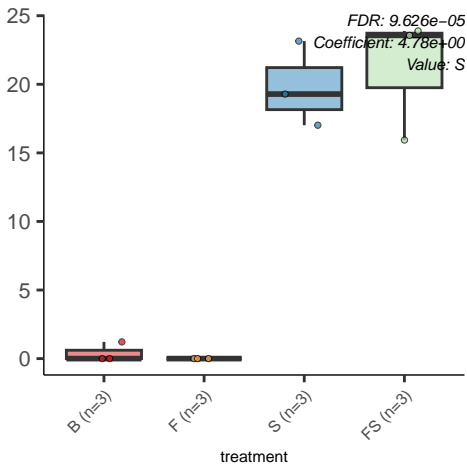
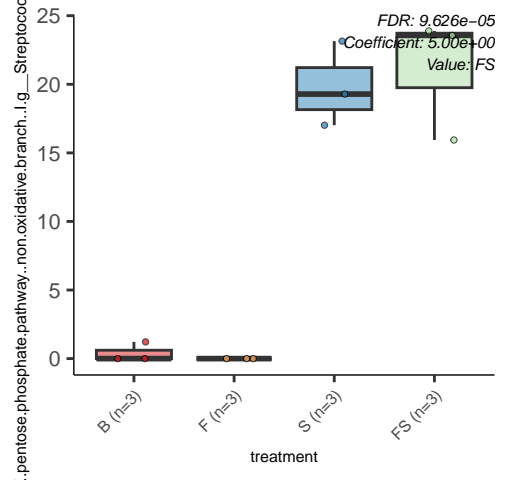
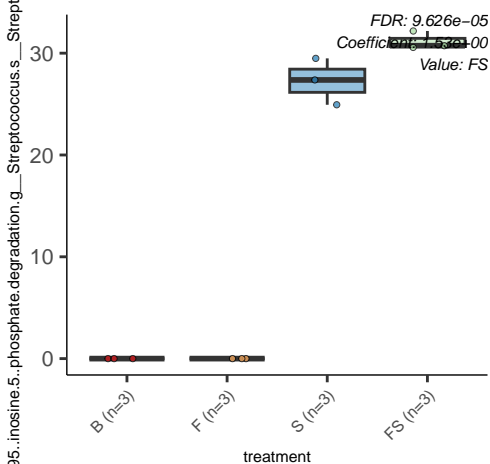
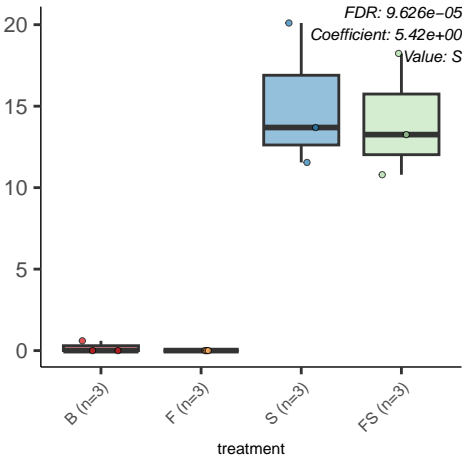


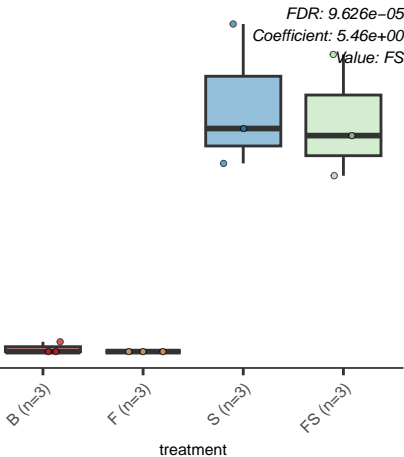
...pentose.phosphate.pathway..non.oxidative.branch...l.g\_\_Streptococcus



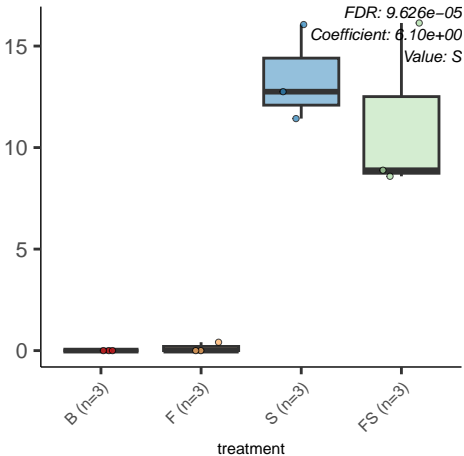




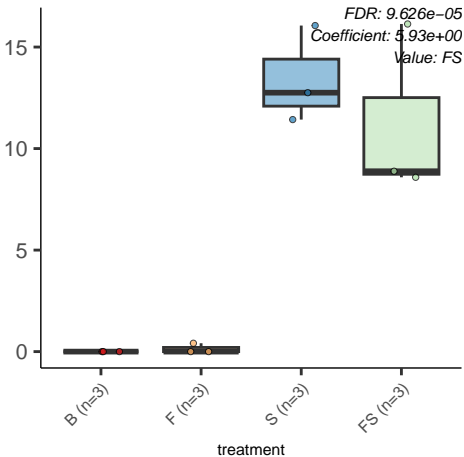




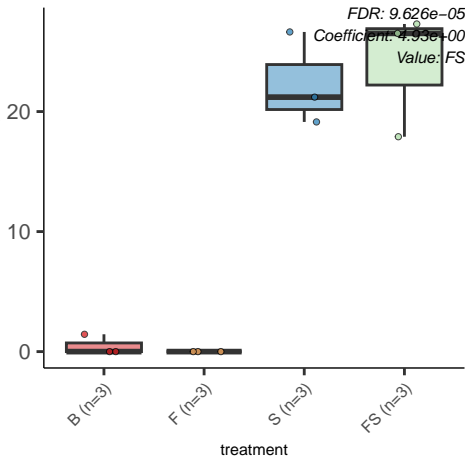
WPWY.7238..sucrose.biosynthesis.II.g\_\_Streptococcus



WY.7238..sucrose.biosynthesis.II.g\_\_Streptococcus

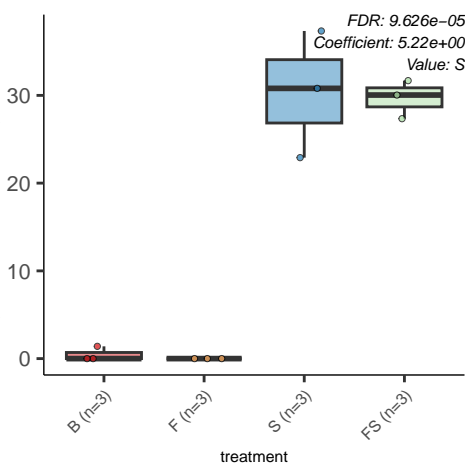


fructose phosphate pathway...non.oxidative.branch..II.g\_\_Streptococcus.

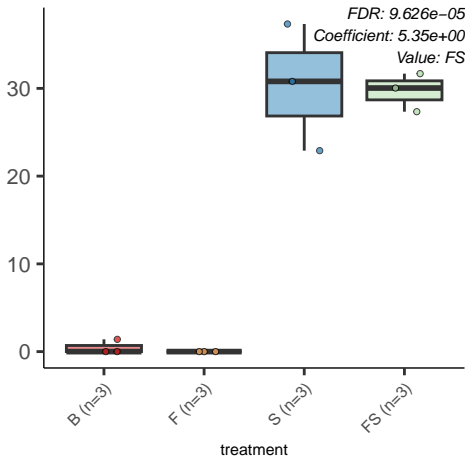




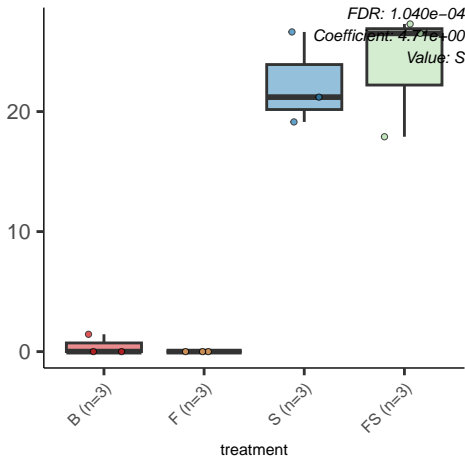
PWY..UDP.N.acetyl.D.glucosamine.biosynthesis.l.g\_\_Streptococcus



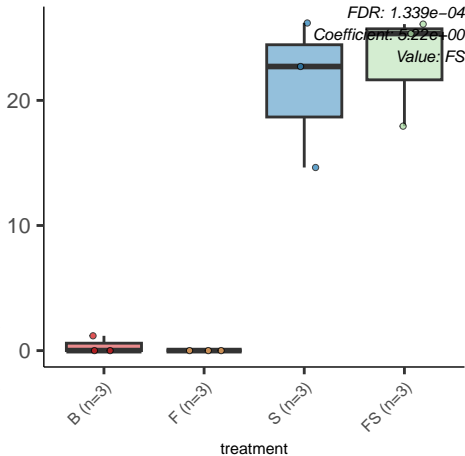
PWY..UDP.N.acetyl.D.glucosamine.biosynthesis.l.g\_\_Streptococcus

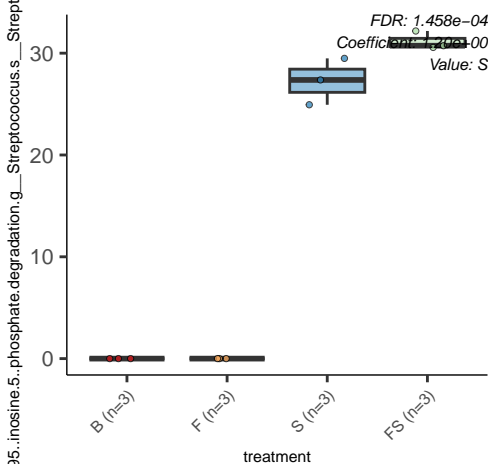


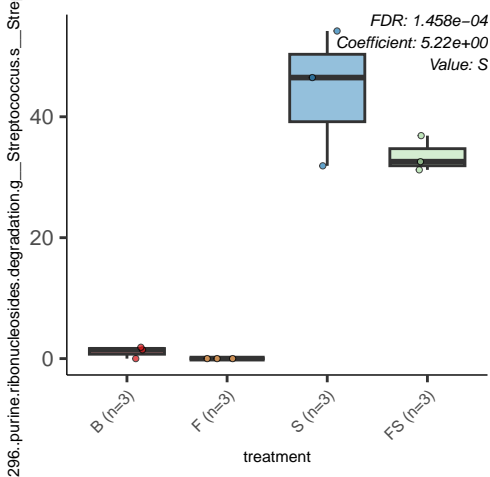
ose.phosphate.pathway..non.oxidative.branch..ll.g\_\_Streptococcus.



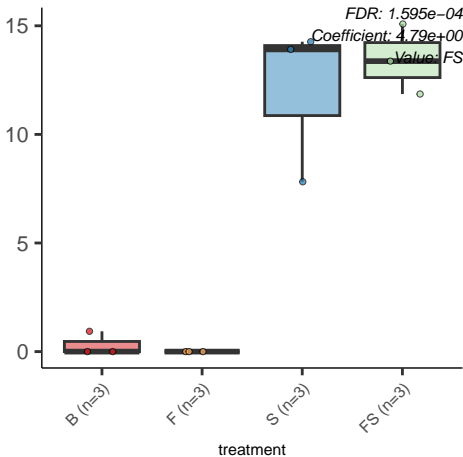
WY.4041...gamma..glutamyl.cycle.g\_\_Streptococcus



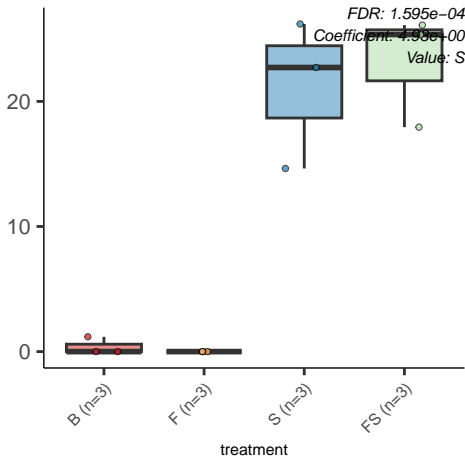




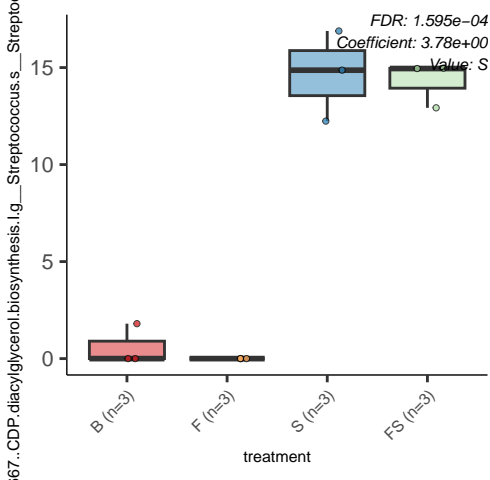
TANA.PWY..L..methionine.biosynthesis.III.g\_\_Streptococcus.s\_\_Streptococcus



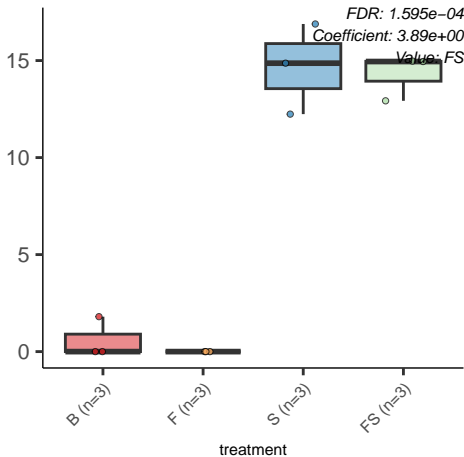
WY.4041...gamma..glutamyl.cycle.g\_\_Streptococcus

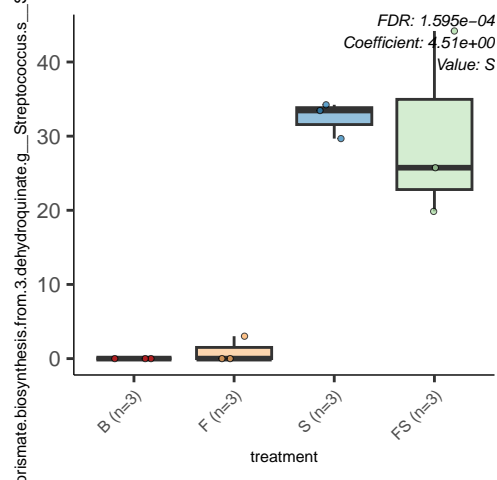


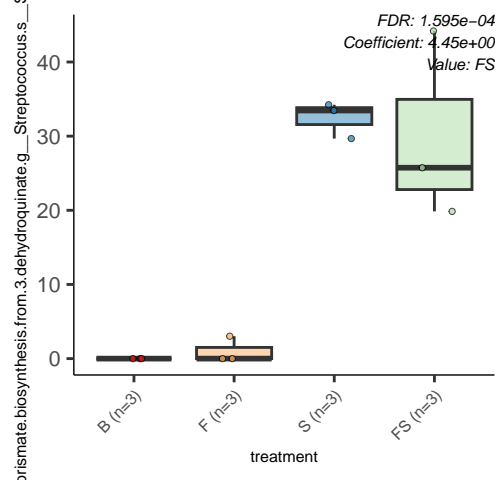


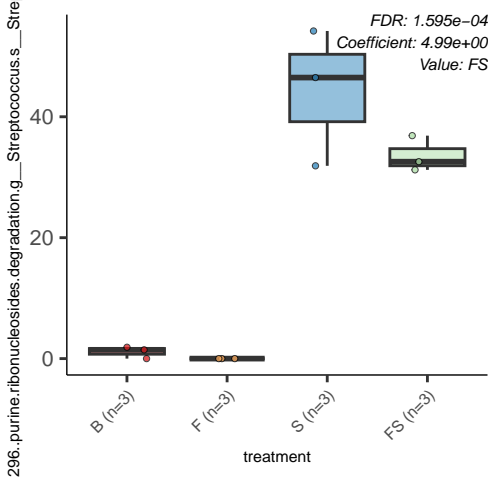


67..CDP.diacylglycerol.biosynthesis.l.g\_\_Streptococcus.s\_\_Strepto

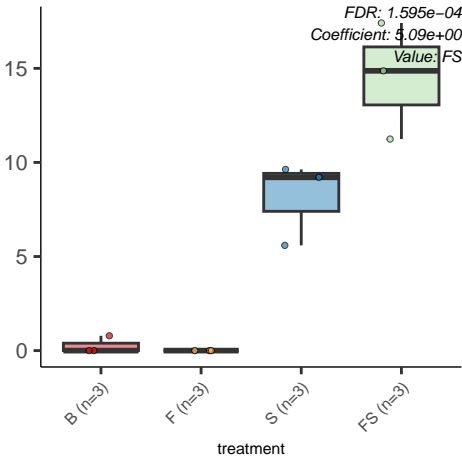




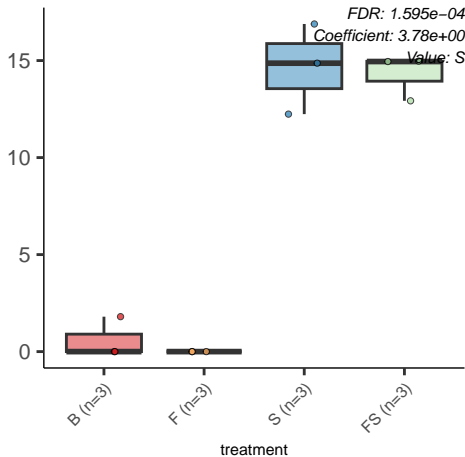


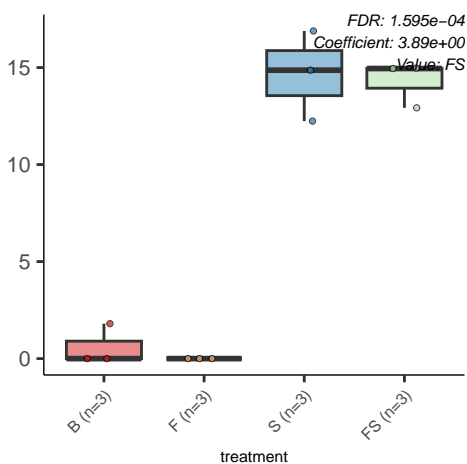


pathway.of.purine.deoxyribonucleosides.degradation.g\_\_Streptococcus

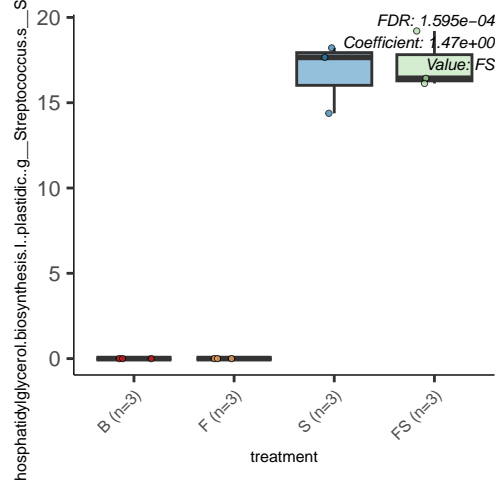


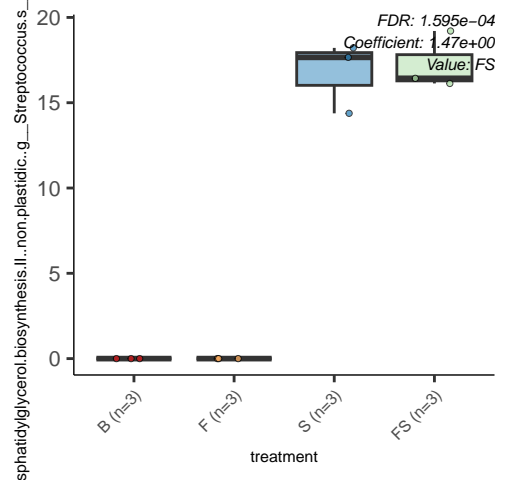
319..CDP.diacylglycerol.biosynthesis.11.g\_\_Streptococcus.s\_\_Streptococcus



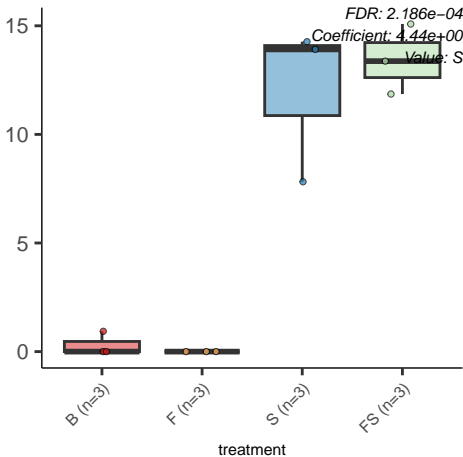


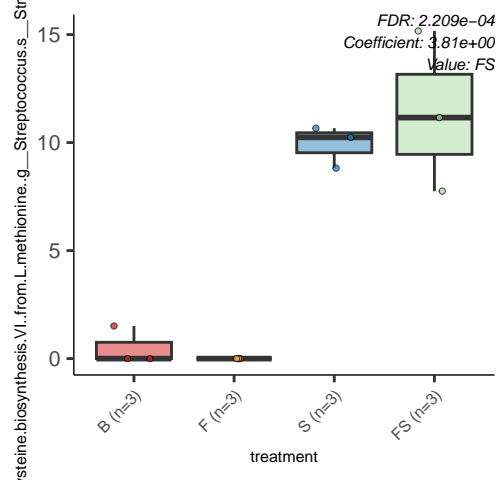


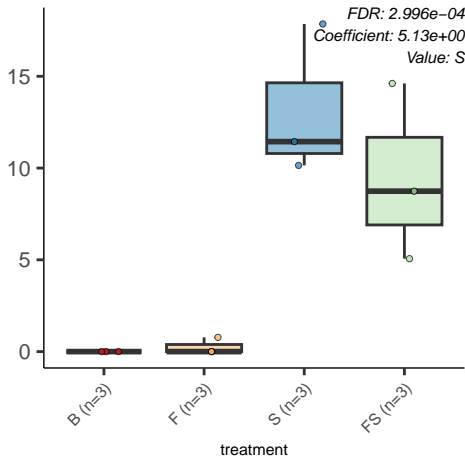


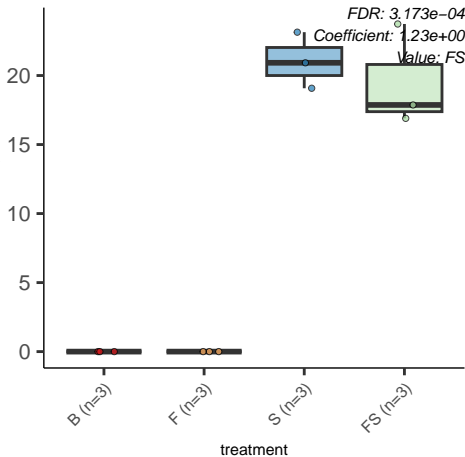


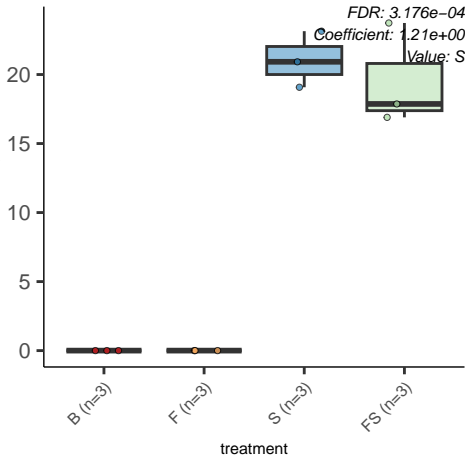
TANA.PWY..L..methionine.biosynthesis.III.g\_\_Streptococcus.s\_\_Streptococcus

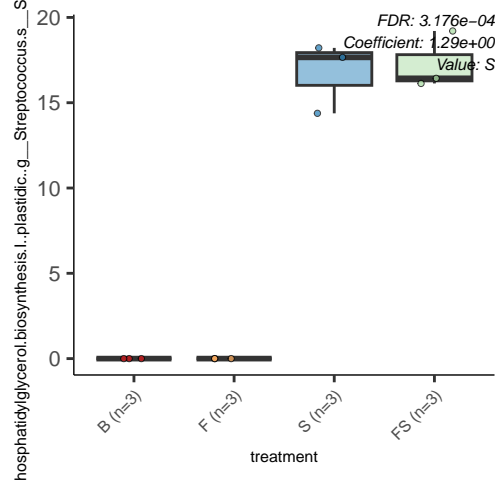




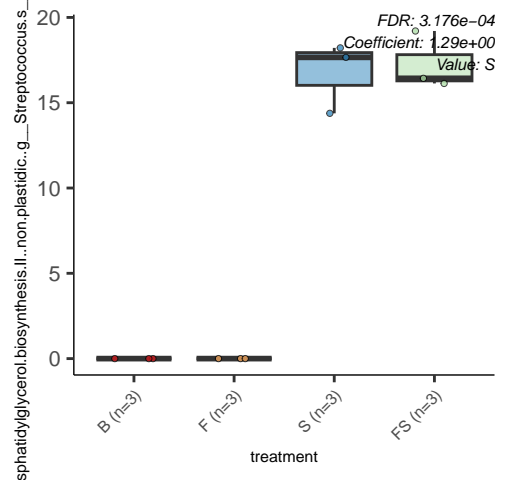




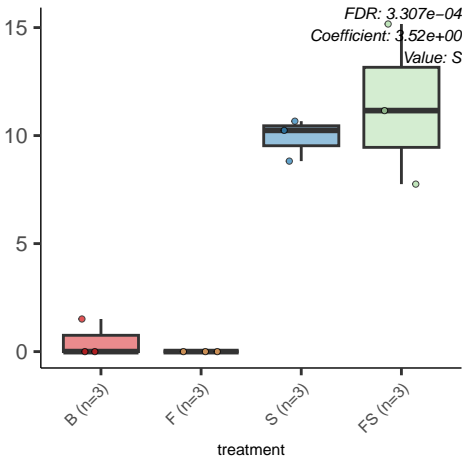




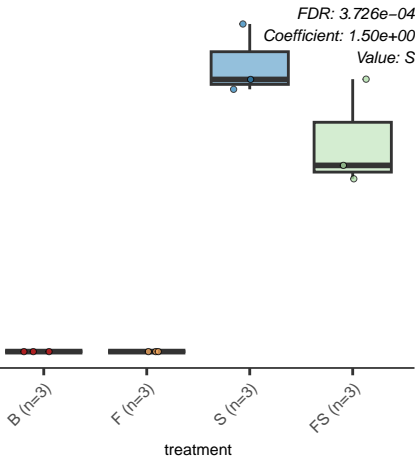


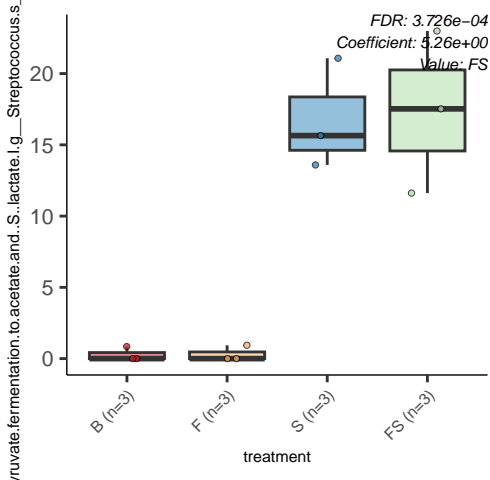


ysteine.biosynthesis.VI..from.L.methionine..g\_\_Streptococcus.s\_\_Str

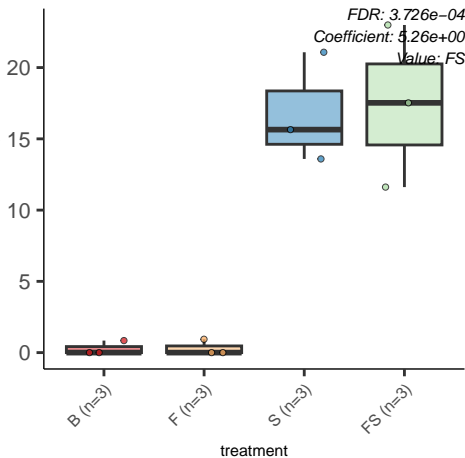


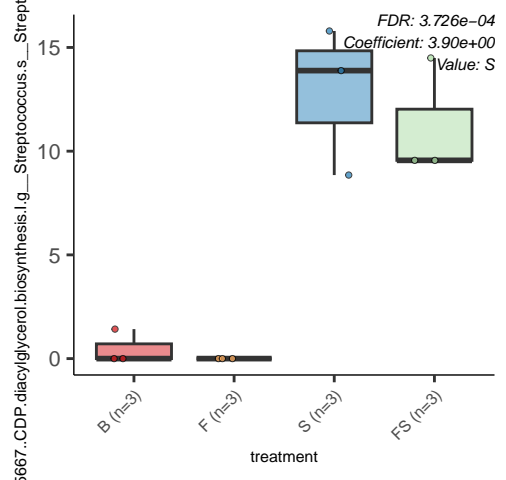
VY..superpathway.of.aromatic.amino.acid.biosynthesis.g\_\_Streptococcus



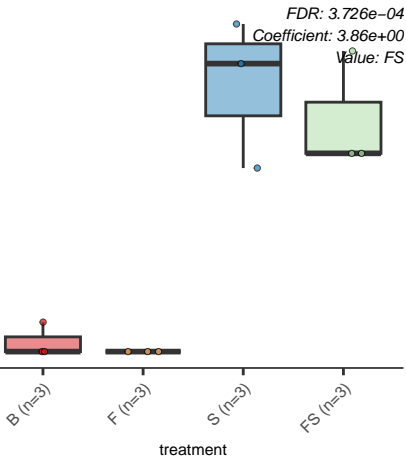


pyruvate, fermentation, to acetate, and lactate. II.g Streptococcus.s

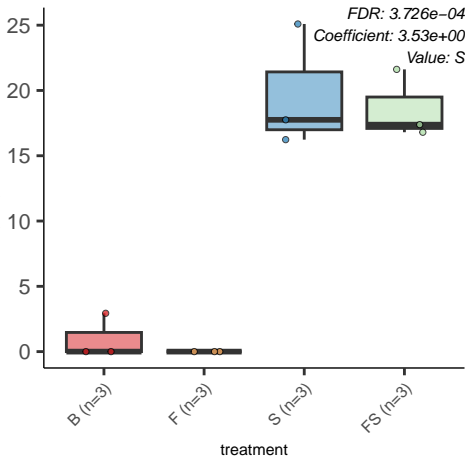




56667..CDP.diacylglycerol.biosynthesis.l.g\_\_Streptococcus.s\_\_Strept

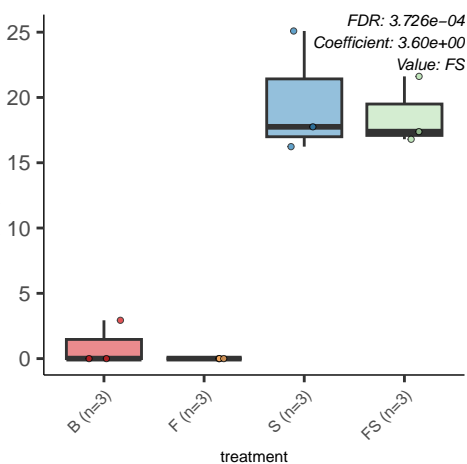


51..S.adenosyl.L.methionine.salvage.l.g\_\_Streptococcus.s\_\_Strepto

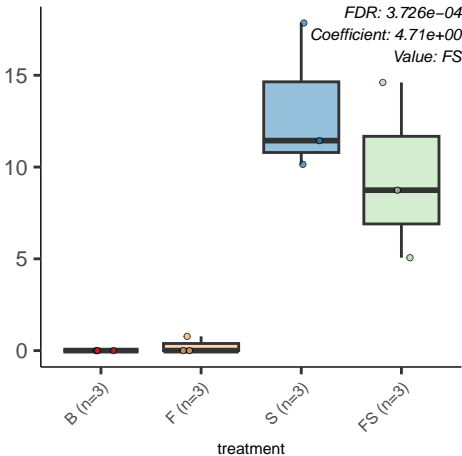




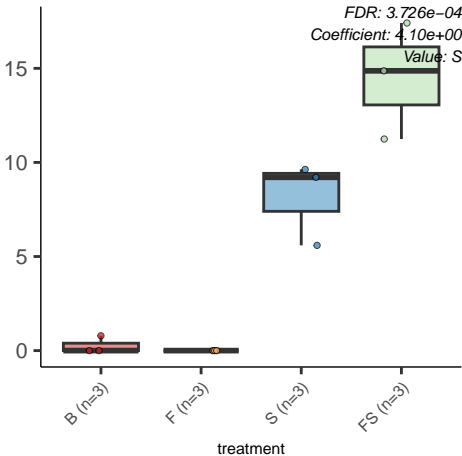
51..S.adenosyl.L.methionine.salvage.l.g\_\_Streptococcus.s\_\_Strepto

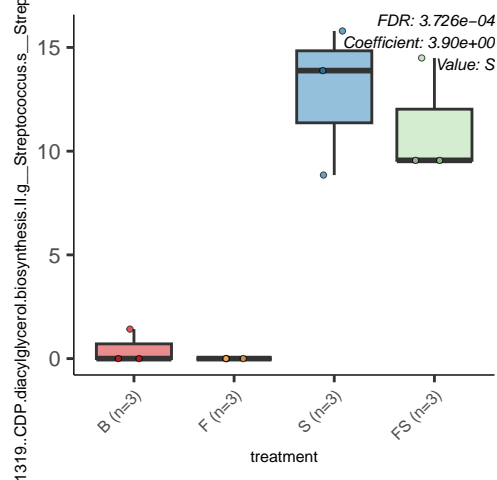


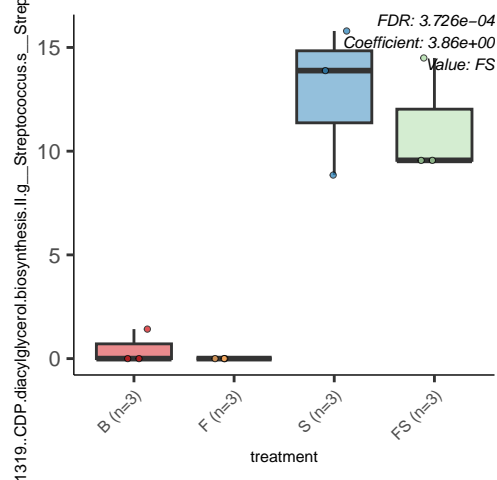
WY.702...L.methionine.biosynthesis.II.g\_\_Streptococcus.s\_\_Streptococcus



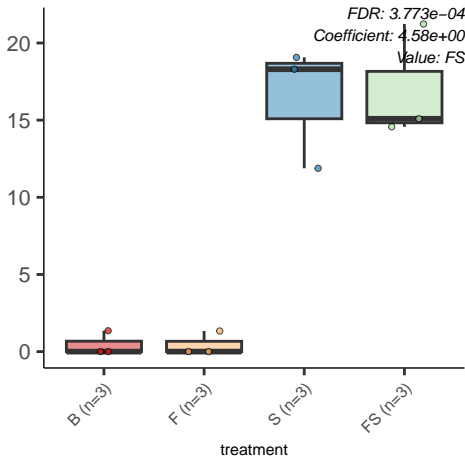
pathway.of.purine.deoxyribonucleosides.degradation.g\_\_Streptococcus



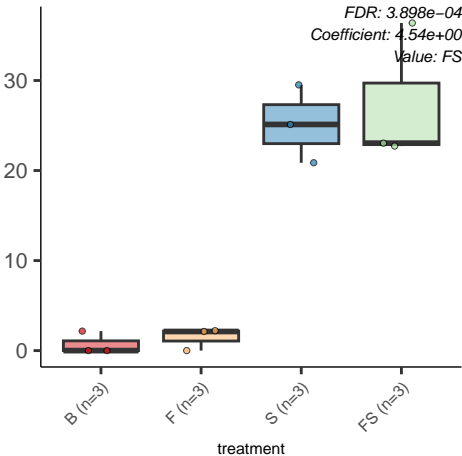


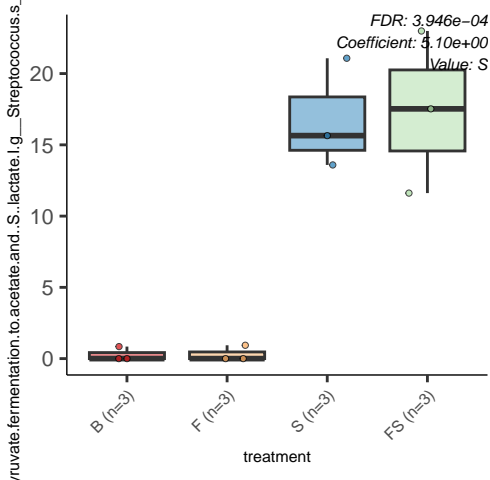


36..seleno.amino.acid.biosynthesis..plants..g\_\_Streptococcus.s\_\_St



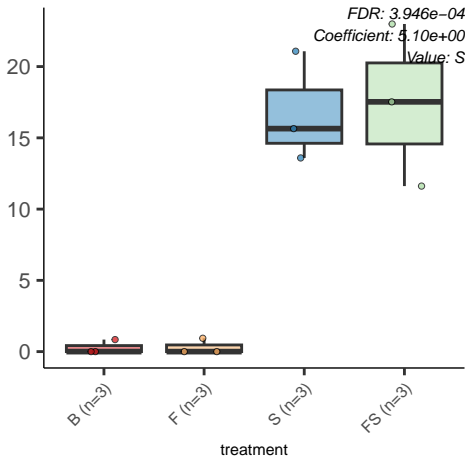
PWY.822..fructan.biosynthesis.g\_\_Streptococcus.s\_\_Streptococcus



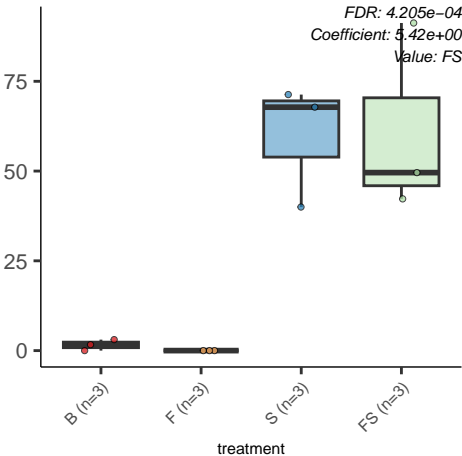


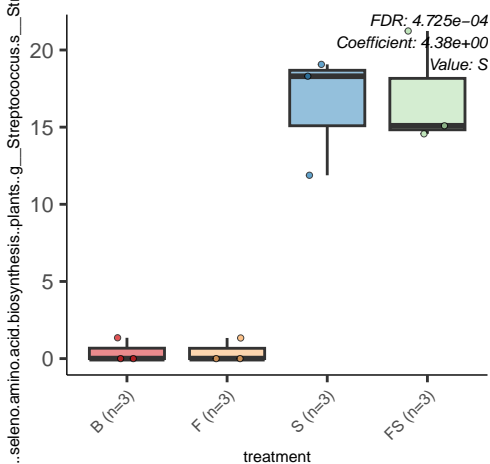


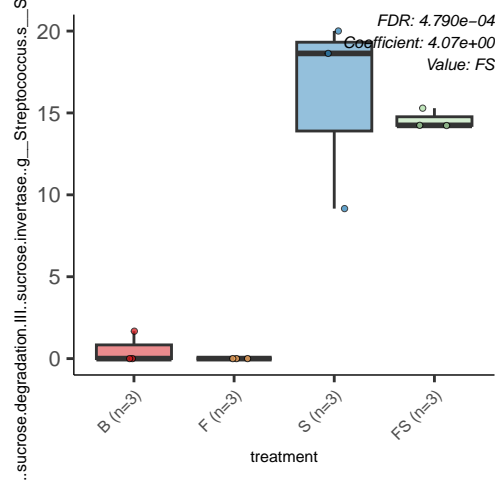
pyruvate, fermentation, to acetate, and lactate. II.g Streptococcus. S



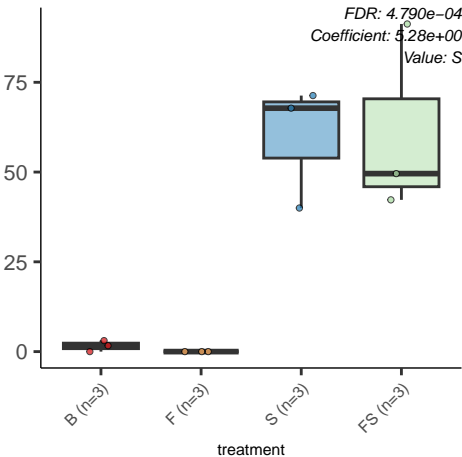
glycan.maturation...meso.diaminopimelate.containing.g\_\_Streptococ



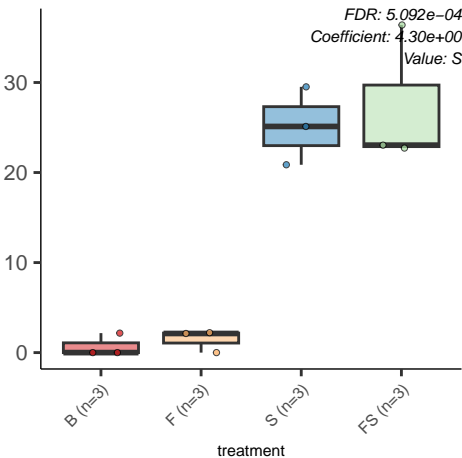


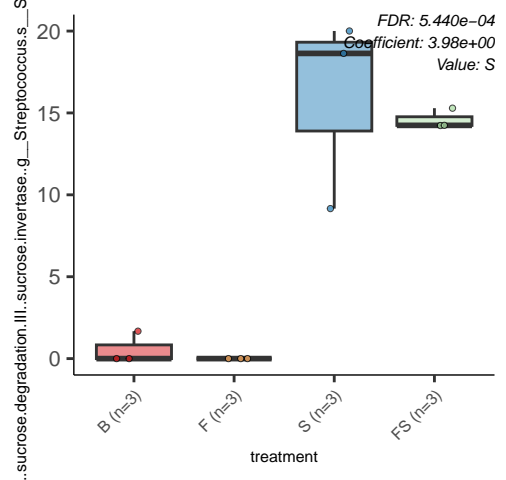


glycan.maturation...meso.diaminopimelate.containing.g\_\_Streptococ

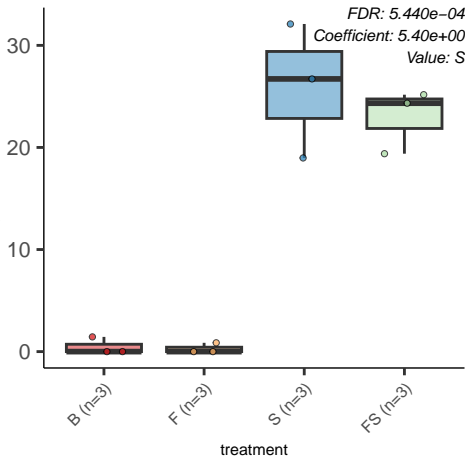


PWY.822..fructan.biosynthesis.g\_\_Streptococcus.s\_\_Streptococcus



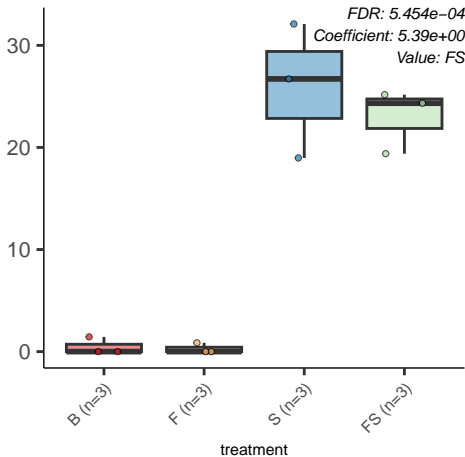


ALSYN.PWY.L.valine.biosynthesis.g\_\_Streptococcus

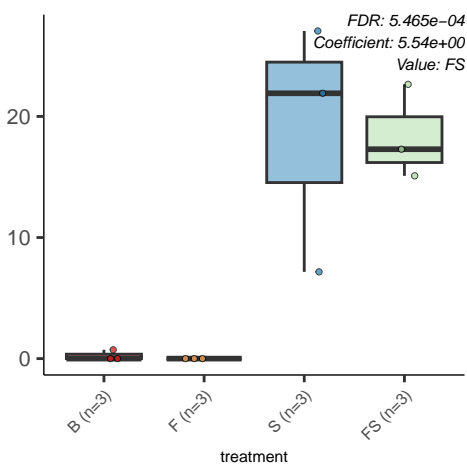


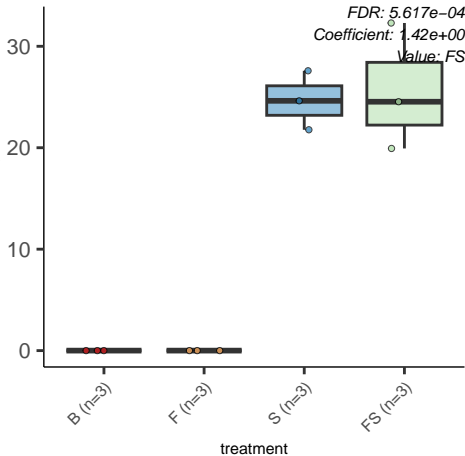


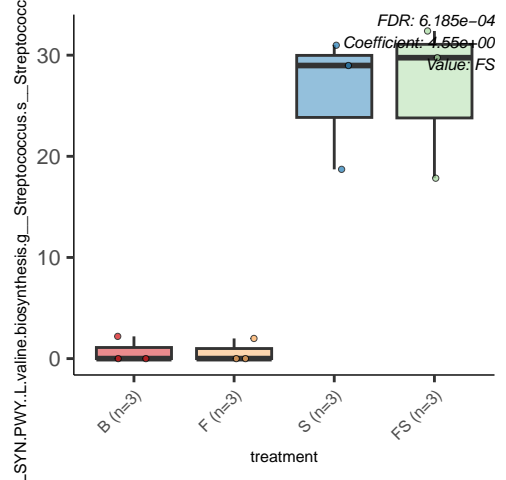
ALSYN.PWY..L.valine.biosynthesis.g\_\_Streptococcus.s\_\_Streptococcus

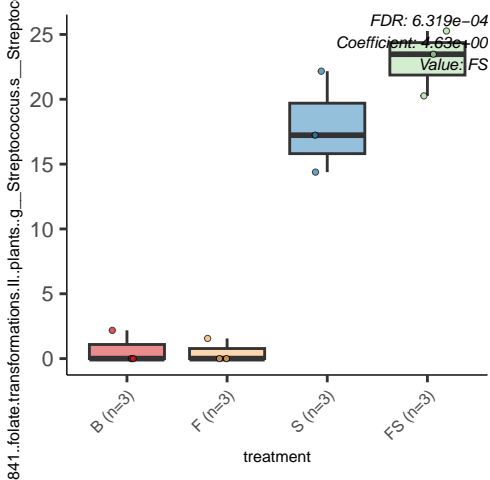


loglycan.maturat...meso.diaminopimelate.containing..g\_\_Streptococ

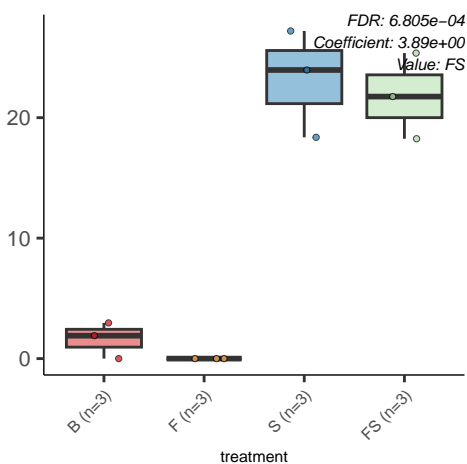




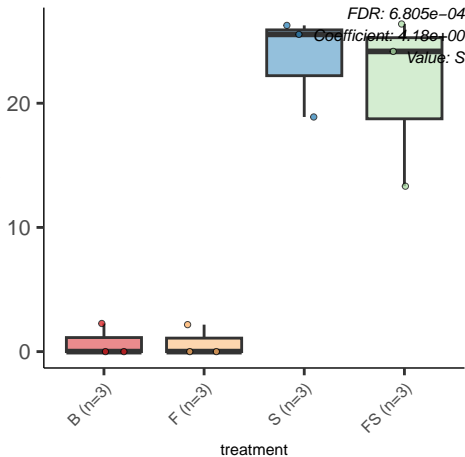




WY..glycogen.biosynthesis.l...from.ADP.D.Glucose..g\_\_Streptococ

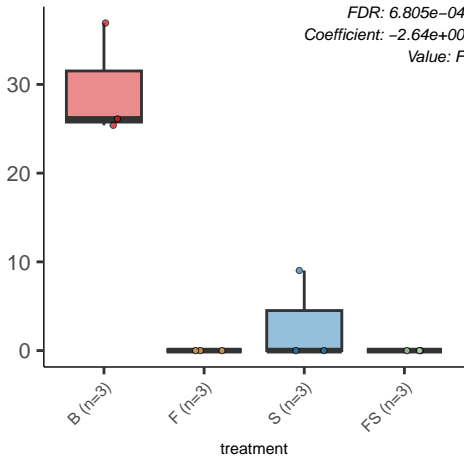


123..inosine.5..phosphate.biosynthesis.l.g\_\_Streptococcus.s\_\_Stre



perpathway.of.unsaturated.fatty.acids.biosynthesis.E.coli.g\_Esch

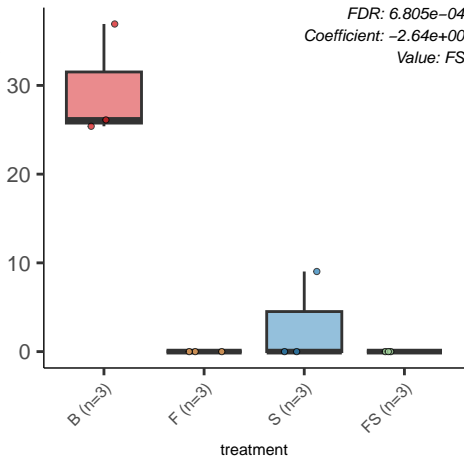
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Coefficient: -2.64e+00  
Value: F

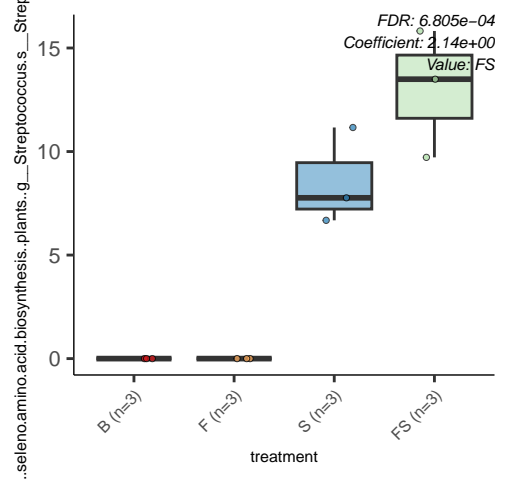




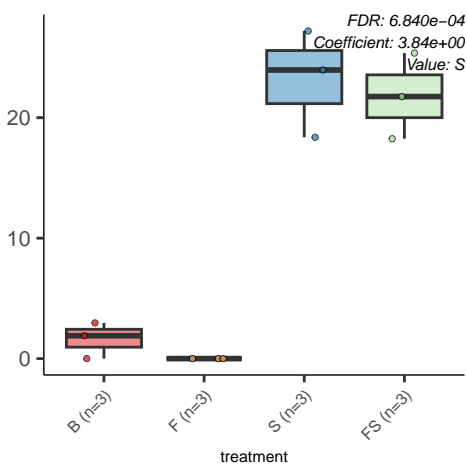
perpathway.of.unsaturated.fatty.acids.biosynthesis.E..coli.g\_Esch

FDR: 6.805e-04  
Coefficient: -2.64e+00  
Value: FS

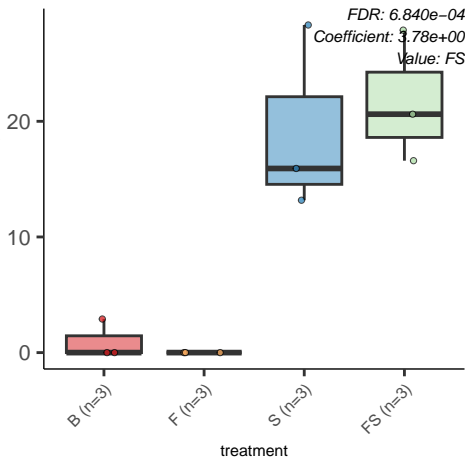


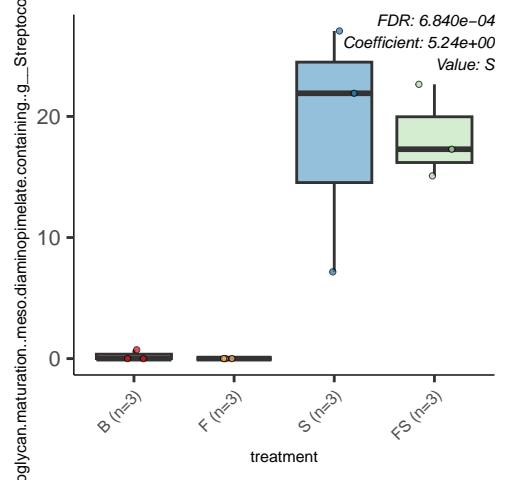


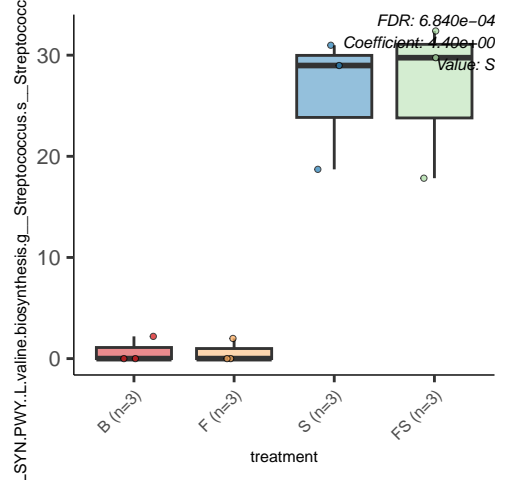
WY..glycogen.biosynthesis.l...from.ADP.D.Glucose..g\_\_Streptococ



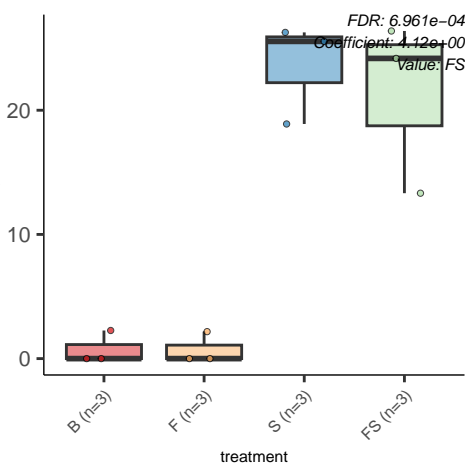
uanosine.ribonucleotides.de.novo.biosynthesis.g\_\_Streptococcus.s

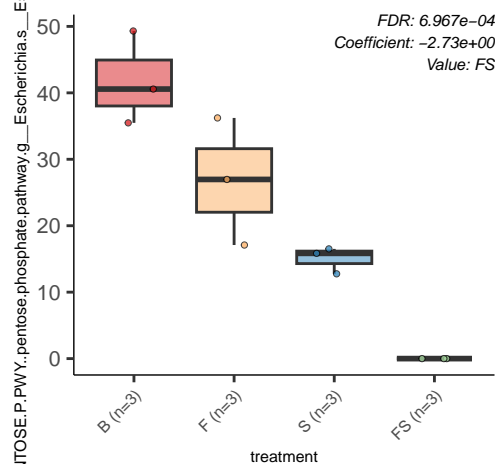




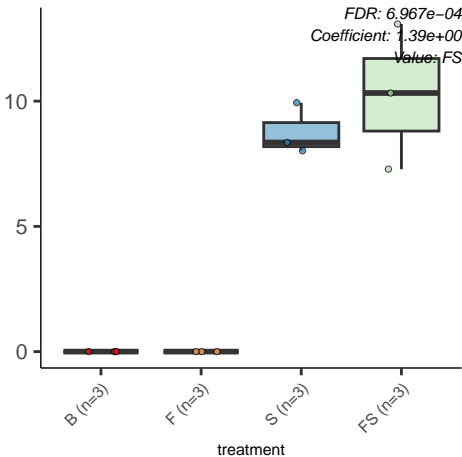


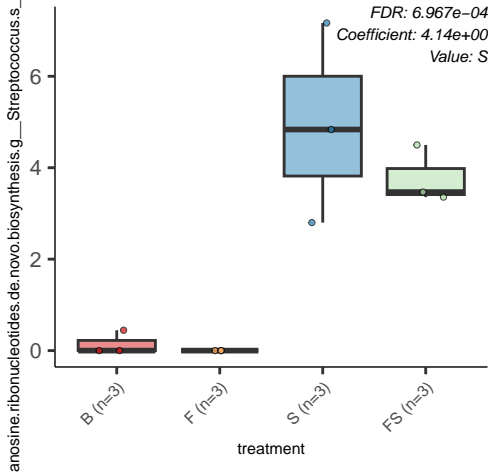
123..inosine.5..phosphate.biosynthesis.l.g\_\_Streptococcus.s\_\_Stre

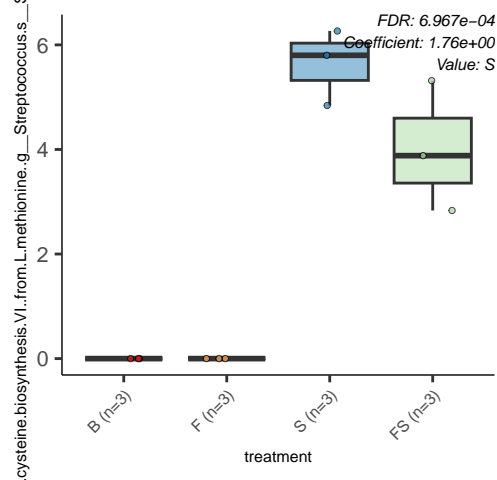




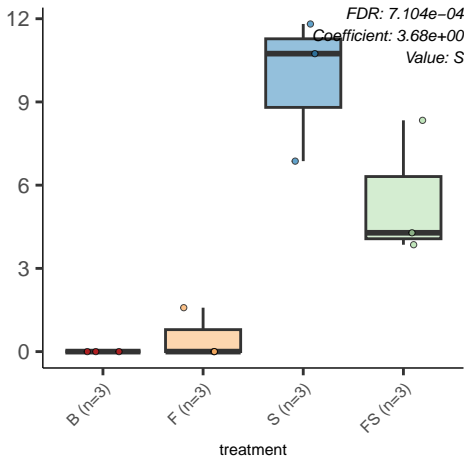


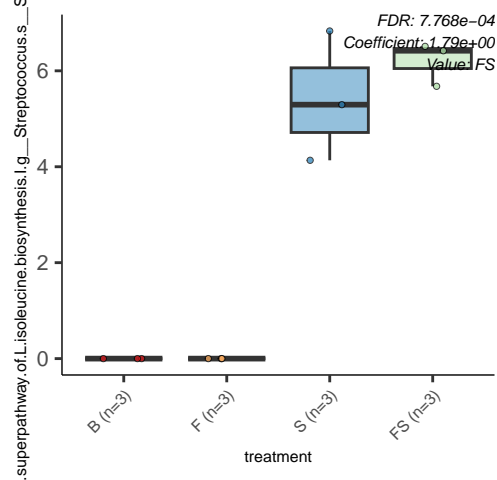


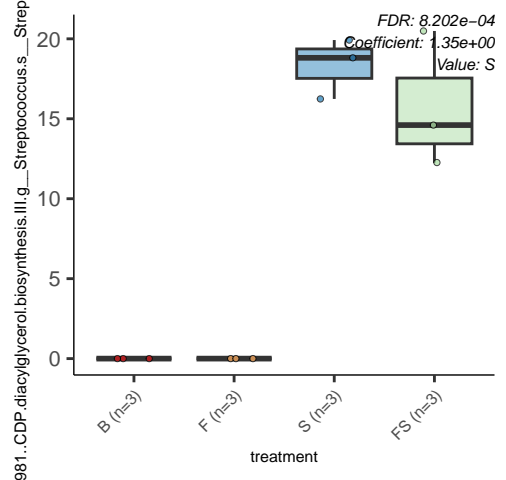




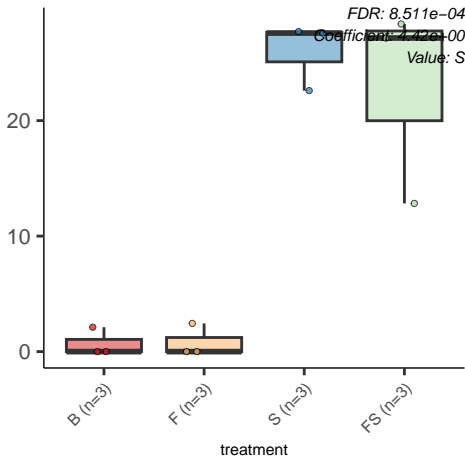
WY.702..L.methionine.biosynthesis.II.g\_\_Streptococcus.s\_\_Streptococcus





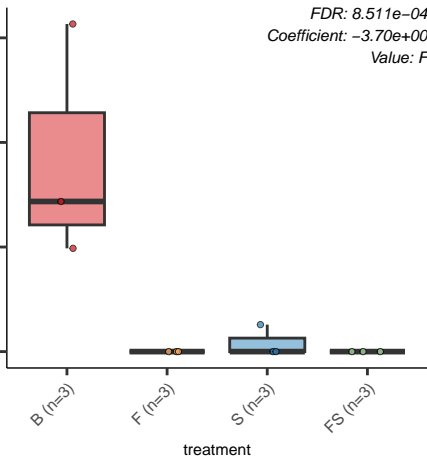


124..inosine.5..phosphate.biosynthesis.II.g\_\_Streptococcus.s\_\_Stre



pyrimidine.deoxyribonucleotides.de.novo.biosynthesis.ll.g\_\_Escherichia

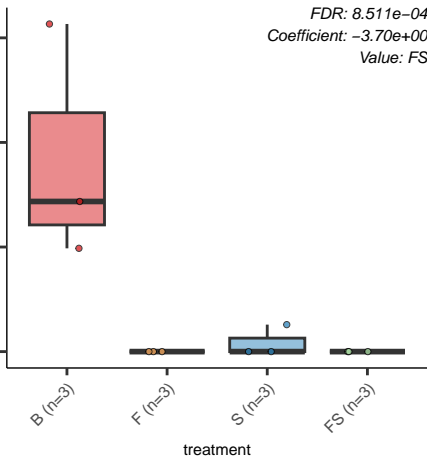
FDR:  $8.511e-04$   
Coefficient:  $-3.70e+00$   
Value: F

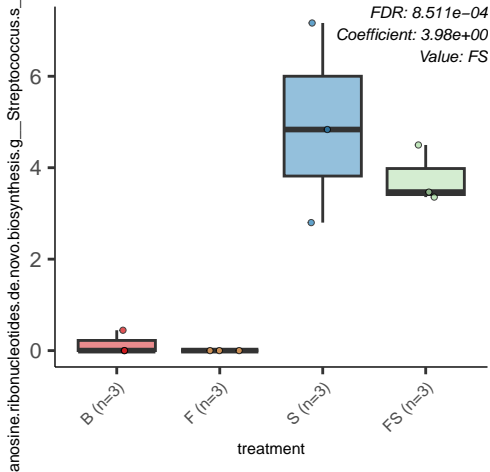




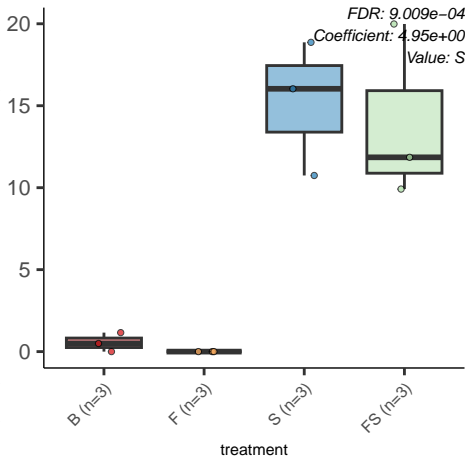
pyrimidine.deoxyribonucleotides.de.novo.biosynthesis.ll.g\_\_Escherichia

FDR: 8.511e-04  
Coefficient: -3.70e+00  
Value: FS

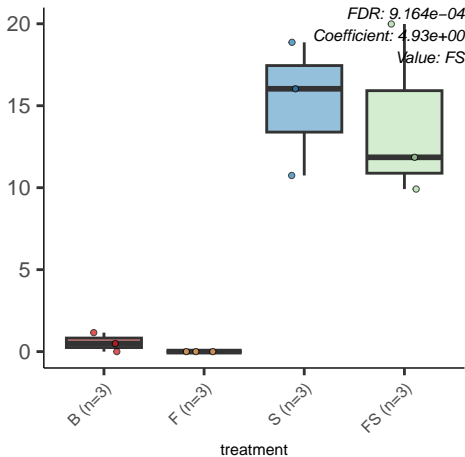


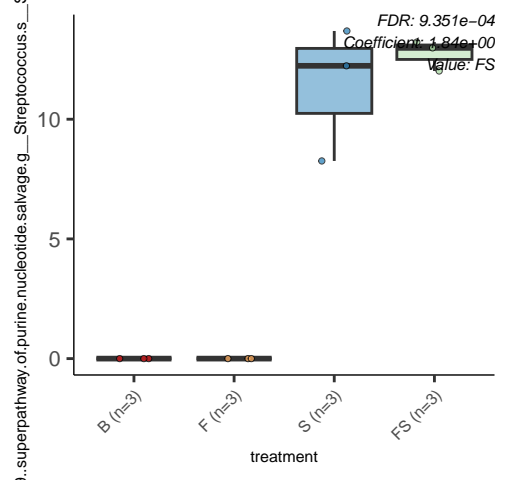


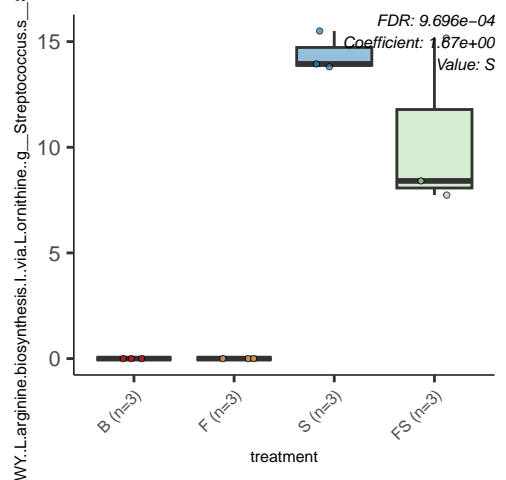
.PWY..glycogen.biosynthesis.l..from.ADP.D.Glucose..g\_\_Streptococ

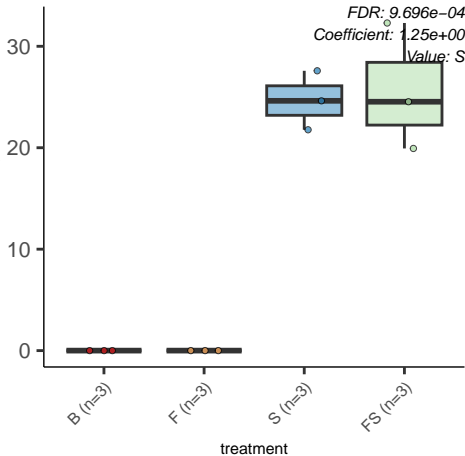


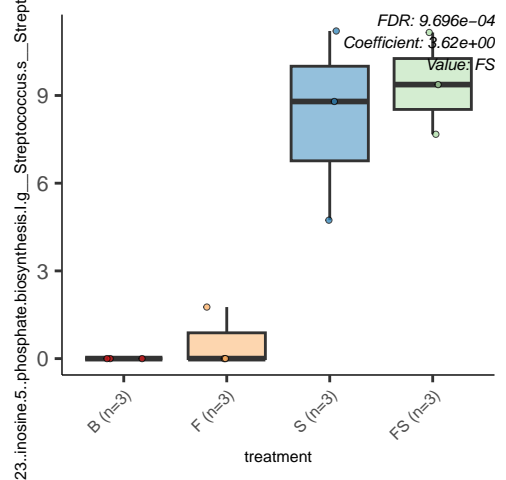
.PWY..glycogen.biosynthesis.l..from.ADP.D.Glucose..g\_\_Streptococ



