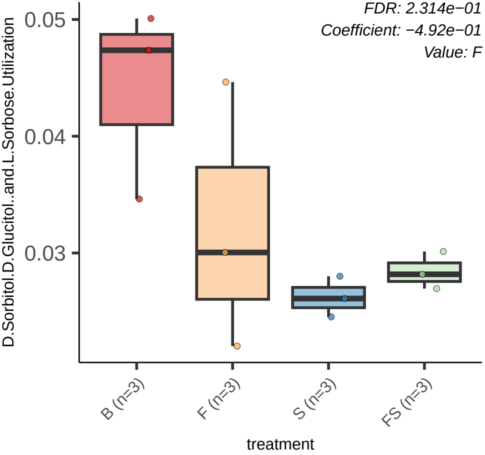

FDR: 2.300e−01
Coefficient: −3.96e−01
Value: S
At1g26220.At1g32070
0.018
0.016
0.014
0.012
0.010
0.008
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

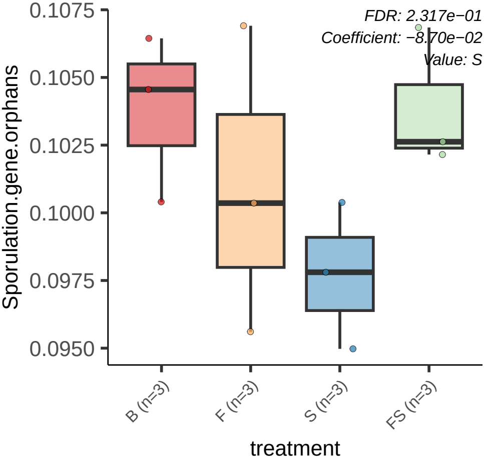

FDR: 2.304e−01
Coefficient: −1.81e−01
Value: S
Steroid.sulfates
0.0425
0.0400
0.0375
0.0350
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

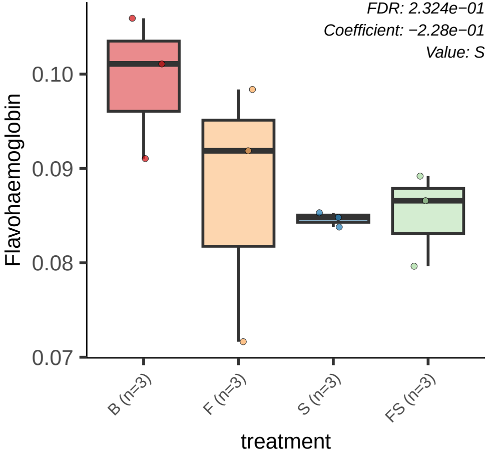

FDR: 2.310e−01
Coefficient: 2.85e−02
Value: F
Bacterial.Cytoskeleton
0.49
0.48
0.47
0.46
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

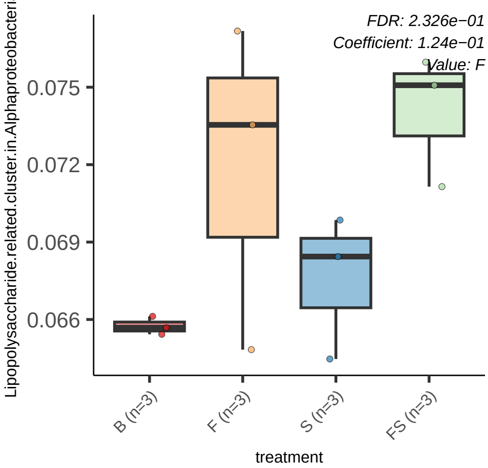

FDR: 2.312e−01
Coefficient: −1.09e−01
Value: FS
N.linked.Glycosylation.in.Bacteria
0.130
0.125
0.120
0.115
0.110
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

