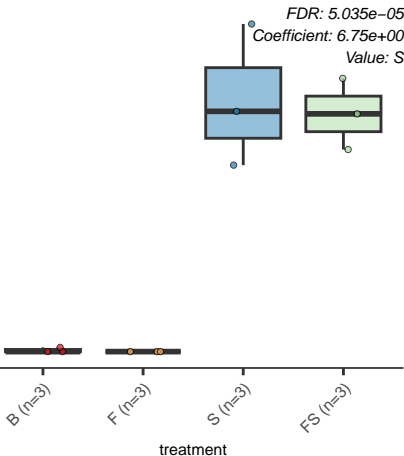
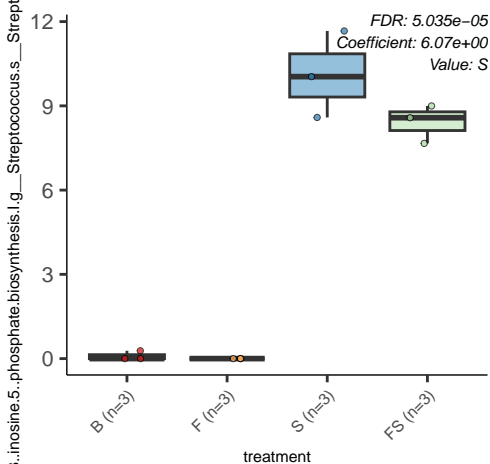
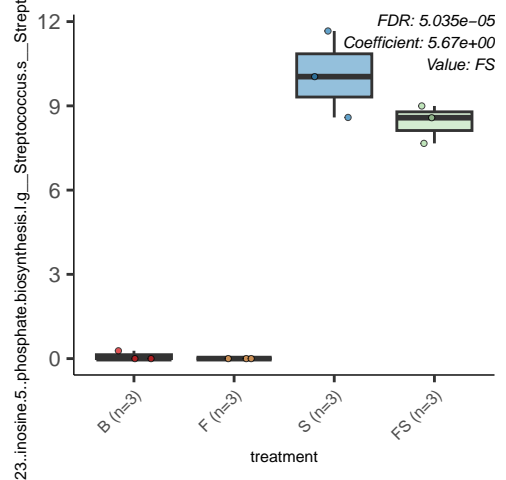
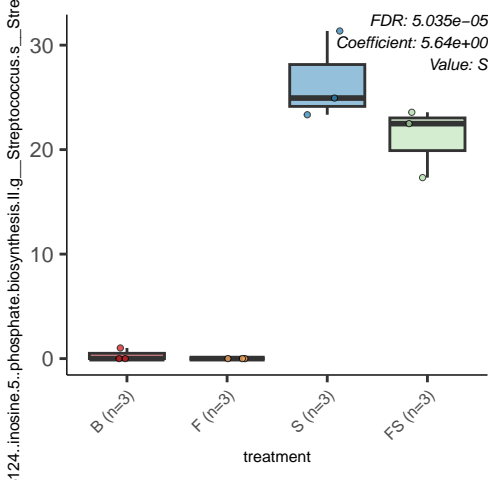


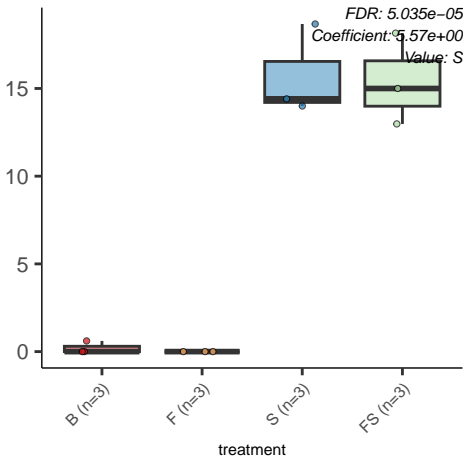
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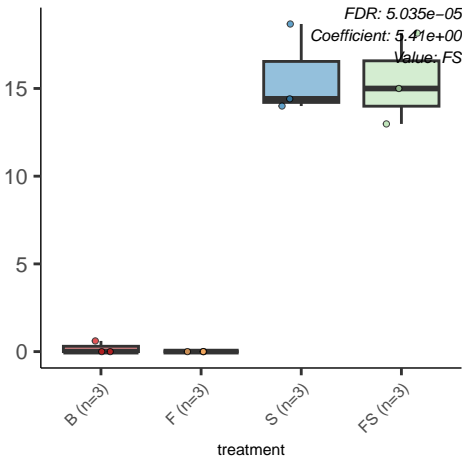


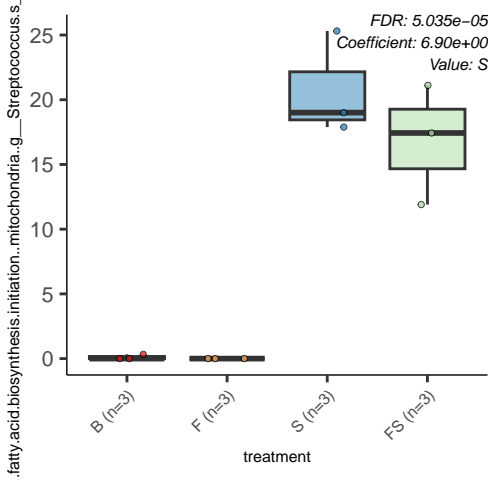


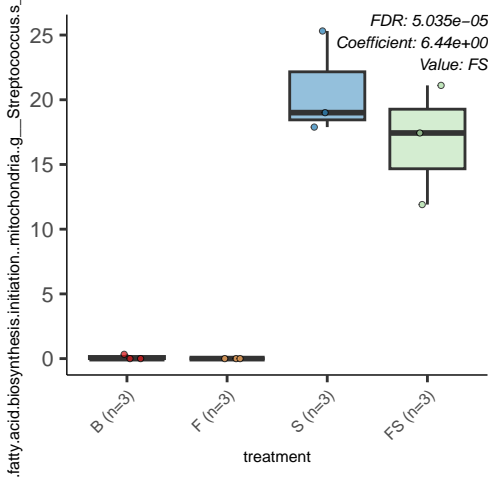


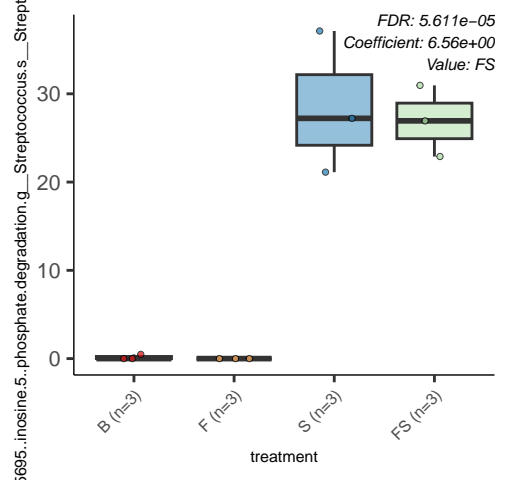


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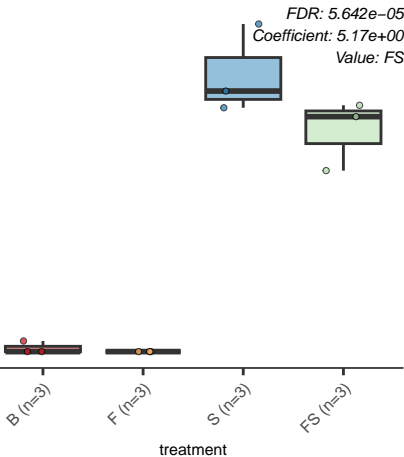


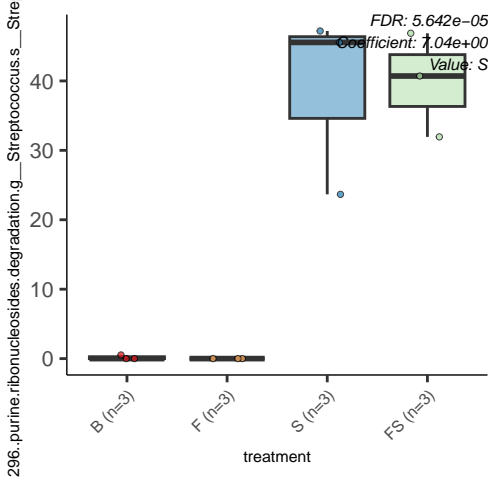


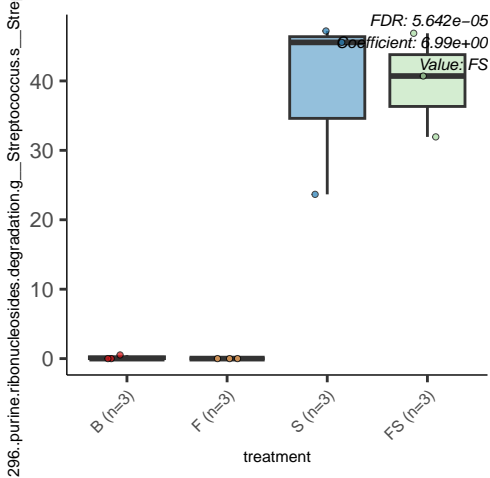


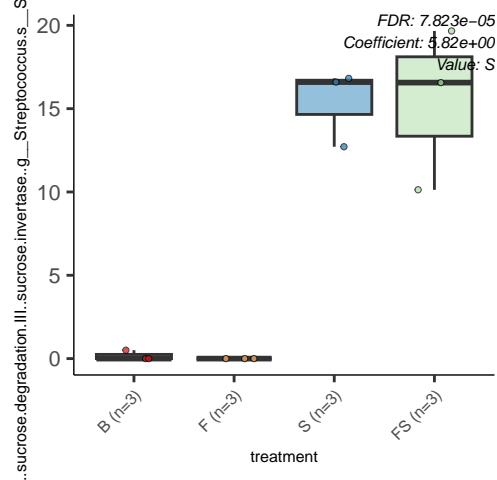


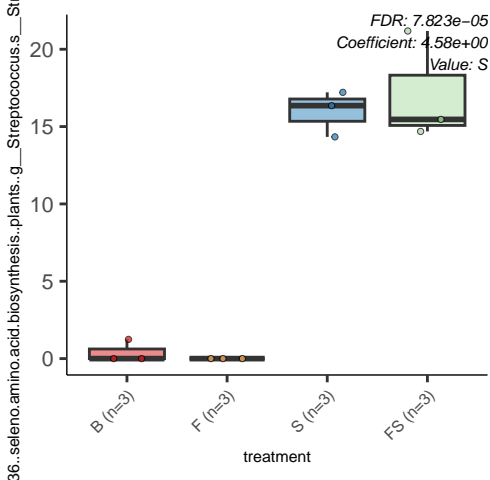
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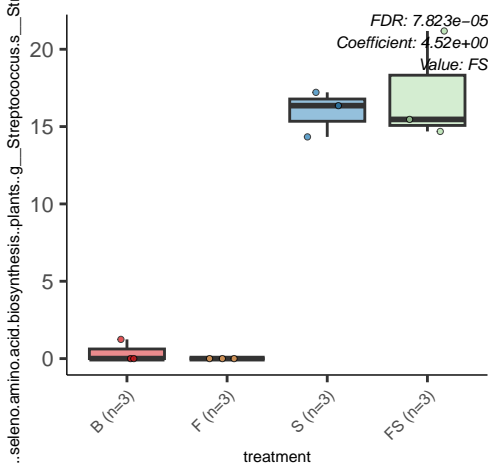




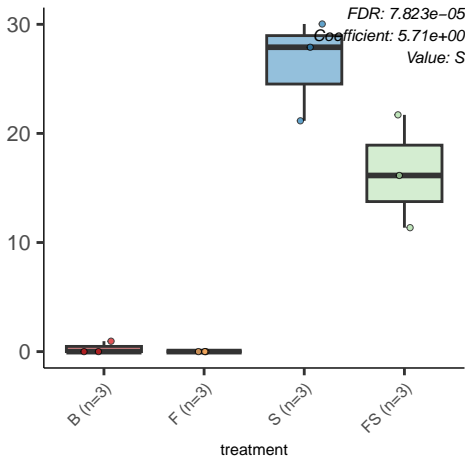




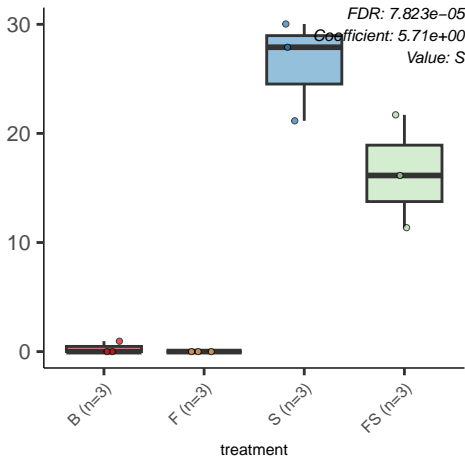


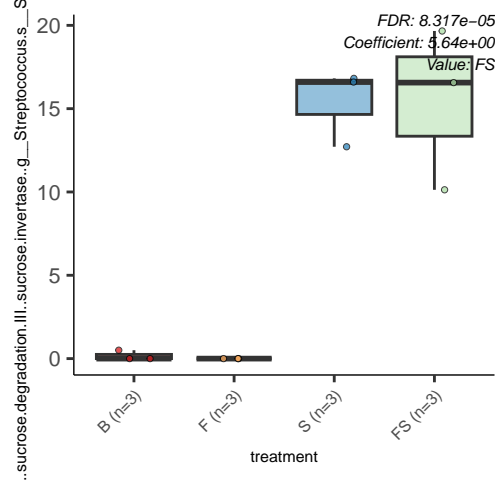


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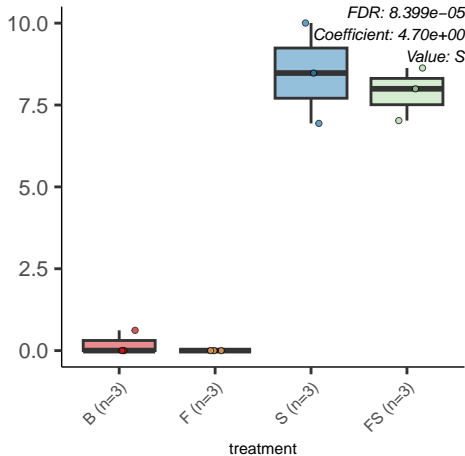


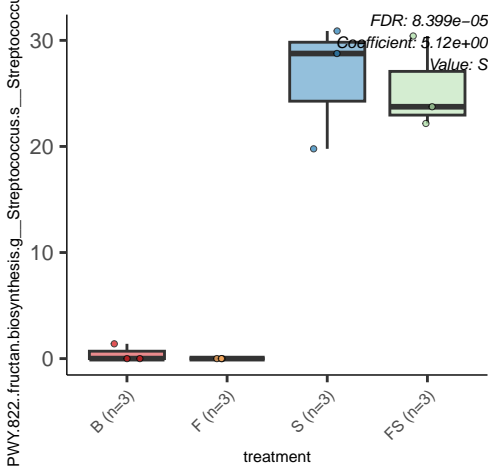
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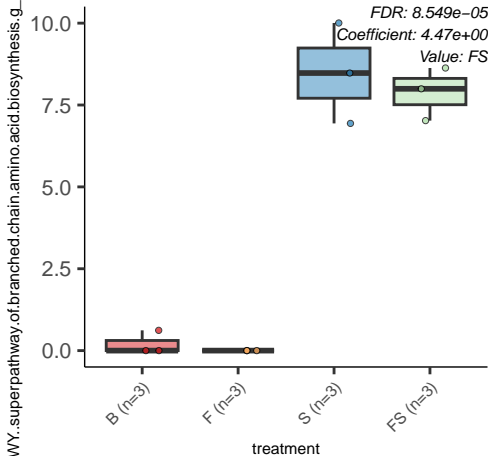


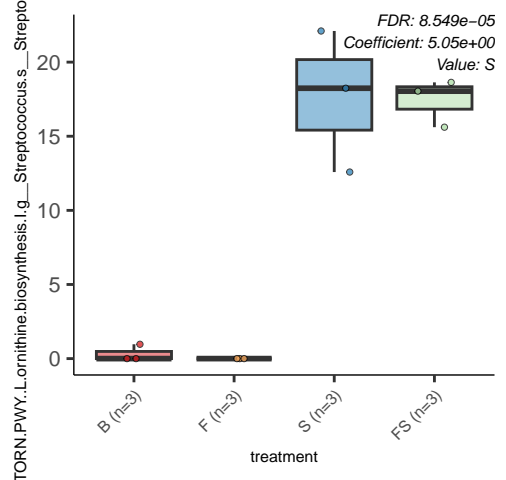


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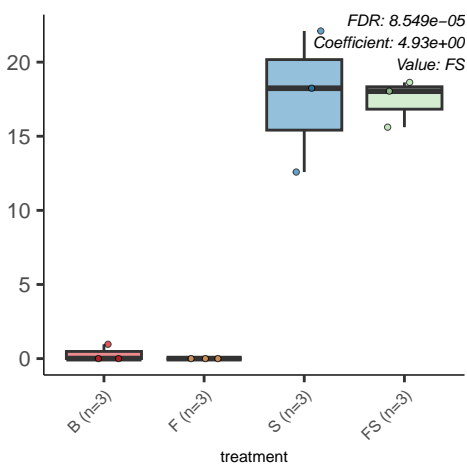




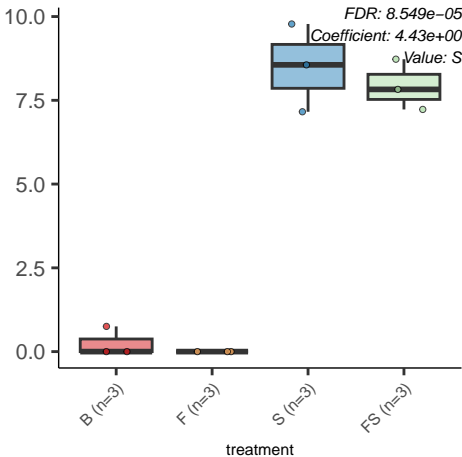




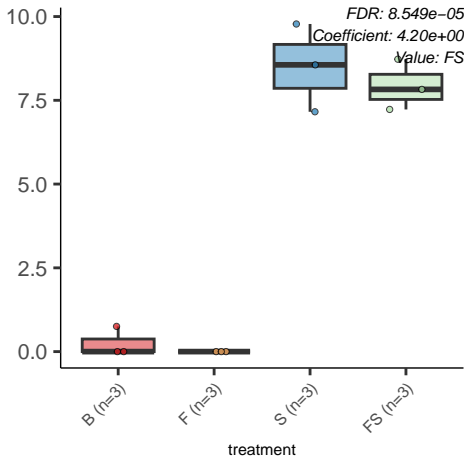
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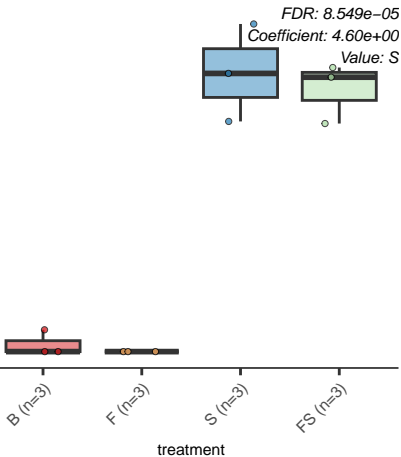


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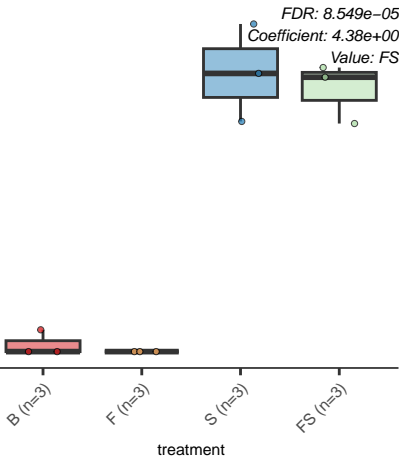


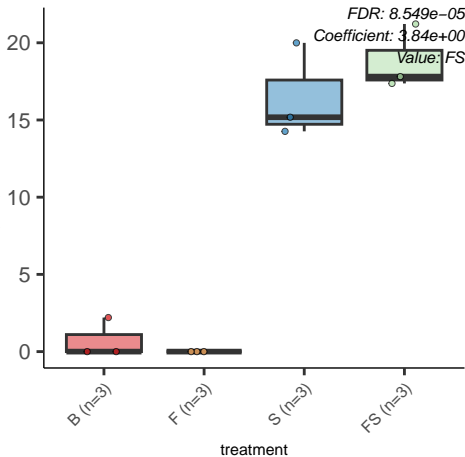
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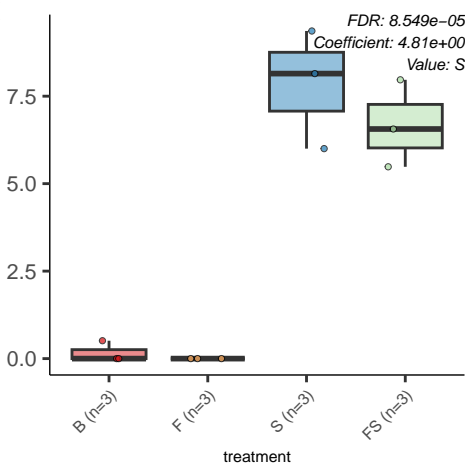


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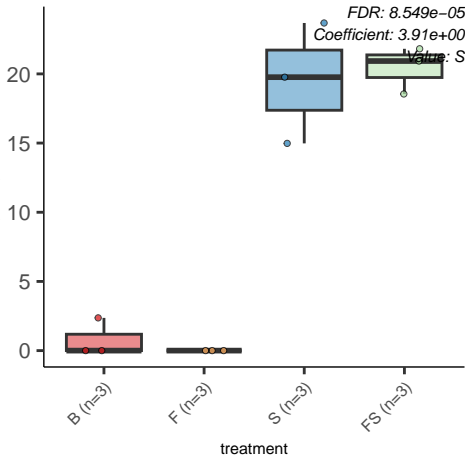




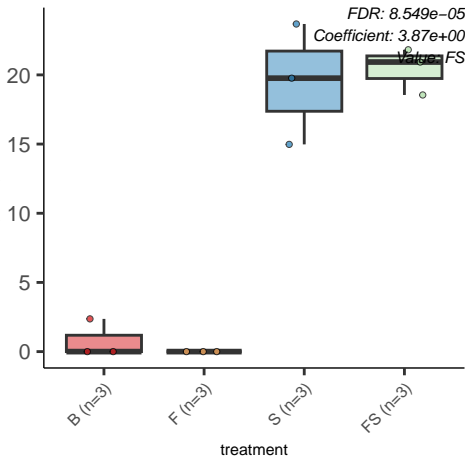
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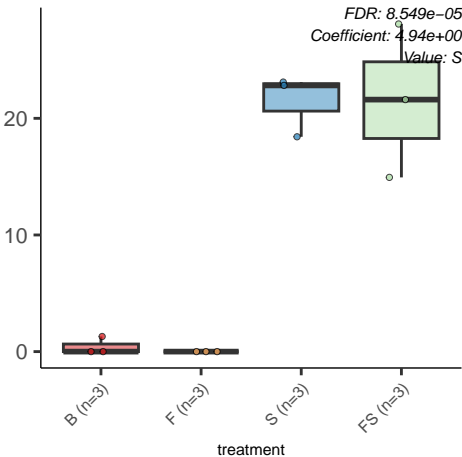
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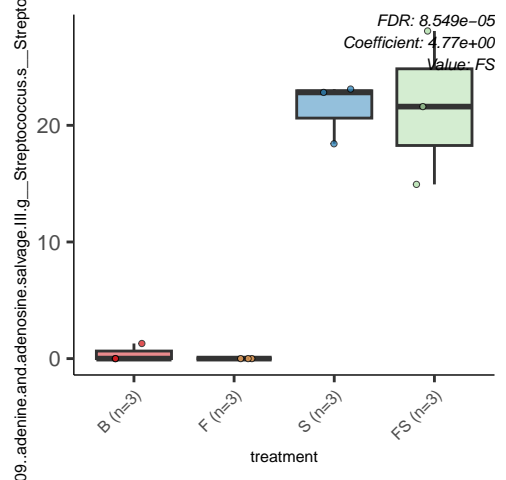


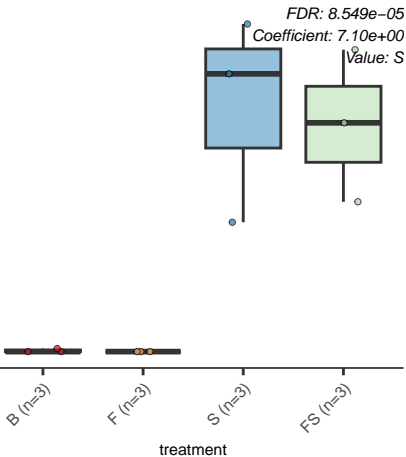
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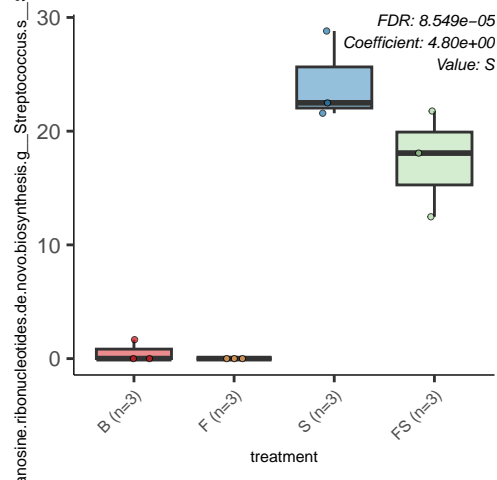


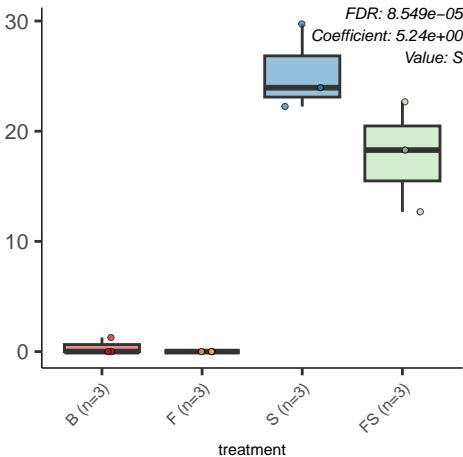
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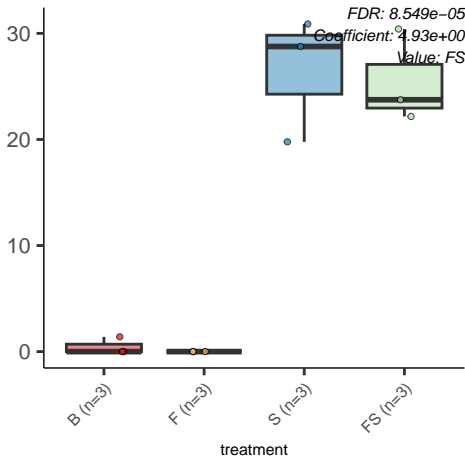


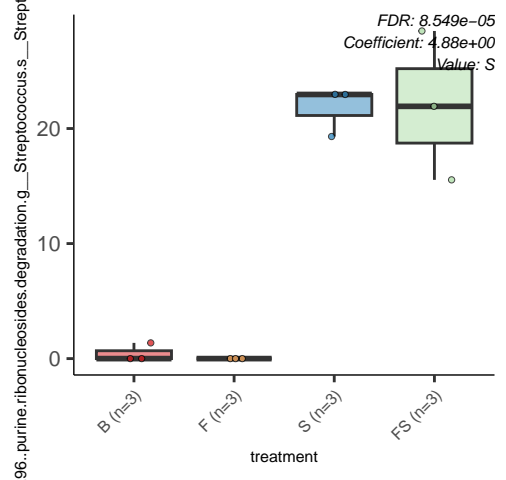


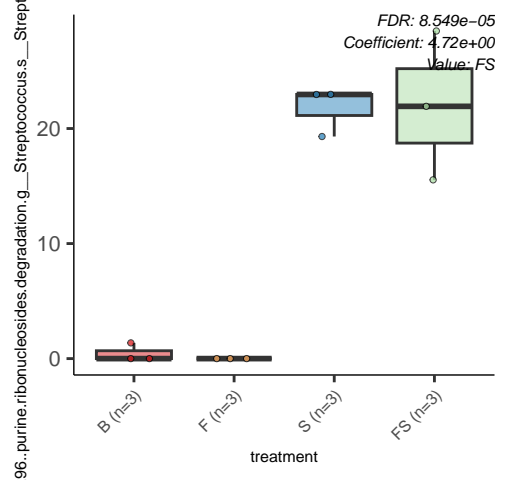




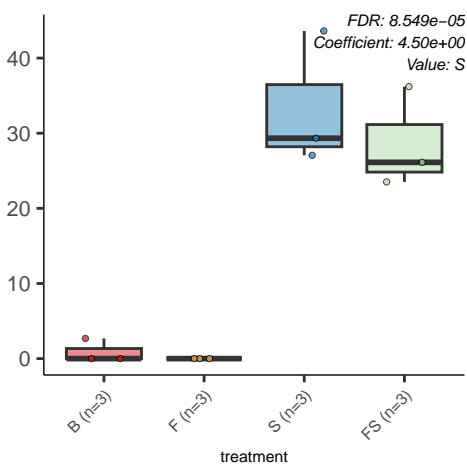
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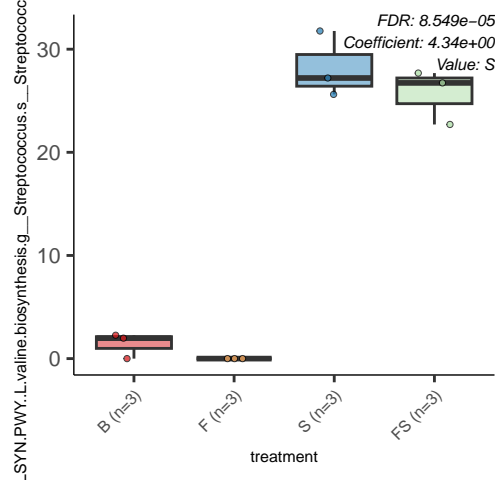




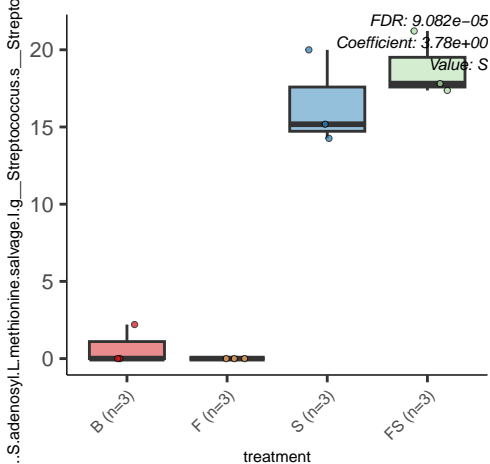


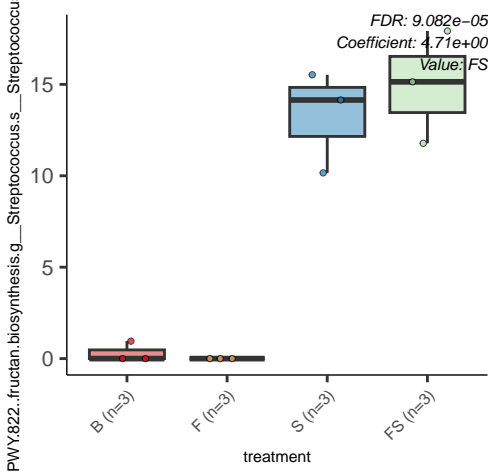
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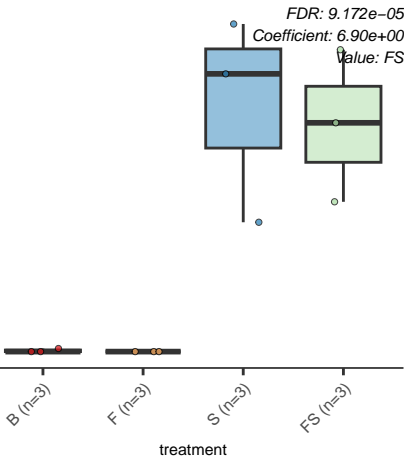


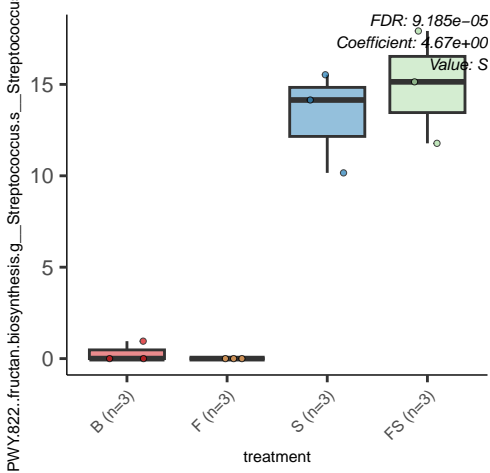


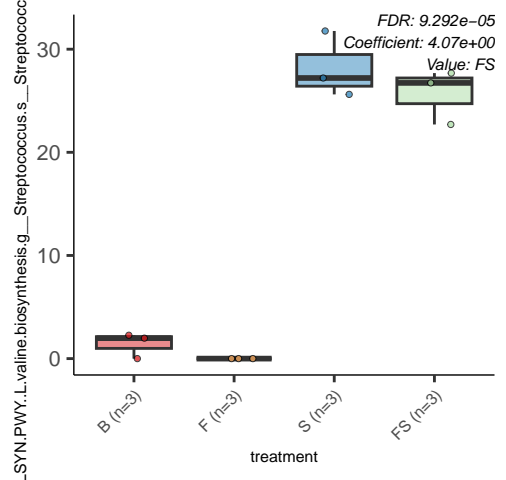
51..S.adenosyl.L.methionine.salvage.l.g__Streptococcus.s__Strepto