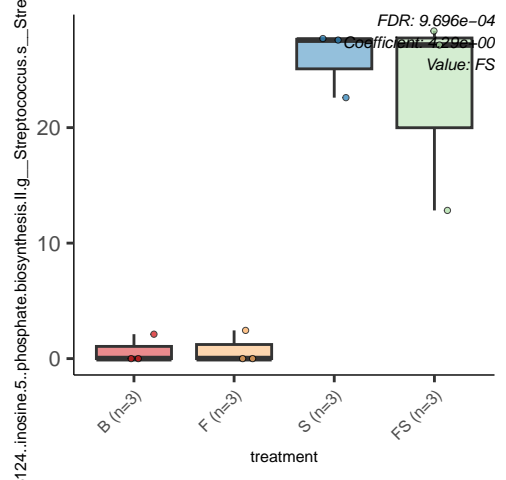


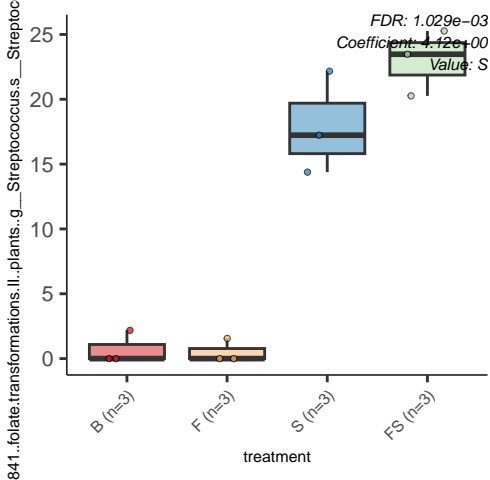


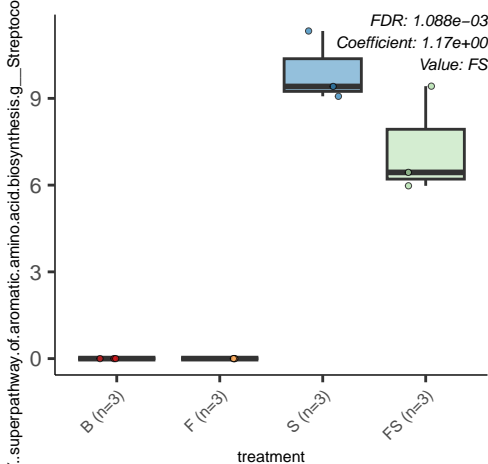




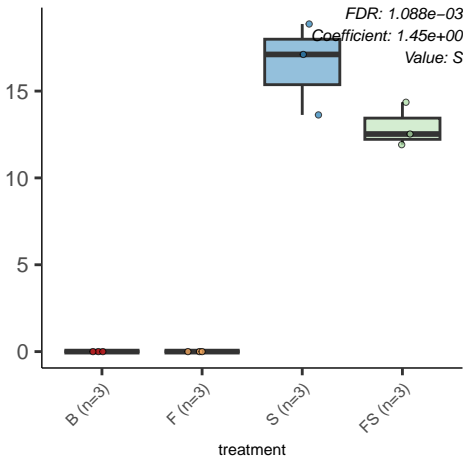




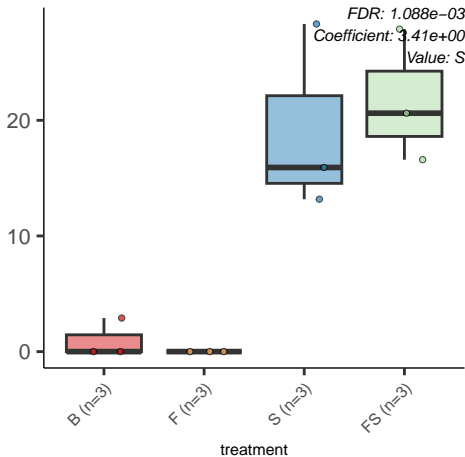


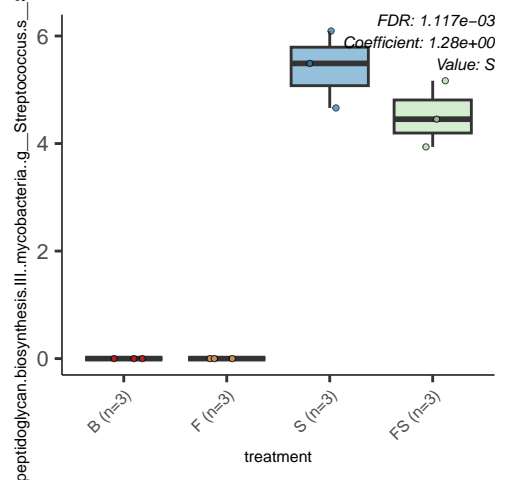


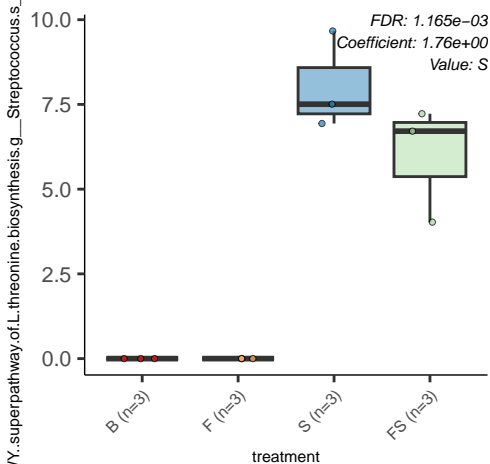
peptidoglycan.biosynthesis.l...meso.diaminopimelate.containing..g\_\_S



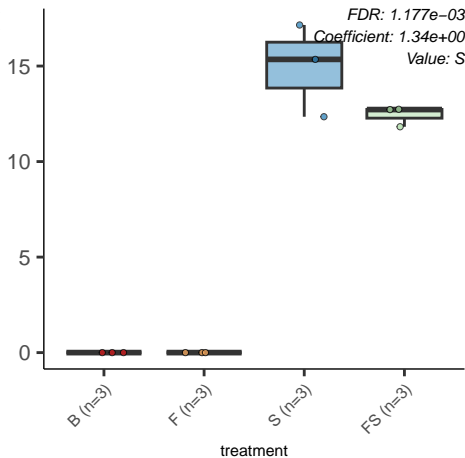
uanosine.ribonucleotides.de.novo.biosynthesis.g\_\_Streptococcus.s





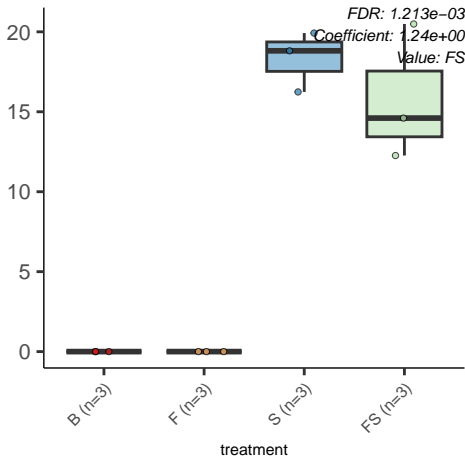


l.pentapeptide.biosynthesis.l..meso.diaminopimelate.containing.g



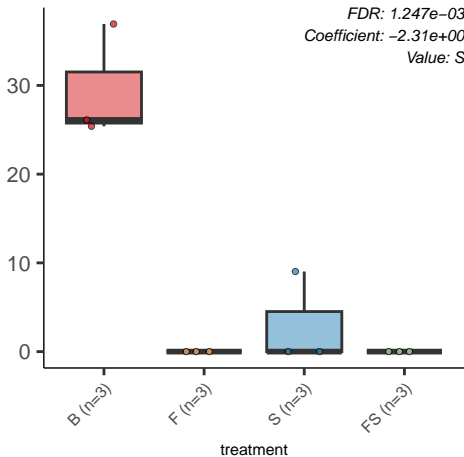


981..CDP.diacylglycerol.biosynthesis.III.g\_\_Streptococcus.s\_\_Strep



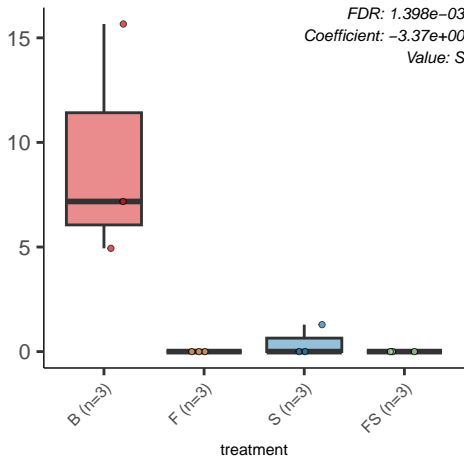
perpathway.of.unsaturated.fatty.acids.biosynthesis..E..coli..g\_\_Esch

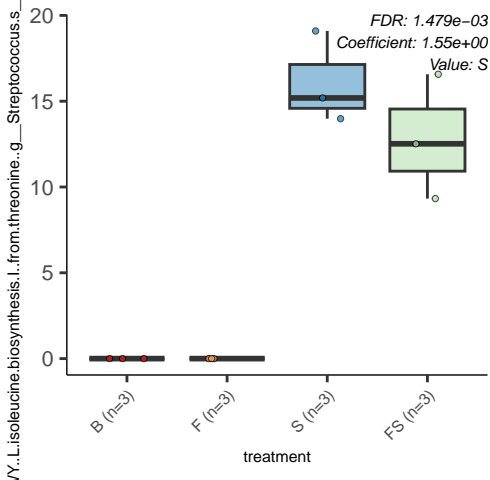
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Coefficient: -2.31e+00  
Value: S

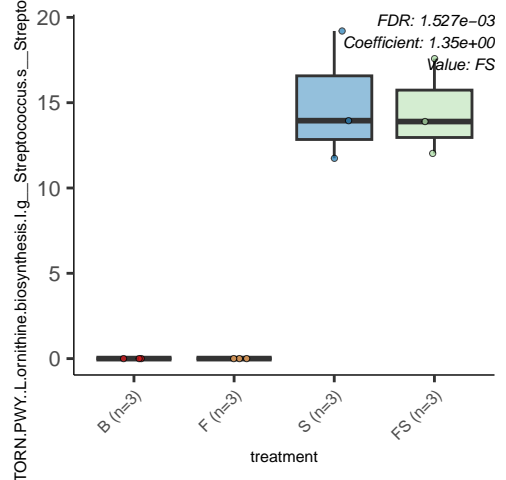


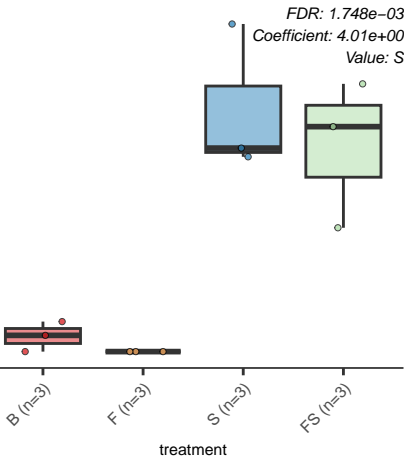
pyrimidine.deoxyribonucleotides.de.novo.biosynthesis.ll.g\_\_Escherichia

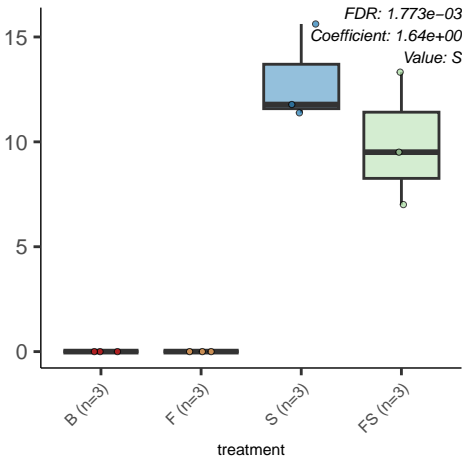
FDR: 1.398e-03  
Coefficient: -3.37e+00  
Value: S



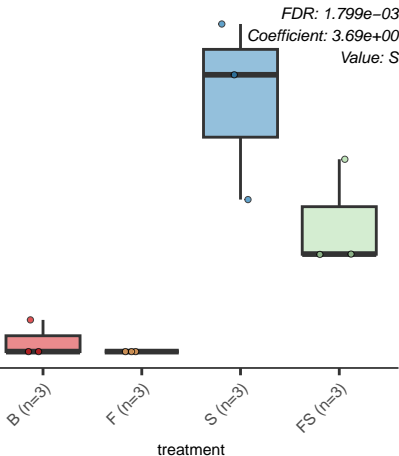






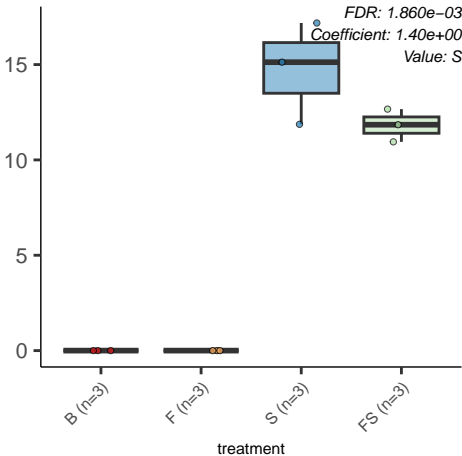


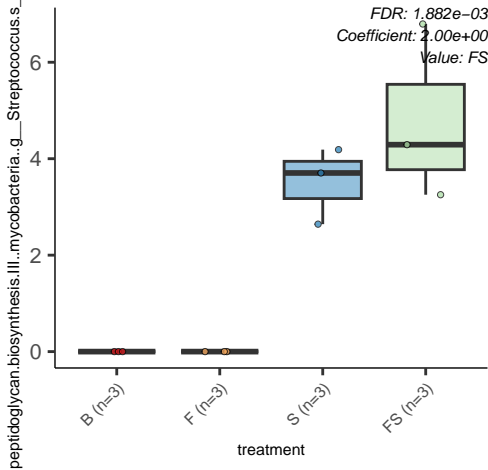
ETANA.PWY..L.methionine.biosynthesis.III.g\_Streptococcus.s\_Str

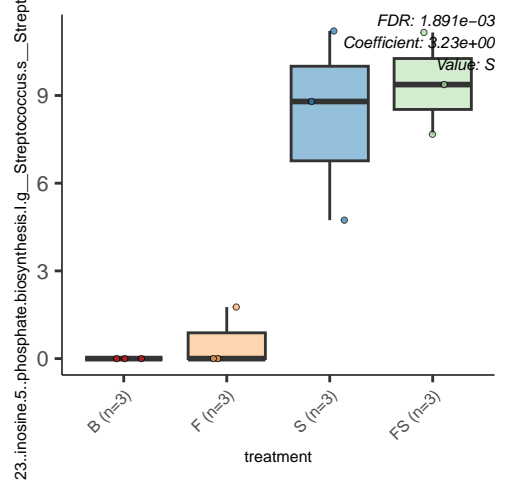


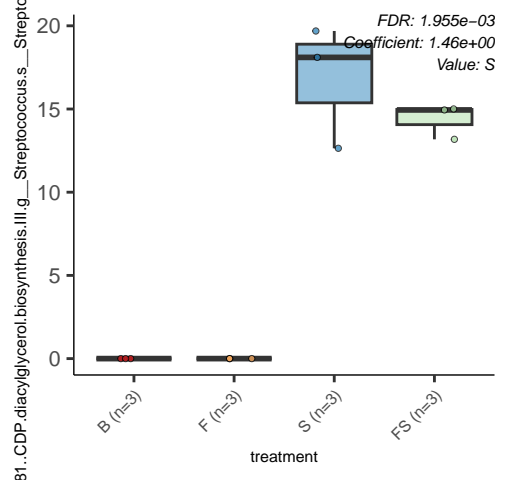


muramoyl.pentapeptide.biosynthesis.II..lysine.containing..g\_\_Strepto

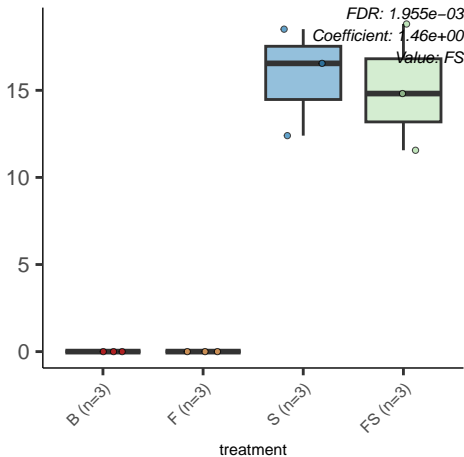




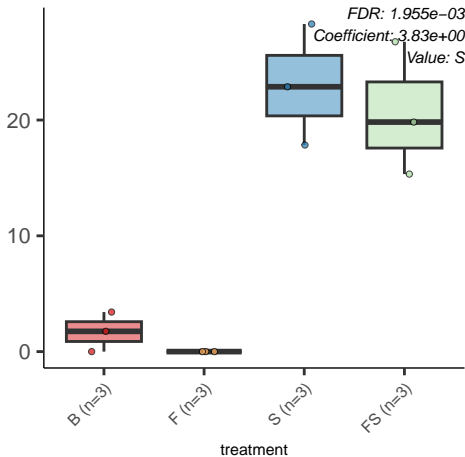


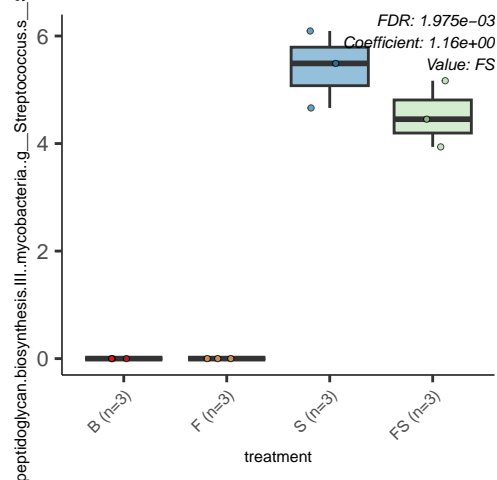


D.galactose.degradation.l...Leloir.pathway..g\_\_Streptococcus.s\_\_Str

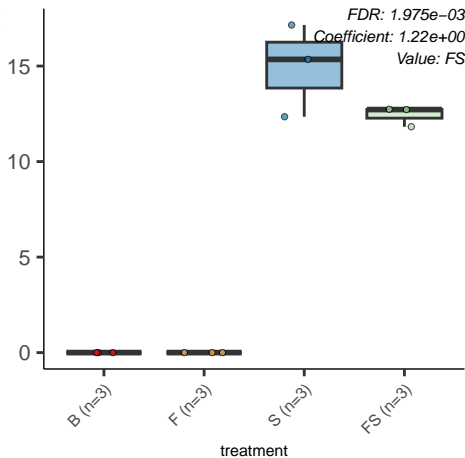


5609..adenine.and.adenosine.salvage.III.g\_\_Streptococcus.s\_\_Streptococcus



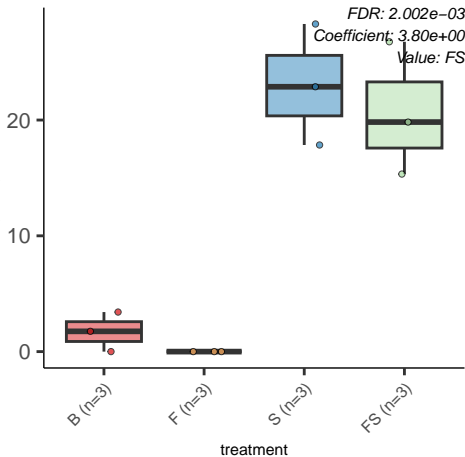


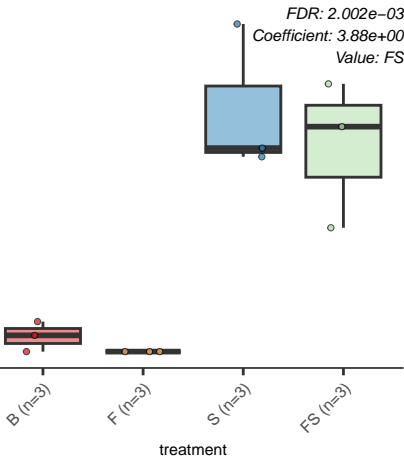
l.pentapeptide.biosynthesis.l..meso.diaminopimelate.containing.g



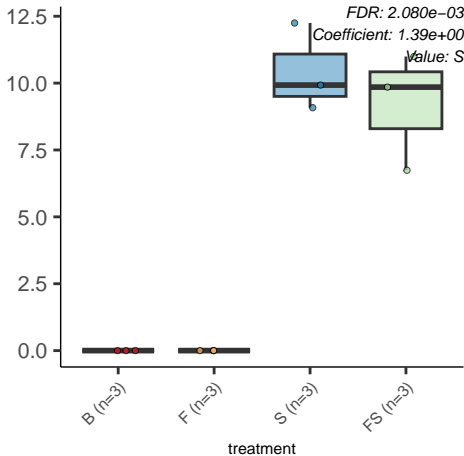


5609..adenine.and.adenosine.salvage.III.g\_\_Streptococcus.s\_\_Streptococcus

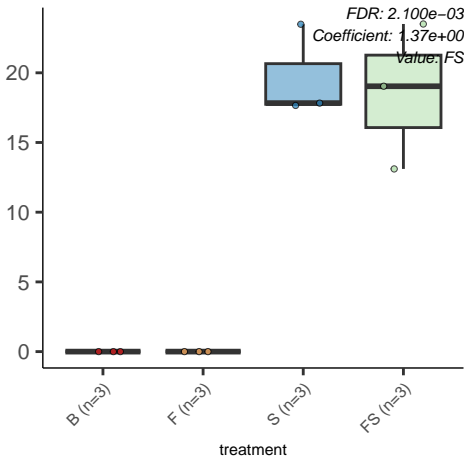


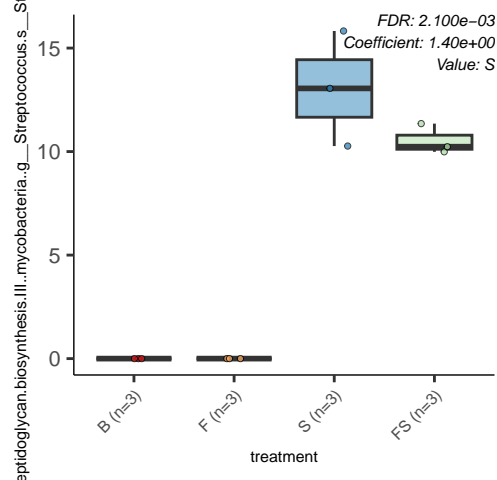


RO.PWY..chorismate.biosynthesis.l.g\_\_Streptococcus.s\_\_Streptococcus

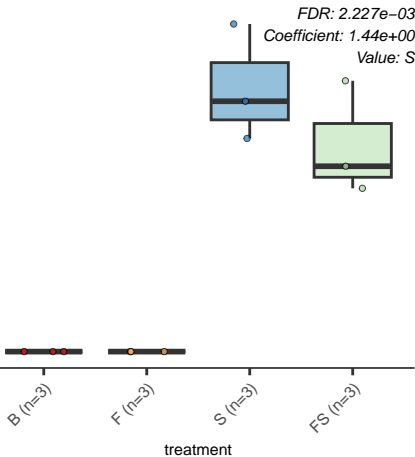


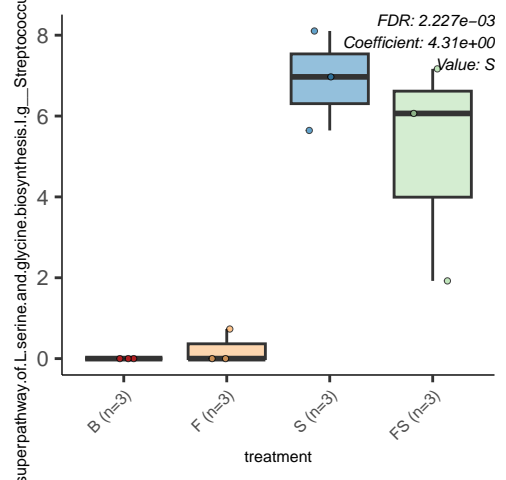
B.PWY..L.arginine.biosynthesis.II..acetyl.cycle..g\_\_Streptococcus.s...

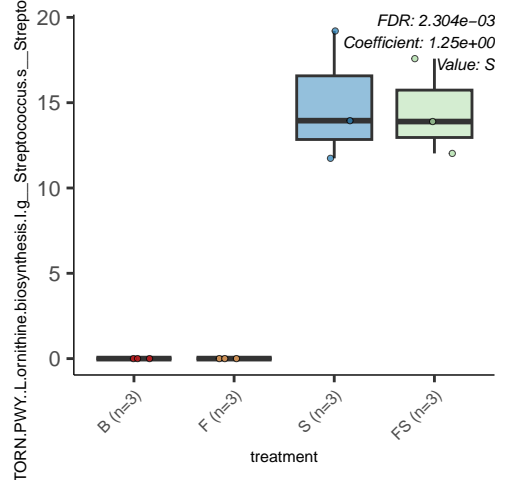




polypentapeptide biosynthesis. III... meso-diaminopimelate, containing...

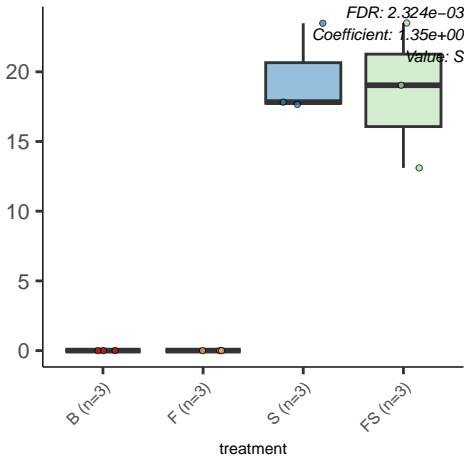




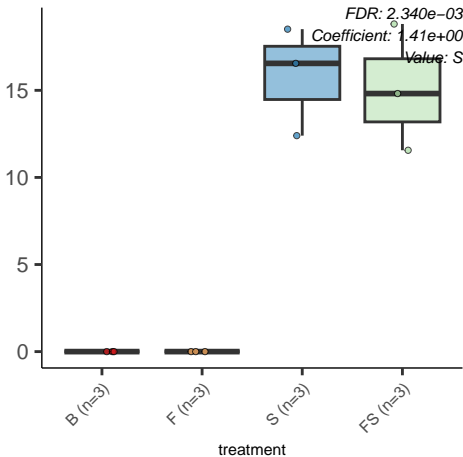


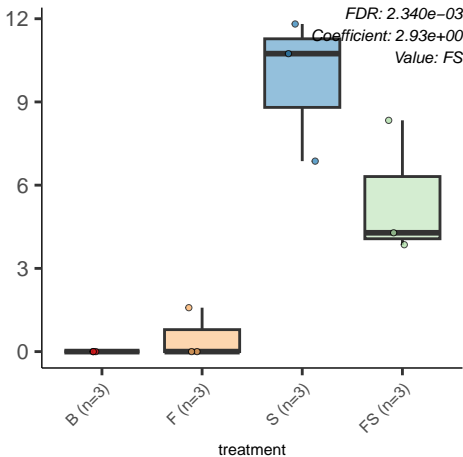


B.PWY..L.arginine.biosynthesis.II..acetyl.cycle..g\_\_Streptococcus.s

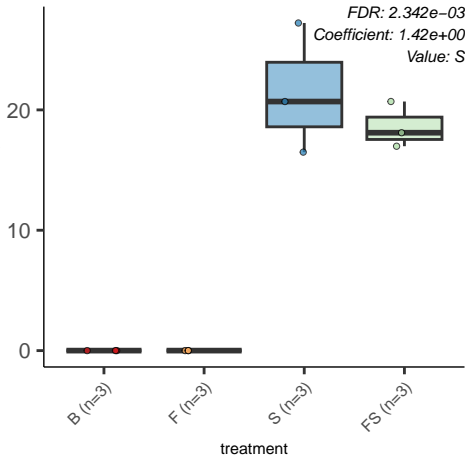


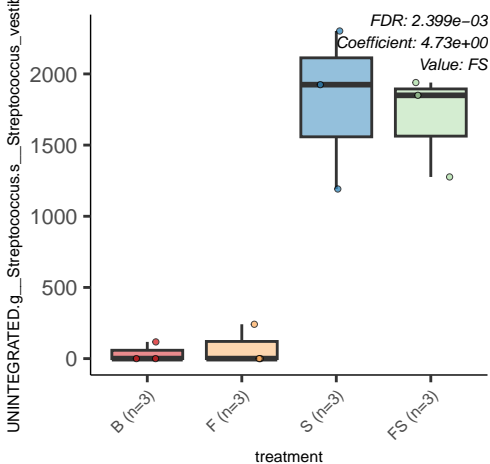
D.galactose.degradation.l...Leloir.pathway..g\_\_Streptococcus.s\_\_Str



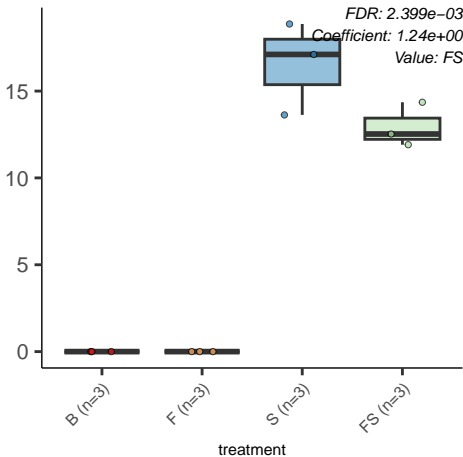


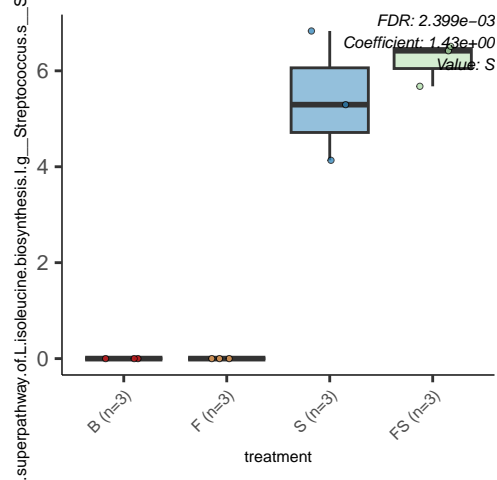
anosine.ribonucleotides.de.novo.biosynthesis.g\_\_Streptococcus.s

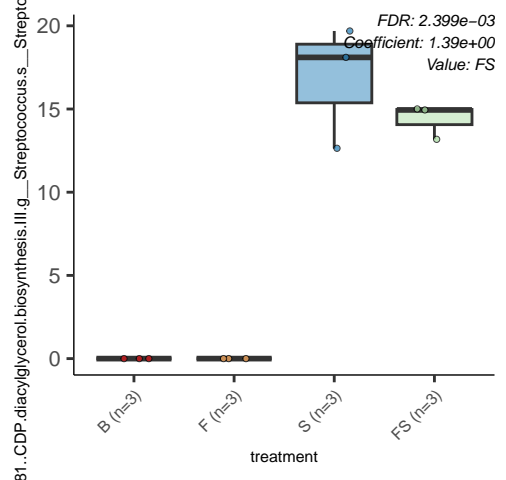




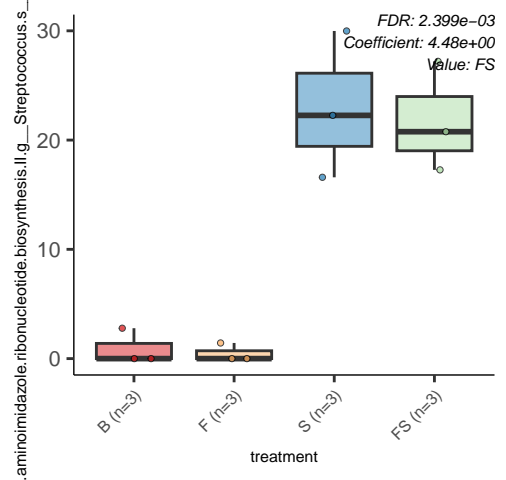
peptidoglycan.biosynthesis.l...meso.diaminopimelate.containing..g\_\_S



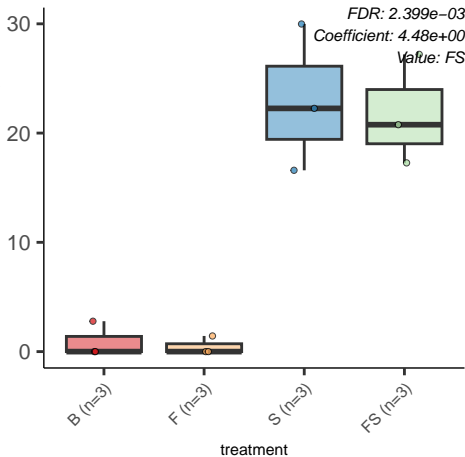


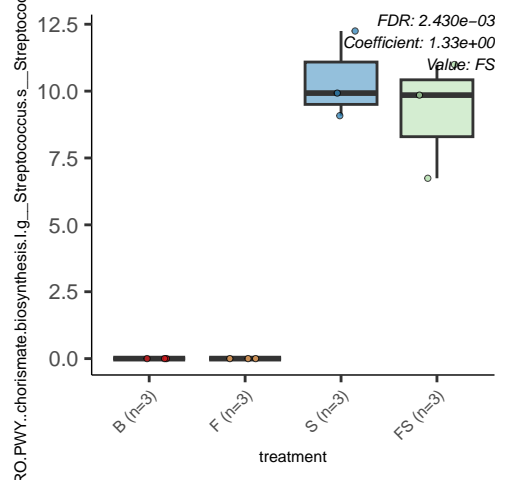




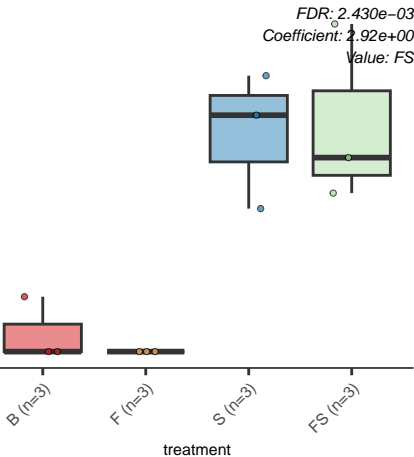


hway.of.5.aminoimidazole.ribonucleotide.biosynthesis.g\_\_Streptococ

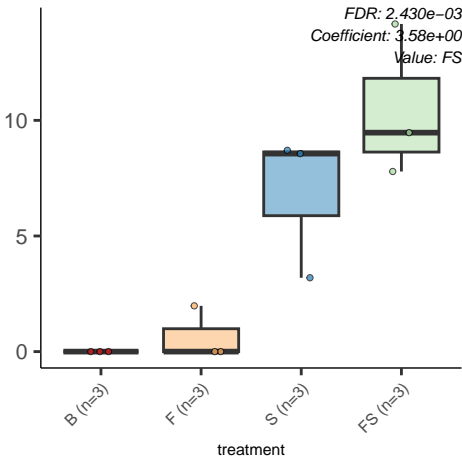


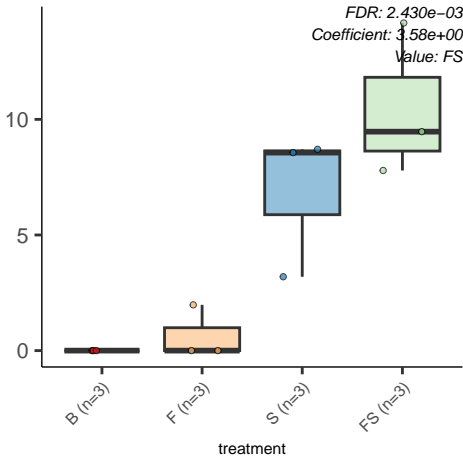


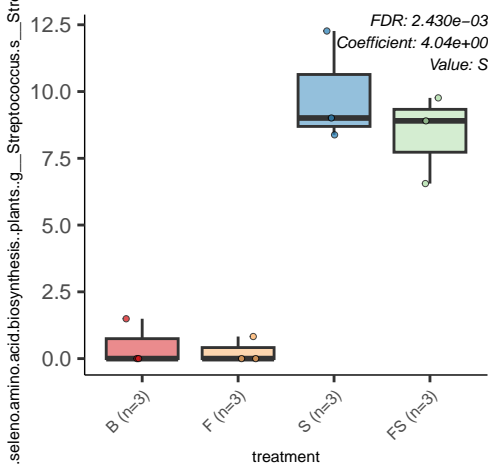
4.PWY..glycogen.biosynthesis.l...from.ADP.D.Glucose..g\_\_Streptococcus

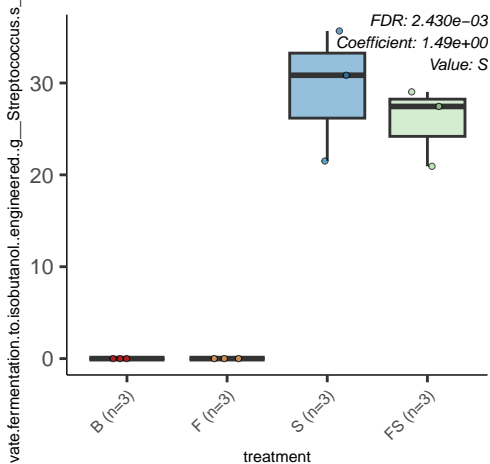


5.aminoimidazole.ribonucleotide.biosynthesis.II.g\_\_Streptococcus.s

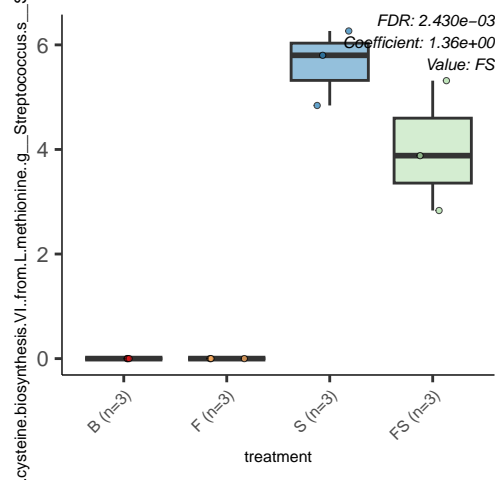




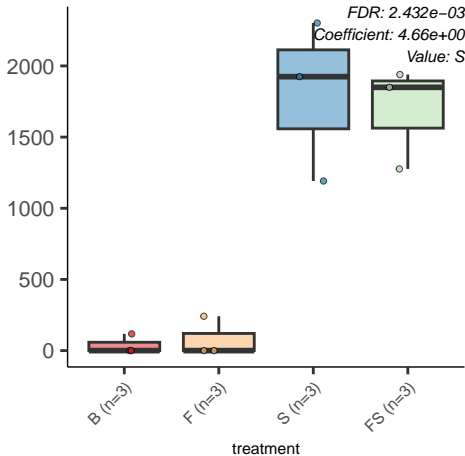




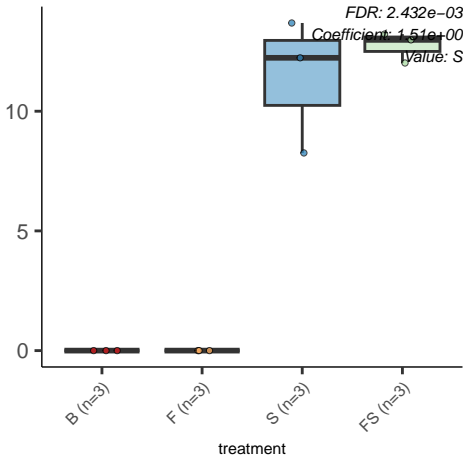


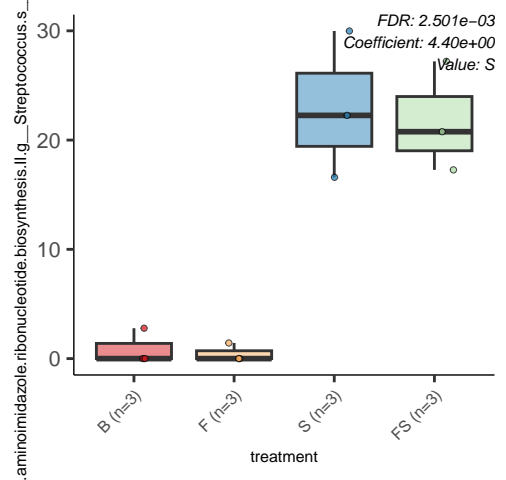


UNINTEGRATED.g\_\_Streptococcus.s\_\_Streptococcus\_vestit

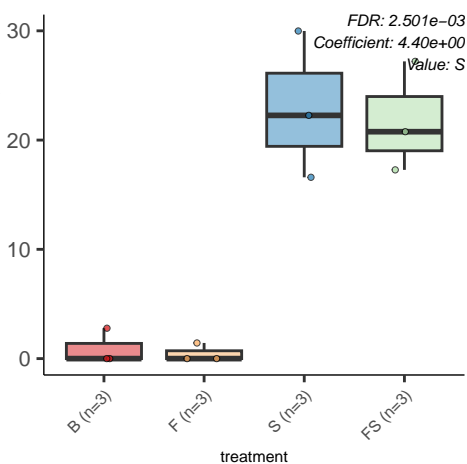


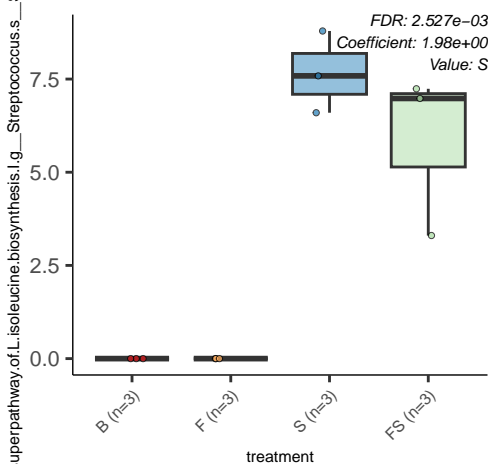
9...superpathway.of.purine.nucleotide.salvage.g\_\_Streptococcus.s...

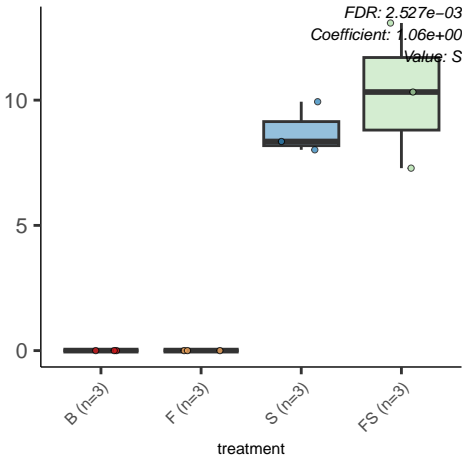




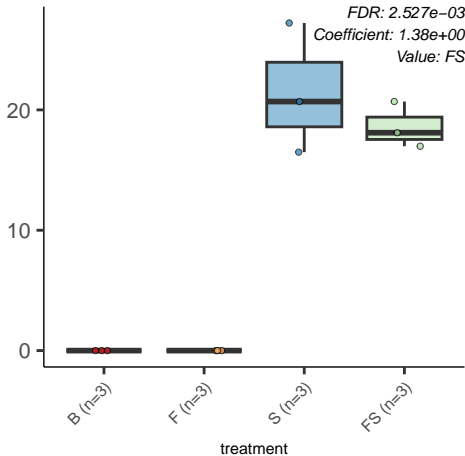
hway.of.5.aminoimidazole.ribonucleotide.biosynthesis.g\_\_Streptococ



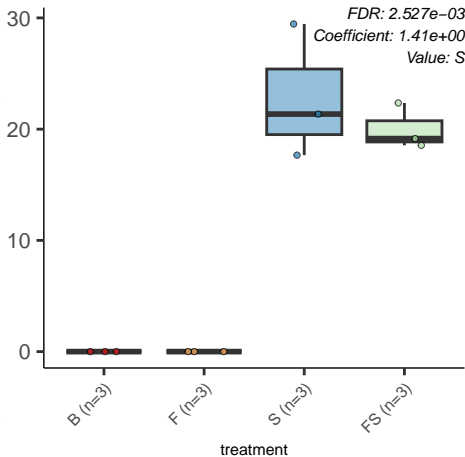


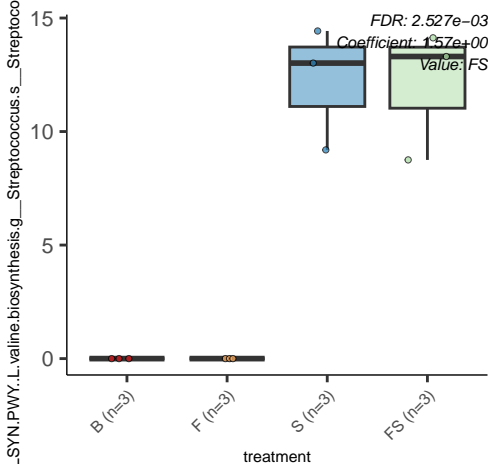


anosine.ribonucleotides.de.novo.biosynthesis.g\_\_Streptococcus.s

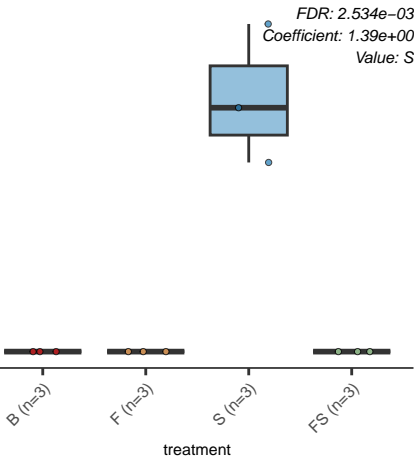




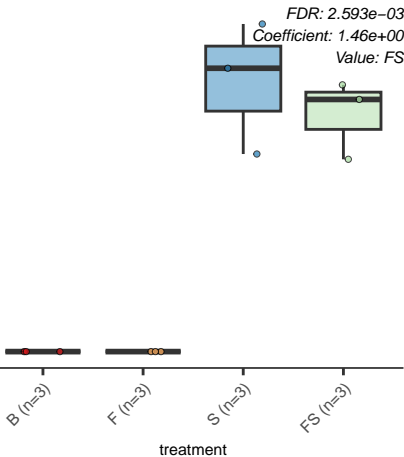


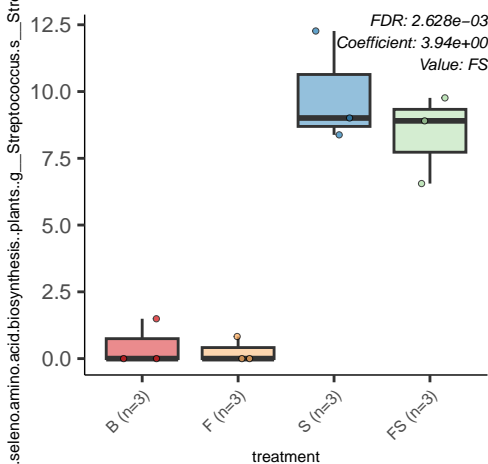


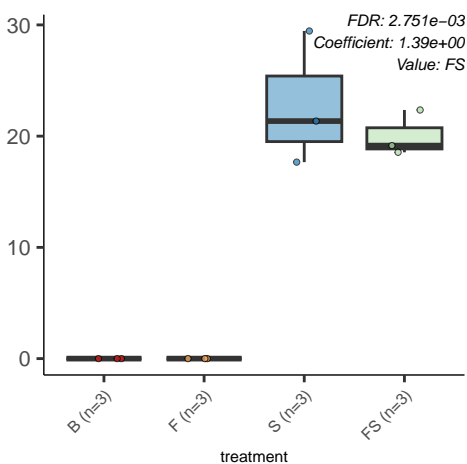
pathway.of.coenzyme.A.biosynthesis.III..mammals.g\_\_Streptococ

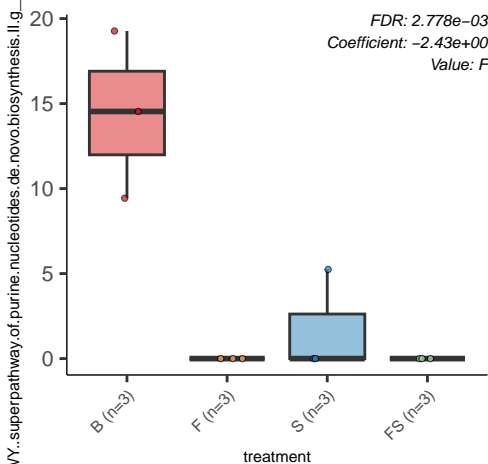


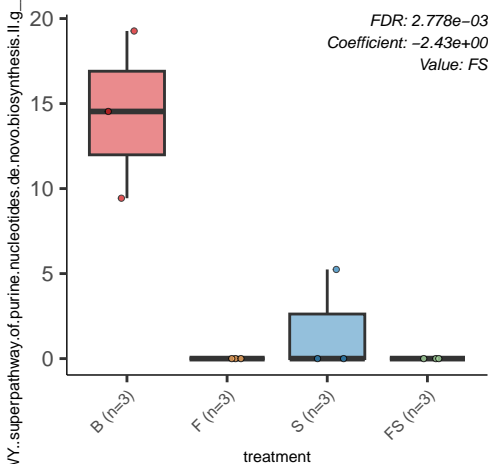
ruvate,fermentation.to.isobutanol..engineered..g\_\_Streptococcus.s\_



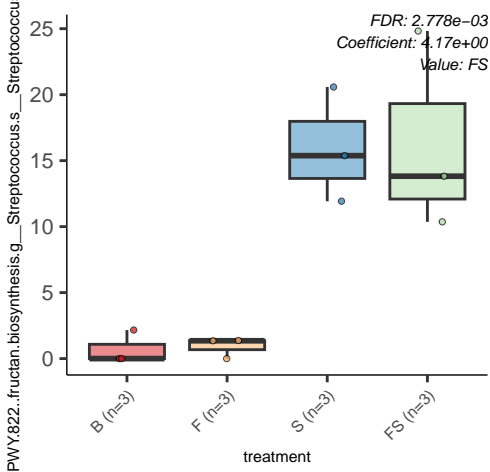


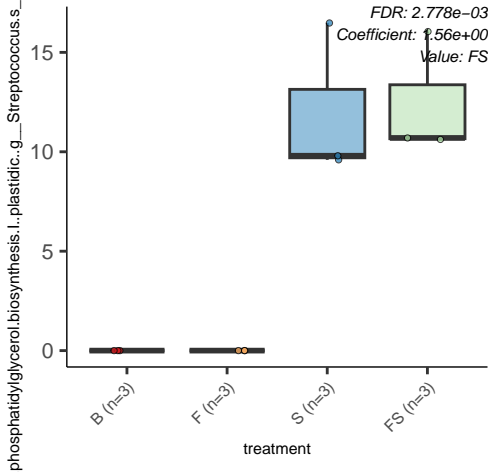




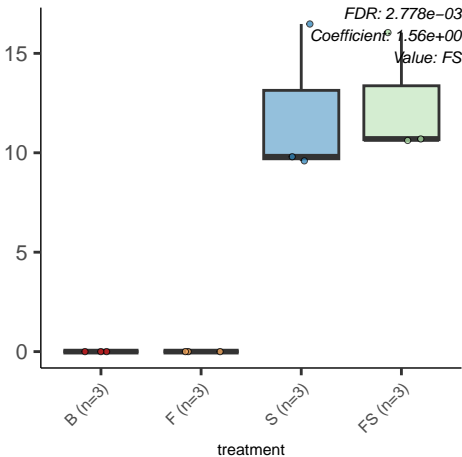


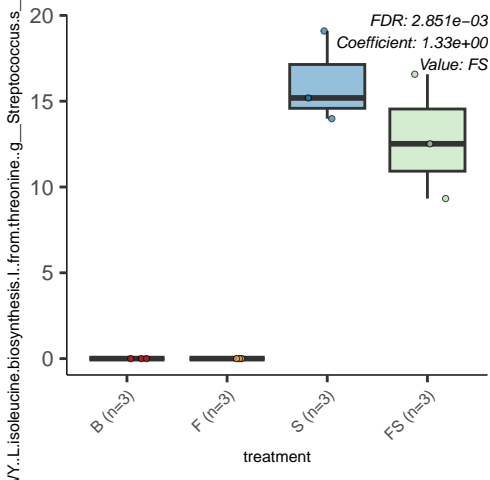


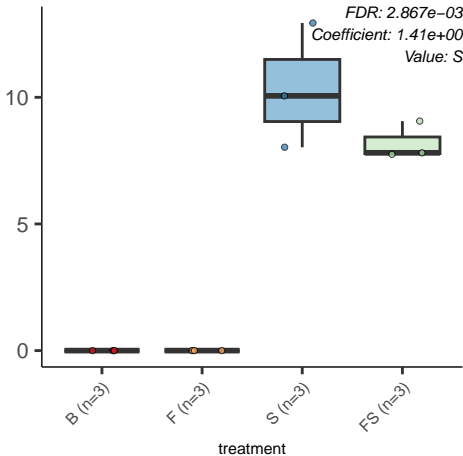


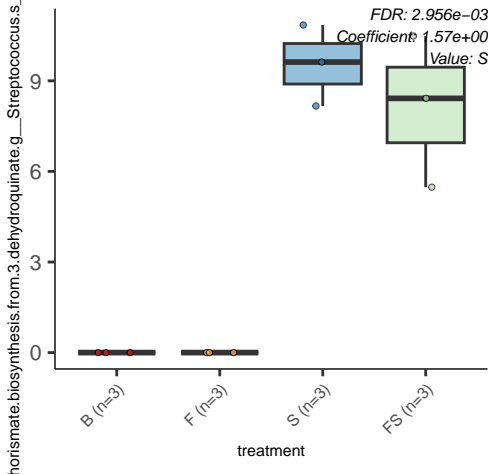


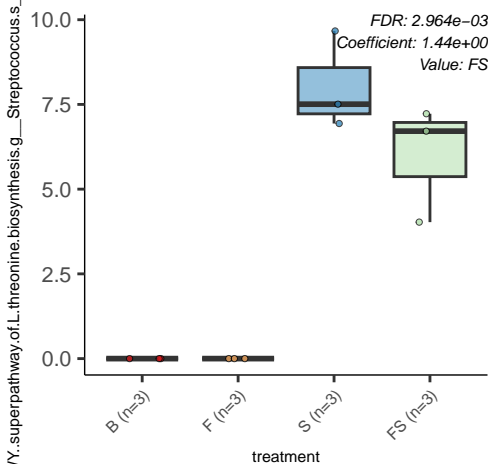
osphatidylglycerol.biosynthesis.ll..non.plastic..g\_\_Streptococcus



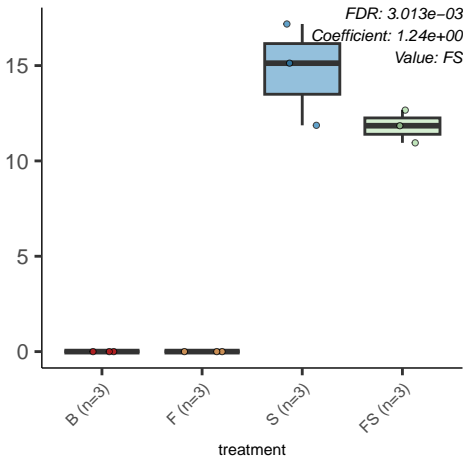






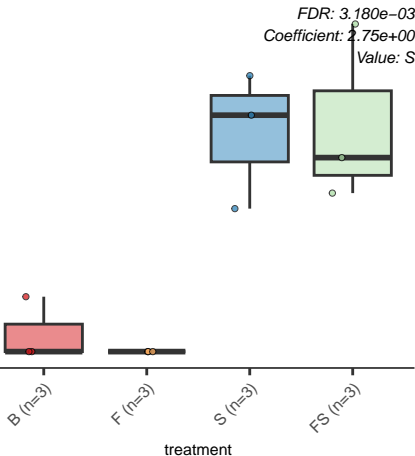


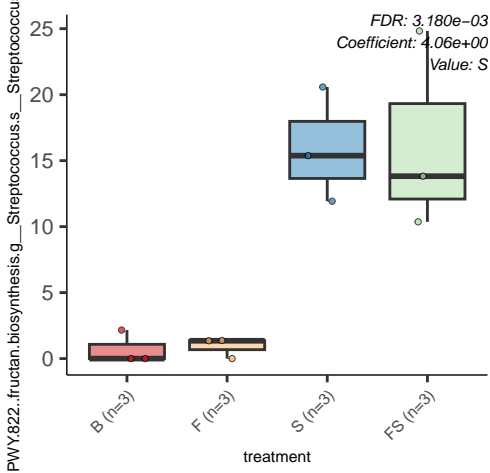
muramoyl.pentapeptide.biosynthesis.11..lysine.containing..g\_\_Strepto



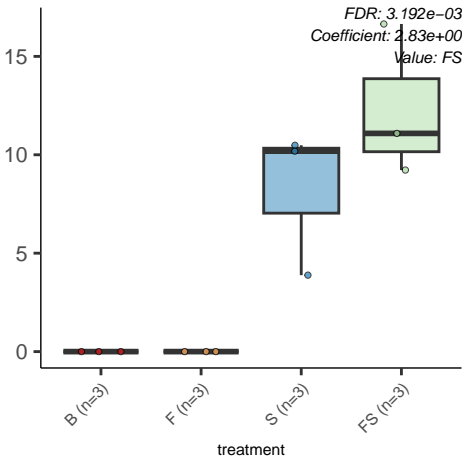


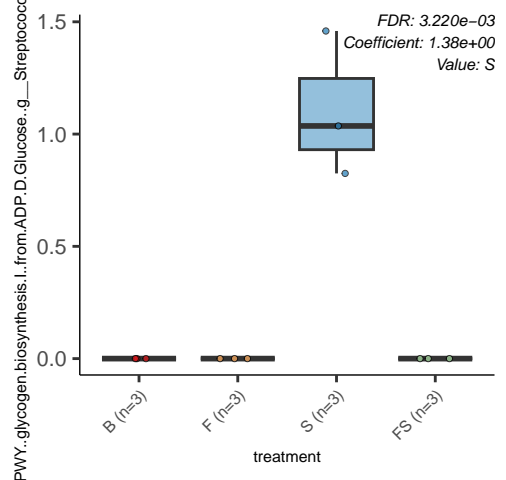
4.PWY..glycogen.biosynthesis.l...from.ADP.D.Glucose..g\_\_Streptococcus

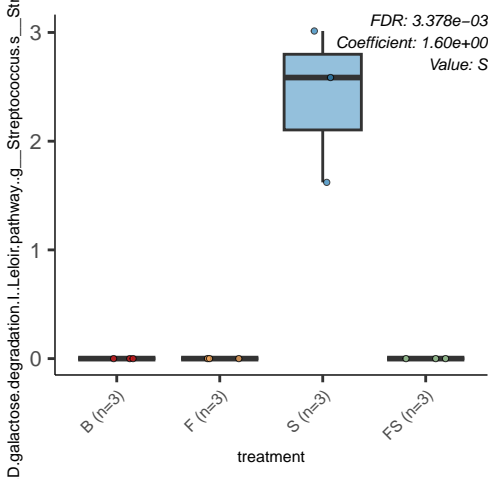


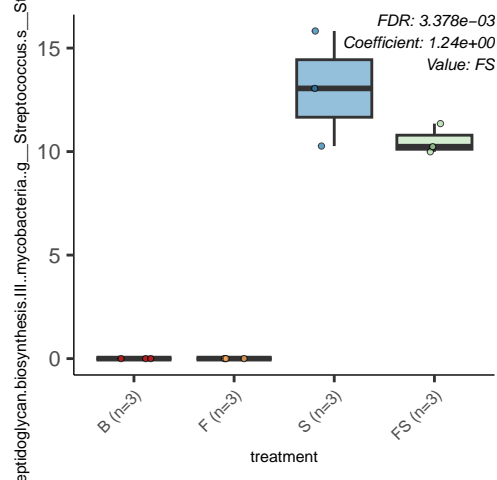


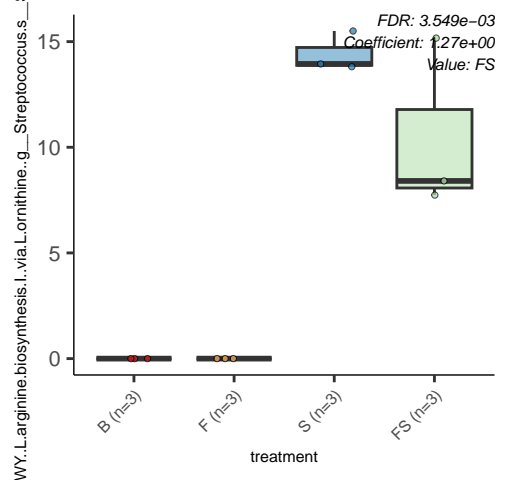
5.aminoimidazole.ribonucleotide.biosynthesis.l.g\_\_Streptococcus.s



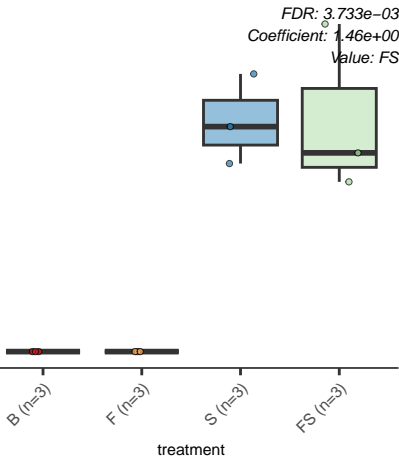




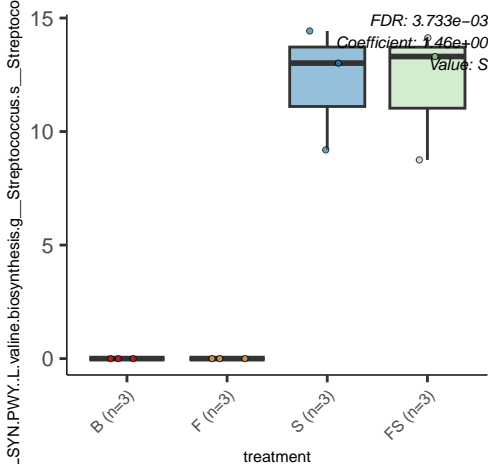




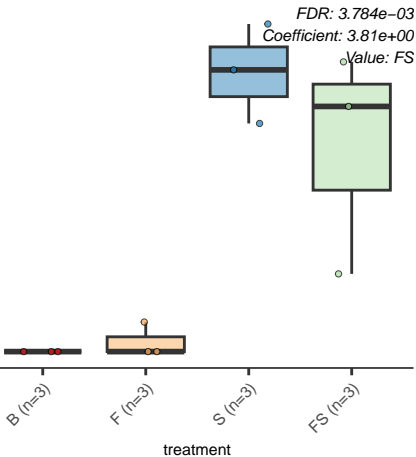
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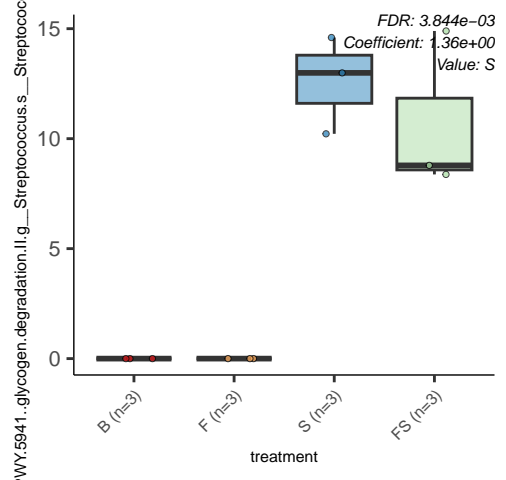






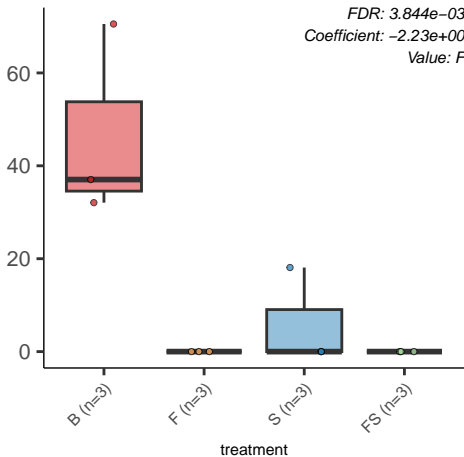
superpathway.of.L.serine.and.glycine.biosynthesis.l.g\_\_Streptococcus





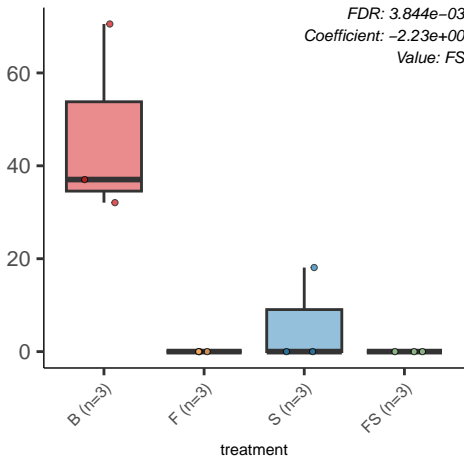
71..palmitate.biosynthesis..type.II.fatty.acid.synthase..g\_\_Escherichia

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Coefficient: -2.23e+00  
Value: F

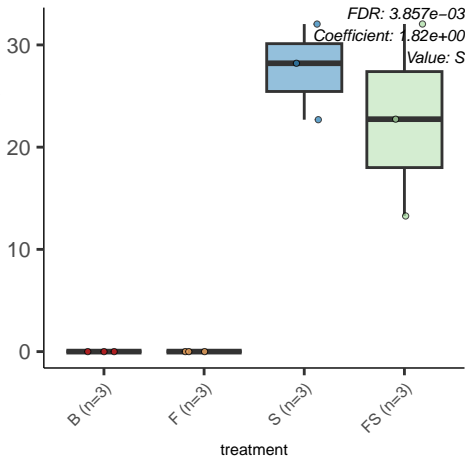


71..palmitate.biosynthesis..type.II.fatty.acid.synthase..g\_\_Escherichia

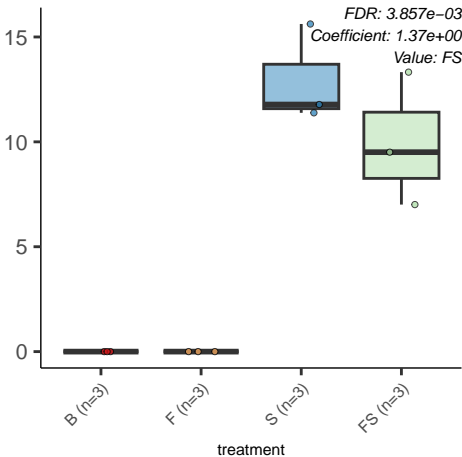
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Coefficient: -2.23e+00  
Value: FS

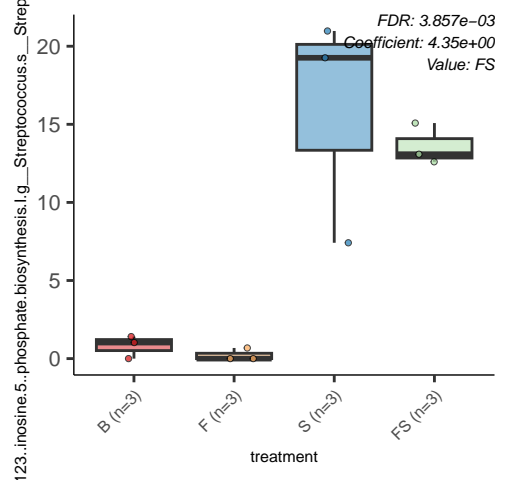


Y..superpathway.of.aromatic.amino.acid.biosynthesis.g\_\_Streptococ

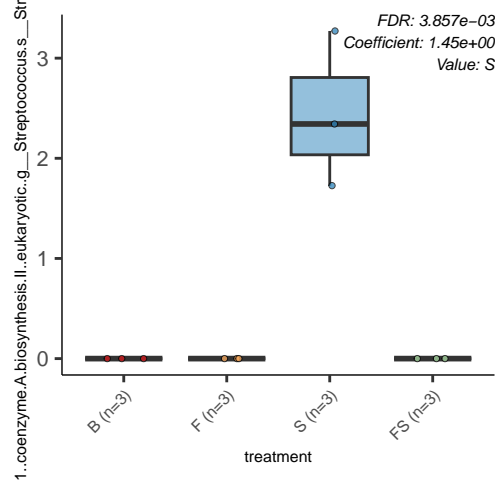


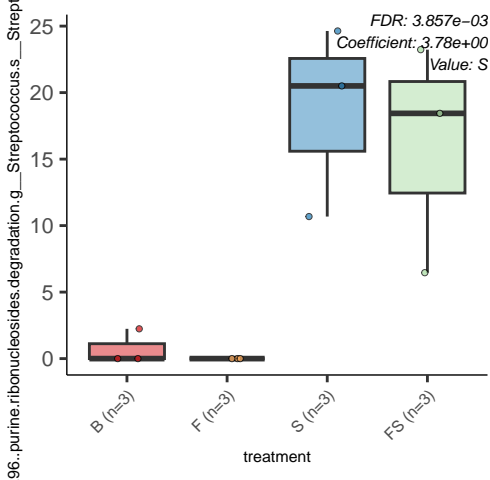
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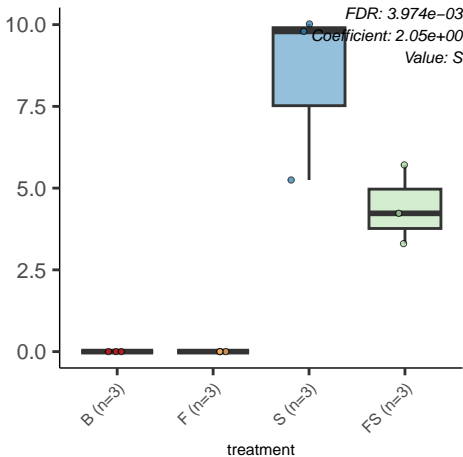




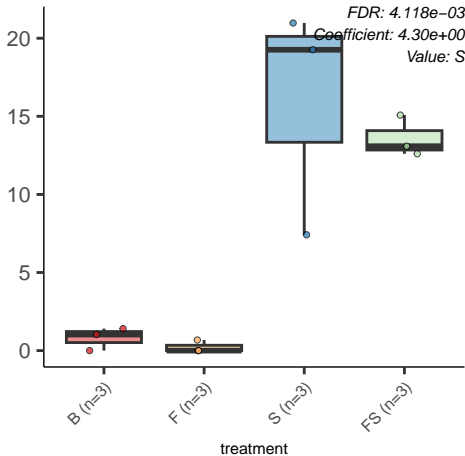


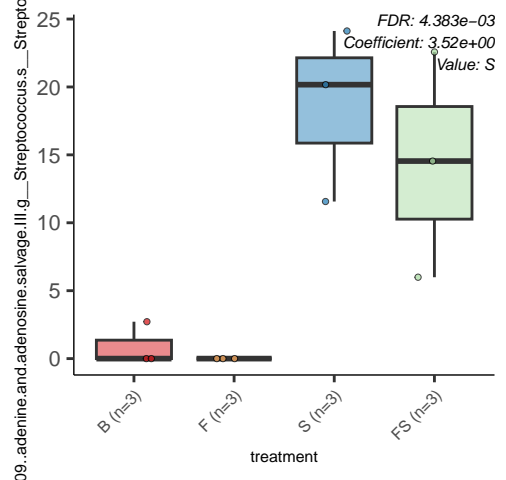


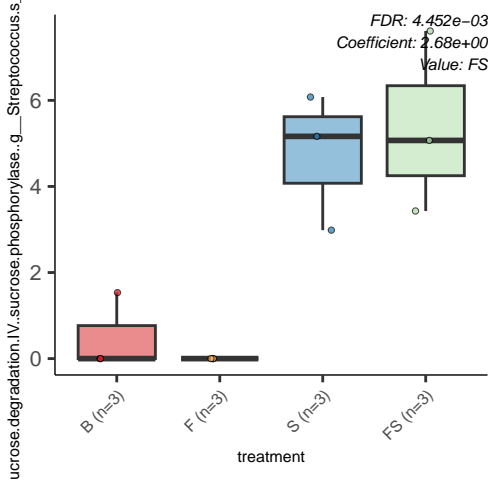
yl.pentapeptide.biosynthesis.III...meso.diaminopimelate.containing...