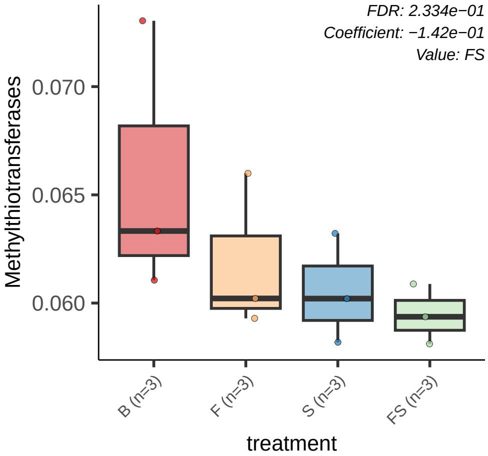

FDR: 2.312e−01
Coefficient: 6.57e−02
Value: F
Nonmevalonate.Branch.of.Isoprenoid.Biosynthesis
0.150
0.145
0.140
0.135
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

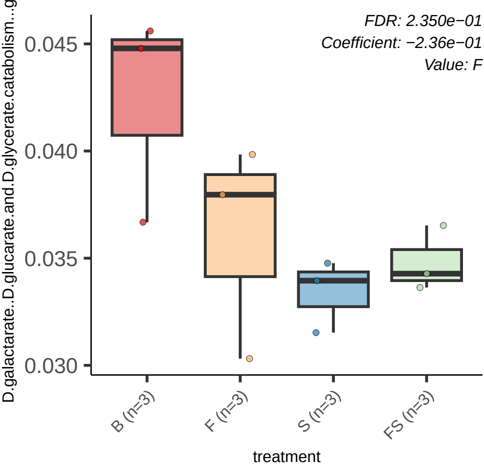

FDR: 2.314e−01
Coefficient: −4.92e−01
Value: F
D.Sorbitol.D.Glucitol..and.L.Sorbose.Utilization
0.05
0.04
0.03
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 2.317e−01
Coefficient: −8.70e−02
Value: S
Sporulation.gene.orphans
0.1075
0.1050
0.1025
0.1000
0.0975
0.0950
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

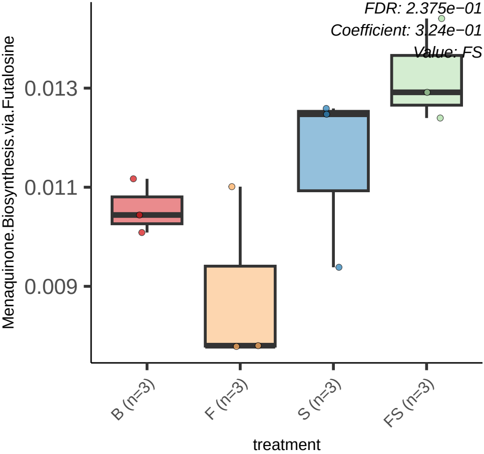

FDR: 2.324e−01
Coefficient: −2.28e−01
Value: S
Flavohaemoglobin
0.10
0.09
0.08
0.07
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

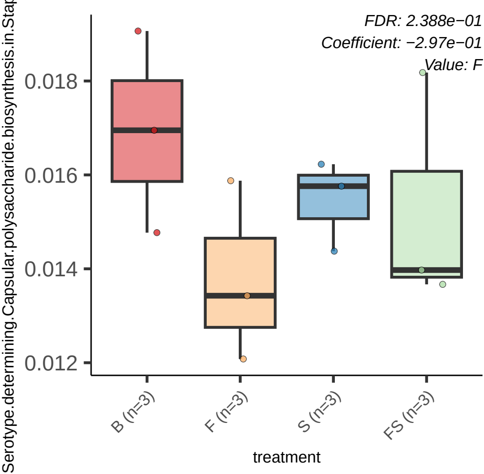

FDR: 2.326e−01
Coefficient: 1.24e−01
Value: F
Lipopolysaccharide.related.cluster.in.Alphaproteobacteri
0.075
0.072
0.069
0.066
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