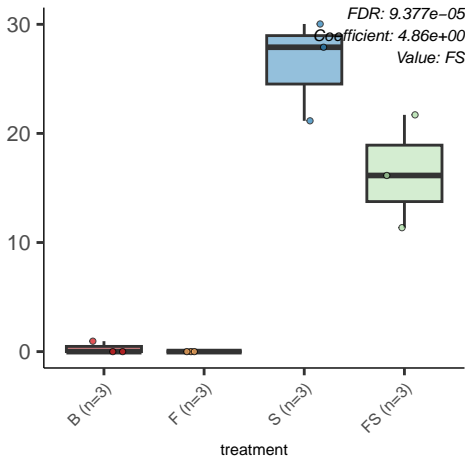




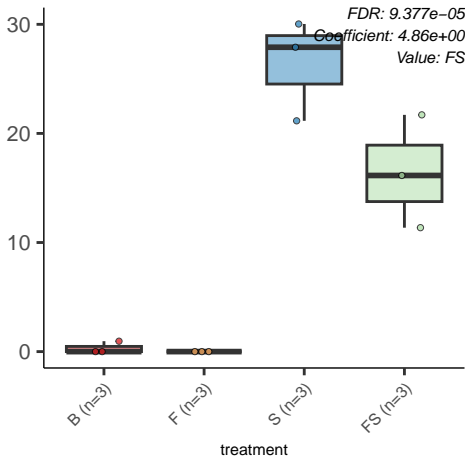


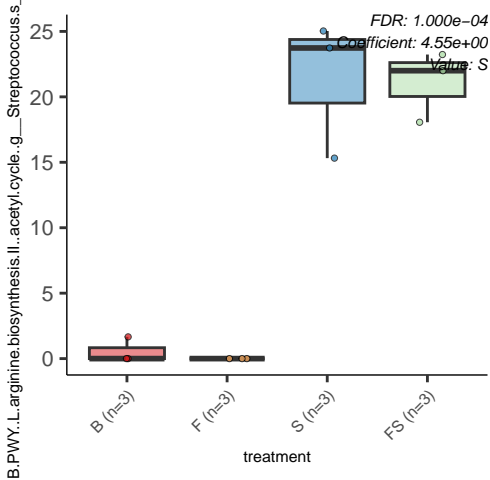


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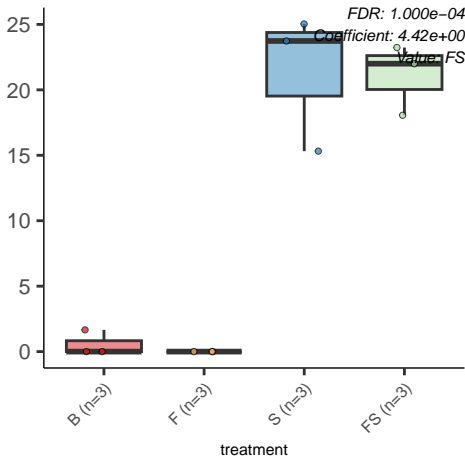


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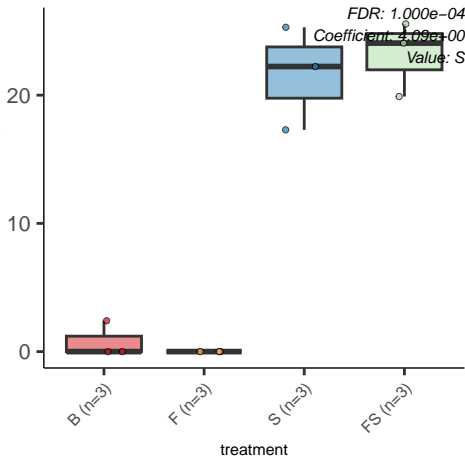




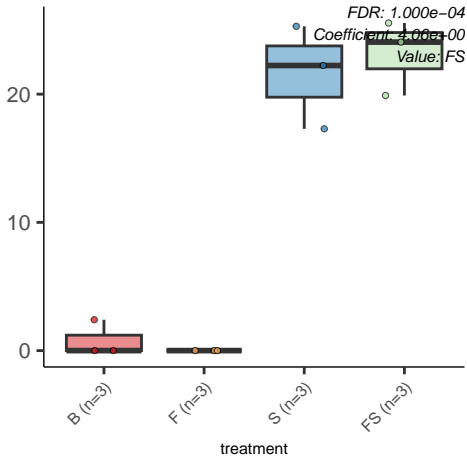
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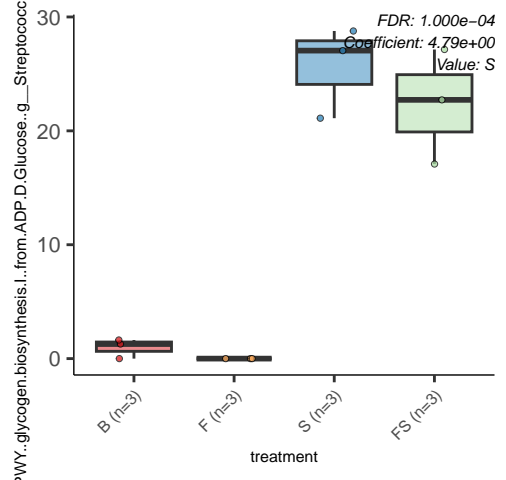


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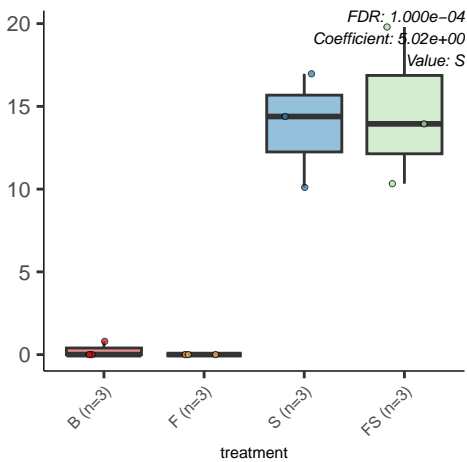


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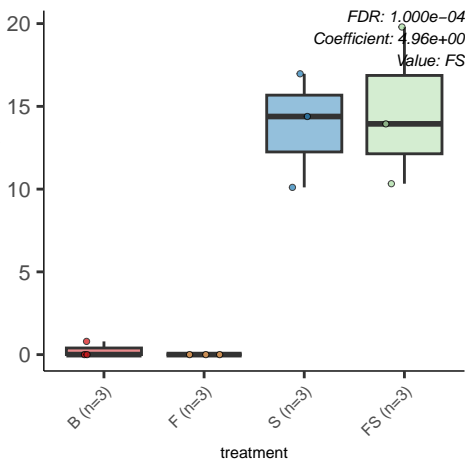


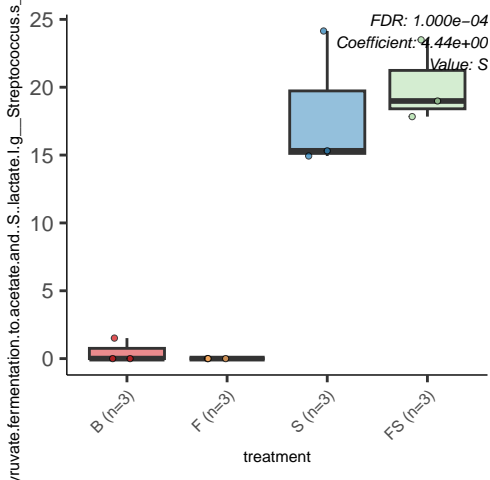


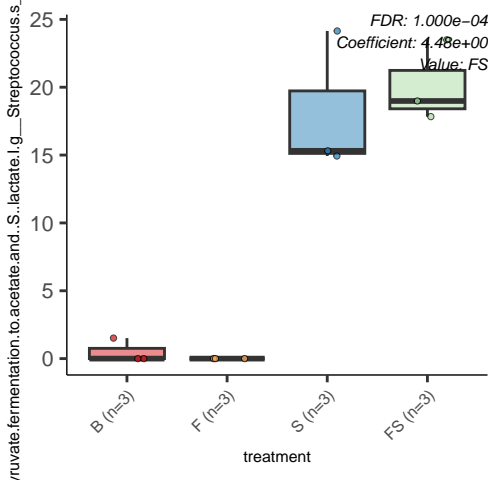
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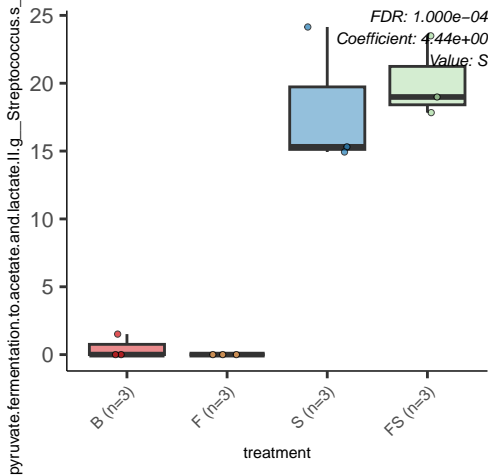


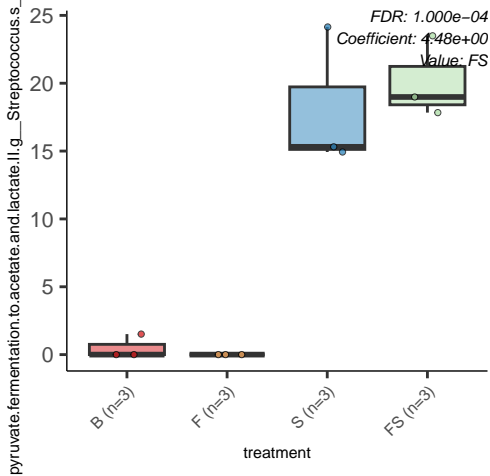
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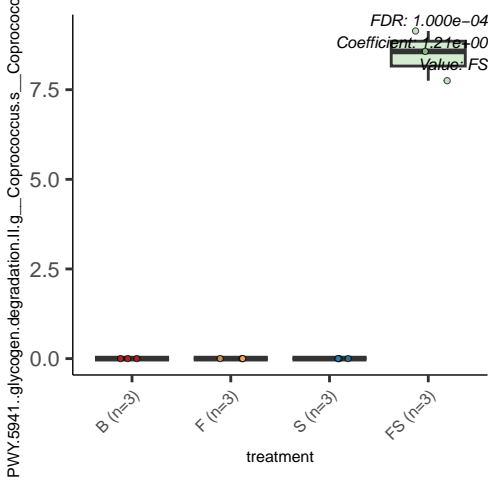




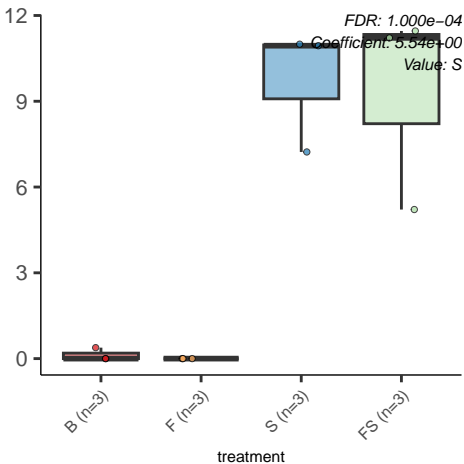


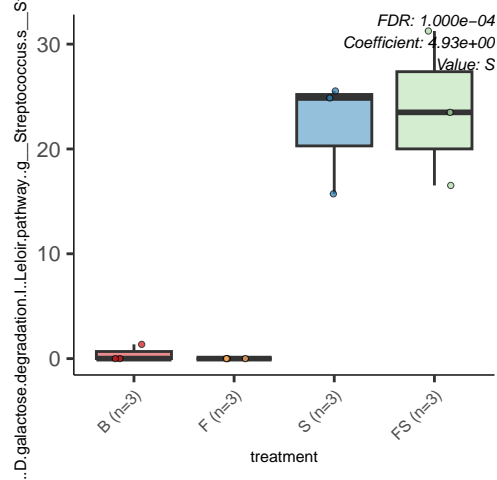




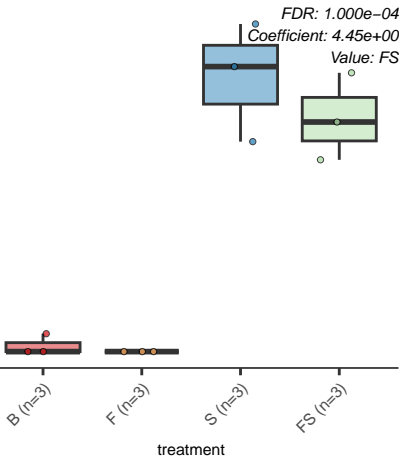


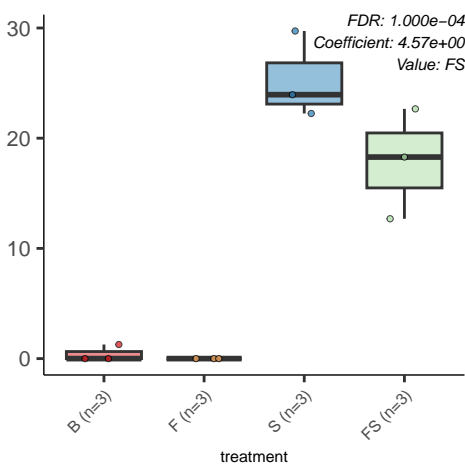
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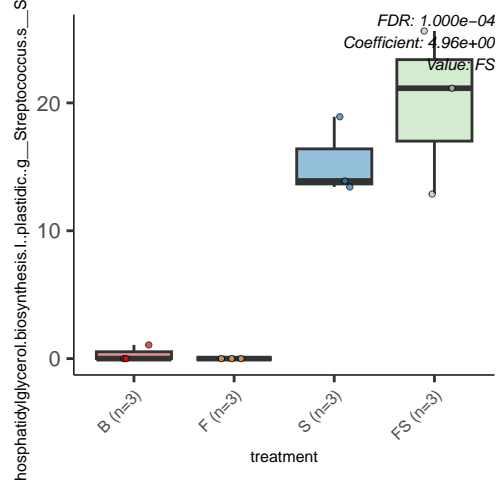


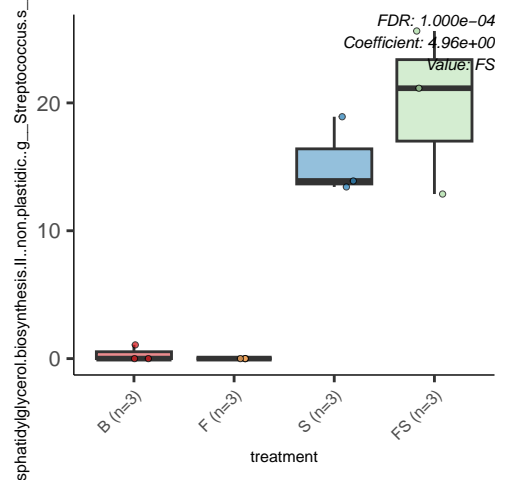


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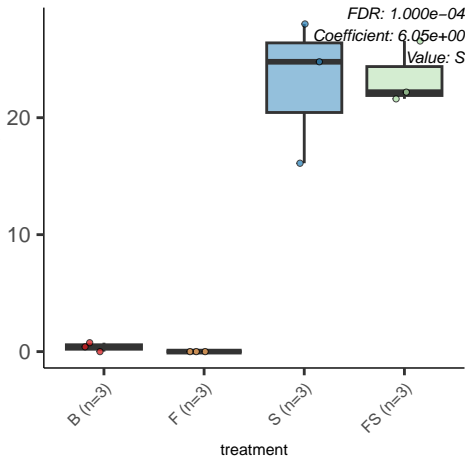




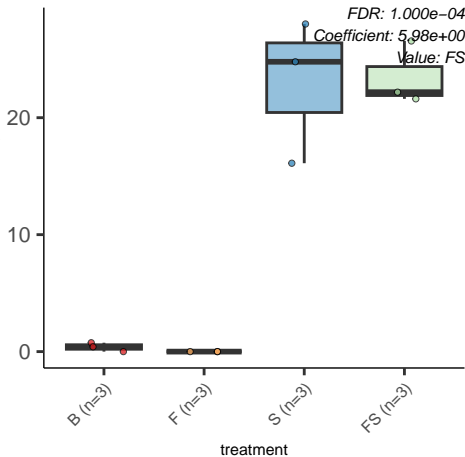




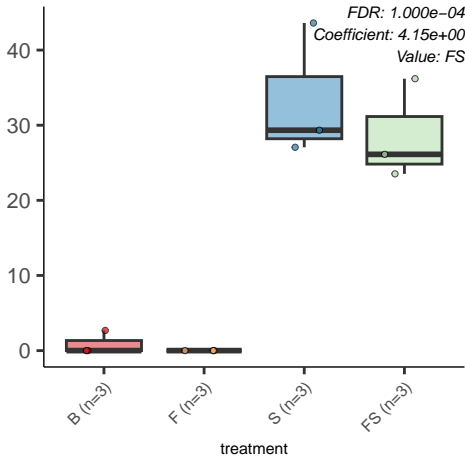
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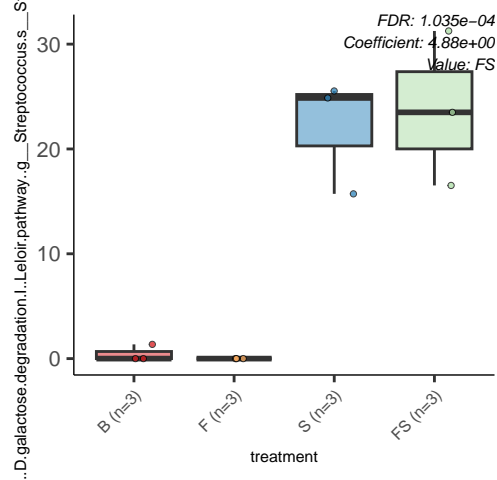


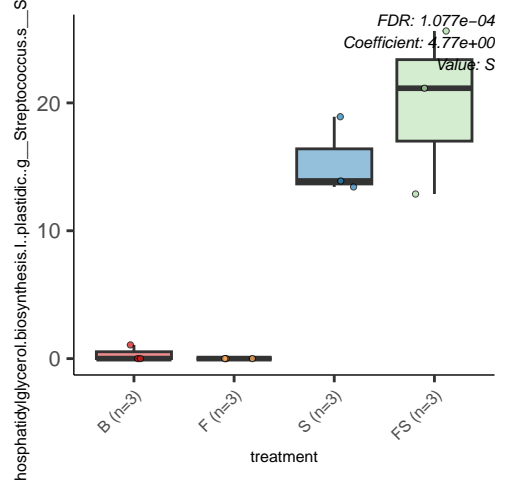
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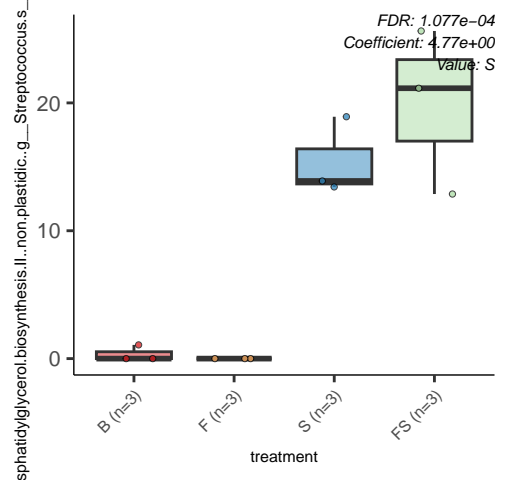


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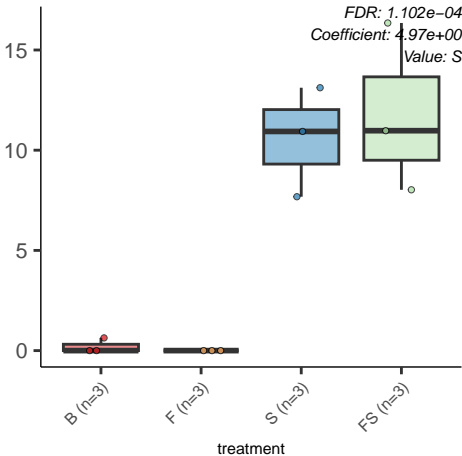


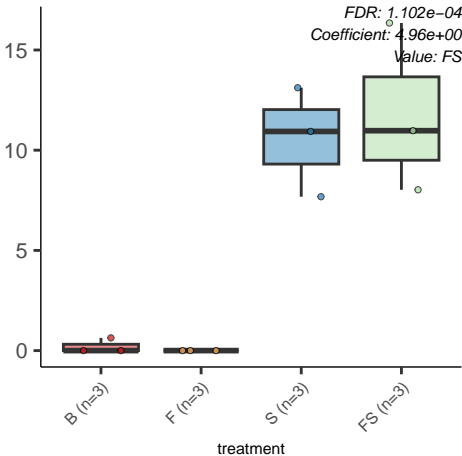


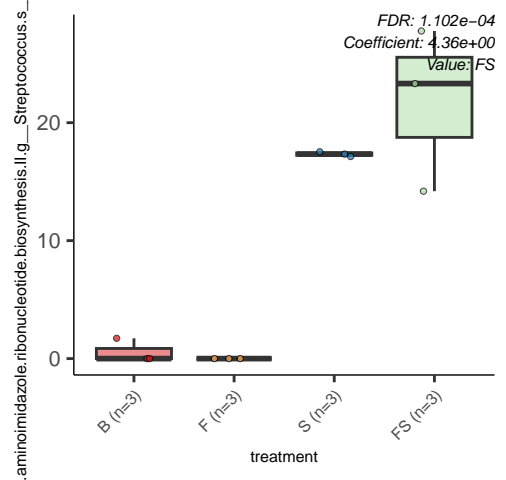




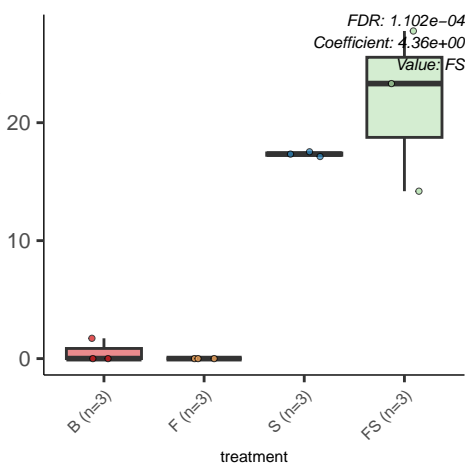
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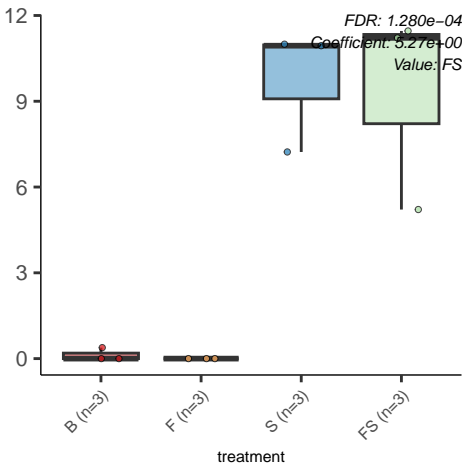


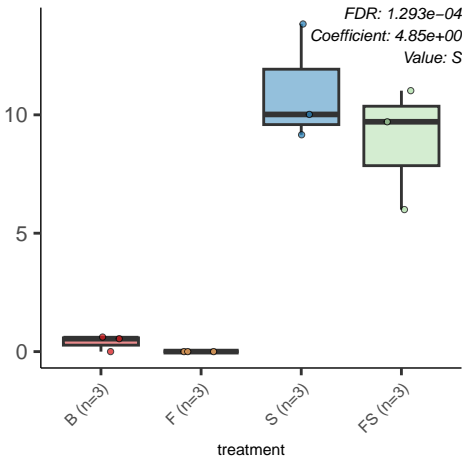


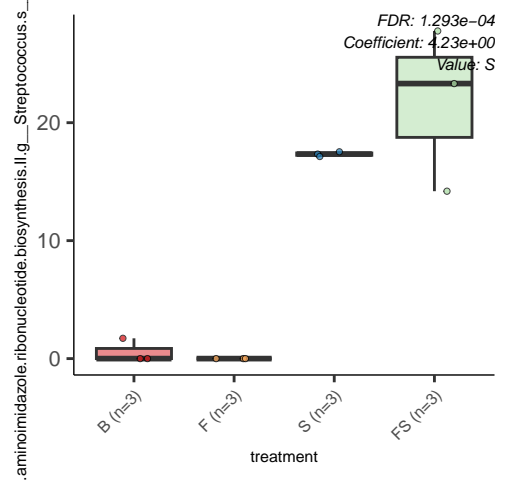
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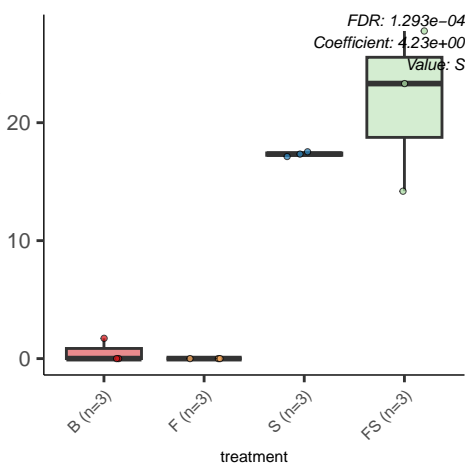
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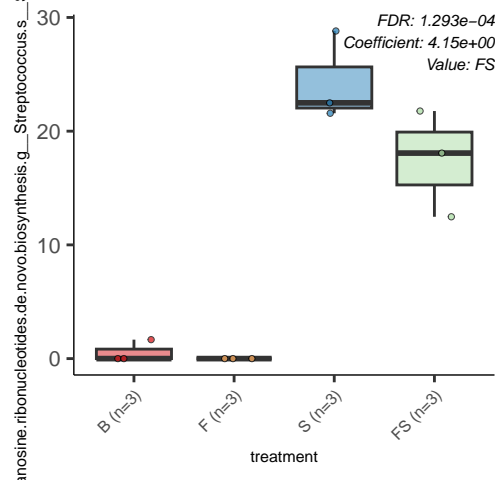




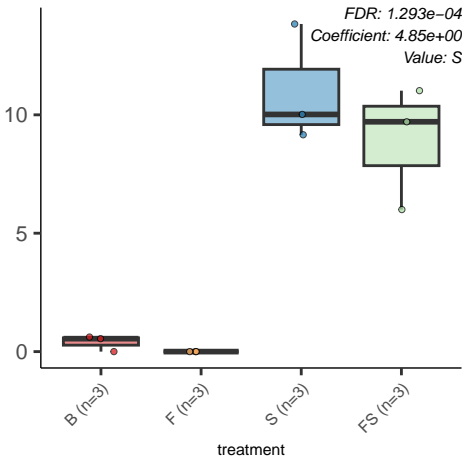


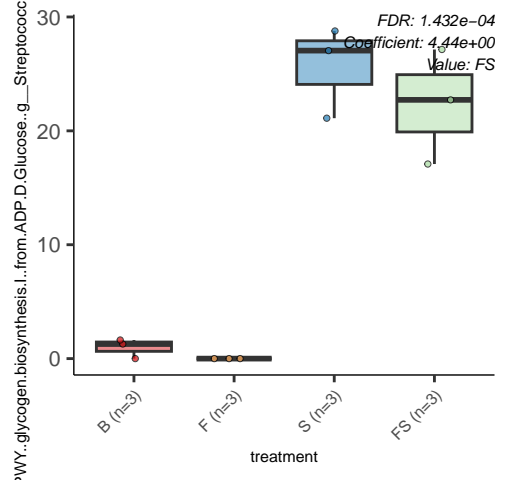
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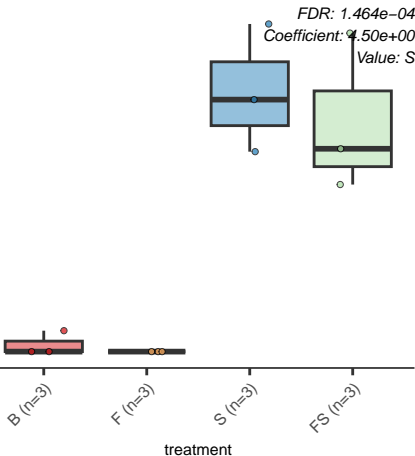




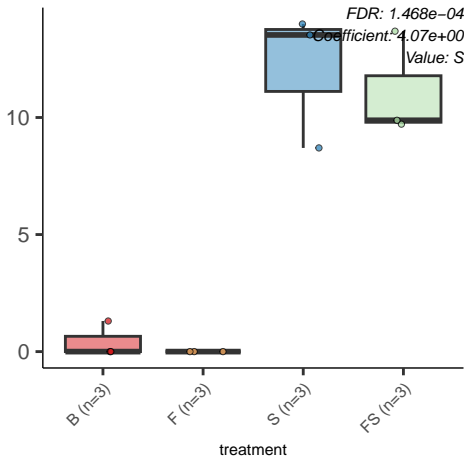
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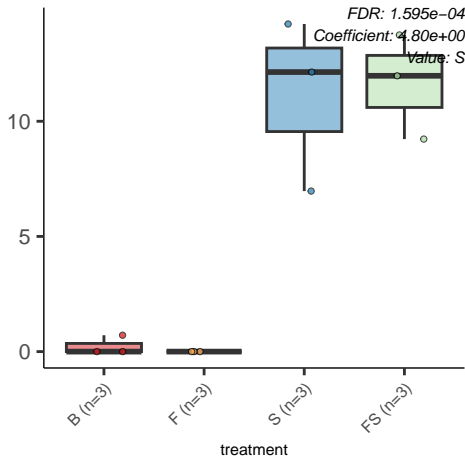


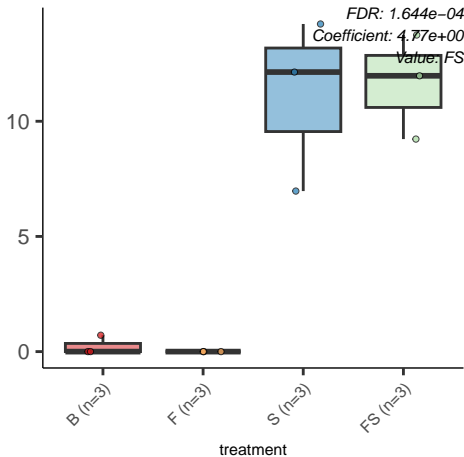




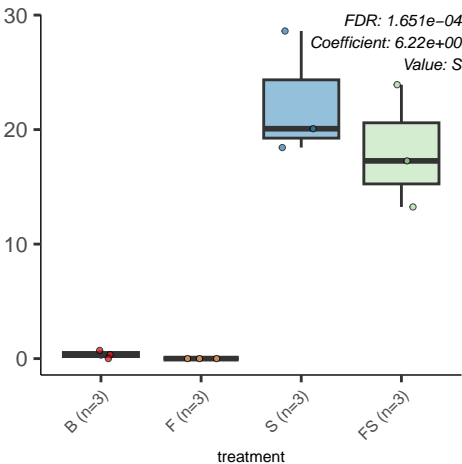
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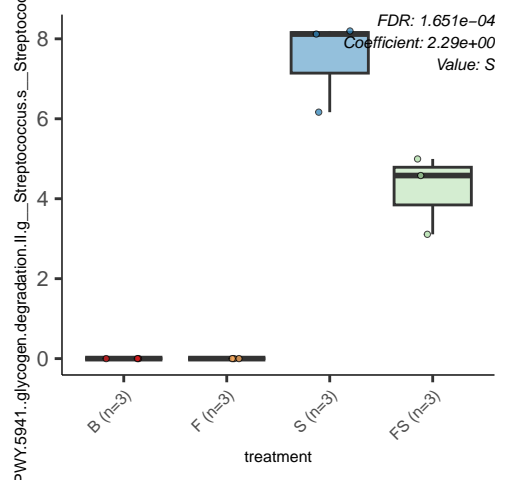




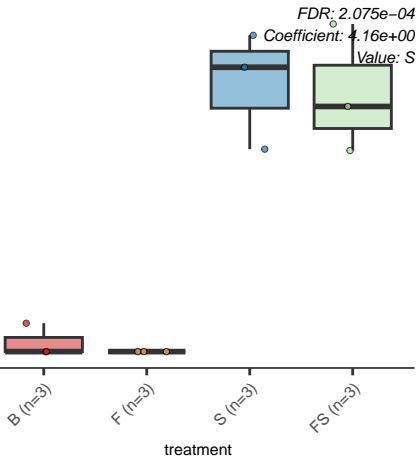


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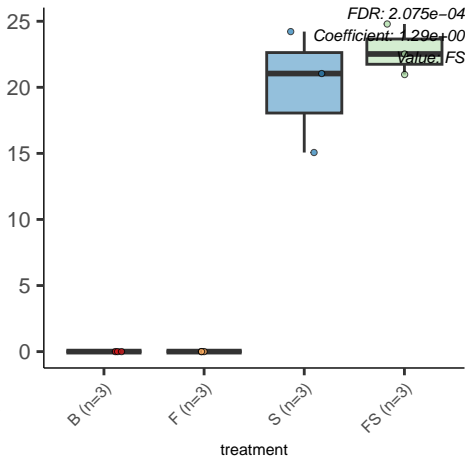




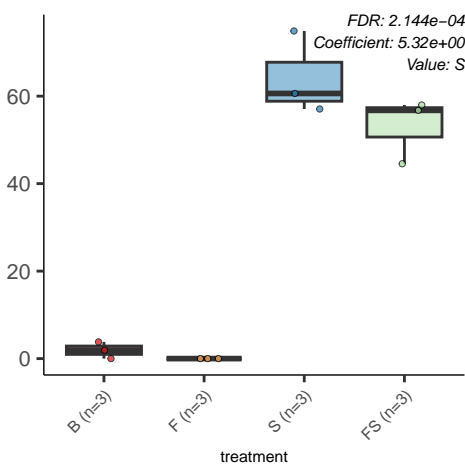
4.PWY..glycogen.biosynthesis.l...from.ADP.D.Glucose..g__Streptococ