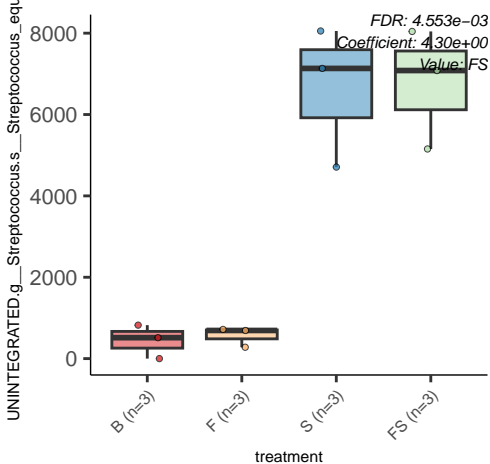


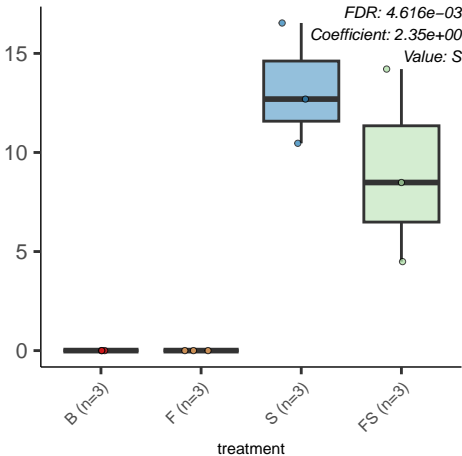
123..inosine.5..phosphate.biosynthesis.l.g\_\_Streptococcus.s\_\_Strep



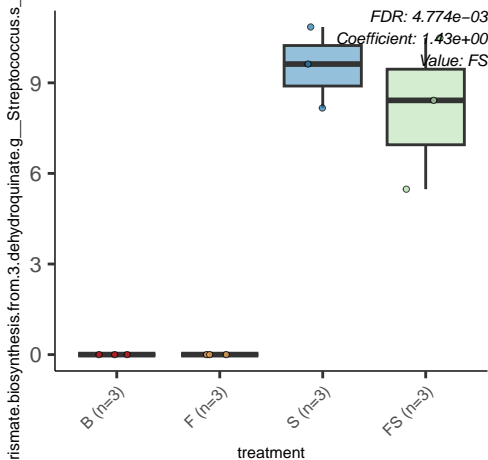




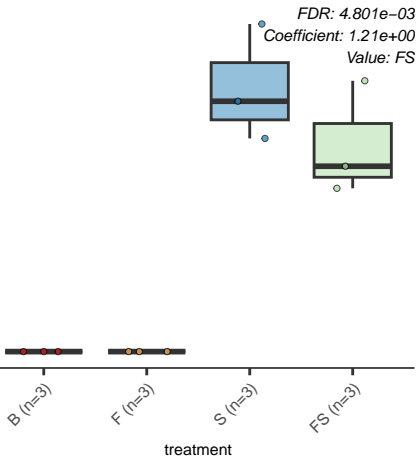




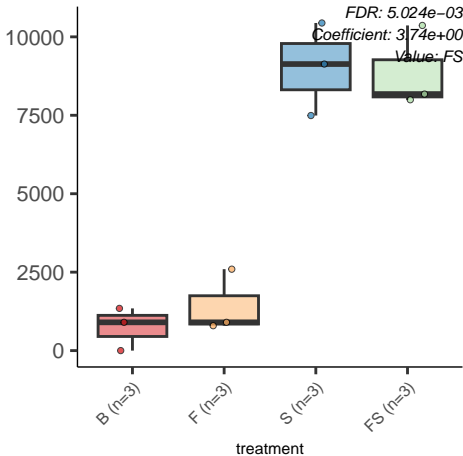




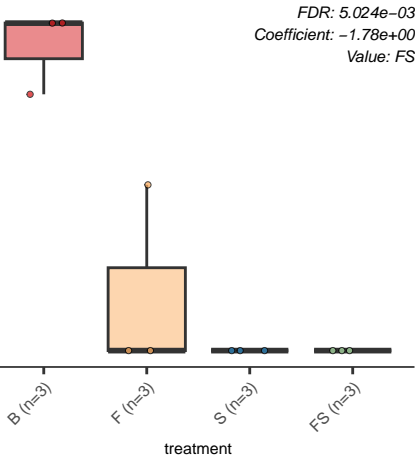
pyl.pentapeptide.biosynthesis.III..meso.diaminopimelate.containing..

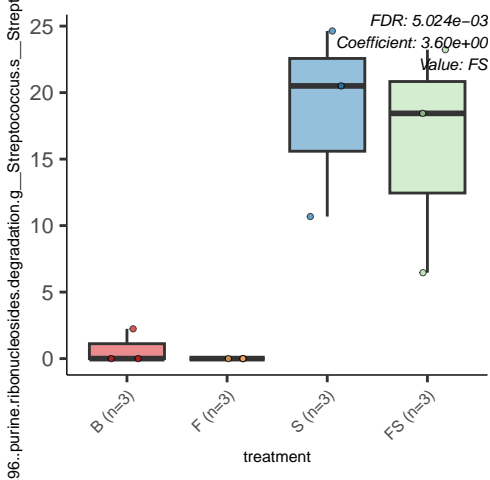


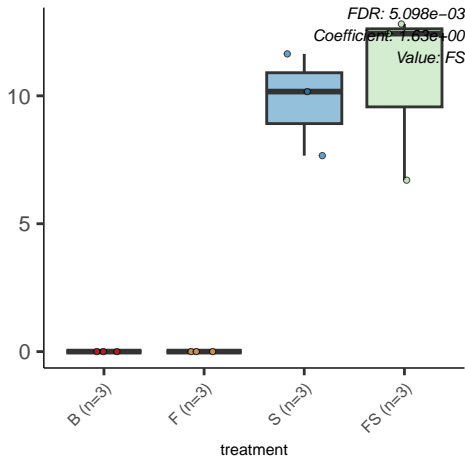
UNINTEGRATED.g\_\_Streptococcus.s\_\_Streptococcus\_pneum

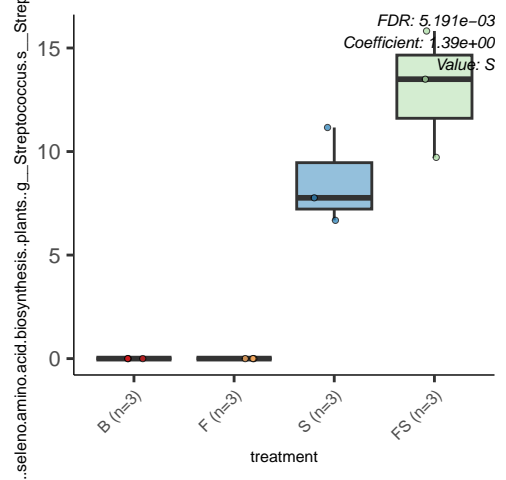






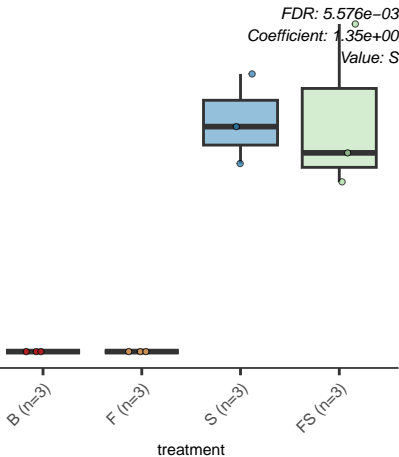


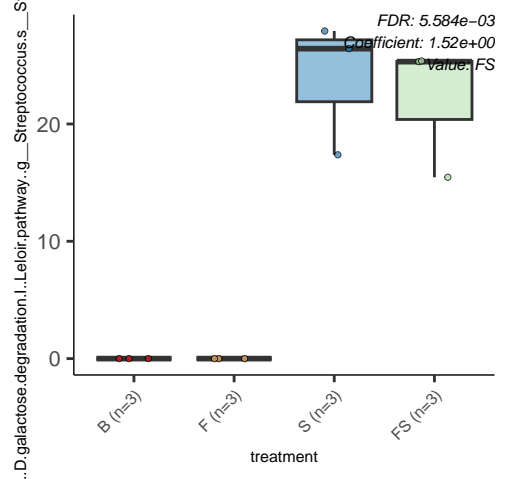


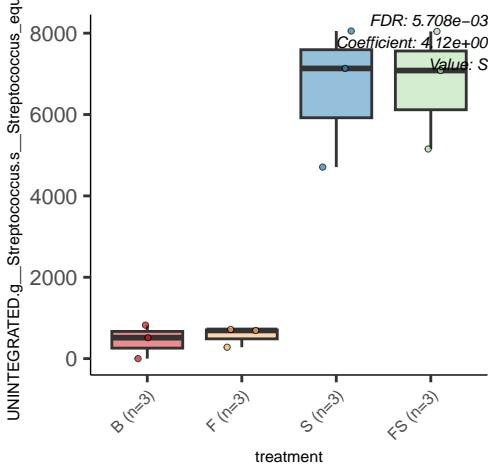


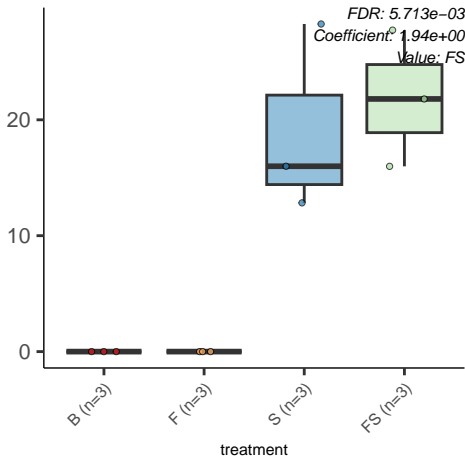


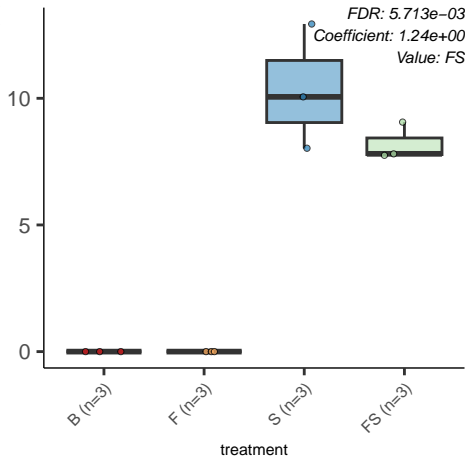
peptidoglycan.biosynthesis.l..meso.diaminopimelate.containing.g

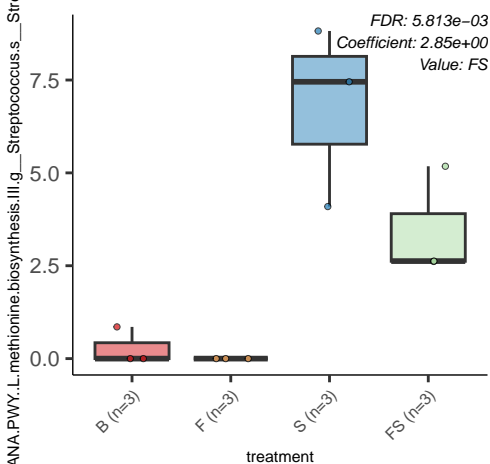


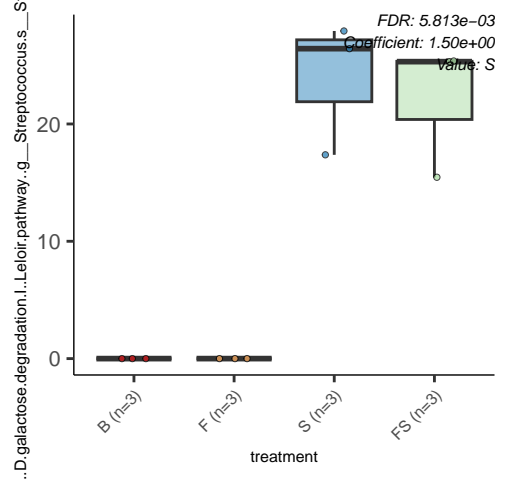




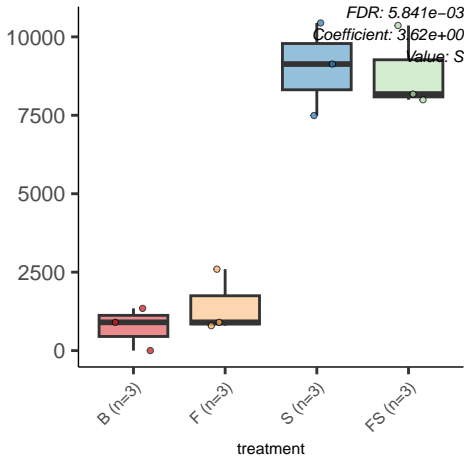






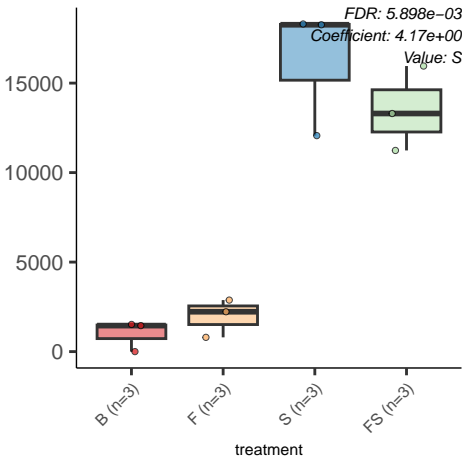


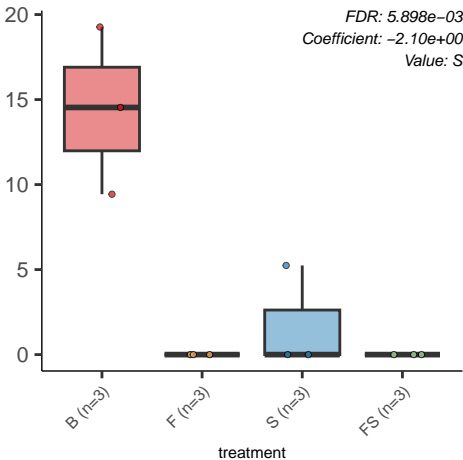
UNINTEGRATED.g\_\_Streptococcus.s\_\_Streptococcus\_pneum

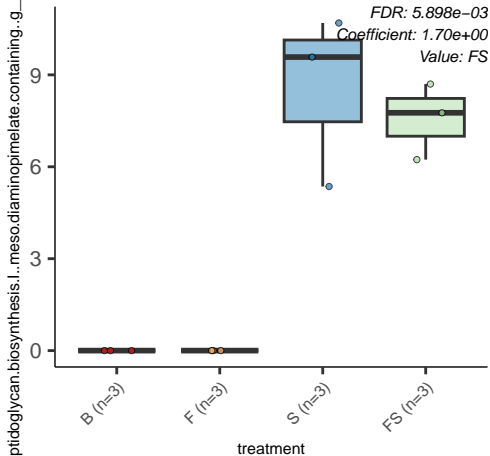




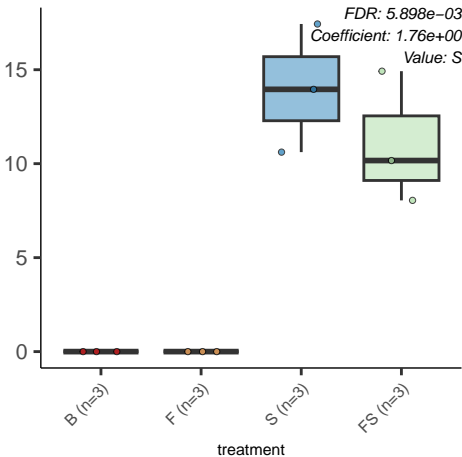
UNINTEGRATED.g\_\_Streptococcus.s\_\_Streptococcus\_saliv

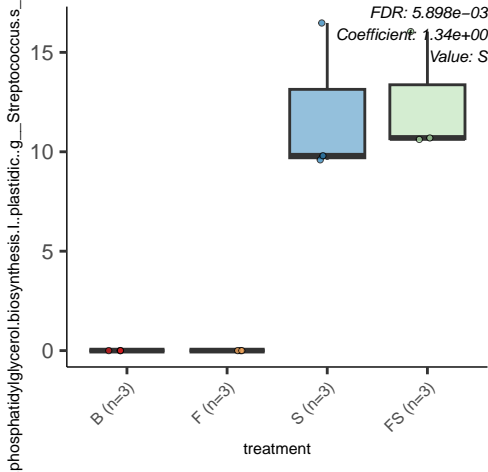


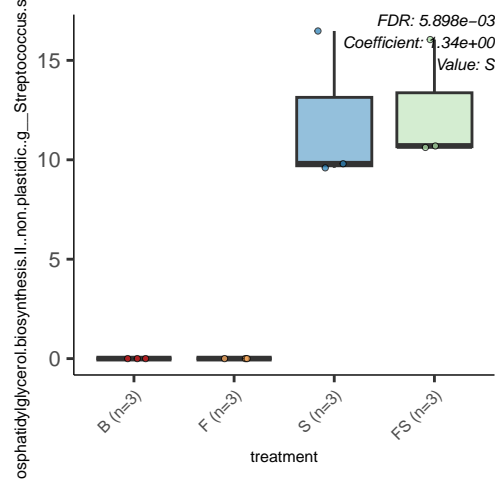


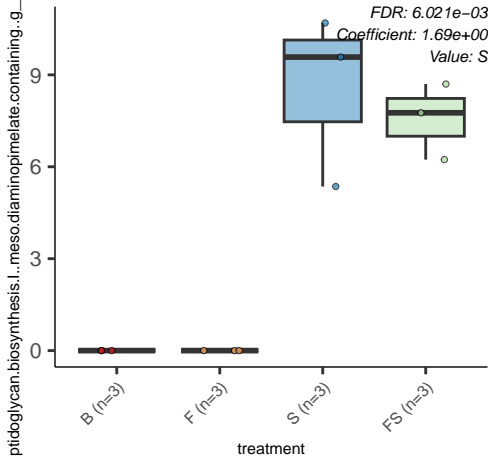


hway.of.adenosine.nucleotides.de.novo.biosynthesis.l.g\_\_Streptococ

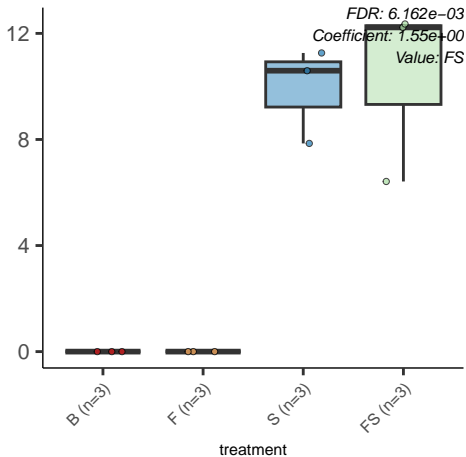




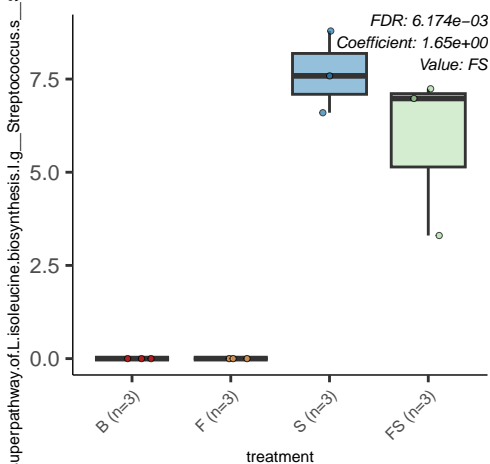


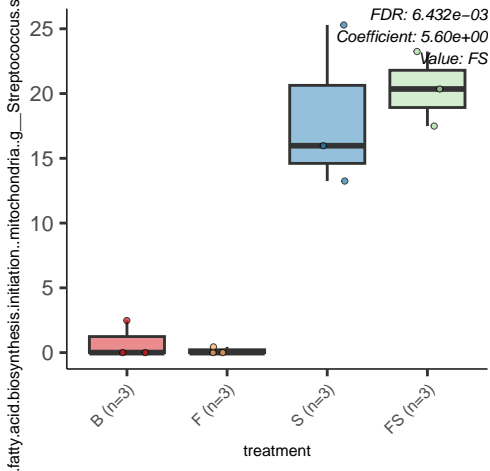


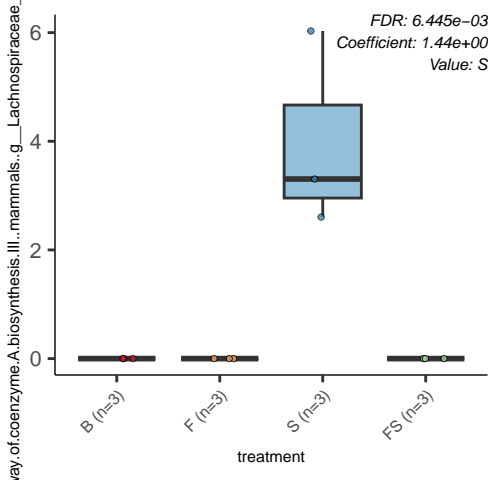
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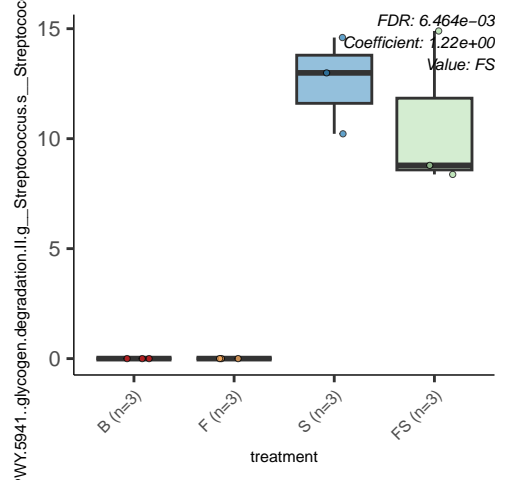


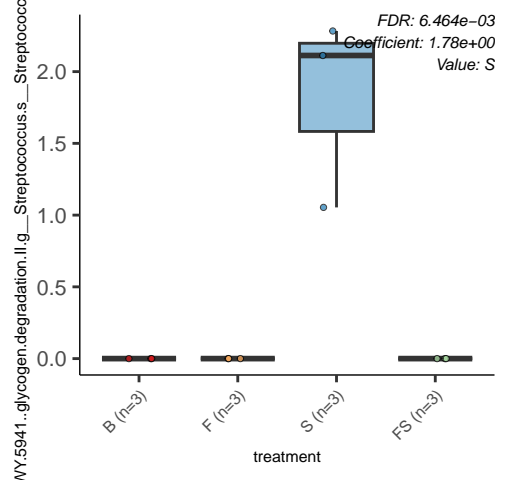




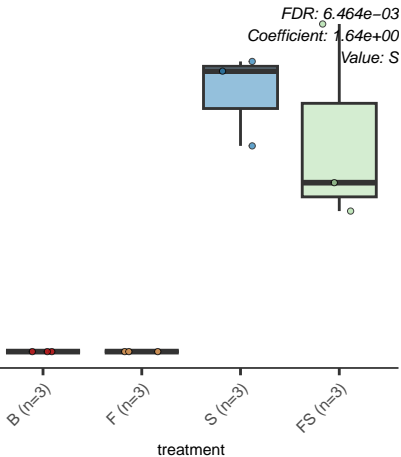


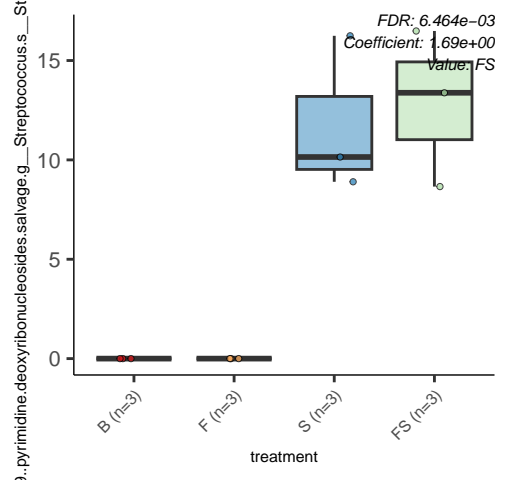






ylmuramoyl.pentapeptide.biosynthesis.II..lysine.containing..g\_\_Strep





PWY1ZNC.1..assimilatory.sulfate.reduction.IV.unclassified

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Coefficient: 2.05e+00  
Value: F

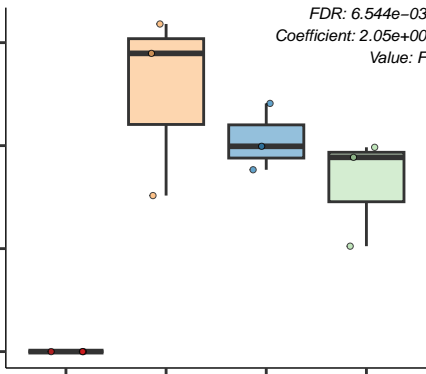
B (n=3)

F (n=3)

S (n=3)

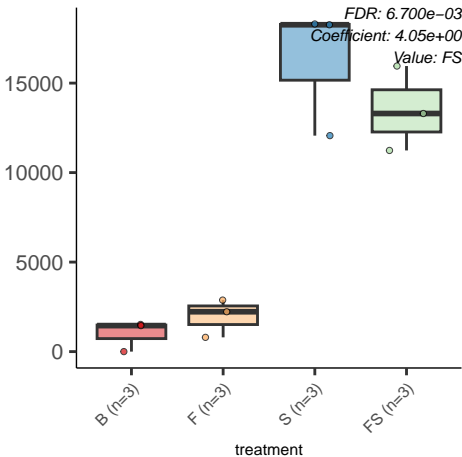
FS (n=3)

treatment

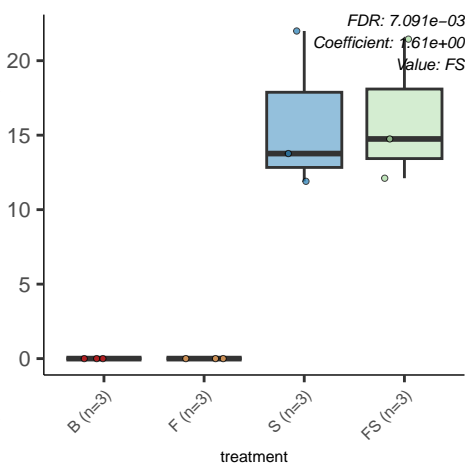


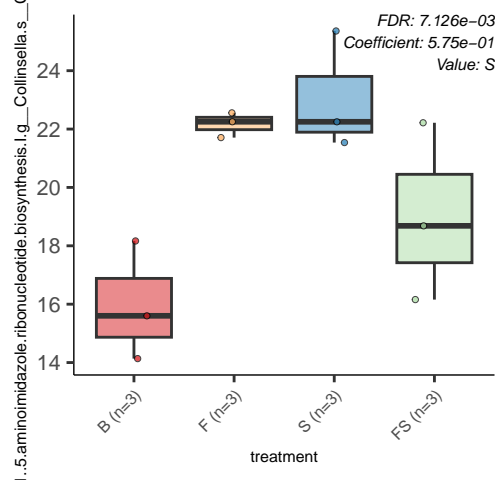


UNINTEGRATED.g\_\_Streptococcus.s\_\_Streptococcus\_saliv

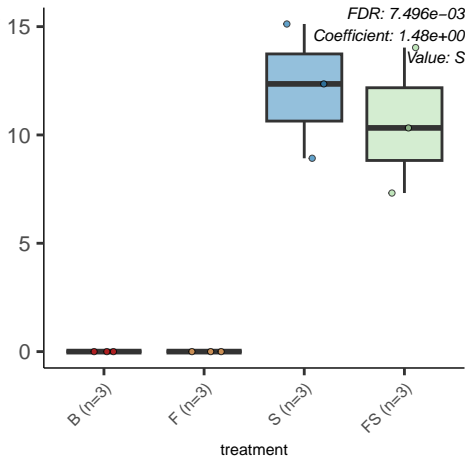


onway.of.guanosine.nucleotides.de.novo.biosynthesis.II.g\_\_Streptococcus

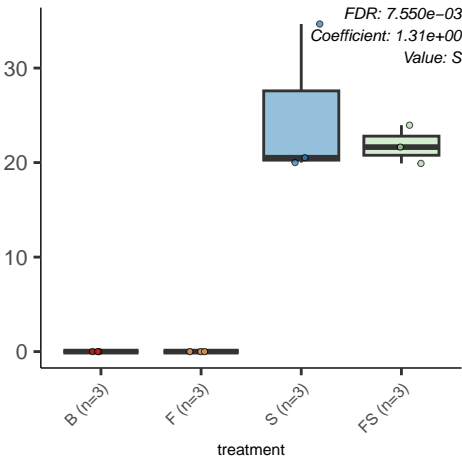




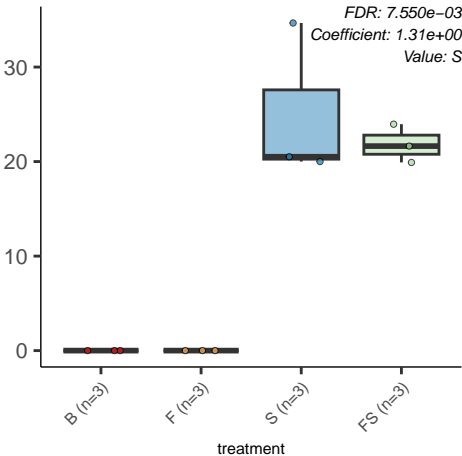
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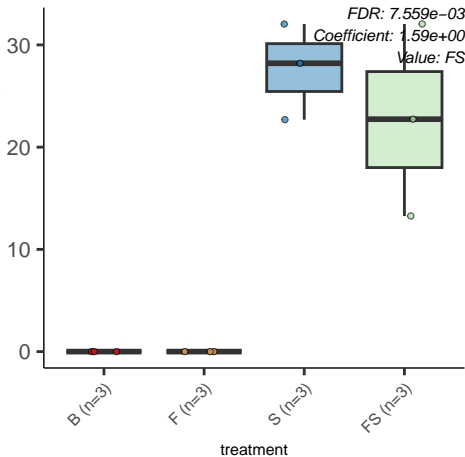
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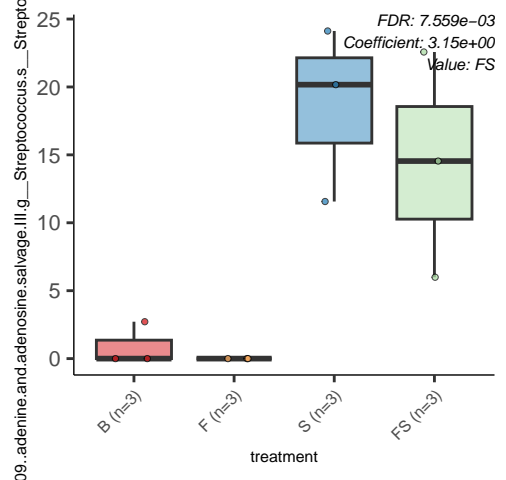


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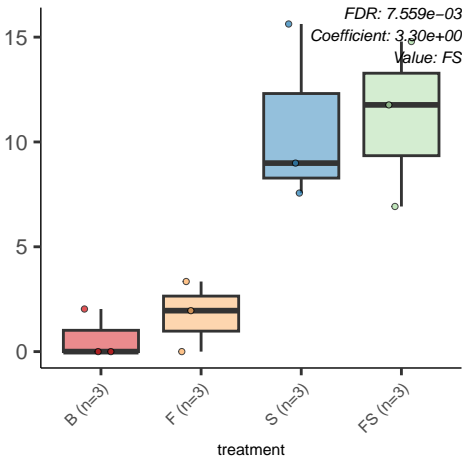
Y..superpathway.of.aromatic.amino.acid.biosynthesis.g\_\_Streptococ



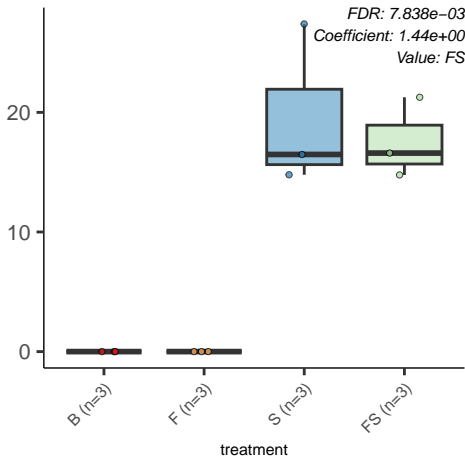


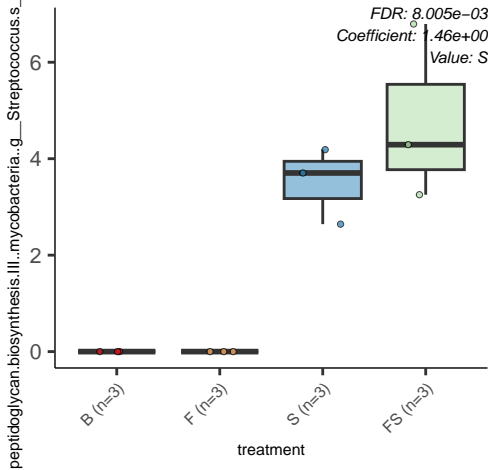


PWY.822..fructan.biosynthesis.g\_\_Streptococcus.s\_\_Streptococcus

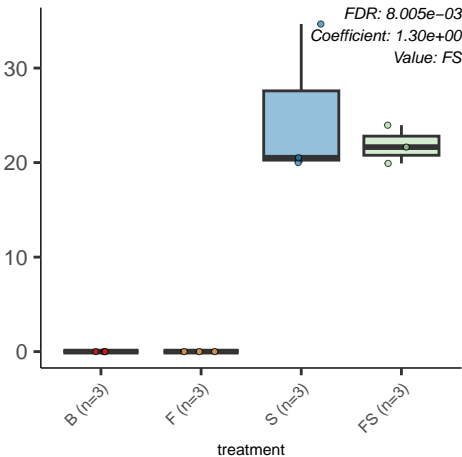


imidine.deoxyribonucleotide.phosphorylation.g\_\_Streptococcus.s\_\_

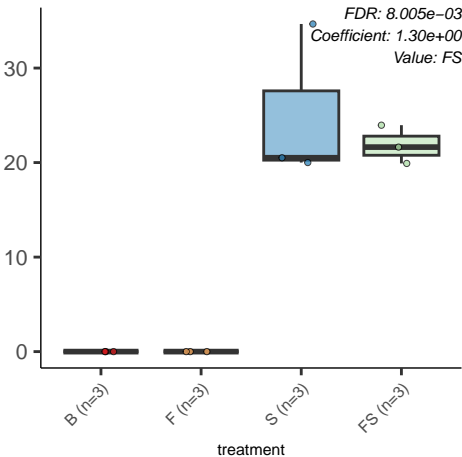


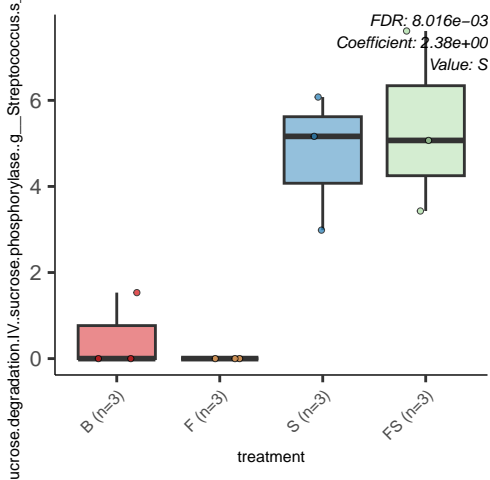


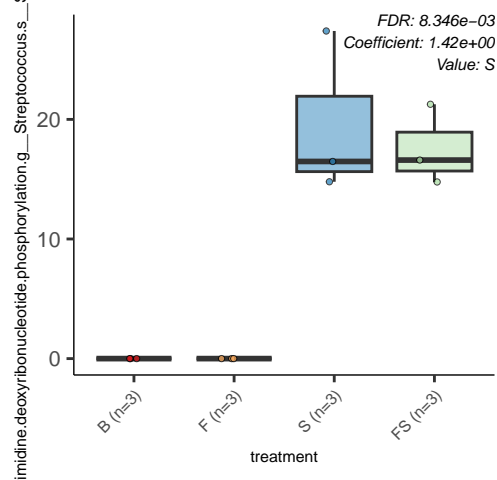
ine.deoxyribonucleotides.de.novo.biosynthesis.ll.g\_\_Streptococcus.

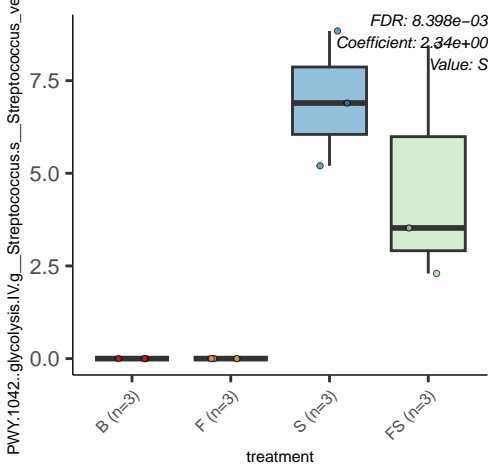


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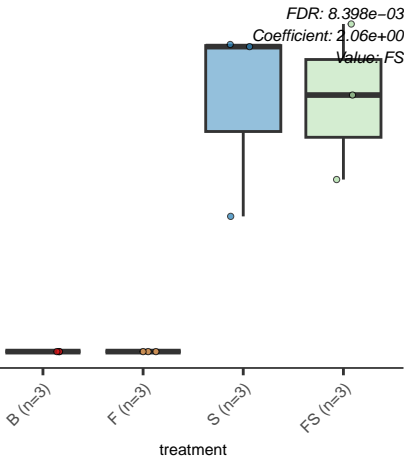




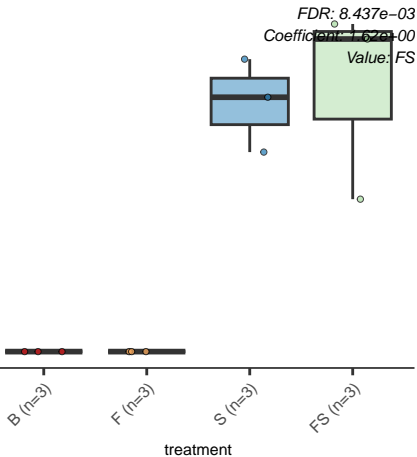




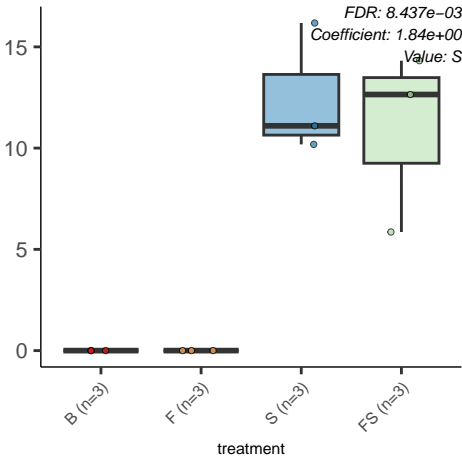
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WY.5103.L.isoleucine.biosynthesis.III.g\_\_Streptococcus.s\_\_Streptococcus

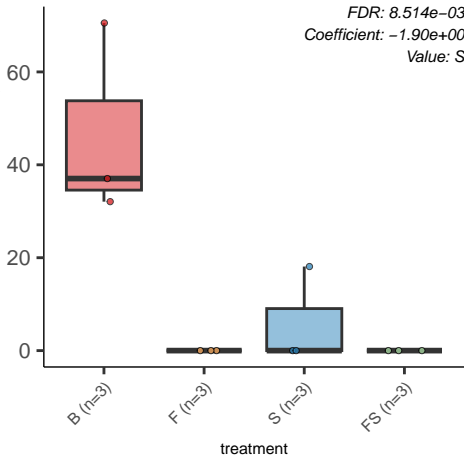


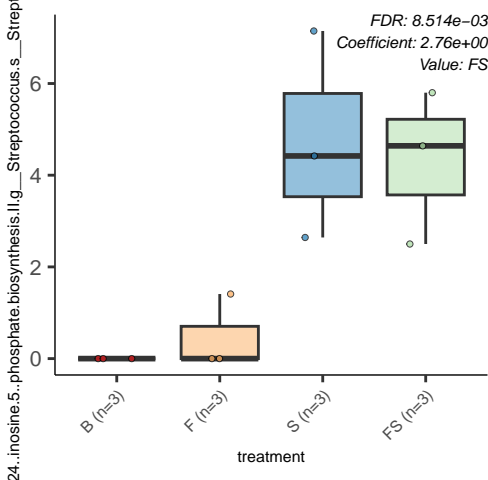
pyruvate.fermentation.to.isobutanol..engineered..g\_\_Streptococcus.s

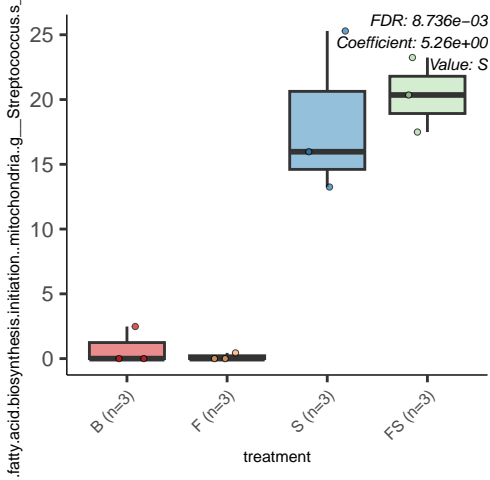


71..palmitate.biosynthesis..type.II.fatty.acid.synthase..g\_\_Escherichia

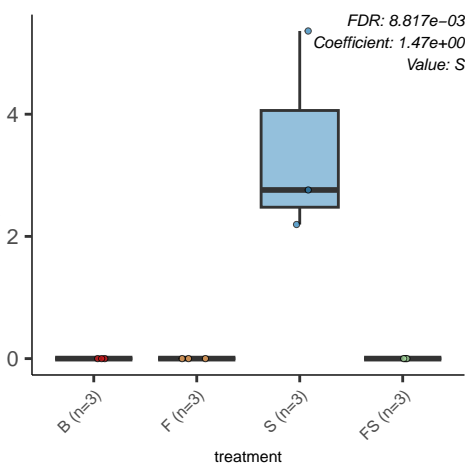
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Coefficient:  $-1.90e+00$   
Value: S



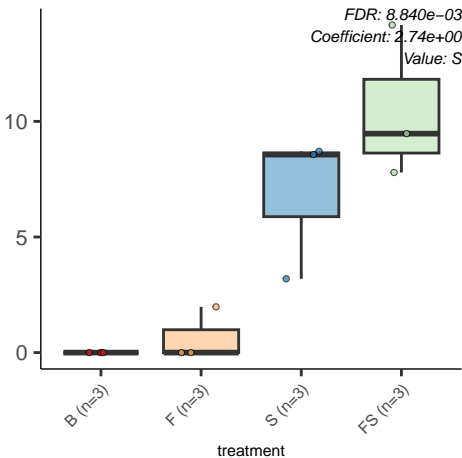




enzyme.A.biosynthesis.II..eukaryotic.g\_\_Lachnospiraceae\_unclassified

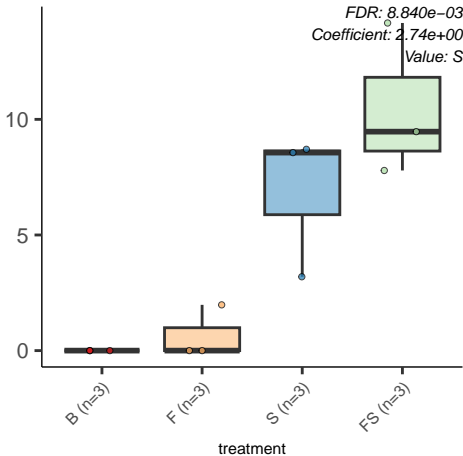


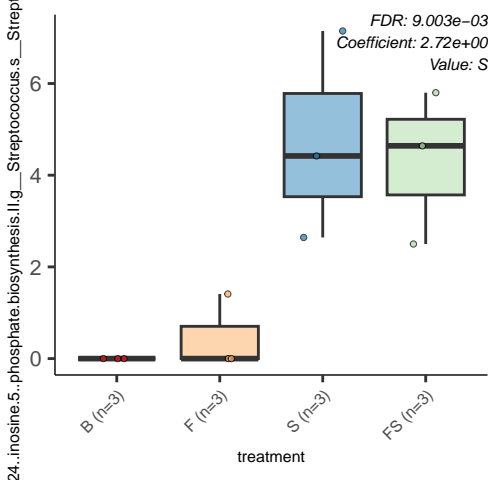
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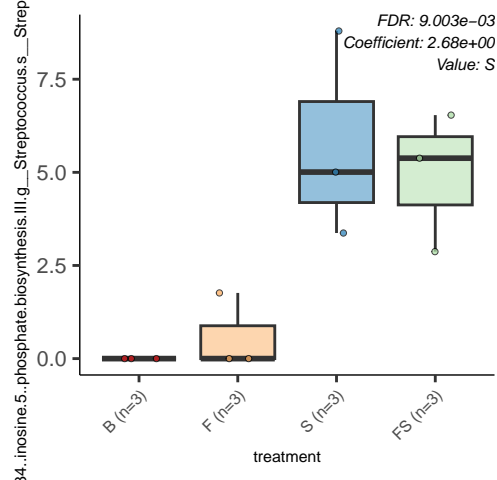


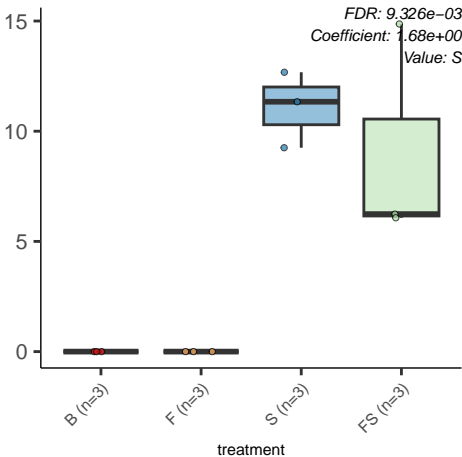


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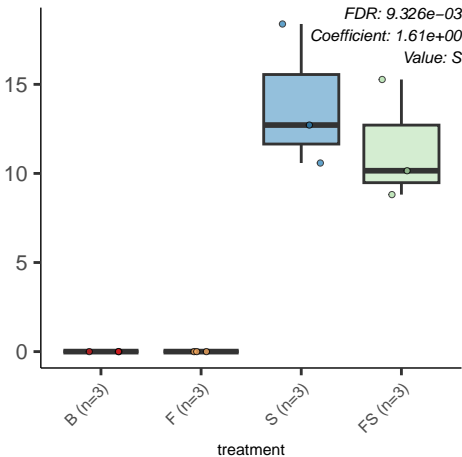






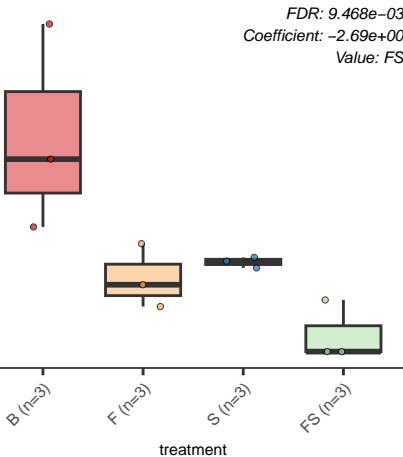


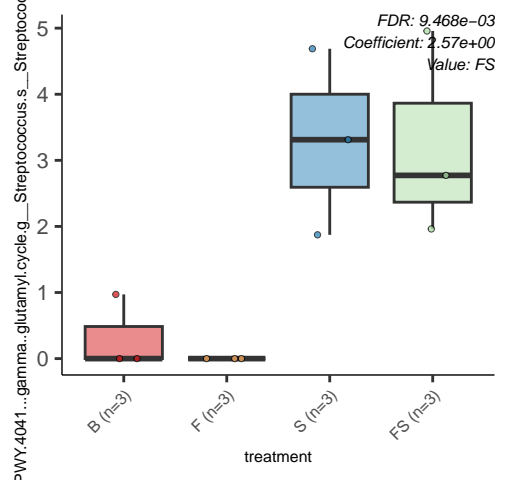
onway.of.adenosine.nucleotides.de.novo.biosynthesis.II.g\_\_Streptococcus



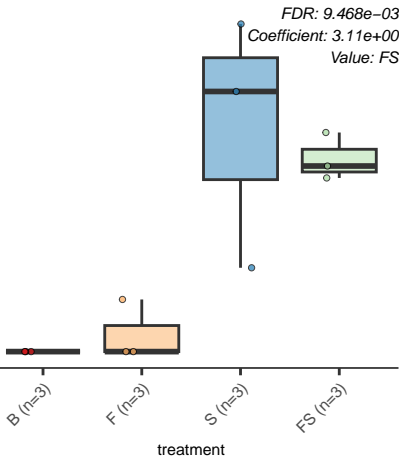
YNTH.PWY..glycogen.biosynthesis.l..from.ADP.D.Glucose.g\_Esch

FDR:  $9.468e-03$   
Coefficient:  $-2.69e+00$   
Value: FS



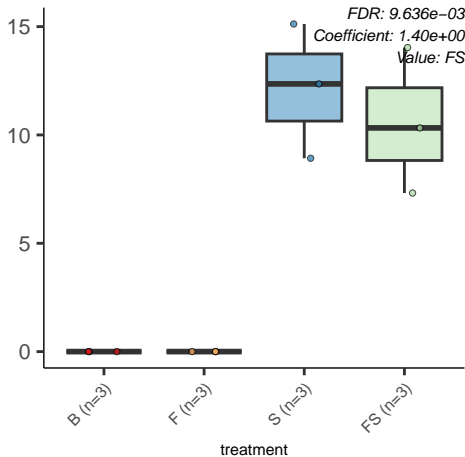


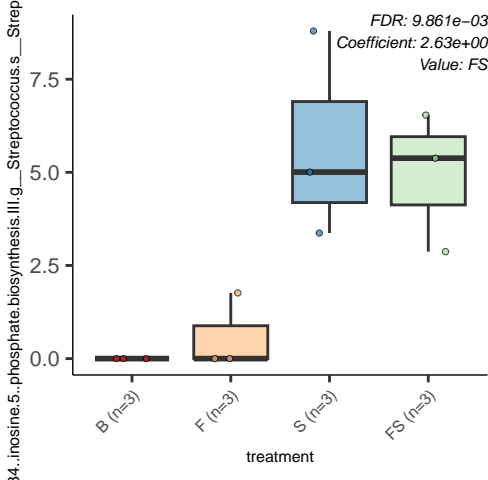
LSYN.PWY..L.valine.biosynthesis.g\_\_Streptococcus.s\_\_Streptococcus



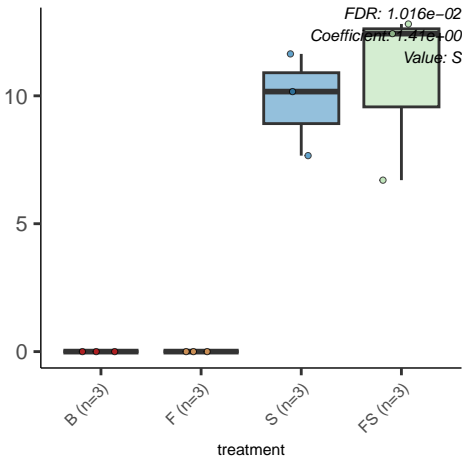


PWY..superpathway.of.branched.chain.amino.acid.biosynthesis.g\_\_S

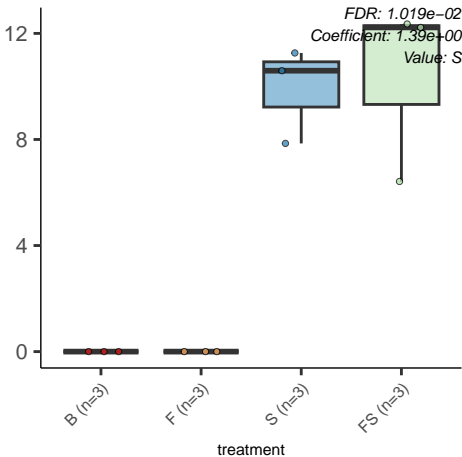




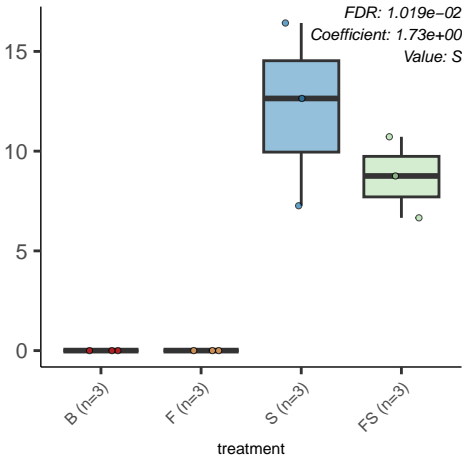
.PWY..superpathway.of.branched.chain.amino.acid.biosynthesis.g



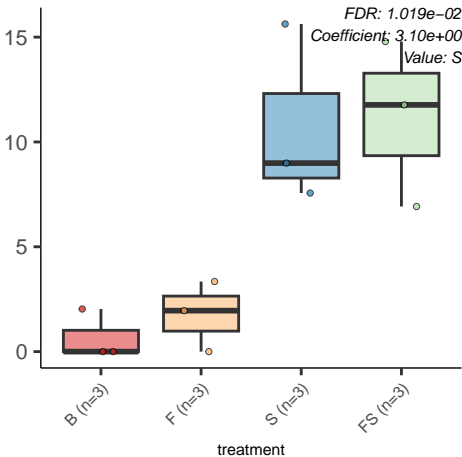
WY.L.isoleucine.biosynthesis.l.from.threonine.g\_\_Streptococcus.s



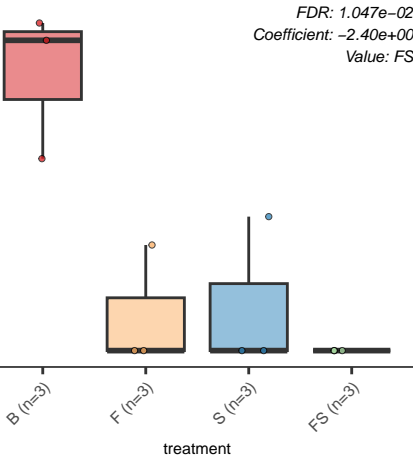
Imuramoyl.pentapeptide.biosynthesis.II..lysine.containing..g\_\_Strept



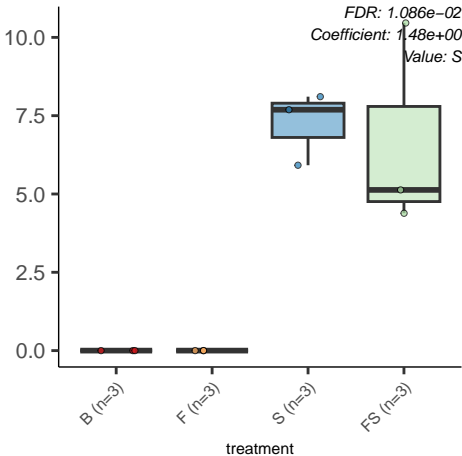
PWY.822..fructan.biosynthesis.g\_\_Streptococcus.s\_\_Streptococcus



CARNMET.PWY..L.carnitine.degradation.l.g\_\_Klebsiella.s\_\_Klebsiella

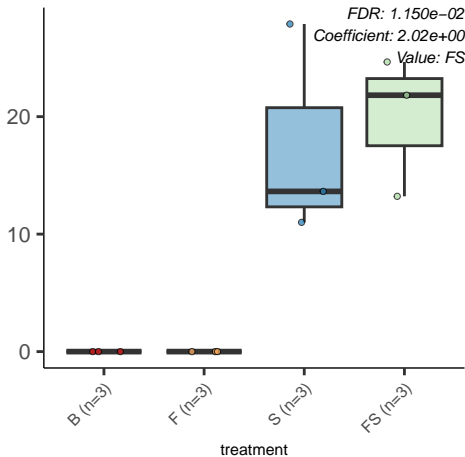


oyl.pentapeptide.biosynthesis.l..meso.diaminopimelate.containing..g

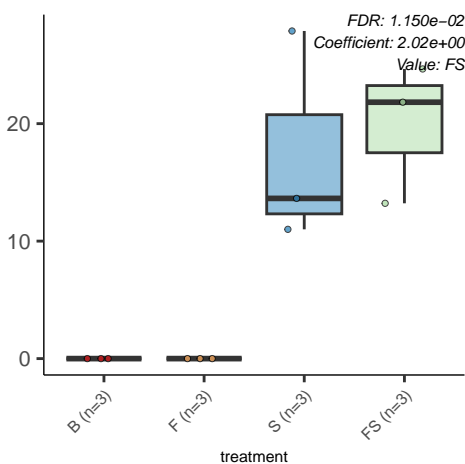


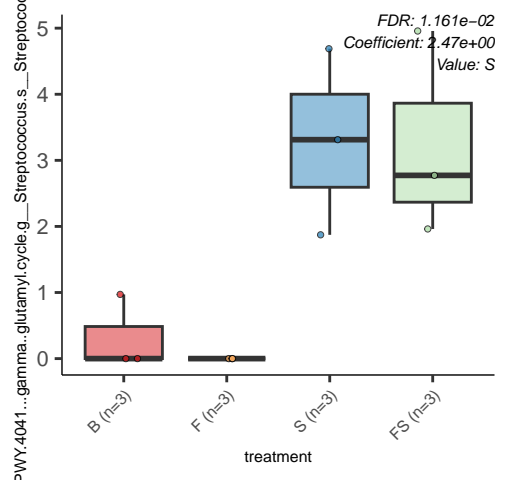


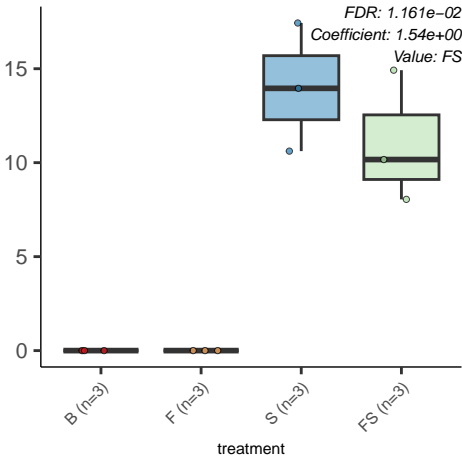
osine.deoxyribonucleotides.de.novo.biosynthesis.II.g\_\_Streptococcus

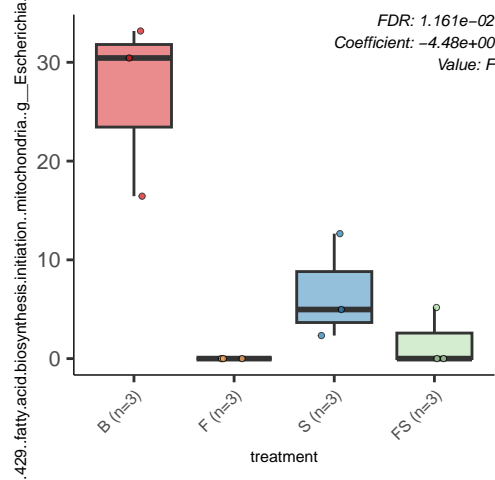


osine.deoxyribonucleotides.de.novo.biosynthesis.ll.g\_\_Streptococcus

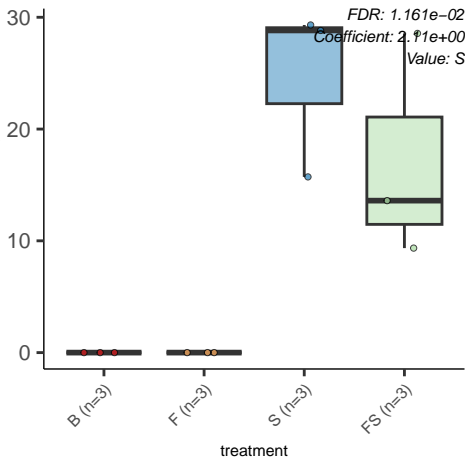


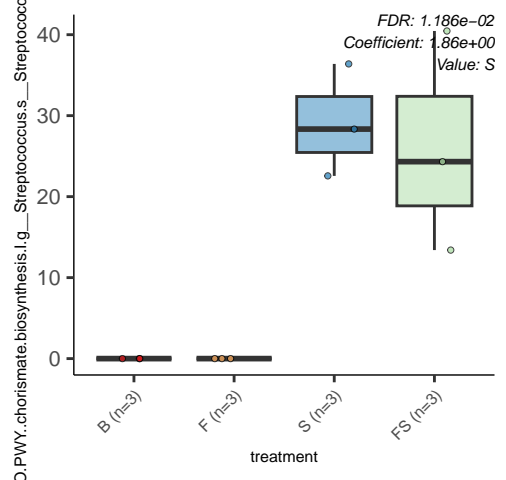




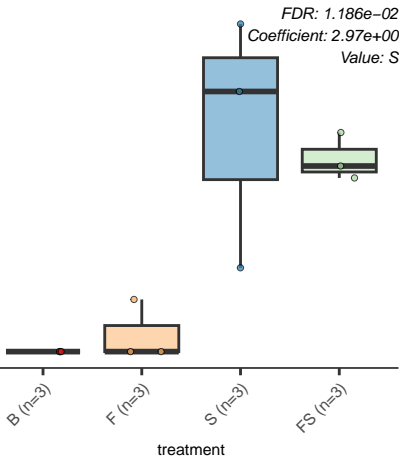


WY..superpathway.of.L.threonine.biosynthesis.g\_\_Streptococcus.s





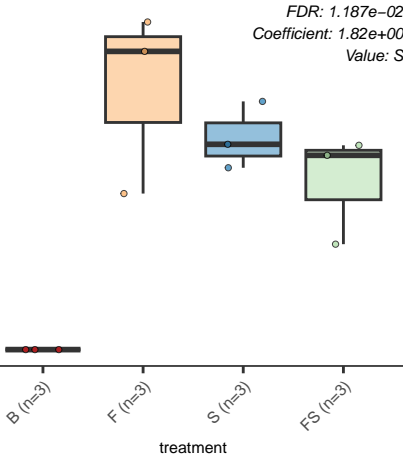
LSYN.PWY..L.valine.biosynthesis.g\_\_Streptococcus.s\_\_Streptococcus



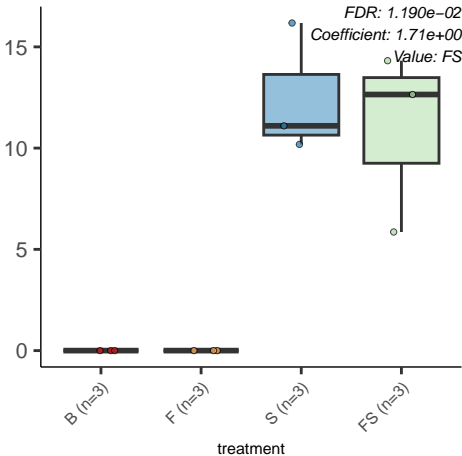


PWY1ZNC.1..assimilatory.sulfate.reduction.IV.unclassified

FDR: 1.187e-02  
Coefficient: 1.82e+00  
Value: S

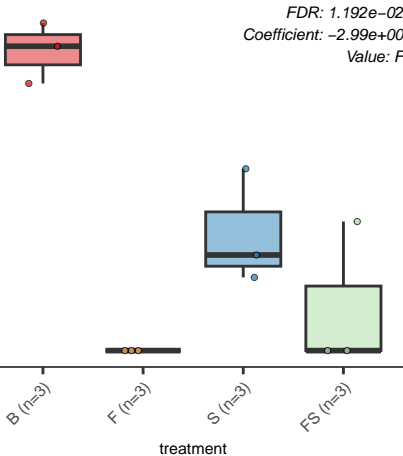


pyruvate.fermentation.to.isobutanol..engineered..g\_\_Streptococcus.s

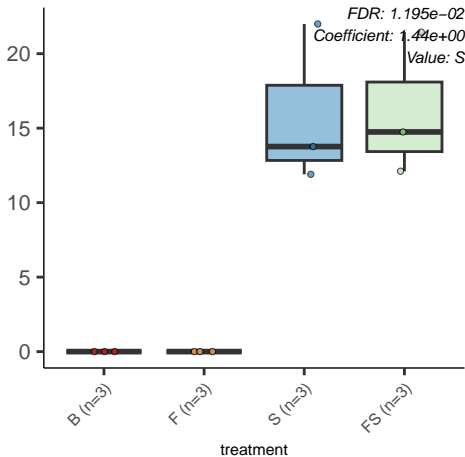


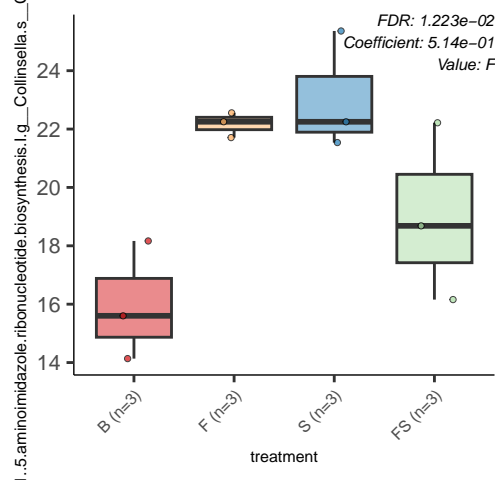
PWY5367..petroselinate.biosynthesis.g\_\_Escherichia.s\_\_Esche

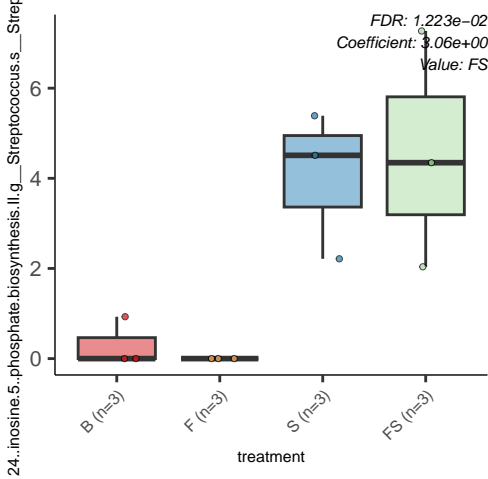
*FDR: 1.192e-02*  
*Coefficient: -2.99e+00*  
*Value: F*



onway.of.guanosine.nucleotides.de.novo.biosynthesis.II.g\_\_Streptococcus

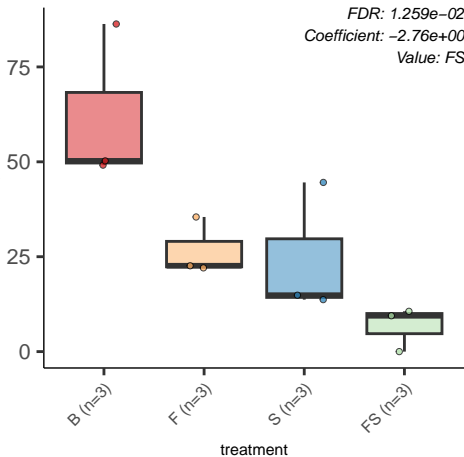


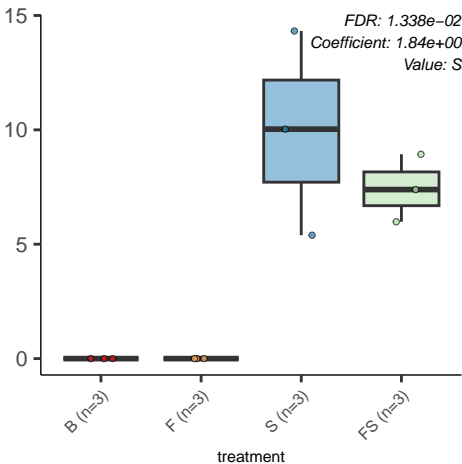




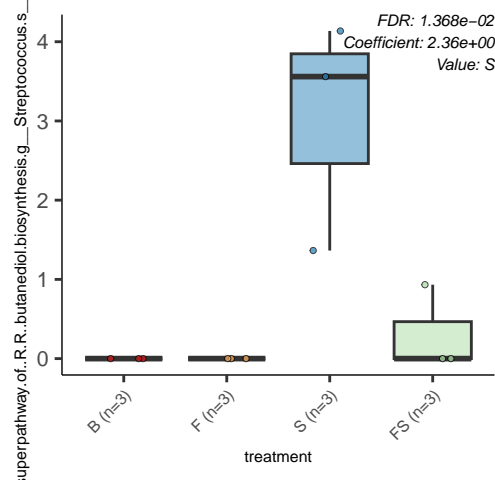
PWY0.1477..ethanolamine.utilization.g\_Escherichia.s\_Escher

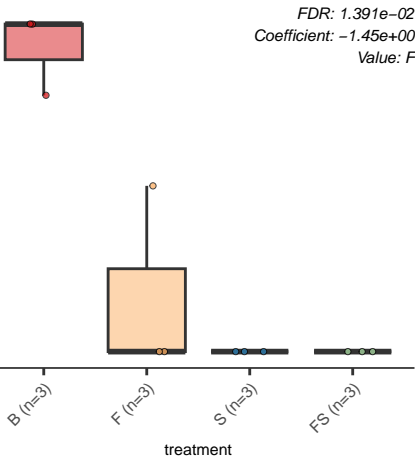
FDR: 1.259e-02  
Coefficient: -2.76e+00  
Value: FS