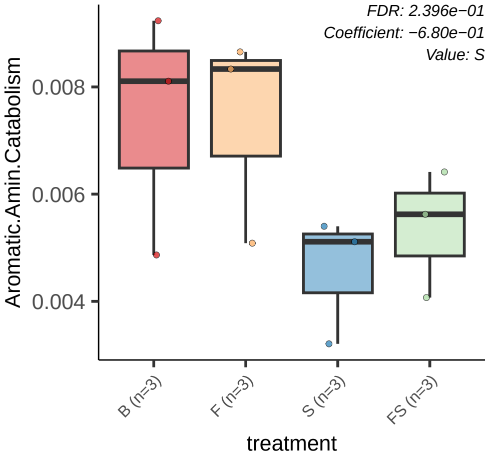

FDR: 2.334e−01
Coefficient: −1.42e−01
Value: FS
Methylthiotransferases
0.070
0.065
0.060
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

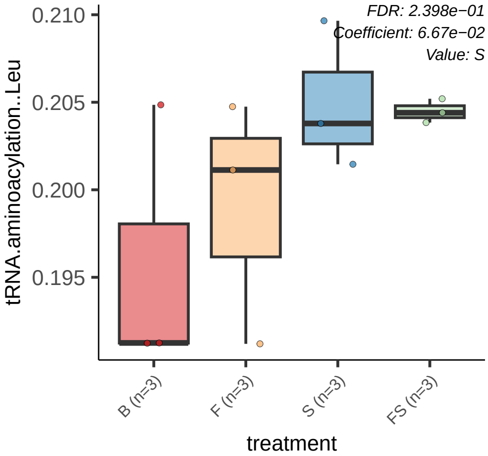


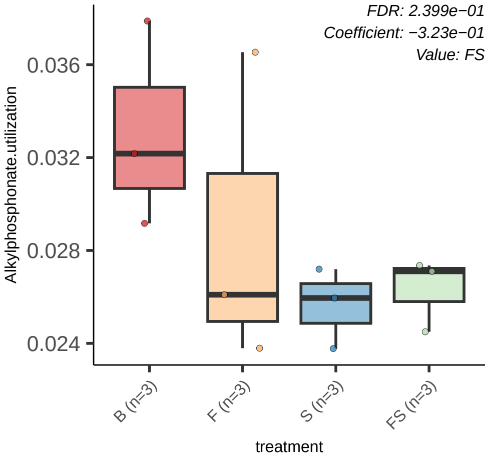
D.galactarate..D.glucarate.and.D.glycerate.catabolism..g
0.045
0.040
0.035
0.030
FDR: 2.350e−01
Coefficient: −2.36e−01
Value: F
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

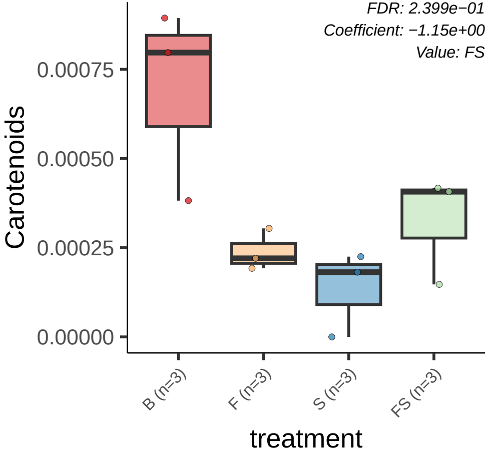

FDR: 2.375e−01
Coefficient: 3.24e−01
Value: FS
Menaquinone.Biosynthesis.via.Futalosine
0.013
0.011
0.009
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

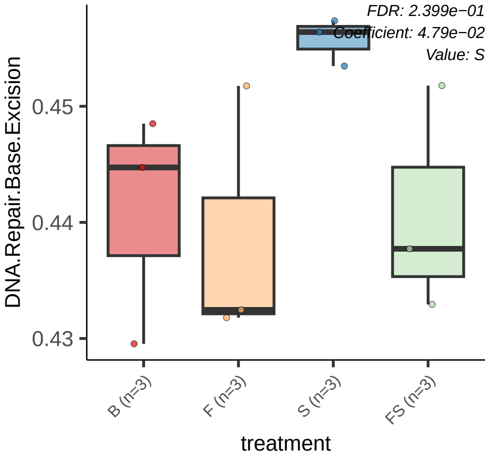

FDR: 2.388e−01
Coefficient: −2.97e−01
Value: F
Serotype.determining.Capsular.polysaccharide.biosynthesis.in.Stap
0.018
0.016
0.014
0.012
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