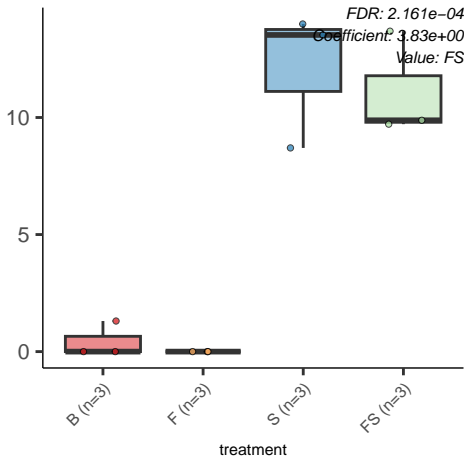
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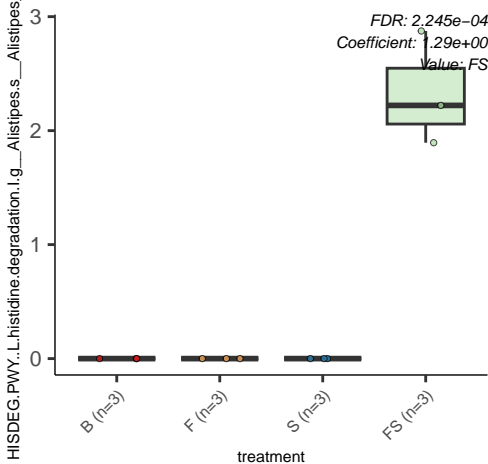


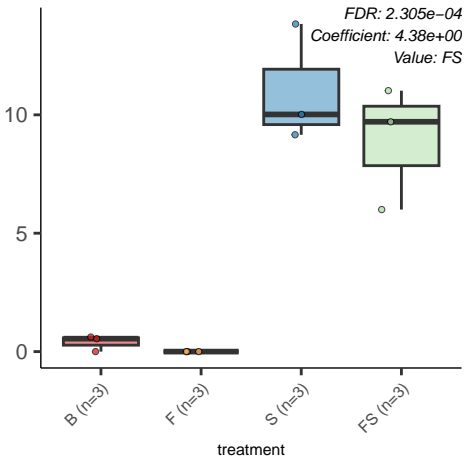
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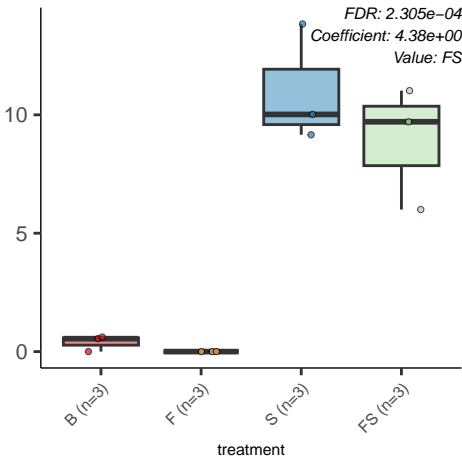
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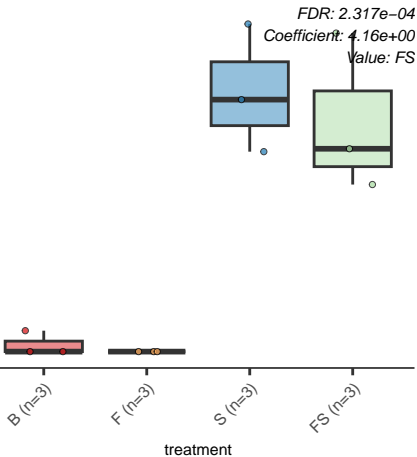


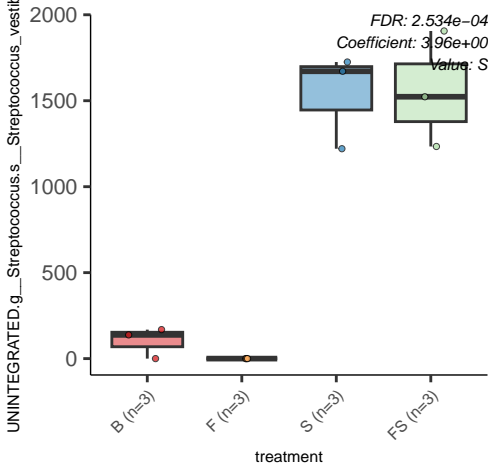


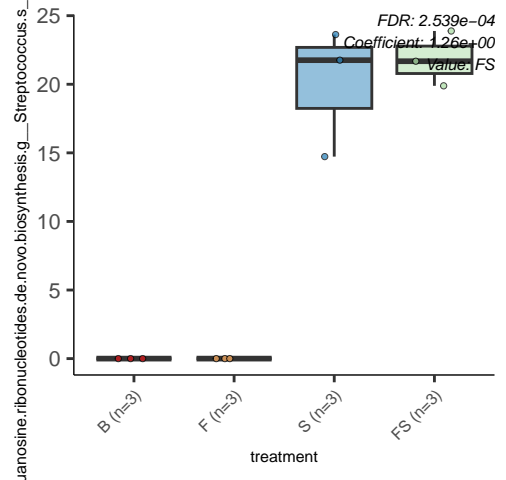


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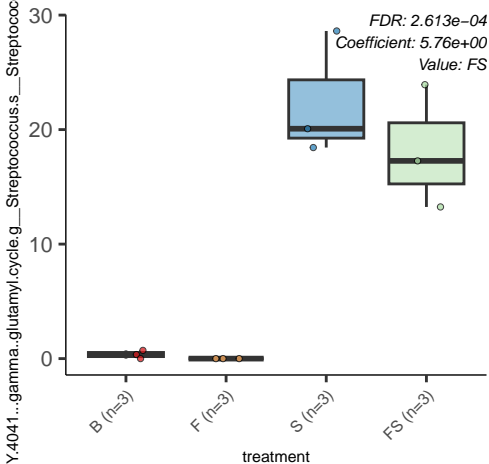


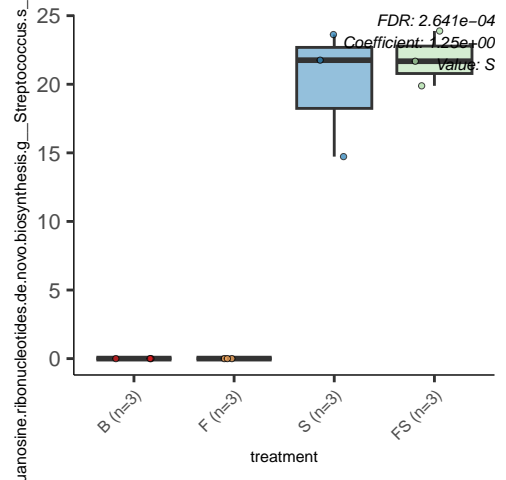




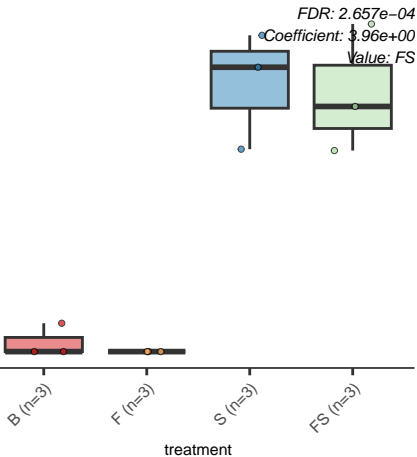


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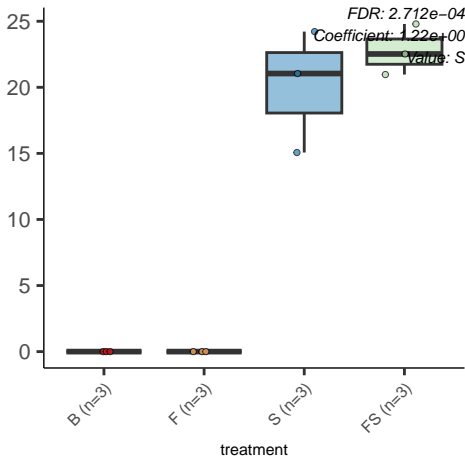




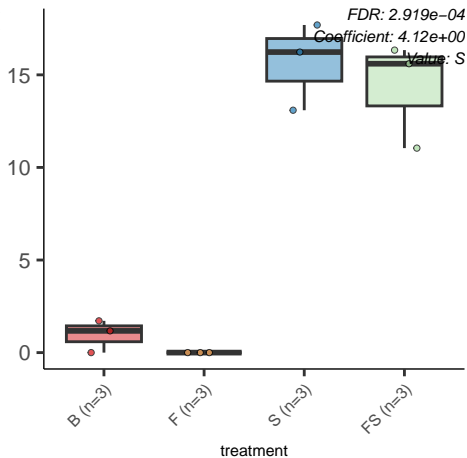
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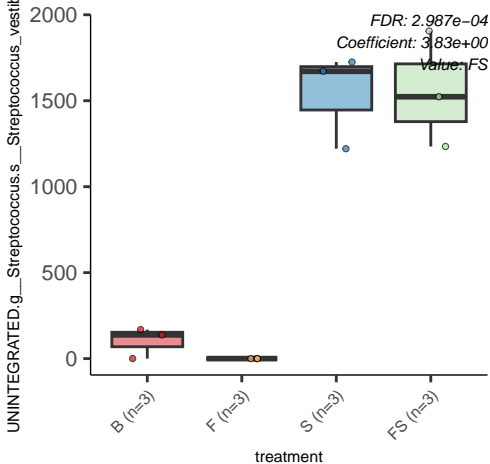


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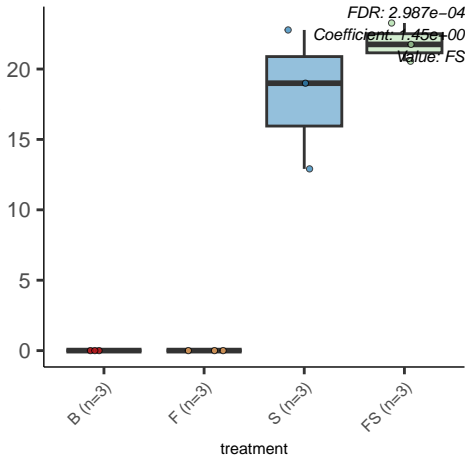


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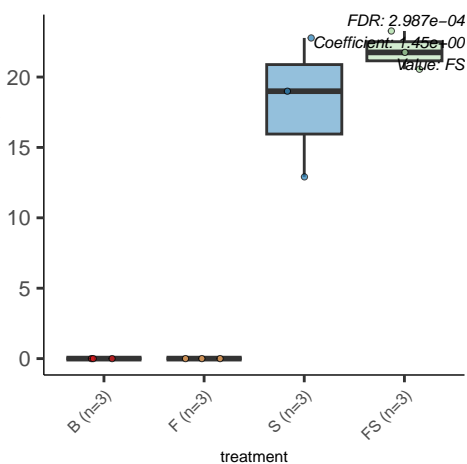


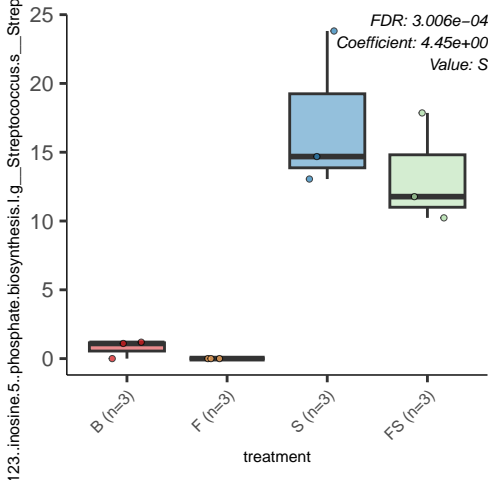


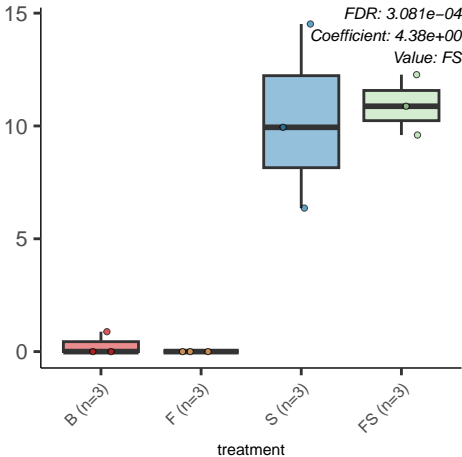
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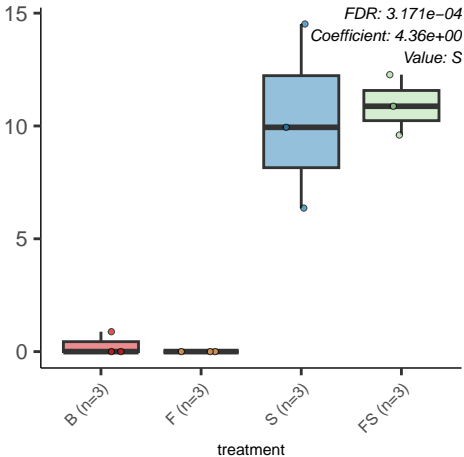


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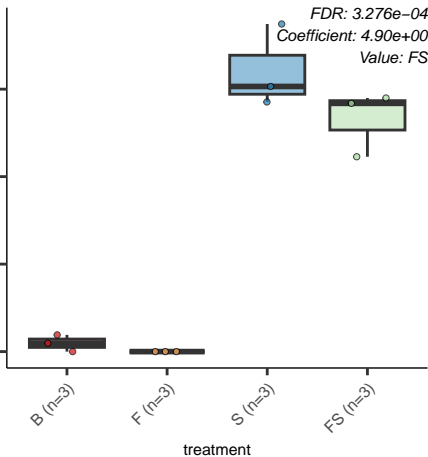


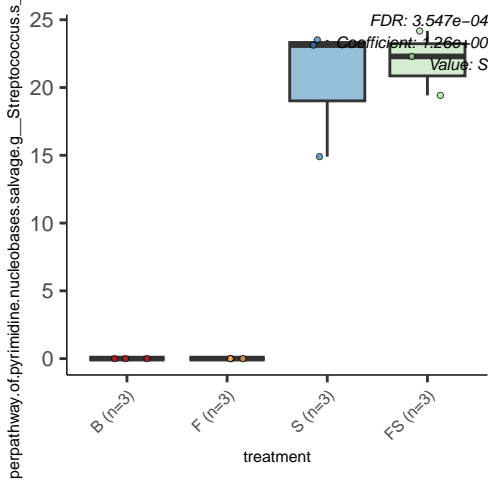


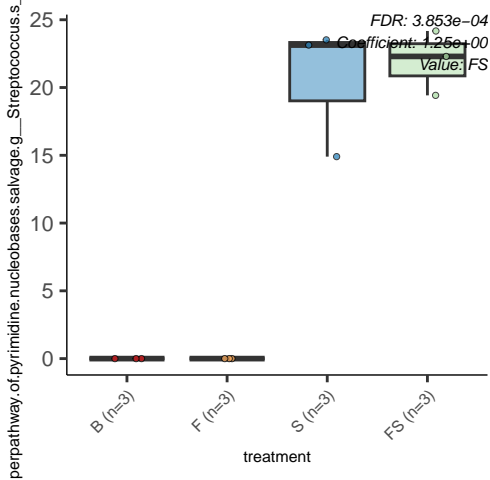




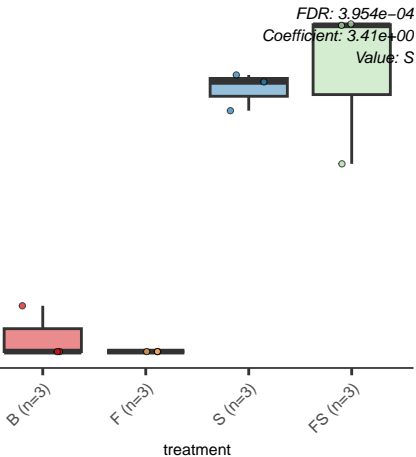
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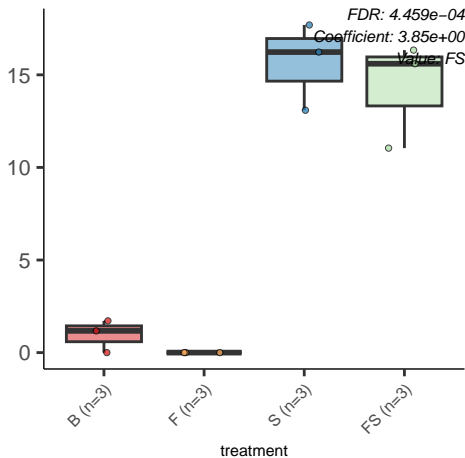




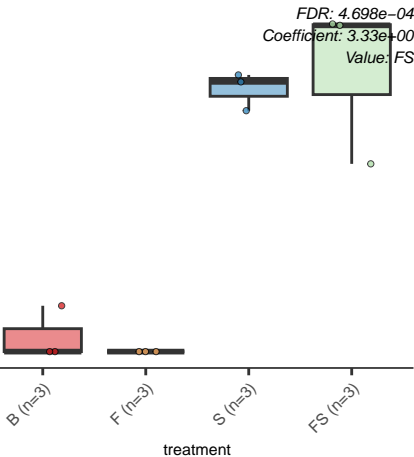
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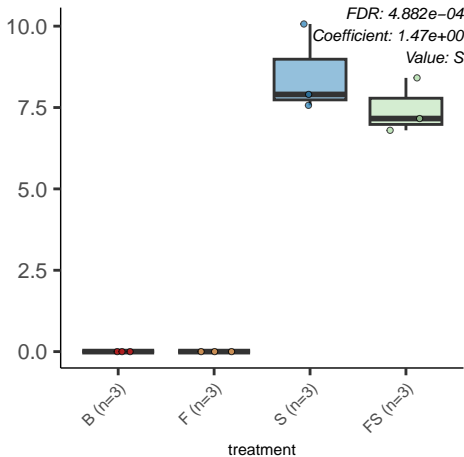
l.pentapeptide.biosynthesis.l..meso.diaminopimelate.containing.g

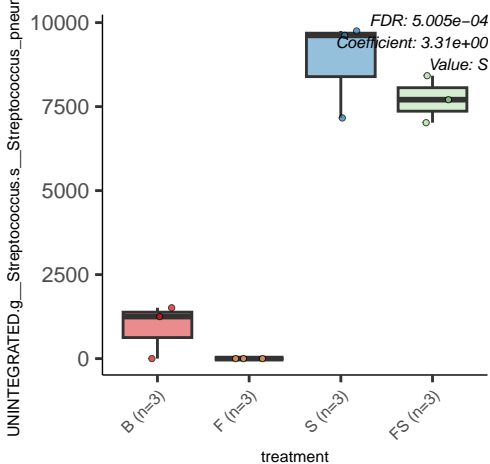


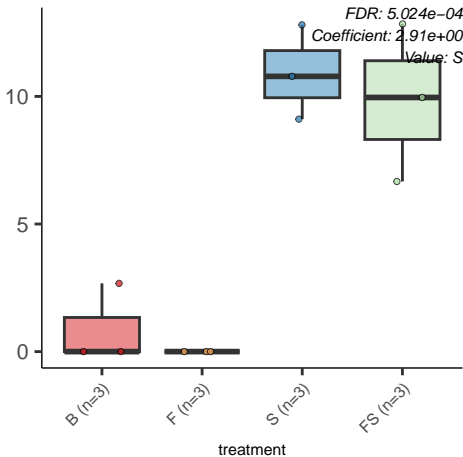
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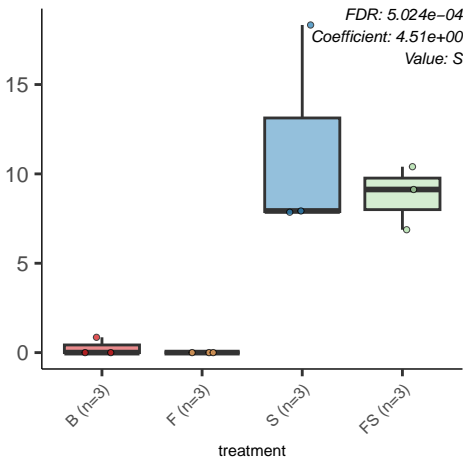
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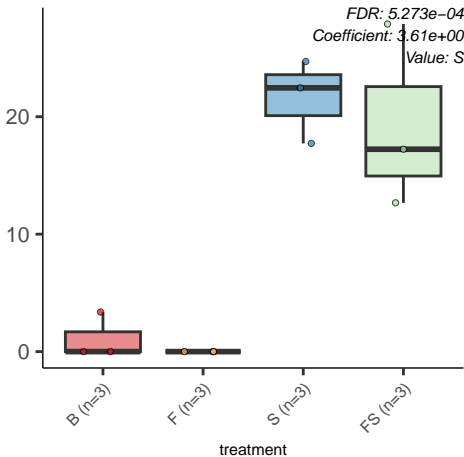


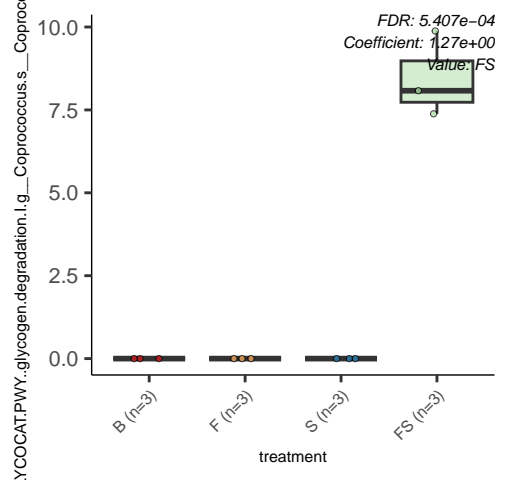


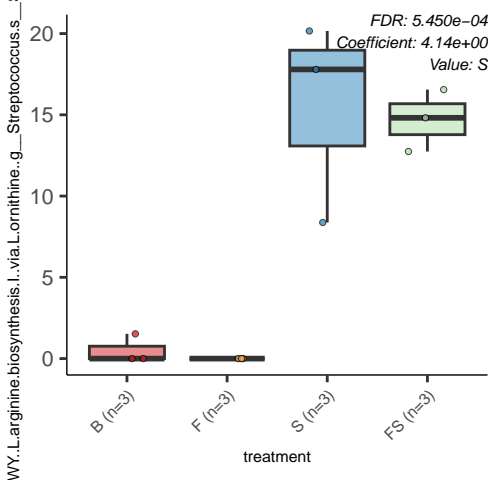


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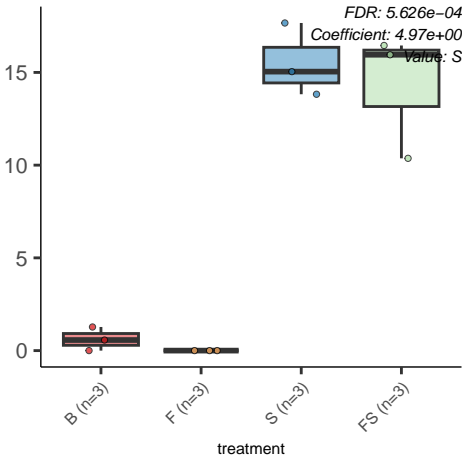




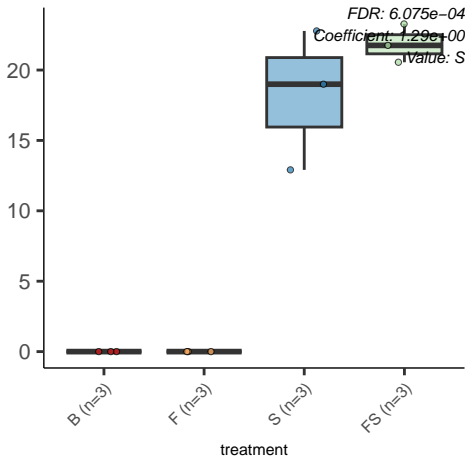




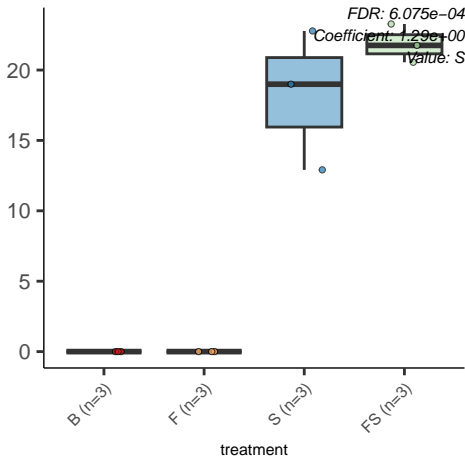
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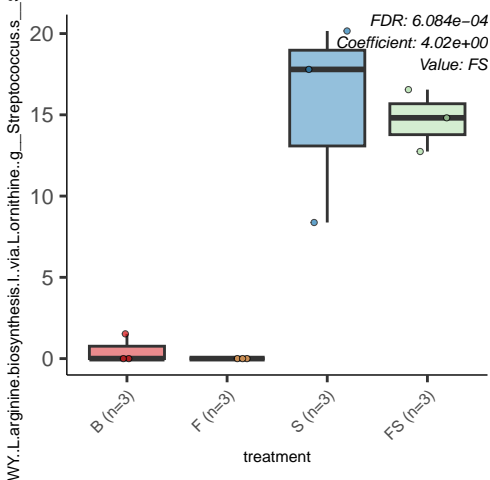


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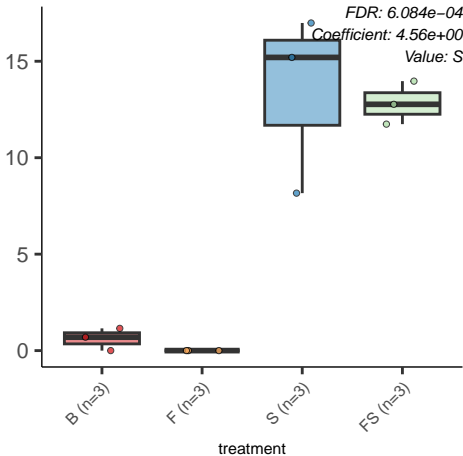


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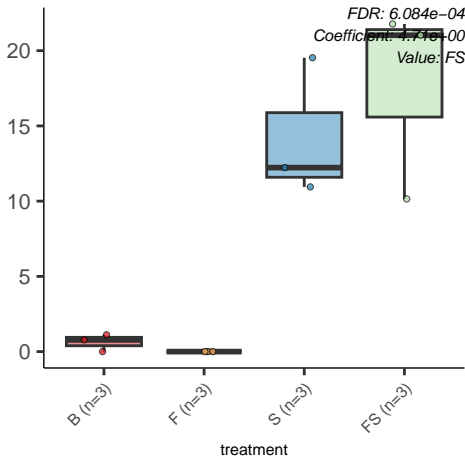




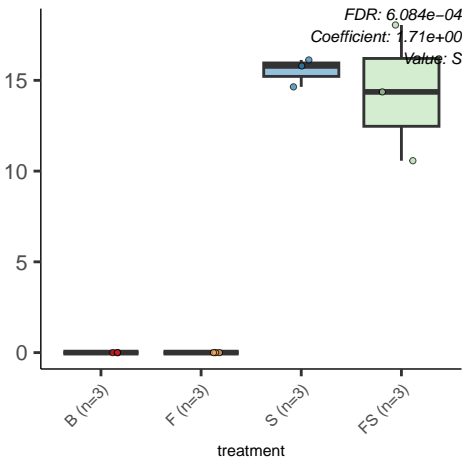
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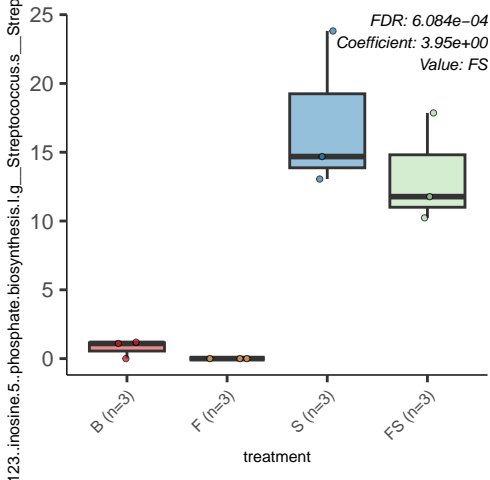


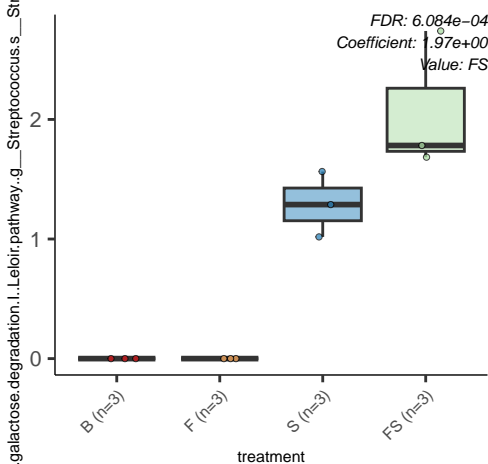
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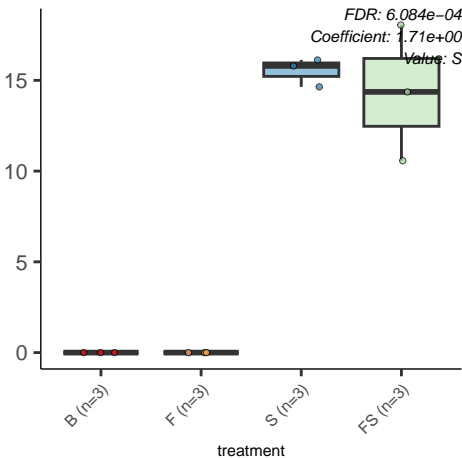
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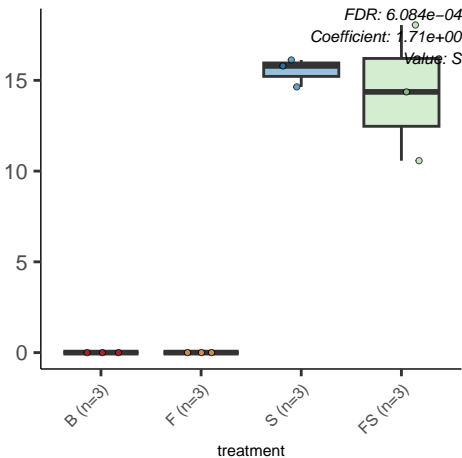




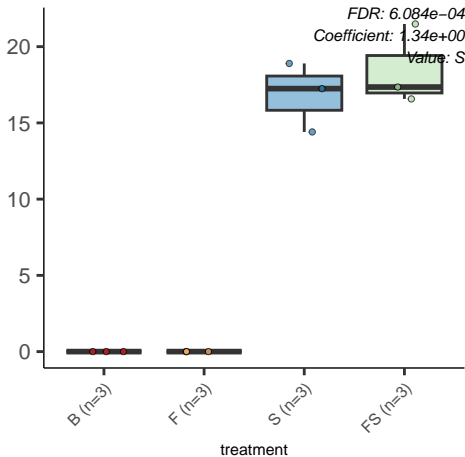
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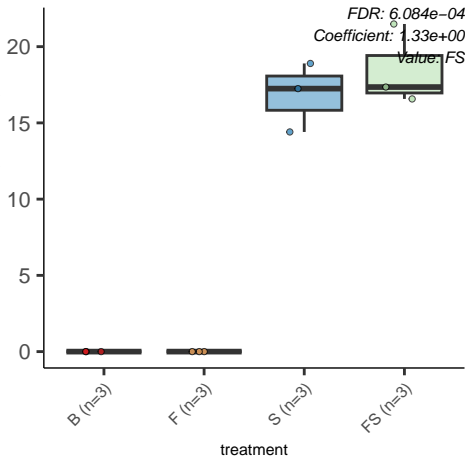
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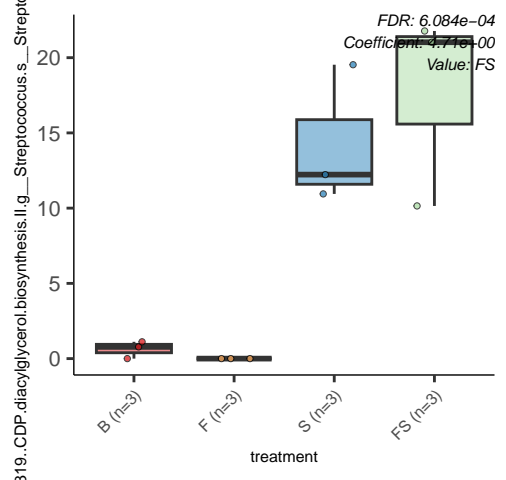


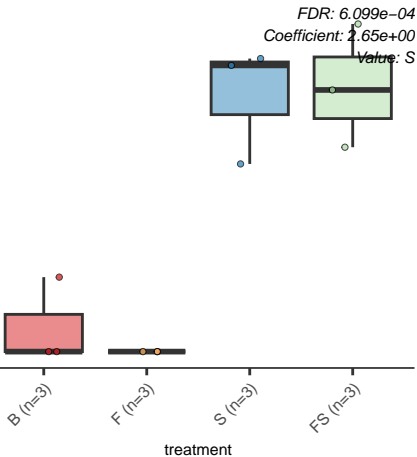
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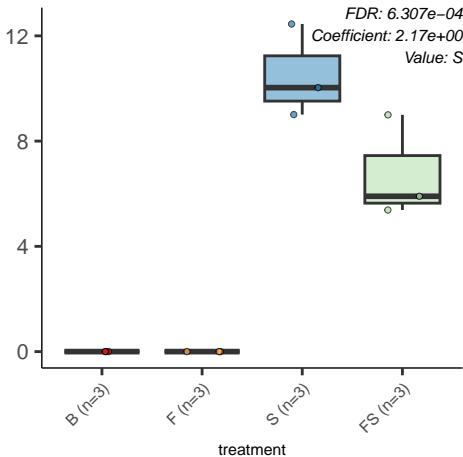
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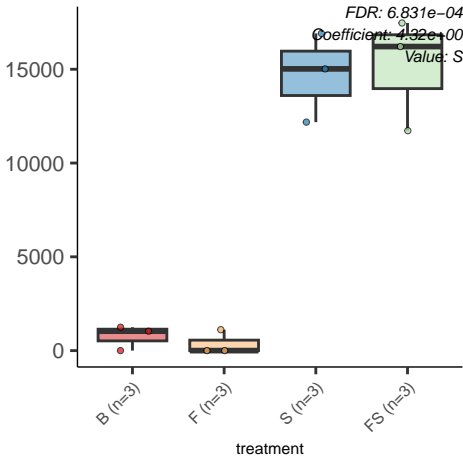