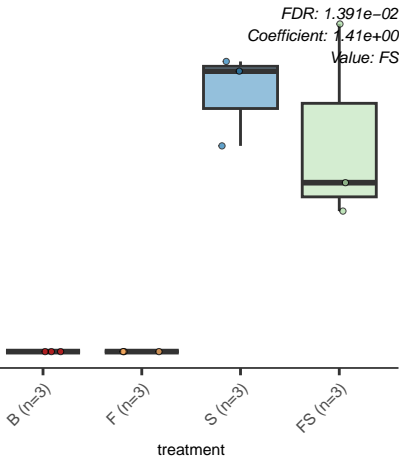




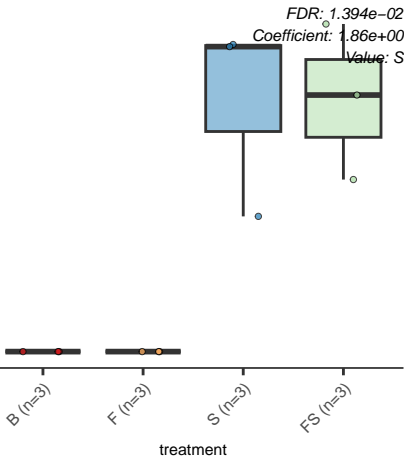




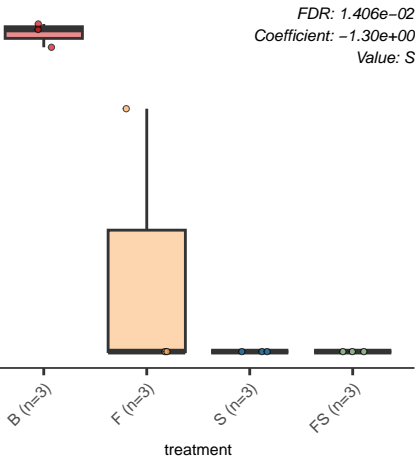
ylmuramoyl.pentapeptide.biosynthesis.II..lysine.containing..g\_\_Strep



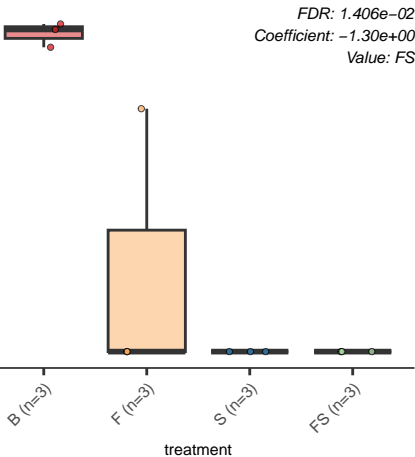
PWY.6703..preQ0.biosynthesis.g\_\_Streptococcus.s\_\_Streptococcus



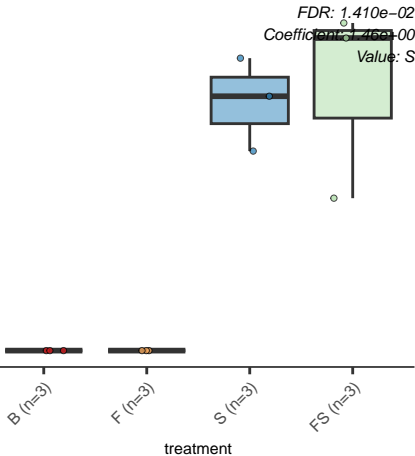
RABCATK12.PWY..D.arabinose.degradation.l.g\_\_Klebsiella.s\_\_Kle



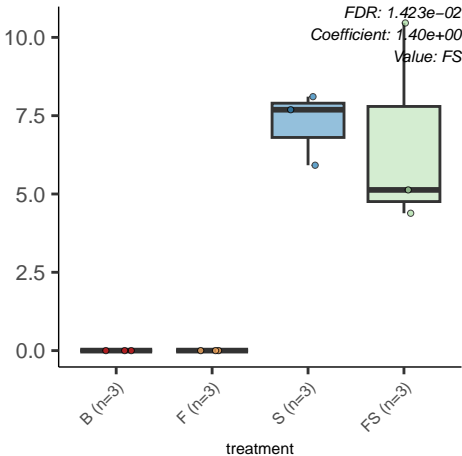
RABCATK12.PWY..D.arabinose.degradation.l.g\_Klebsiella.s\_Kle



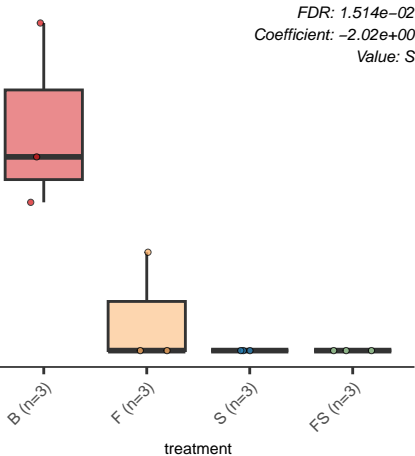
WY.5103.L.isoleucine.biosynthesis.III.g\_\_Streptococcus.s\_\_Streptococcus



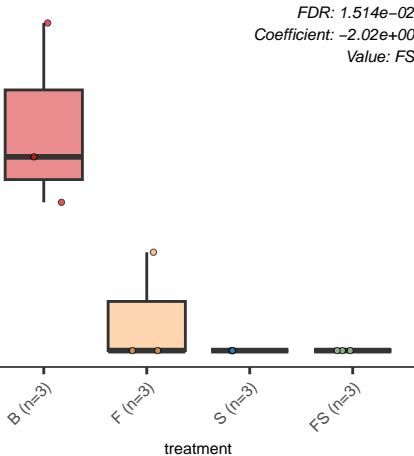
oyl.pentapeptide.biosynthesis.l..meso.diaminopimelate.containing..g

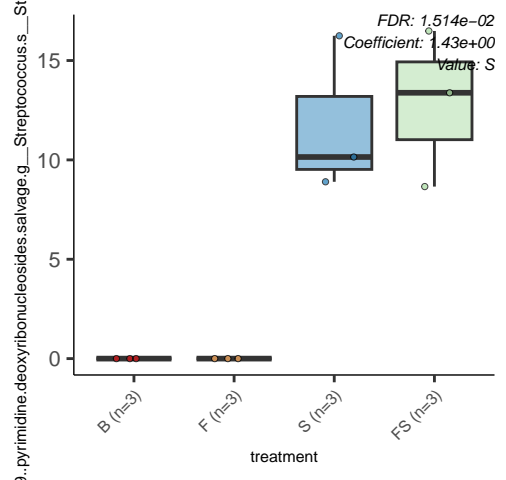




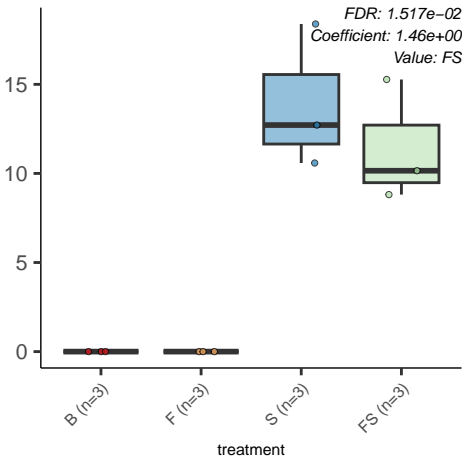


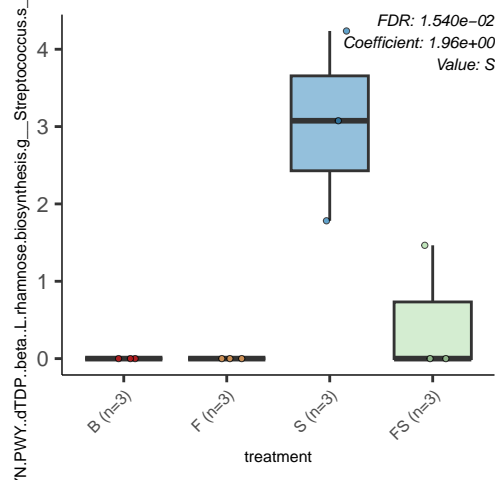
EG.PWY..superpathway.of.glycol.metabolism.and.degradation.g\_E



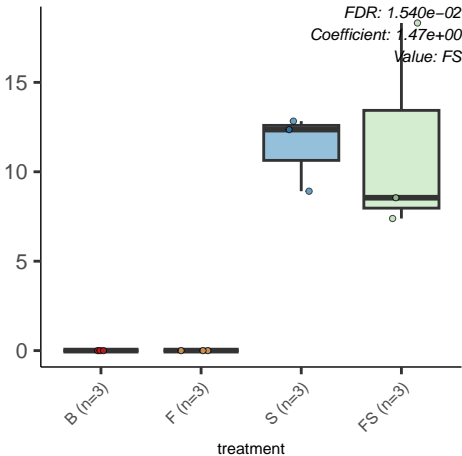


onway.of.adenosine.nucleotides.de.novo.biosynthesis.ll.g\_\_Streptococ

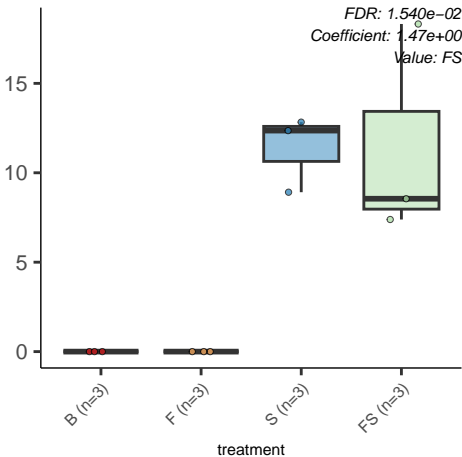




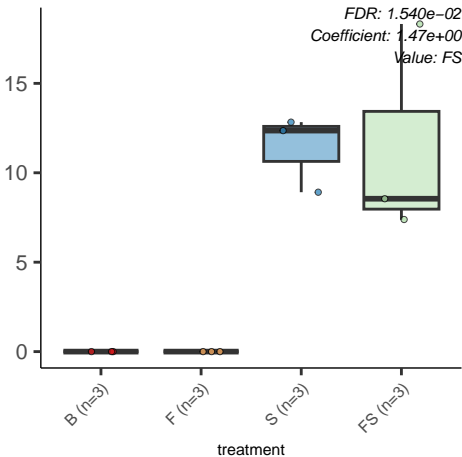
PWY.5686..UMP.biosynthesis.l.g\_\_Streptococcus.s\_\_Streptococcus



PWY.7790..UMP.biosynthesis.ll.g\_\_Streptococcus.s\_\_Streptococcus

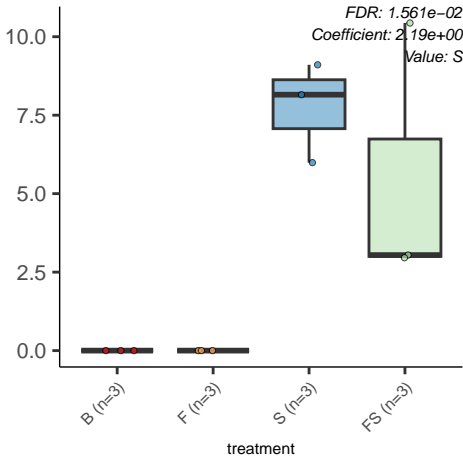


PWY.7791..UMP.biosynthesis.III.g\_\_Streptococcus.s\_\_Streptococcus

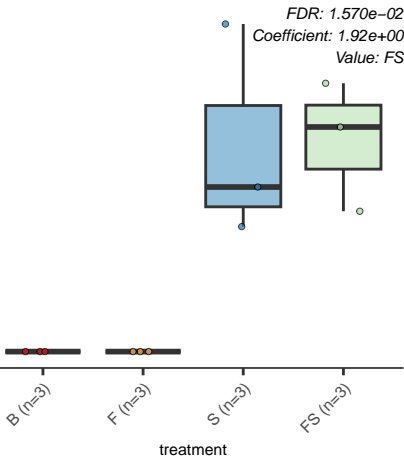




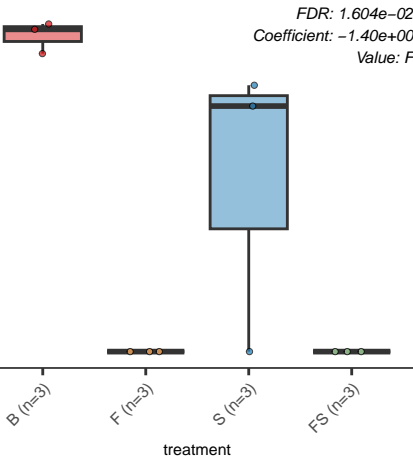
6700..queuosine.biosynthesis.l..de.novo..g\_\_Streptococcus.s\_\_Strept



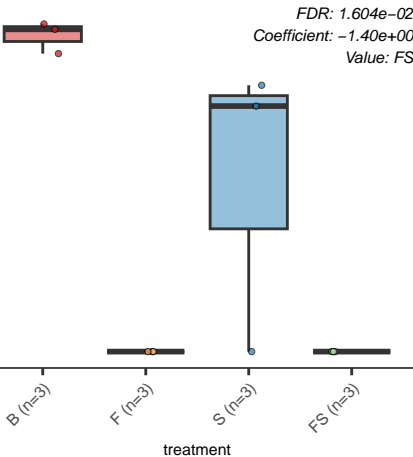
perpathway.of.pyrimidine.nucleobases.salvage.g\_\_Streptococcus.s.



P108.PWY..pyruvate.fermentation.to.propanoate.l.unclassified

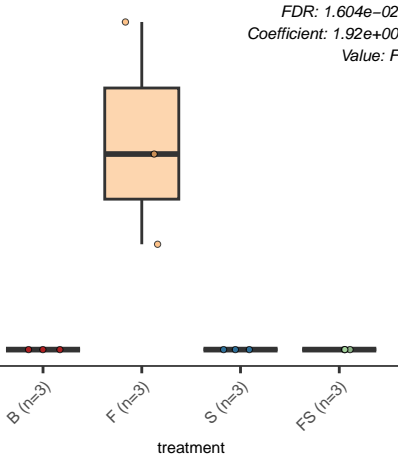


P108.PWY..pyruvate.to.propanoate.l.unclassified



denosine.deoxyribonucleotides.de.novo.biosynthesis.II.g\_\_Bacteroid

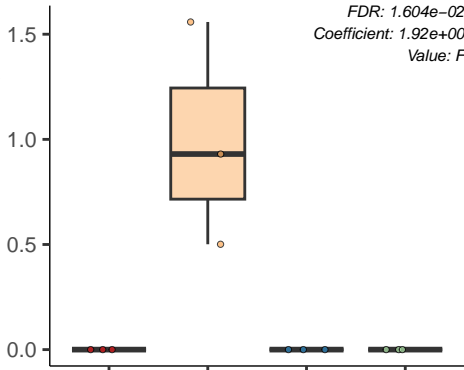
*FDR: 1.604e-02*  
*Coefficient: 1.92e+00*  
*Value: F*



FS (n=3)

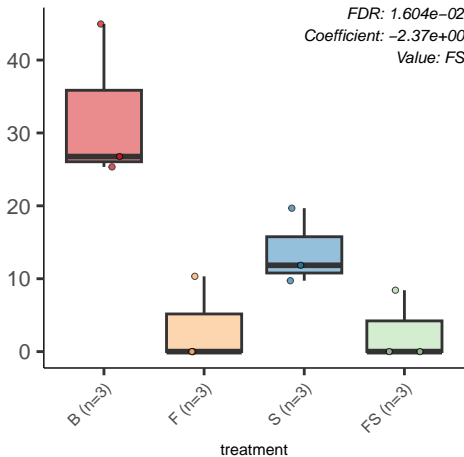
treatment

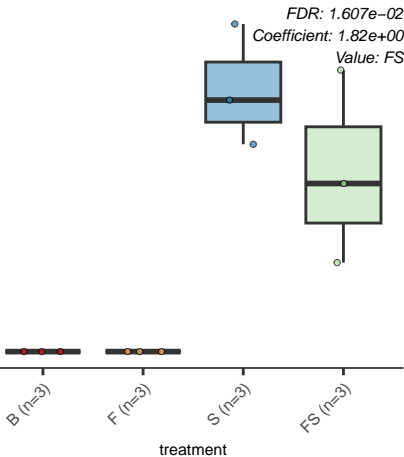
FDR: 1.604e-02  
Coefficient: 1.92e+00  
Value: F



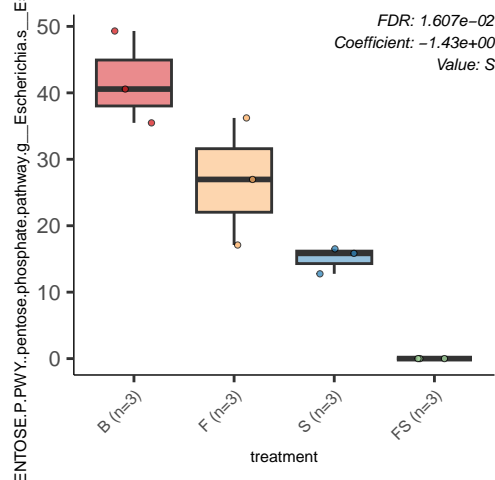
7400..L.arginine.biosynthesis.IV..archaeobacteria..g\_Escherichia.s

FDR: 1.604e-02  
Coefficient: -2.37e+00  
Value: FS



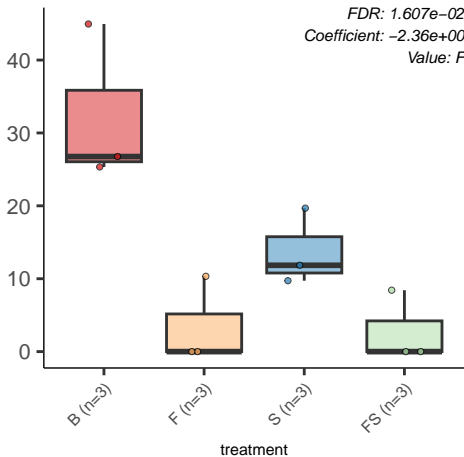


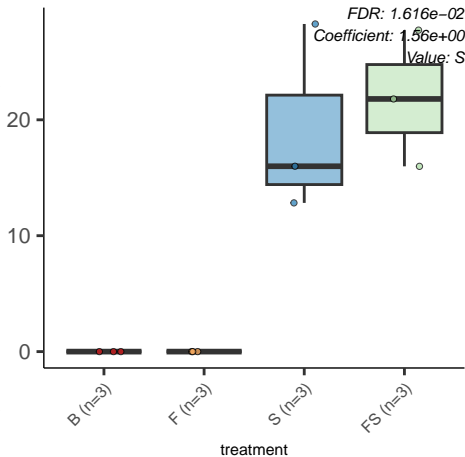


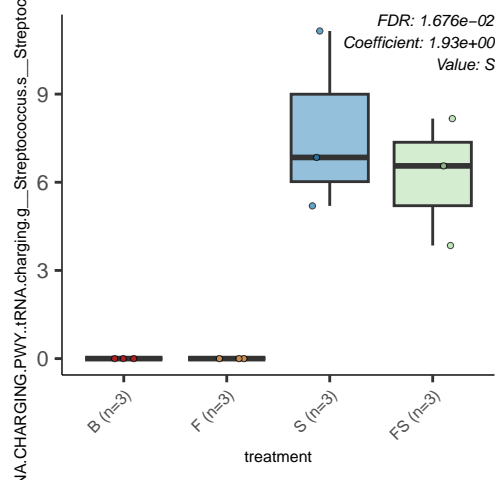


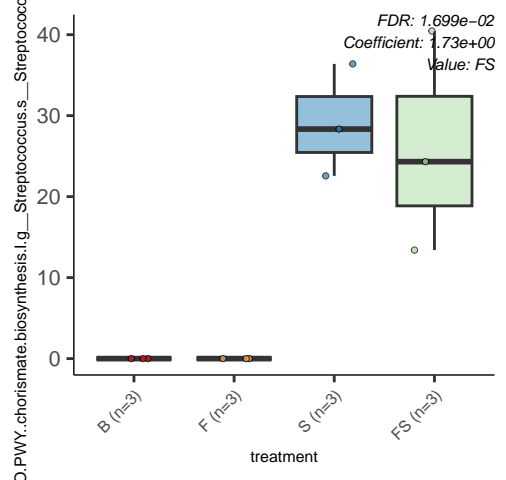
7400..L.arginine.biosynthesis.IV..archaeobacteria..g\_Escherichia.s

FDR: 1.607e-02  
Coefficient: -2.36e+00  
Value: F

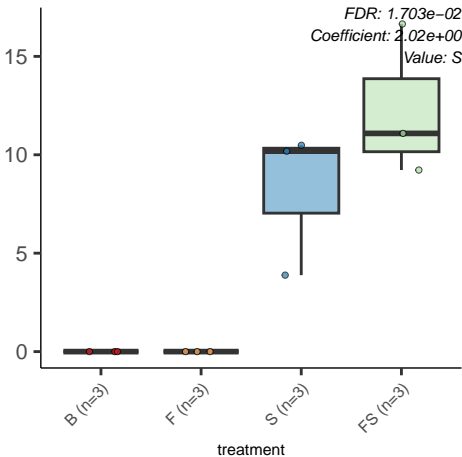






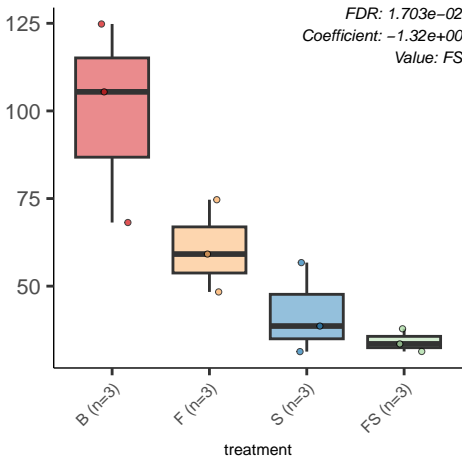


5.aminoimidazole.ribonucleotide.biosynthesis.l.g\_\_Streptococcus.s

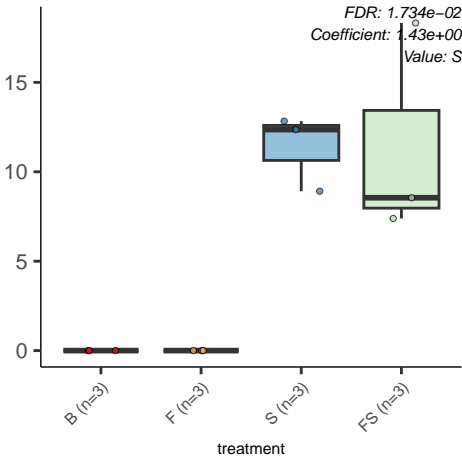


peptidoglycan.maturation...meso.diaminopimelate.containing..g\_\_Esch

FDR:  $1.703e-02$   
Coefficient:  $-1.32e+00$   
Value: FS

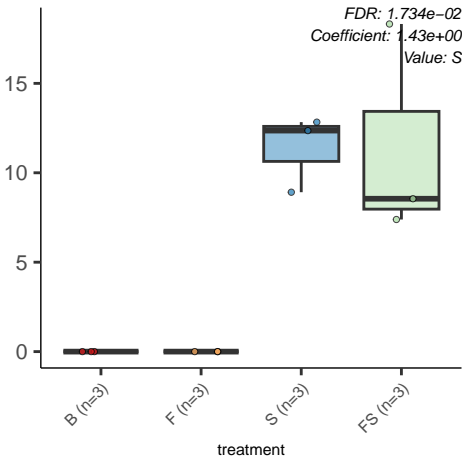


PWY.5686..UMP.biosynthesis.l.g\_\_Streptococcus.s\_\_Streptococcus

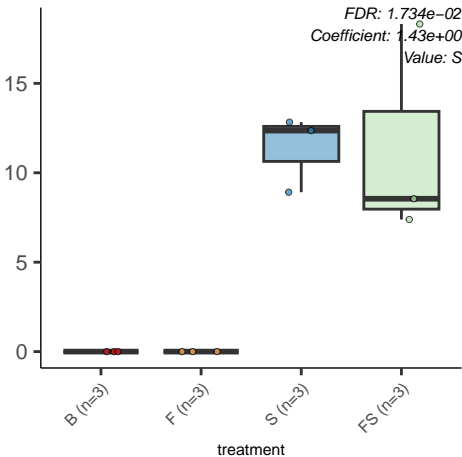


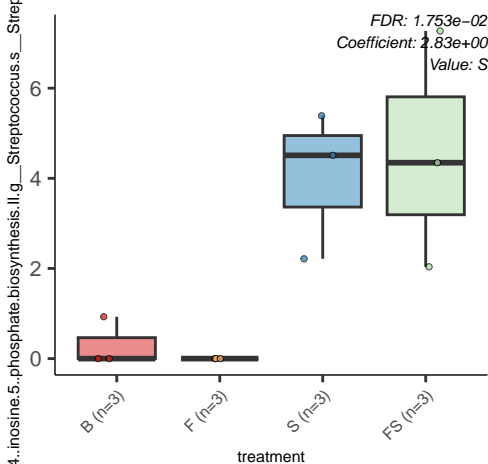


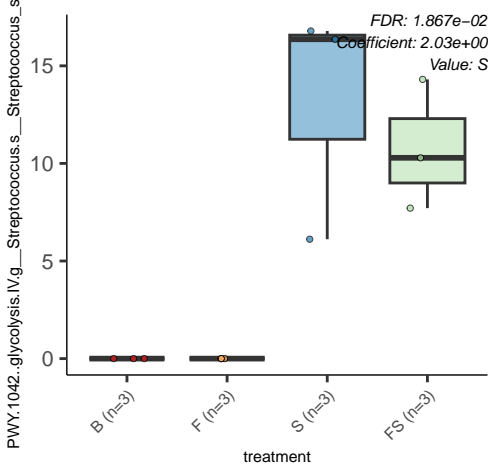
PWY.7790..UMP.biosynthesis.ll.g\_\_Streptococcus.s\_\_Streptococcus



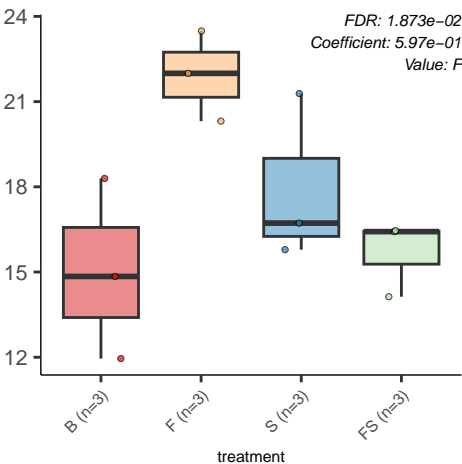
PWY.7791..UMP.biosynthesis.III.g\_\_Streptococcus.s\_\_Streptococcus



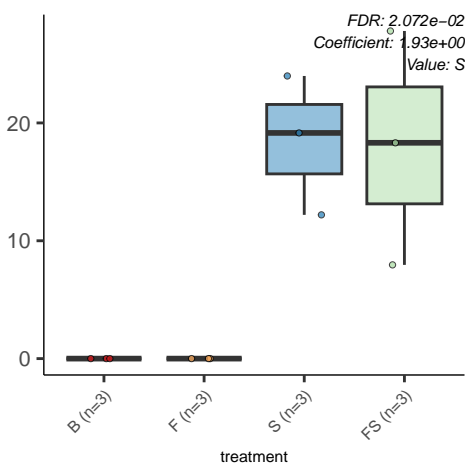


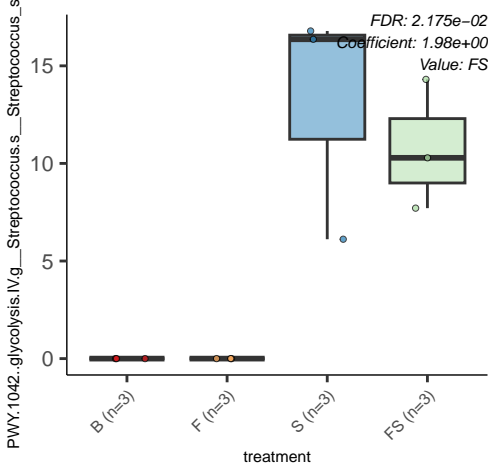


ETANA.PWY..L.methionine.biosynthesis.III.g\_\_Bifidobacterium.s\_\_Bi

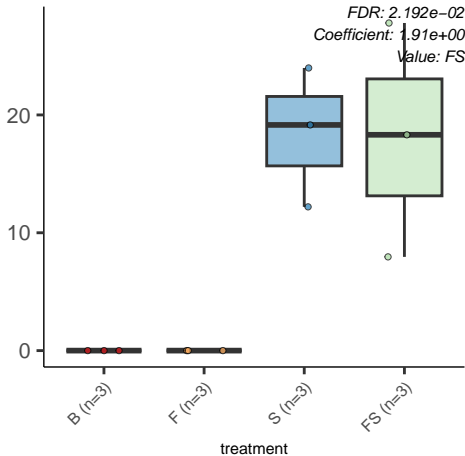


YN.PWY..dTDP..beta..L.rhamnose.biosynthesis.g\_\_Streptococcus.s





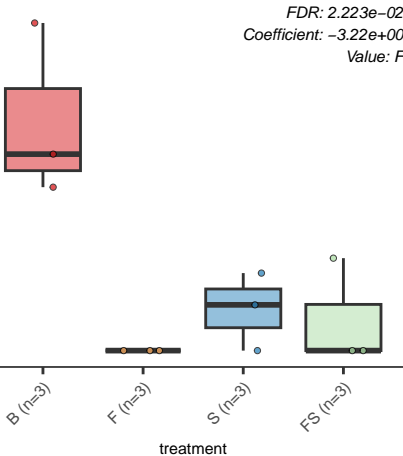
YN.PWY..dTDP..beta..L.rhamnose.biosynthesis.g\_\_Streptococcus.s



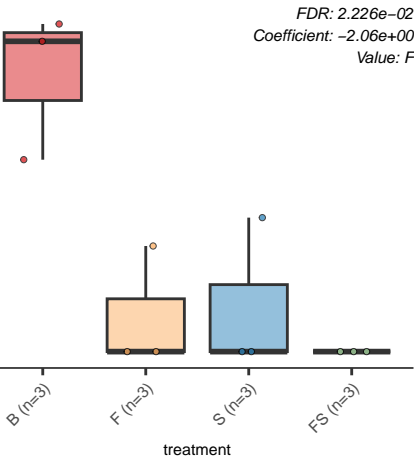


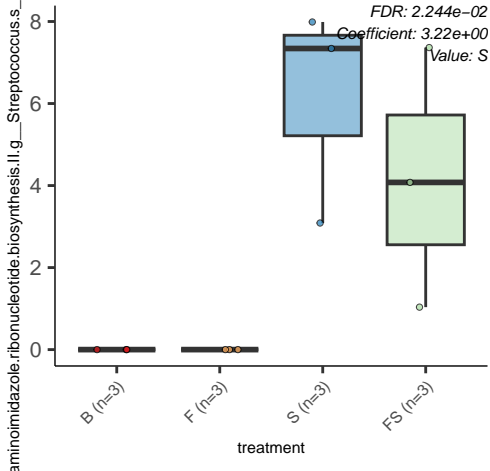
PWY.2942..L.lysine.biosynthesis.Ill.g\_Escherichia.s\_Escherichia

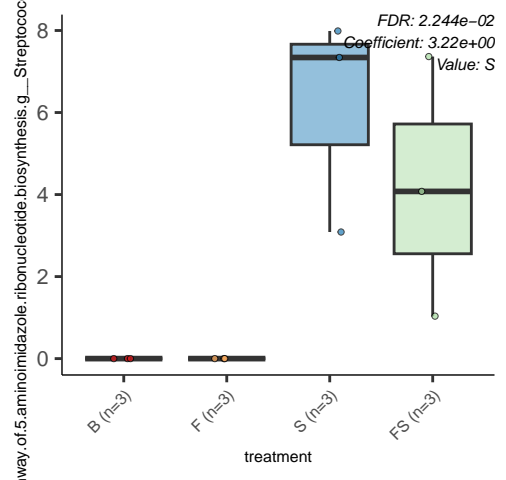
FDR: 2.223e-02  
Coefficient: -3.22e+00  
Value: F

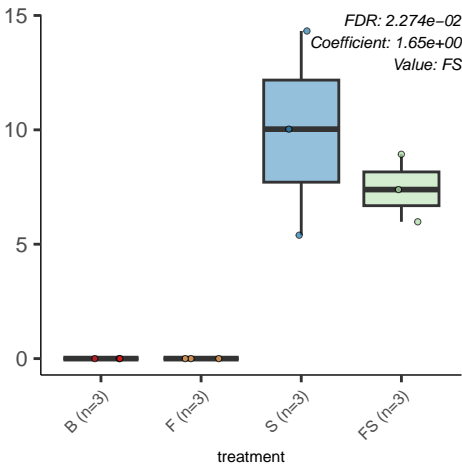


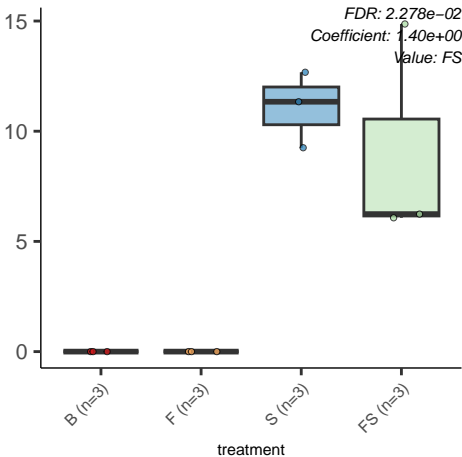
CARNMET.PWY..L.carnitine.degradation.l.g\_\_Klebsiella.s\_\_Klebsiella

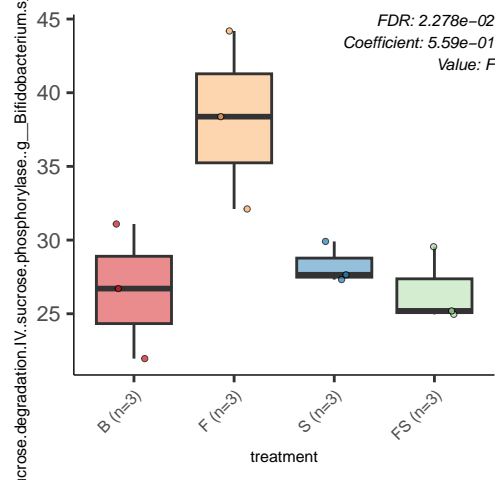




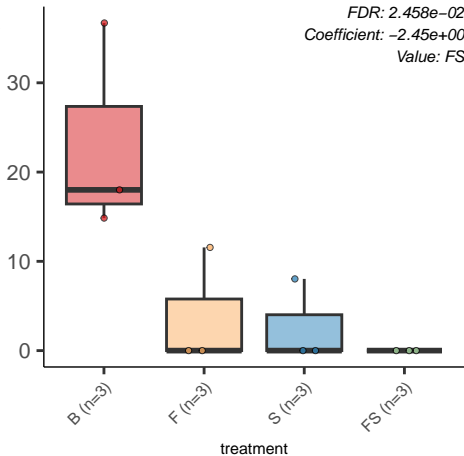








FDR: 2.458e-02  
Coefficient: -2.45e+00  
Value: FS





PWY1ZNC.1..assimilatory.sulfate.reduction.IV.unclassified

FDR: 2.471e-02  
Coefficient: 1.57e+00  
Value: FS

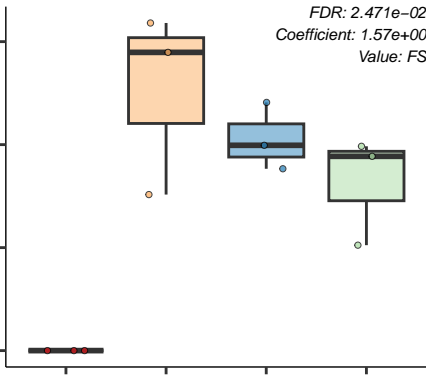
B (n=3)

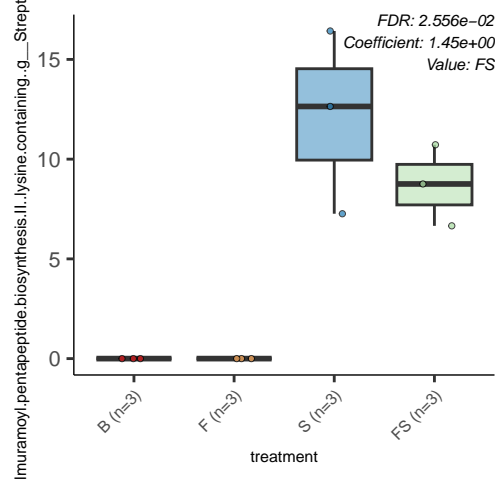
F (n=3)

S (n=3)

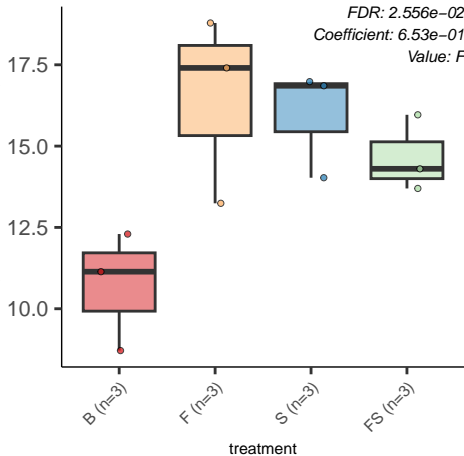
FS (n=3)

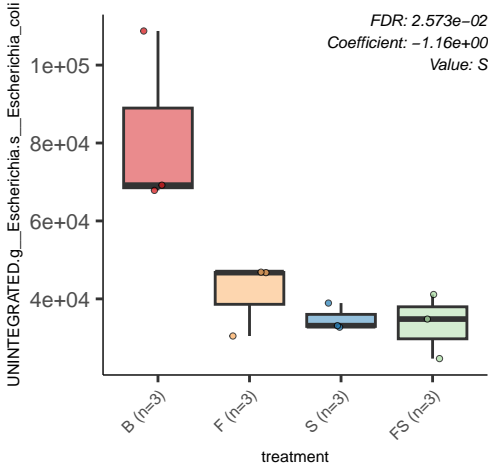
treatment



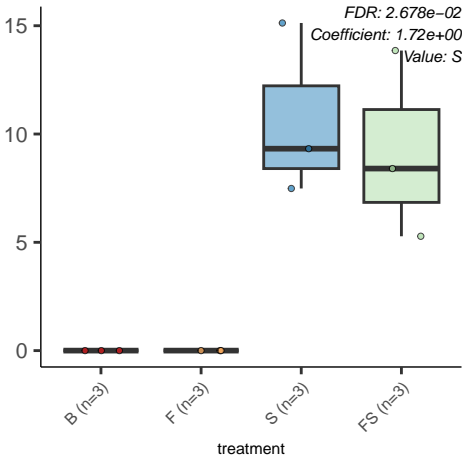


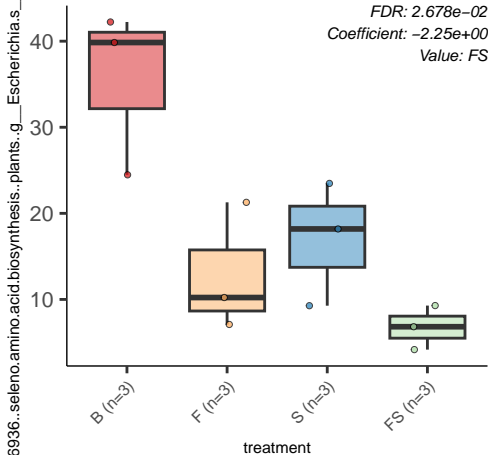
FDR: 2.556e-02  
Coefficient: 6.53e-01  
Value: F

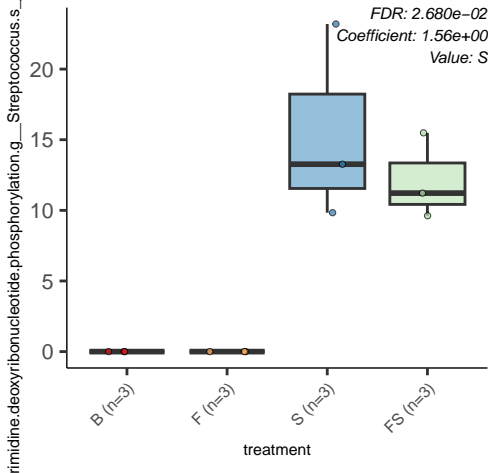


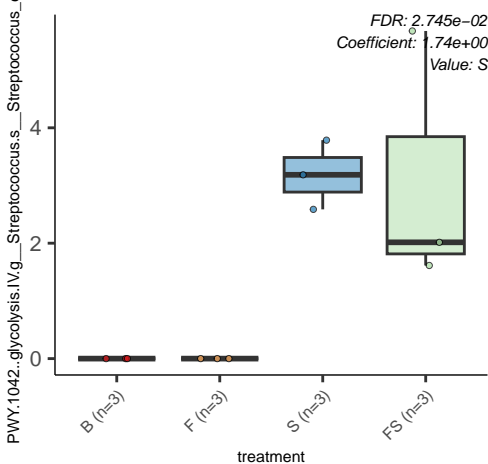


700..queuosine.biosynthesis.l..de.novo.g\_\_Streptococcus.s\_\_Strep

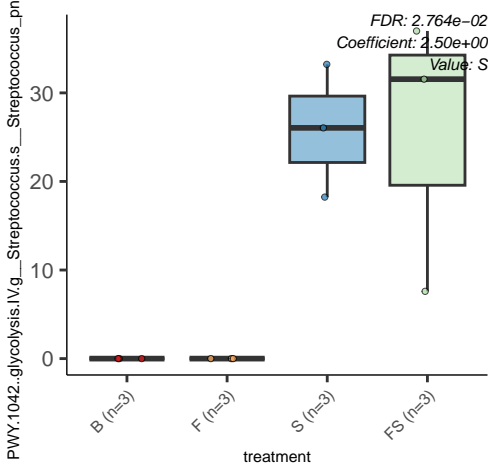




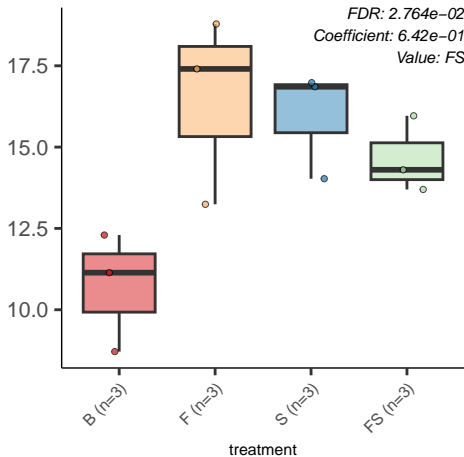




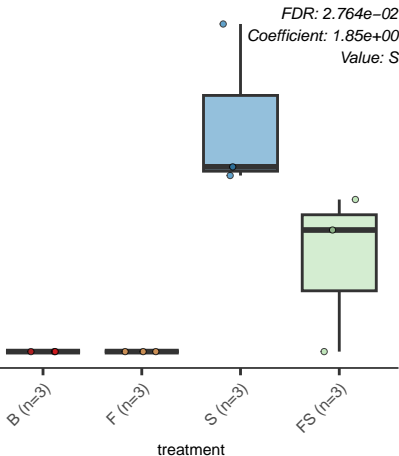




FDR: 2.764e-02  
Coefficient: 6.42e-01  
Value: FS



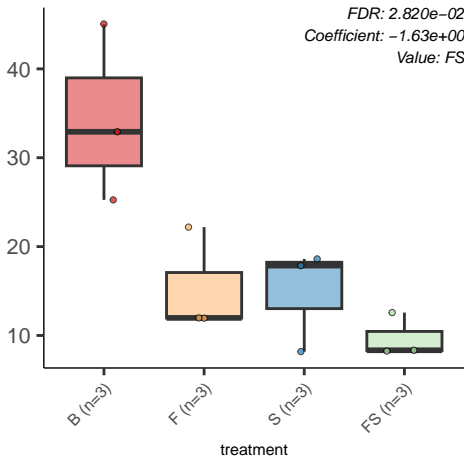
WY..UDP.N.acetyl.D.glucosamine.biosynthesis.l.g\_\_Streptococcus.s





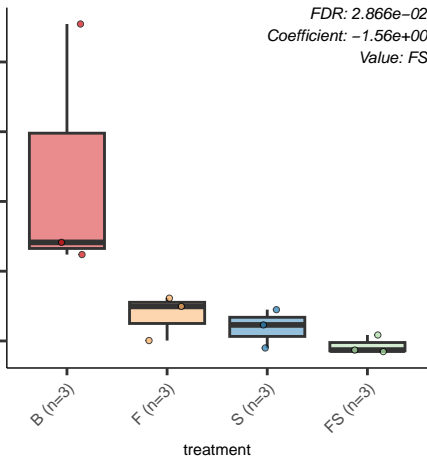
OSER.METSYN.PWY..L.methionine.biosynthesis.l.g\_\_Escherichia.s

*FDR: 2.820e-02*  
*Coefficient: -1.63e+00*  
*Value: FS*

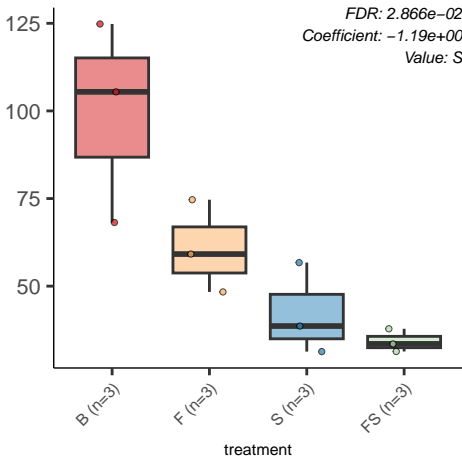


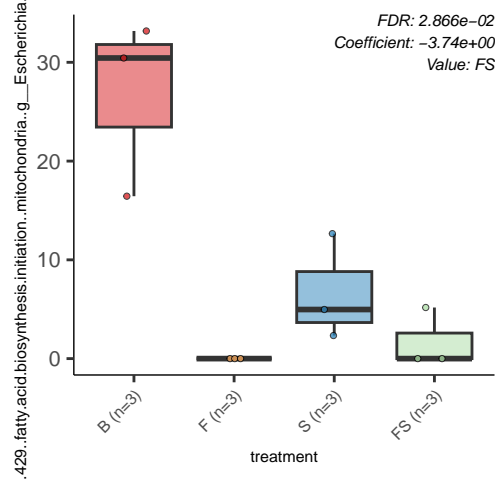
superpathway.of.L.homoserine.and.L.methionine.biosynthesis.g\_Es

FDR: 2.866e-02  
Coefficient: -1.56e+00  
Value: FS



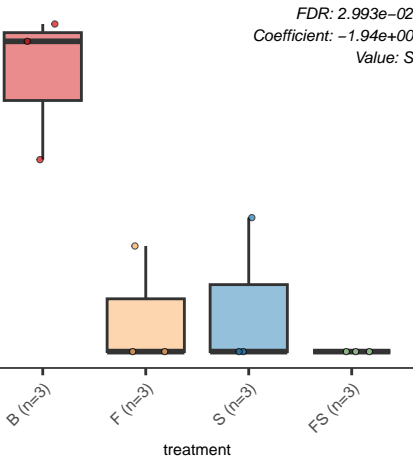
FDR: 2.866e-02  
Coefficient: -1.19e+00  
Value: S



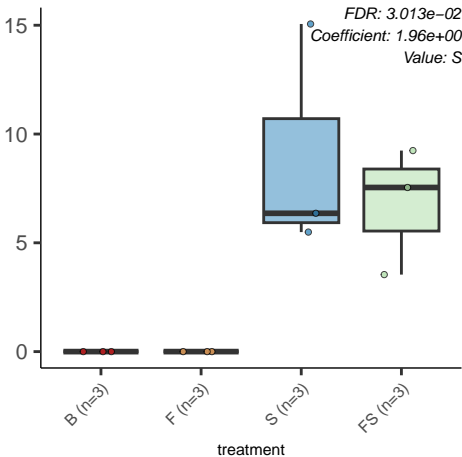


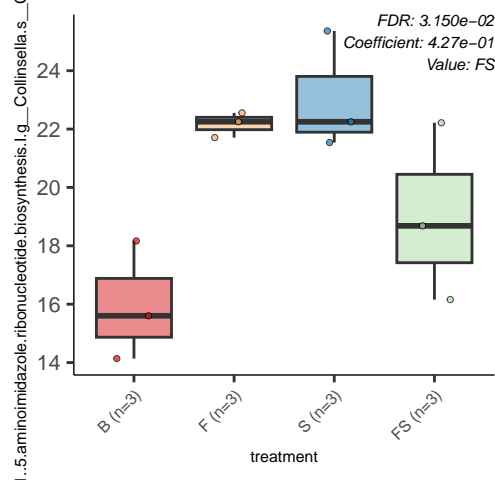


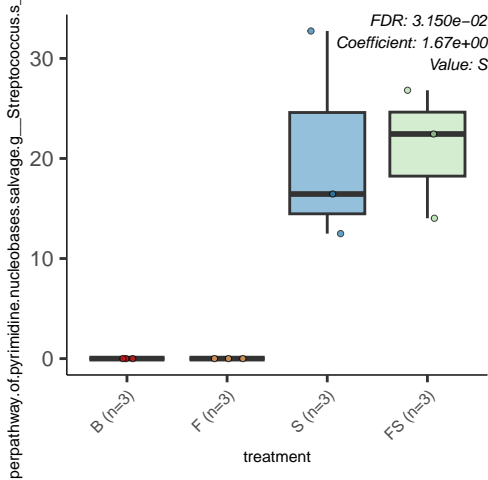
CARNMET.PWY..L.carnitine.degradation.l.g\_\_Klebsiella.s\_\_Klebsiella



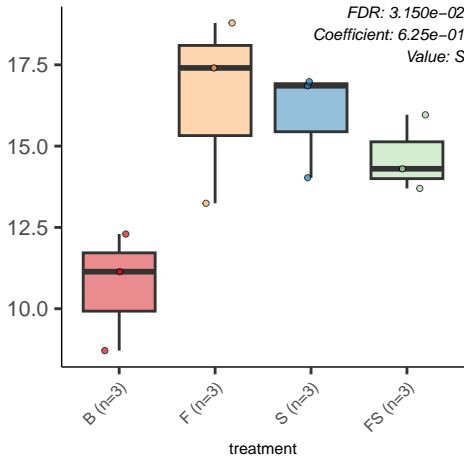
cysteine.biosynthesis.Vl..from.L.methionine..g\_\_Streptococcus.s\_\_S

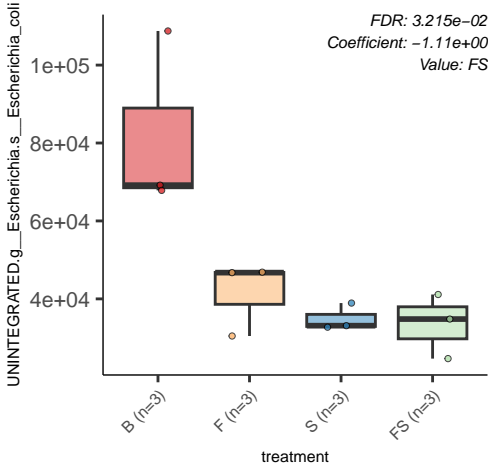




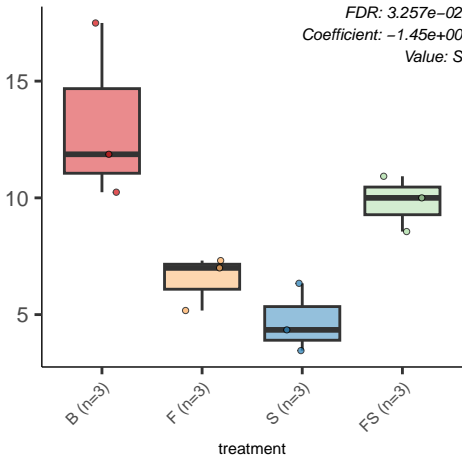


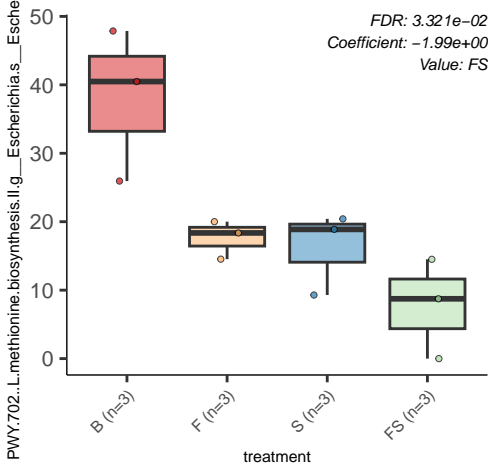
FDR: 3.150e-02  
Coefficient: 6.25e-01  
Value: S





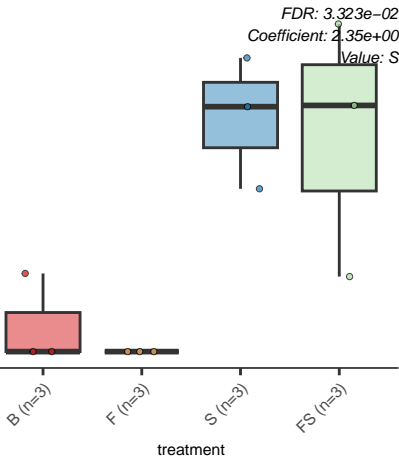
FDR: 3.257e-02  
Coefficient: -1.45e+00  
Value: S



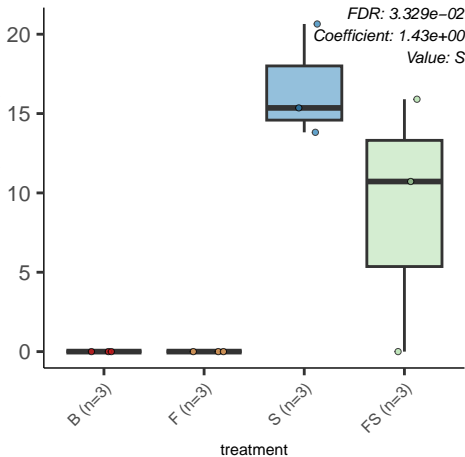




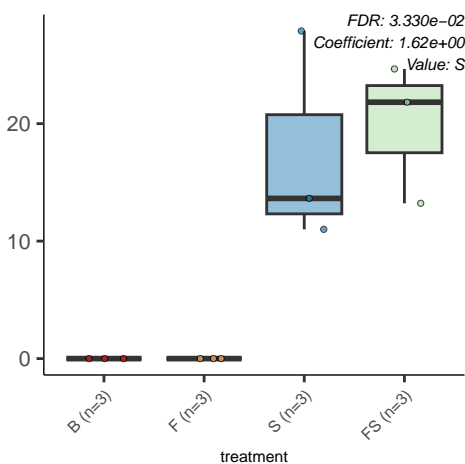
WY.4041...gamma..glutamyl.cycle.g\_\_Streptococcus.s\_\_Streptococcus



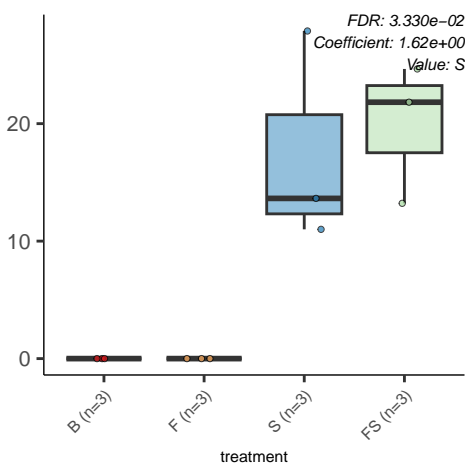
WY.7237..myo...chiro...and.scyllo.inositol.degradation.g\_\_Blautia.s



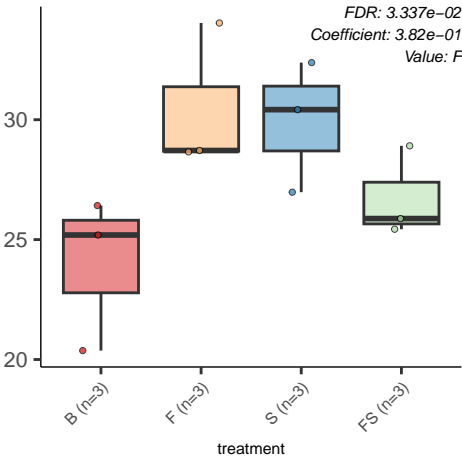
osine.deoxyribonucleotides.de.novo.biosynthesis.ll.g\_\_Streptococcus



osine.deoxyribonucleotides.de.novo.biosynthesis.ll.g\_\_Streptococcus

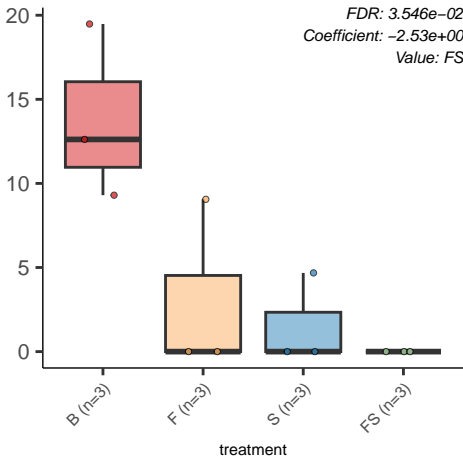


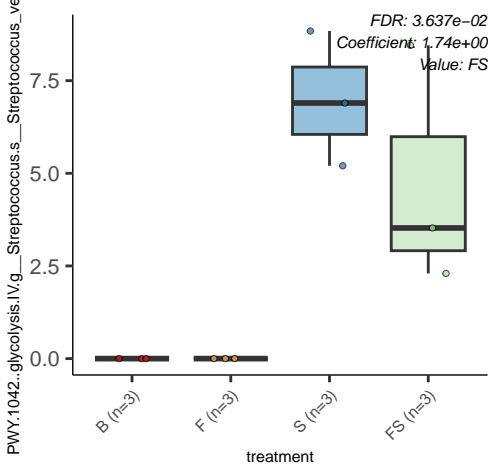
PWY.5941..glycogen.degradation.ll.g\_\_Collinsella.s\_\_Collinsella\_a

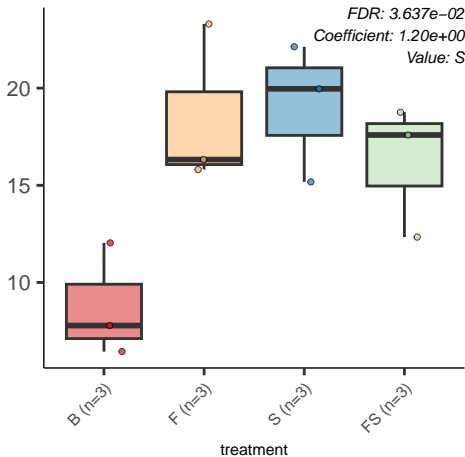


perpathway.of.purine.nucleotides.de.novo.biosynthesis.l.g\_\_Escher

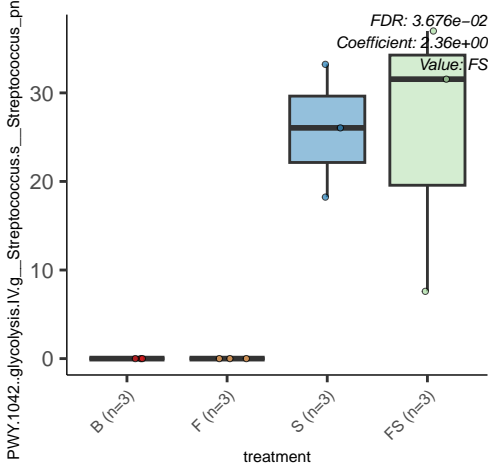
*FDR: 3.546e-02*  
*Coefficient: -2.53e+00*  
*Value: FS*

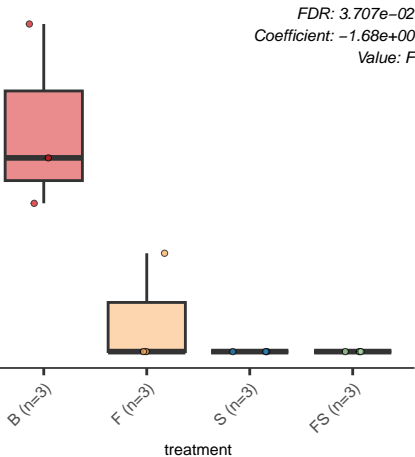




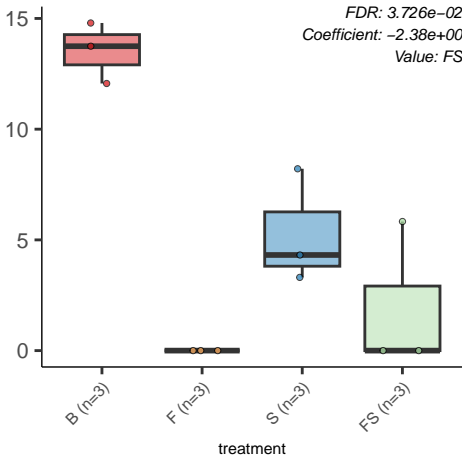


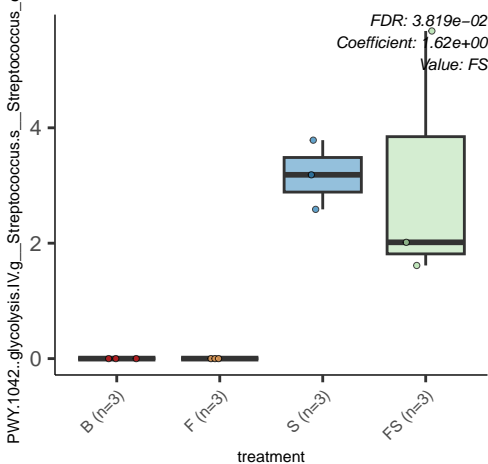




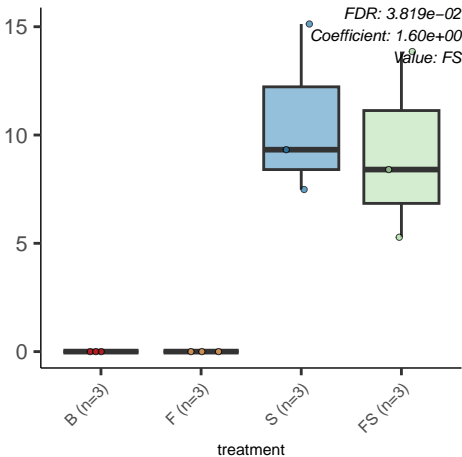


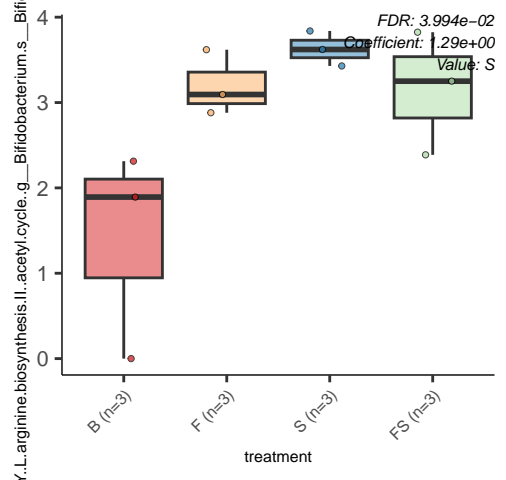
PWY5367..petroselinate.biosynthesis.g\_Escherichia.s\_Esche



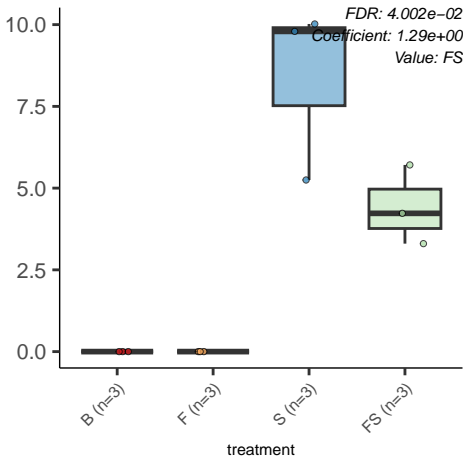


700..queuosine.biosynthesis.l..de.novo.g\_\_Streptococcus.s\_\_Strep

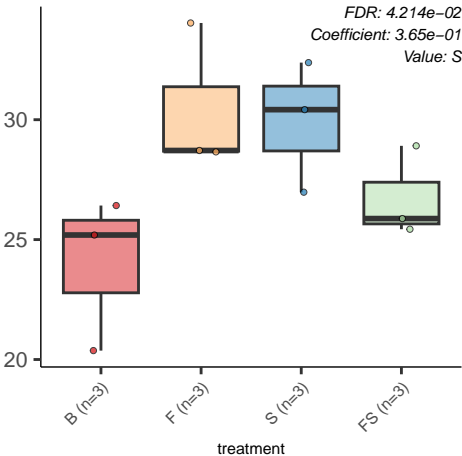




yl.pentapeptide.biosynthesis.III...meso.diaminopimelate.containing...