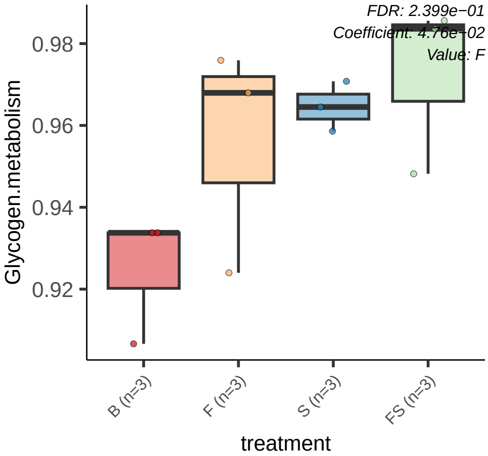

FDR: 2.396e−01
Coefficient: −6.80e−01
Value: S
Aromatic.Amin.Catabolism
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

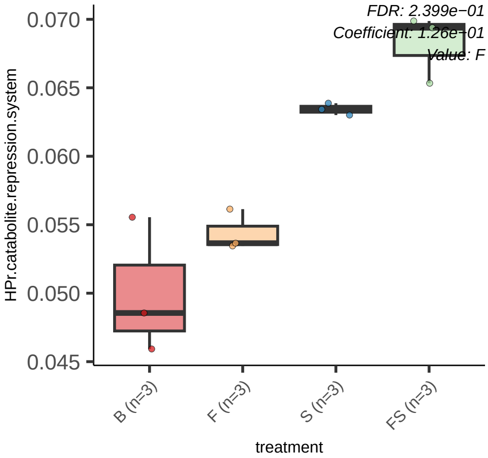

FDR: 2.398e−01
Coefficient: 6.67e−02
Value: S
tRNA.aminoacylation..Leu
0.210
0.205
0.200
0.195
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

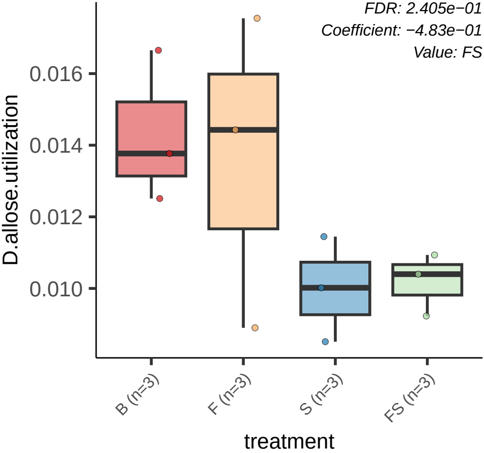

FDR: 2.399e−01
Coefficient: −3.23e−01
Value: FS
Alkylphosphonate.utilization
0.036
0.032
0.028
0.024
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

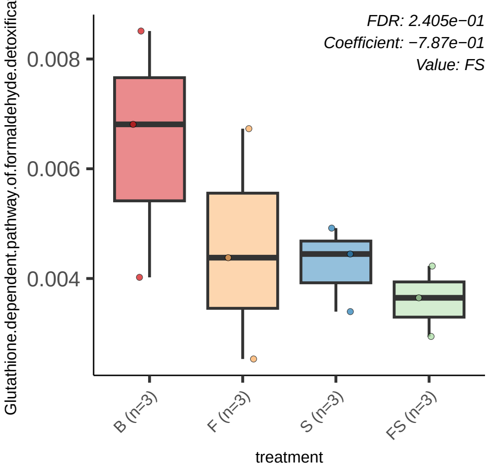

FDR: 2.399e−01
Coefficient: −1.15e+00
Value: FS
Carotenoids
0.00075
0.00050
0.00025
0.00000
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