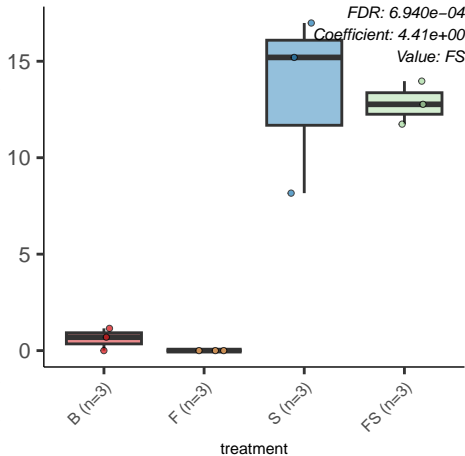
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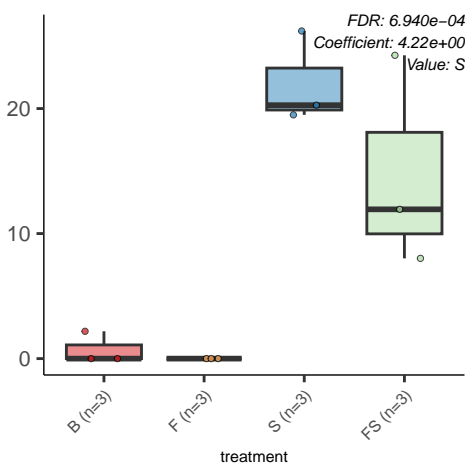
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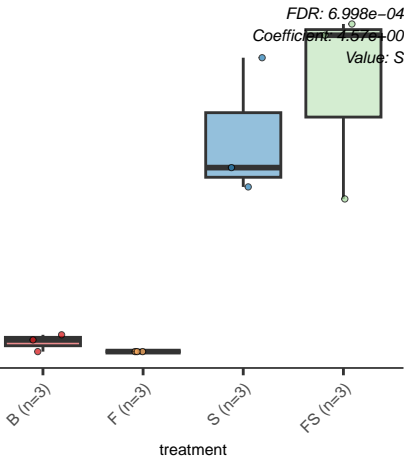
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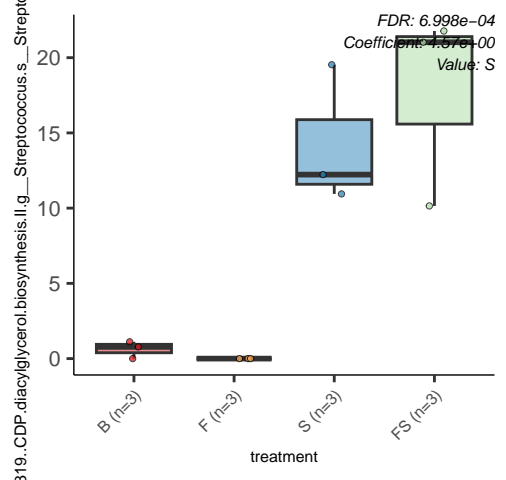


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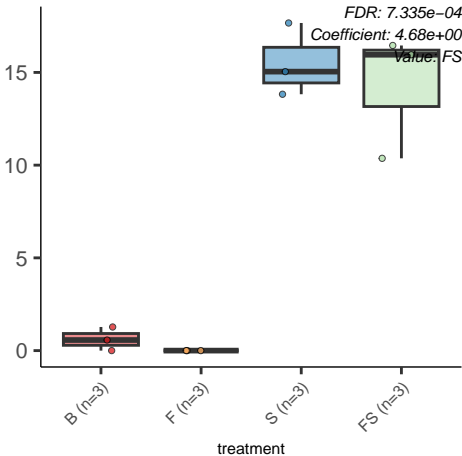


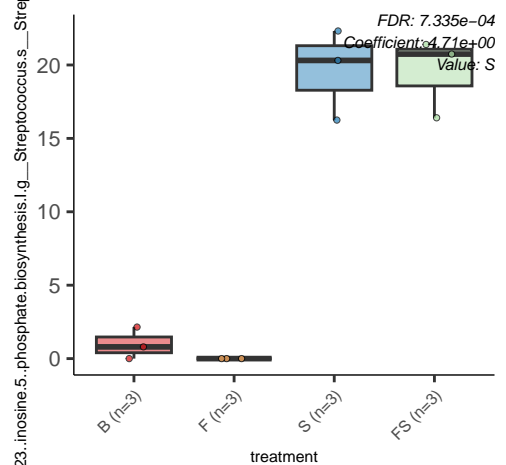
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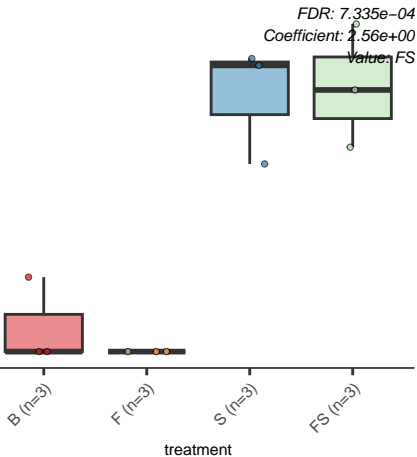


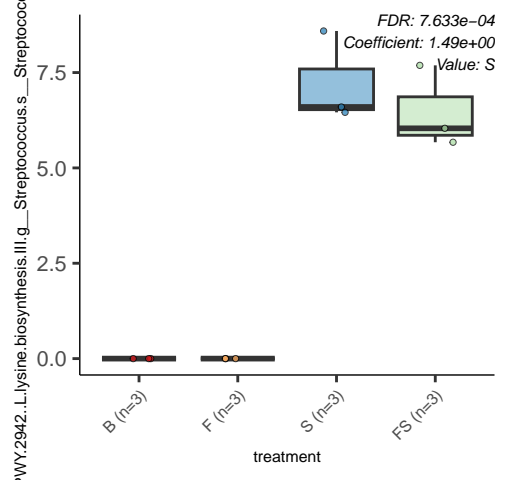


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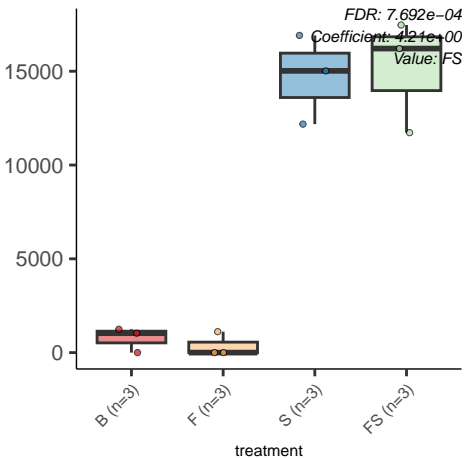




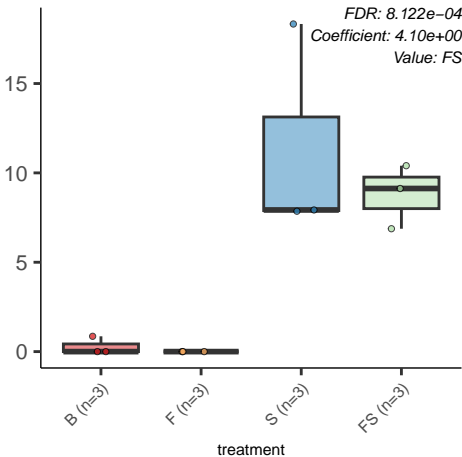


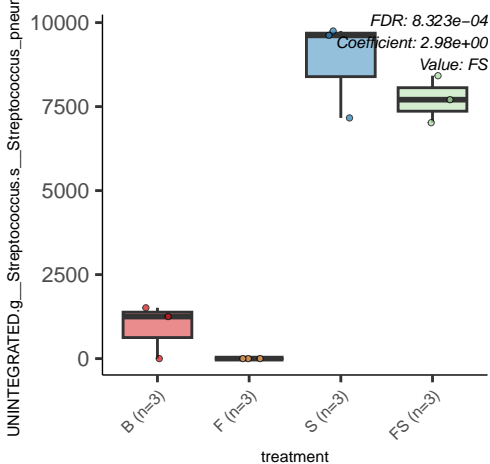


UNINTEGRATED.g__Streptococcus.s__Streptococcus_saliv

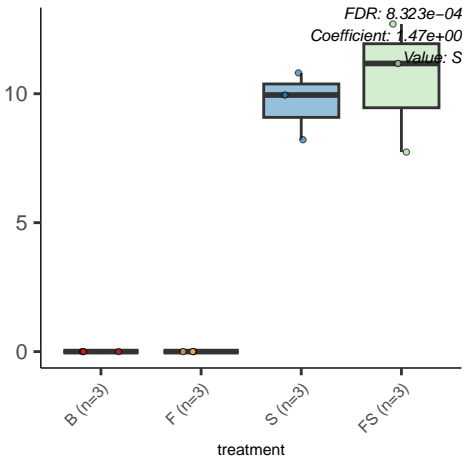


5.aminoimidazole.ribonucleotide.biosynthesis.l.g__Streptococcus.s

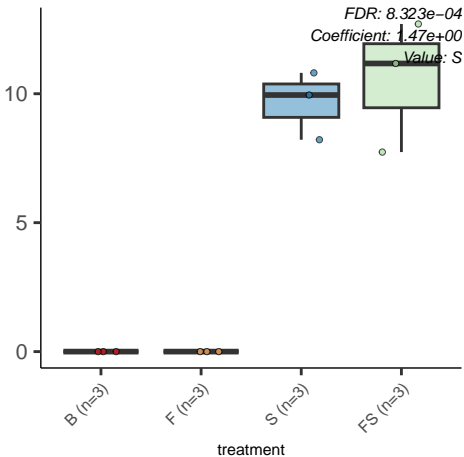


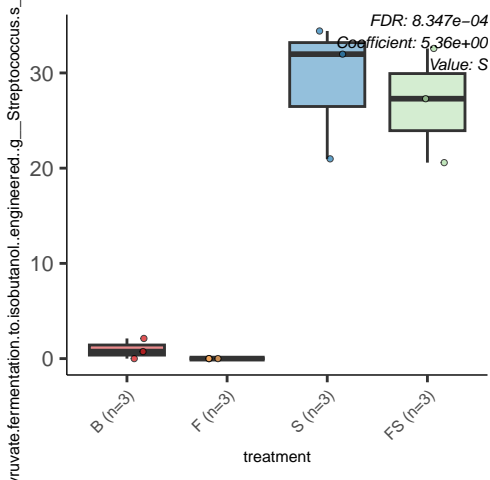


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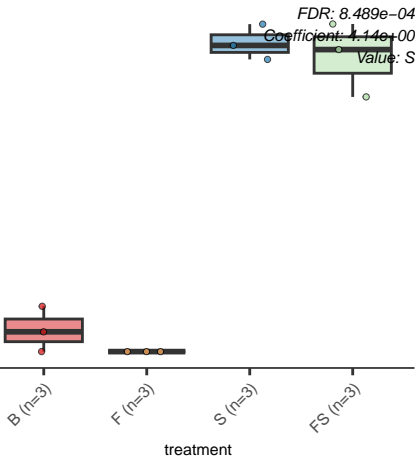


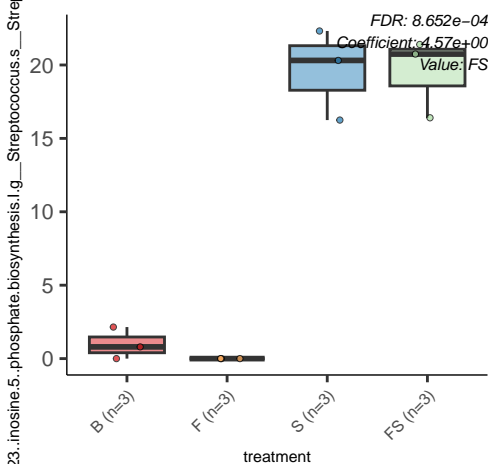
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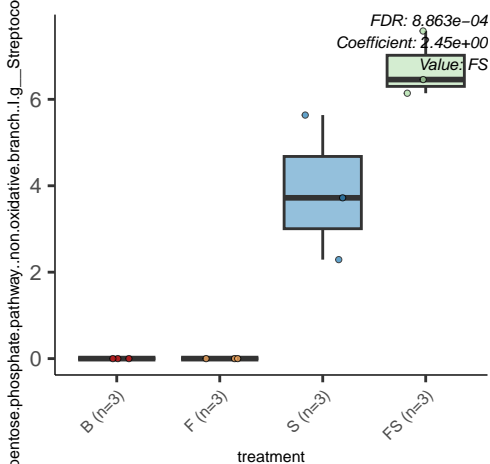


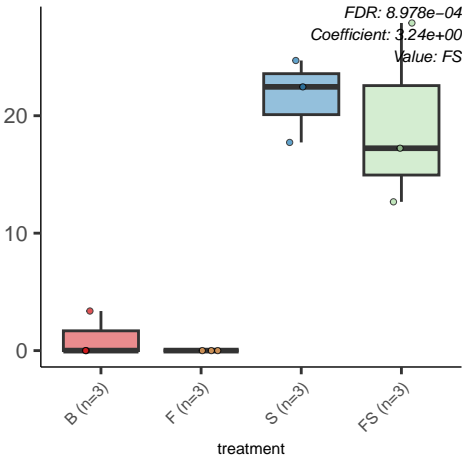


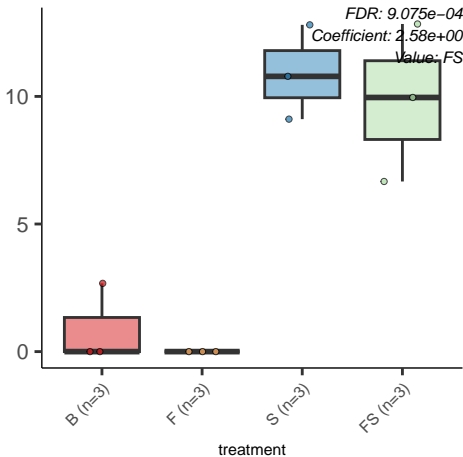
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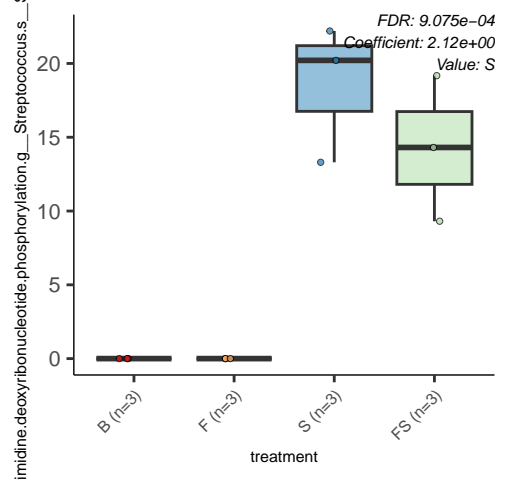




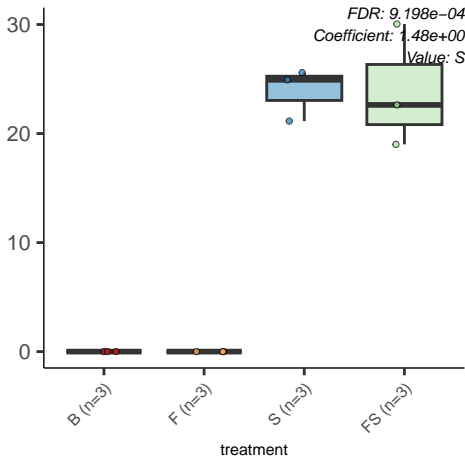




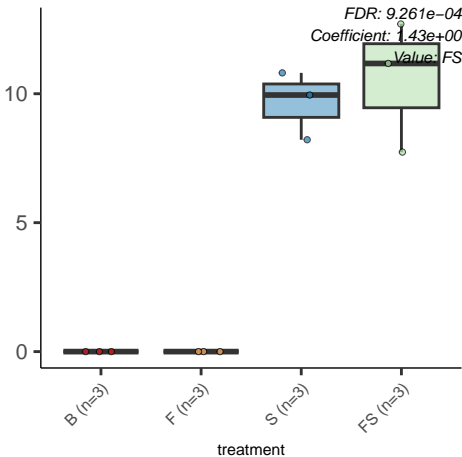




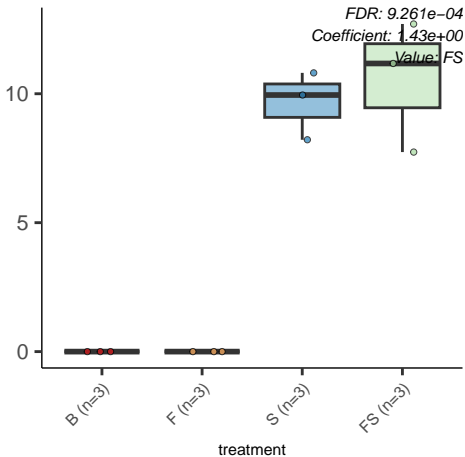
Y..superpathway.of.aromatic.amino.acid.biosynthesis.g__Streptococ

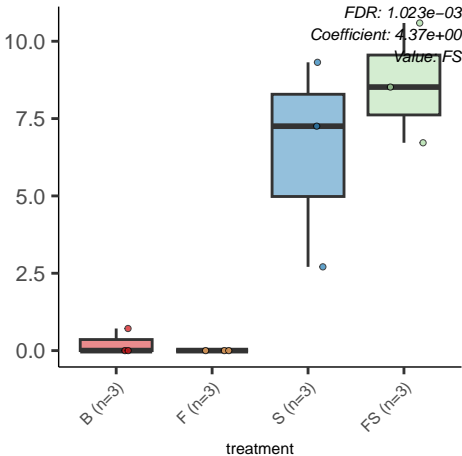


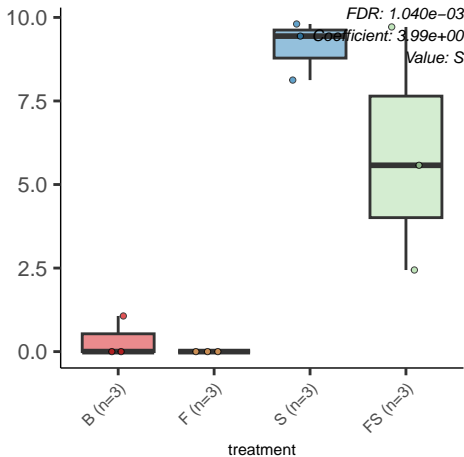
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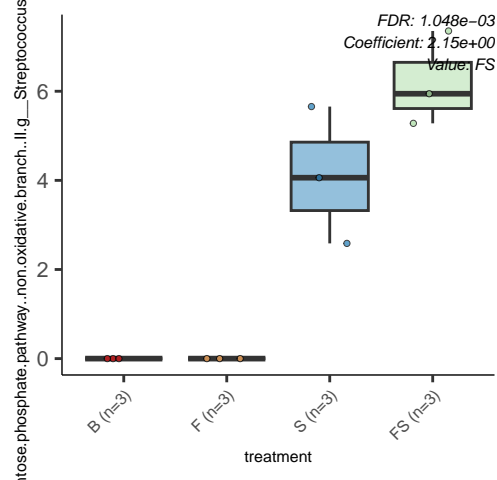


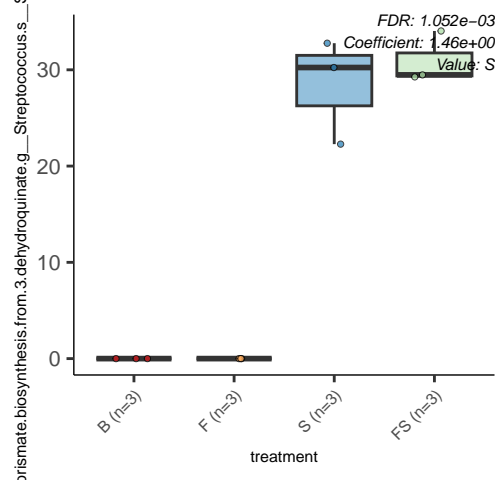
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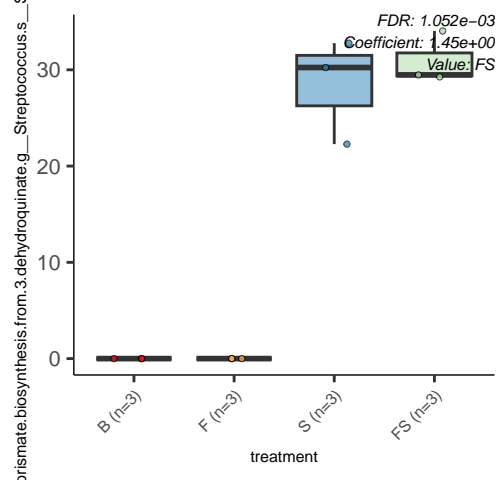


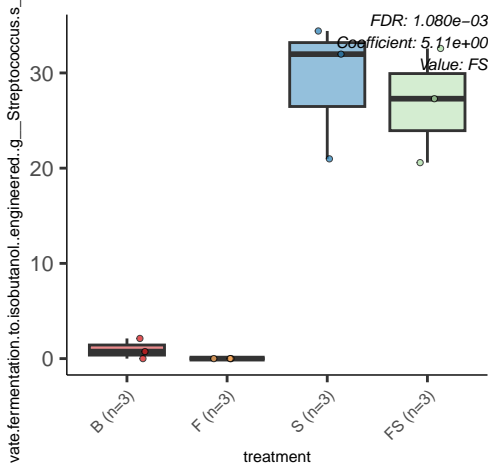


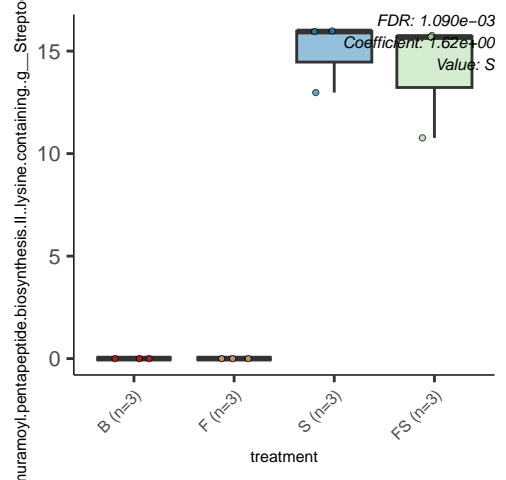


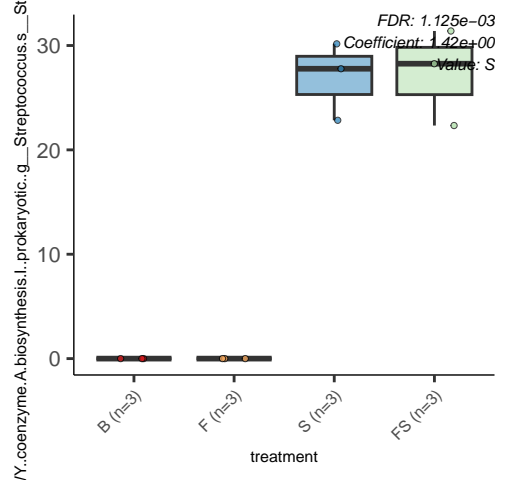




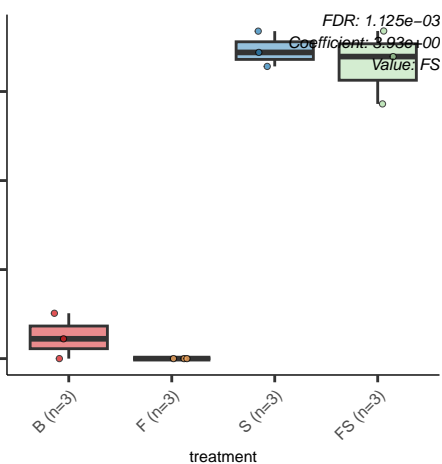


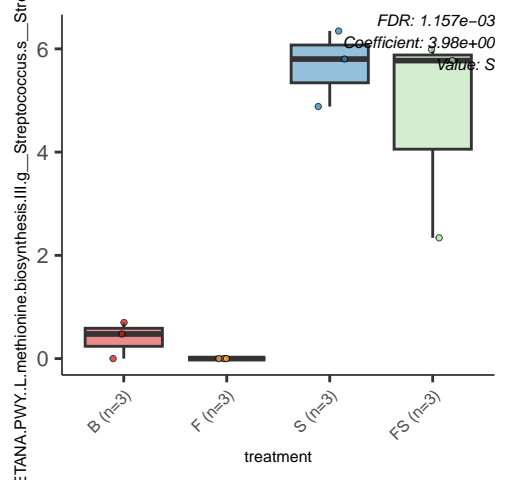


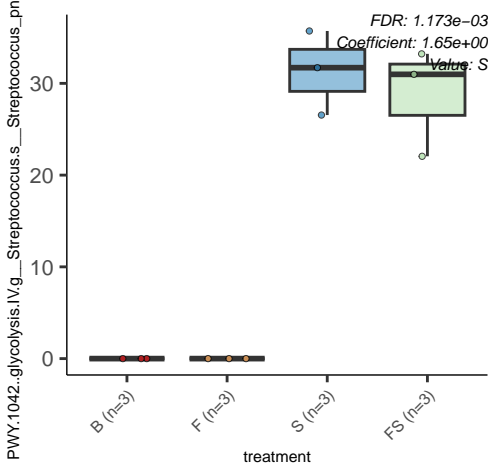




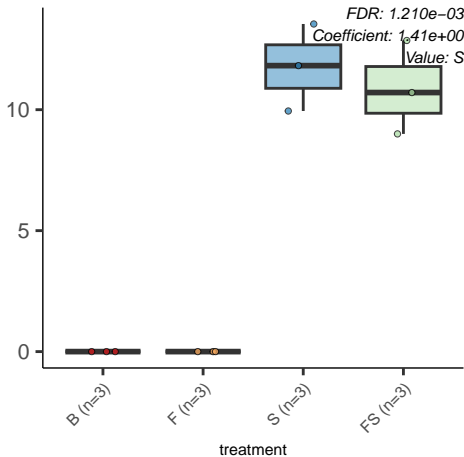
pyruvate.fermentation.to.isobutanol..engineered..g__Streptococcus.s

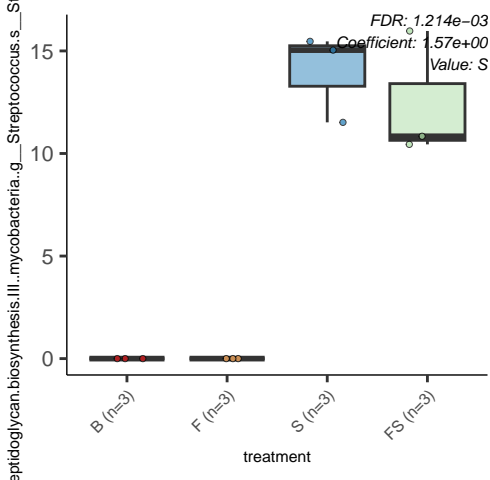


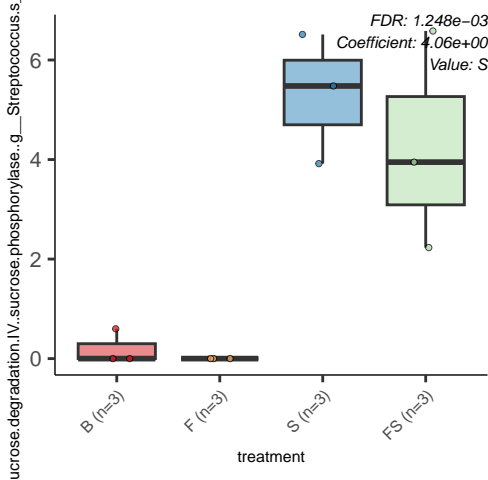


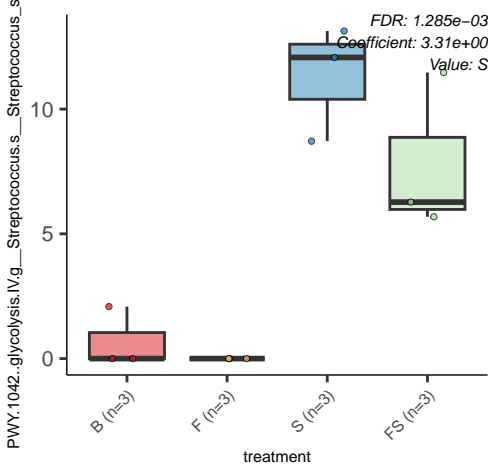


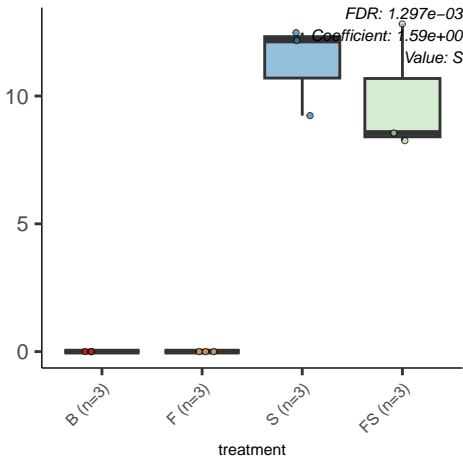
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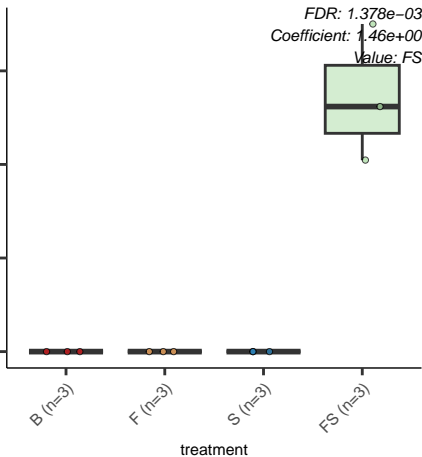




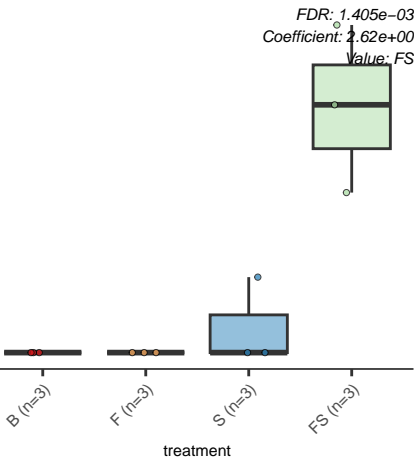




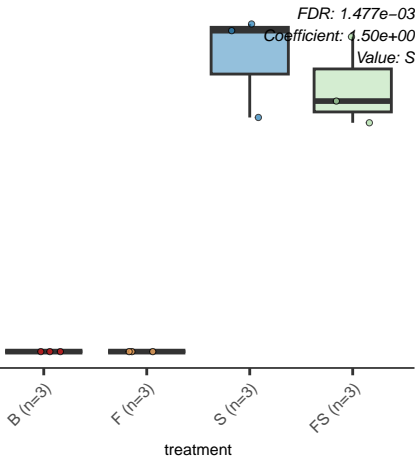


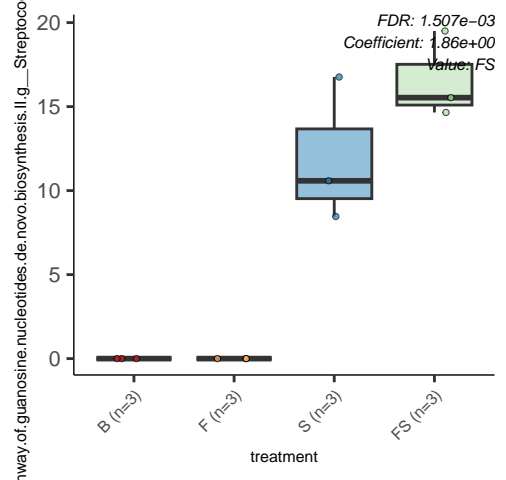


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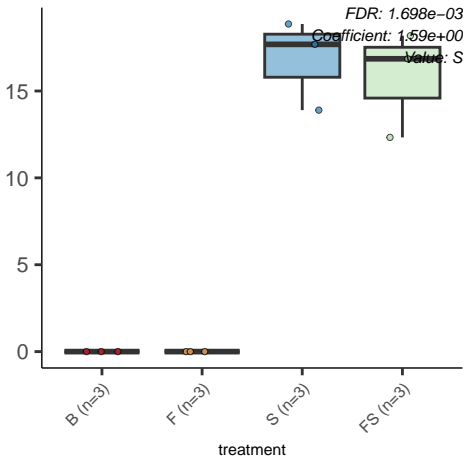


ylmuramoyl.pentapeptide.biosynthesis.II..lysine.containing..g__Strep

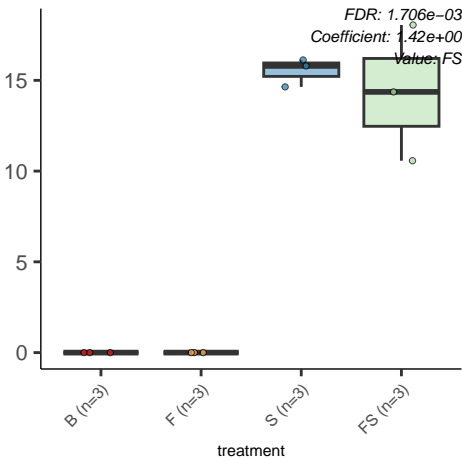




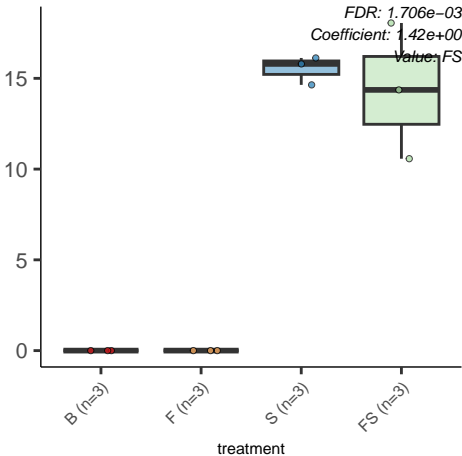
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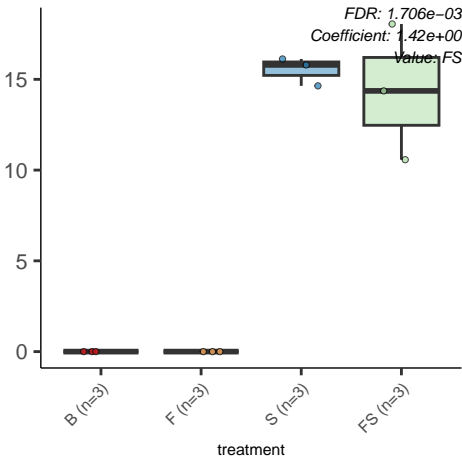
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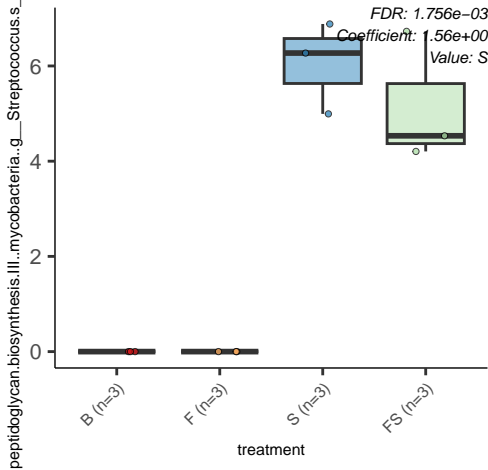