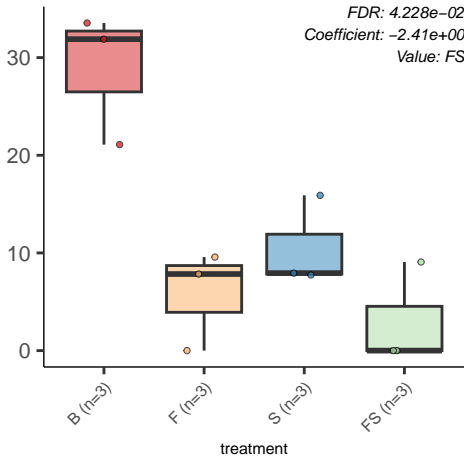
PWY.5941..glycogen.degradation.ll.g\_\_Collinsella.s\_\_Collinsella\_a

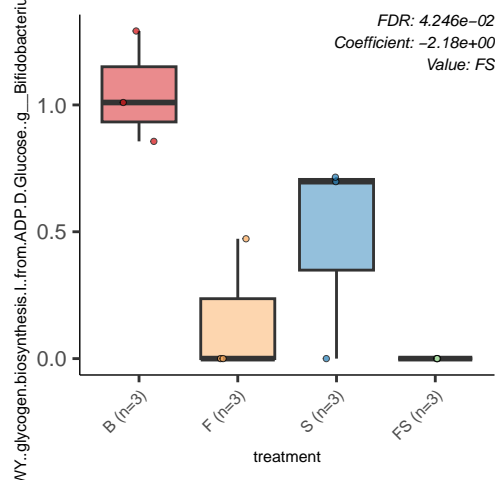




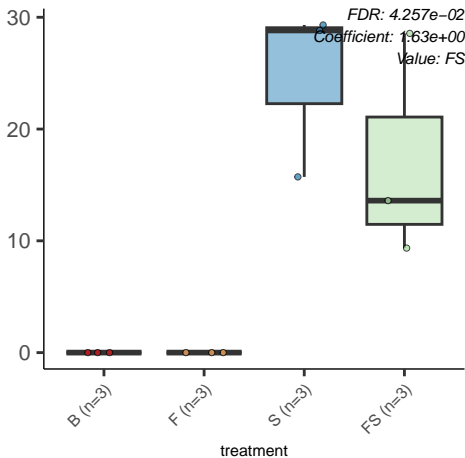
54..L.arginine.biosynthesis.III...via.N.acetyl.L.citrulline..g\_\_Escherichia

FDR: 4.228e-02  
Coefficient: -2.41e+00  
Value: FS

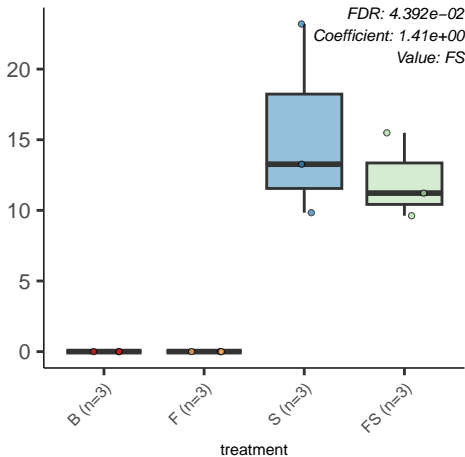




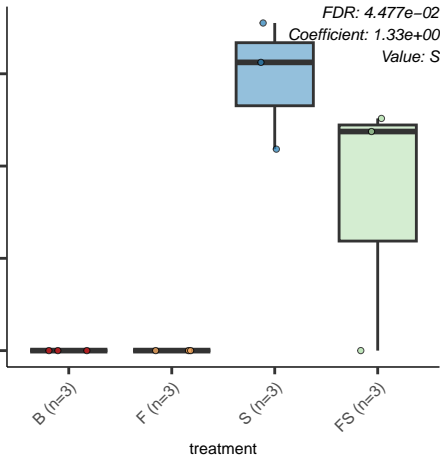
WY..superpathway.of.L.threonine.biosynthesis.g\_\_Streptococcus.s



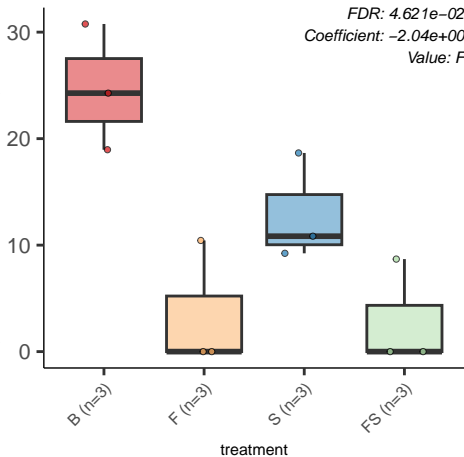
rimidine.deoxyribonucleotide.phosphorylation.g\_\_Streptococcus.s



erpathway.of.coenzyme.A.biosynthesis.Ill...mammals..g\_\_Streptococ

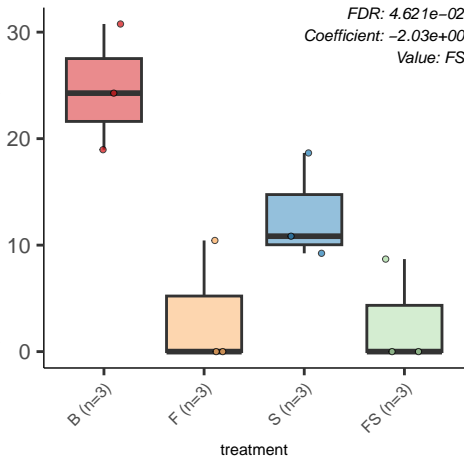


FDR:  $4.621e-02$   
Coefficient:  $-2.04e+00$   
Value: F

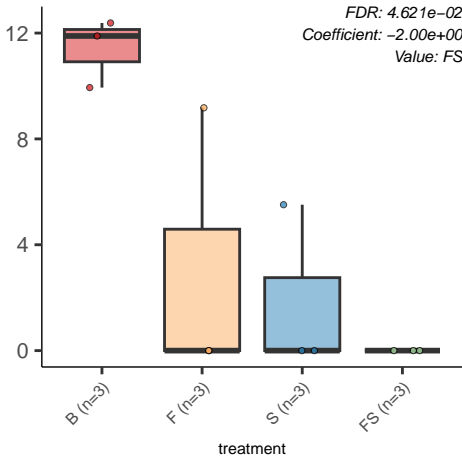


NBSUB.PWY..L.arginine.biosynthesis.II..acetyl.cycle..g\_\_Escherichia

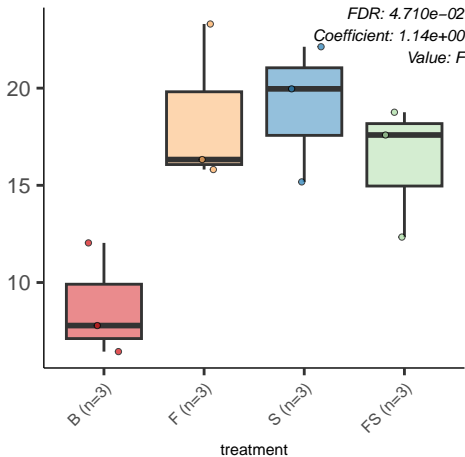
FDR: 4.621e-02  
Coefficient: -2.03e+00  
Value: FS



08..superpathway.of.pyrimidine.nucleobases.salvage.g\_\_Escherichia

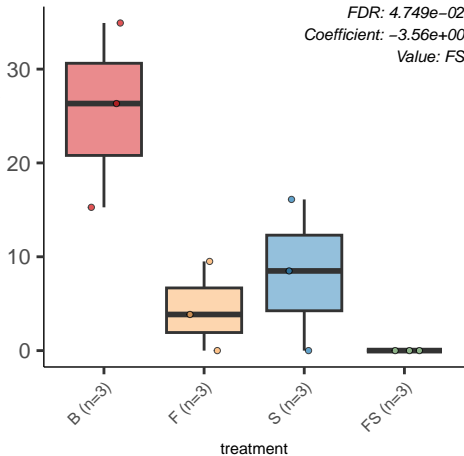




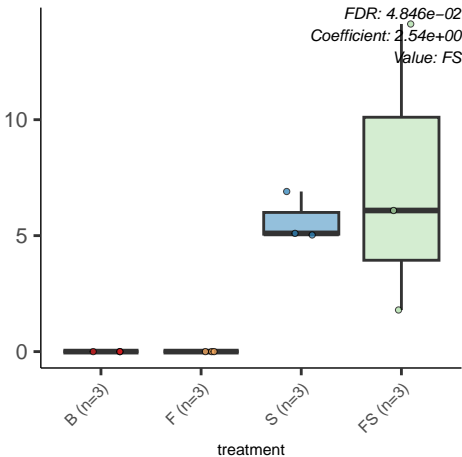


SYN.PWY..colanic.acid.building.blocks.biosynthesis.g\_\_Escherichia

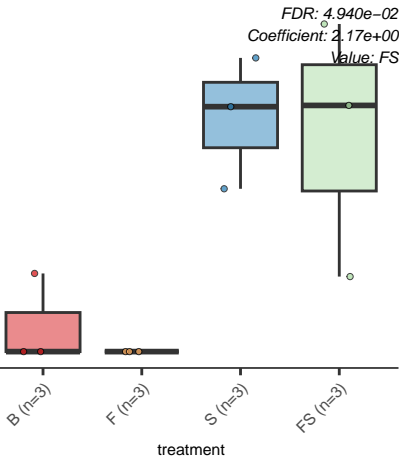
FDR: 4.749e-02  
Coefficient: -3.56e+00  
Value: FS

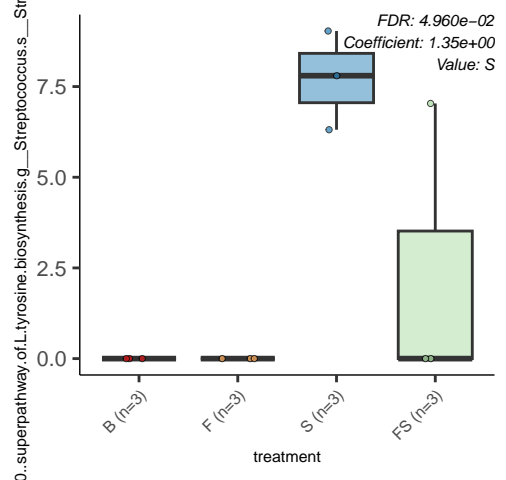


WPY.2941..L-lysine.biosynthesis.II.g\_\_Streptococcus

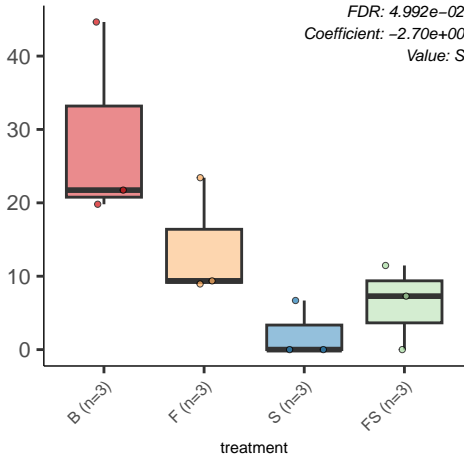


WY.4041...gamma..glutamyl.cycle.g\_\_Streptococcus

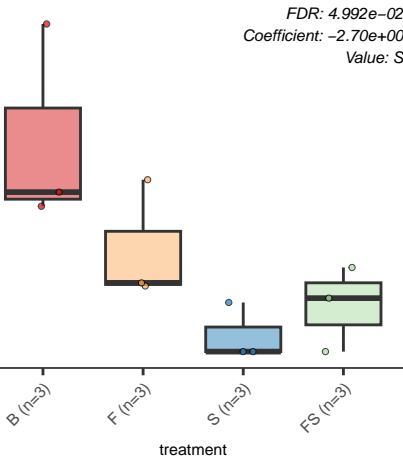




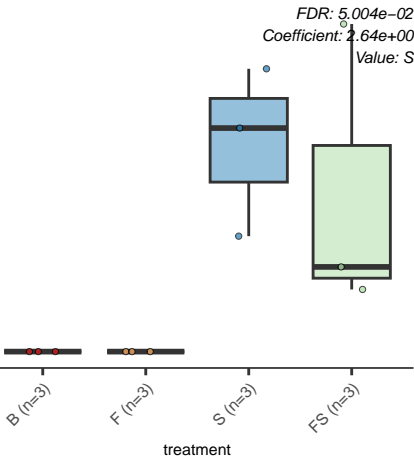
*FDR: 4.992e-02*  
*Coefficient: -2.70e+00*  
*Value: S*



FDR:  $4.992e-02$   
Coefficient:  $-2.70e+00$   
Value: S

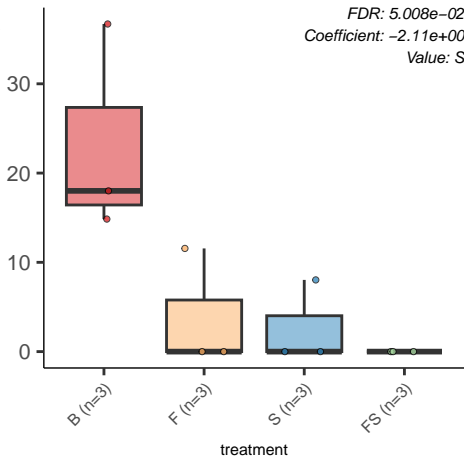


guanosine.ribonucleotides.de.novo.biosynthesis.g\_\_Streptococcus.s

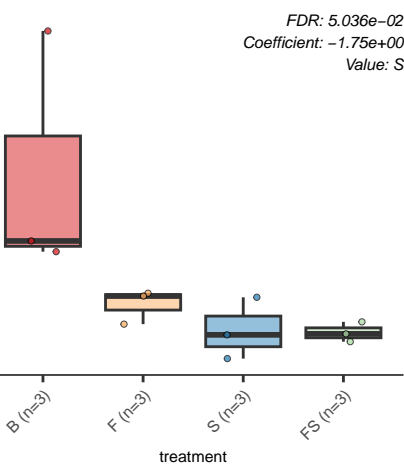




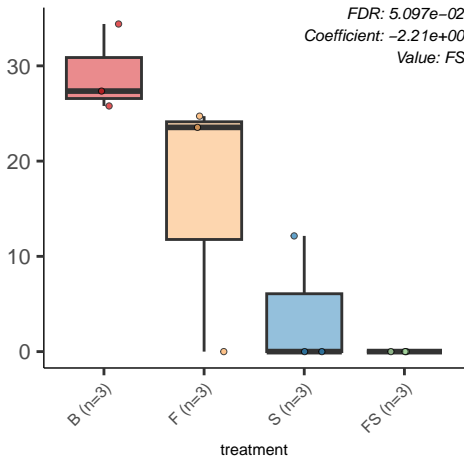
FDR:  $5.008e-02$   
Coefficient:  $-2.11e+00$   
Value: S



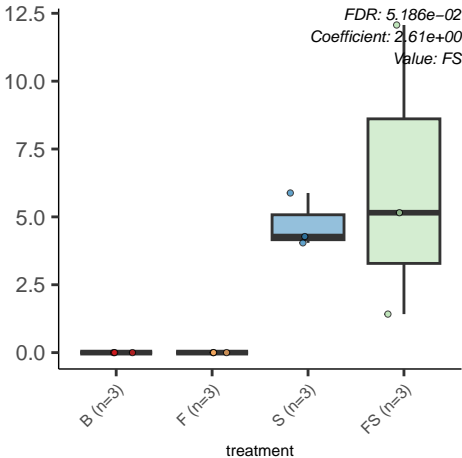
perpathway.of.L.methionine.biosynthesis..transsulfuration..g\_Esch



FDR: 5.097e-02  
Coefficient: -2.21e+00  
Value: FS

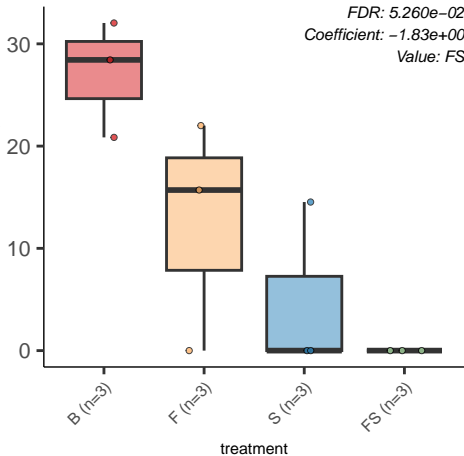


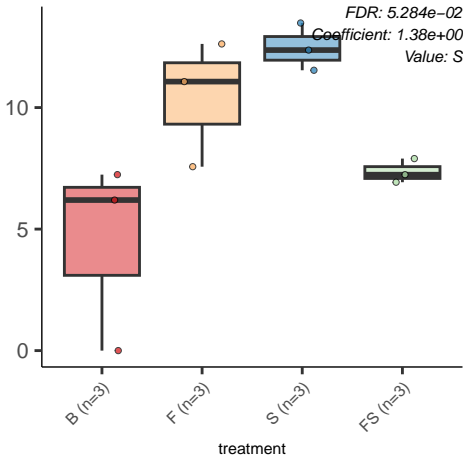
WY.2942...L.lysine.biosynthesis.III.g\_\_Streptococcus

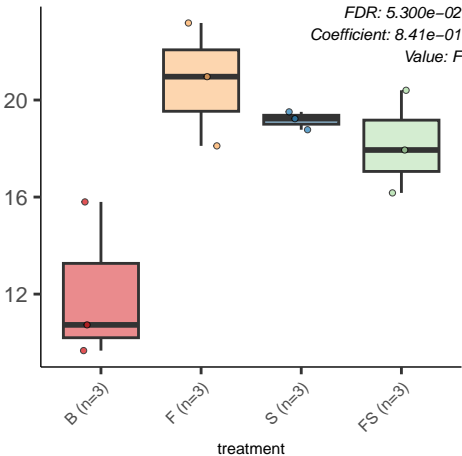


TTIN.BIOSYNTHESIS.PWY..biotin.biosynthesis.l.g\_Escherichia.s

FDR: 5.260e-02  
Coefficient: -1.83e+00  
Value: FS

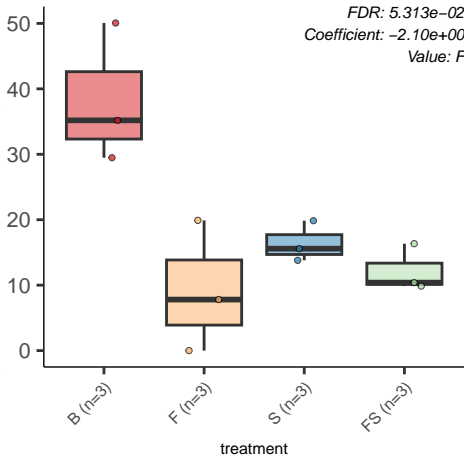




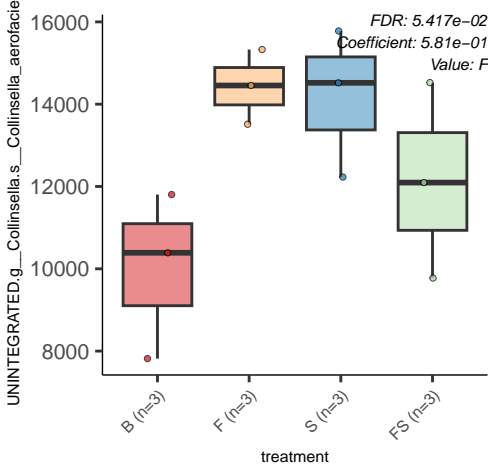


YN.PWY..L-arginine.biosynthesis.l..via.L-ornithine.g\_\_Escherichia.s

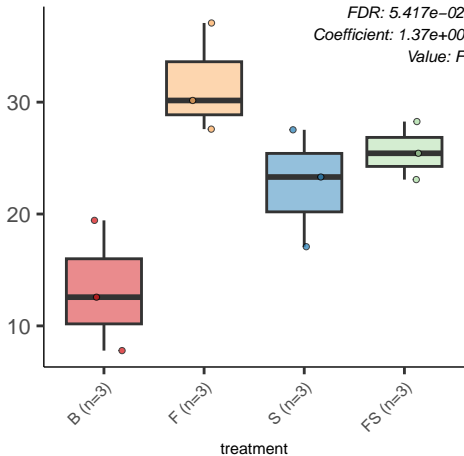
FDR:  $5.313e-02$   
Coefficient:  $-2.10e+00$   
Value: F

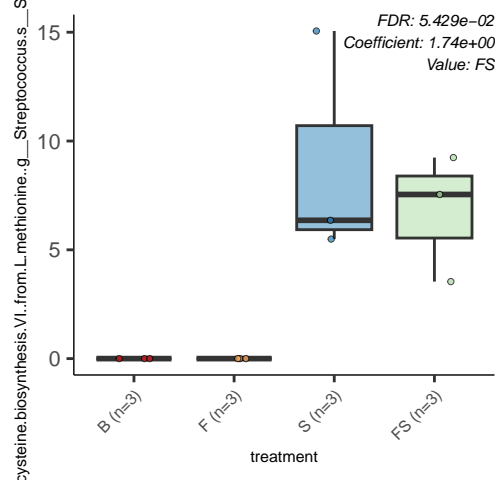




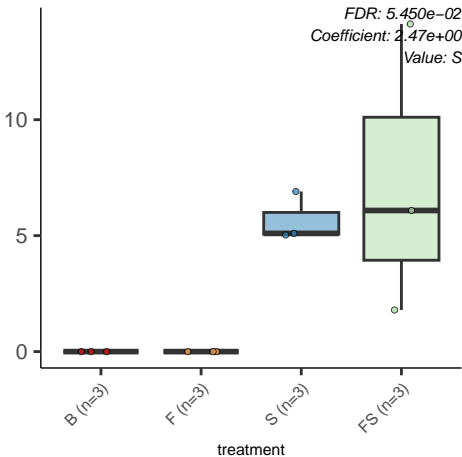


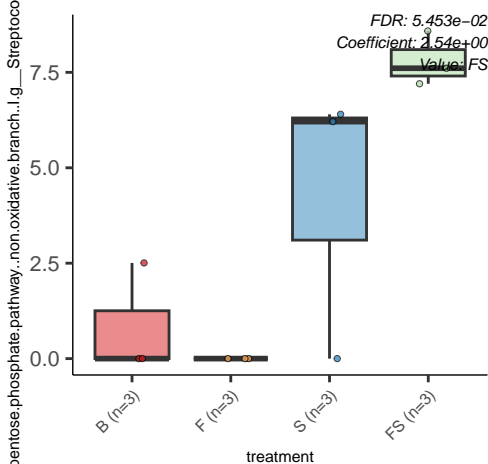
FDR: 5.417e-02  
Coefficient: 1.37e+00  
Value: F





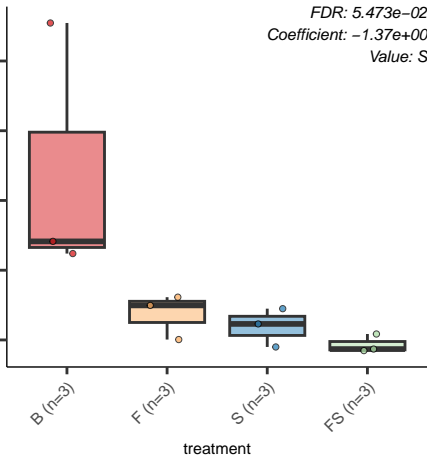
WPY.2941..L-lysine.biosynthesis.II.g\_\_Streptococcus



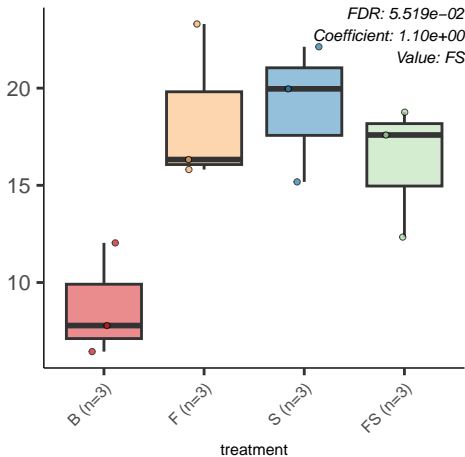


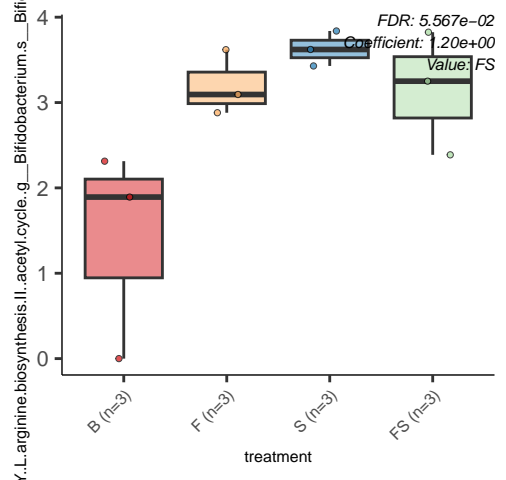
superpathway.of.L.homoserine.and.L.methionine.biosynthesis.g\_Es

FDR:  $5.473e-02$   
Coefficient:  $-1.37e+00$   
Value: S

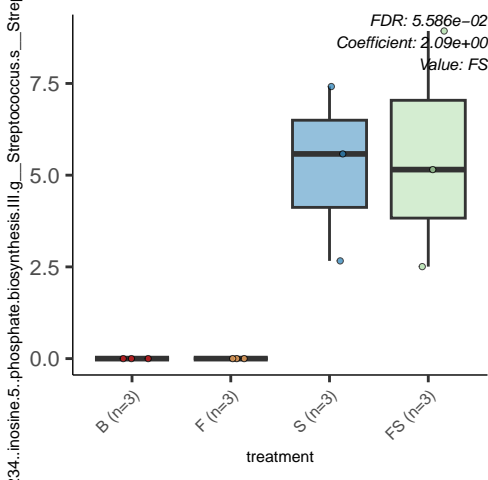


YWY.7977..L.methionine.biosynthesis.IV.g\_Collinsella.s\_Collinsella

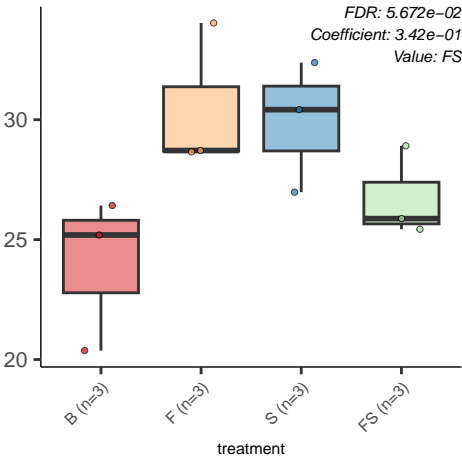






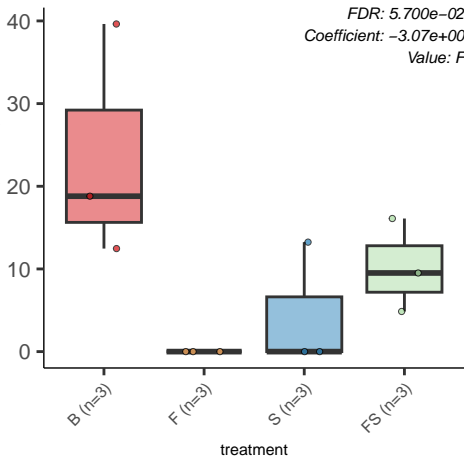


PWY.5941..glycogen.degradation.ll.g\_\_Collinsella.s\_\_Collinsella\_a

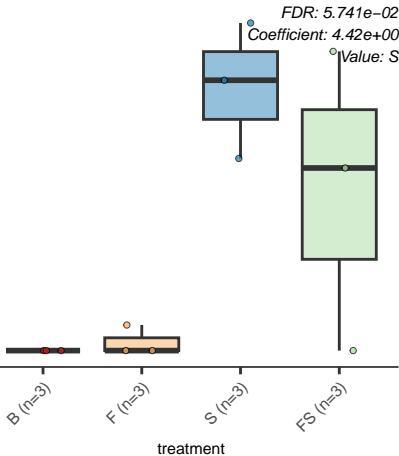


Y.5189..tetrapyrrole.biosynthesis.II...from.glycine..g\_\_Escherichia.s

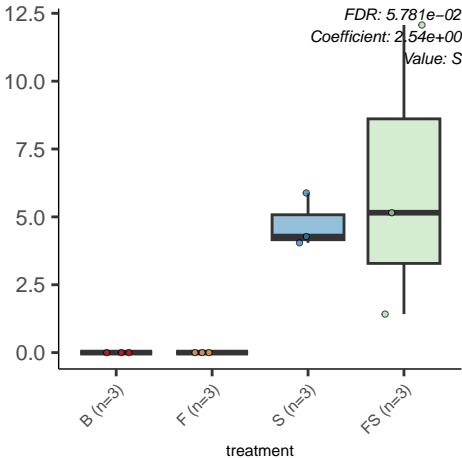
FDR: 5.700e-02  
Coefficient: -3.07e+00  
Value: F

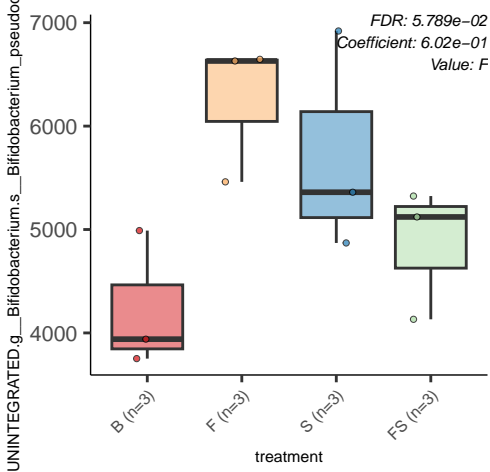


PWY.7238..sucrose.biosynthesis.ll.g\_\_Streptococcus



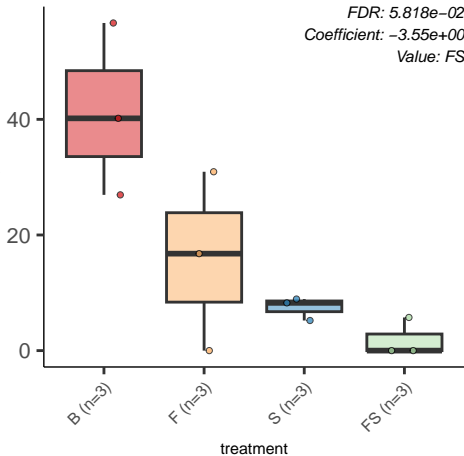
WY.2942...L.lysine.biosynthesis.III.g\_\_Streptococcus.s\_\_Streptococcus



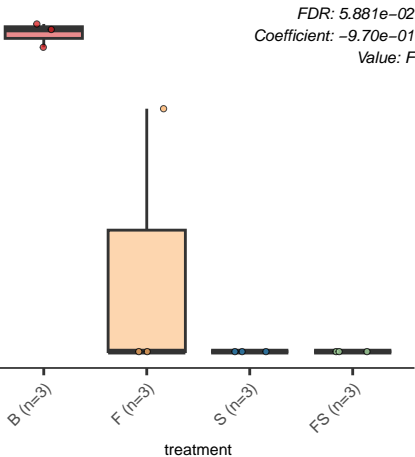


PWY.5973..cis.vaccinate.biosynthesis.g\_Escherichia.s\_Esche

FDR: 5.818e-02  
Coefficient: -3.55e+00  
Value: FS

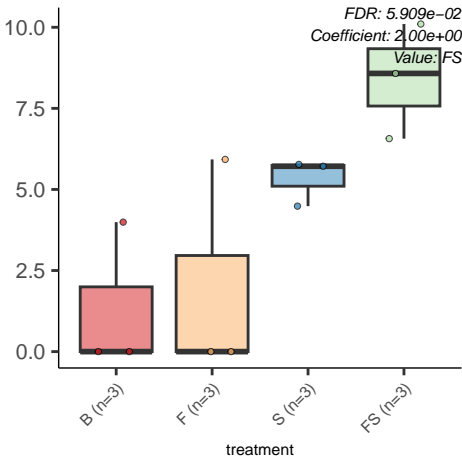


RABCATK12.PWY..D.arabinose.degradation.l.g\_Klebsiella.s\_Kle

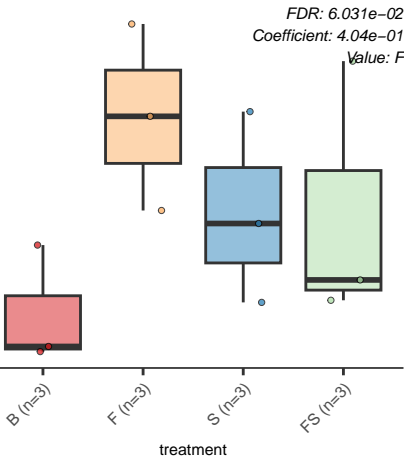


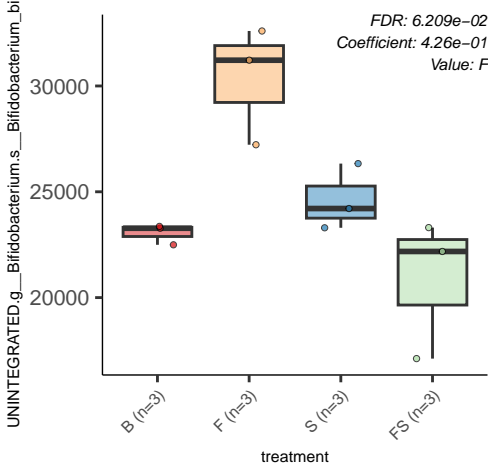


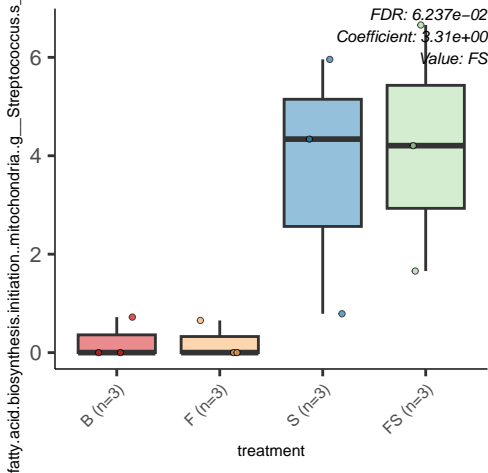
HEME.BIOSYNTHESIS.II...heme.b.biosynthesis.I...aerobic...unc

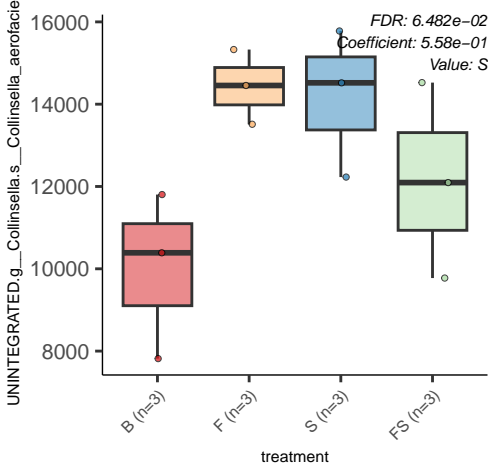


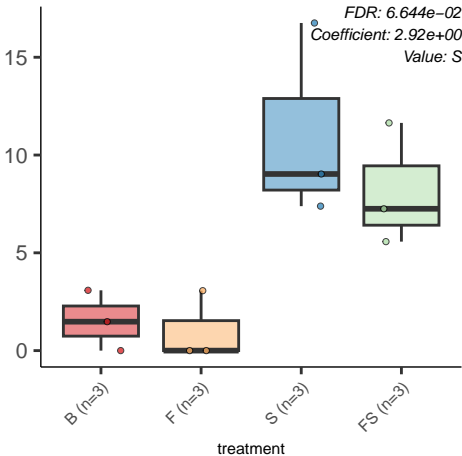
pentapeptide.biosynthesis.l...meso.diaminopimelate.containing...g\_E











UNINTEGRATED.g\_Escherichia.s\_Escherichia\_coli

FDR:  $6.698e-02$   
Coefficient:  $-9.46e-01$   
Value: F

B (n=3)

F (n=3)

S (n=3)

FS (n=3)

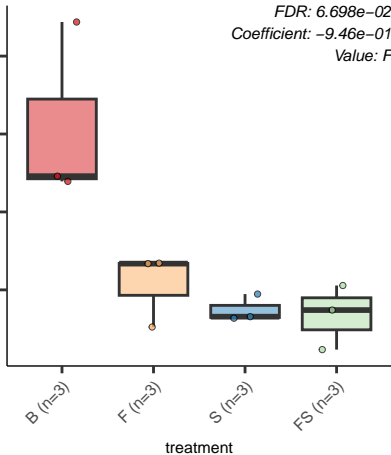
treatment

$1e+05$

$8e+04$

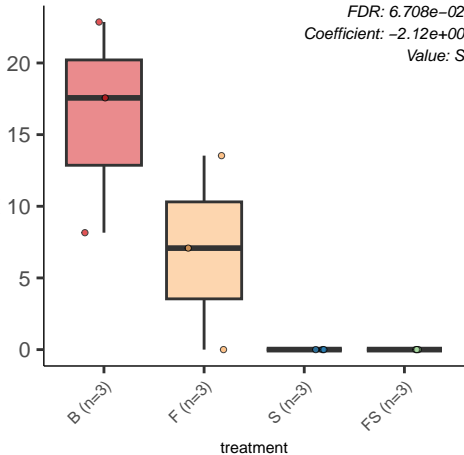
$6e+04$

$4e+04$



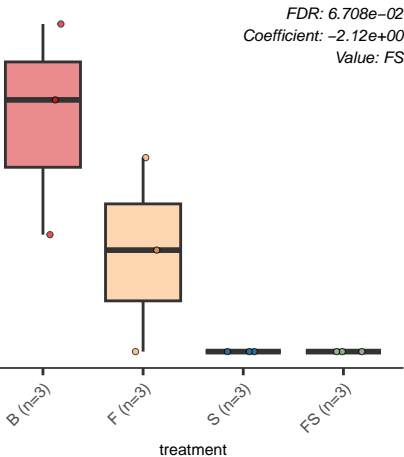
PWY0.1479..tRNA.processing.g\_Escherichia.s\_Escherich

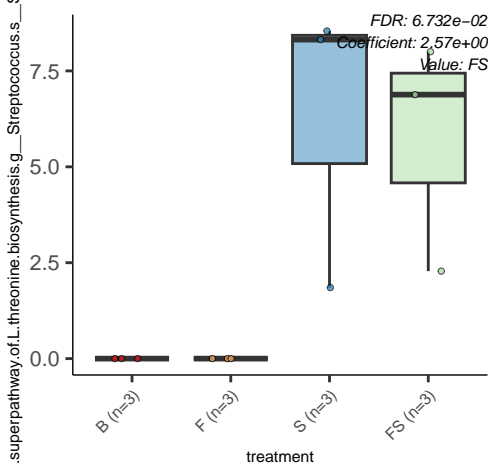
FDR: 6.708e-02  
Coefficient: -2.12e+00  
Value: S

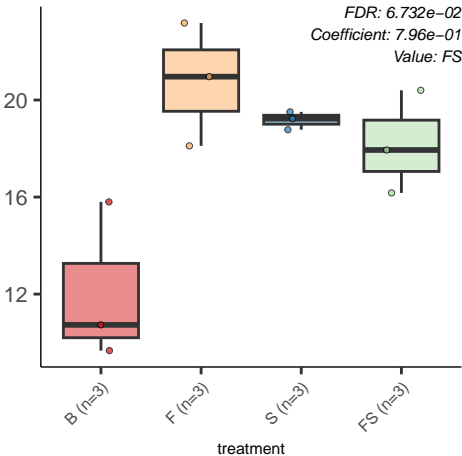




PWY0.1479..tRNA.processing.g\_Escherichia.s\_Escherich

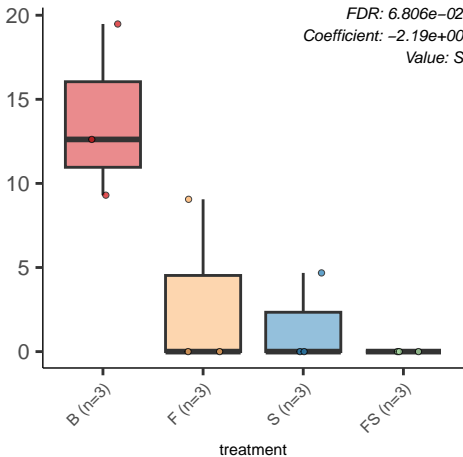




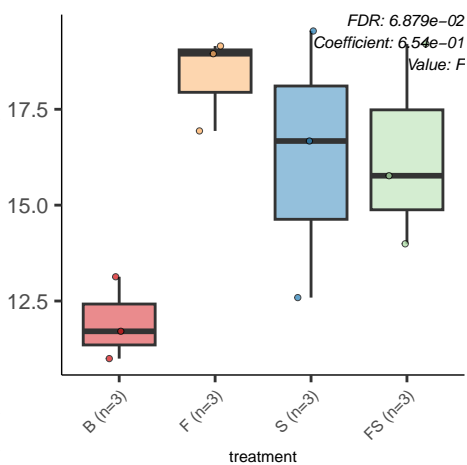


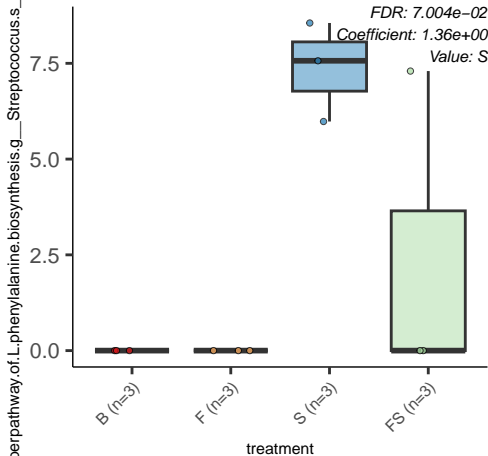
perpathway.of.purine.nucleotides.de.novo.biosynthesis.l.g\_\_Escher

FDR:  $6.806e-02$   
Coefficient:  $-2.19e+00$   
Value: S



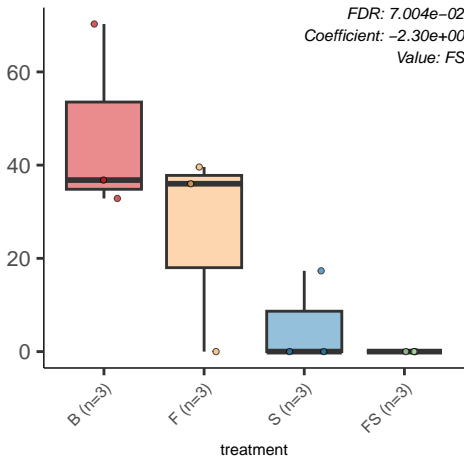
Y..glycogen.biosynthesis.l...from.ADP.D.Glucose..g\_\_Faecalibacter

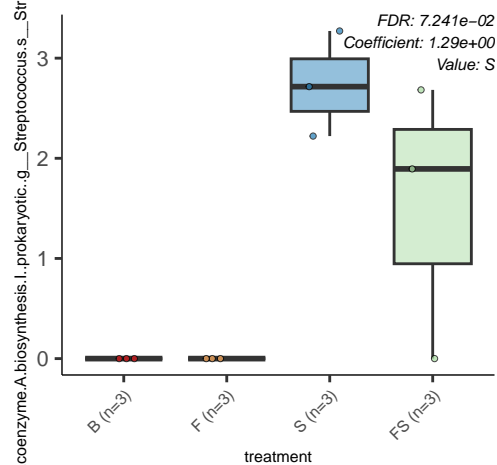




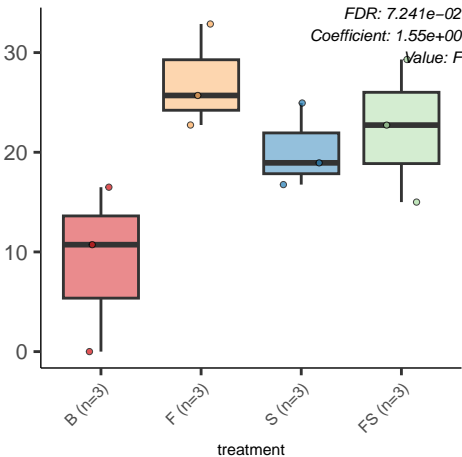
pWY.7664..oleate.biosynthesis.IV..anaerobic..g\_Escherichia.s\_Es

FDR:  $7.004e-02$   
Coefficient:  $-2.30e+00$   
Value: FS

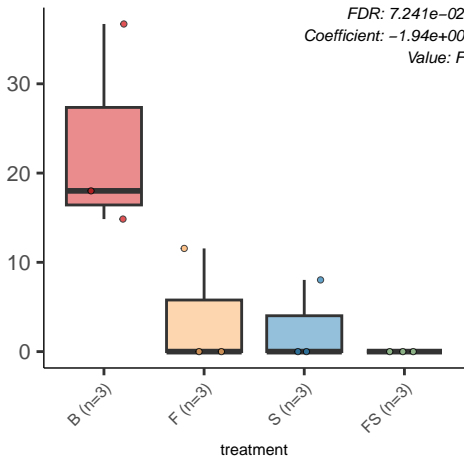


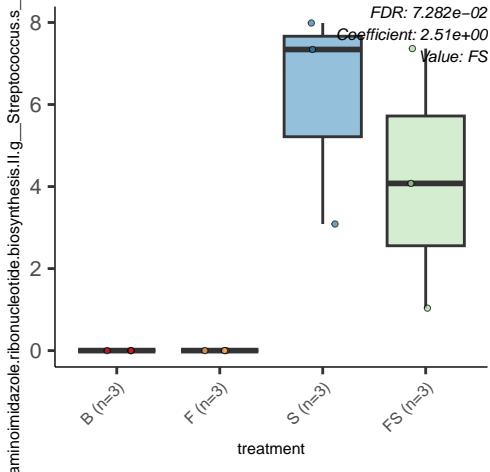


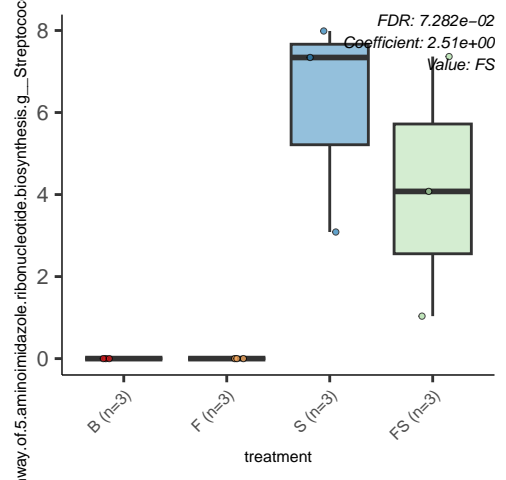




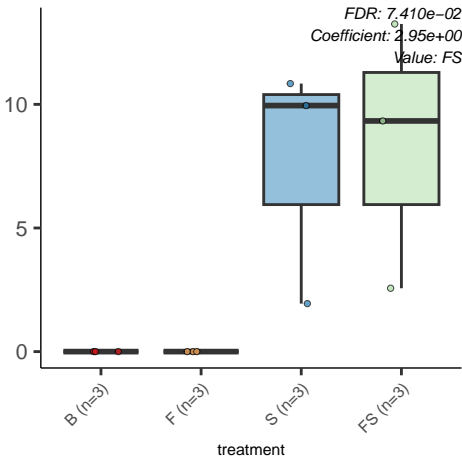
FDR:  $7.241e-02$   
Coefficient:  $-1.94e+00$   
Value: F







7.702.L.methionine.biosynthesis.II.g\_\_Streptococcus.s\_\_Streptococcus



PANTO.PWY..phosphopantothenate.biosynthesis.l.unclass

FDR: 7.417e-02  
Coefficient: 7.17e-01  
Value: F

21  
18  
15  
12

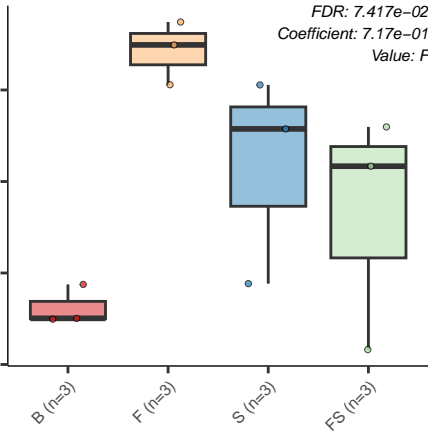
B (n=3)

F (n=3)

S (n=3)

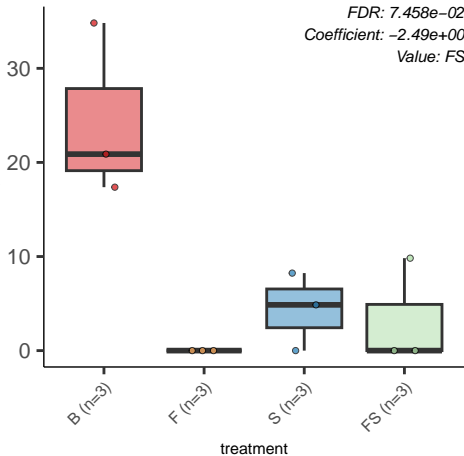
FS (n=3)

treatment

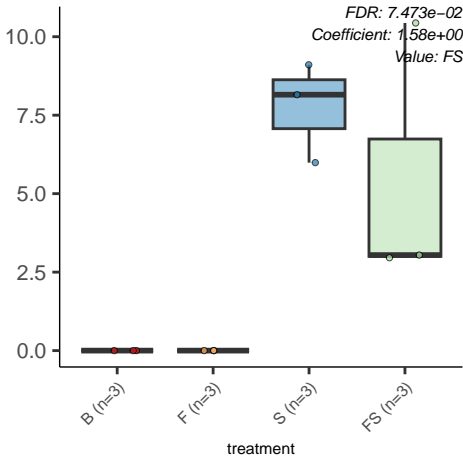


PWY.2942..L.lysine.biosynthesis.Ill.g\_\_Escherichia.s\_\_Escheri

FDR:  $7.458e-02$   
Coefficient:  $-2.49e+00$   
Value: FS

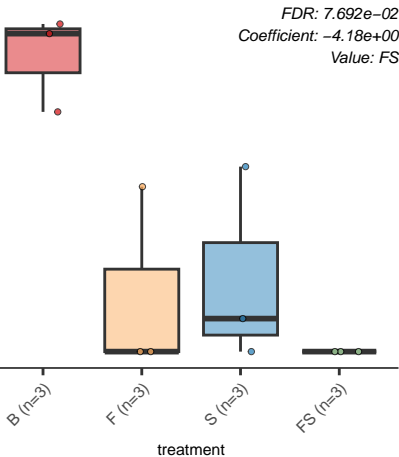


5700..queuosine.biosynthesis.l..de.novo..g\_\_Streptococcus.s\_\_Streptococcus

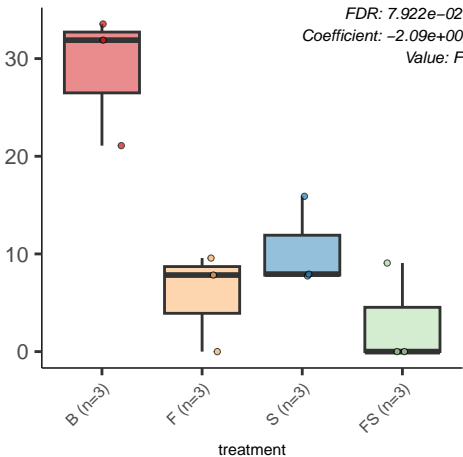


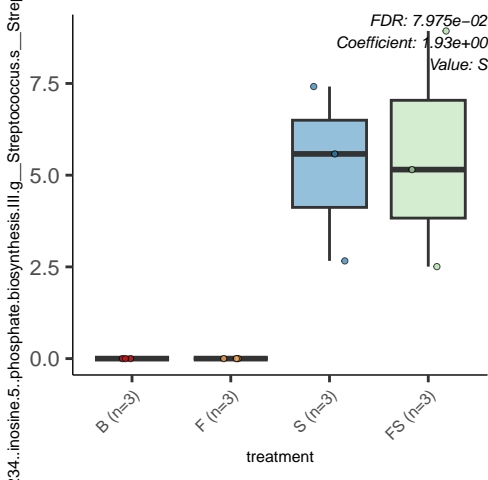


97..pyrimidine.deoxyribonucleotide.phosphorylation.g\_\_Escherichia



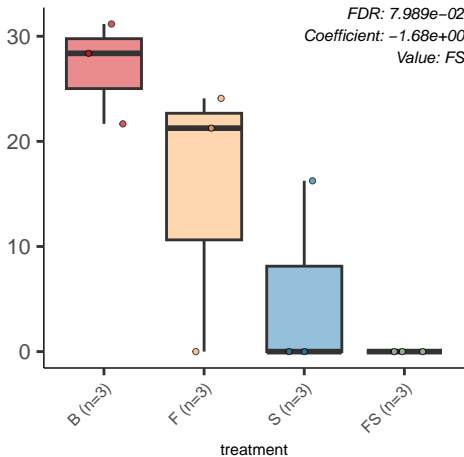
54..L.arginine.biosynthesis.III...via.N.acetyl.L.citrulline..g\_\_Escherichia

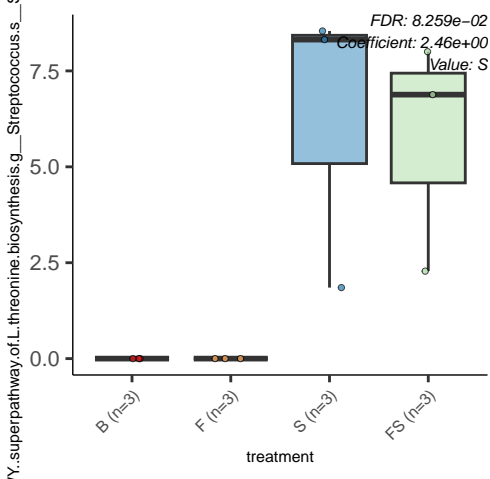


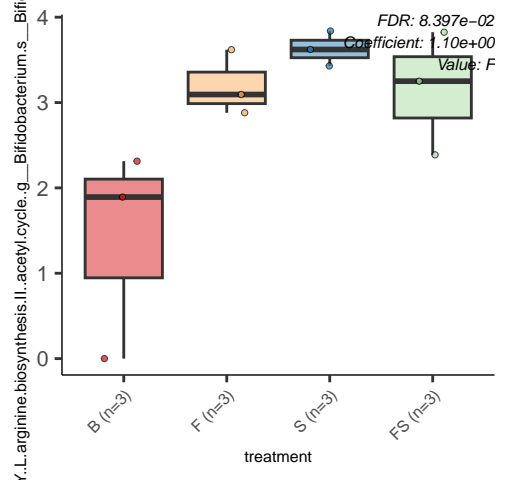


Y.6519...8.amino.7.oxononanoate.biosynthesis.l.g\_Escherichia.s

*FDR: 7.989e-02*  
*Coefficient: -1.68e+00*  
*Value: FS*

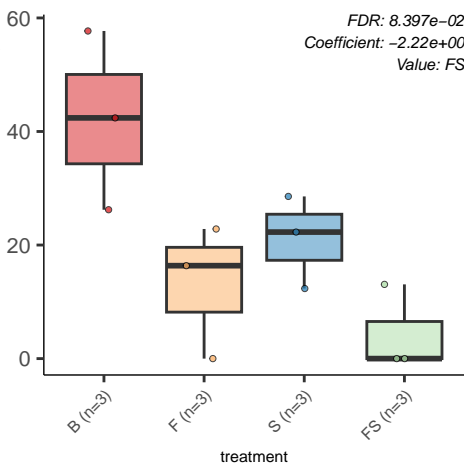




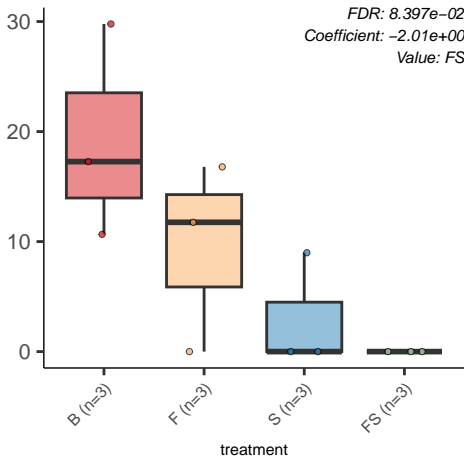


pwY..superpathway.of.phospholipid.biosynthesis.l...bacteria..g\_\_Esc

FDR: 8.397e-02  
Coefficient: -2.22e+00  
Value: FS



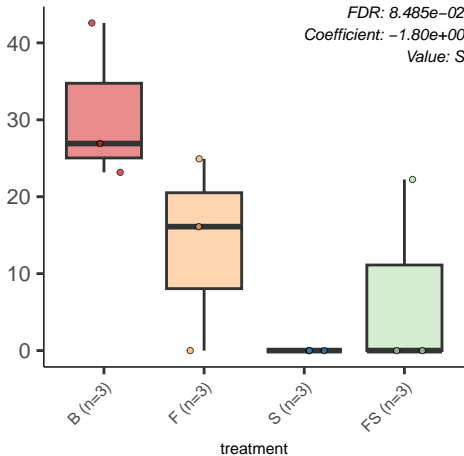
FDR:  $8.397e-02$   
Coefficient:  $-2.01e+00$   
Value: FS





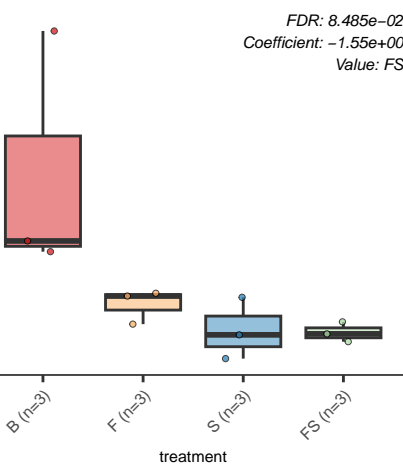
AGLYCOLYSIS.PWY.glycolysis.III..from.glucose.g\_Escherichia.s

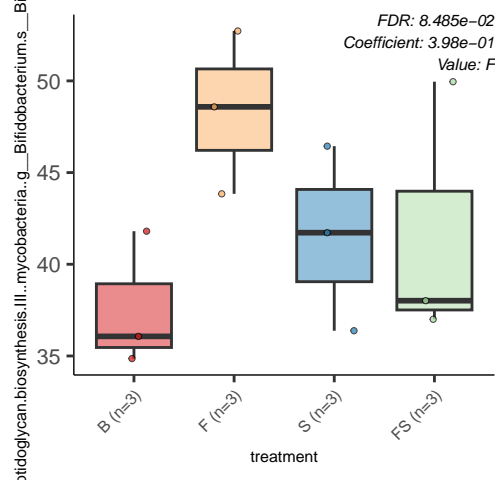
FDR:  $8.485e-02$   
Coefficient:  $-1.80e+00$   
Value: S



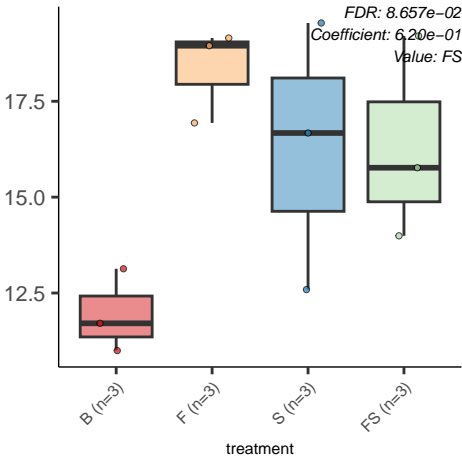
perpathway.of.L.methionine.biosynthesis..transsulfuration..g\_Esch

FDR:  $8.485e-02$   
Coefficient:  $-1.55e+00$   
Value: FS

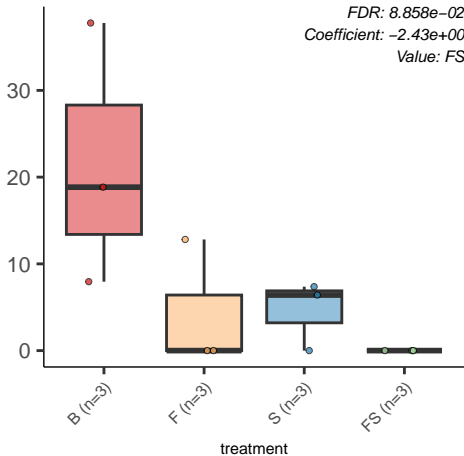


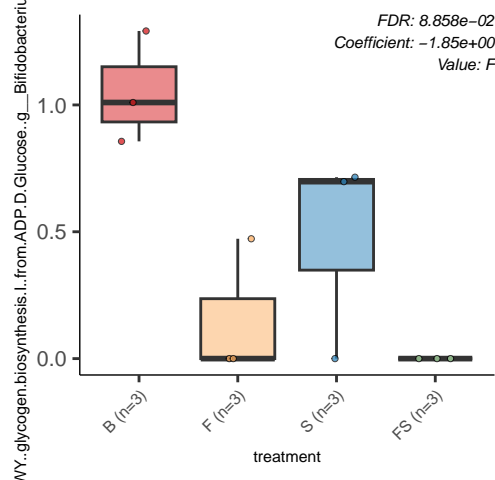


Y..glycogen.biosynthesis.l...from.ADP.D.Glucose..g\_\_Faecalibacter

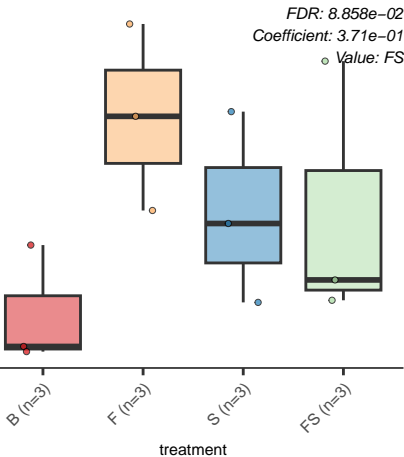


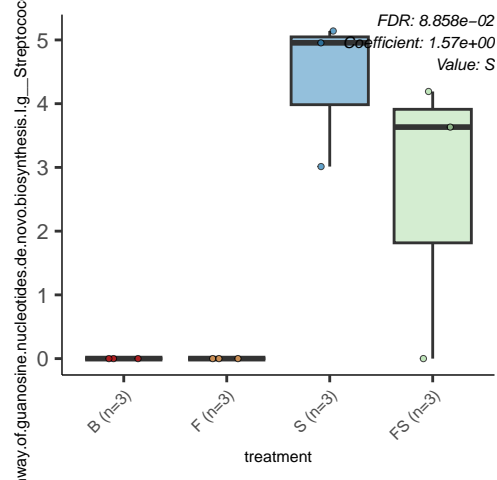
FDR:  $8.858e-02$   
Coefficient:  $-2.43e+00$   
Value: FS



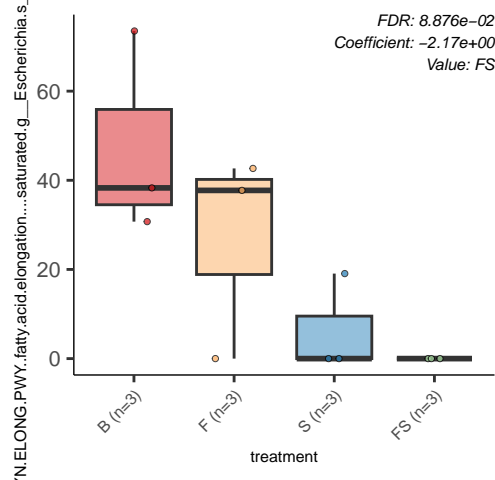


pentapeptide.biosynthesis.l...meso.diaminopimelate.containing..g\_E

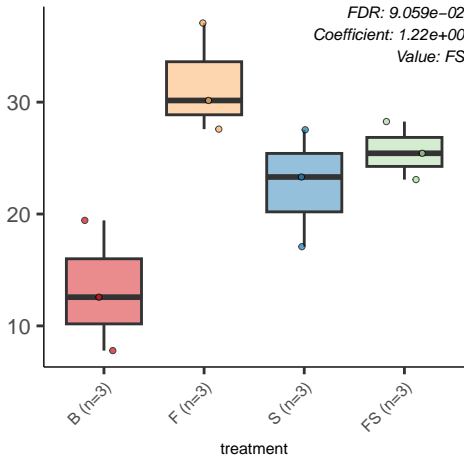


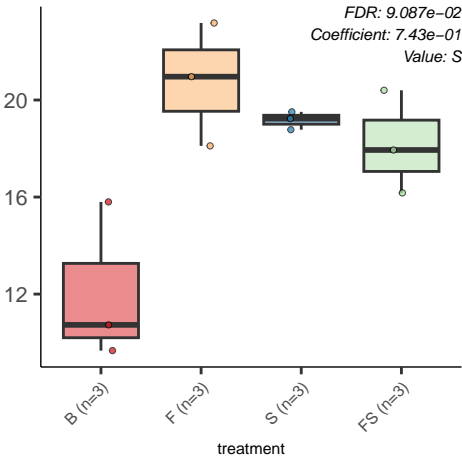


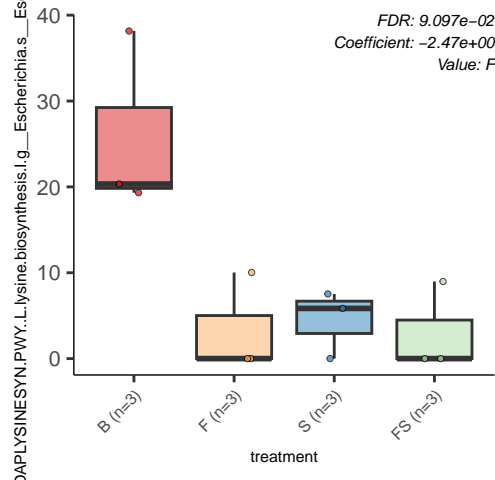


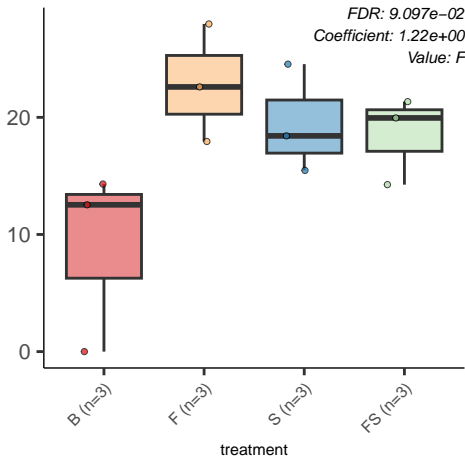


FDR:  $9.059e-02$   
Coefficient:  $1.22e+00$   
Value: FS

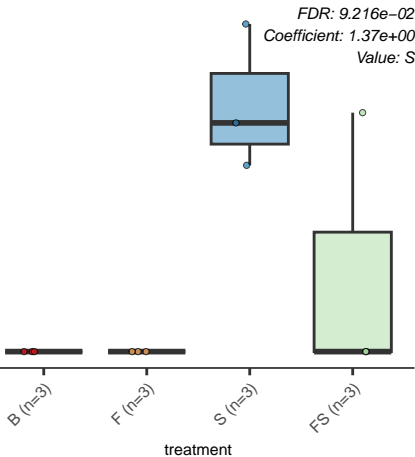


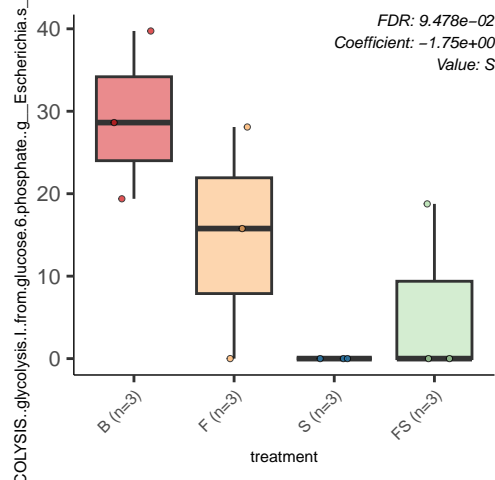






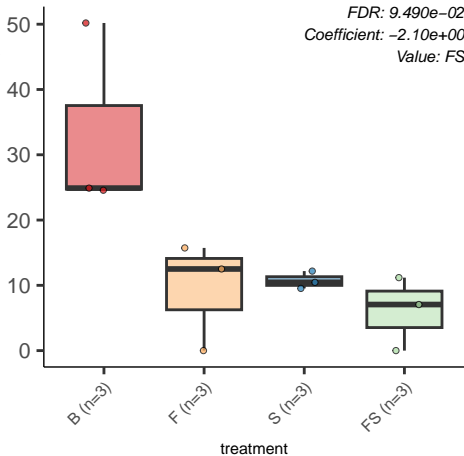
ORN.PWY..L.ornithine.biosynthesis.l.g\_\_Streptococcus.s\_\_Streptococcus



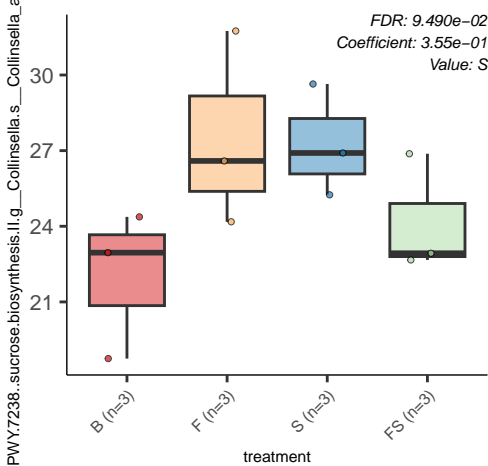


Y. superpathway.of.S.adenosyl.L.methionine.biosynthesis.g\_Esche

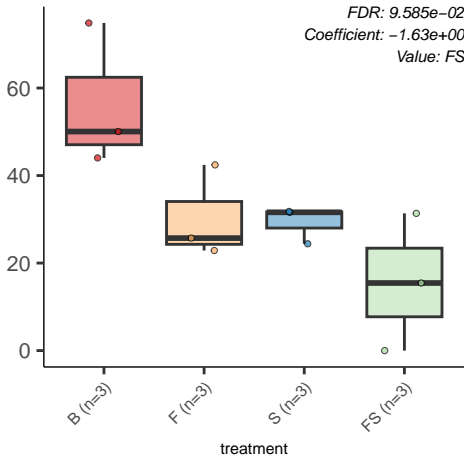
FDR:  $9.490e-02$   
Coefficient:  $-2.10e+00$   
Value: FS



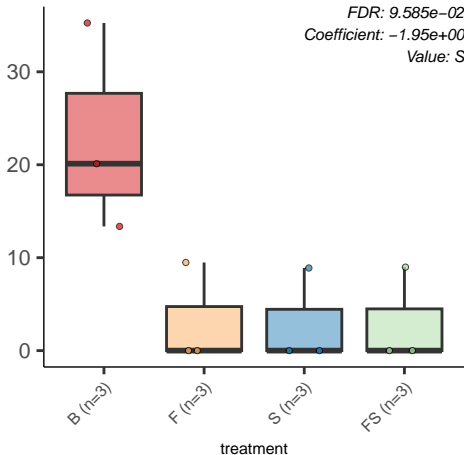




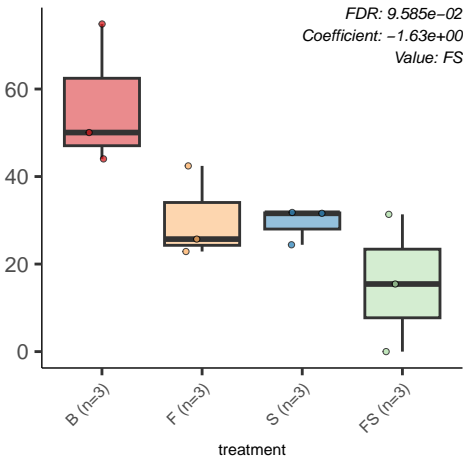
FDR:  $9.585e-02$   
Coefficient:  $-1.63e+00$   
Value: FS

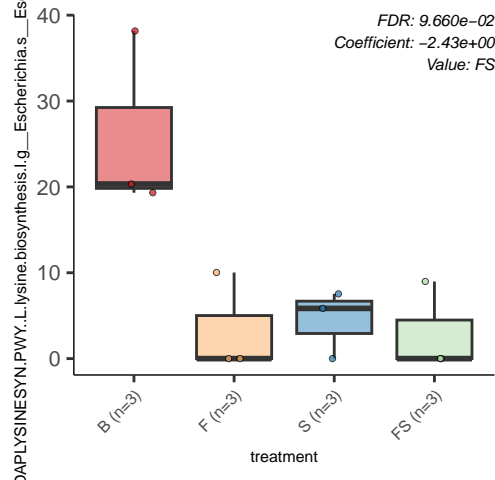


FDR:  $9.585e-02$   
Coefficient:  $-1.95e+00$   
Value: S



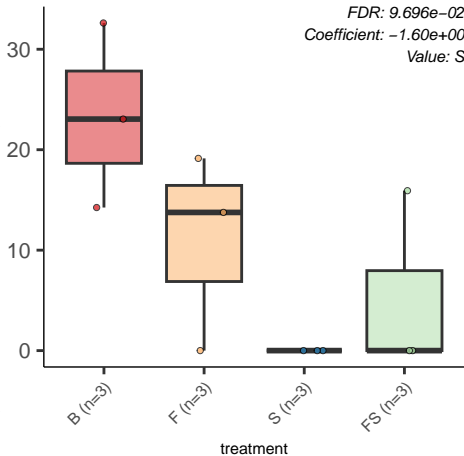
WY0.1319..CDP..diacylglycerol.biosynthesis.II.g\_Escherichia.s\_Es

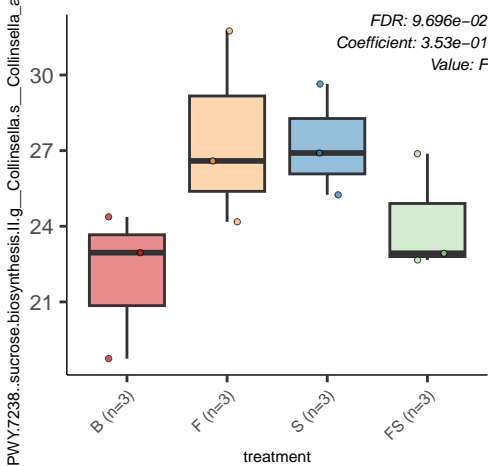


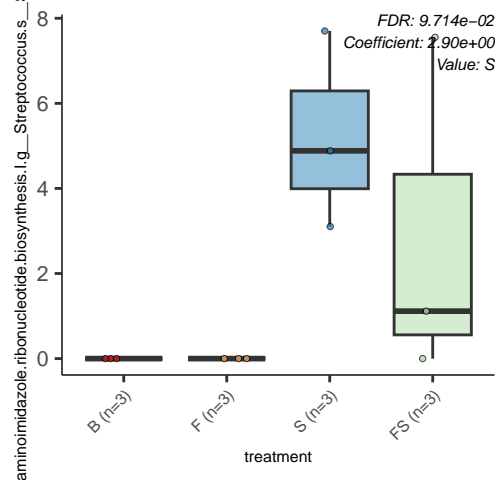


Y.5484..glycolysis.II..from.fructose.6.phosphate.g\_Escherichia.s

*FDR: 9.696e-02*  
*Coefficient: -1.60e+00*  
*Value: S*

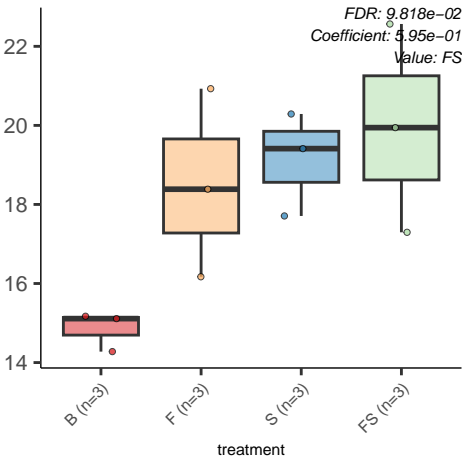






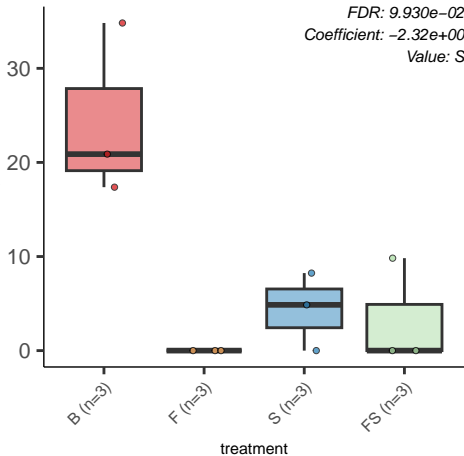


Y..UDP.N.acetyl.D.glucosamine.biosynthesis.l.g\_\_Catenibacterium.