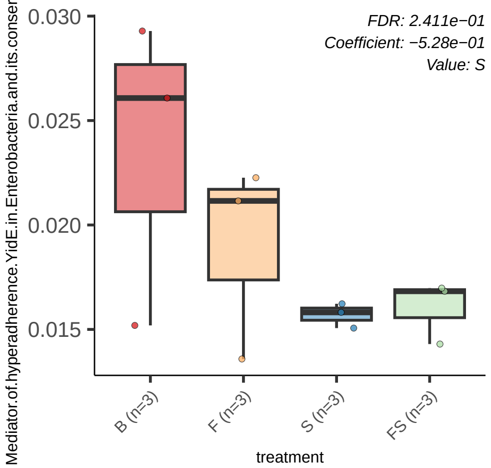

FDR: 2.399e−01
Coefficient: 4.79e−02
Value: S
DNA.Repair.Base.Excision
0.45
0.44
0.43
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

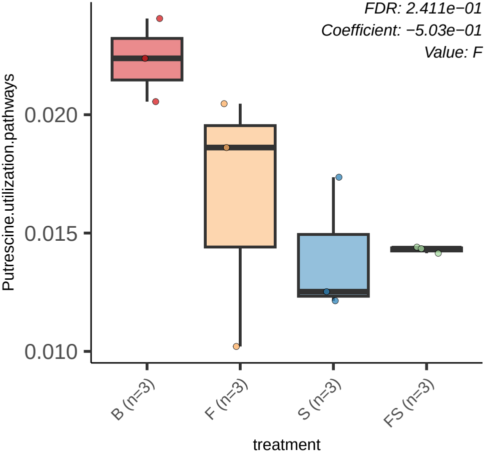

FDR: 2.399e−01
Coefficient: 4.76e−02
Value: F
Glycogen.metabolism
0.98
0.96
0.94
0.92
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

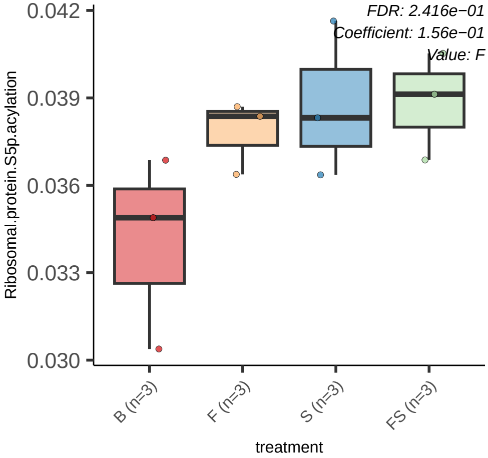

FDR: 2.399e−01
Coefficient: 1.26e−01
Value: F
HPr.catabolite.repression.system
0.070
0.065
0.060
0.055
0.050
0.045
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

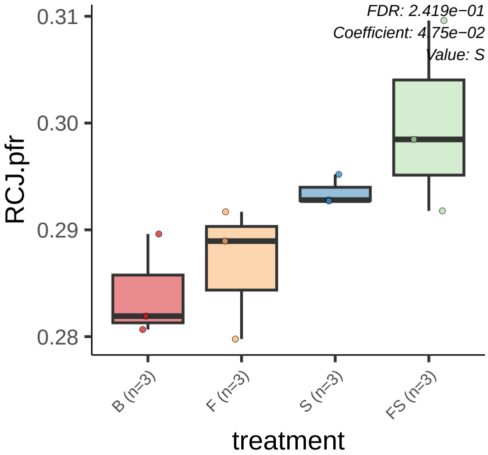

FDR: 2.405e−01
Coefficient: −4.83e−01
Value: FS
D.allose.utilization
0.016
0.014
0.012
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