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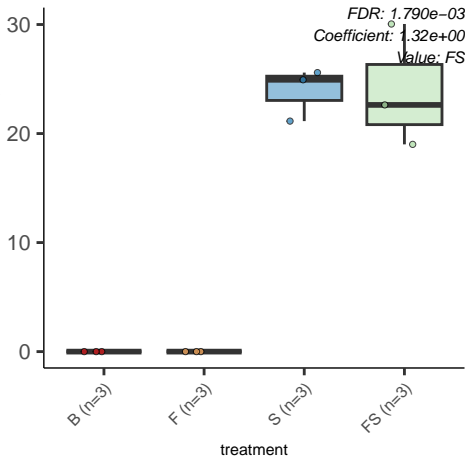


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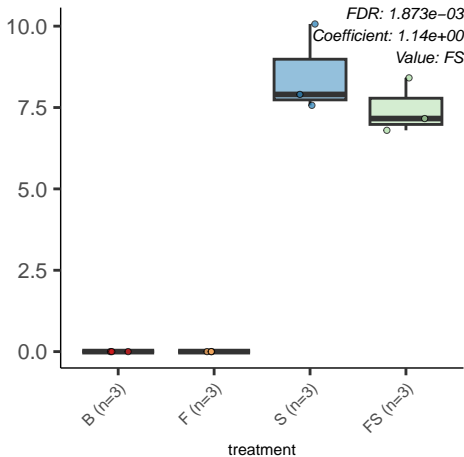




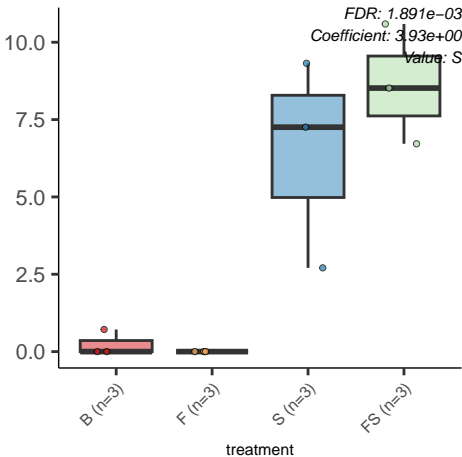
Y..superpathway.of.aromatic.amino.acid.biosynthesis.g__Streptococ

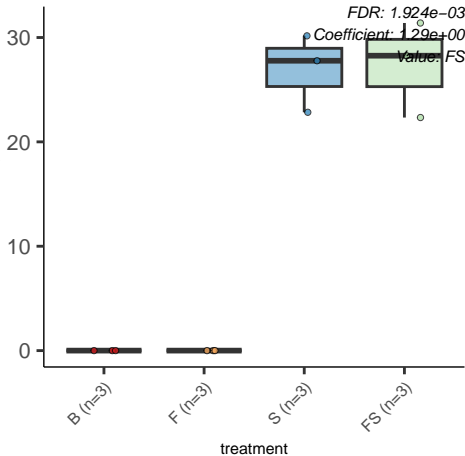


pwY.2941..L-lysine.biosynthesis.II.g__Streptococcus.s__Streptococcus

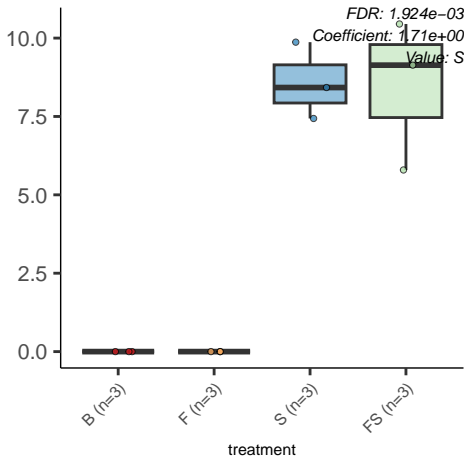


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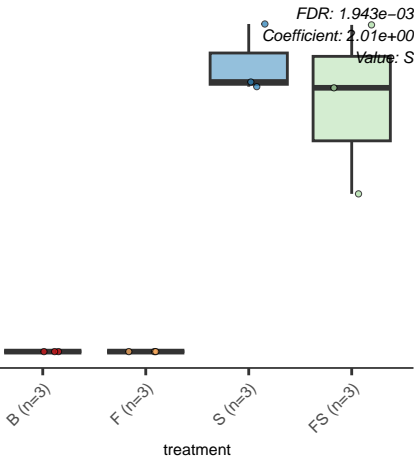


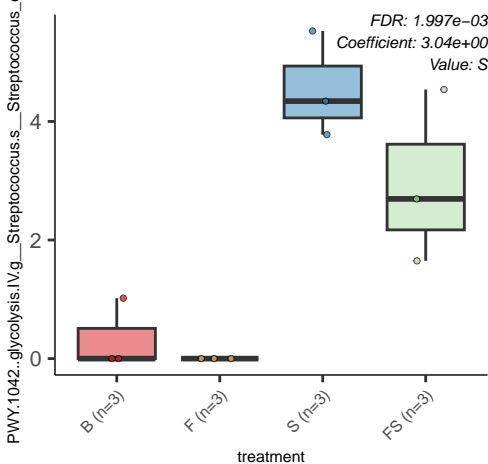


NA.CHARGING.PWY.tRNA.charging.g__Streptococcus.s__Streptococcus

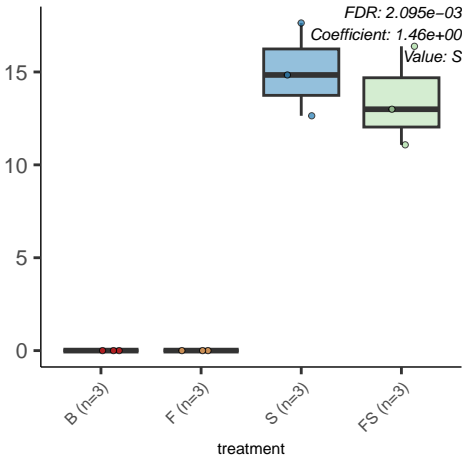


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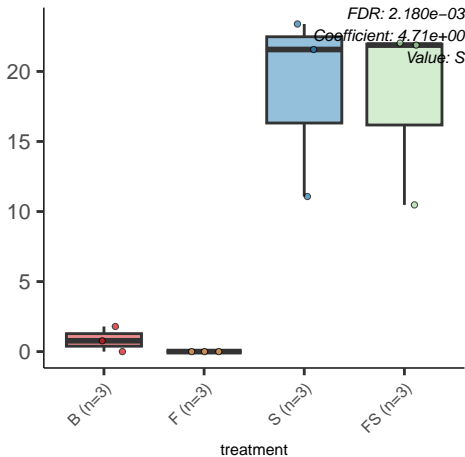




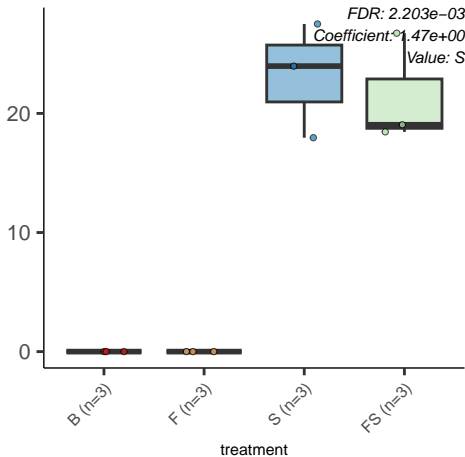
se.phosphate.pathway..non.oxidative.branch..ll.g__Streptococcus.s

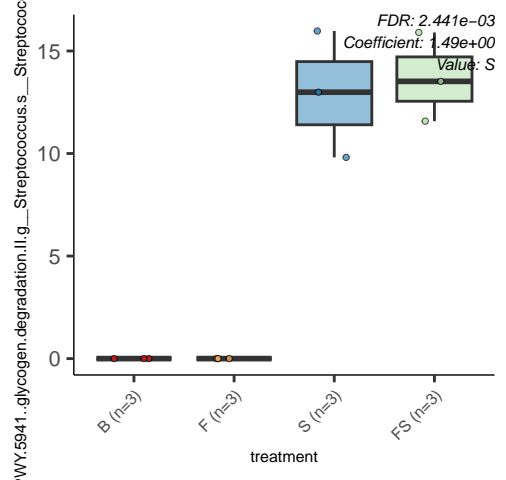


81..CDP.diacylglycerol.biosynthesis.III.g__Streptococcus.s__Strepto

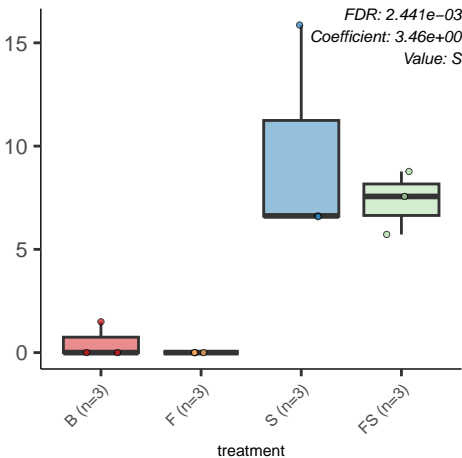


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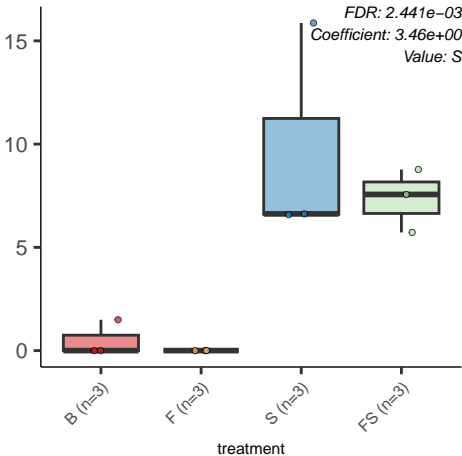


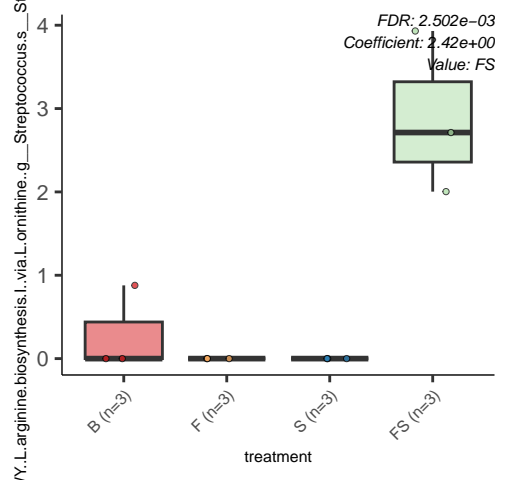


5.aminoimidazole.ribonucleotide.biosynthesis.II.g__Streptococcus.s

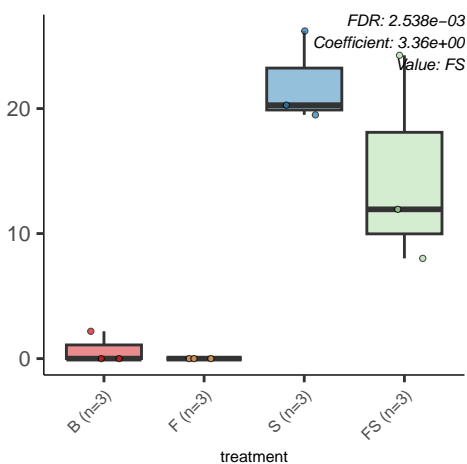


thway.of.5.aminoimidazole.ribonucleotide.biosynthesis.g__Streptococcus

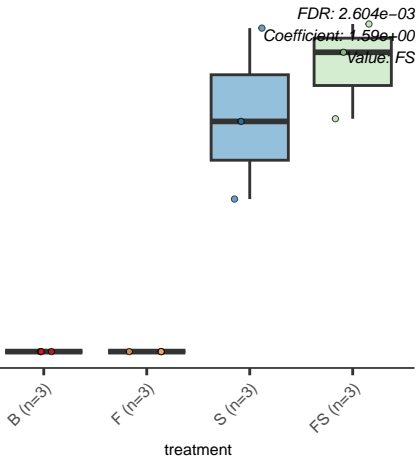


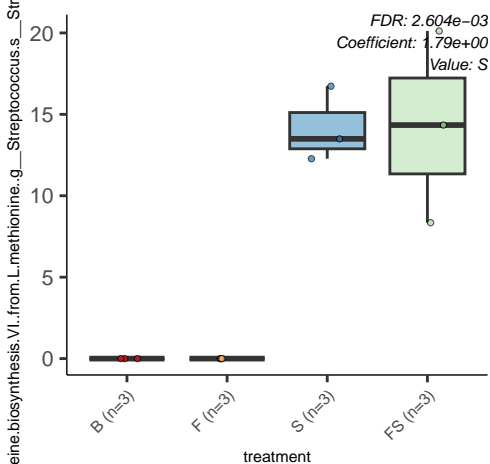


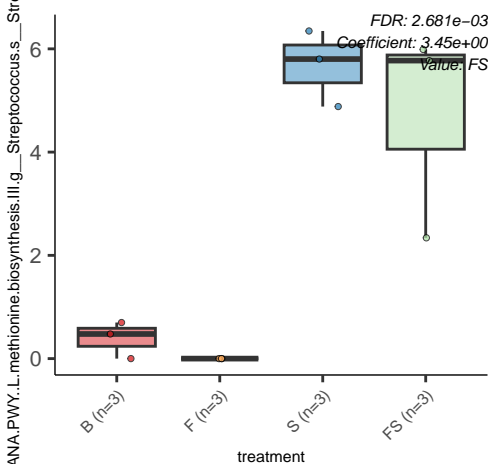
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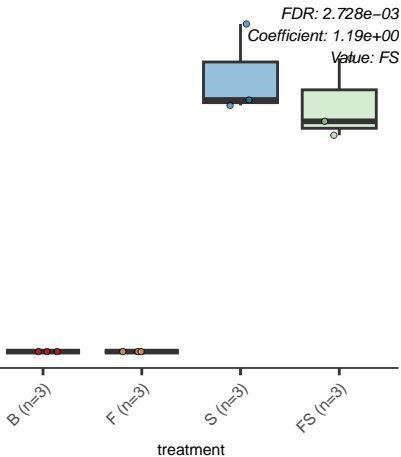
yl.pentapeptide.biosynthesis.III...meso.diaminopimelate.containing...g

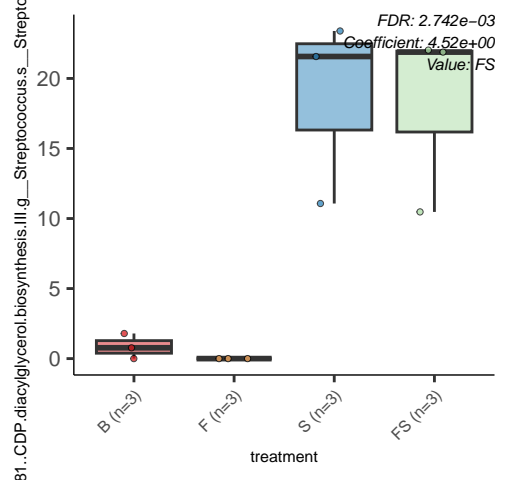


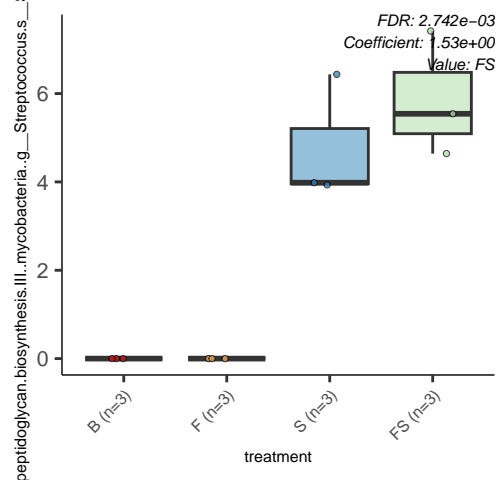


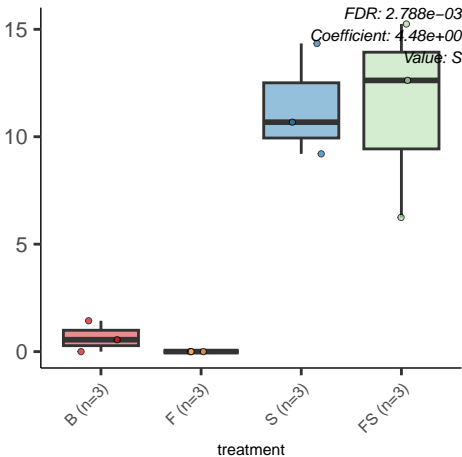


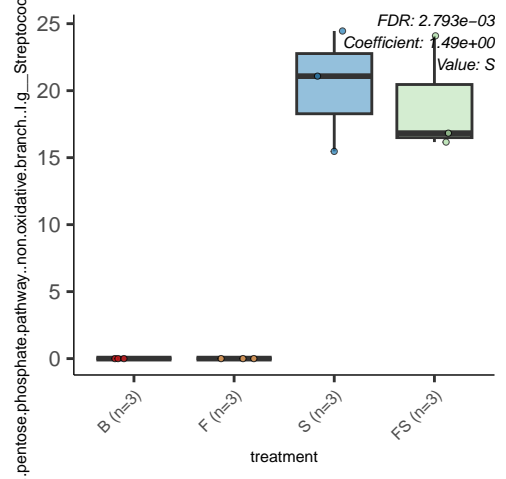
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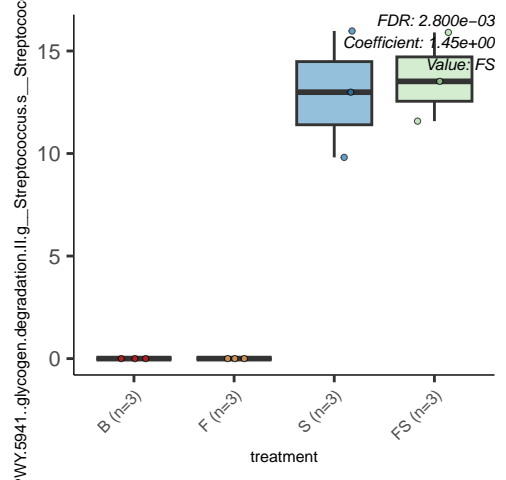


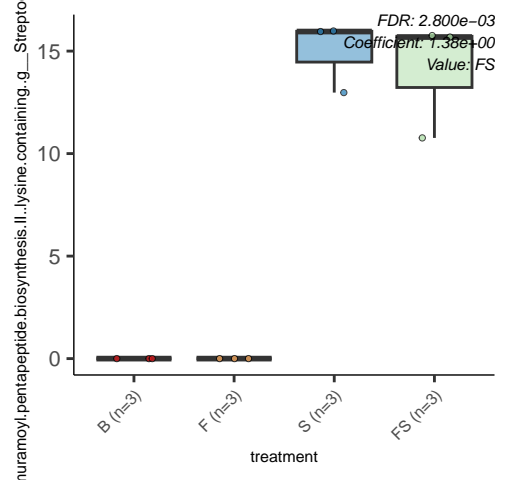




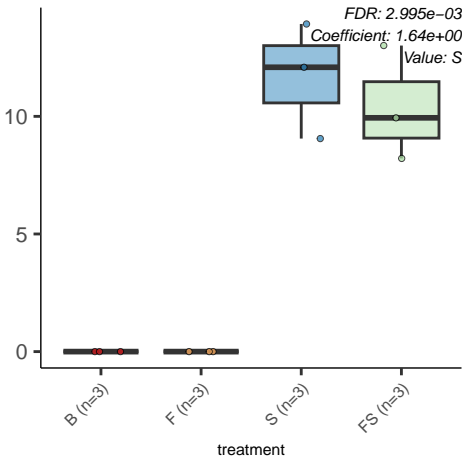


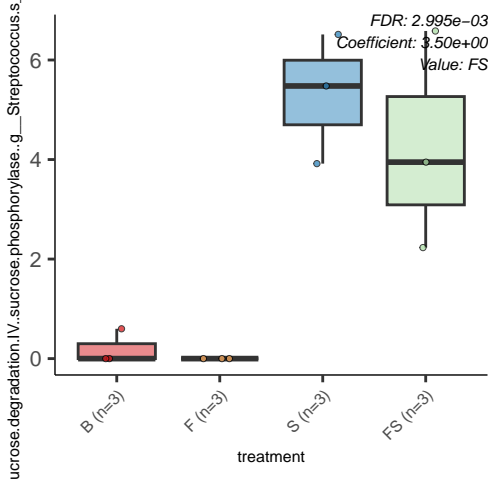


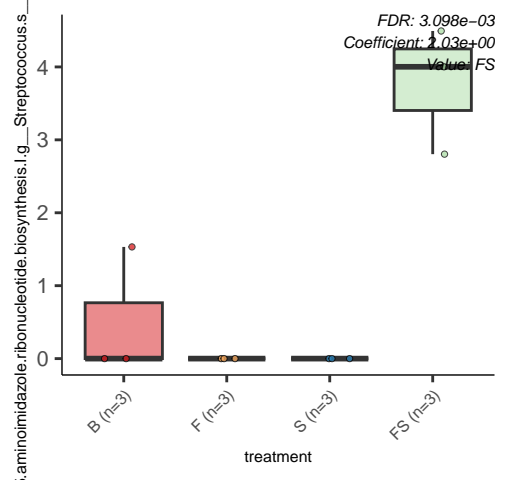


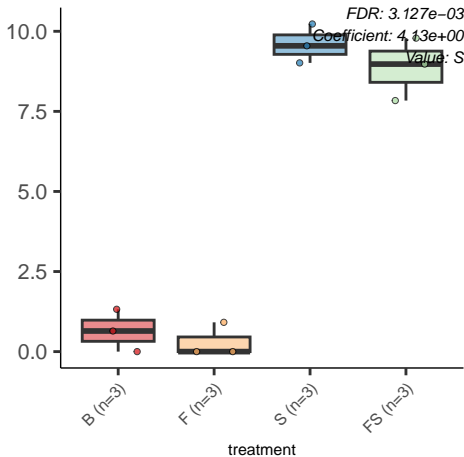


RO.PWY..chorismate.biosynthesis.l.g__Streptococcus.s__Streptococcus

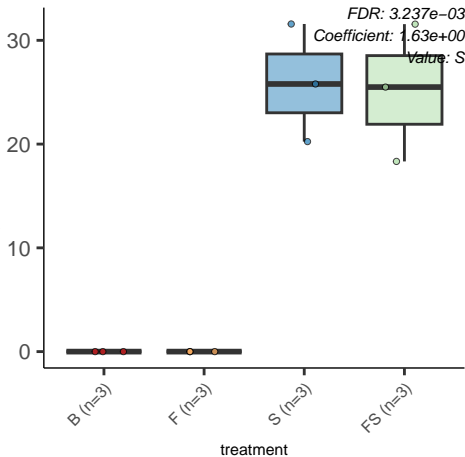


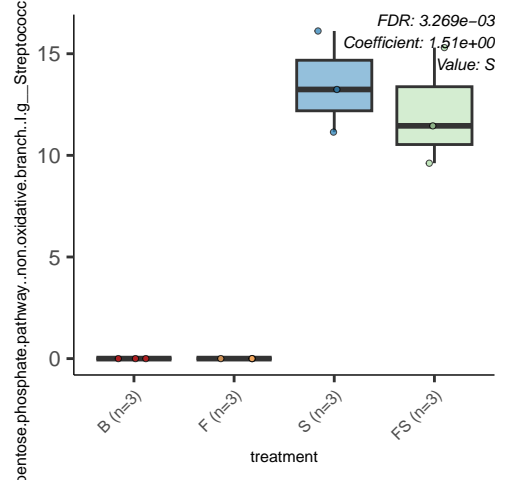


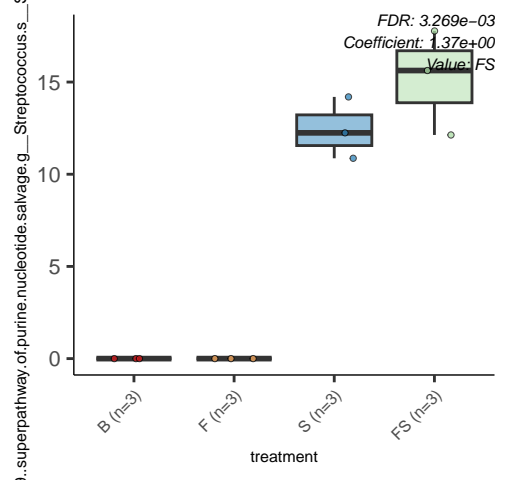


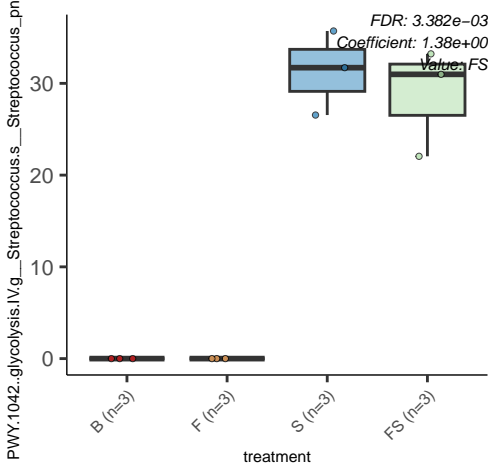


O.PWY.chorismate.biosynthesis.l.g__Streptococcus

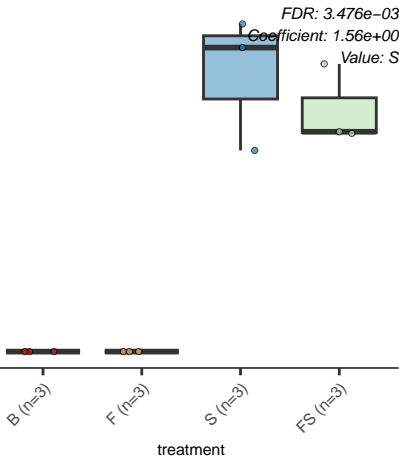


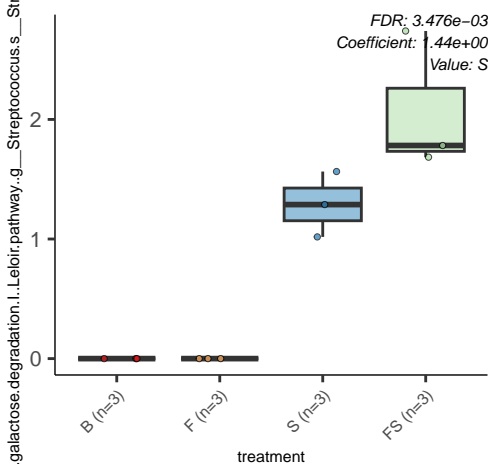


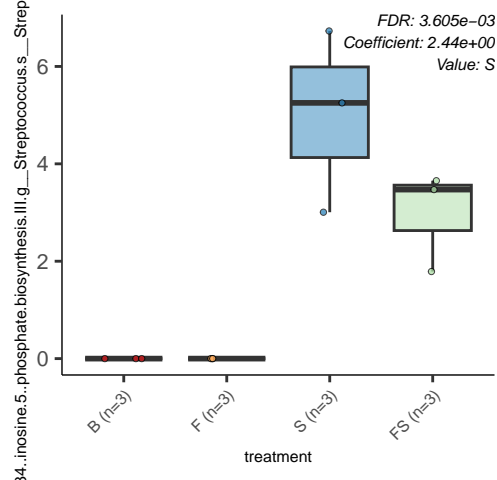




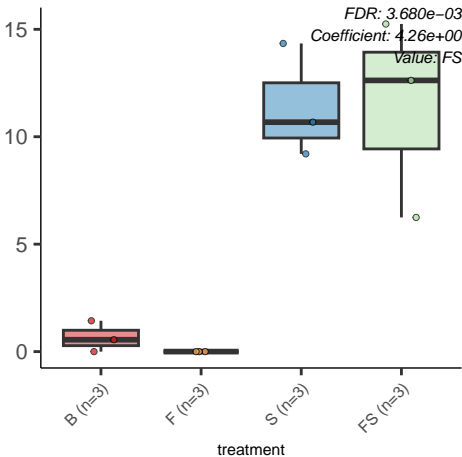
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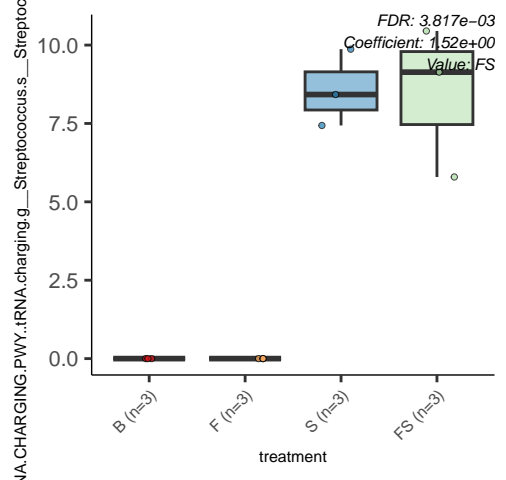




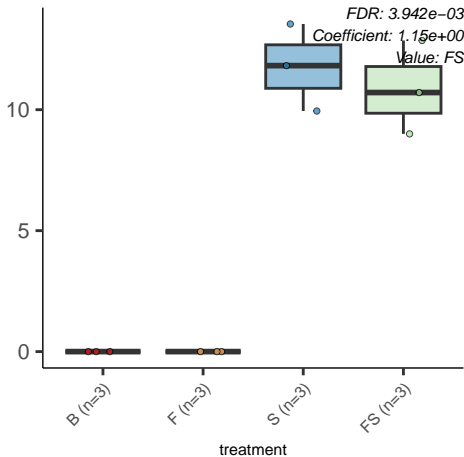


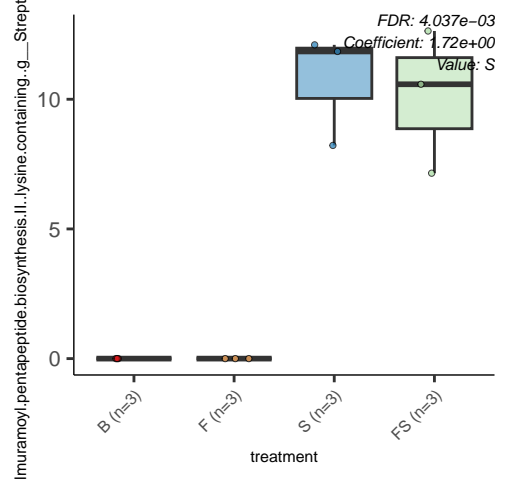
WY.702..L.methionine.biosynthesis.II.g__Streptococcus.s__Streptococcus



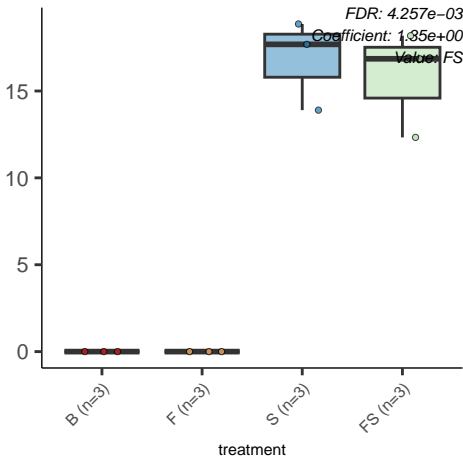


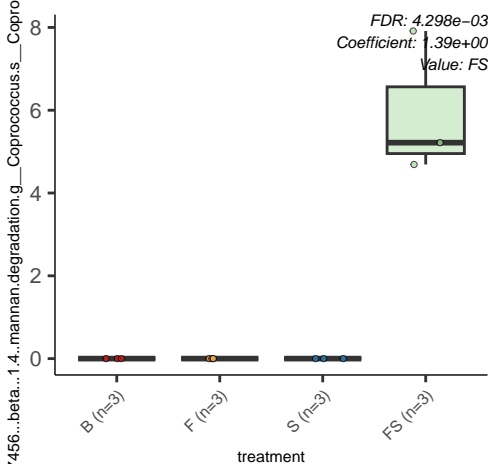
thorismate, biosynthesis, from, 3, dehydroquinate, g__ Streptococcus, s