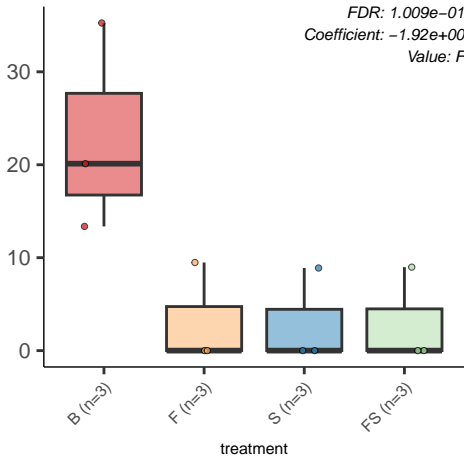


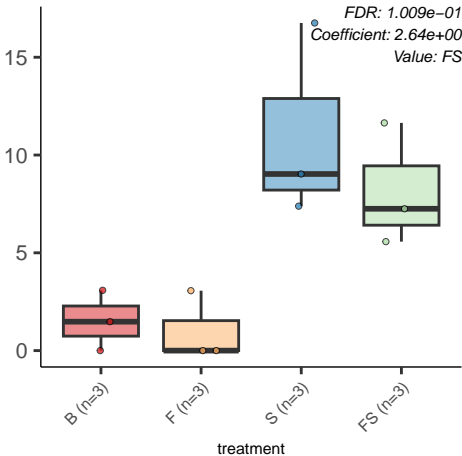
PWY.2942..L.lysine.biosynthesis.Ill.g\_\_Escherichia.s\_\_Escheri

FDR:  $9.930e-02$   
Coefficient:  $-2.32e+00$   
Value: S

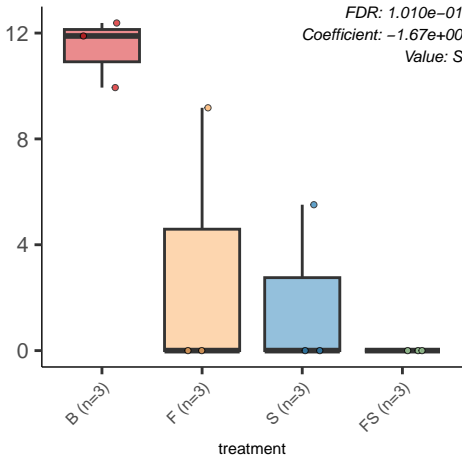


FDR: 1.009e-01  
Coefficient: -1.92e+00  
Value: F



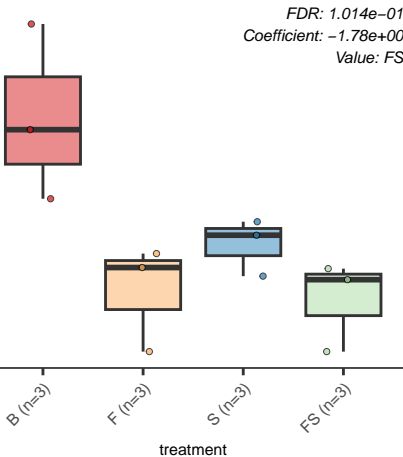


08..superpathway.of.pyrimidine.nucleobases.salvage.g\_\_Escherichia

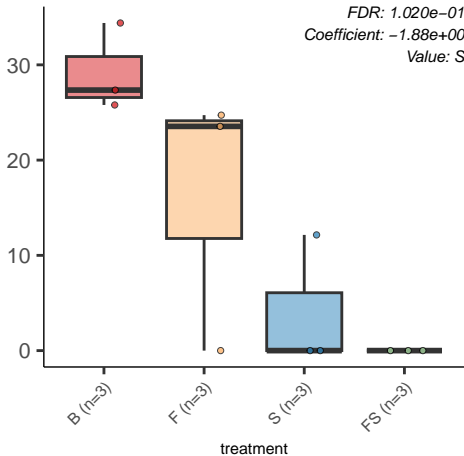


PWY.4041...gamma..glutamyl.cycle.g\_\_Escherichia.s\_\_Escheri

*FDR: 1.014e-01*  
*Coefficient: -1.78e+00*  
*Value: FS*



FDR: 1.020e-01  
Coefficient: -1.88e+00  
Value: S

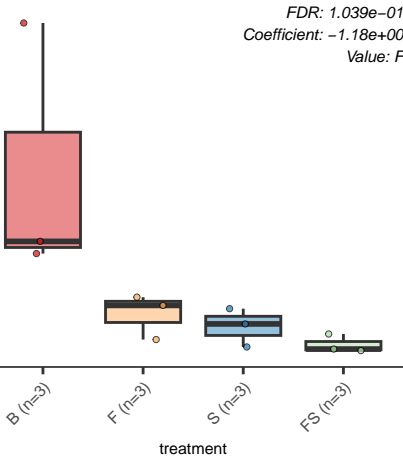




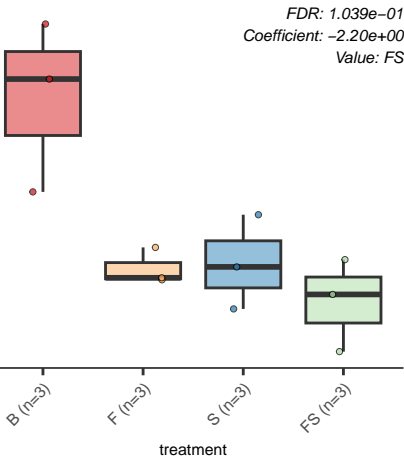


superpathway.of.L.homoserine.and.L.methionine.biosynthesis.g\_Es

FDR: 1.039e-01  
Coefficient: -1.18e+00  
Value: F

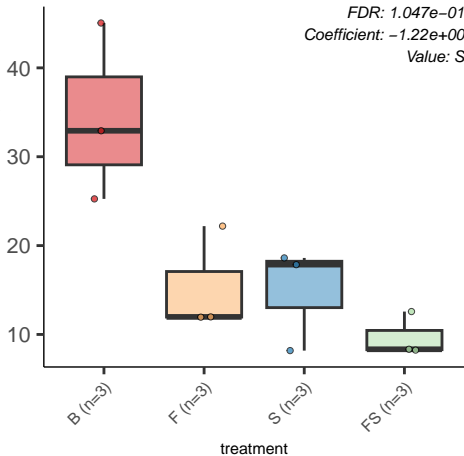


WY.6151..S.adenosyl.L.methionine.salvage.l.g\_Escherichia.s\_Es

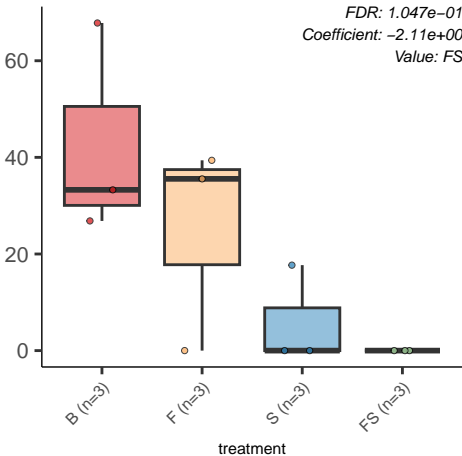


OSER.METSYN.PWY..L.methionine.biosynthesis.l.g\_\_Escherichia.s

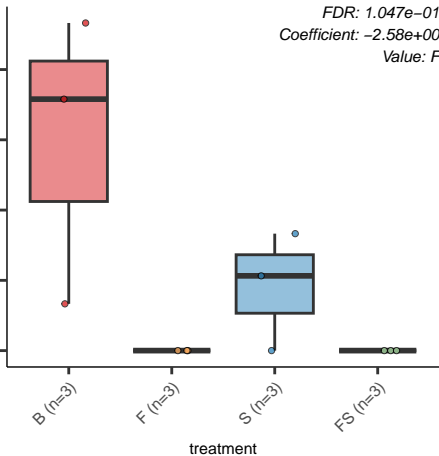
FDR: 1.047e-01  
Coefficient: -1.22e+00  
Value: S

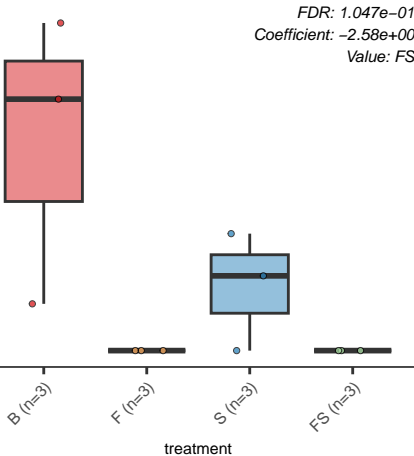


...palmitoleate.biosynthesis.l.from..5Z...dodec.5.enoate..g\_\_Escheric

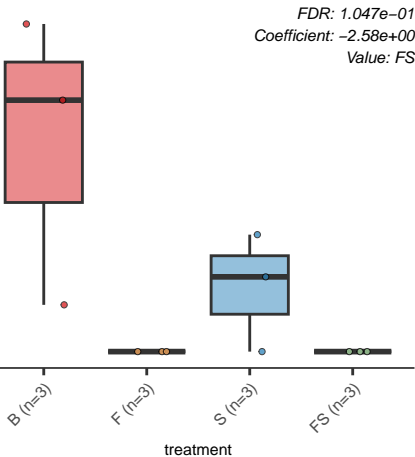


FDR: 1.047e-01  
Coefficient: -2.58e+00  
Value: F



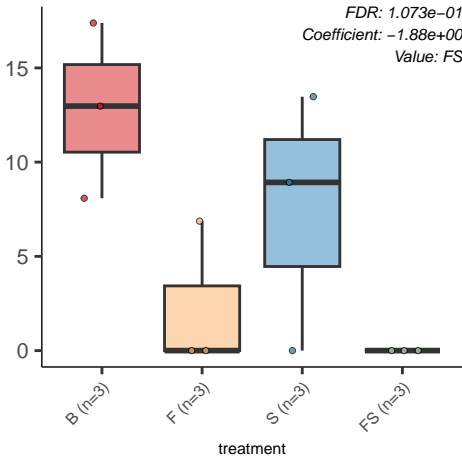


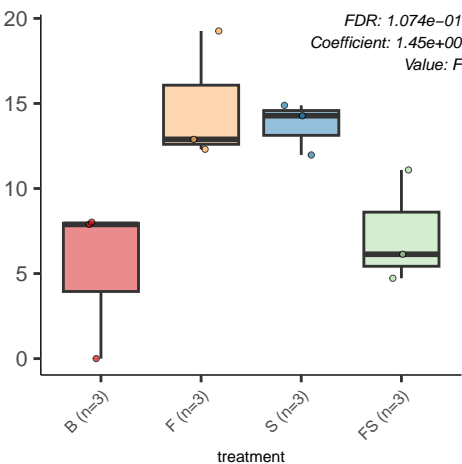


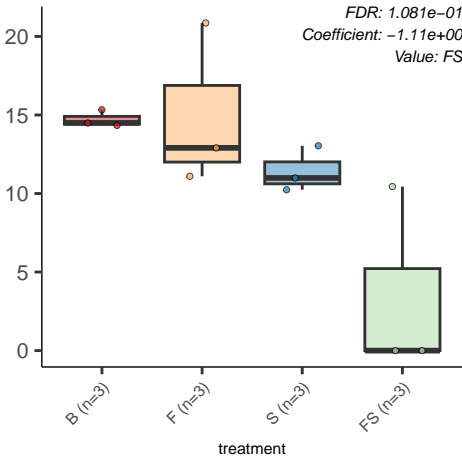




#AMSYN.PWY..dTDP..beta..L.rhamnose.biosynthesis.g\_\_Escherich

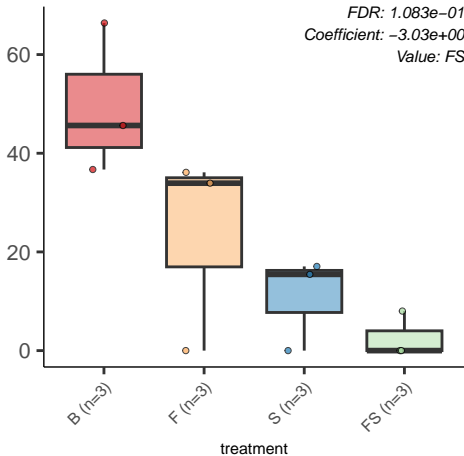


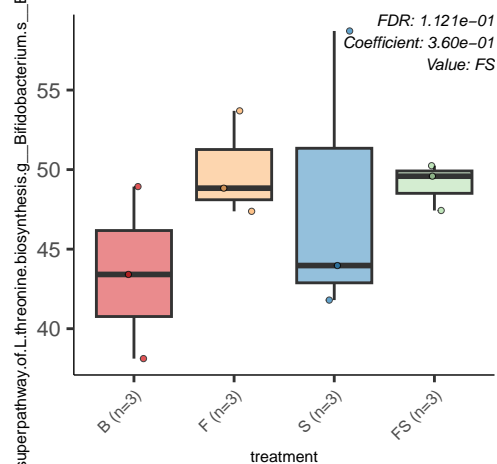




PWY0.862....5Z..dodecenoate.biosynthesis.l.g\_\_Escherichia.s\_\_Esc

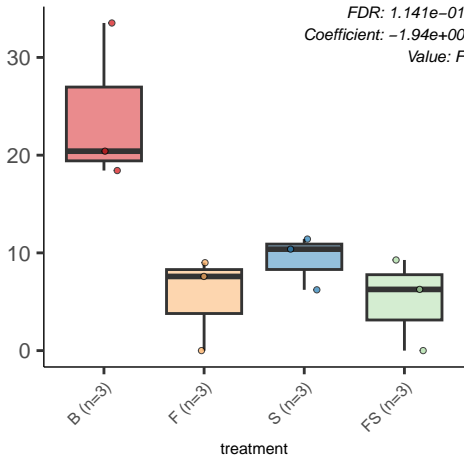
*FDR: 1.083e-01*  
*Coefficient: -3.03e+00*  
*Value: FS*



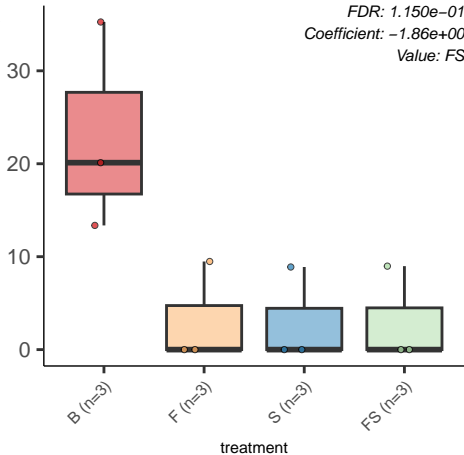


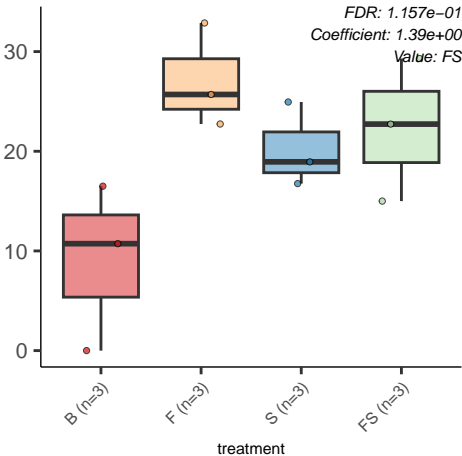
PWY.7977..L.methionine.biosynthesis.IV.g\_Escherichia.s\_Esch

*FDR: 1.141e-01*  
*Coefficient: -1.94e+00*  
*Value: F*



FDR: 1.150e-01  
Coefficient: -1.86e+00  
Value: FS

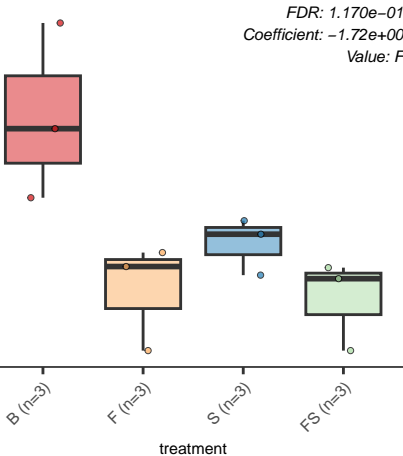




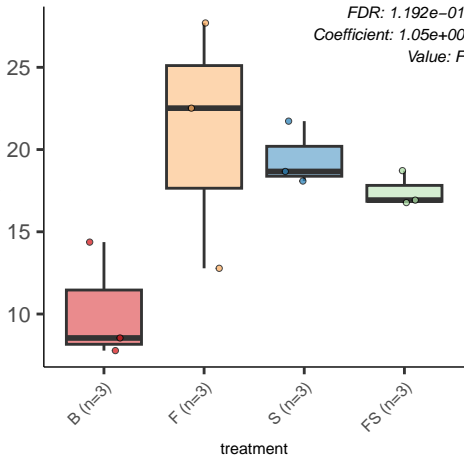


PWY.4041...gamma..glutamyl.cycle.g\_\_Escherichia.s\_\_Escheri

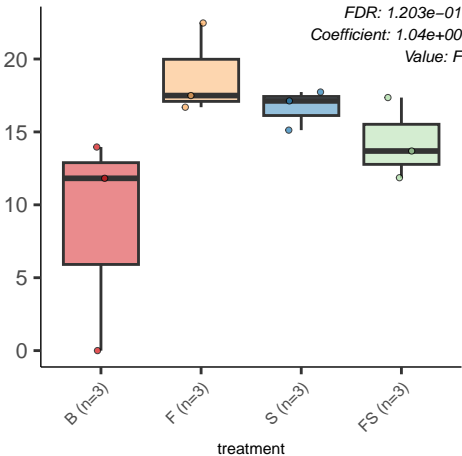
*FDR: 1.170e-01*  
*Coefficient: -1.72e+00*  
*Value: F*



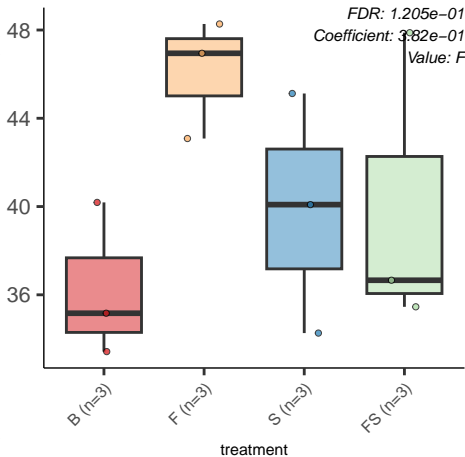
FDR: 1.192e-01  
Coefficient: 1.05e+00  
Value: F



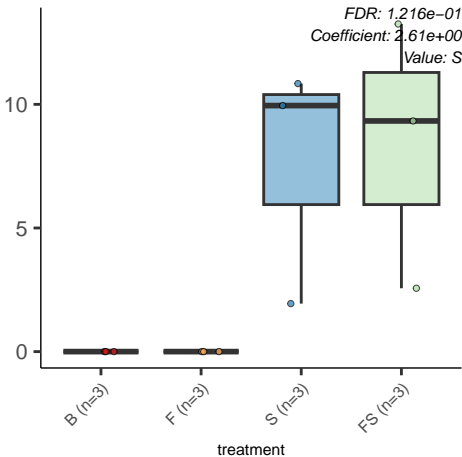
Y..peptidoglycan.biosynthesis.l..meso.diaminopimelate.containing..g



btidglycan.biosynthesis.l..meso.diaminopimelate.containing..g\_\_Bifidobacterium

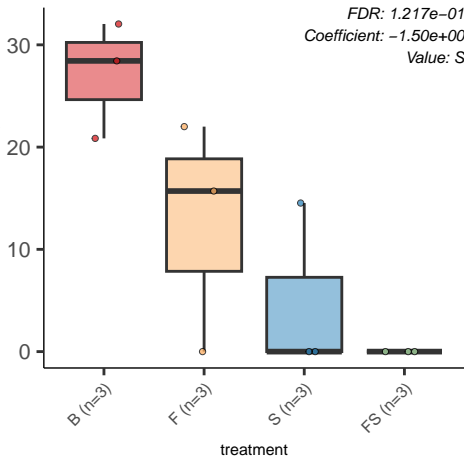


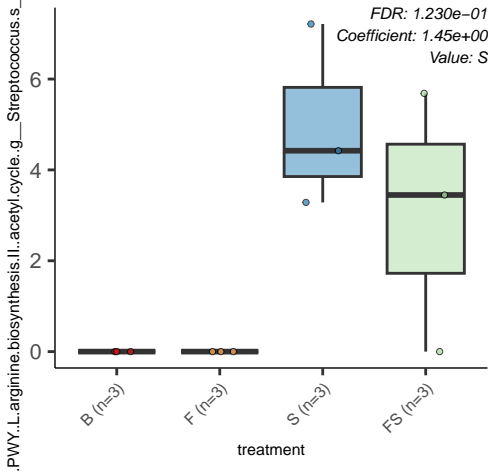
702.L.methionine.biosynthesis.II.g\_\_Streptococcus

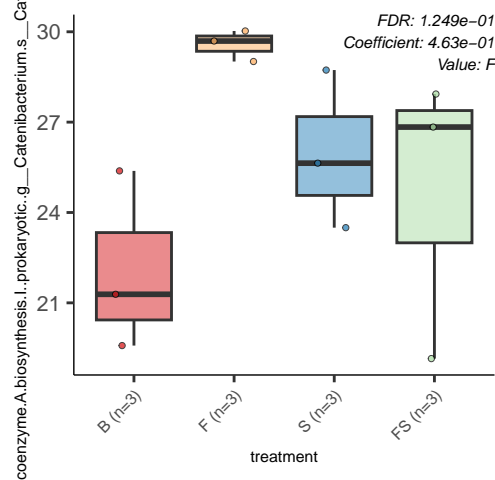


TTIN.BIOSYNTHESIS.PWY..biotin.biosynthesis.l.g\_Escherichia.s

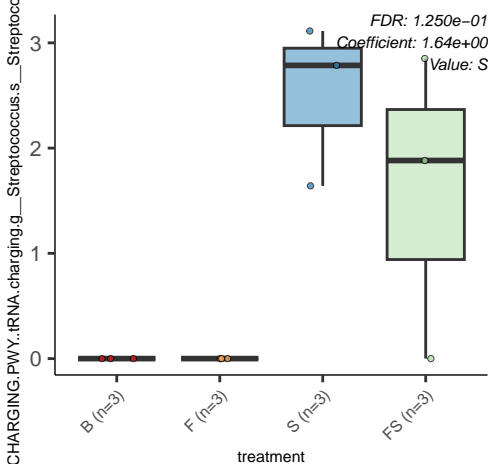
FDR: 1.217e-01  
Coefficient: -1.50e+00  
Value: S



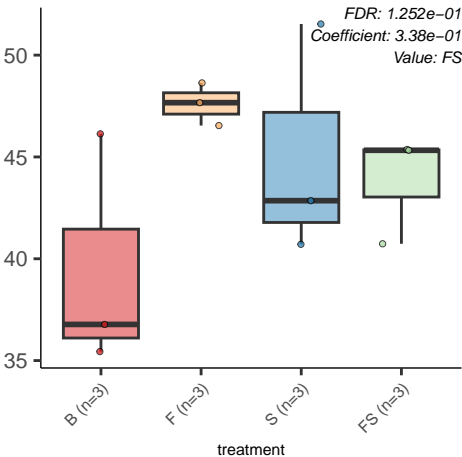


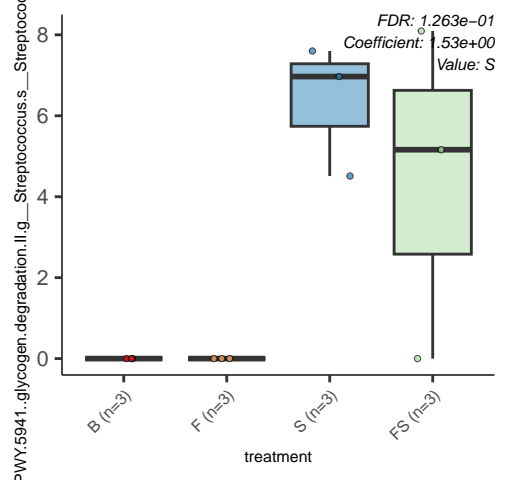






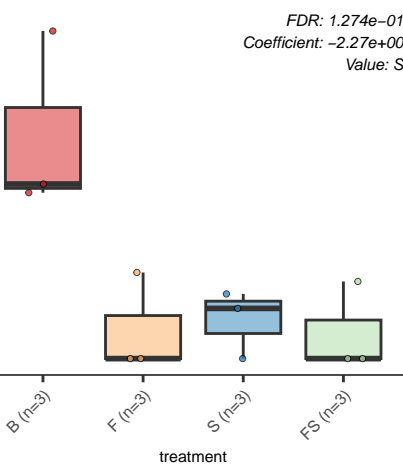
uperpathway.of.L.serine.and.glycine.biosynthesis.l.g\_\_Bifidobacteriu



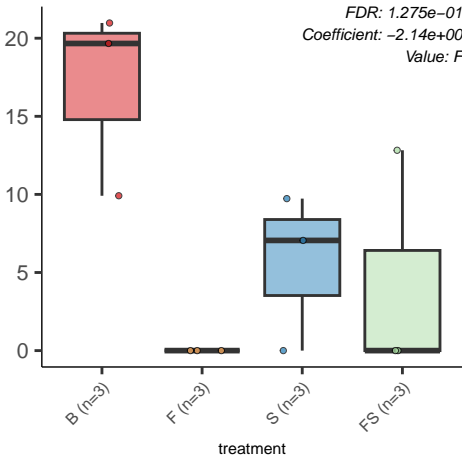


DAPLYSINESYN.PWY..L.lysine.biosynthesis.l.g\_\_Escherichia.s\_\_Es

FDR: 1.274e-01  
Coefficient: -2.27e+00  
Value: S

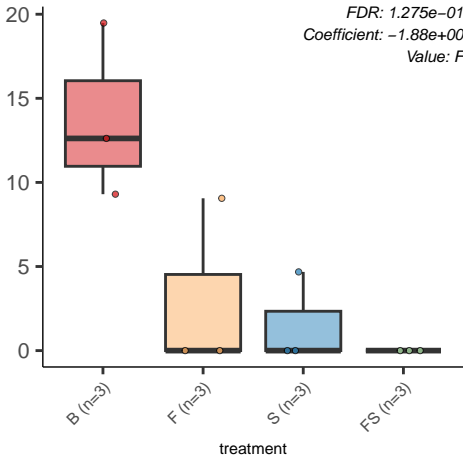


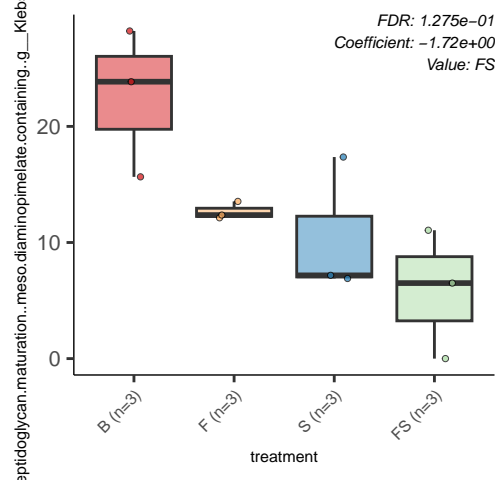
erpathway.of.adenosine.nucleotides.de.novo.biosynthesis.l.g\_Esch

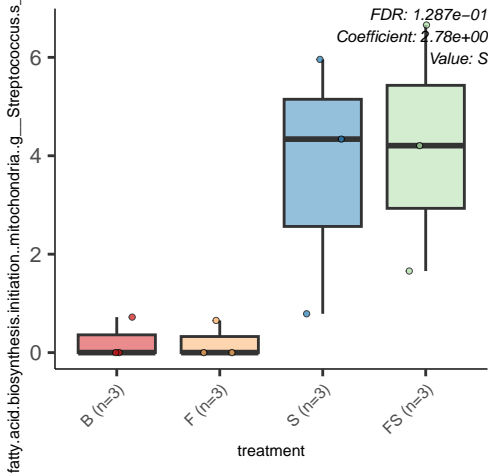


perpathway.of.purine.nucleotides.de.novo.biosynthesis.l.g\_\_Escher

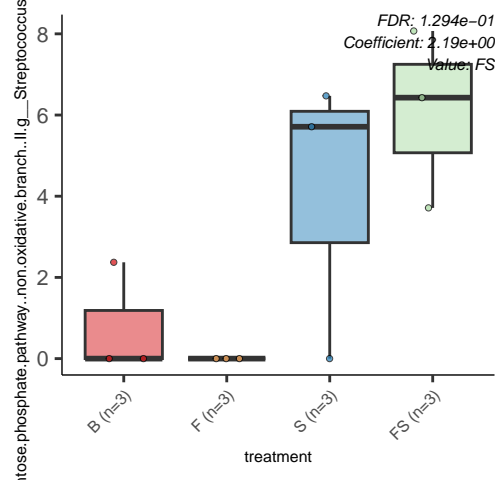
*FDR: 1.275e-01*  
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*Value: F*





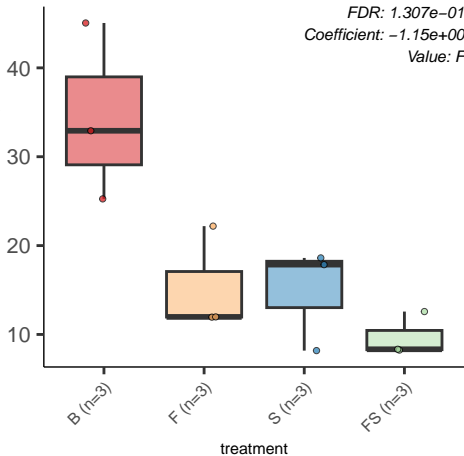


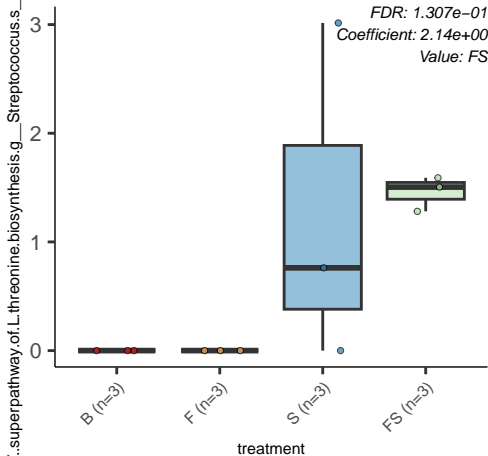




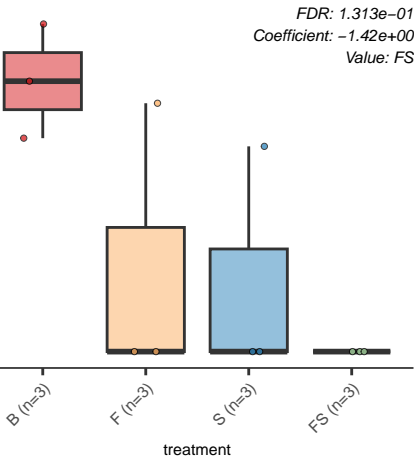
OSER.METSYN.PWY..L.methionine.biosynthesis.l.g\_\_Escherichia.s

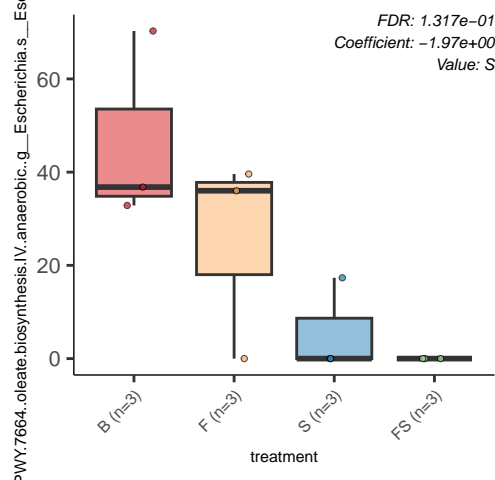
*FDR: 1.307e-01*  
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*Value: F*





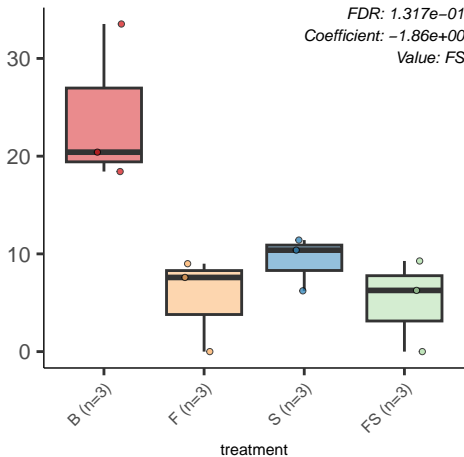
CARNMET.PWY..L.carnitine.degradation.l.g\_Escherichia.s\_Esch

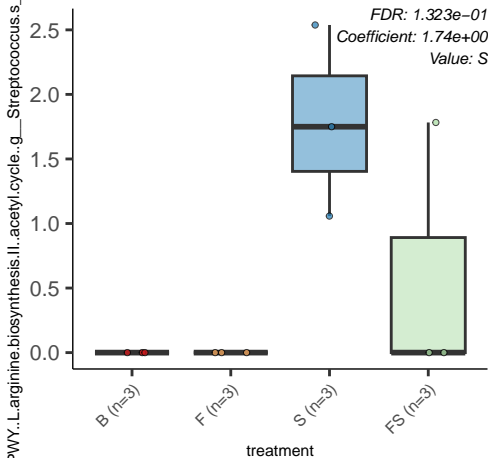




PWY.7977..L.methionine.biosynthesis.IV.g\_Escherichia.s\_Esch

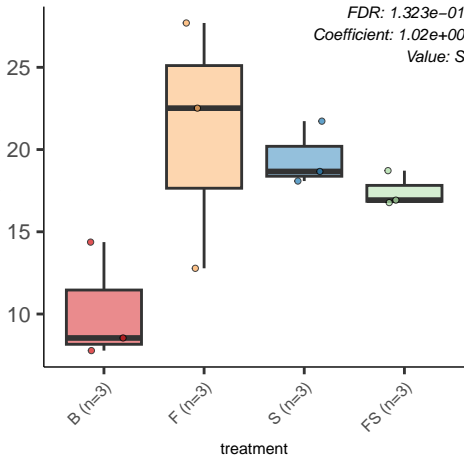
FDR: 1.317e-01  
Coefficient: -1.86e+00  
Value: FS





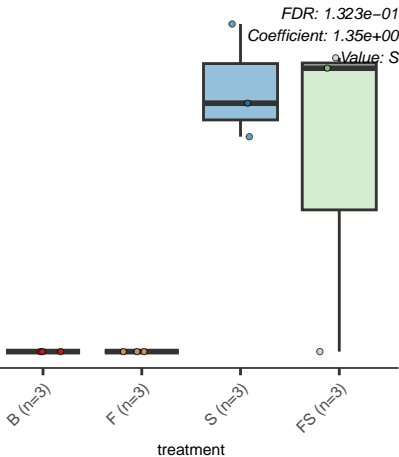
WY.6609..adenine.and.adenosine.salvage.III.g\_\_Roseburia.s\_\_Rose

*FDR: 1.323e-01*  
*Coefficient: 1.02e+00*  
*Value: S*



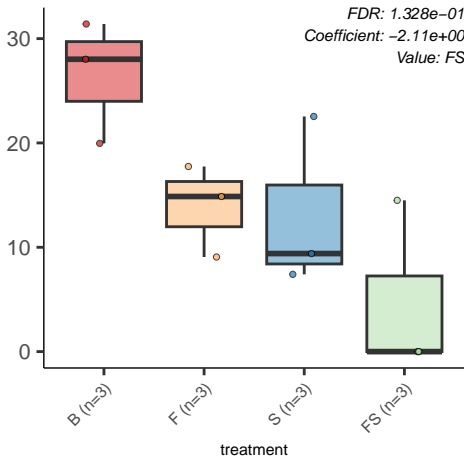


way.of.adenosine.nucleotides.de.novo.biosynthesis.l.g\_\_Streptococ

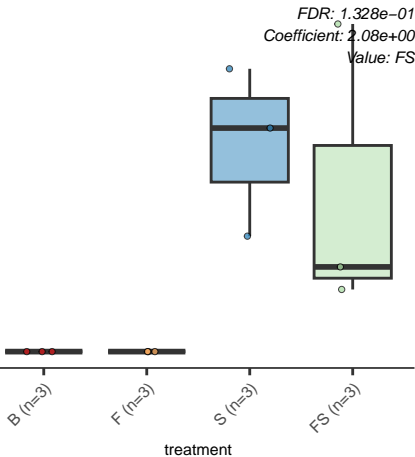


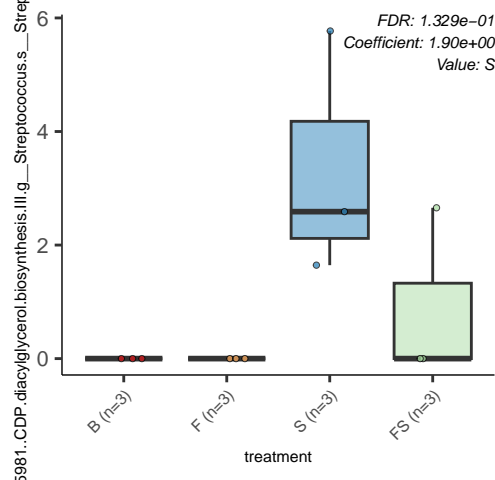
METAB.PWY..glucose.and.glucose.1.phosphate.degradation.g\_Esch

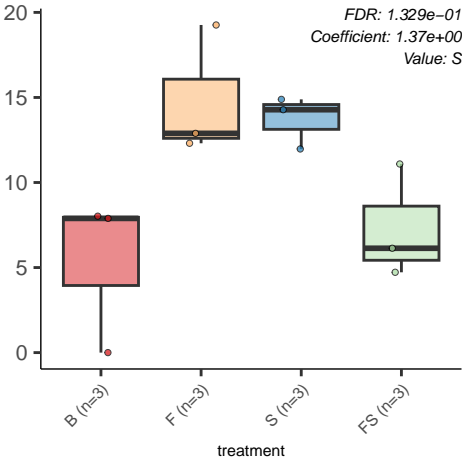
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Coefficient: -2.11e+00  
Value: FS

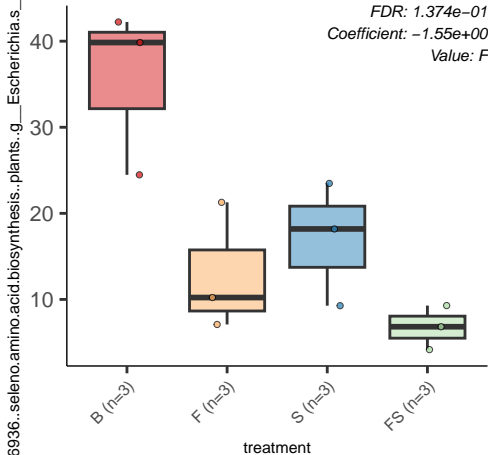


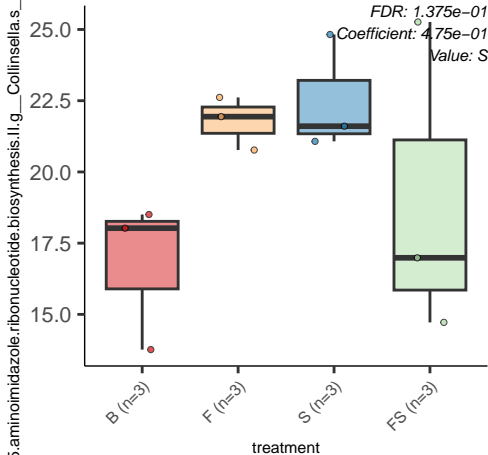
guanosine.ribonucleotides.de.novo.biosynthesis.g\_\_Streptococcus.s



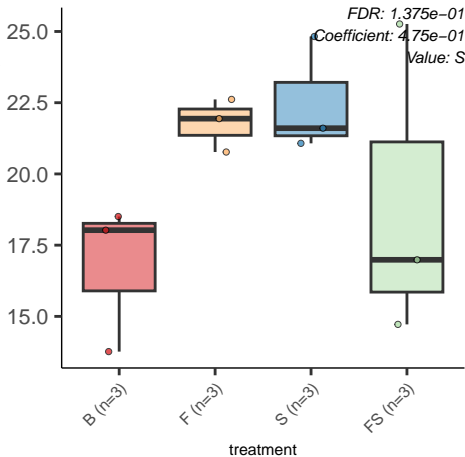








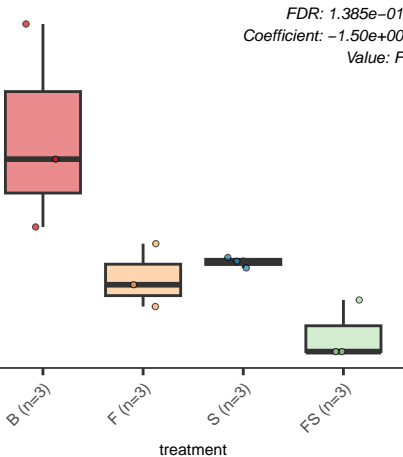
pathway.of.5.aminoimidazole.ribonucleotide.biosynthesis.g\_collins



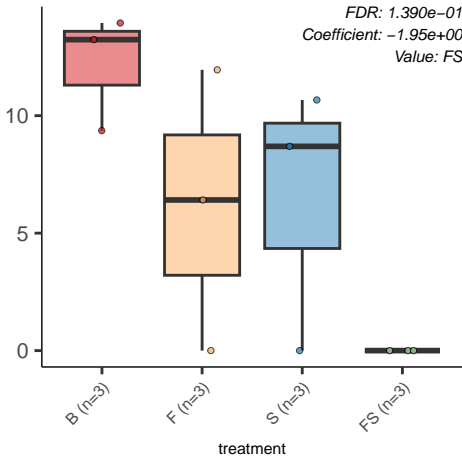


YNTH.PWY..glycogen.biosynthesis.l..from.ADP.D.Glucose.g\_Esch

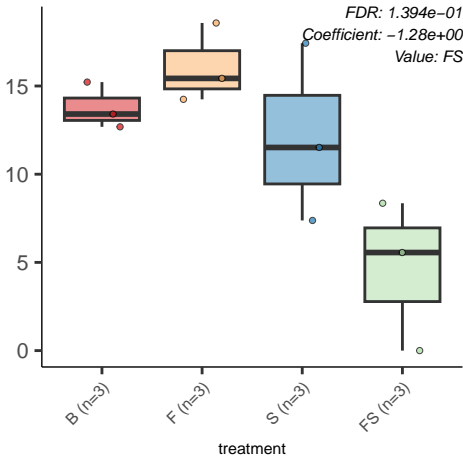
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Value: F

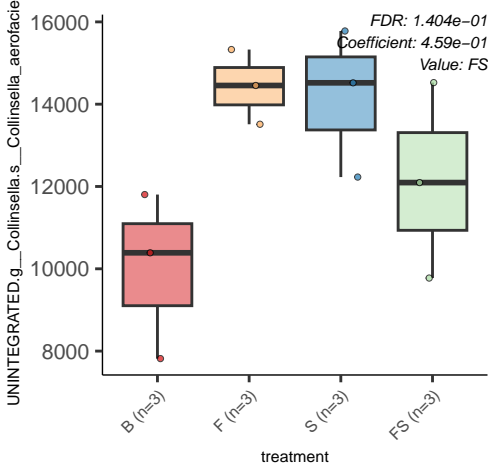


P185.PWY..formaldehyde.assimilation.III..dihydroxyacetone.cycle.



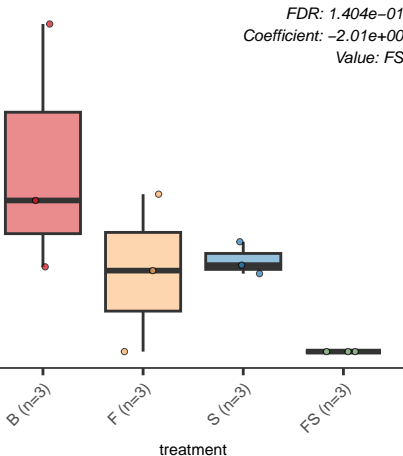
FRUCAT.PWY.homolactic.fermentation.g\_\_Catenibacterium.s\_\_Cate



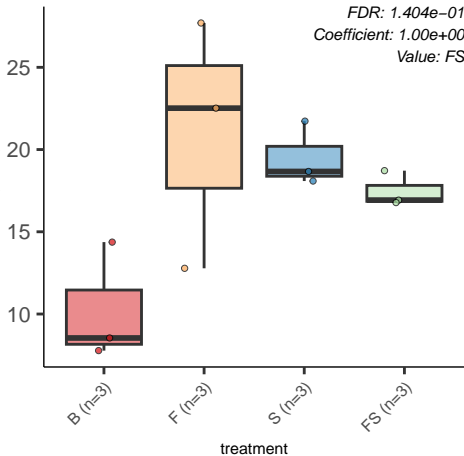


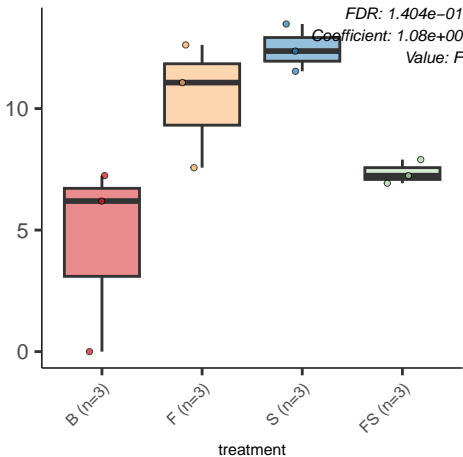
PWY.5659..GDP.mannose.biosynthesis.g\_Escherichia.s\_Esche

FDR: 1.404e-01  
Coefficient: -2.01e+00  
Value: FS

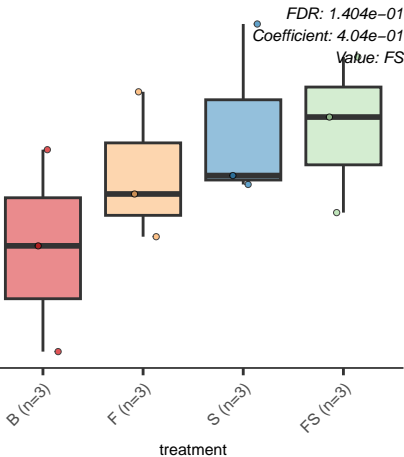


FDR: 1.404e-01  
Coefficient: 1.00e+00  
Value: FS



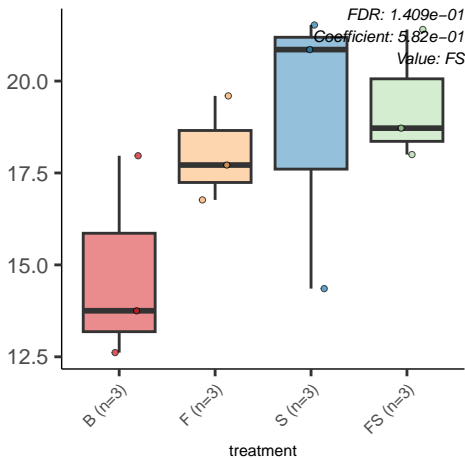


VALSYN.PWY..L.valine.biosynthesis.g\_\_Blautia.s\_\_Blautia\_w



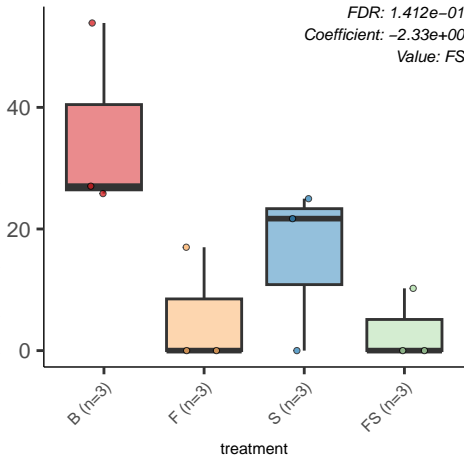


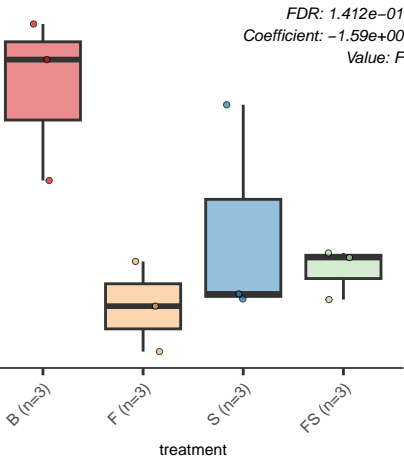
O.antigen.building.blocks.biosynthesis.E..coli..g\_\_Catenibacterium.



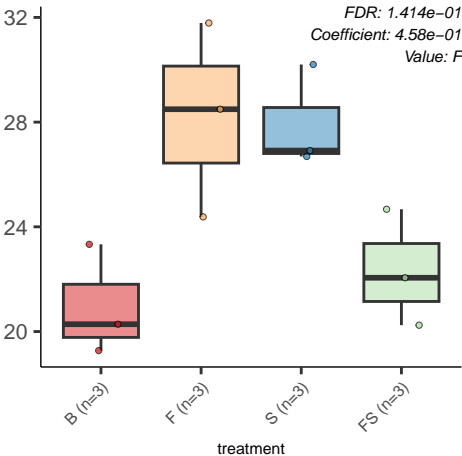
PWY.5941..glycogen.degradation.ll.g\_\_Escherichia.s\_\_Escheri

FDR: 1.412e-01  
Coefficient: -2.33e+00  
Value: FS



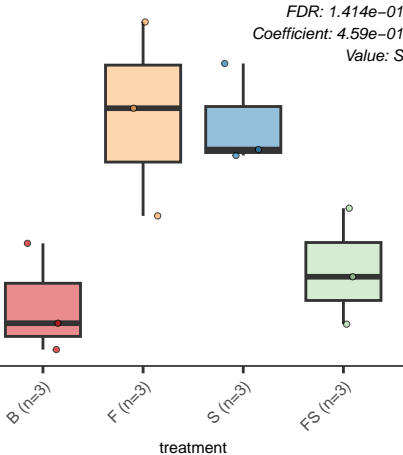


PWY.5941..glycogen.degradation.ll.g\_\_Roseburia.s\_\_Roseburia

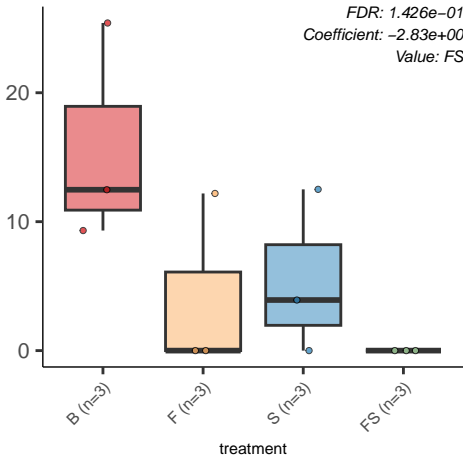


PWY.5941..glycogen.degradation.ll.g\_\_Roseburia.s\_\_Roseburia

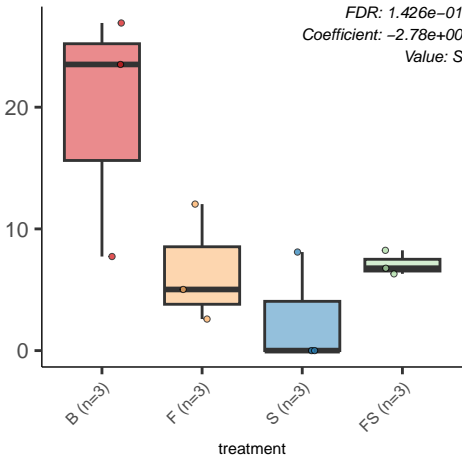
FDR: 1.414e-01  
Coefficient: 4.59e-01  
Value: S



FDR: 1.426e-01  
Coefficient: -2.83e+00  
Value: FS

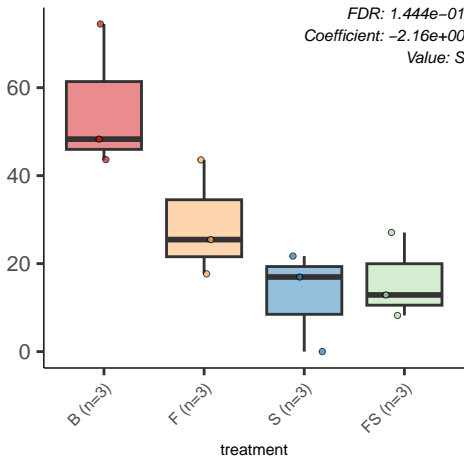


WY.6123...inosine.5..phosphate.biosynthesis.l.g\_Escherichia.s\_Es



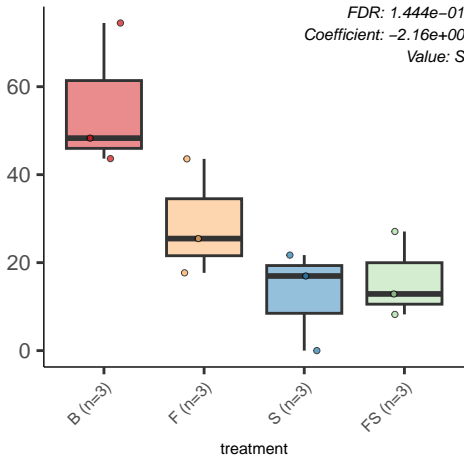
LACTARDEG.PWY..D.galactarate.degradation.l.g\_Escherichia.s

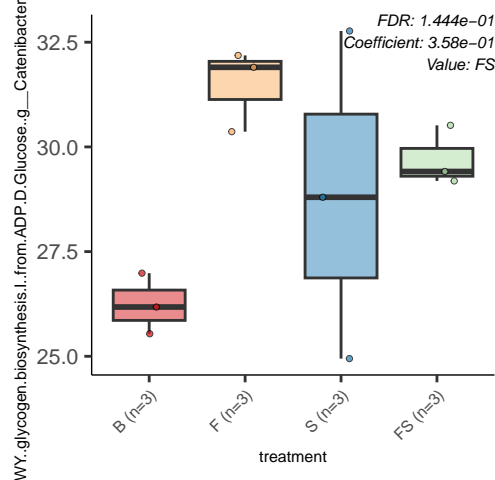
FDR: 1.444e-01  
Coefficient: -2.16e+00  
Value: S





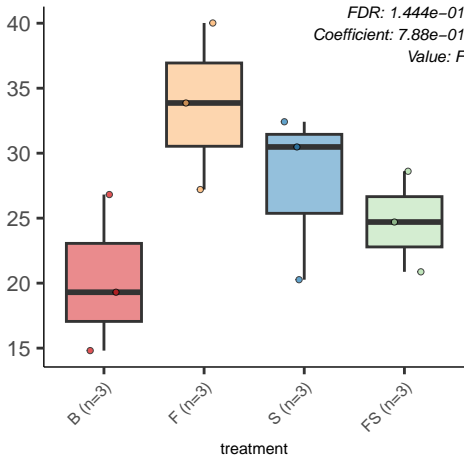
FDR: 1.444e-01  
Coefficient: -2.16e+00  
Value: S





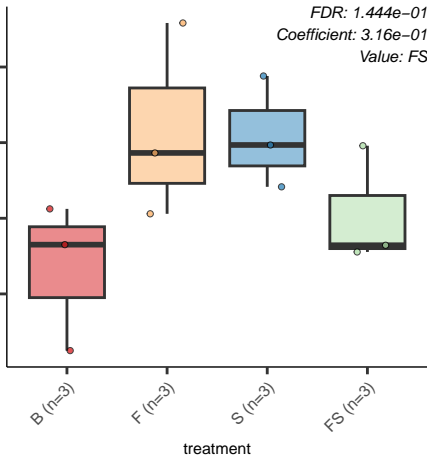
PWY.6163..chorismate.biosynthesis.from.3.dehydroquinate.uno

*FDR: 1.444e-01*  
*Coefficient: 7.88e-01*  
*Value: F*

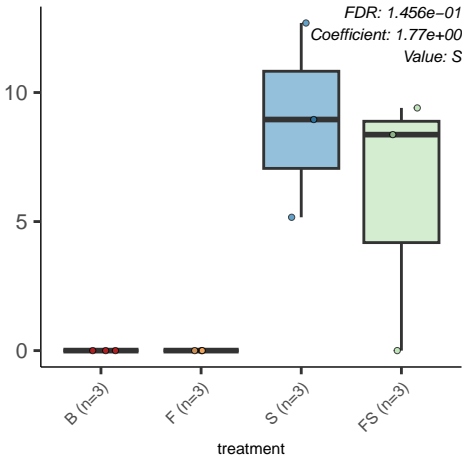


PWY.7238..sucrose.biosynthesis.II.g\_\_Collinsella.s\_\_Collinsella\_s

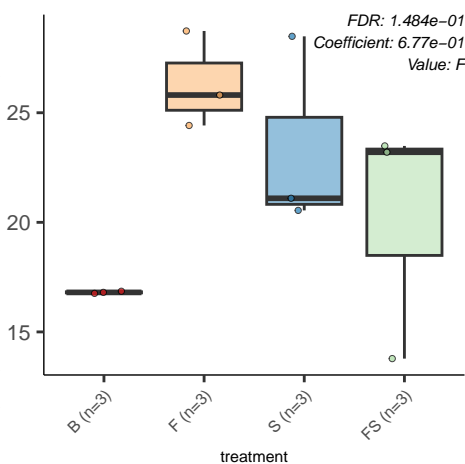
FDR: 1.444e-01  
Coefficient: 3.16e-01  
Value: FS

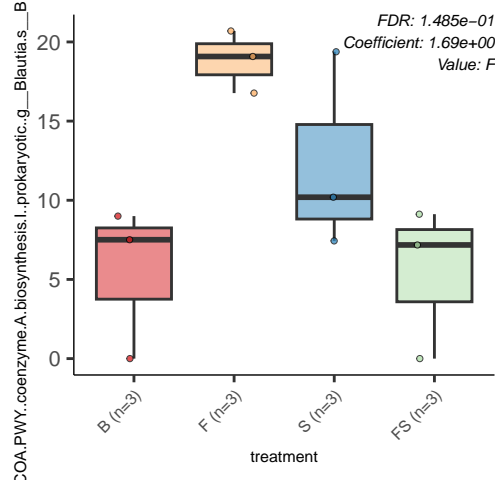


SYN.PWY..L.histidine.biosynthesis.g\_\_Streptococcus.s\_\_Streptococcus

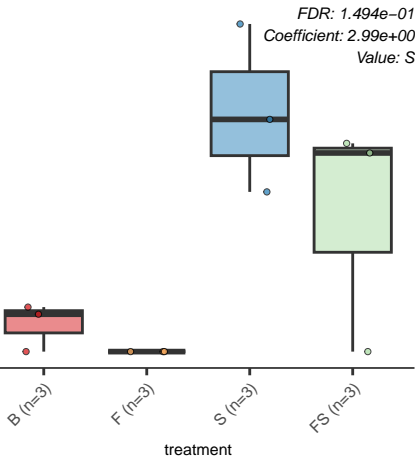


TH.PWY..glycogen.biosynthesis.l..from.ADP.D.Glucose..g\_\_Collinse



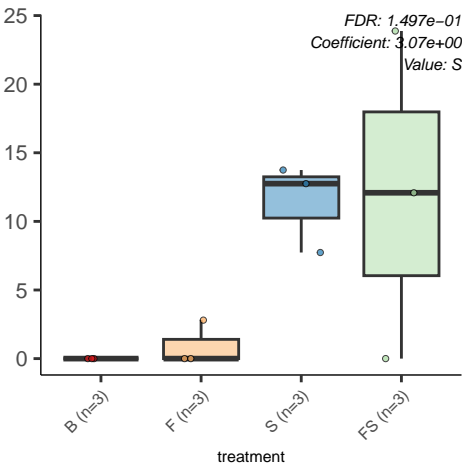


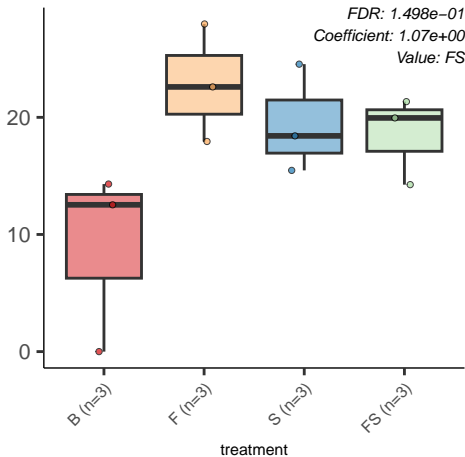
ETANA.PWY..L\_methionine.biosynthesis.III.g\_\_Streptococcus.s\_\_St





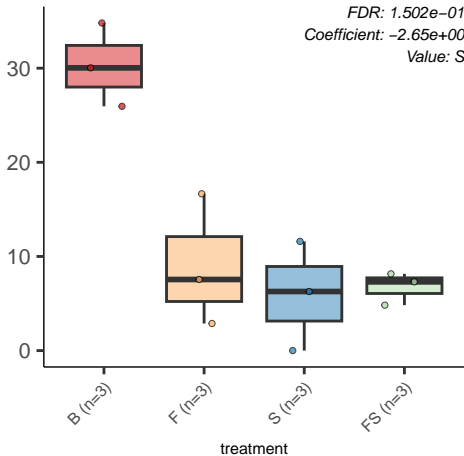
WY.7238...sucrose.biosynthesis.II.g\_\_Streptococcus





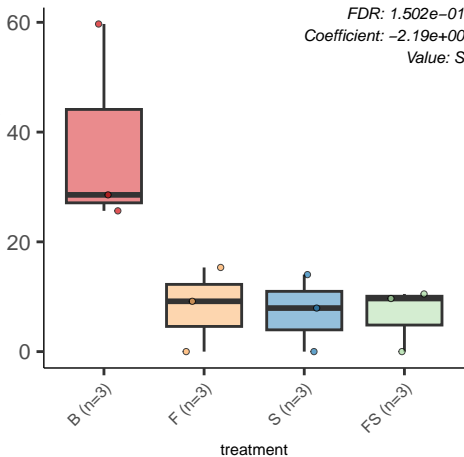
siLUCARDEG.PWY..D.glucarate.degradation..l.g\_Escherichia.s\_Es

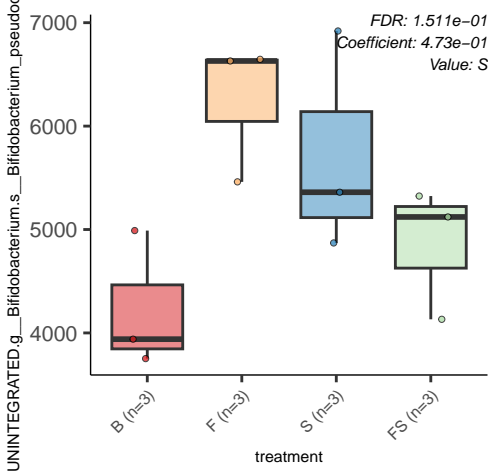
FDR: 1.502e-01  
Coefficient: -2.65e+00  
Value: S



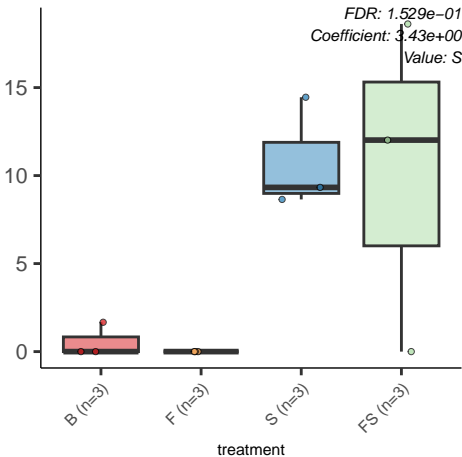
3001..superpathway.of.L.isoleucine.biosynthesis.l.g\_\_Escherichia.s

FDR: 1.502e-01  
Coefficient: -2.19e+00  
Value: S

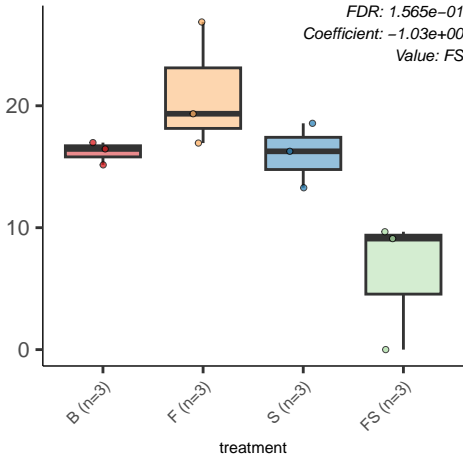




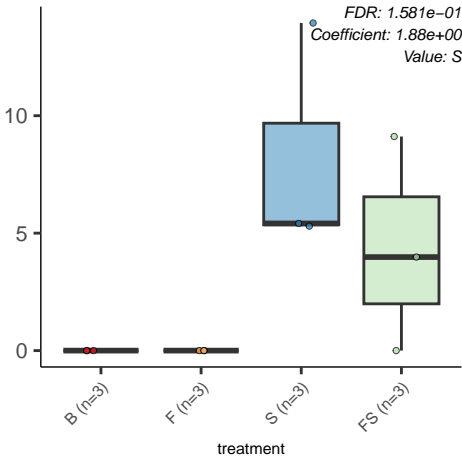
se.phosphate.pathway..non.oxidative.branch..ll.g\_\_Streptococcus.s



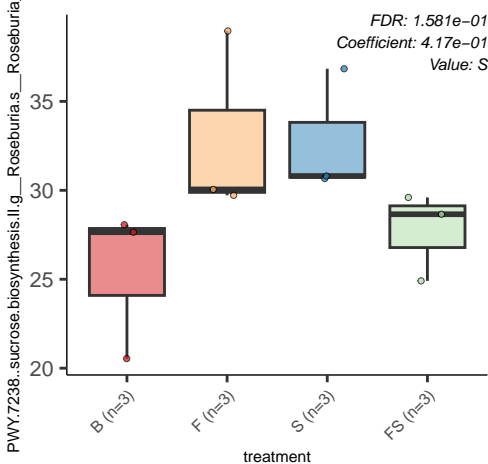
FDR: 1.565e-01  
Coefficient: -1.03e+00  
Value: FS



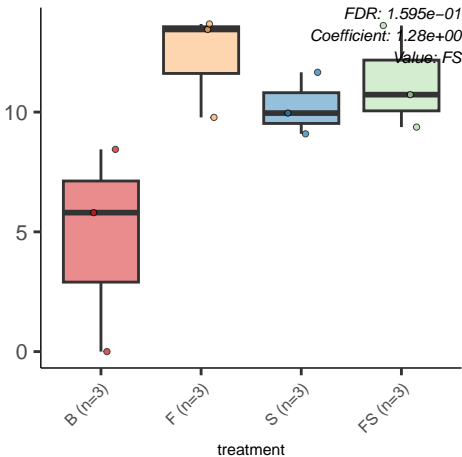
PWY.6703..preQ0.biosynthesis.g\_\_Streptococcus.s\_\_Streptococcus



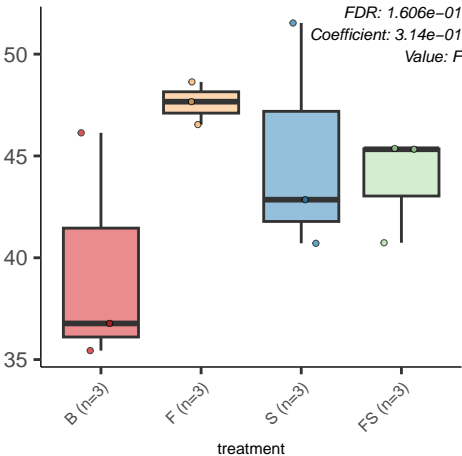




PWY.6527..stachyose.degradation.g\_\_Roseburia.s\_\_Roseburia

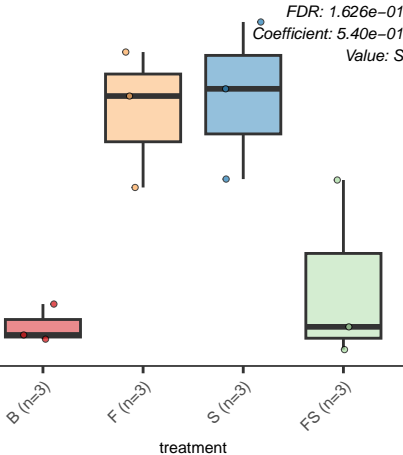


uperpathway.of.L.serine.and.glycine.biosynthesis.l.g\_\_Bifidobacteriu

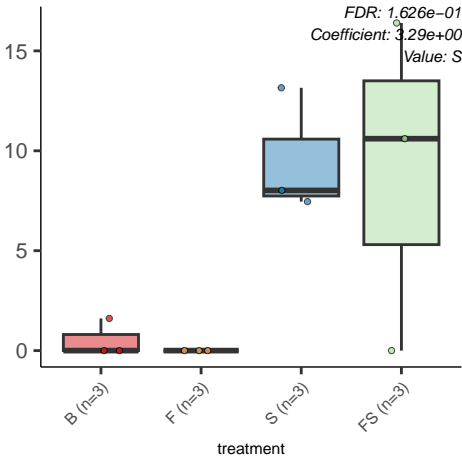


ARO.PWY..chorismate.biosynthesis.l.g\_\_Roseburia.s\_\_Roseburia

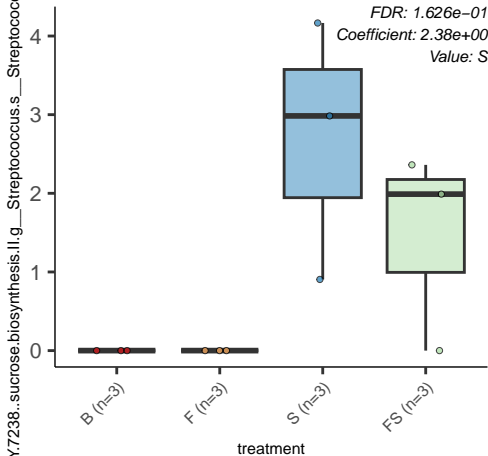
FDR: 1.626e-01  
Coefficient: 5.40e-01  
Value: S