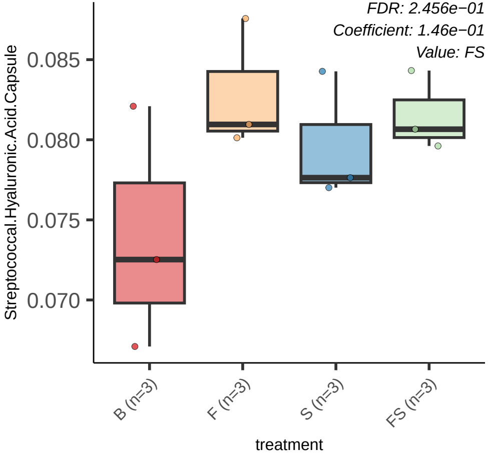

FDR: 2.405e−01
Coefficient: −7.87e−01
Value: FS
Glutathione.dependent.pathway.of.formaldehyde.detoxifica
0.008
0.006
0.004
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

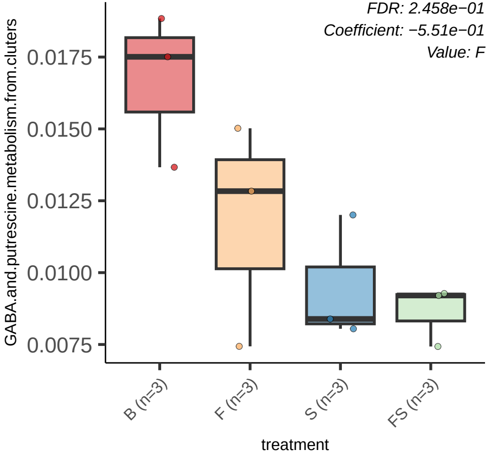

FDR: 2.411e−01
Coefficient: −5.28e−01
Value: S
Mediator.of.hyperadherence.YidE.in.Enterobacteria.and.its.conser
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

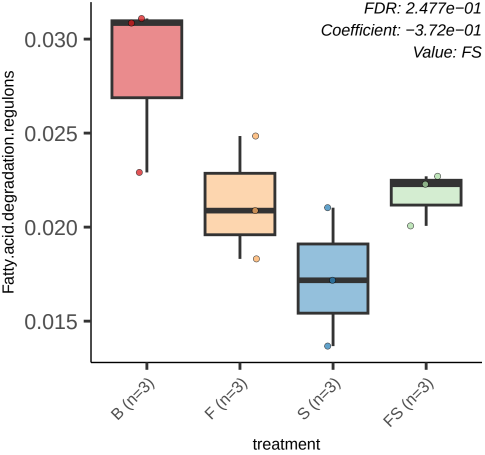

FDR: 2.411e−01
Coefficient: −5.03e−01
Value: F
Putrescine.utilization.pathways
0.020
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

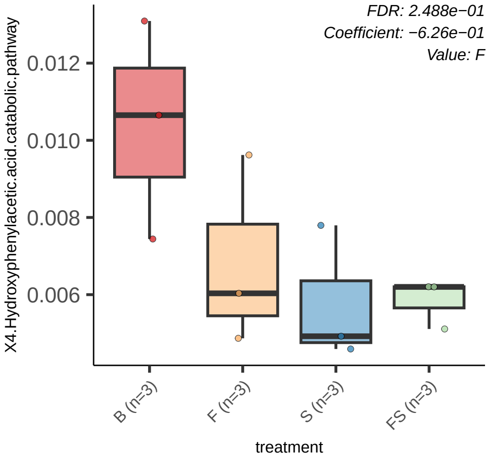

FDR: 2.416e−01
Coefficient: 1.56e−01
Value: F
Ribosomal.protein.S5p.acylation
0.042
0.039
0.036
0.033
0.030
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