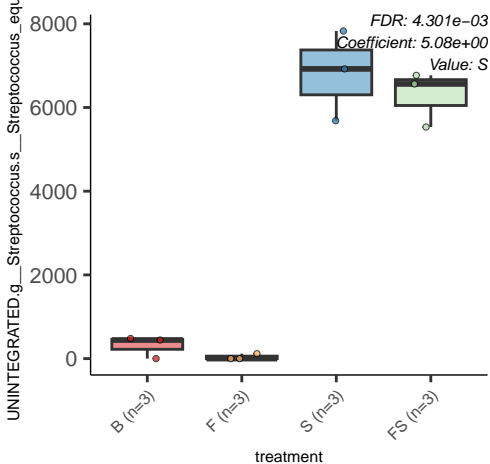


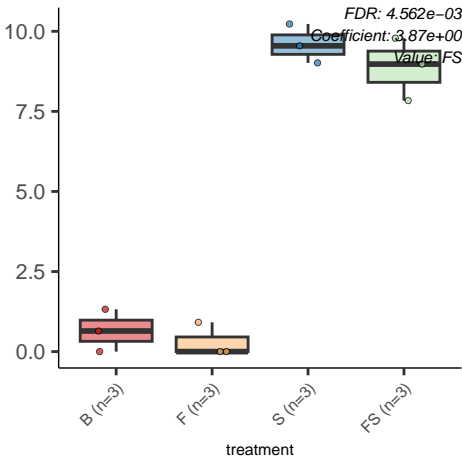


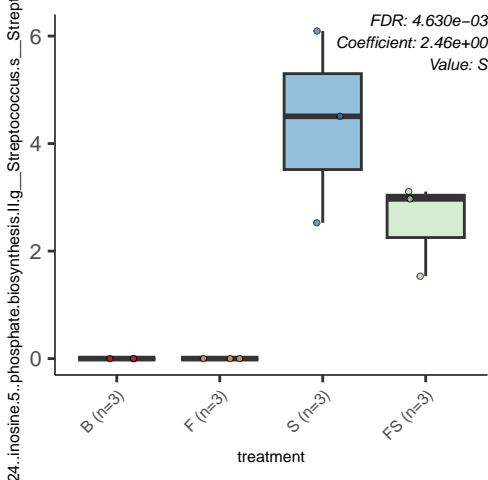
peptidoglycan.biosynthesis.l...meso.diaminopimelate.containing..g__S

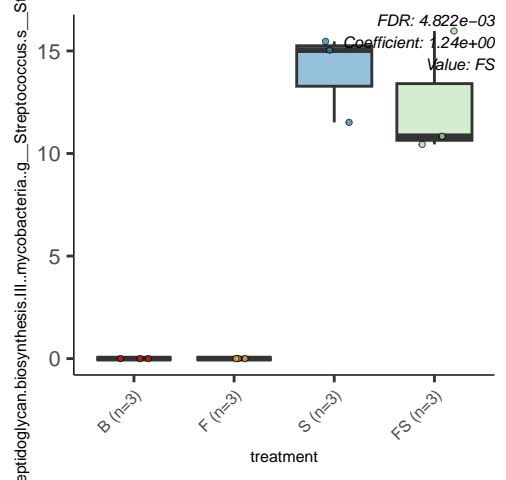


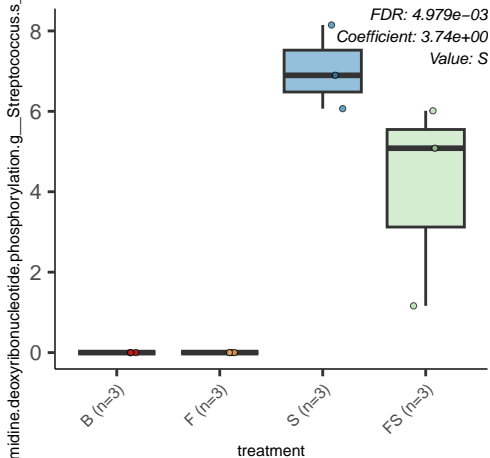


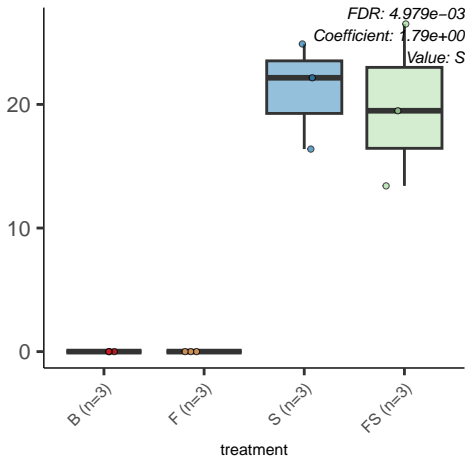




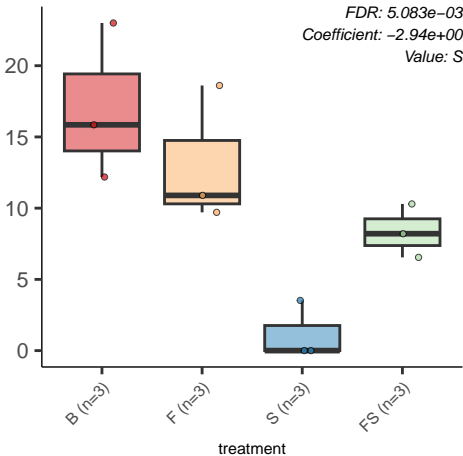




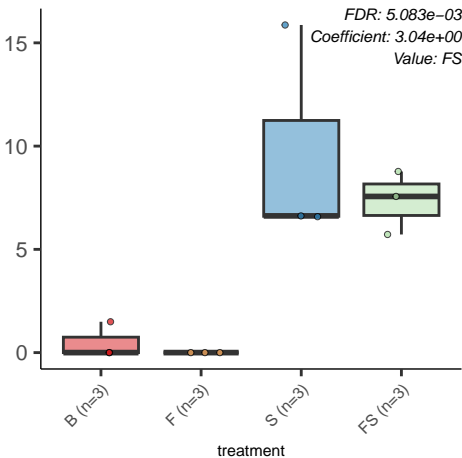




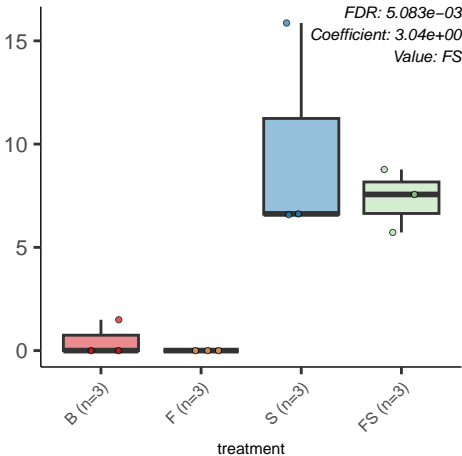
#AMSYN.PWY..dTDP..beta..L.rhamnose.biosynthesis.g_Escherich



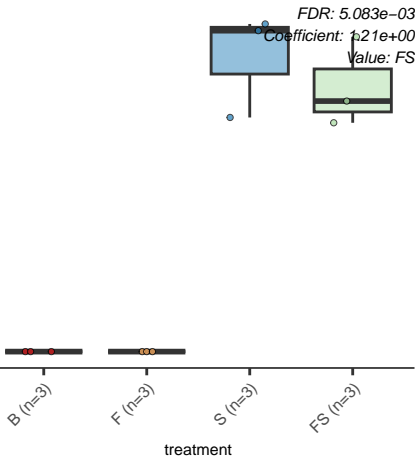
5.aminoimidazole.ribonucleotide.biosynthesis.II.g__Streptococcus.s

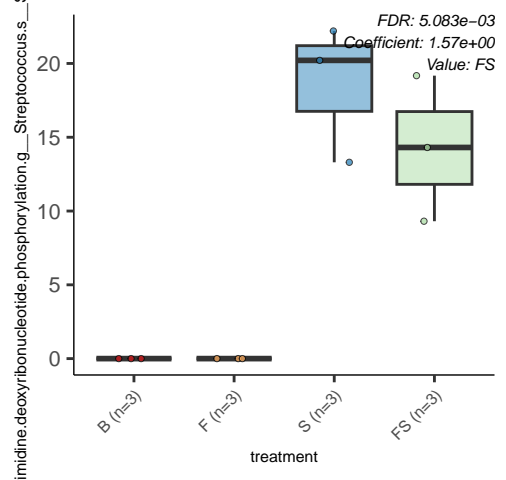


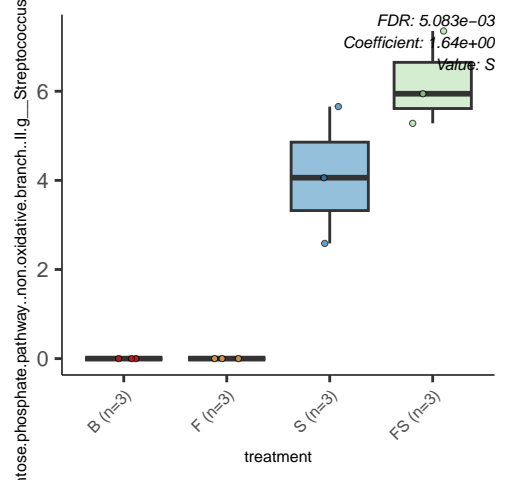
thway.of.5.aminoimidazole.ribonucleotide.biosynthesis.g__Streptococcus

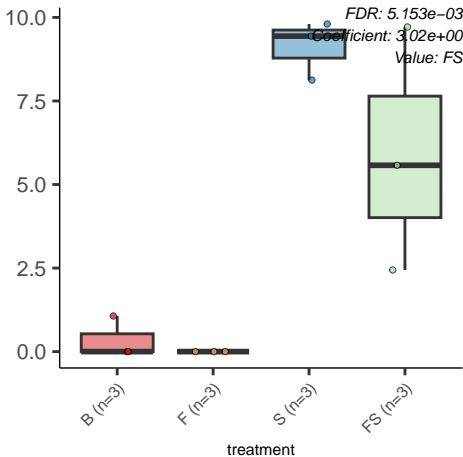


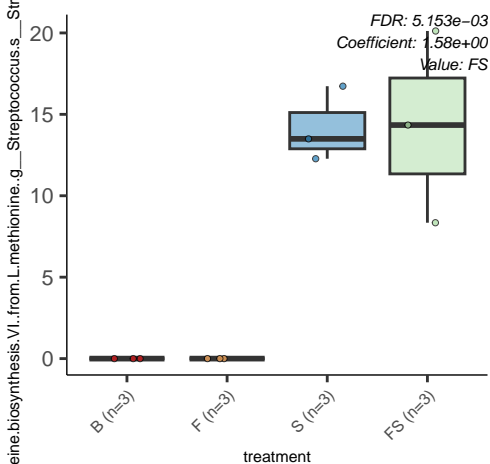
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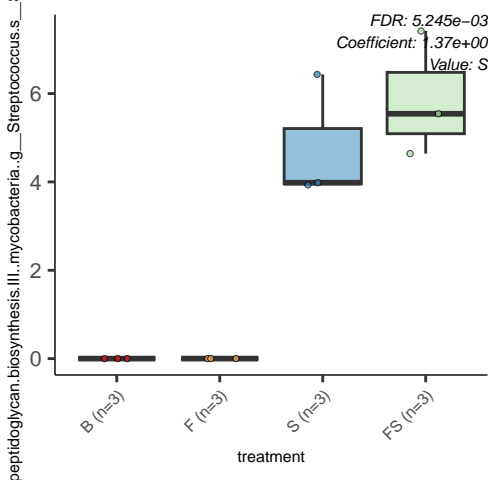




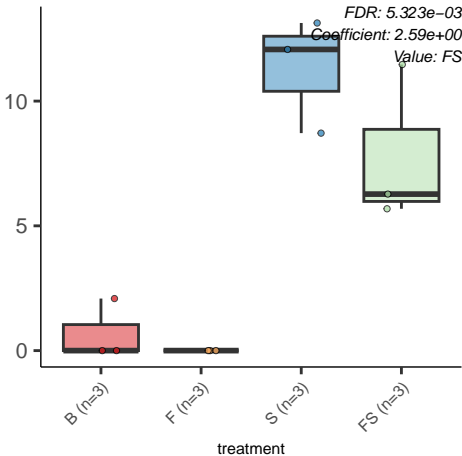


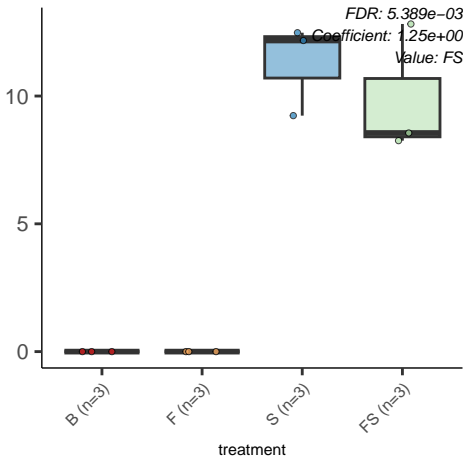




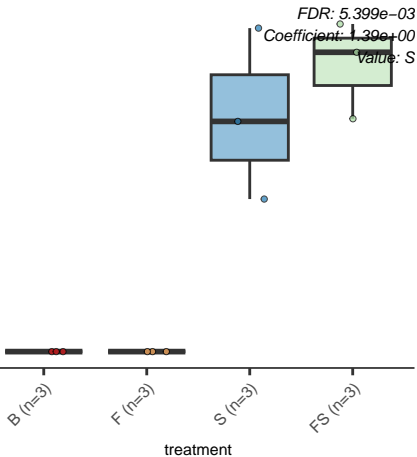


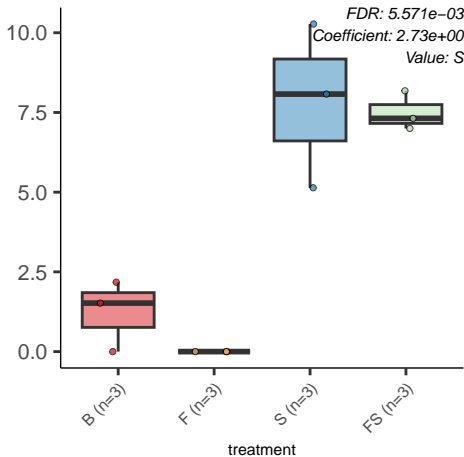
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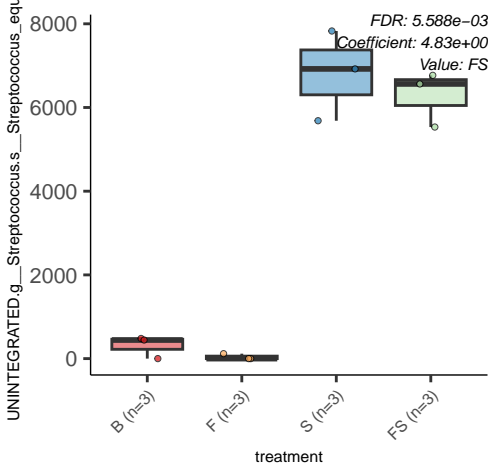


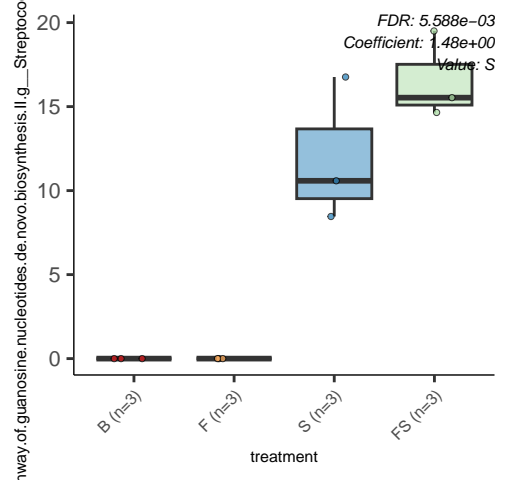


yl.pentapeptide.biosynthesis.III...meso.diaminopimelate.containing...g

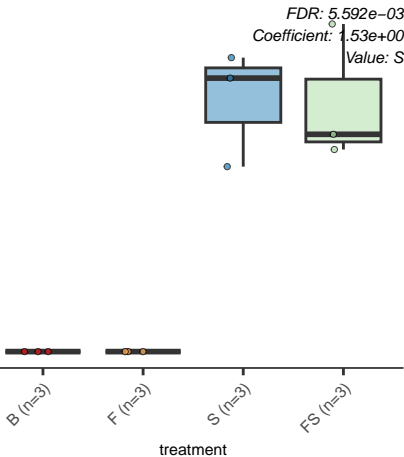


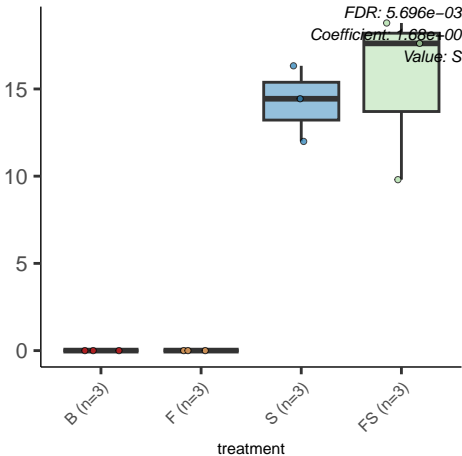


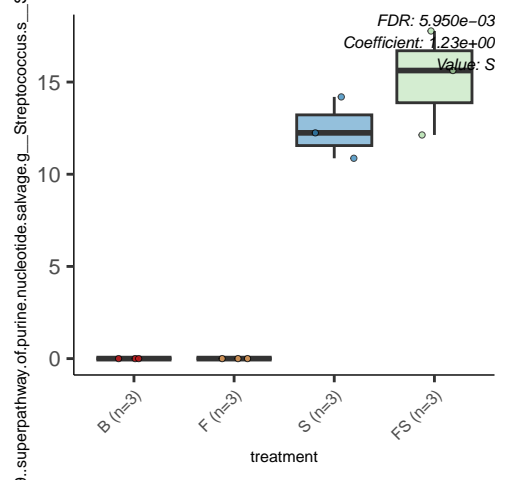


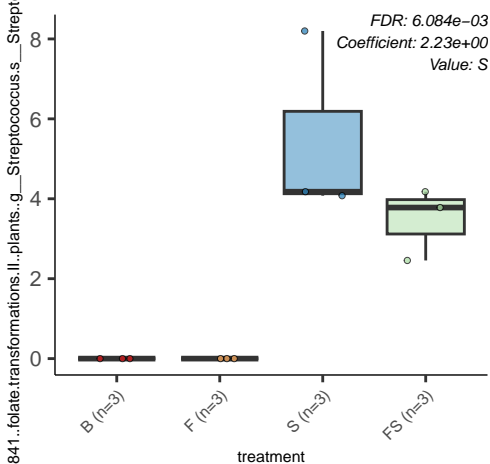


PWY.6703..preQ0.biosynthesis.g__Streptococcus.s__Streptococcus

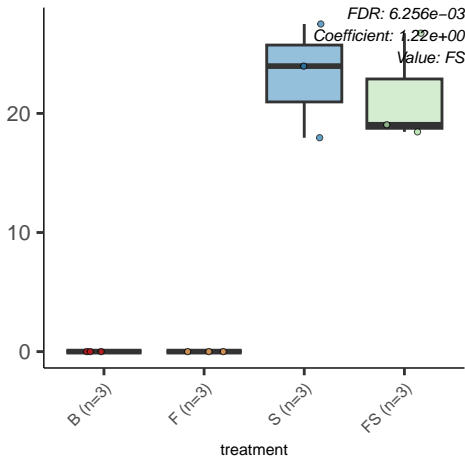


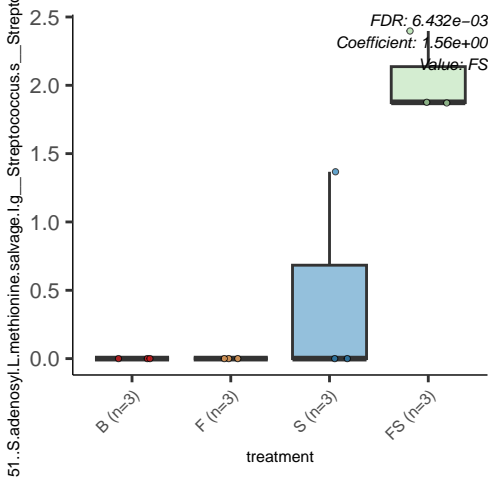




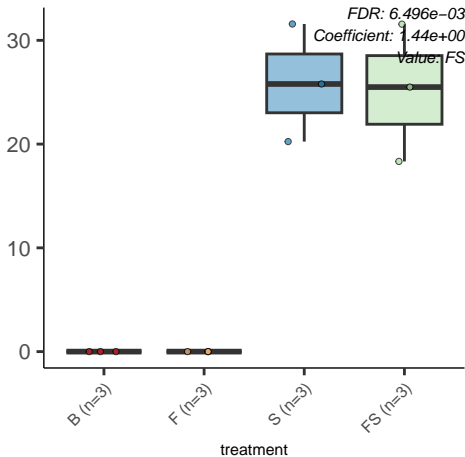


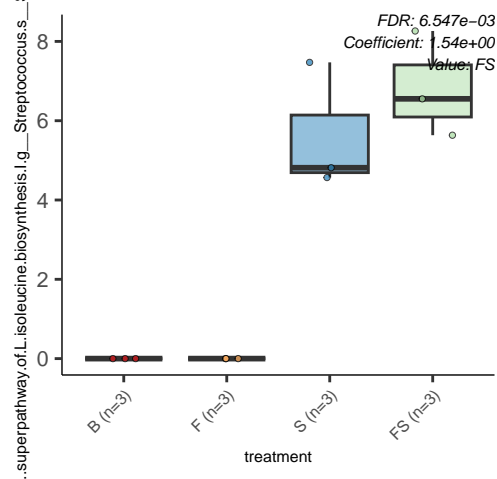
ose.phosphate.pathway..non.oxidative.branch..ll.g__Streptococcus.

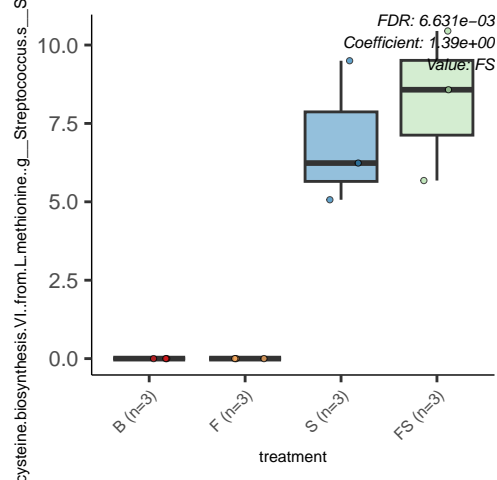




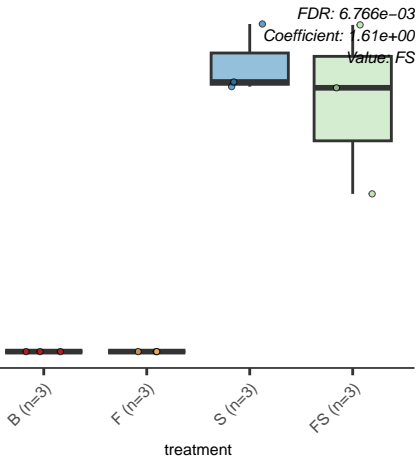
O.PWY.chorismate.biosynthesis.l.g__Streptococcus

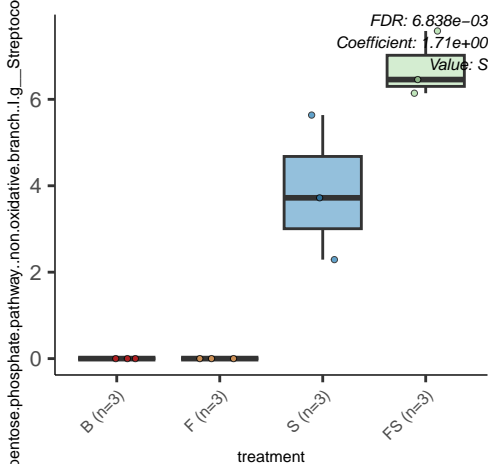


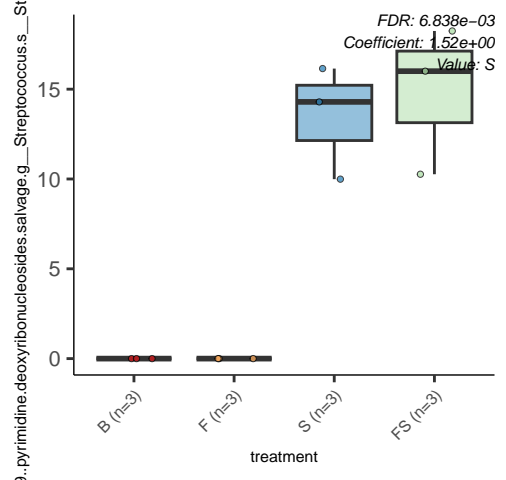




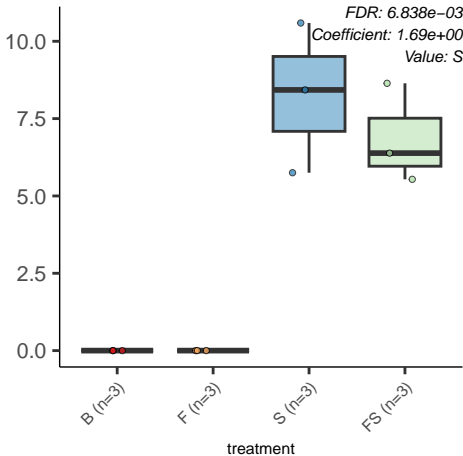
PWY.6703..preQ0.biosynthesis.g__Streptococcus.s__Streptococcus

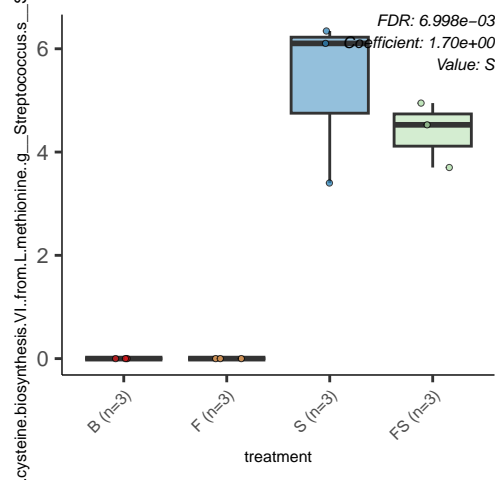


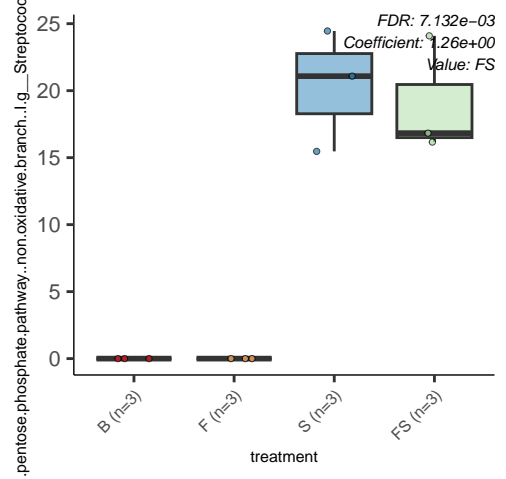


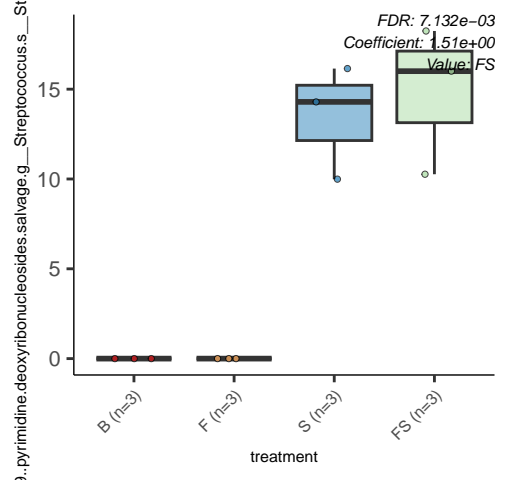


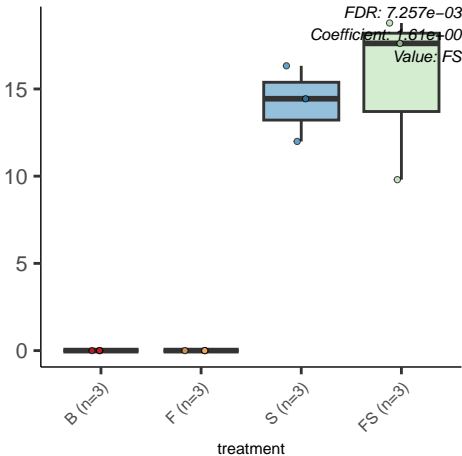
polypentapeptide biosynthesis. III... meso-diaminopimelate, containing...