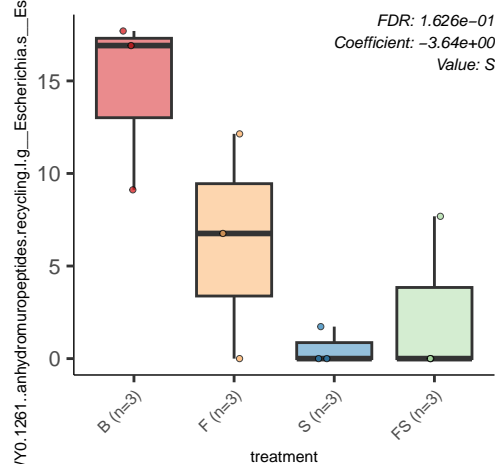


pentose.phosphate.pathway..non.oxidative.branch..l.g\_\_Streptococ

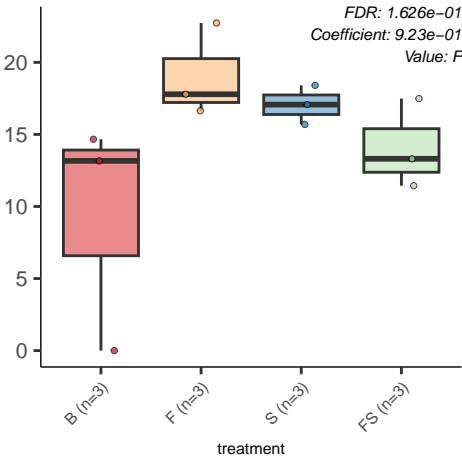


WY.7238..sucrose.biosynthesis.II.g\_\_Streptococcus.s\_\_Streptococcus



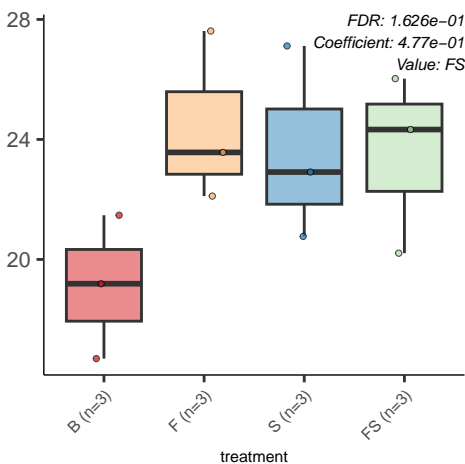


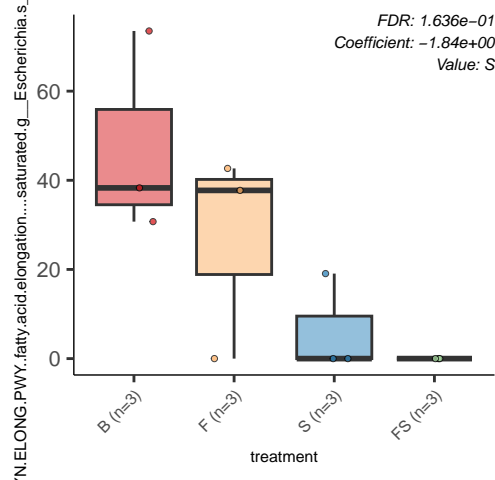
5..peptidoglycan.biosynthesis.III..mycobacteria..g\_\_Collinsella.s\_\_C





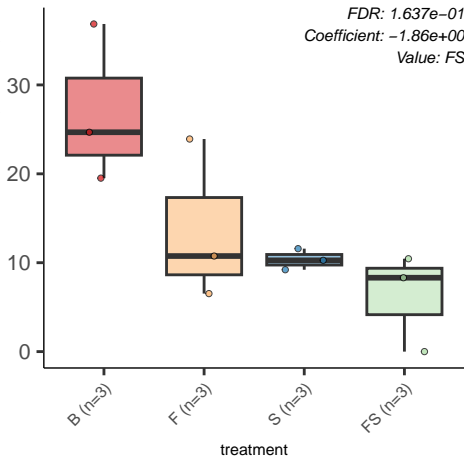
N.PWY..UDP.N.acetyl.D.glucosamine.biosynthesis.l.g\_\_Collinsella.s



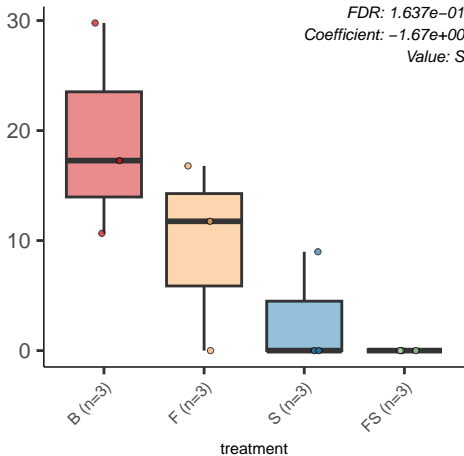


perpathway.of.pyrimidine.deoxyribonucleosides.degradation.g\_Esc

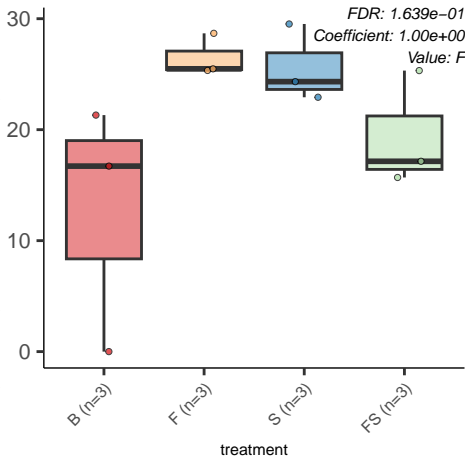
FDR: 1.637e-01  
Coefficient: -1.86e+00  
Value: FS



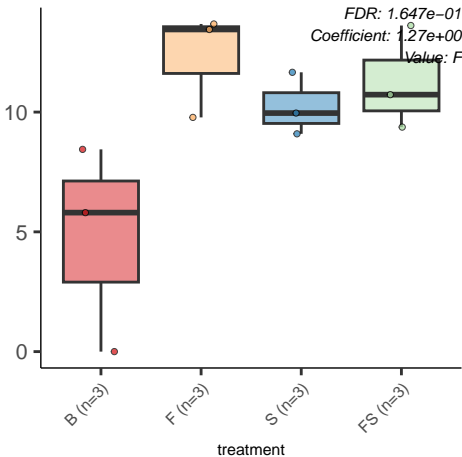
FDR: 1.637e-01  
Coefficient: -1.67e+00  
Value: S



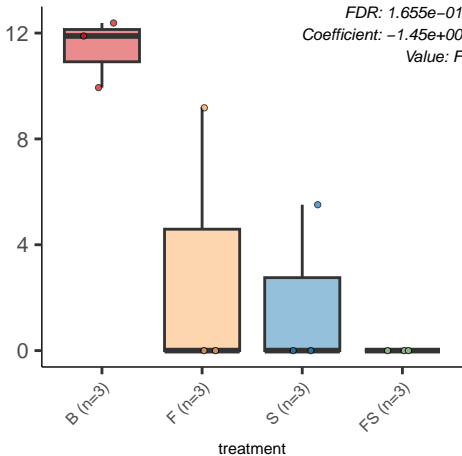
2pWY..O.antigen.building.blocks.biosynthesis..E..coli..g\_\_Collinsella.s

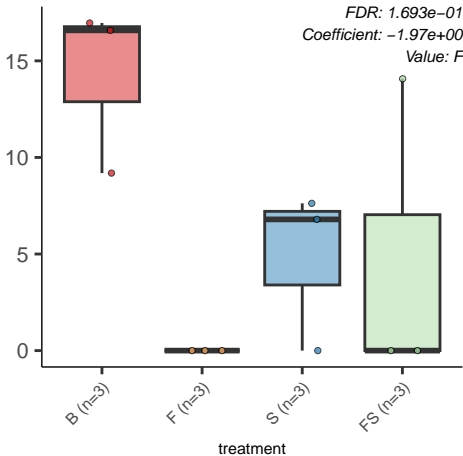


PWY.6527..stachyose.degradation.g\_\_Roseburia.s\_\_Roseburia

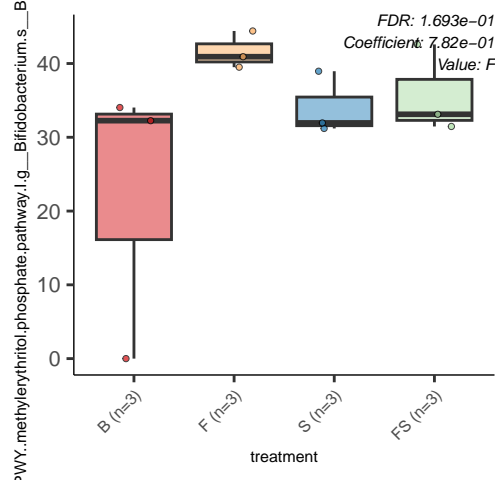


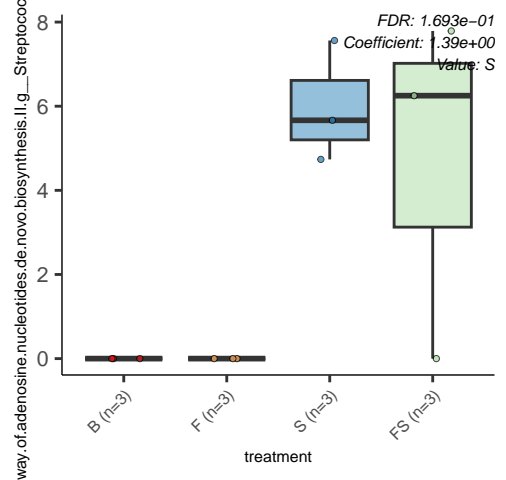
08..superpathway.of.pyrimidine.nucleobases.salvage.g\_\_Escherichia

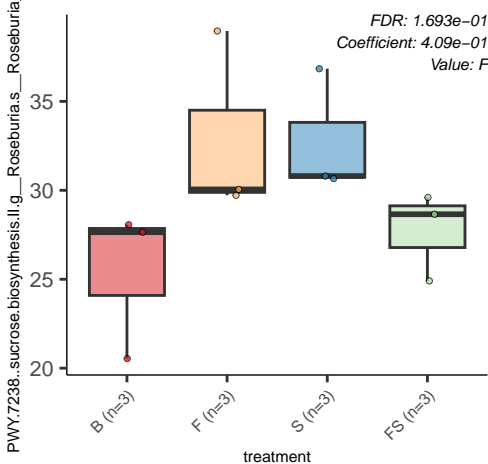


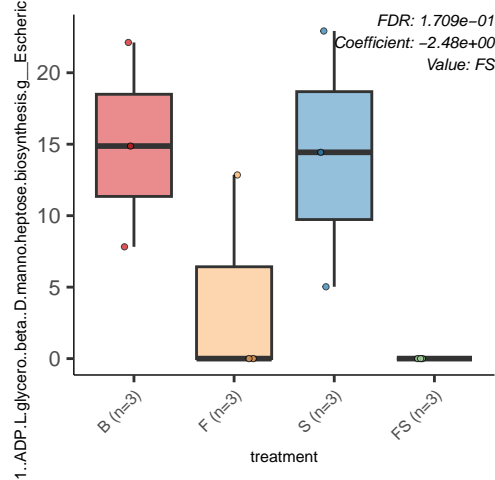






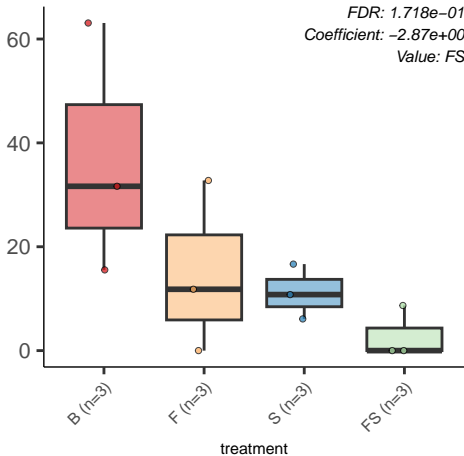






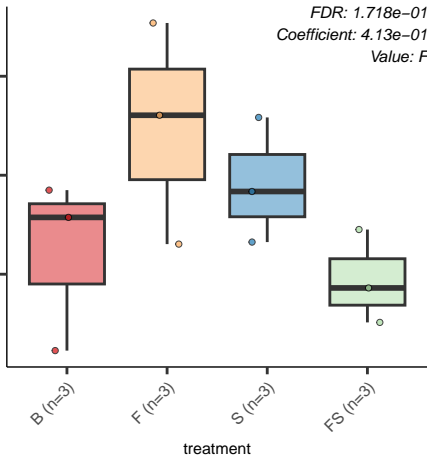
5989..stearate.biosynthesis.II..bacteria.and.plants..g\_\_Escherichia.s

FDR: 1.718e-01  
Coefficient: -2.87e+00  
Value: FS

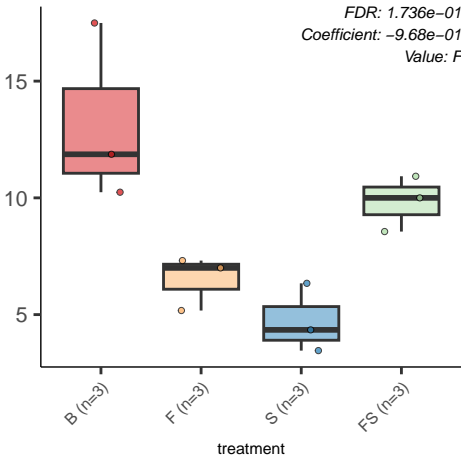


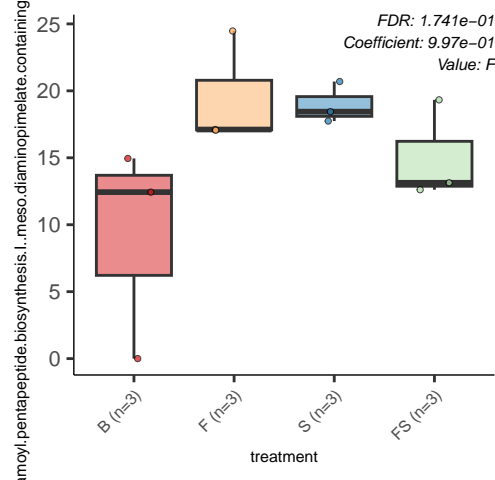
151..S.adenosyl.L.methionine.salvage.l.g\_\_Bifidobacterium.s\_\_Bifid

*FDR: 1.718e-01*  
*Coefficient: 4.13e-01*  
*Value: F*



FDR: 1.736e-01  
Coefficient: -9.68e-01  
Value: F

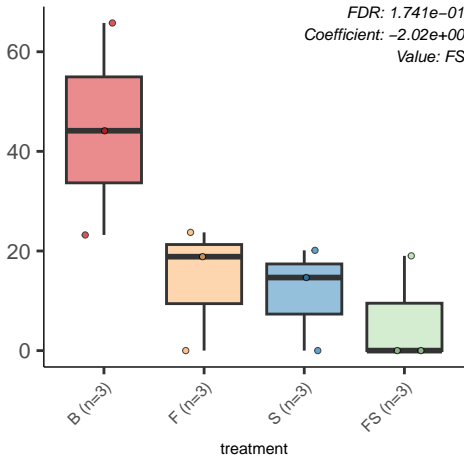






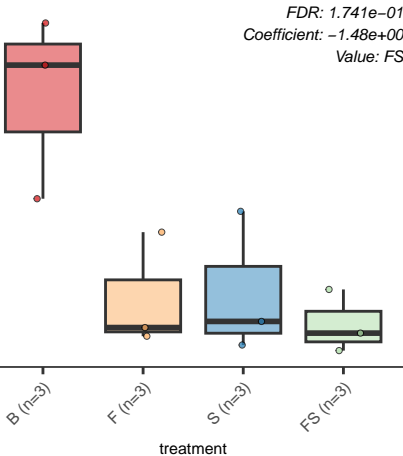
SYN.PWY..UDP.N.acetyl.D.glucosamine.biosynthesis.l.g\_\_Escherich

FDR: 1.741e-01  
Coefficient: -2.02e+00  
Value: FS



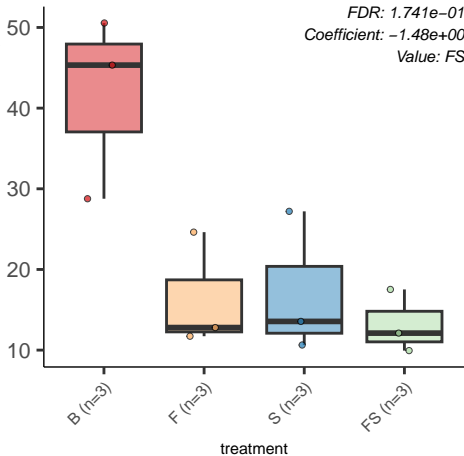
22...5.aminoimidazole.ribonucleotide.biosynthesis.II.g\_\_Escherichia

FDR: 1.741e-01  
Coefficient: -1.48e+00  
Value: FS



erpathway.of.5.aminoimidazole.ribonucleotide.biosynthesis.g\_Esch

*FDR: 1.741e-01*  
*Coefficient: -1.48e+00*  
*Value: FS*



PWY.6936..seleno.amino.acid.biosynthesis..plants..unclass

FDR: 1.754e-01  
Coefficient: 1.14e+00  
Value: FS

30  
20  
10

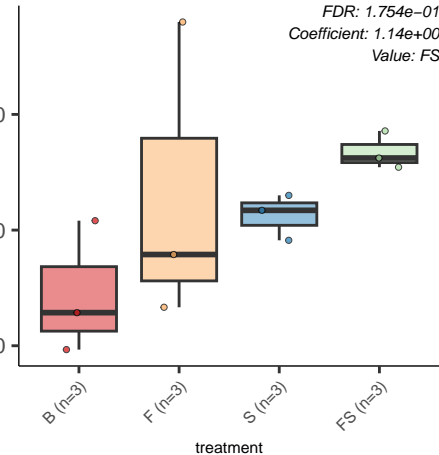
B (n=3)

F (n=3)

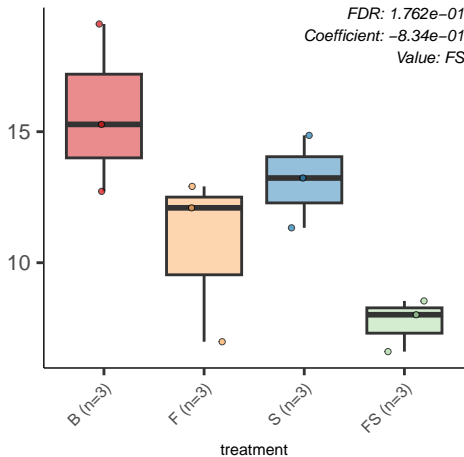
S (n=3)

FS (n=3)

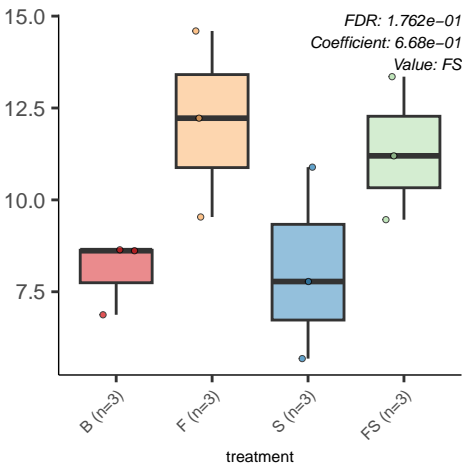
treatment



FDR: 1.762e-01  
Coefficient: -8.34e-01  
Value: FS

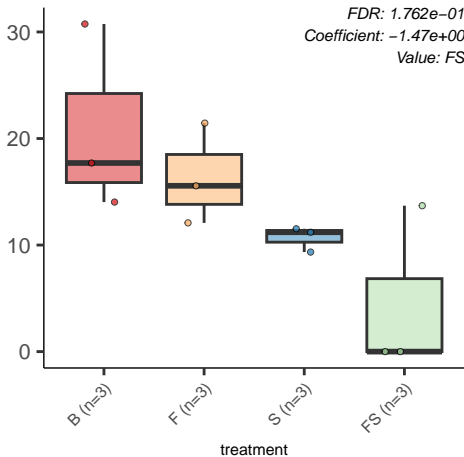


PWY.6123..inosine.5..phosphate.biosynthesis.l.g\_\_Blautia.s\_\_Blaut



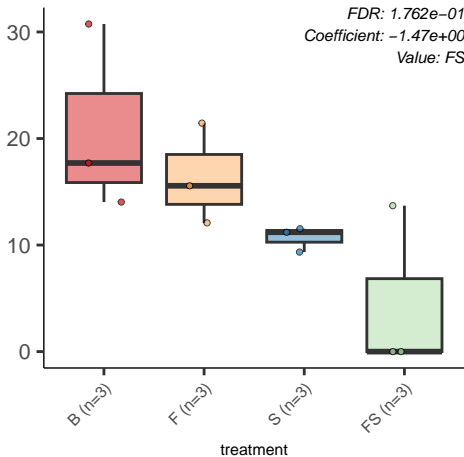
PWY4FS.7..phosphatidylglycerol.biosynthesis.l..plastidic..unc

FDR: 1.762e-01  
Coefficient: -1.47e+00  
Value: FS



PWY4FS.8..phosphatidylglycerol.biosynthesis.II..non.plasticidic.ur

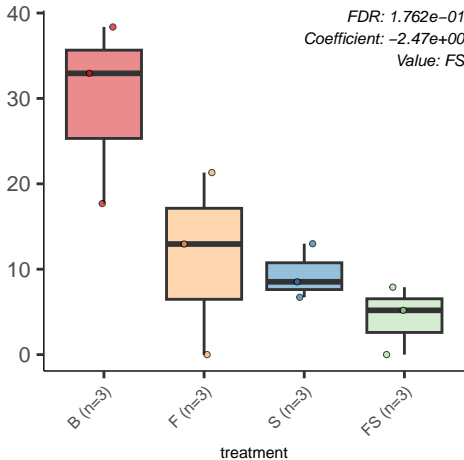
FDR: 1.762e-01  
Coefficient: -1.47e+00  
Value: FS



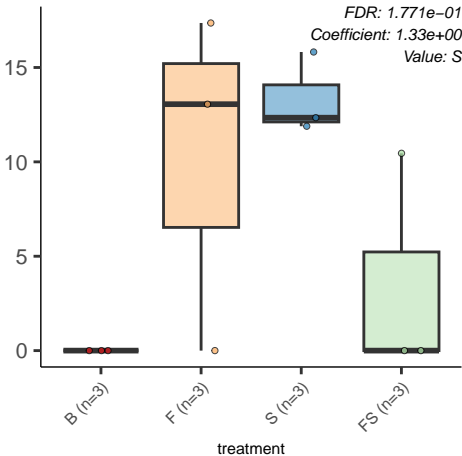


L.PWY..superpathway.of.L.serine.and.glycine.biosynthesis.l.g\_Esch

FDR: 1.762e-01  
Coefficient: -2.47e+00  
Value: FS

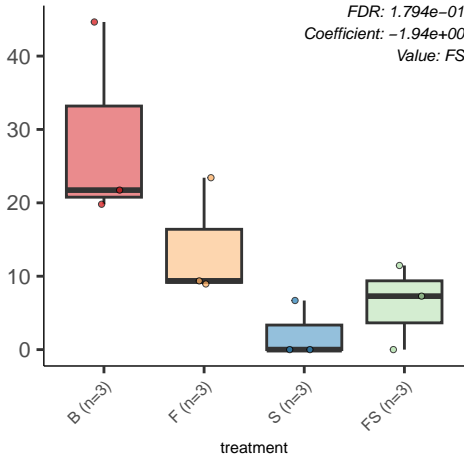


yl.pentapeptide.biosynthesis.Ill...meso.diaminopimelate.containing..g



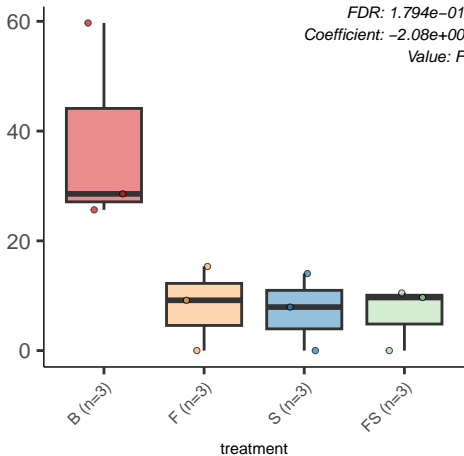
GLIPASYN.PWY..lipid.IVA.biosynthesis..E..coli..g\_Escherichia.s

FDR: 1.794e-01  
Coefficient: -1.94e+00  
Value: FS



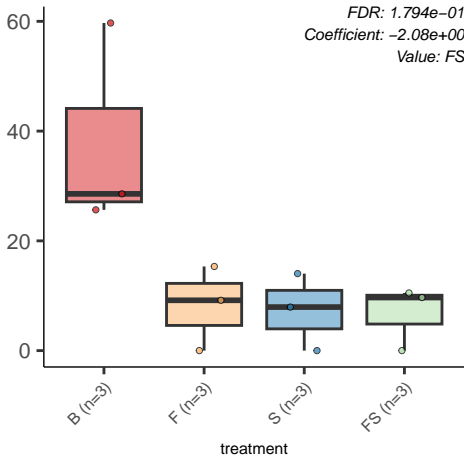
3001..superpathway.of.L.isoleucine.biosynthesis.l.g\_\_Escherichia.s

FDR: 1.794e-01  
Coefficient: -2.08e+00  
Value: F



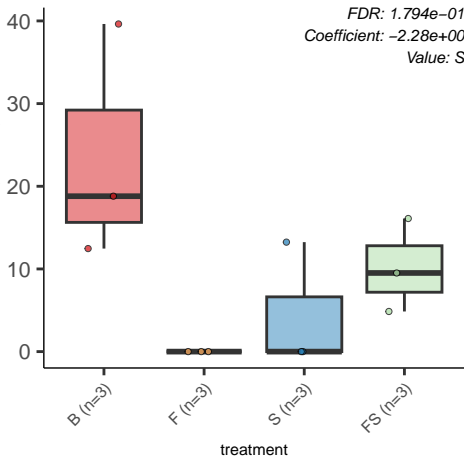
3001..superpathway.of.L.isoleucine.biosynthesis.l.g\_\_Escherichia.s

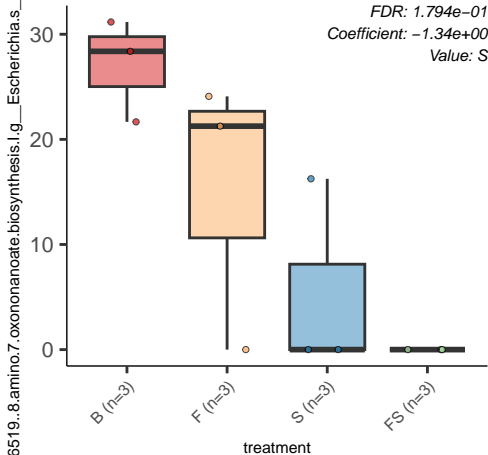
FDR: 1.794e-01  
Coefficient: -2.08e+00  
Value: FS



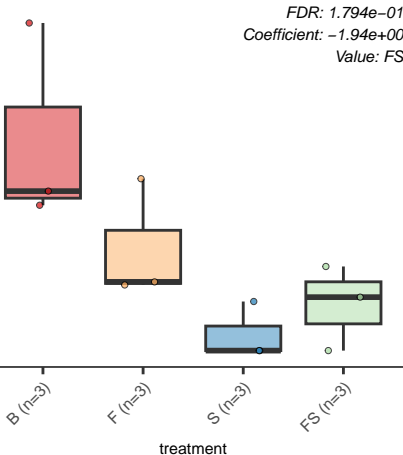
Y.5189..tetrapyrrole.biosynthesis.II...from.glycine..g\_\_Escherichia.s

FDR: 1.794e-01  
Coefficient: -2.28e+00  
Value: S

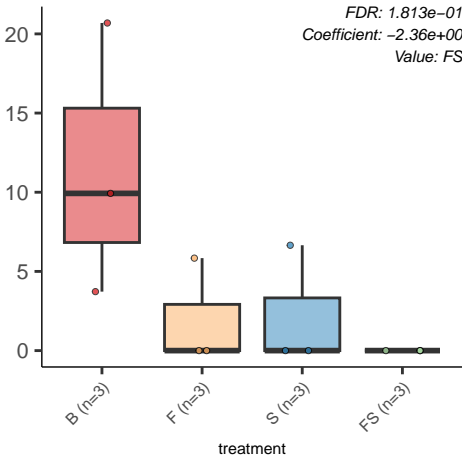


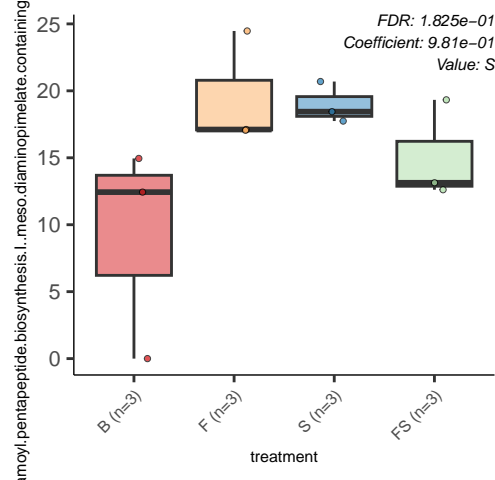


FDR: 1.794e-01  
Coefficient: -1.94e+00  
Value: FS

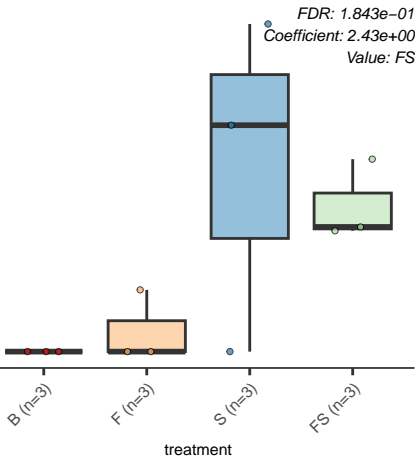






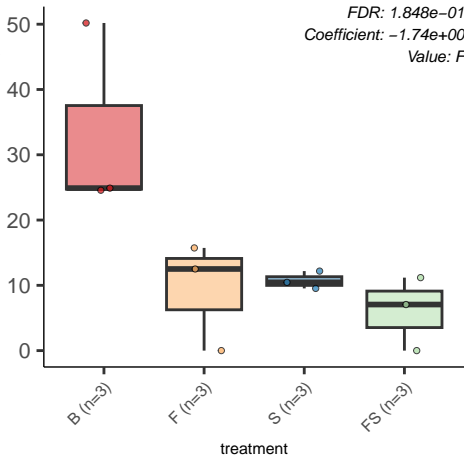


Y.702..L.methionine.biosynthesis.II.g\_\_Streptococcus.s\_\_Streptococcus



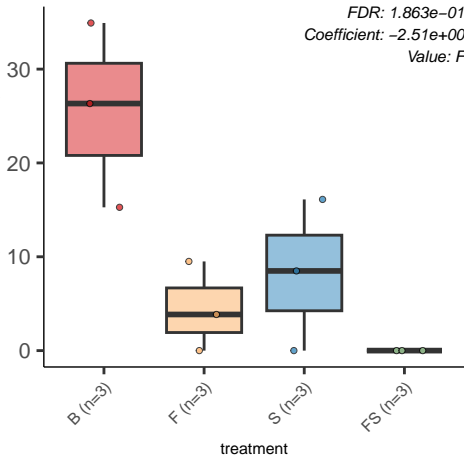
Y.Y.superpathway.of.S.adenosyl.L.methionine.biosynthesis.g\_Esche

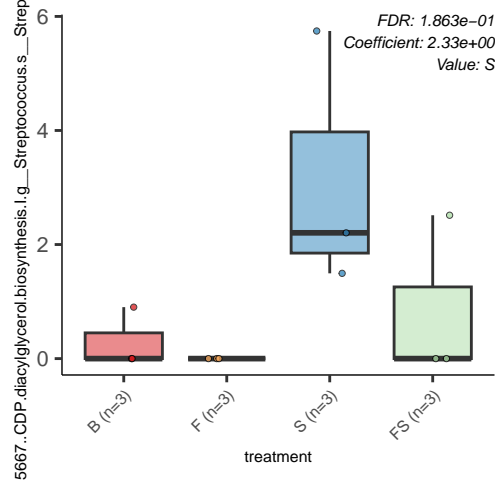
FDR: 1.848e-01  
Coefficient: -1.74e+00  
Value: F



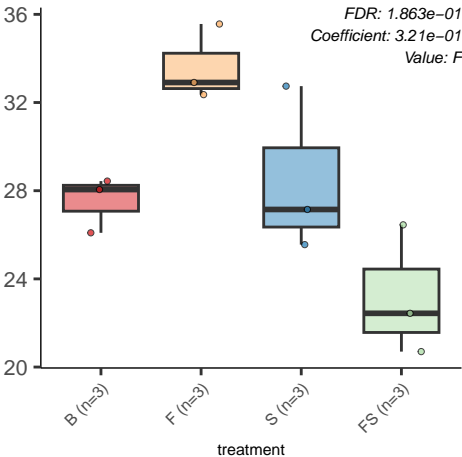
SYN.PWY..colanic.acid.building.blocks.biosynthesis.g\_\_Escherichia

FDR: 1.863e-01  
Coefficient: -2.51e+00  
Value: F

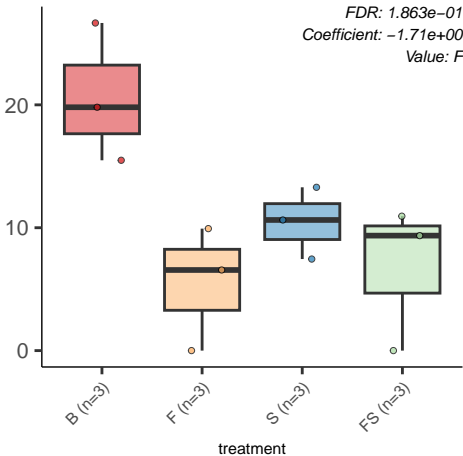




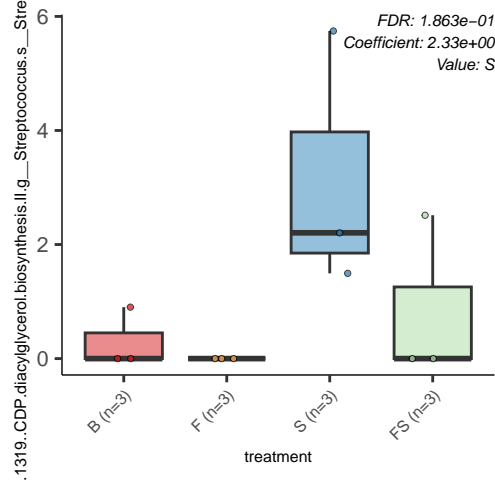
WY.7238..sucrose.biosynthesis.ll.g\_\_Bifidobacterium.s\_\_Bifidobact

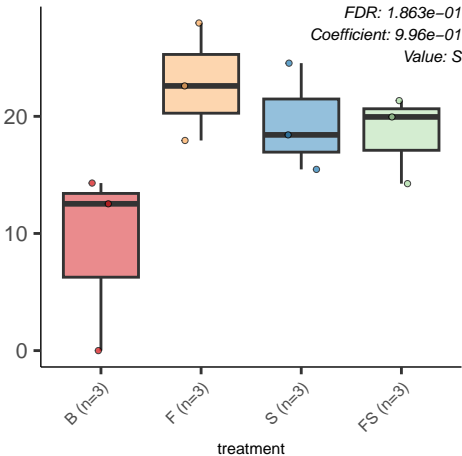


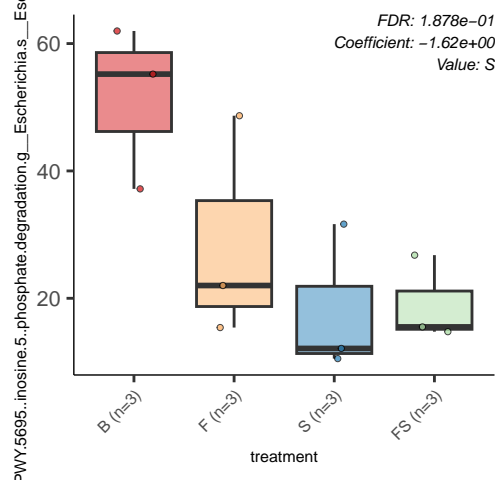
l9..L..cysteine.biosynthesis.Vl..from.L..methionine..g\_\_Escherichia.s...

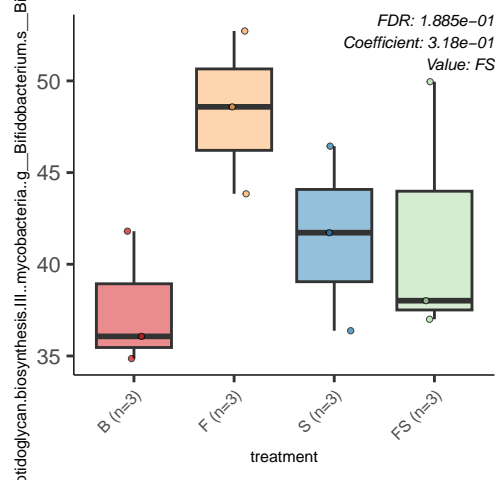






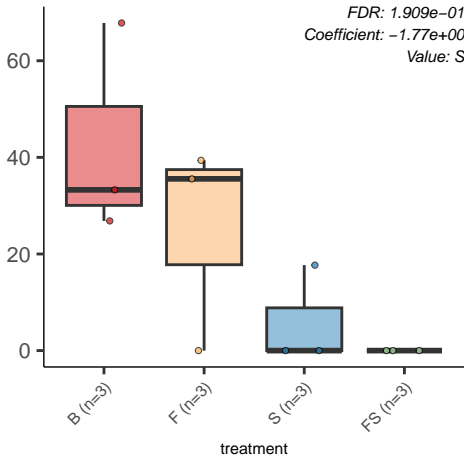




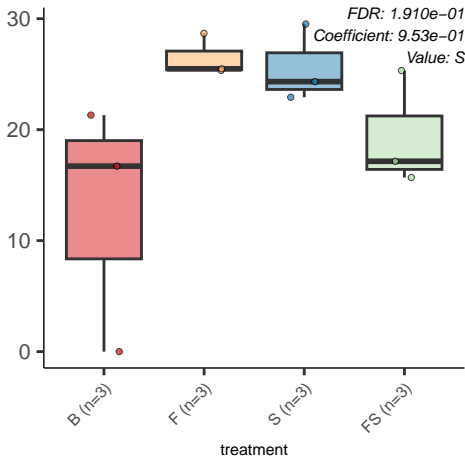


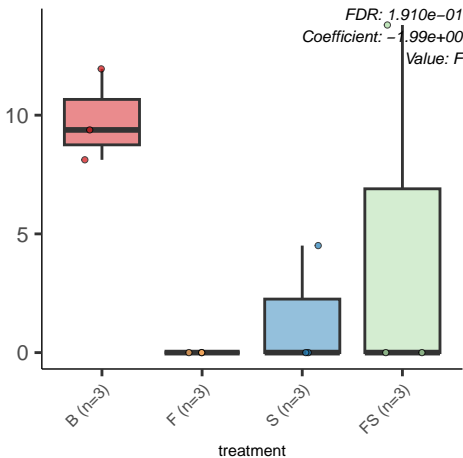
...palmitoleate.biosynthesis.l.from..5Z...dodec.5.enoate..g\_\_Escheria

FDR: 1.909e-01  
Coefficient: -1.77e+00  
Value: S



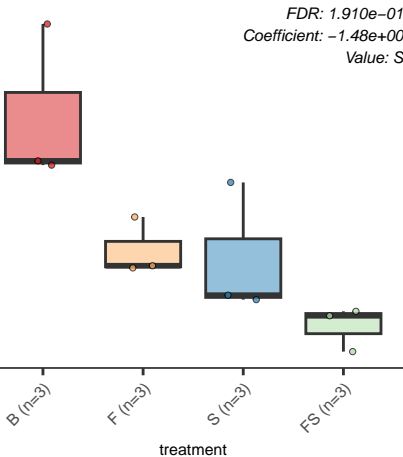
2pWY..O.antigen.building.blocks.biosynthesis..E..coli..g\_\_Collinsella.s





PWY0.1477..ethanolamine.utilization.g\_Escherichia.s\_Escher

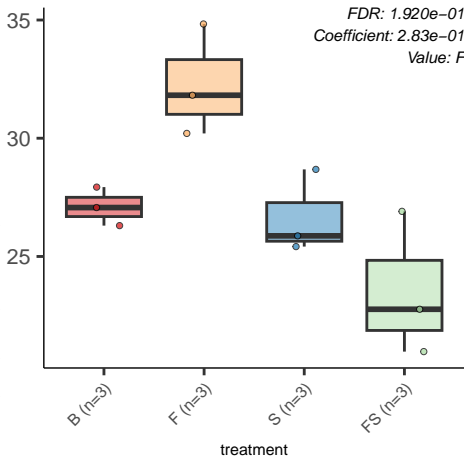
FDR: 1.910e-01  
Coefficient: -1.48e+00  
Value: S





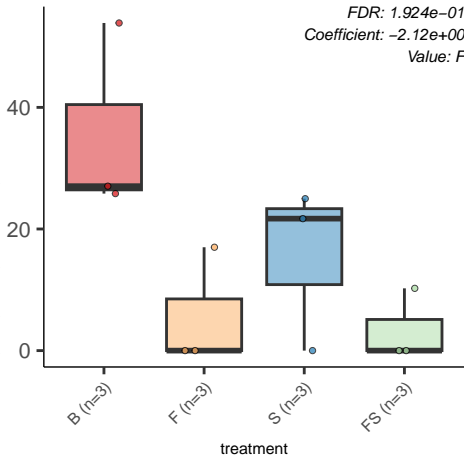
WY.5941..glycogen.degradation.ll.g\_\_Bifidobacterium.s\_\_Bifidobact

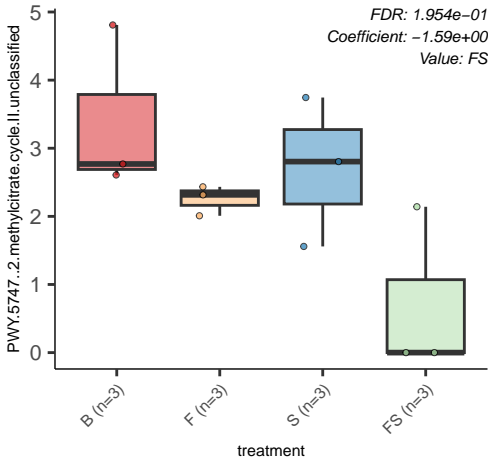
*FDR: 1.920e-01*  
*Coefficient: 2.83e-01*  
*Value: F*

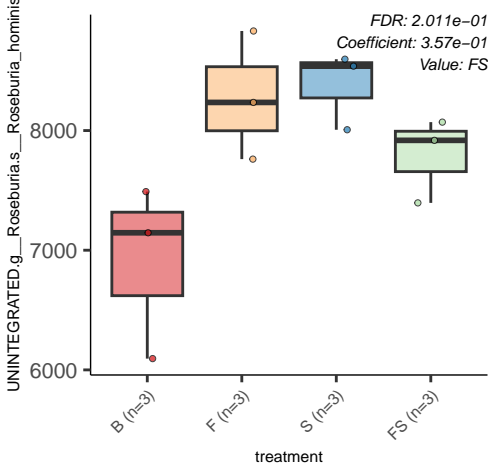


PWY.5941..glycogen.degradation.ll.g\_\_Escherichia.s\_\_Escheri

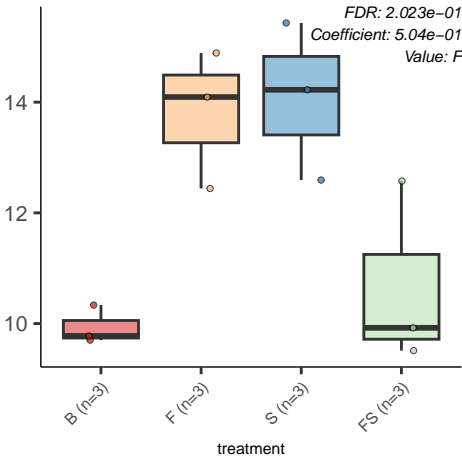
*FDR: 1.924e-01*  
*Coefficient: -2.12e+00*  
*Value: F*

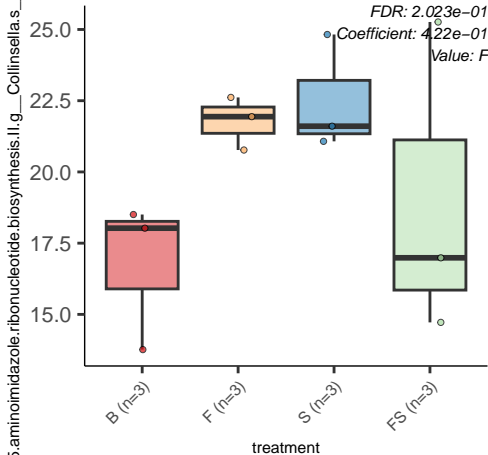




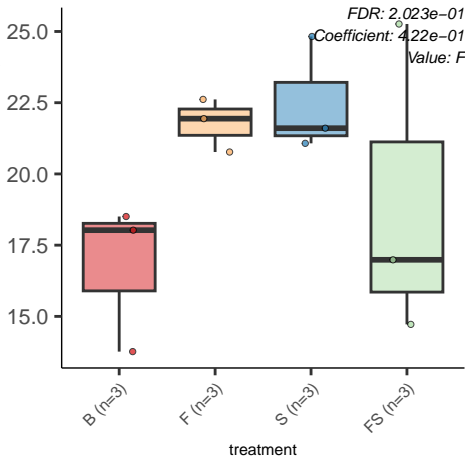


ARO.PWY..chorismate.biosynthesis.l.g\_\_Roseburia.s\_\_Roseburia

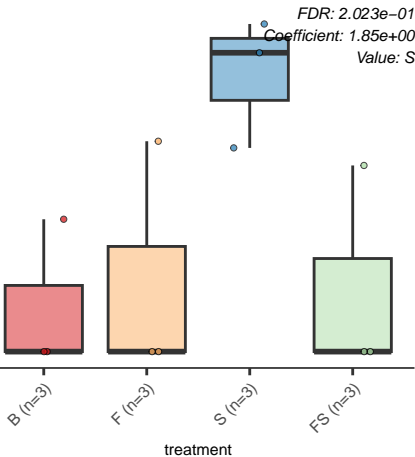




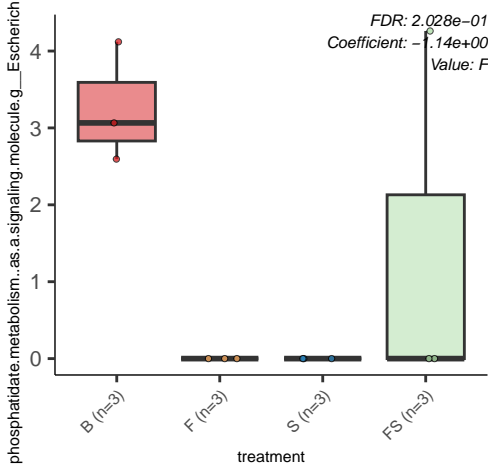
pathway.of.5.aminoimidazole.ribonucleotide.biosynthesis.g\_collins

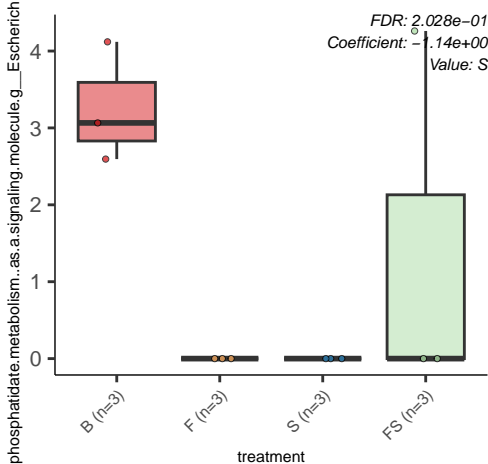


N2.PWY..flavin.biosynthesis.l..bacteria.and.plants..g\_\_Bacteroides.s



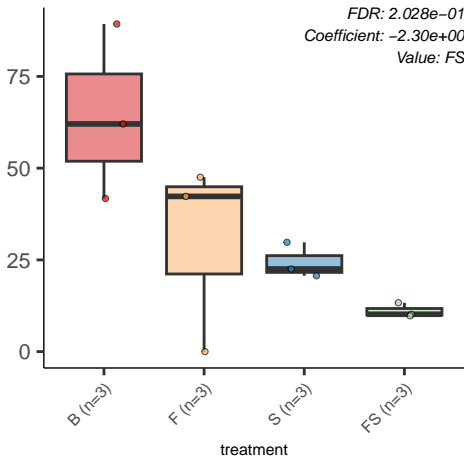






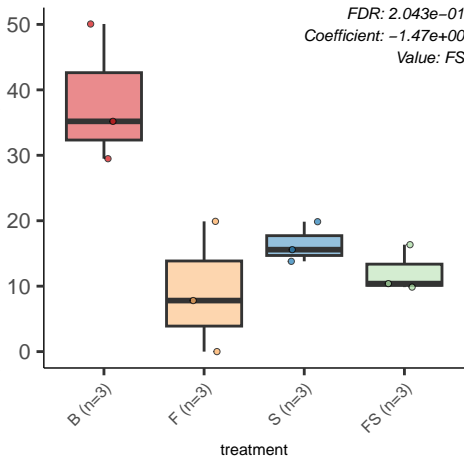
WY.7663..gondate.biosynthesis..anaerobic..g\_\_Escherichia.s\_\_Es

FDR: 2.028e-01  
Coefficient: -2.30e+00  
Value: FS



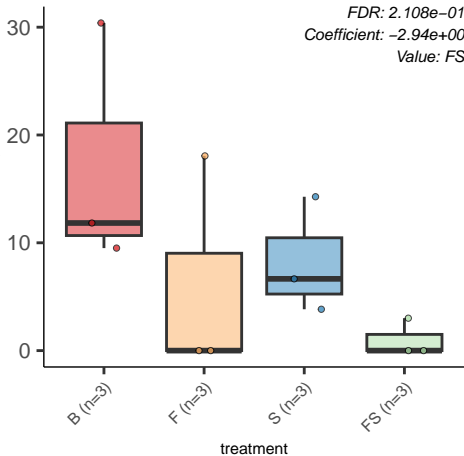
YN.PWY..L-arginine.biosynthesis.l..via.L-ornithine.g\_\_Escherichia.s

FDR: 2.043e-01  
Coefficient: -1.47e+00  
Value: FS



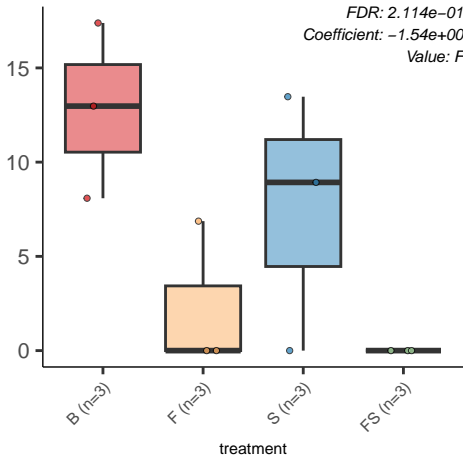
PWY.3841...folate.transformations.II..plants.g\_Escherichia.s\_Esc

FDR: 2.108e-01  
Coefficient: -2.94e+00  
Value: FS

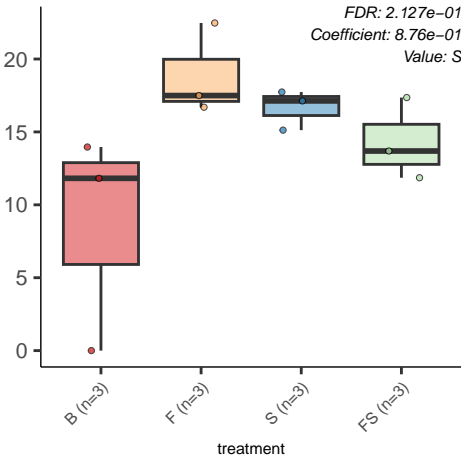


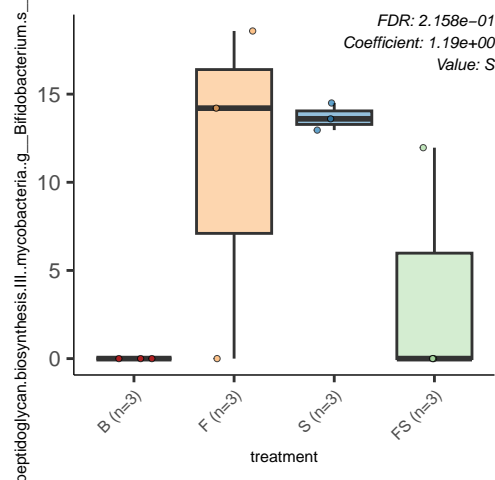
#AMSYN.PWY..dTDP..beta..L.rhamnose.biosynthesis.g\_\_Escherich

FDR: 2.114e-01  
Coefficient: -1.54e+00  
Value: F



Y..peptidoglycan.biosynthesis.l..meso.diaminopimelate.containing..g

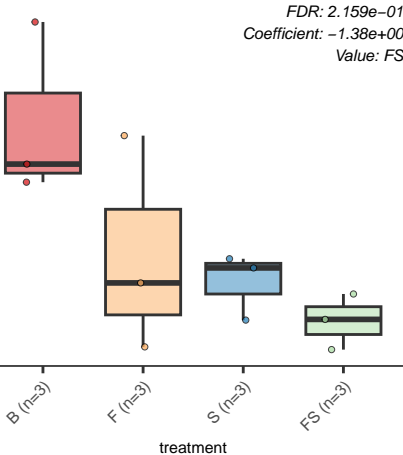


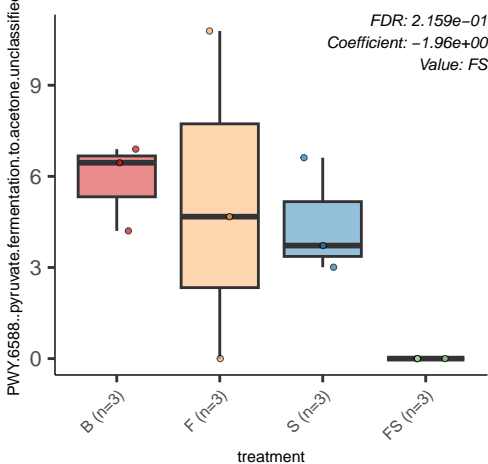




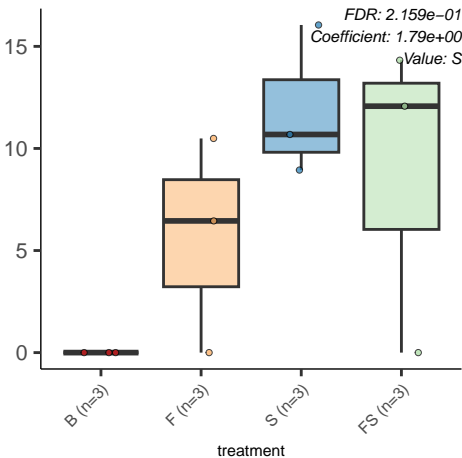
GLUTORN.PWY..L.ornithine.biosynthesis.l.g\_Escherichia.s\_Esc

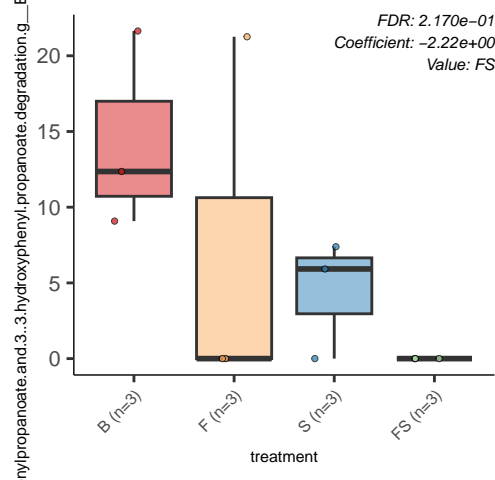
FDR: 2.159e-01  
Coefficient: -1.38e+00  
Value: FS





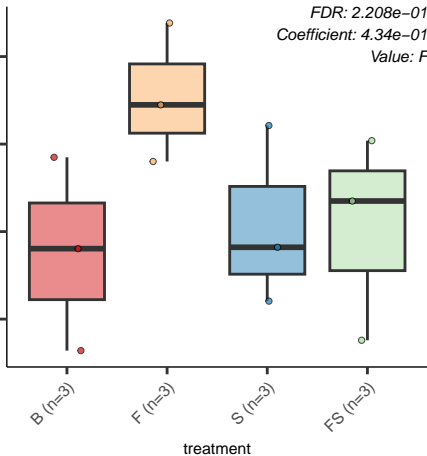
a.phosphate.formation.from.pyrithiamine.and.oxythiamine..yeast..g

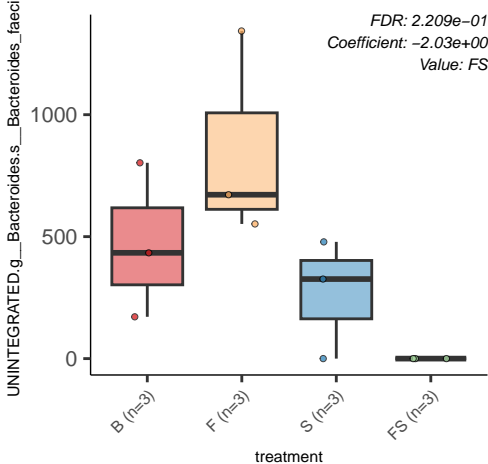




ucose.degradation.IV..sucrose.phosphorylase..g\_\_Bifidobacterium.s

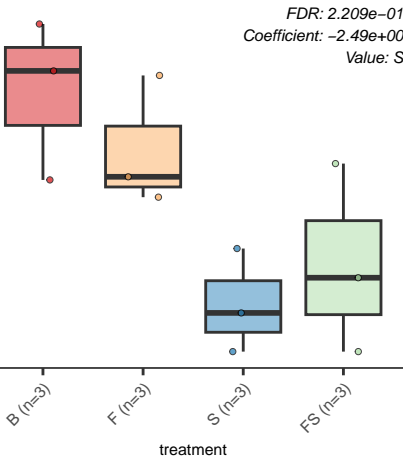
*FDR: 2.208e-01*  
*Coefficient: 4.34e-01*  
*Value: F*

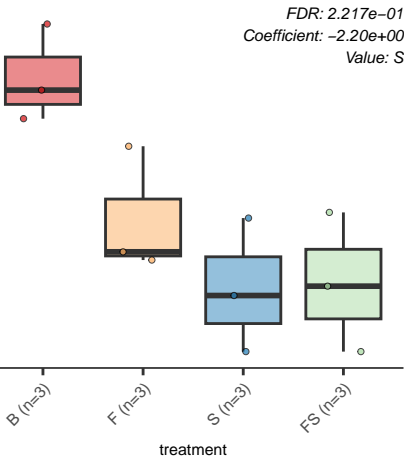




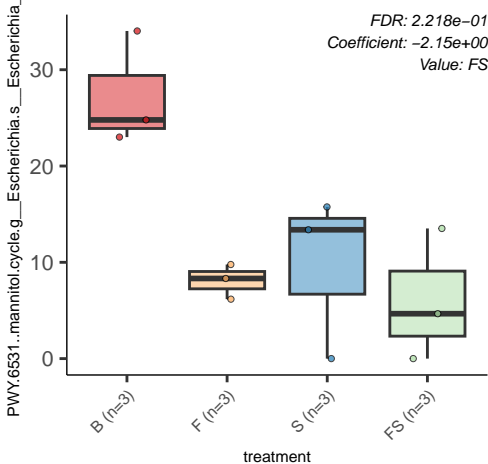
ARO.PWY..chorismate.biosynthesis.l.g\_Escherichia.s\_Escher

FDR: 2.209e-01  
Coefficient: -2.49e+00  
Value: S

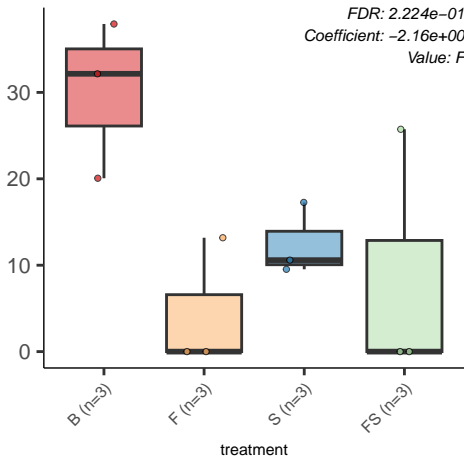


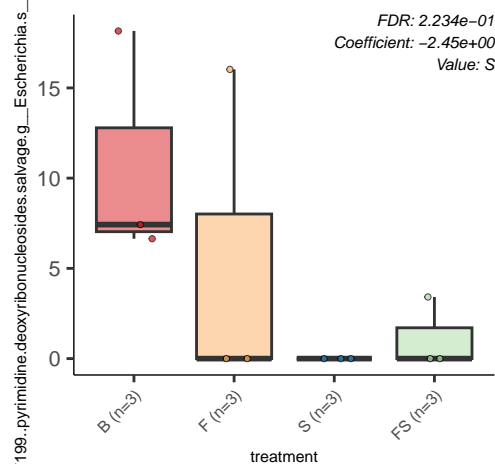


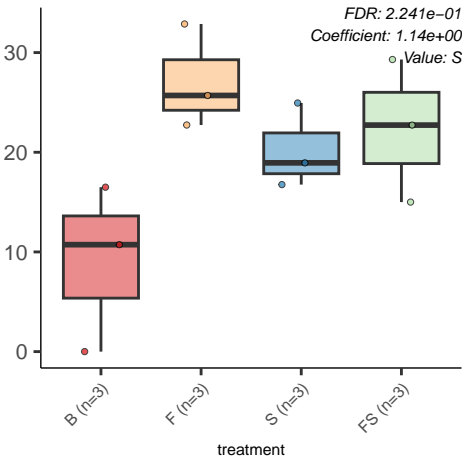




FDR: 2.224e-01  
Coefficient: -2.16e+00  
Value: F







FUCCAT.PWY..fucose.degradation.g\_\_Klebsiella.s\_\_Klebsiella\_

B (n=3)

 $F(n=3)$  $S(n=3)$ 

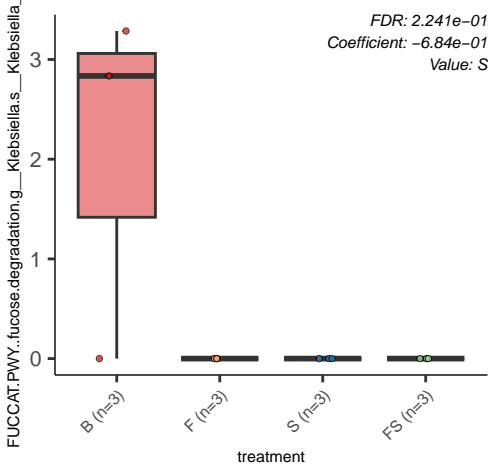
FS (n=3)

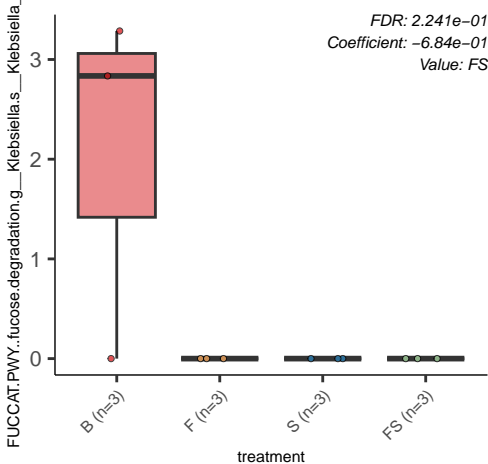
treatment

*FDR: 2.241e-01*

Coefficient:  $-6.84e-01$

Value:  $F$





PWY..heme.b.biosynthesis.II..oxygen.independent..g\_\_Escherichia.

FDR: 2.241e-01  
Coefficient: -1.62e+00  
Value: F

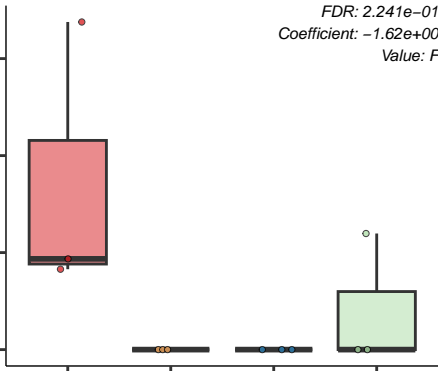
B (n=3)

F (n=3)

S (n=3)

FS (n=3)

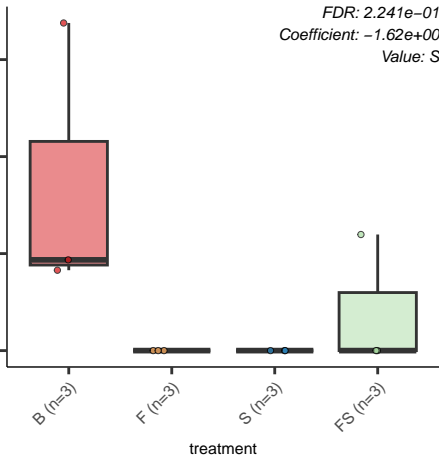
treatment



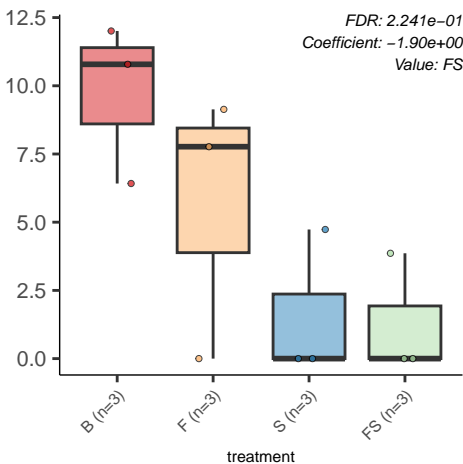


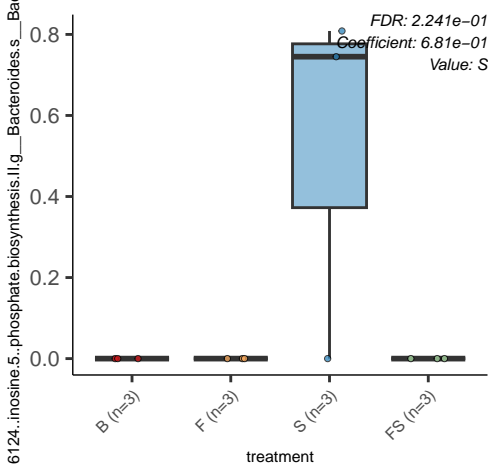
PWY..heme.b.biosynthesis.II..oxygen.independent..g\_\_Escherichia.s.