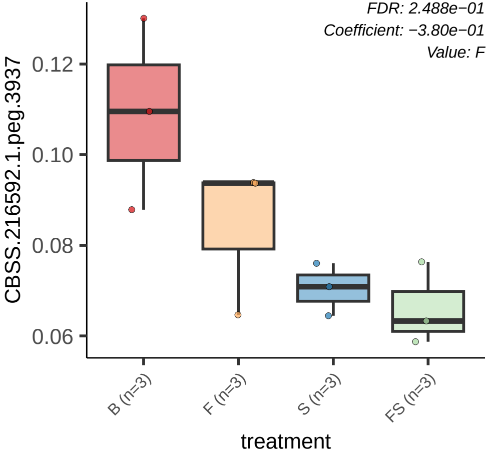

FDR: 2.419e−01
Coefficient: 4.75e−02
Value: S
RCJ.pfr
0.31
0.30
0.29
0.28
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

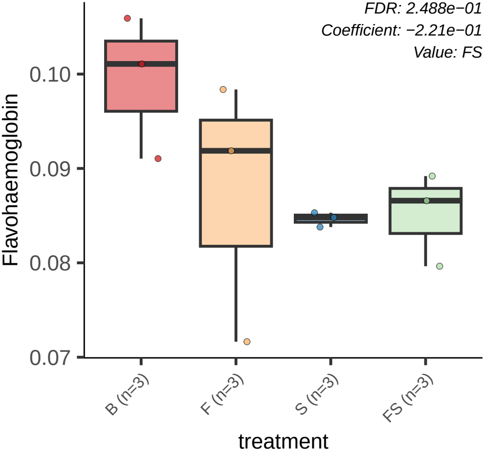

FDR: 2.456e−01
Coefficient: 1.46e−01
Value: FS
Streptococcal.Hyaluronic.Acid.Capsule
0.085
0.080
0.075
0.070
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

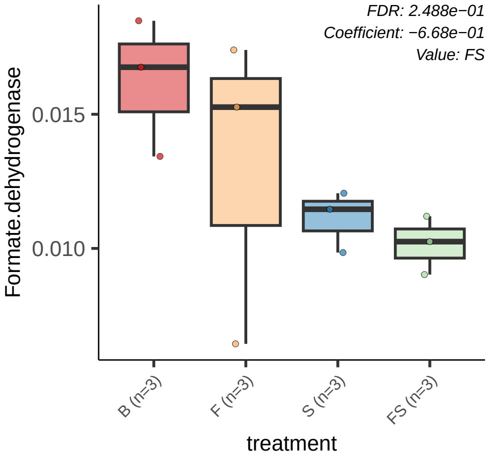

FDR: 2.458e−01
Coefficient: −5.51e−01
Value: F
GABA.and.putrescine.metabolism.from.cluters
0.0175
0.0150
0.0125
0.0100
0.0075
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

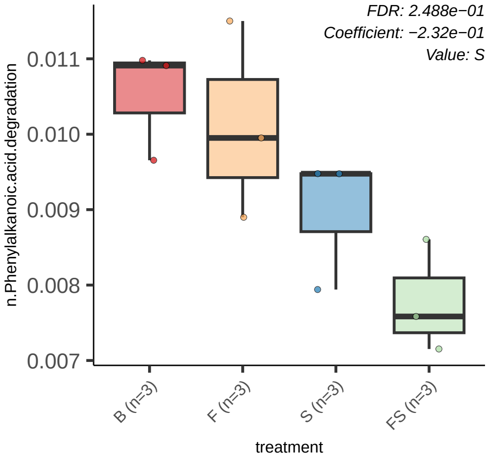

FDR: 2.477e−01
Coefficient: −3.72e−01
Value: FS
Fatty.acid.degradation.regulons
0.030
0.025
0.020
0.015
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

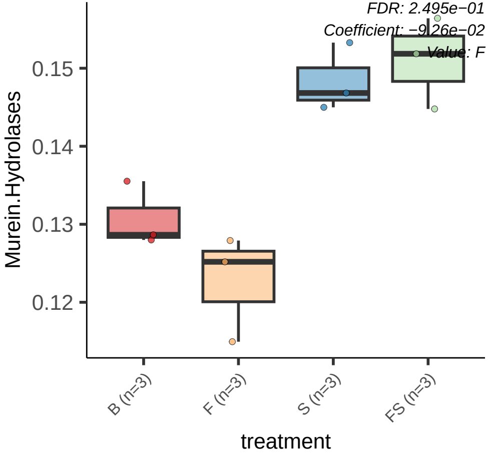

FDR: 2.488e−01
Coefficient: −6.26e−01
Value: F
X4.Hydroxyphenylacetic.acid.catabolic.pathway
0.012
0.010
0.008
0.006
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