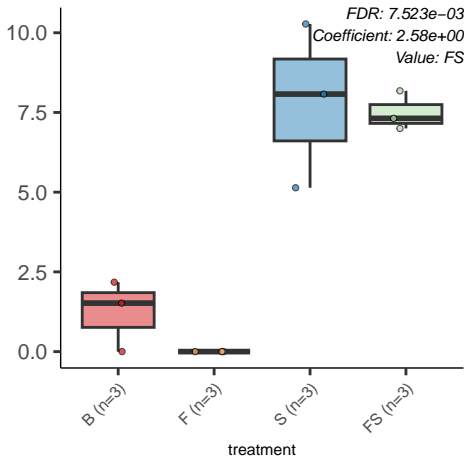




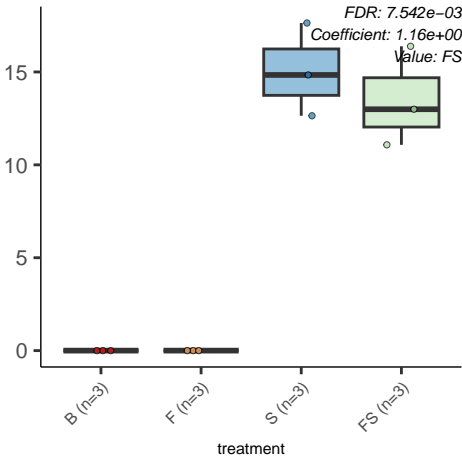




WY.4041...gamma..glutamyl.cycle.g__Streptococcus.s__Streptococcus

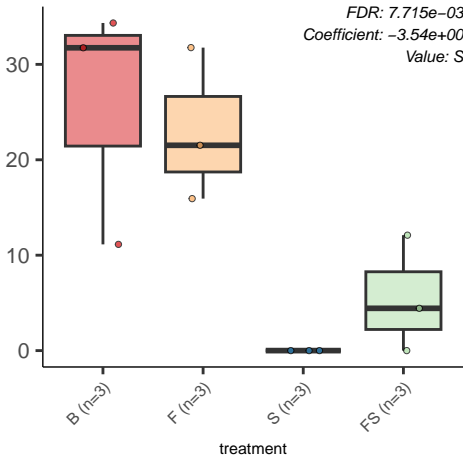


se.phosphate.pathway..non.oxidative.branch..ll.g__Streptococcus.s

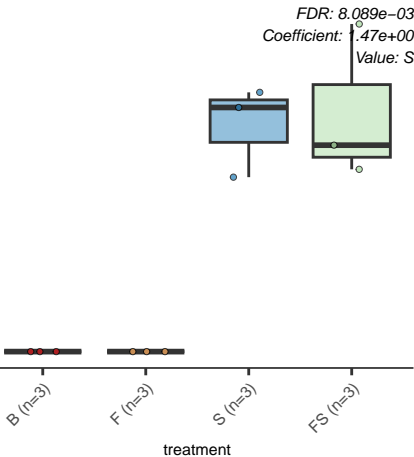


WY.6609..adenine.and.adenosine.salvage.III.g__Escherichia.s__Es

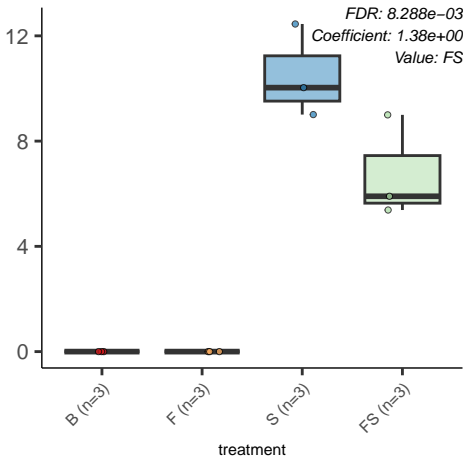
FDR: $7.715e-03$
Coefficient: $-3.54e+00$
Value: S

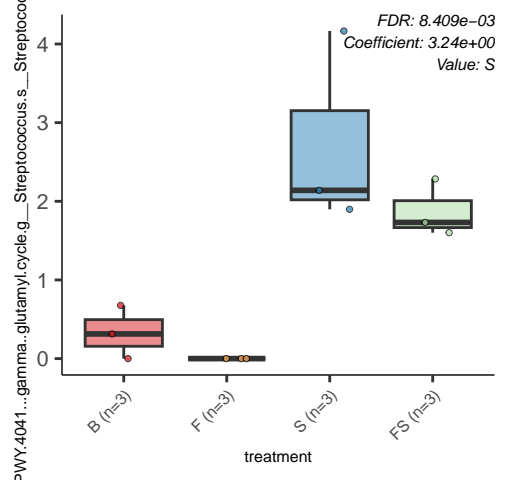


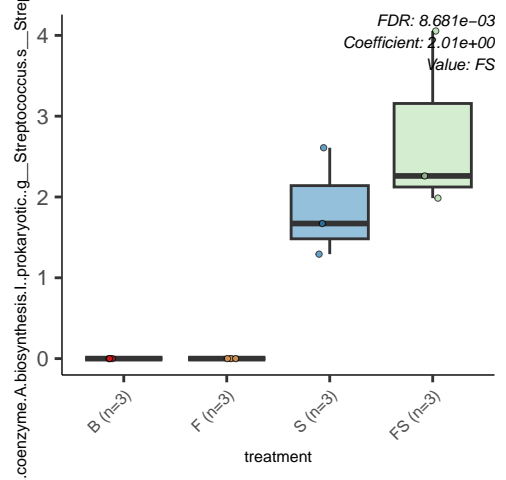
peptidoglycan.biosynthesis.l...meso.diaminopimelate.containing...g

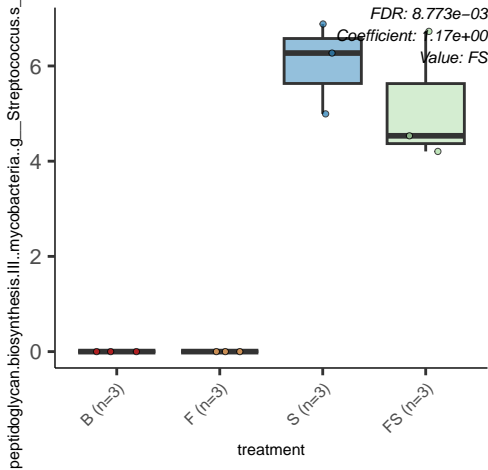


6700..queuosine.biosynthesis.l..de.novo..g___Streptococcus.s___Streptococcus

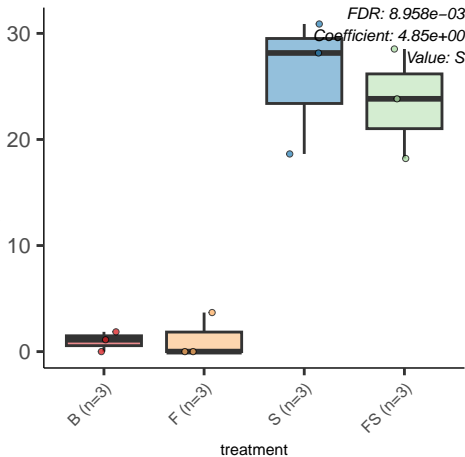


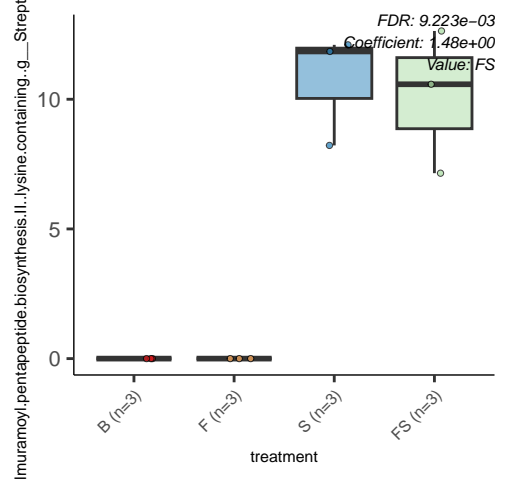




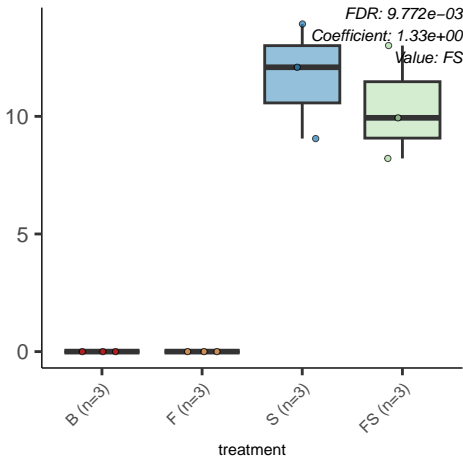


ALSYN.PWY..L.valine.biosynthesis.g__Streptococcus.s__Streptococcus

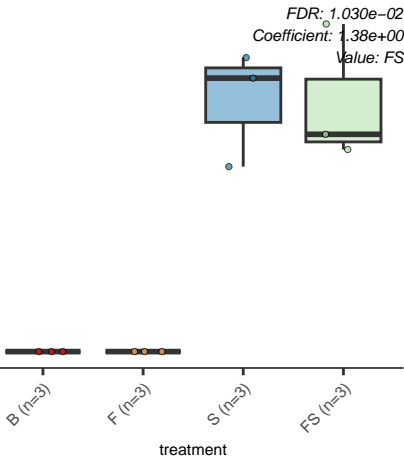




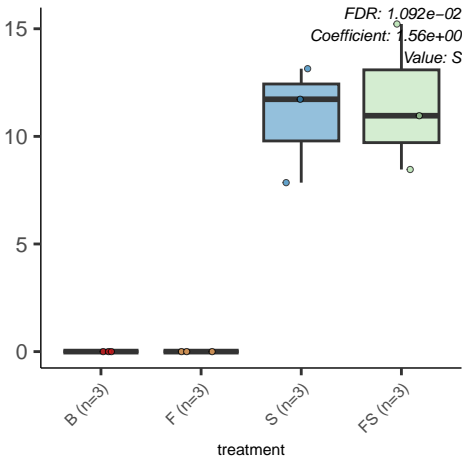
RO.PWY..chorismate.biosynthesis.l.g__Streptococcus.s__Streptococcus



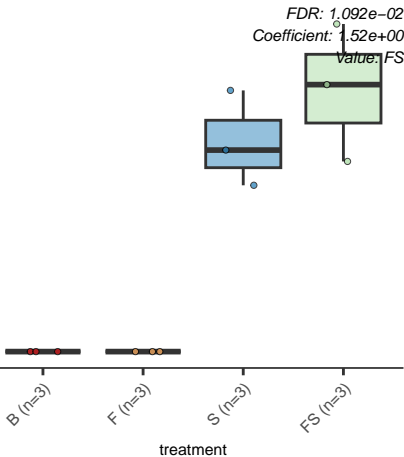
PWY.6703..preQ0.biosynthesis.g__Streptococcus.s__Streptococcus

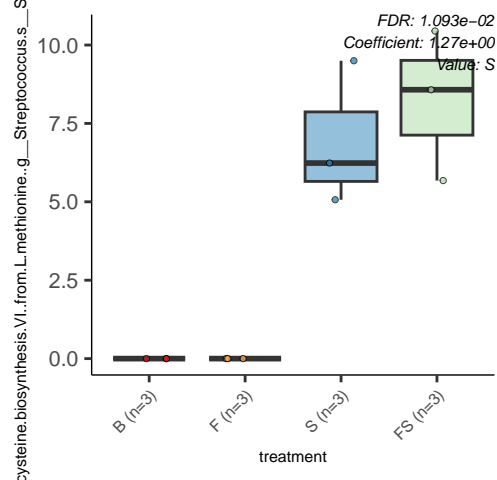


PWY..superpathway.of.branched.chain.amino.acid.biosynthesis.g__S

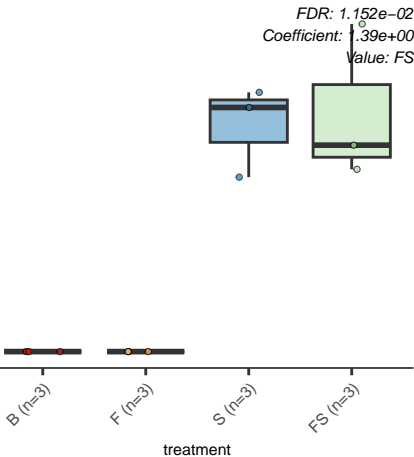


onway.of.adenosine.nucleotides.de.novo.biosynthesis.ll.g__Streptococcus

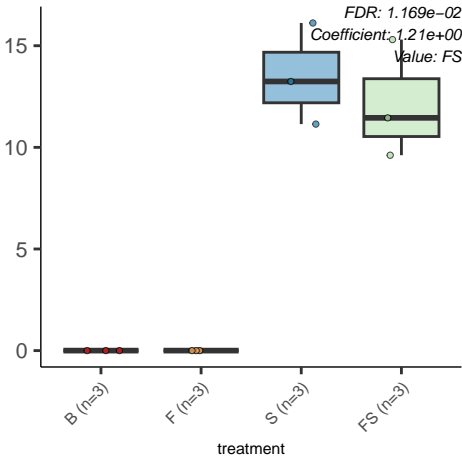


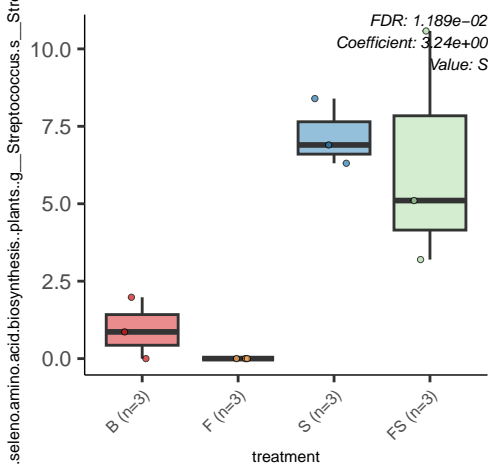


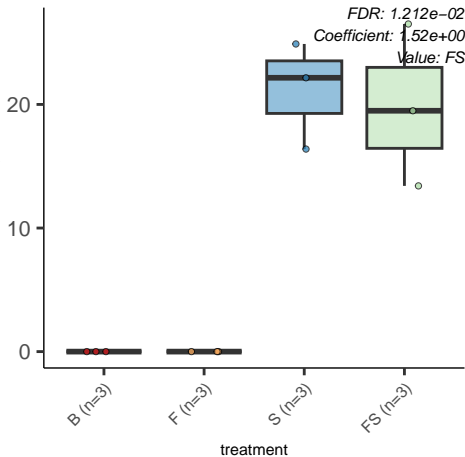
peptidoglycan.biosynthesis.l...meso.diaminopimelate.containing..g

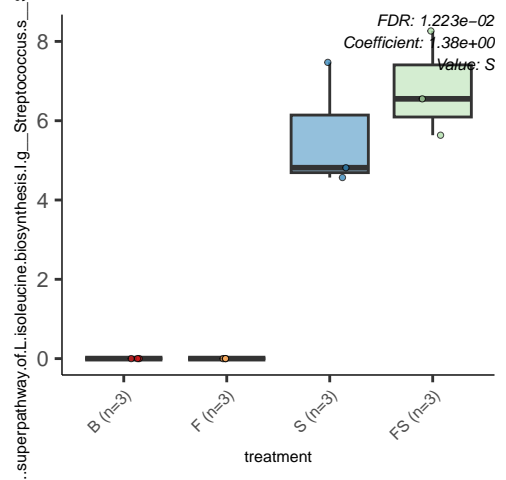


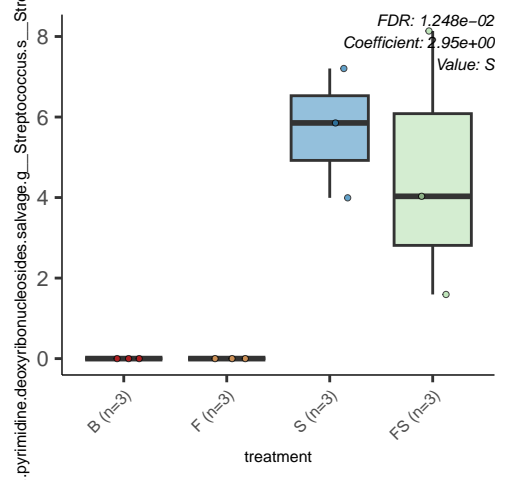
pentose.phosphate.pathway..non.oxidative.branch...l.g__Streptococ



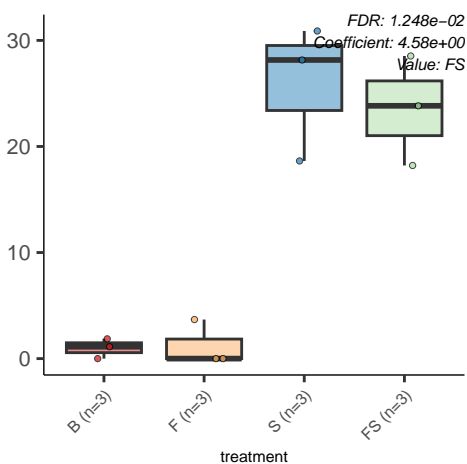




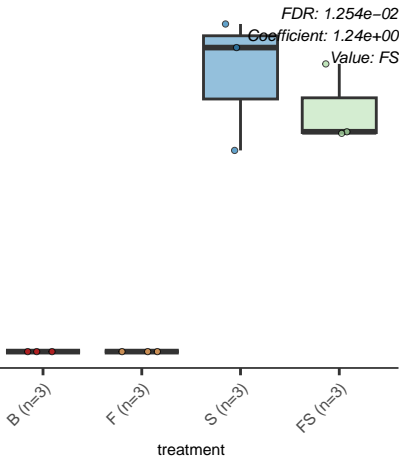


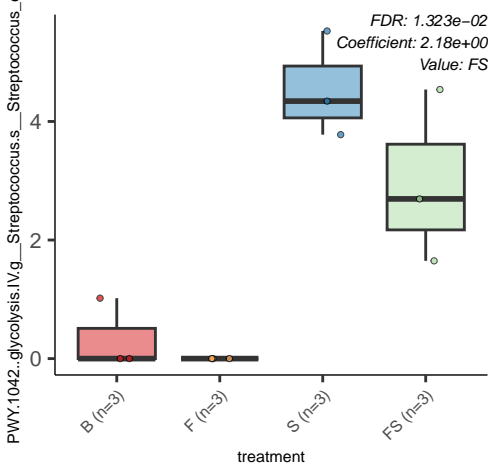


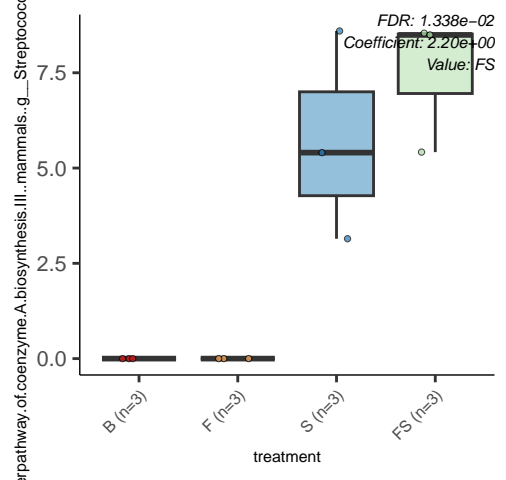
ALSYN.PWY..L.valine.biosynthesis.g__Streptococcus.s__Streptococcus



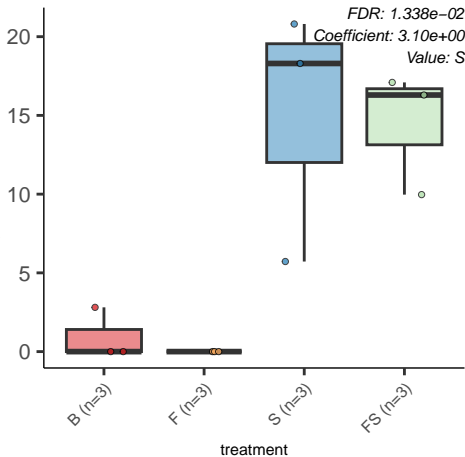
peptidoglycan.biosynthesis.l..meso.diaminopimelate.containing..g



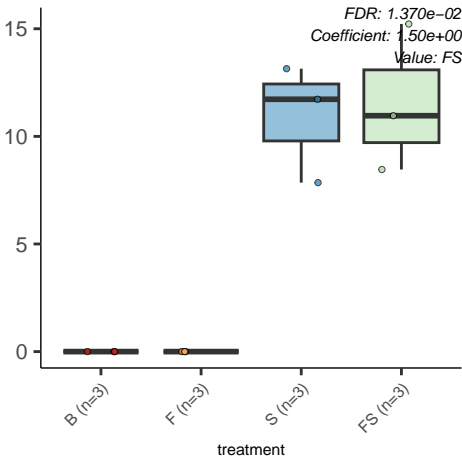




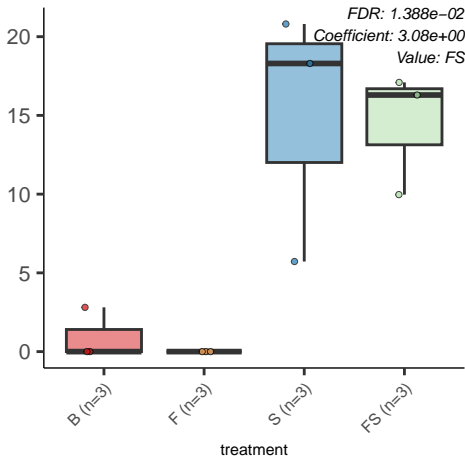
WY.7238...sucrose.biosynthesis.II.g__Streptococcus



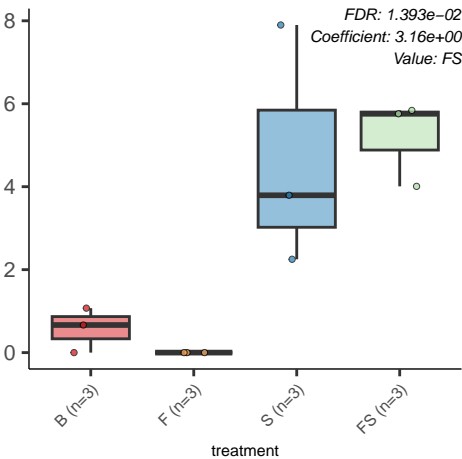
PWY..superpathway.of.branched.chain.amino.acid.biosynthesis.g__S



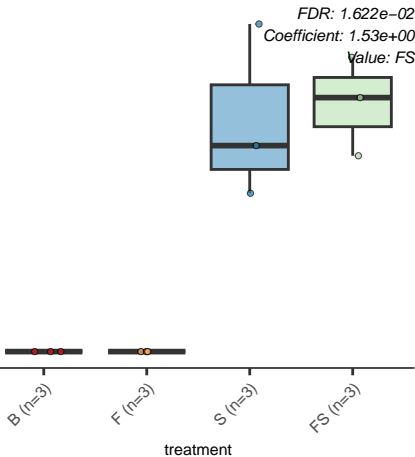
WY.7238...sucrose.biosynthesis.II.g__Streptococcus



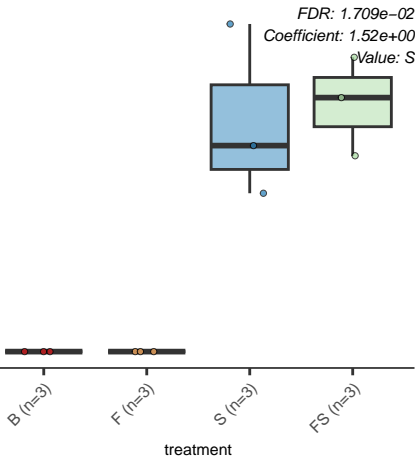
fatty.acid.biosynthesis.initiation...mitochondria..g__Streptococcus.s

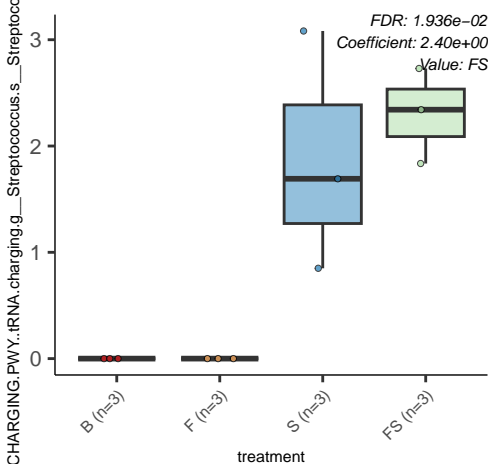


SYN.PWY..L.histidine.biosynthesis.g__Streptococcus.s__Streptococcus

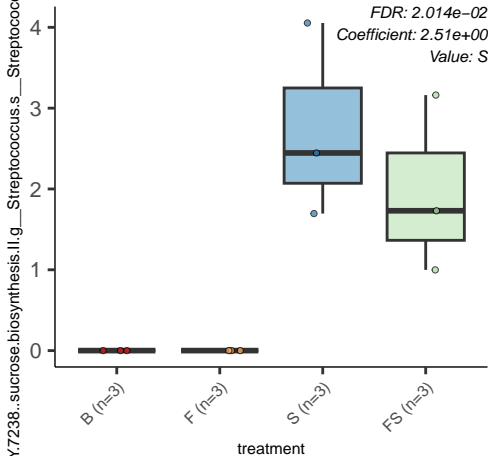


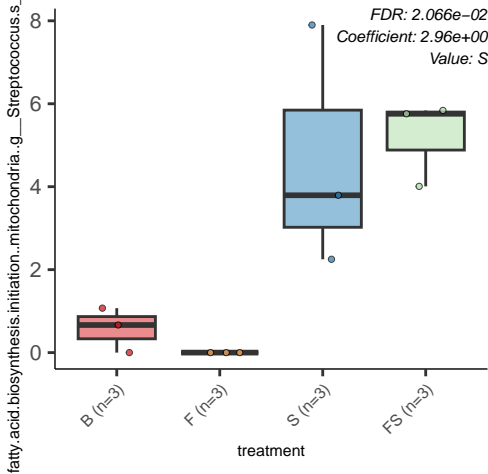
SYN.PWY..L.histidine.biosynthesis.g__Streptococcus.s__Streptococcus



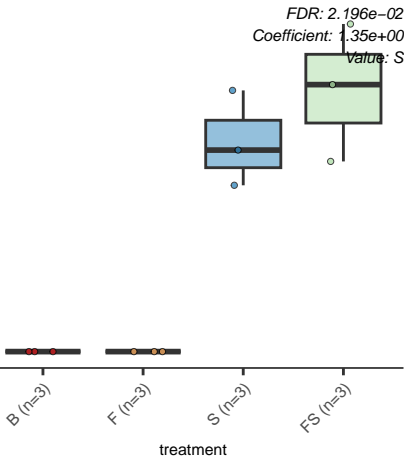


WY.7238..sucrose.biosynthesis.ll.g__Streptococcus.s__Streptococcus

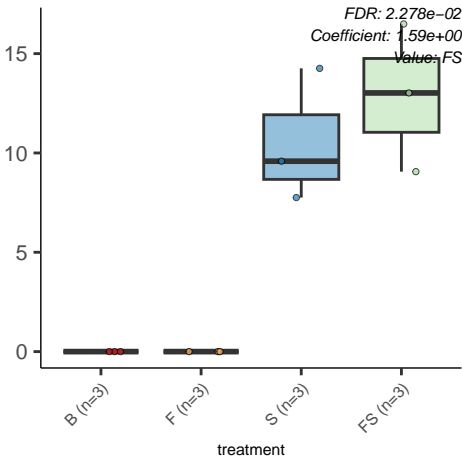


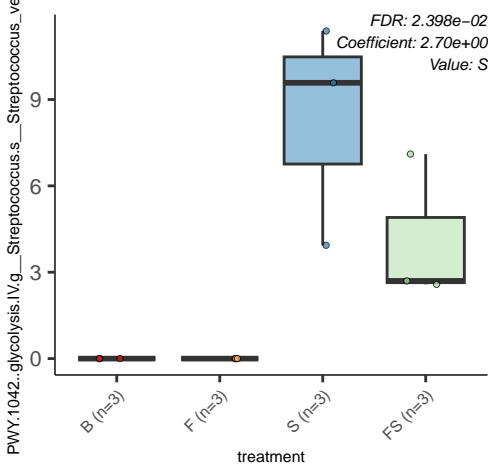


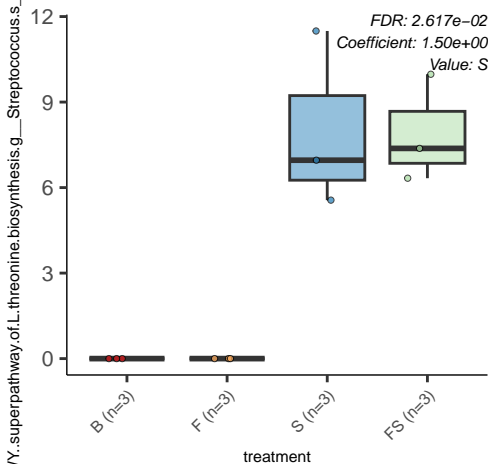
onway.of.adenosine.nucleotides.de.novo.biosynthesis.II.g__Streptococ

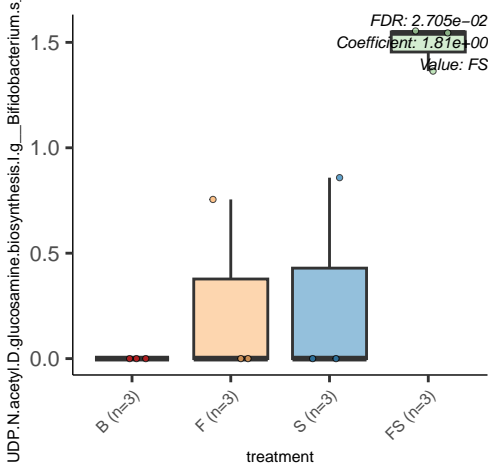


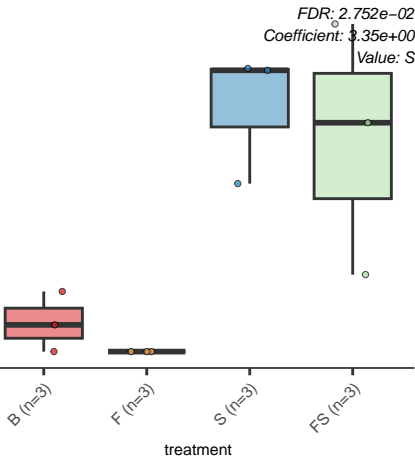
hway.of.adenosine.nucleotides.de.novo.biosynthesis.l.g__Streptococ

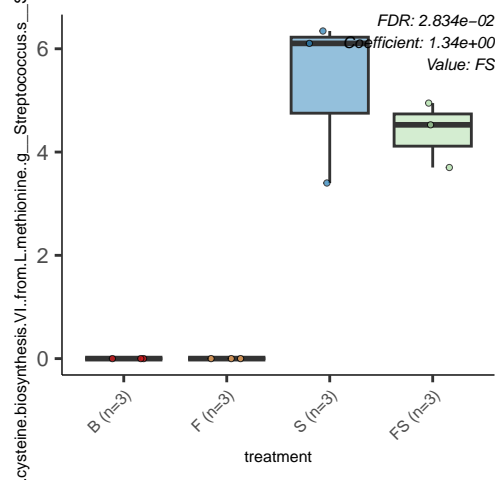


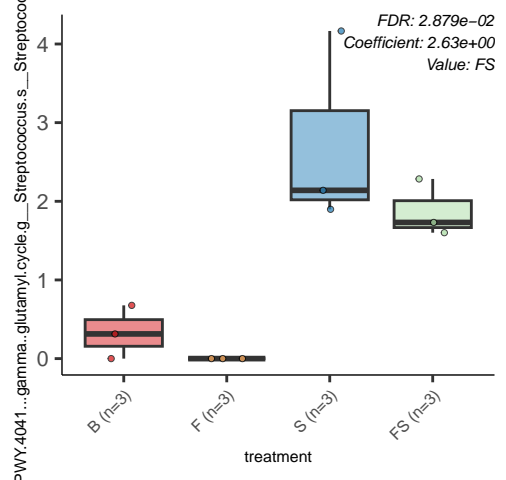




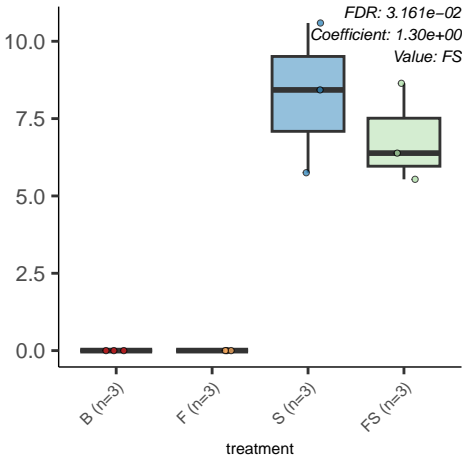


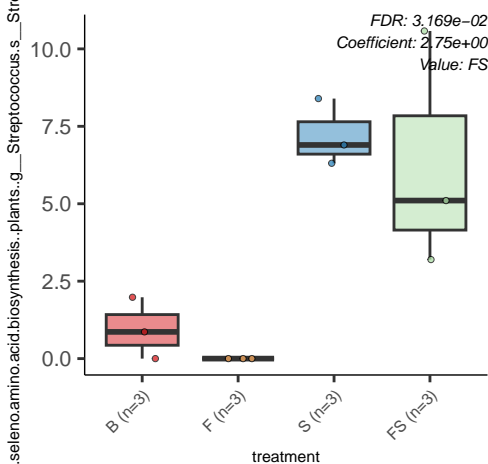


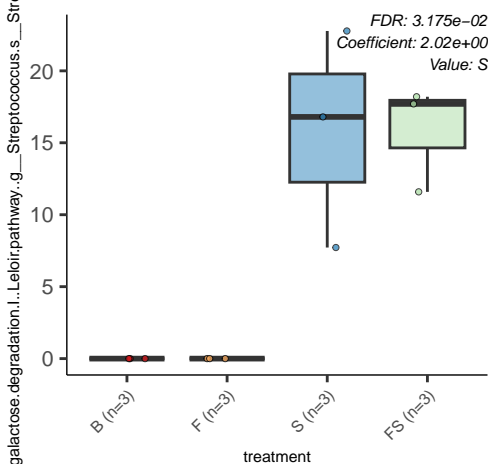




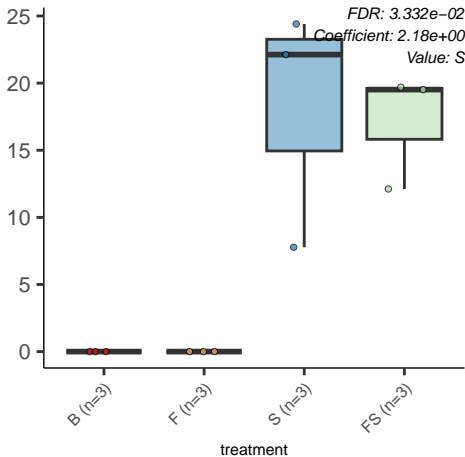
pyl.pentapeptide.biosynthesis.III...meso.diaminopimelate.containing...