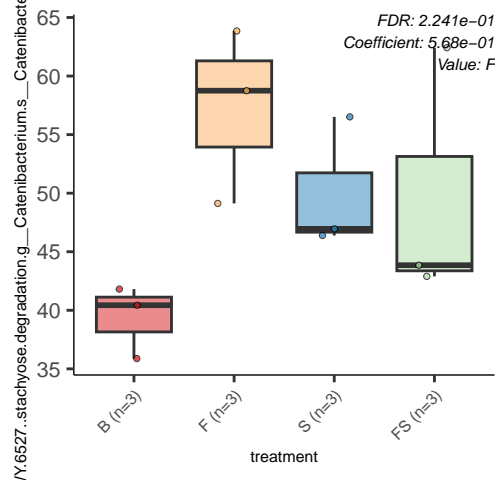
*FDR: 2.241e-01*  
*Coefficient: -1.62e+00*  
*Value: S*

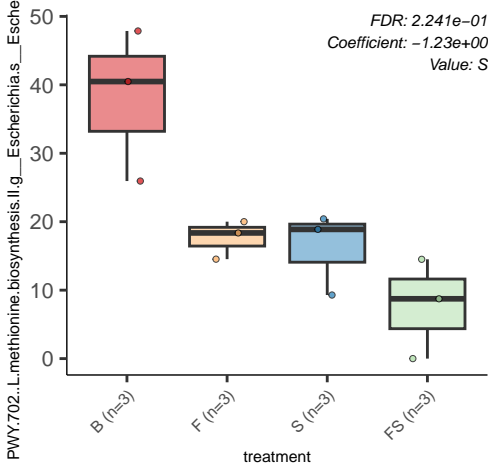


HESIS.II.NAD.salvage.pathway.III.to.nicotinamide.riboside.g\_Esc

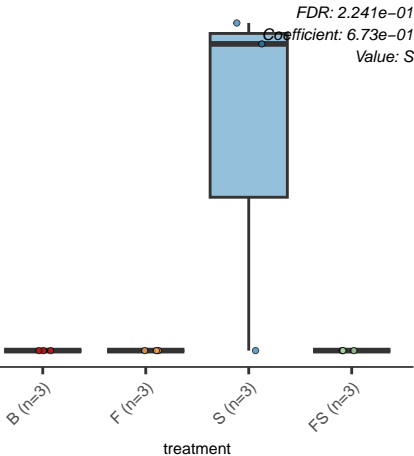


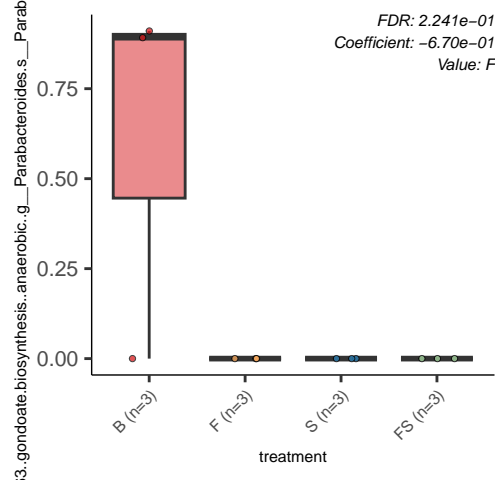


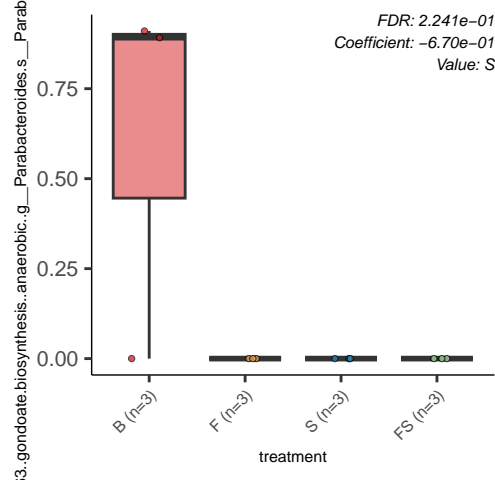




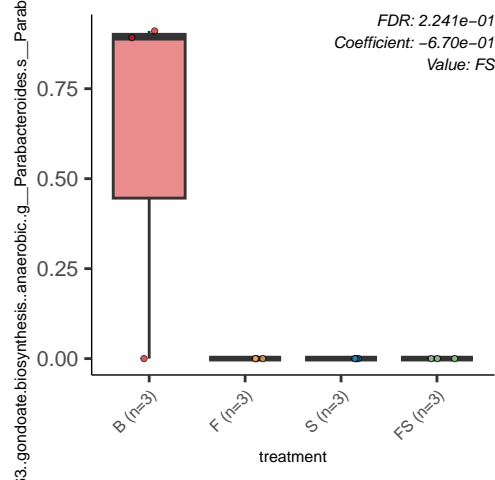
thway.of.guanosine.nucleotides.de.novo.biosynthesis.l.g\_\_Streptococcus

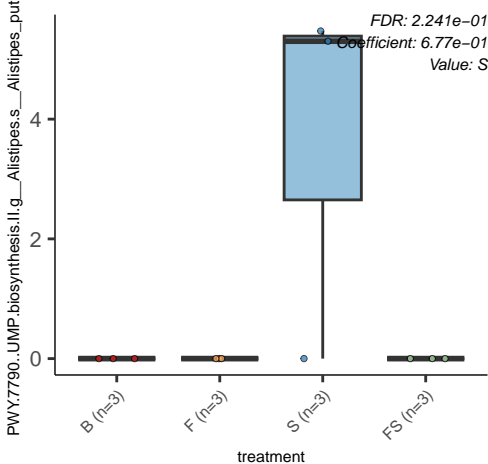


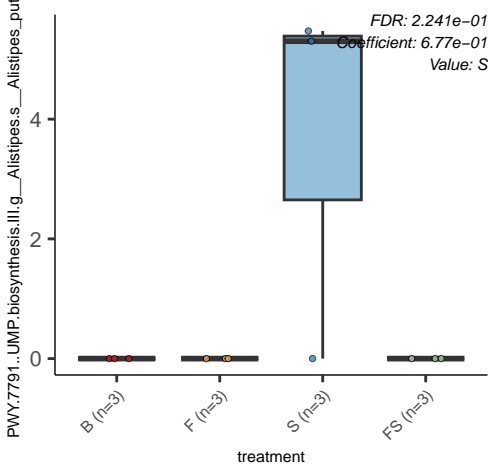




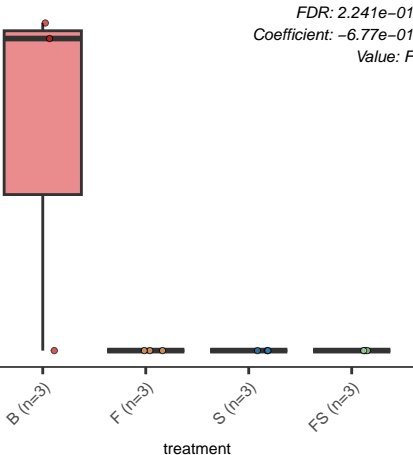




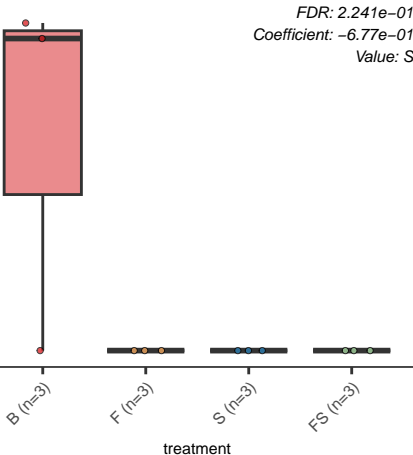




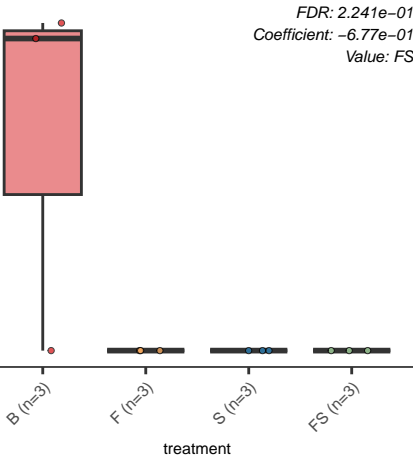
PWY.7820..teichuronic.acid.biosynthesis..B..subtilis.168..uncle



PWY.7820..teichuronic.acid.biosynthesis..B..subtilis.168..uncle

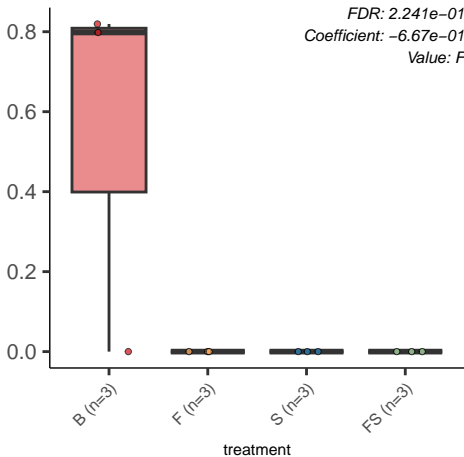


PWY.7820..teichuronic.acid.biosynthesis..B..subtilis.168..uncle

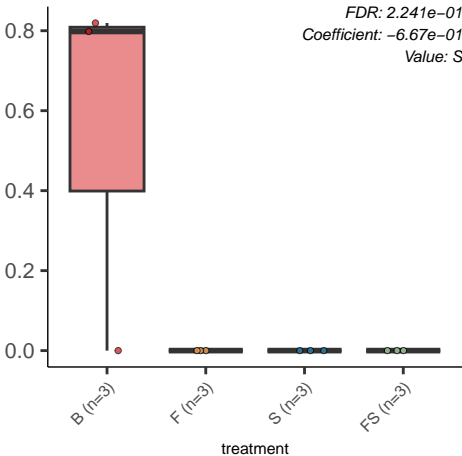


PWY.7977..L.methionine.biosynthesis.IV.g\_\_Bacteroides.s\_\_Bacter

*FDR: 2.241e-01*  
*Coefficient: -6.67e-01*  
*Value: F*



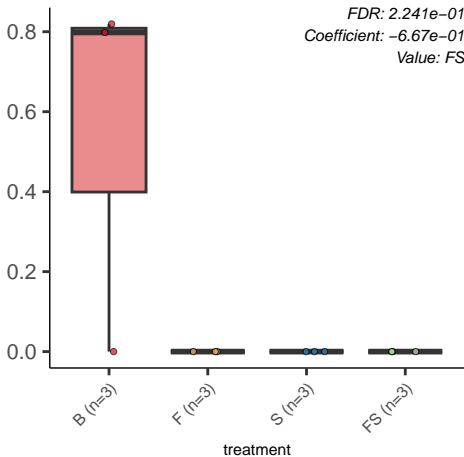
PWY.7977..L.methionine.biosynthesis.IV.g\_\_Bacteroides.s\_\_Bacter

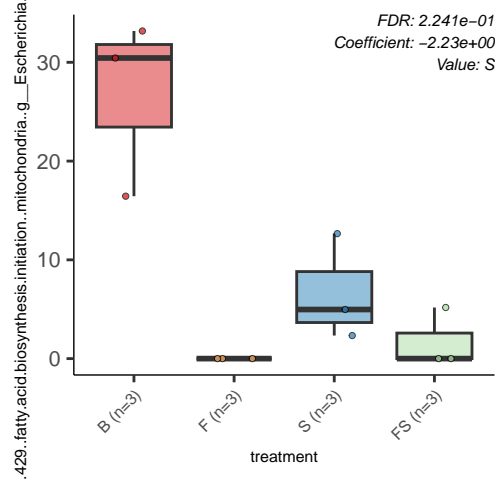




PWY.7977..L.methionine.biosynthesis.IV.g\_\_Bacteroides.s\_\_Bacter

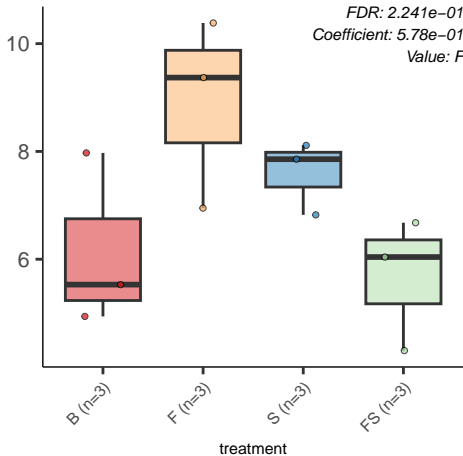
*FDR: 2.241e-01*  
*Coefficient: -6.67e-01*  
*Value: FS*





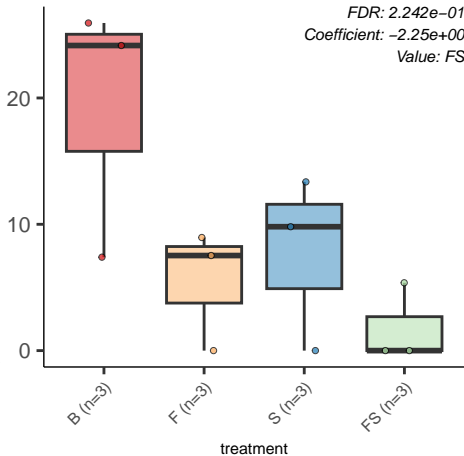
N.PWY..superpathway.of.L.serine.and.glycine.biosynthesis.l.g\_\_Bla

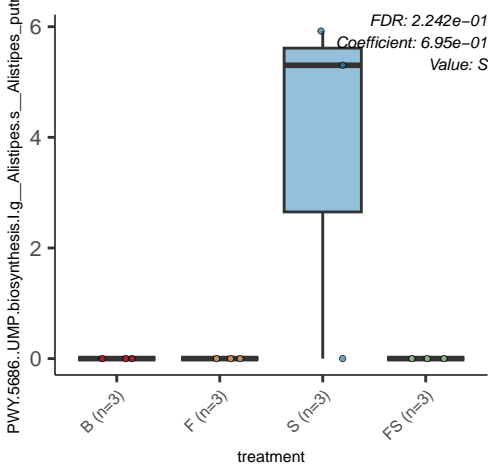
FDR: 2.241e-01  
Coefficient: 5.78e-01  
Value: F



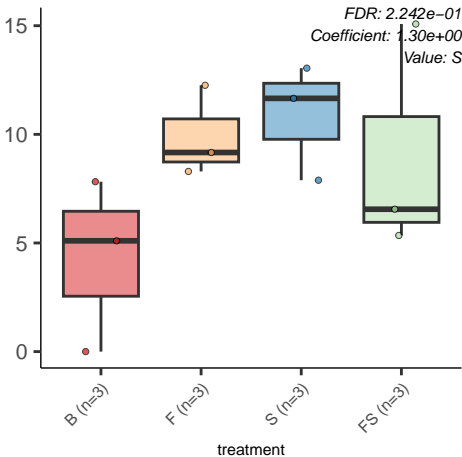
84..sucrose.degradation.IV..sucrose.phosphorylase.g\_\_Escherichia

FDR: 2.242e-01  
Coefficient: -2.25e+00  
Value: FS

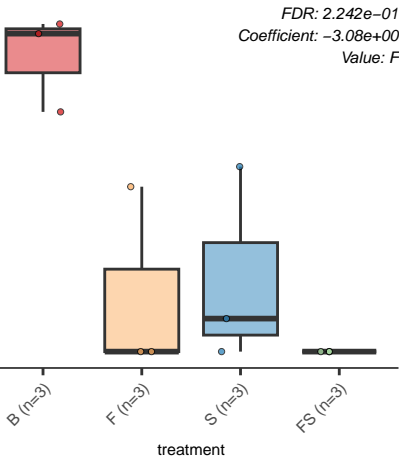




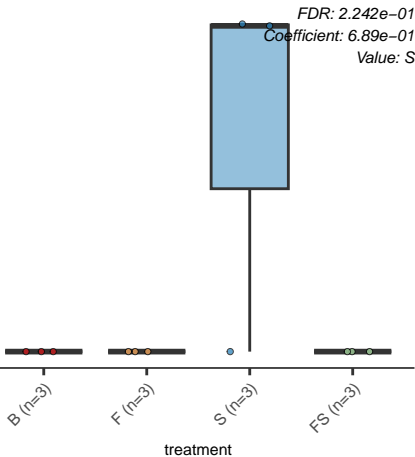
41.glycogen.degradation.ll.g\_\_Bifidobacterium.s\_\_Bifidobacterium



97..pyrimidine.deoxyribonucleotide.phosphorylation.g\_\_Escherichia



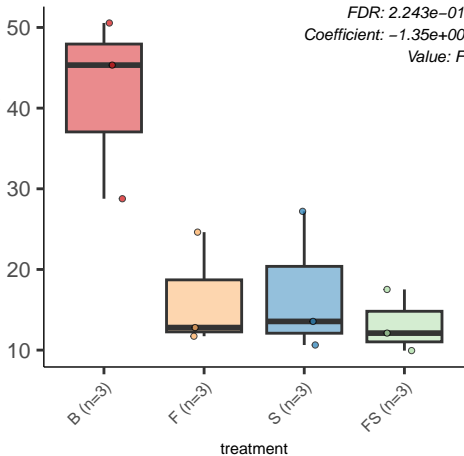
thway.of.adenosine.nucleotides.de.novo.biosynthesis.l.g\_\_Streptococcus





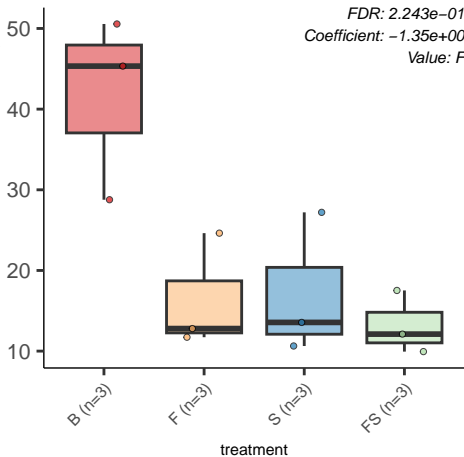
22..5.aminoimidazole.ribonucleotide.biosynthesis.ll.g\_\_Escherichia

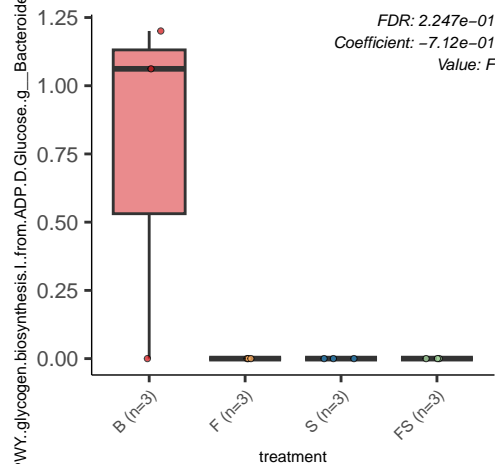
*FDR: 2.243e-01*  
*Coefficient: -1.35e+00*  
*Value: F*

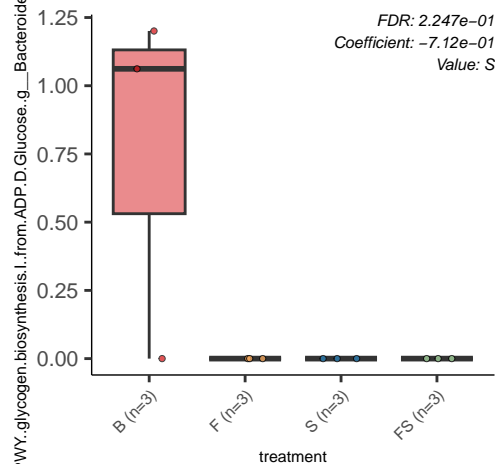


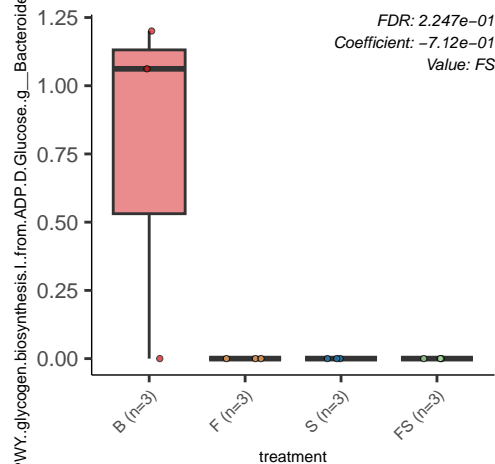
erpathway.of.5.aminoimidazole.ribonucleotide.biosynthesis.g\_Esch

*FDR: 2.243e-01*  
*Coefficient: -1.35e+00*  
*Value: F*

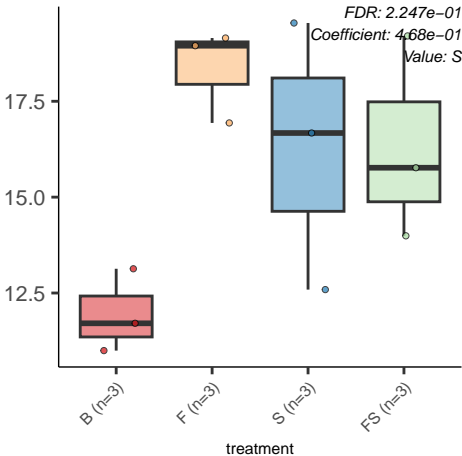


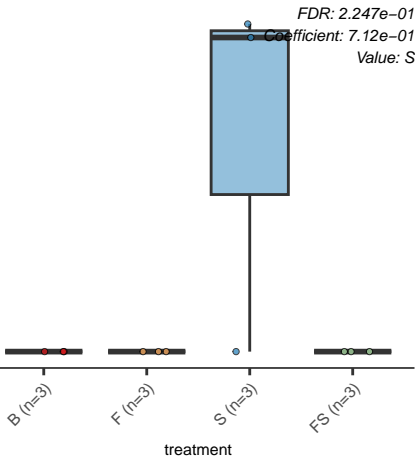




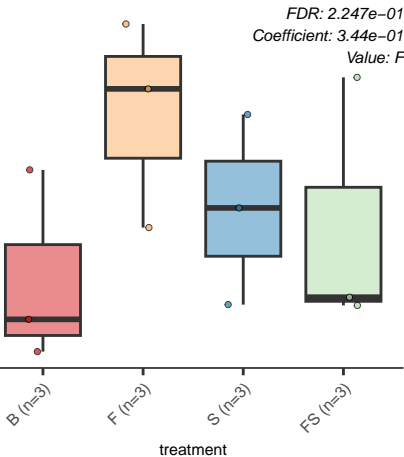


VY..glycogen.biosynthesis.l...from.ADP.D.Glucose..g\_\_Faecalibacter





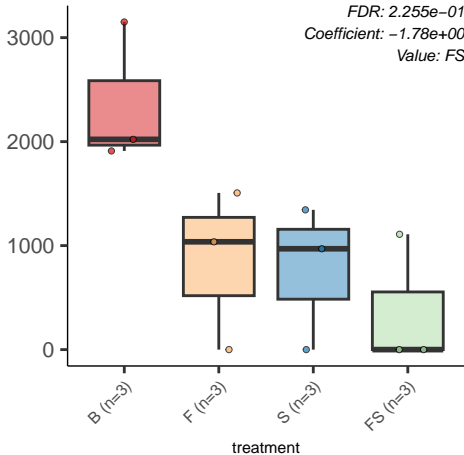
uramoyl.pentapeptide.biosynthesis.II...lysine.containing..g\_\_Bifidobac

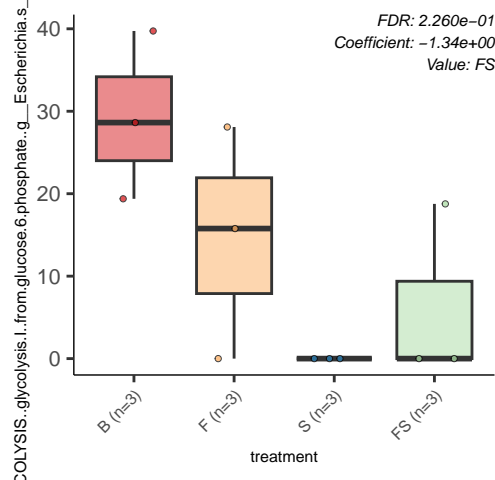




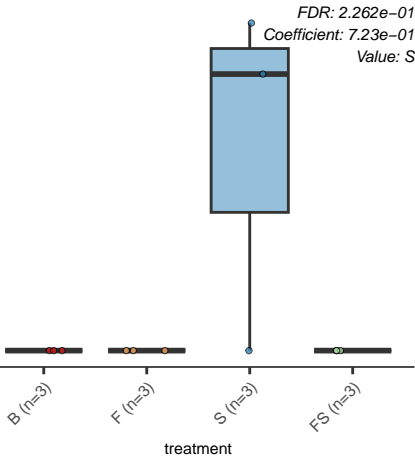
UNINTEGRATED.g\_\_Bacteroides.s\_\_Bacteroides\_stercor

FDR: 2.255e-01  
Coefficient: -1.78e+00  
Value: FS

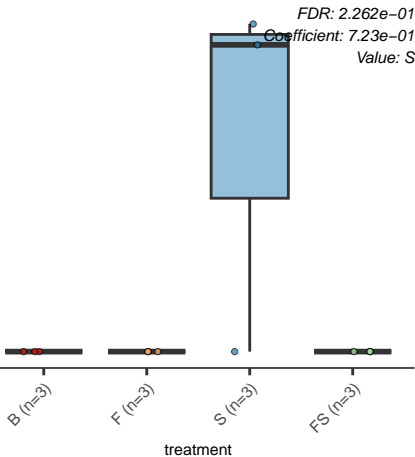




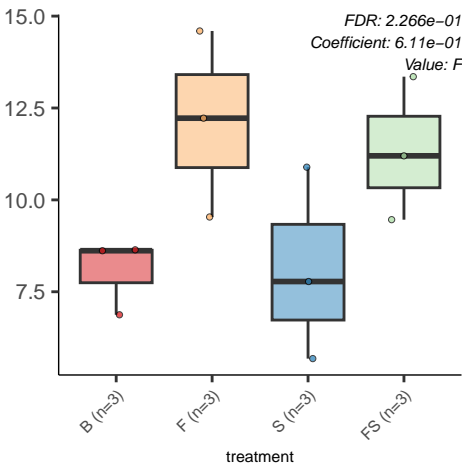
thway.of.adenosine.nucleotides.de.novo.biosynthesis.ll.g\_\_Streptococcus

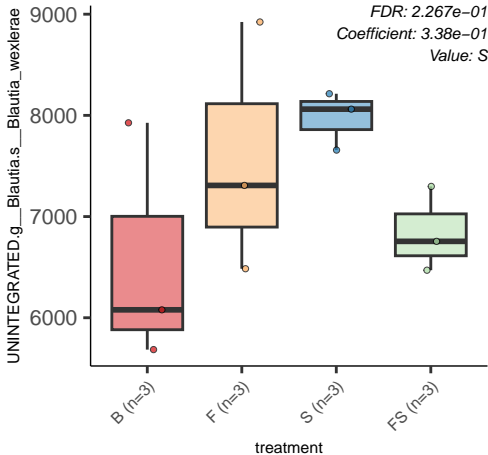


PWY.6703..preQ0.biosynthesis.g\_\_Streptococcus.s\_\_Streptococcus

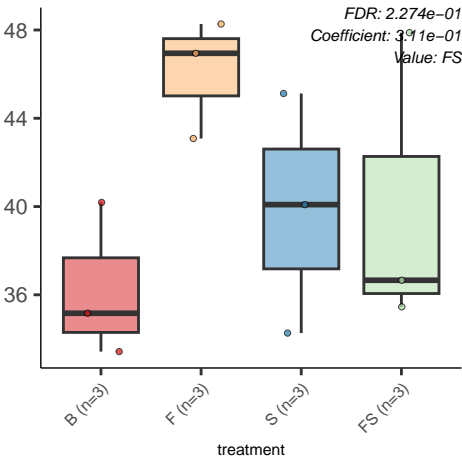


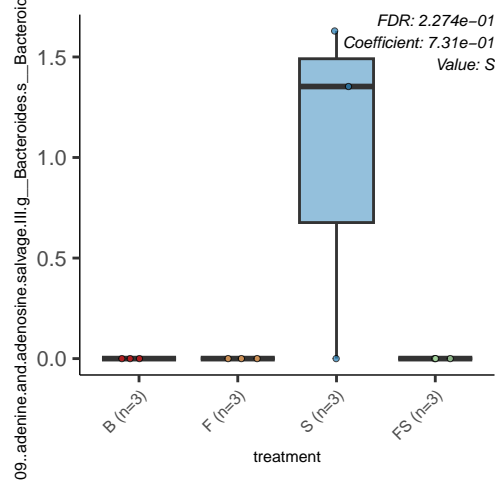
PWY.6123..inosine.5..phosphate.biosynthesis.l.g\_\_Blautia.s\_\_Blau





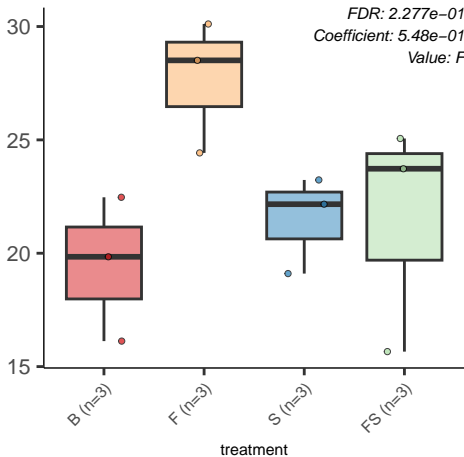
btidoglycan.biosynthesis.l..meso.diaminopimelate.containing..g\_\_Bifid

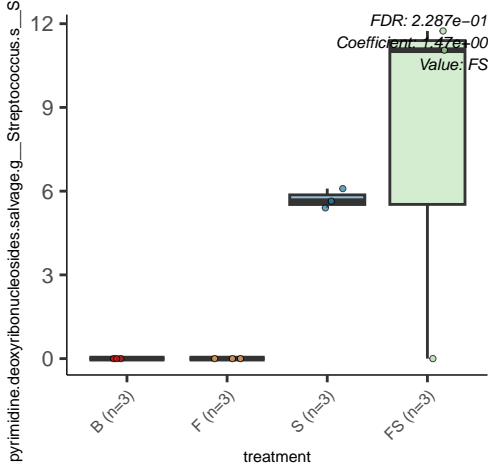






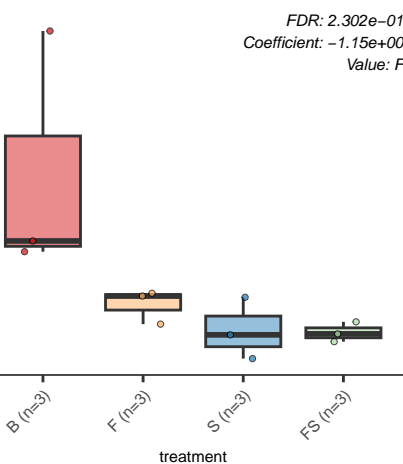
FDR: 2.277e-01  
Coefficient: 5.48e-01  
Value: F



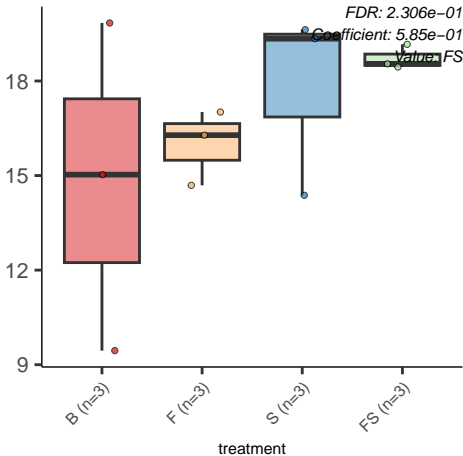


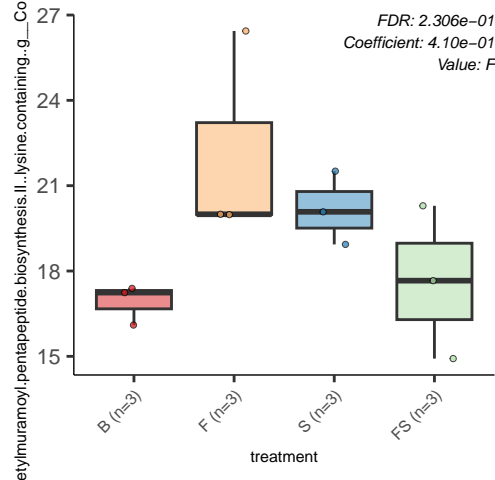
perpathway.of.L.methionine.biosynthesis..transsulfuration..g\_Esch

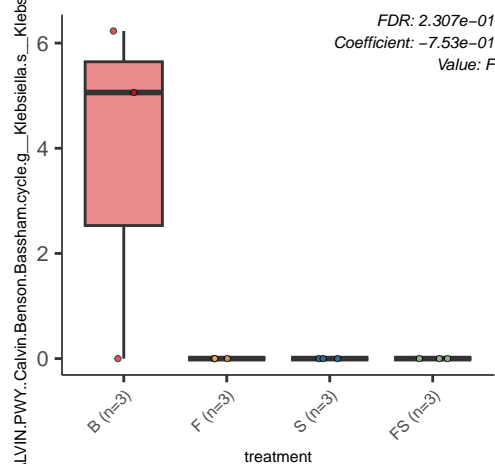
*FDR: 2.302e-01*  
*Coefficient: -1.15e+00*  
*Value: F*

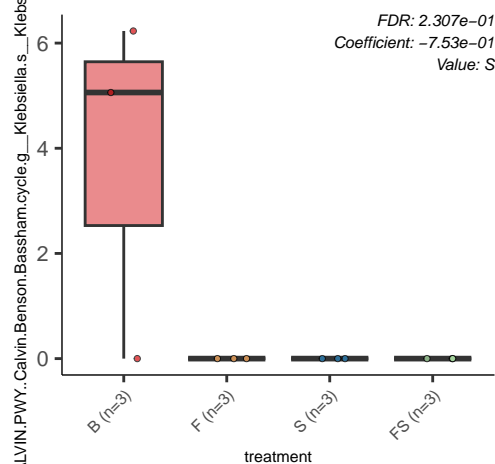


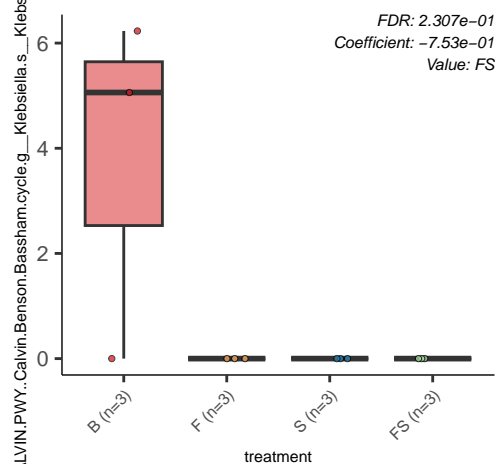
J.PWY.dTDP..beta..L.rhamnose.biosynthesis.g\_\_Catenibacterium.s



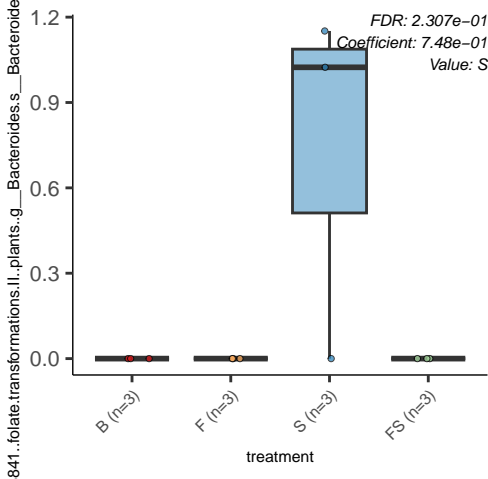


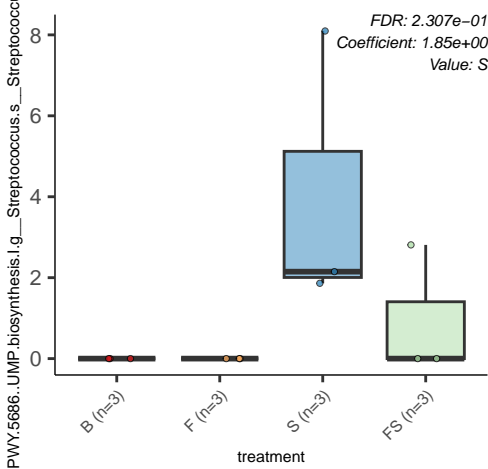


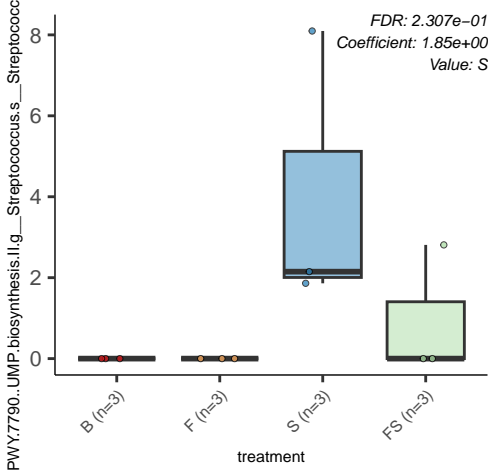


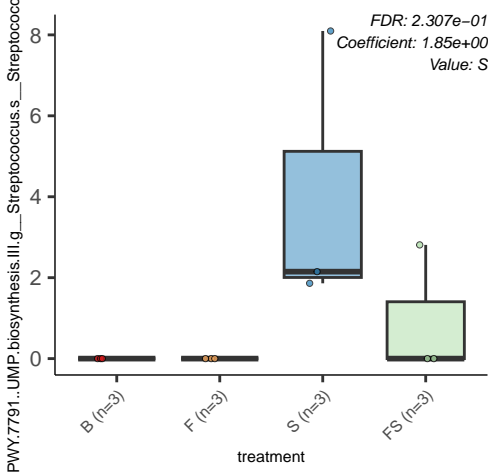


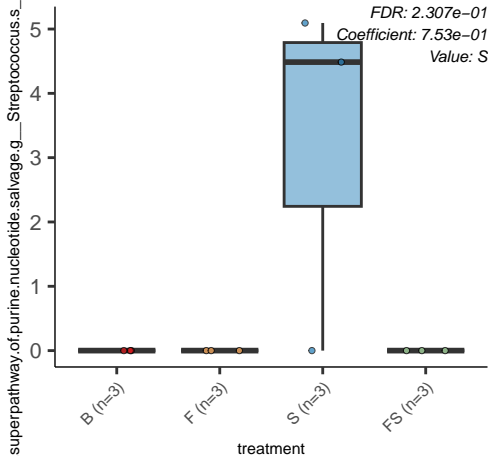


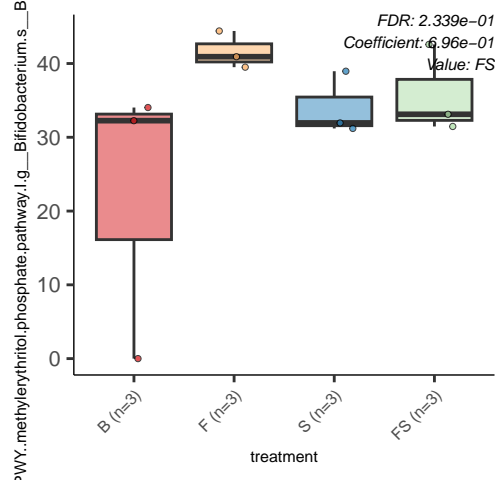


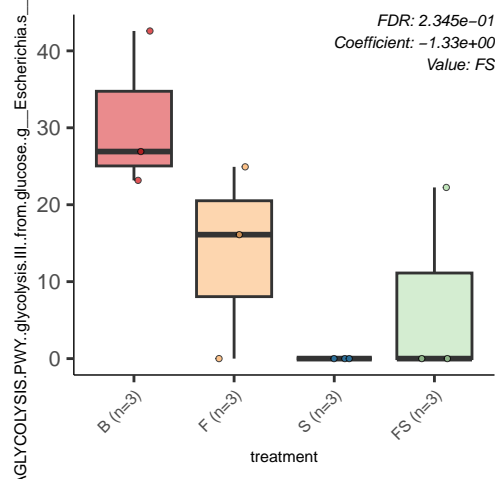






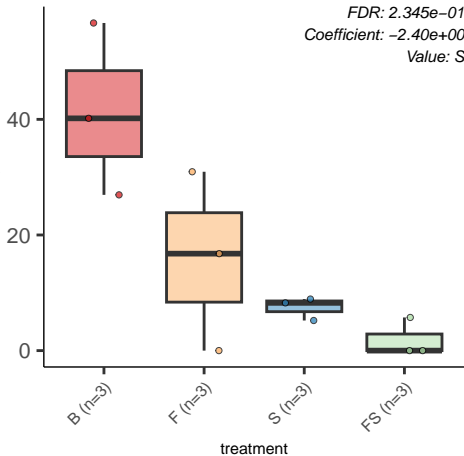






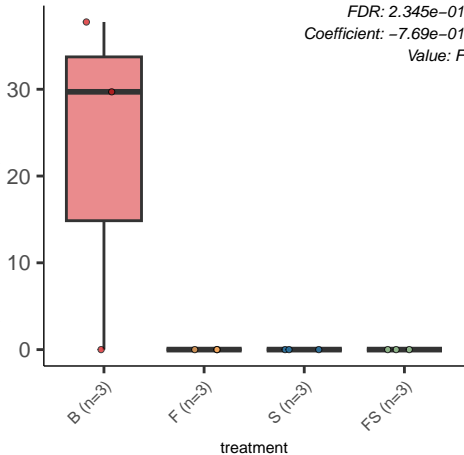
PWY.5973..cis.vaccinate.biosynthesis.g\_Escherichia.s\_Esche

FDR: 2.345e-01  
Coefficient: -2.40e+00  
Value: S



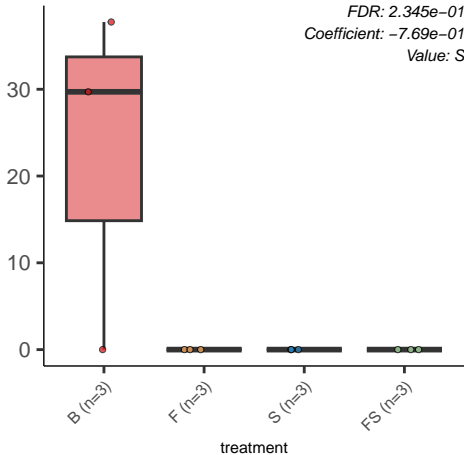


FDR: 2.345e-01  
Coefficient: -7.69e-01  
Value: F



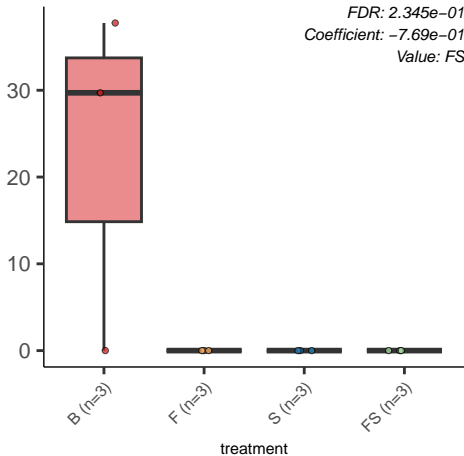
01..superpathway.of.glucose.and.xylose.degradation.g\_\_Escherichia

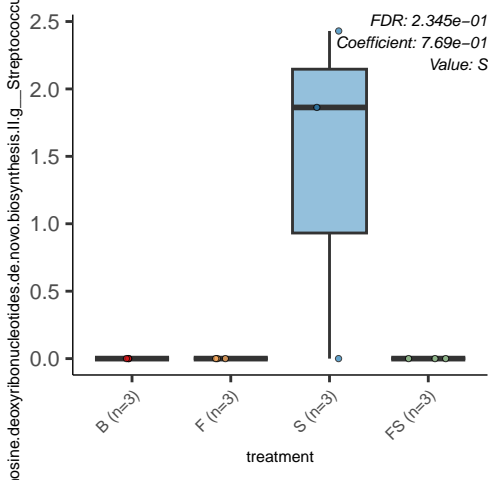
FDR: 2.345e-01  
Coefficient: -7.69e-01  
Value: S

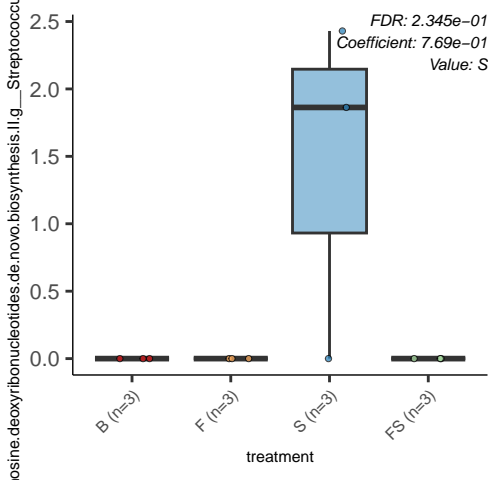


01..superpathway.of.glucose.and.xylose.degradation.g\_\_Escherichia

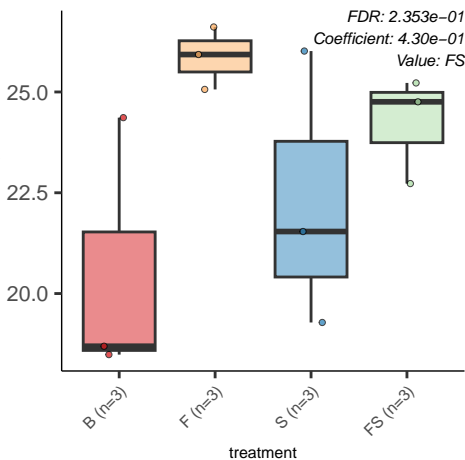
FDR: 2.345e-01  
Coefficient: -7.69e-01  
Value: FS



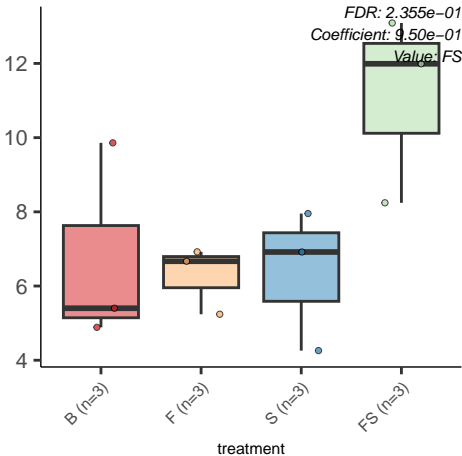


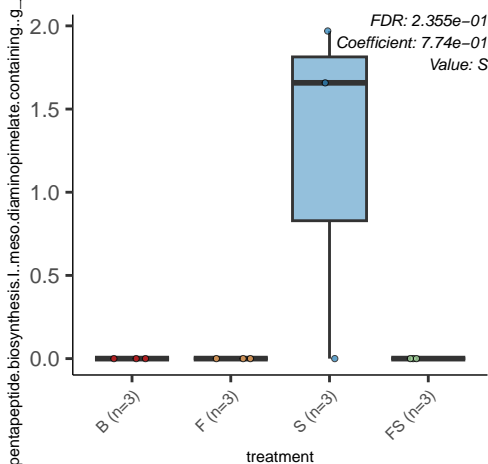


atty.acid.biosynthesis.initiation...mitochondria.g\_\_Catenibacterium.s

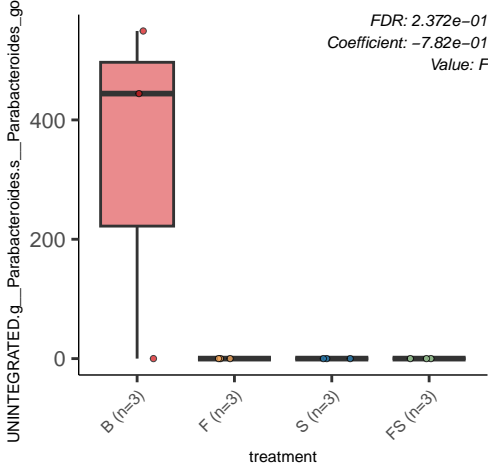


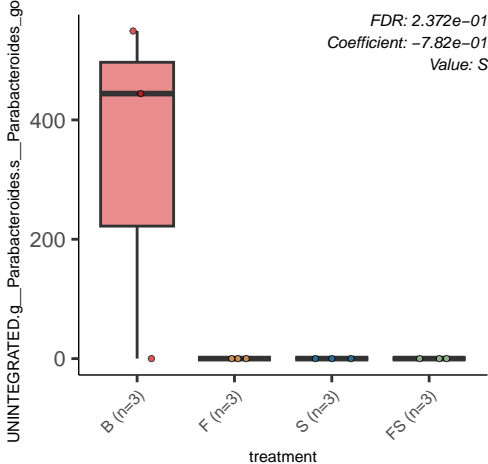
mate.biosynthesis.from.3.dehydroquinate.g\_\_Lachnospiraceae\_unclassified

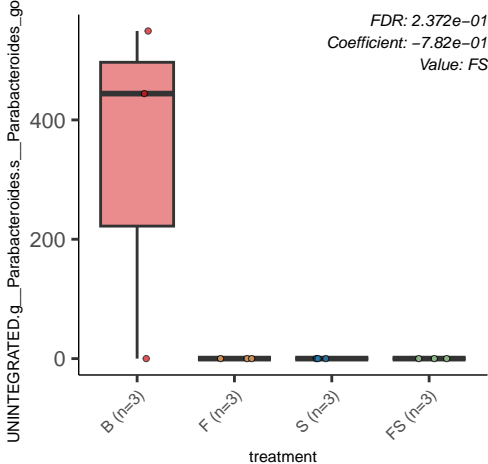






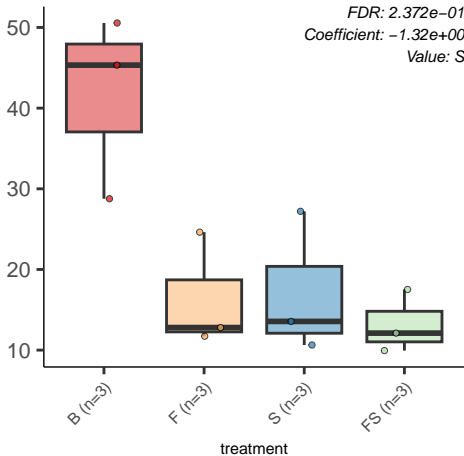






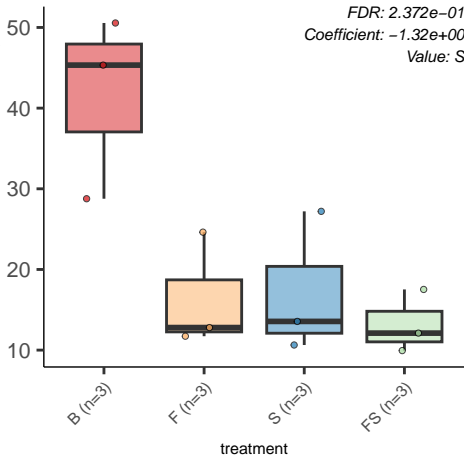
22..5.aminoimidazole.ribonucleotide.biosynthesis.ll.g\_\_Escherichia

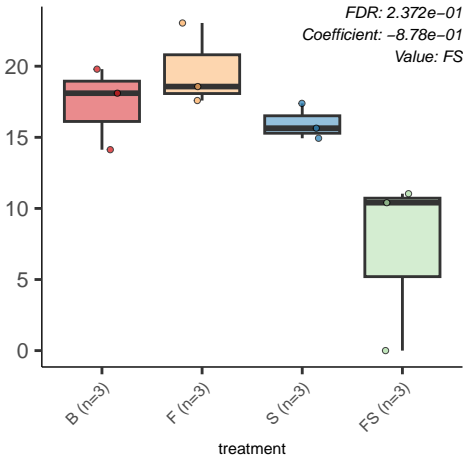
FDR: 2.372e-01  
Coefficient: -1.32e+00  
Value: S



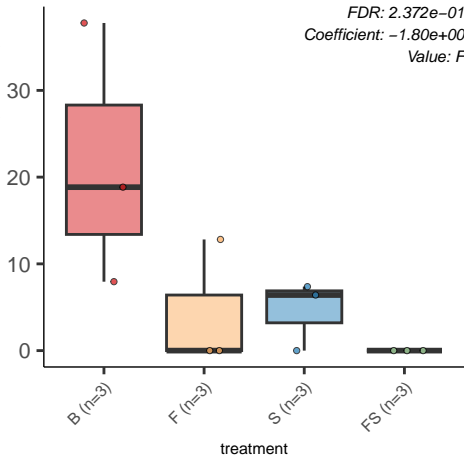
erpathway.of.5.aminoimidazole.ribonucleotide.biosynthesis.g\_Esch

FDR: 2.372e-01  
Coefficient: -1.32e+00  
Value: S



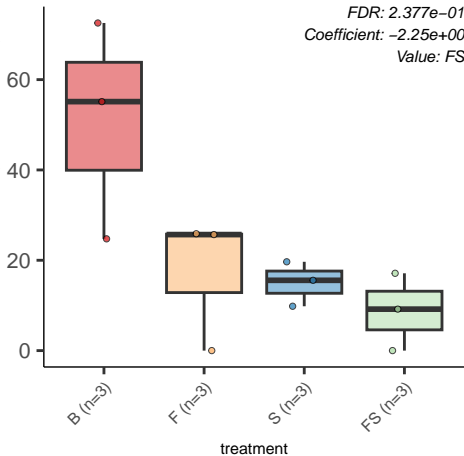


FDR: 2.372e-01  
Coefficient: -1.80e+00  
Value: F



superpathway.of.L.aspartate.and.L.asparagine.biosynthesis.g\_Esc

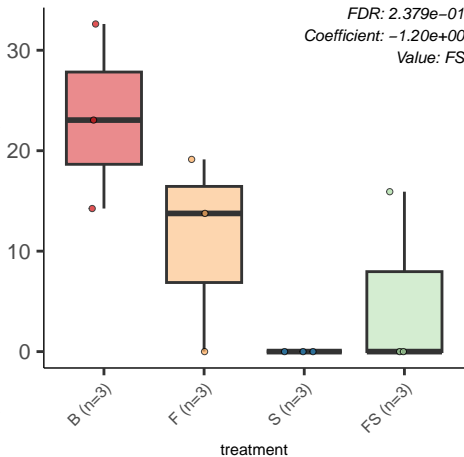
FDR: 2.377e-01  
Coefficient: -2.25e+00  
Value: FS





Y.5484..glycolysis.II..from.fructose.6.phosphate..g\_Escherichia.s

FDR: 2.379e-01  
Coefficient: -1.20e+00  
Value: FS



ARO.PWY..chorismate.biosynthesis.l.unclassified

FDR: 2.380e-01  
Coefficient: 4.42e-01  
Value: F

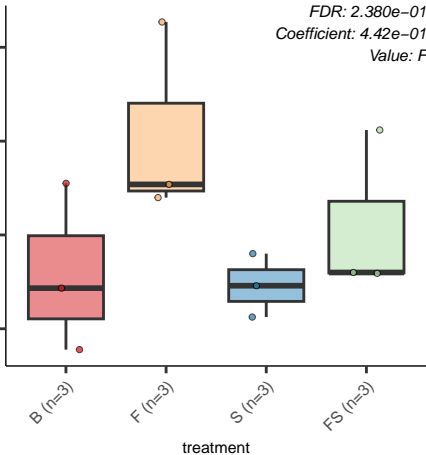
B (n=3)

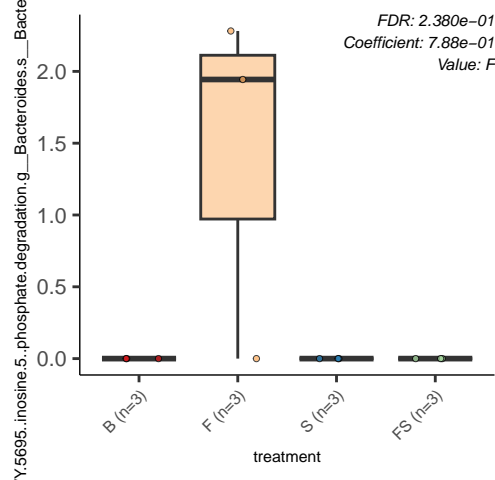
F (n=3)

S (n=3)

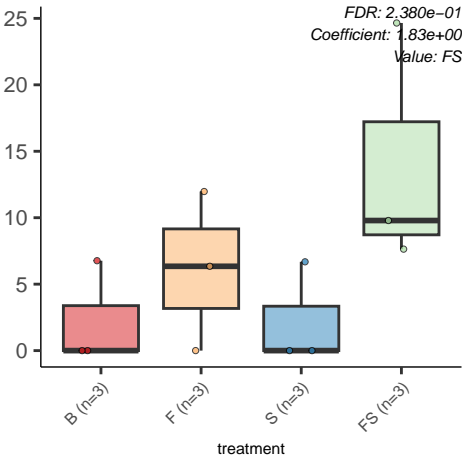
FS (n=3)

treatment

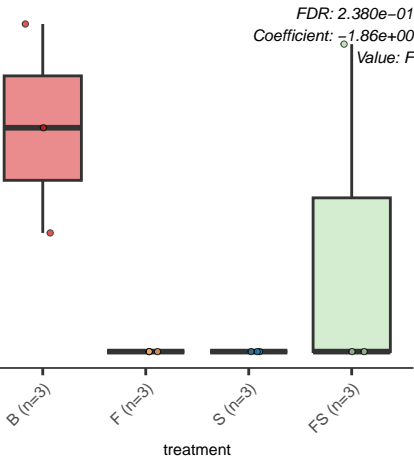




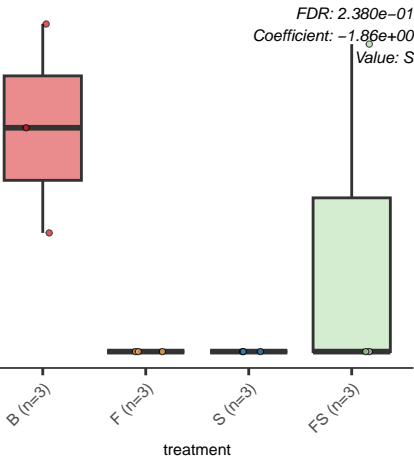
PWY.6897..thiamine.diphosphate.salvage.II.unclassified



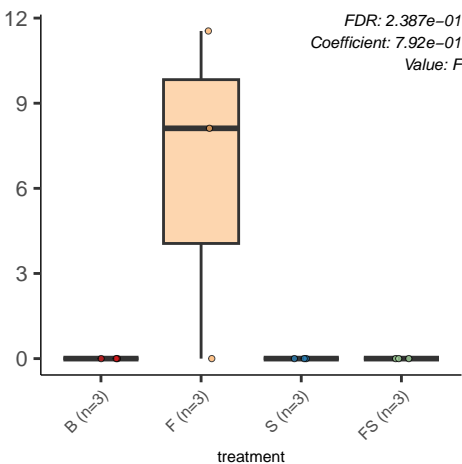
9..phosphatide.metabolism...as.a.signaling.molecule.g\_\_Klebsiella.

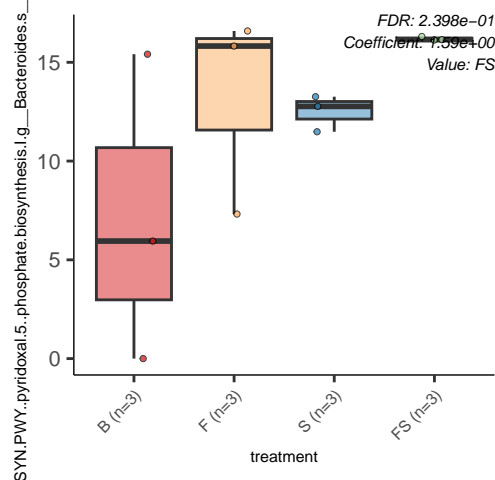


9..phosphatide.metabolism...as.a.signaling.molecule.g\_\_Klebsiella.



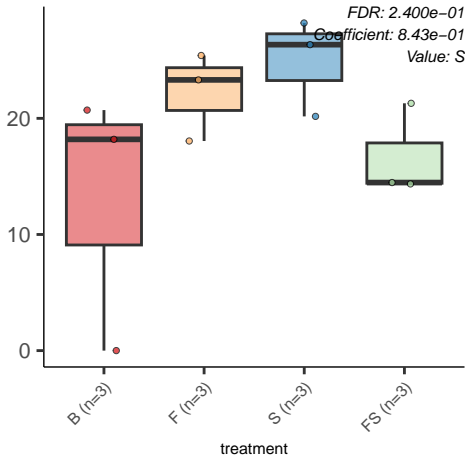
way.of.UDP.glucose.derived.O.antigen.building.blocks.biosynthesis.g



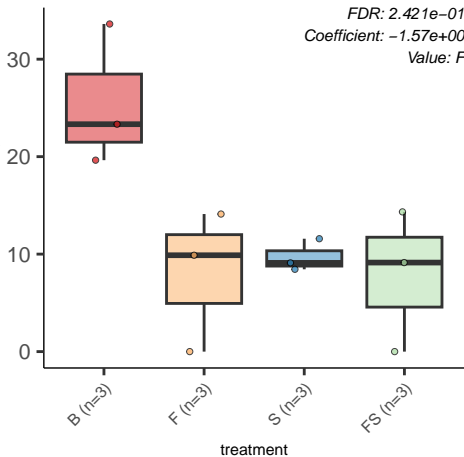




...guanosine.ribonucleotides.de.novo.biosynthesis.g\_\_Collinsella.s

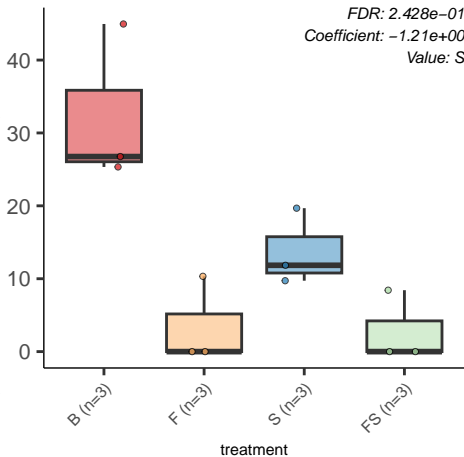


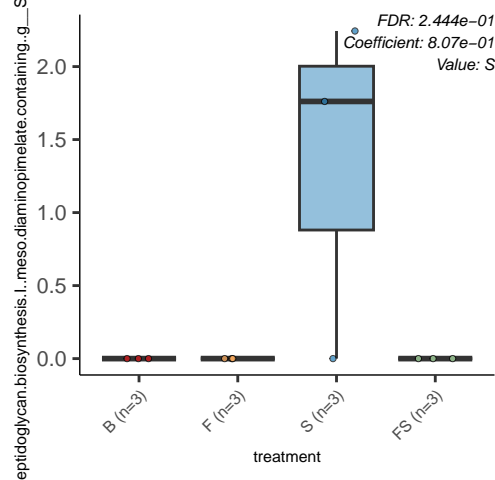
FDR:  $2.421e-01$   
Coefficient:  $-1.57e+00$   
Value: F

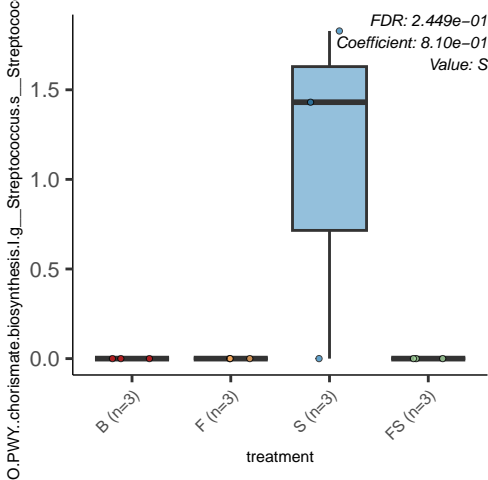


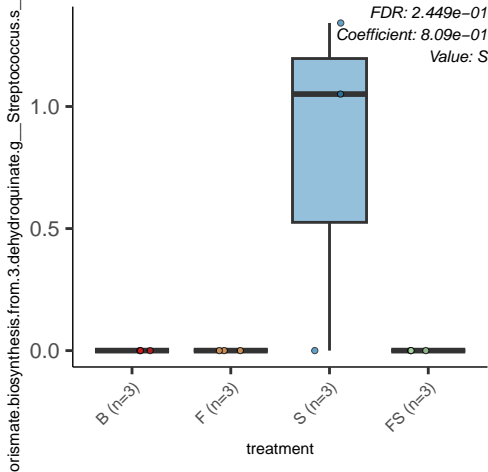
7400..L.arginine.biosynthesis.IV..archaeobacteria.g\_Escherichia.s

*FDR: 2.428e-01*  
*Coefficient: -1.21e+00*  
*Value: S*

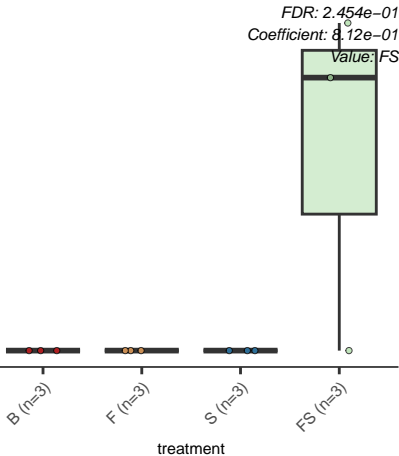






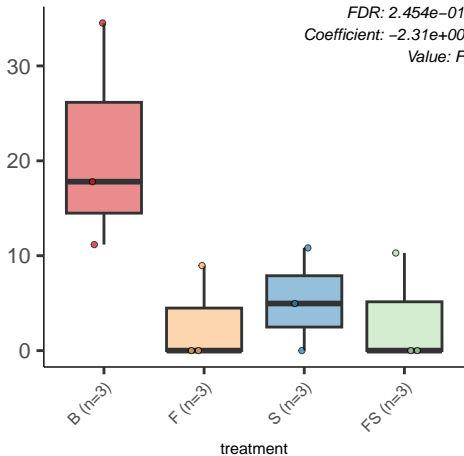


WY.4041...gamma...glutamyl.cycle.g\_\_Streptococcus.s\_\_Streptococcus



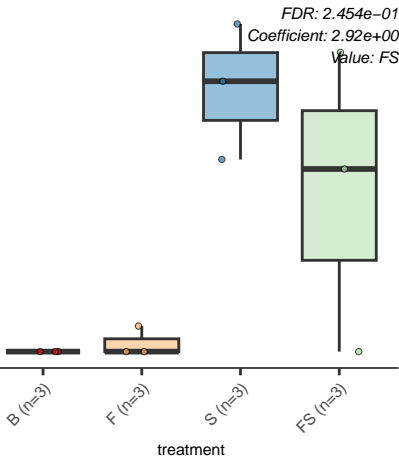
PWY.5097..L.lysine.biosynthesis.VI.g\_Escherichia.s\_Escherichia

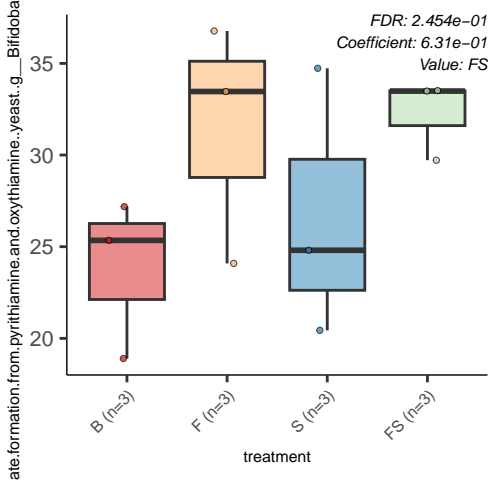
FDR: 2.454e-01  
Coefficient: -2.31e+00  
Value: F



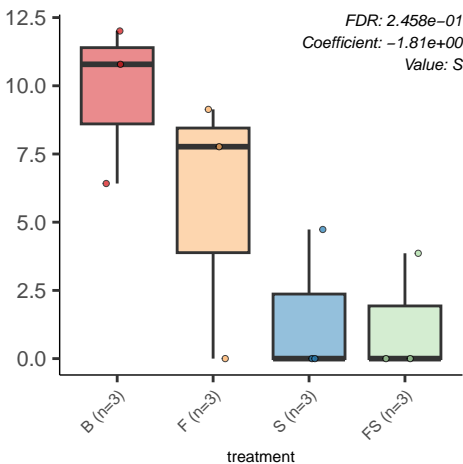


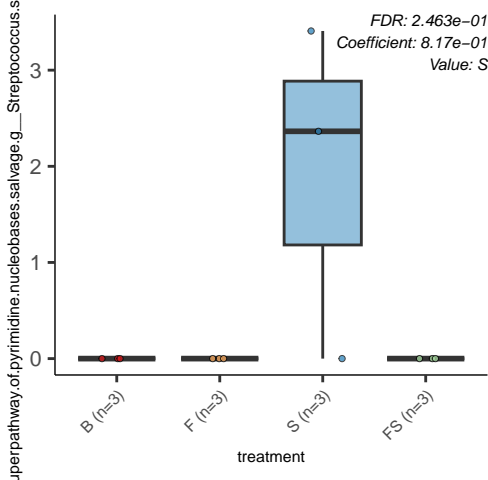
PWY.7238..sucrose.biosynthesis.II.g\_\_Streptococcus.s\_\_Streptococcus

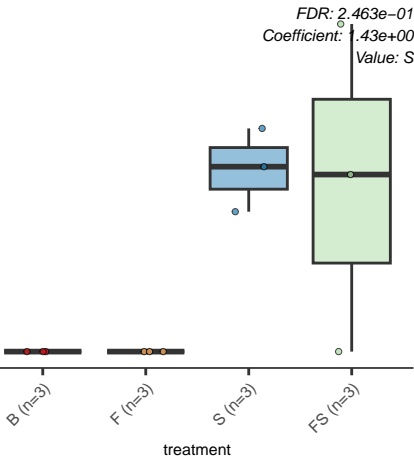


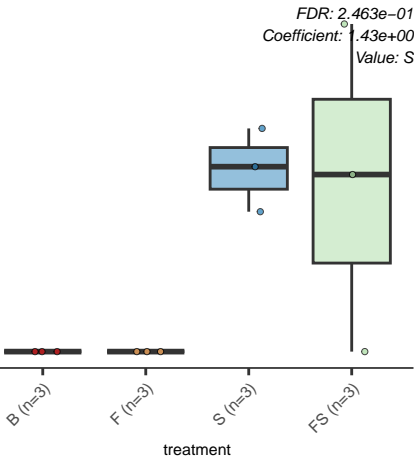


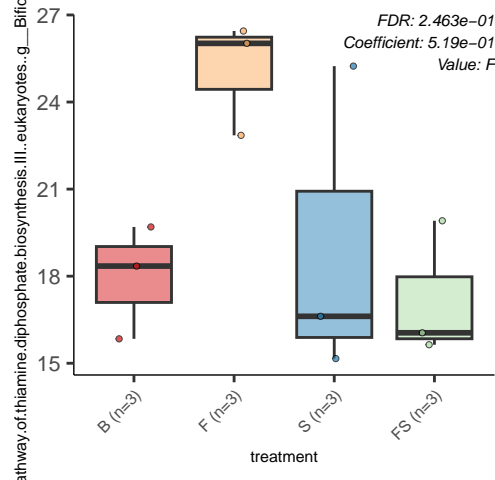
HESIS.II.NAD.salvage.pathway.III..to.nicotinamide.riboside.g\_Esc

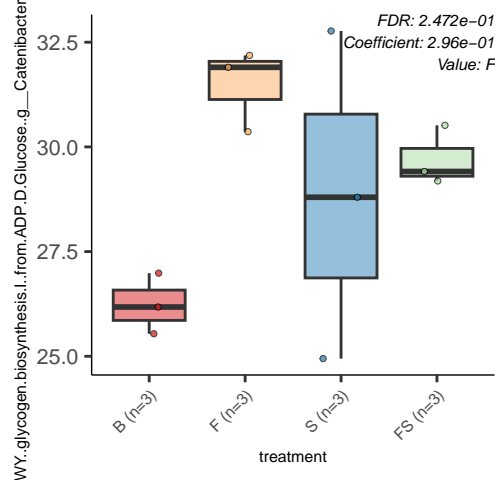






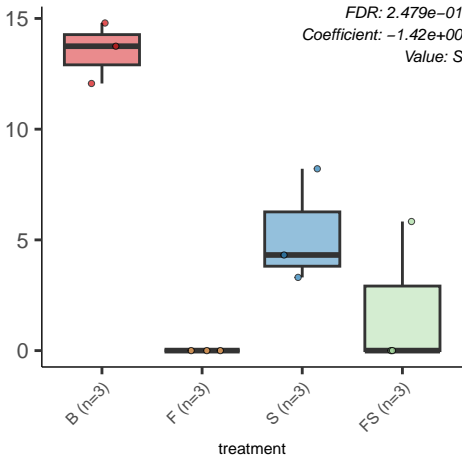


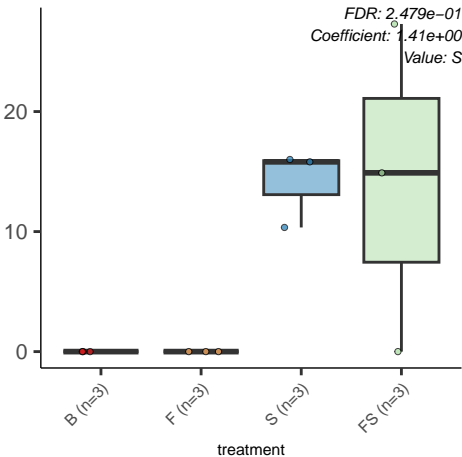






PWY5367..petroselinate.biosynthesis.g\_Escherichia.s\_Esche





PWY.7238..sucrose.biosynthesis.ll.g\_\_Ruminococcus.s\_\_Ruminococcus