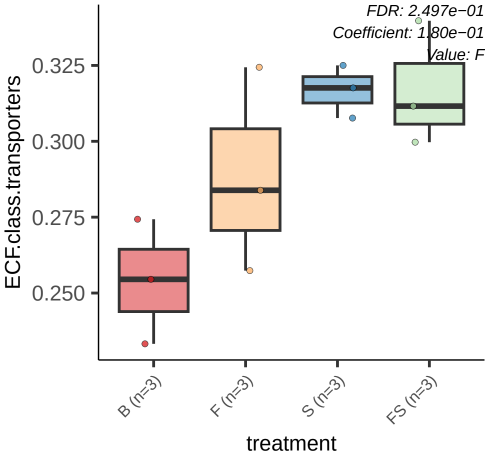

FDR: 2.488e−01
Coefficient: −3.80e−01
Value: F
CBSS.216592.1.peg.3937
0.12
0.10
0.08
0.06
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

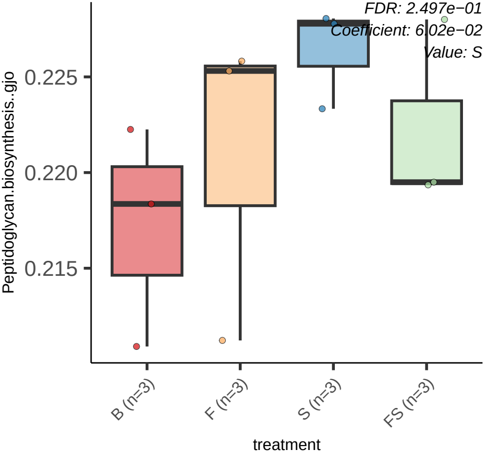

FDR: 2.488e−01
Coefficient: −2.21e−01
Value: FS
Flavohaemoglobin
0.10
0.09
0.08
0.07
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment

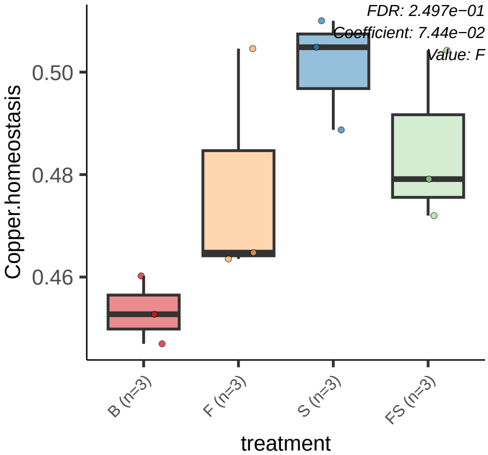

FDR: 2.488e−01
Coefficient: −6.68e−01
Value: FS
Formate.dehydrogenase
0.015
0.010
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 2.488e−01
Coefficient: −2.32e−01
Value: S
n.Phenylalkanoic.acid.degradation
0.011
0.010
0.009
0.008
0.007
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 2.495e−01
Coefficient: −9.26e−02
Value: F
Murein.Hydrolases
0.15
0.14
0.13
0.12
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 2.497e−01
Coefficient: 1.80e−01
Value: F
ECF.class.transporters
0.325
0.300
0.275
0.250
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 2.497e−01
Coefficient: 6.02e−02
Value: S
Peptidoglycan.biosynthesis..gjo
0.225
0.220
0.215
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment


FDR: 2.497e−01
Coefficient: 7.44e−02
Value: F
Copper.homeostasis
0.50
0.48
0.46
B (n=3)
F (n=3)
S (n=3)
FS (n=3)
treatment