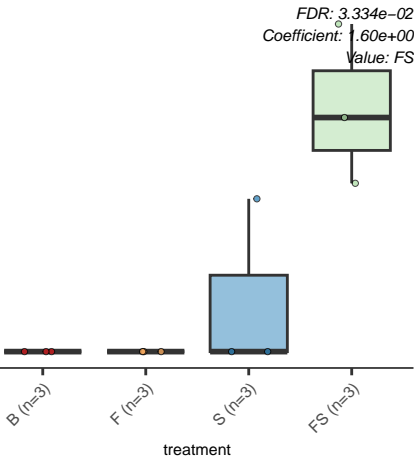


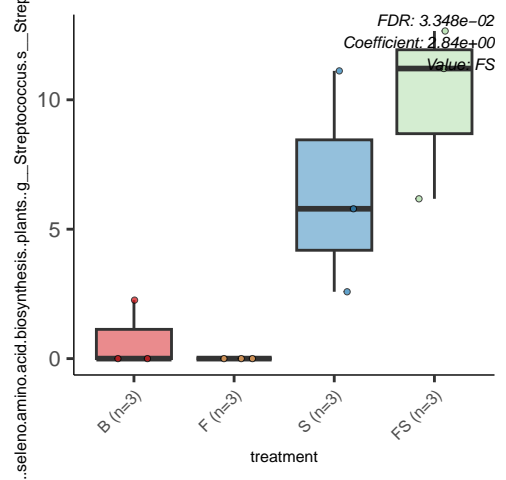


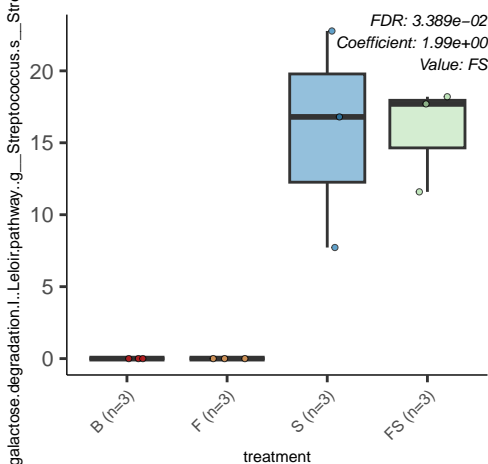
WY.5941..glycogen.degradation.ll.g__Streptococcus.s__Streptococcus

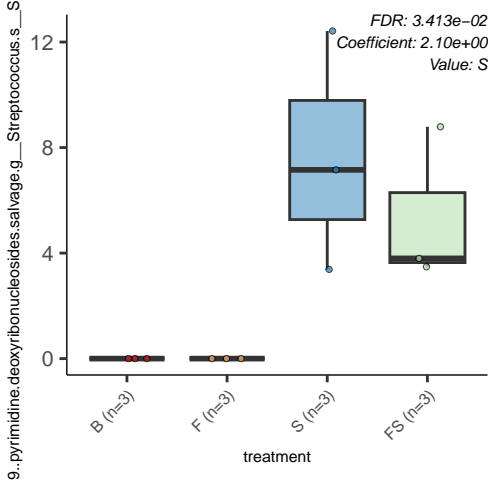


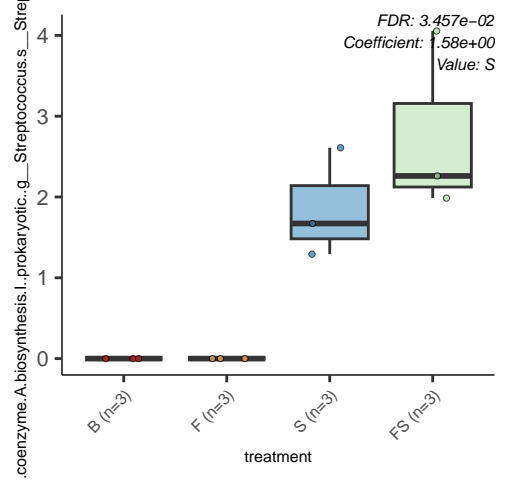
TANA.PWY..L.methionine.biosynthesis.III.g__Streptococcus.s__Stre



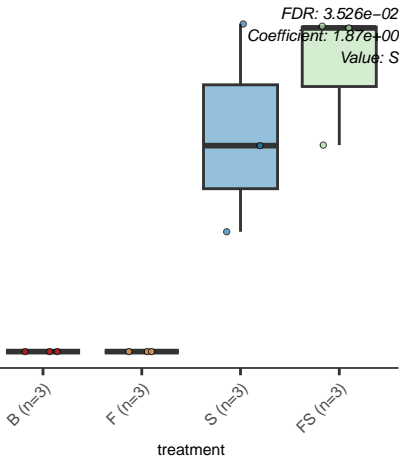




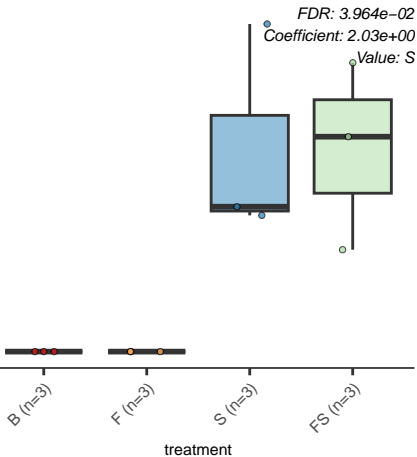




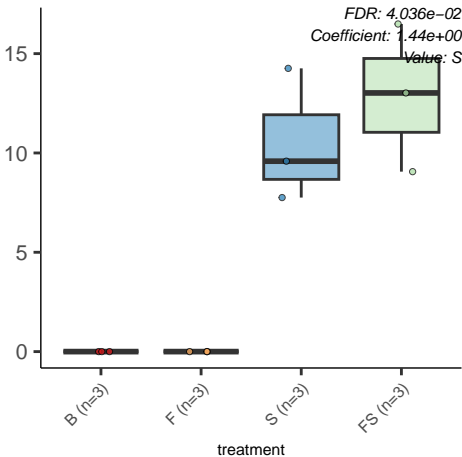
erpathway.of.coenzyme.A.biosynthesis.Ill...mammals..g__Streptococ

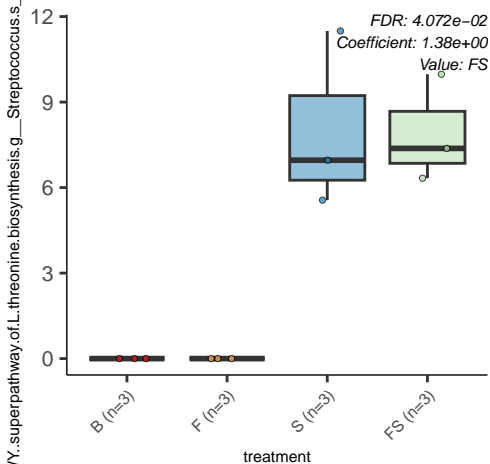


superpathway.of.L.serine.and.glycine.biosynthesis.l.g__Streptococcus

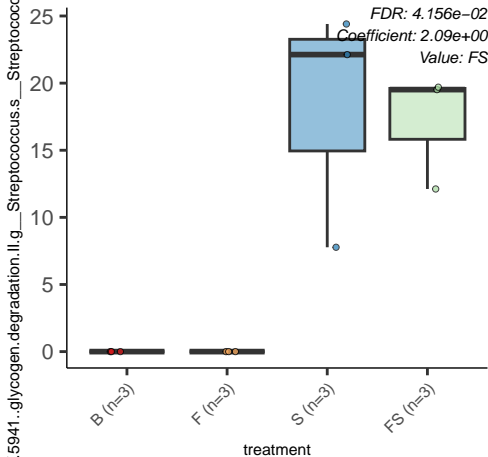


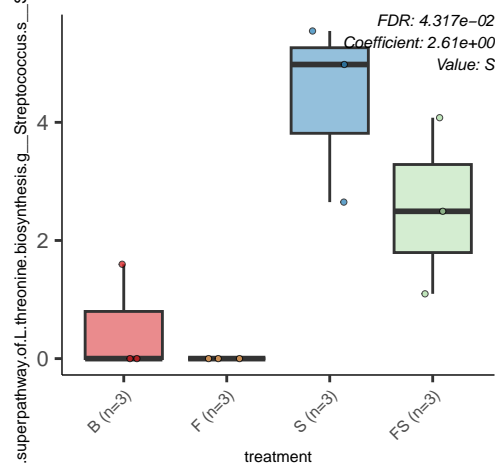
hway.of.adenosine.nucleotides.de.novo.biosynthesis.l.g__Streptococ

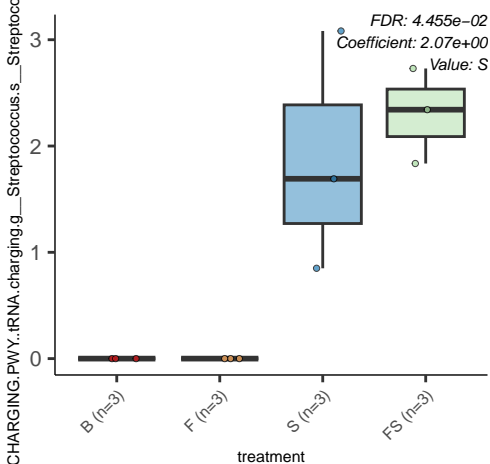


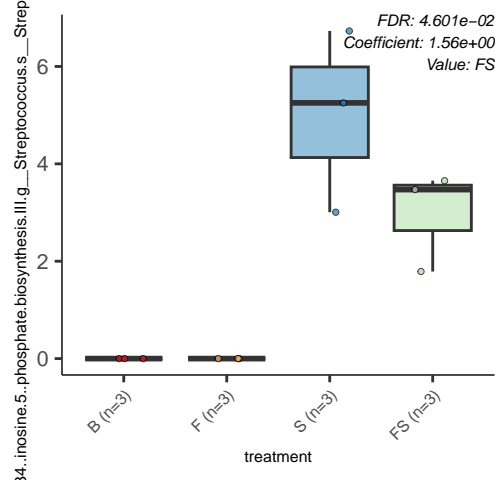


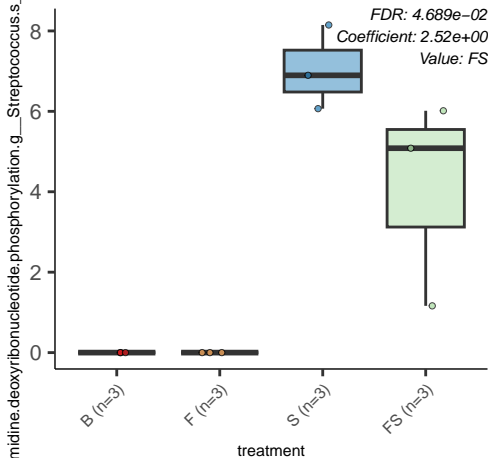
WY.5941..glycogen.degradation.ll.g__Streptococcus.s__Streptococcus

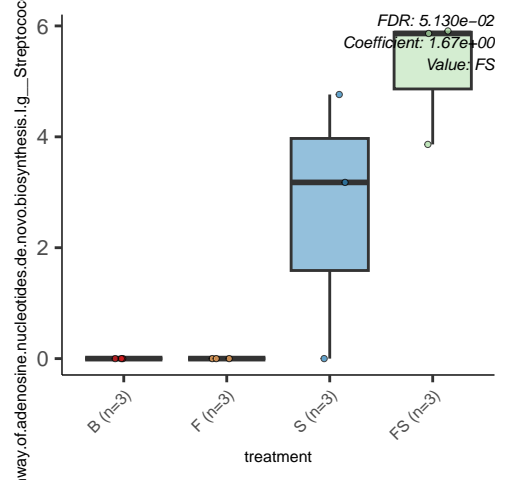


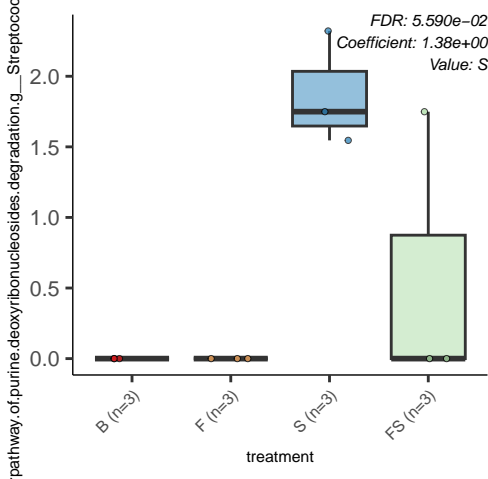


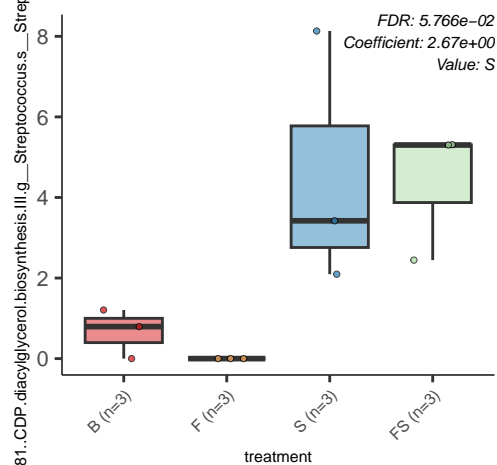


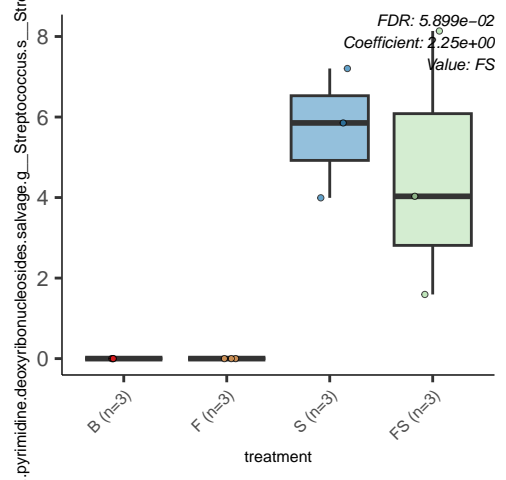




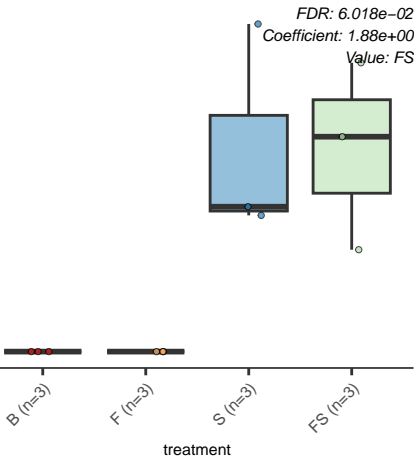




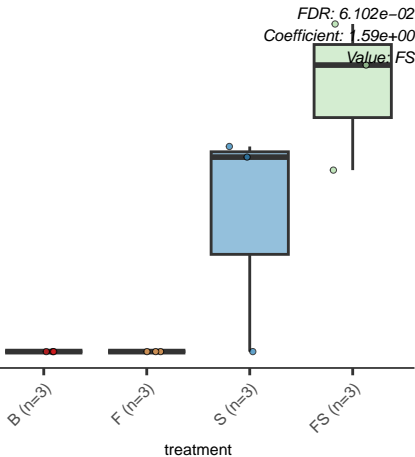


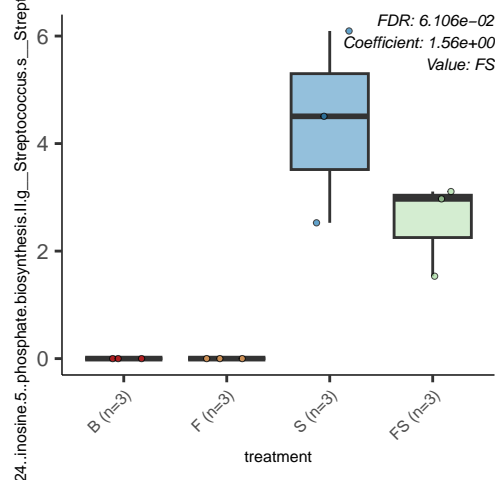


superpathway.of.L.serine.and.glycine.biosynthesis.l.g__Streptococcus

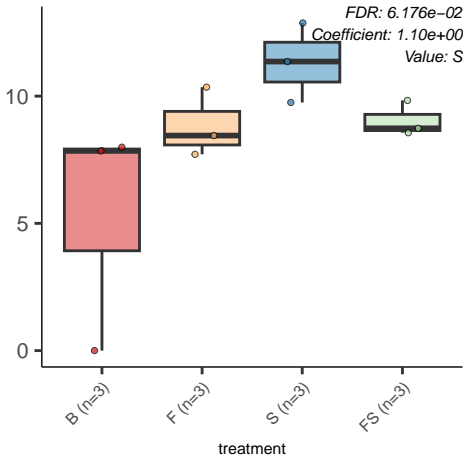


P108.PWY..pyruvate.to.propanoate.l.unclassified

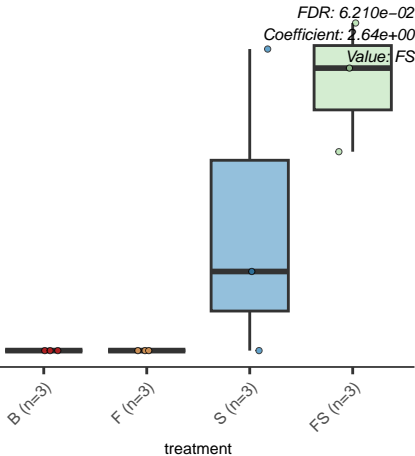




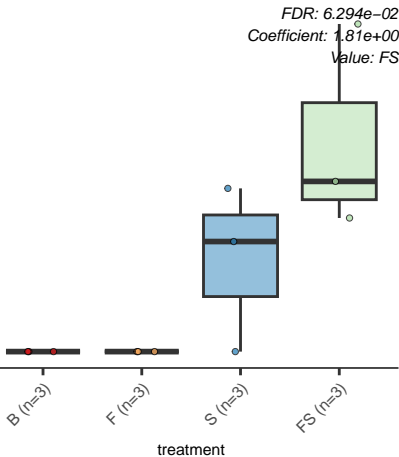
SYN.PWY..L.isoleucine.biosynthesis.l...from.threonine..g__Blautia.s

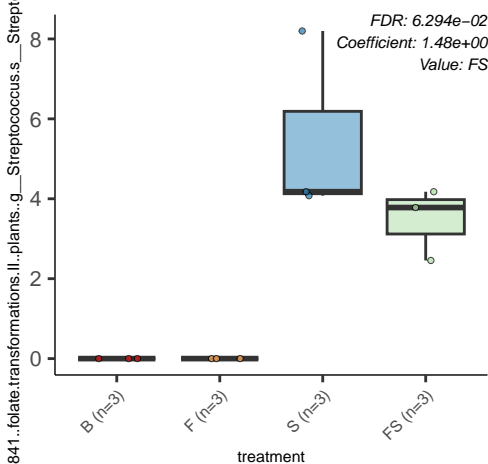


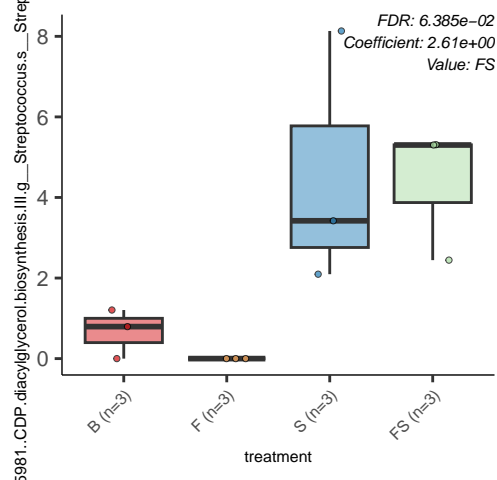
ORN.PWY..L.ornithine.biosynthesis.l.g__Streptococcus.s__Streptococcus



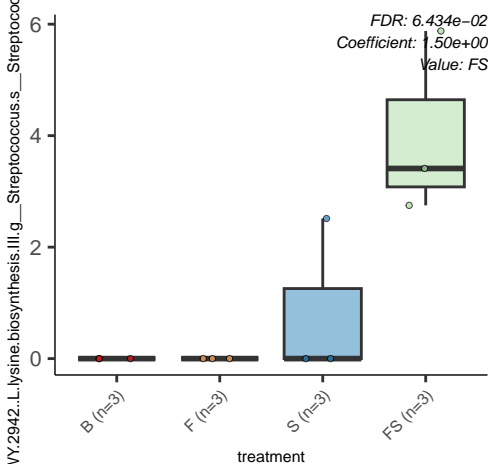
superpathway.of..R.R..butanediol.biosynthesis.g__Streptococcus.s

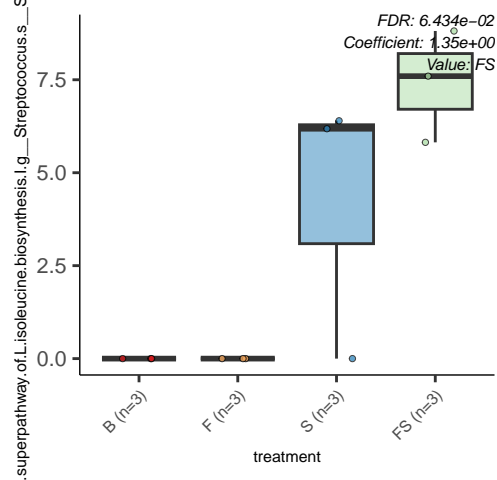






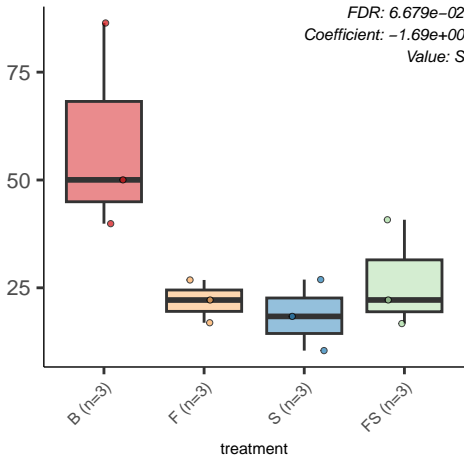
PWY.2942.L.lysine.biosynthesis.III.g__Streptococcus.s__Streptococcus

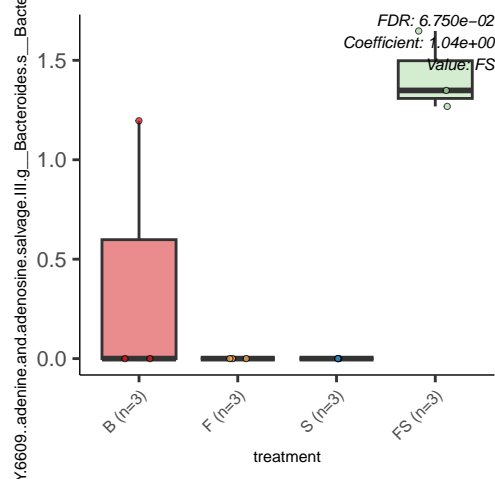




VALSYN.PWY..L.valine.biosynthesis.g_Escherichia.s_Escher

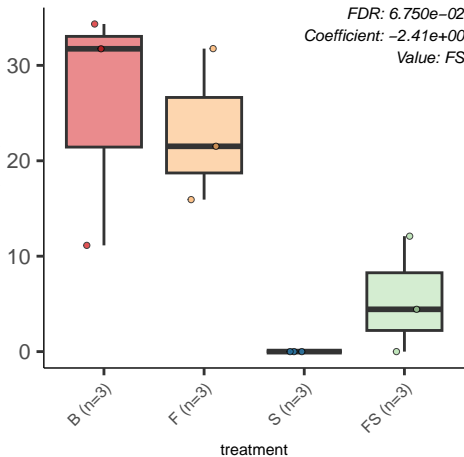
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Coefficient: $-1.69e+00$
Value: S



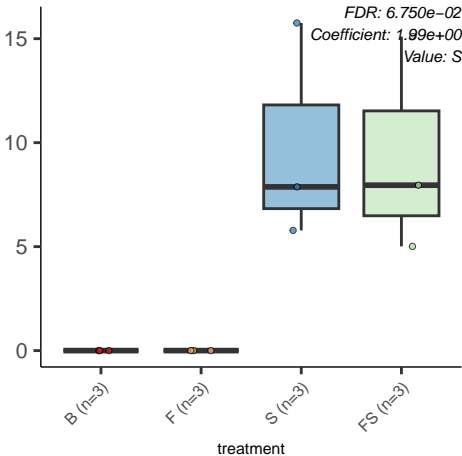


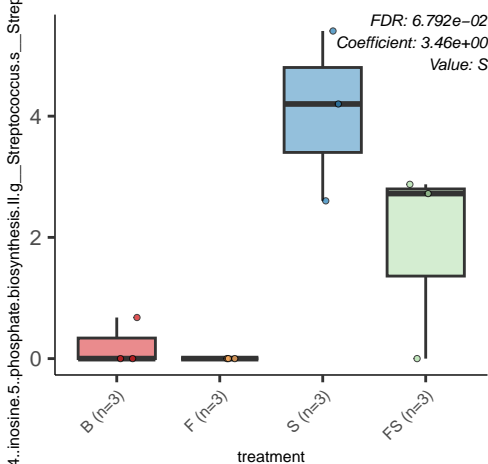
WY.6609..adenine.and.adenosine.salvage.III.g__Escherichia.s__Es

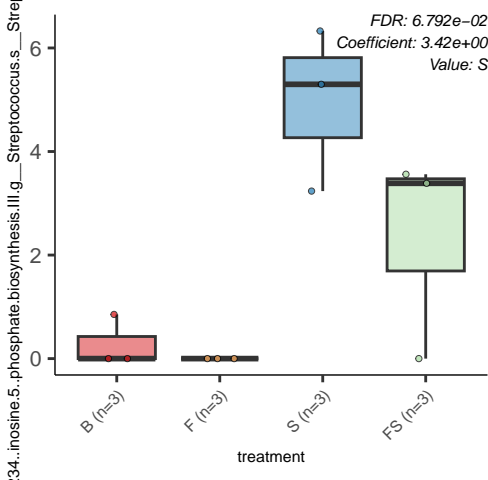
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Coefficient: $-2.41e+00$
Value: FS



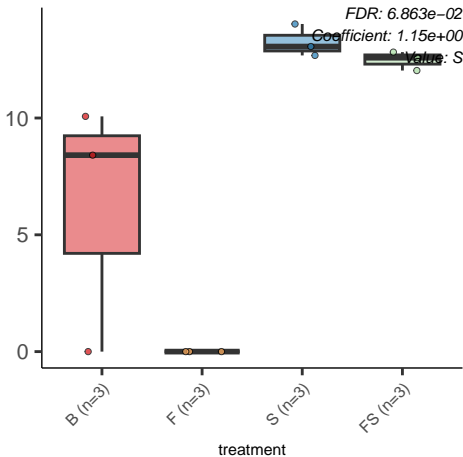
700..queuosine.biosynthesis.l..de.novo.g__Streptococcus.s__Strep



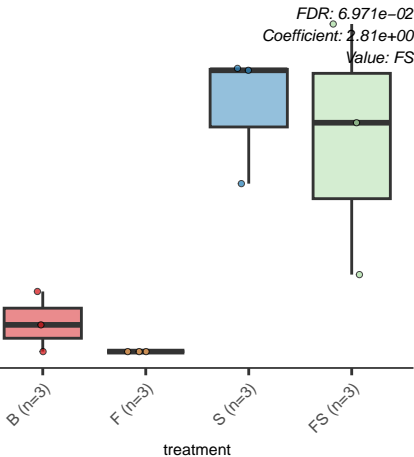


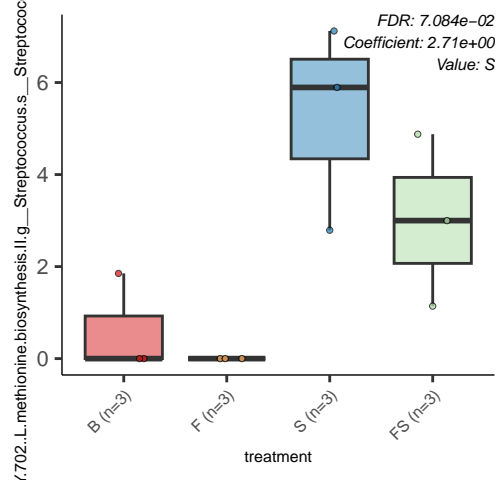


hway.of.adenosylcobalamin.salvage.from.cobinamide.l.g__Faecalib



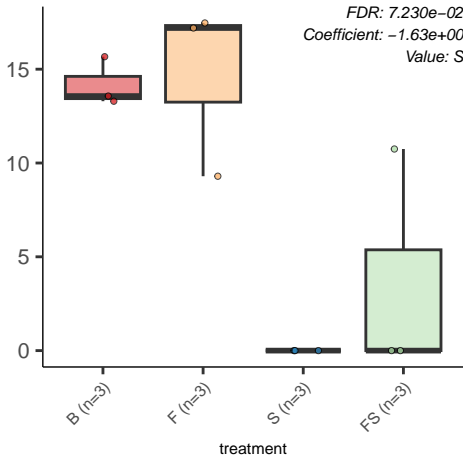
ETANA.PWY..L_methionine.biosynthesis.III.g__Streptococcus.s__St

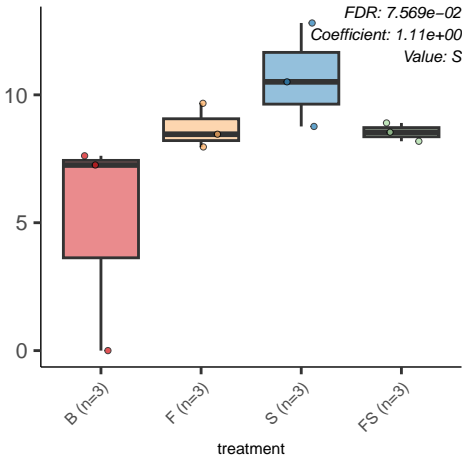


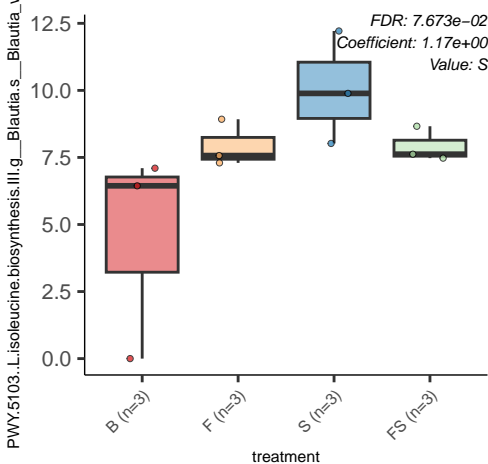


PWY.7234..inosine.5..phosphate.biosynthesis.III.unclassified

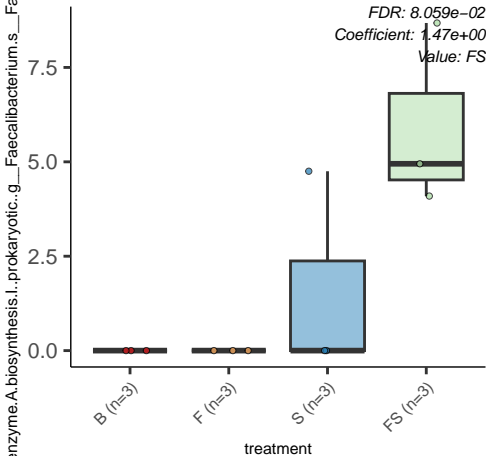
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Coefficient: -1.63e+00
Value: S

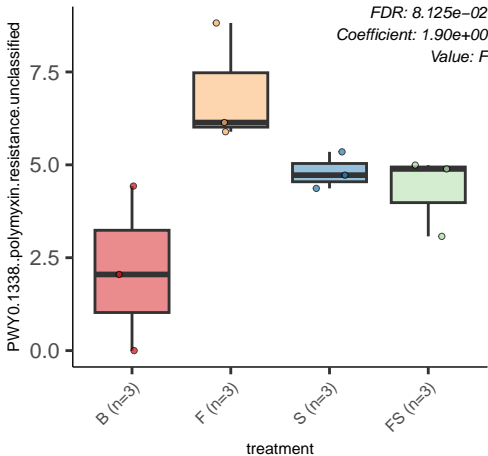




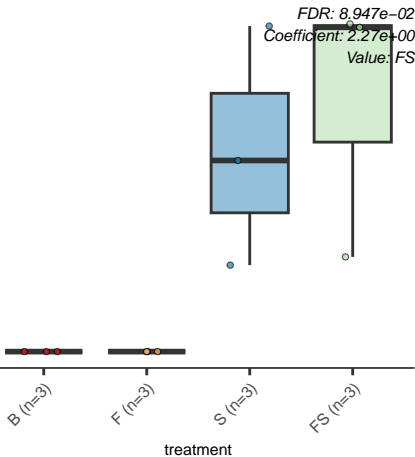


coenzyme.A.biosynthesis.l.prokaryotic.g__Faecalibacterium.s__Fae

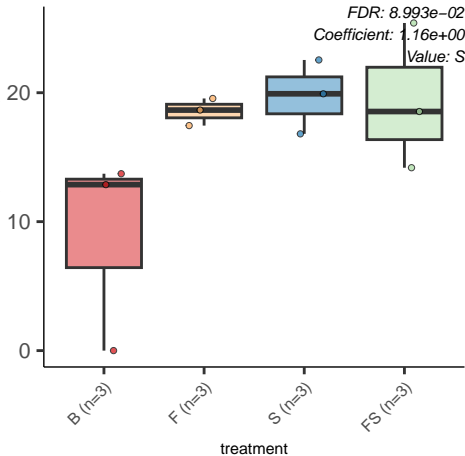


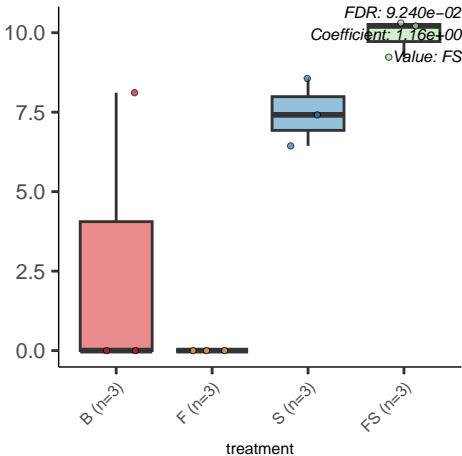


guanosine.ribonucleotides.de.novo.biosynthesis.g__Streptococcus.s



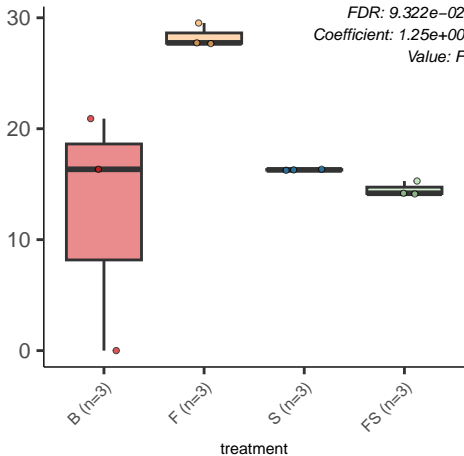
LACTOSECAT.PWY..lactose.and.galactose.degradation..l.uncle

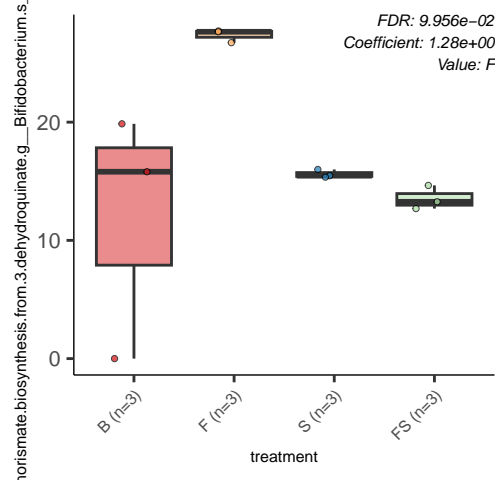


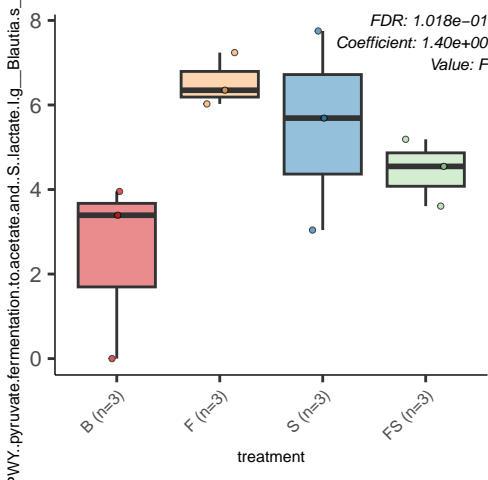


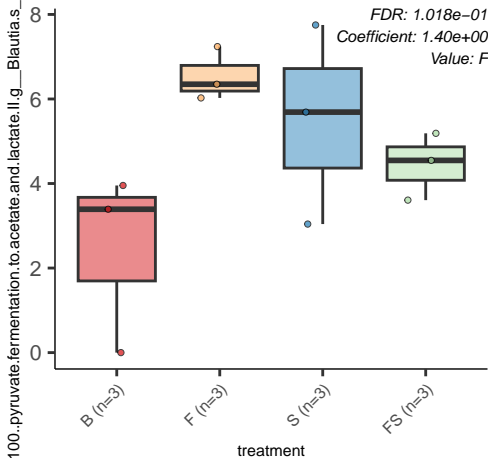
RO.PWY..chorismate.biosynthesis.l.g__Bifidobacterium.s__Bifidoba

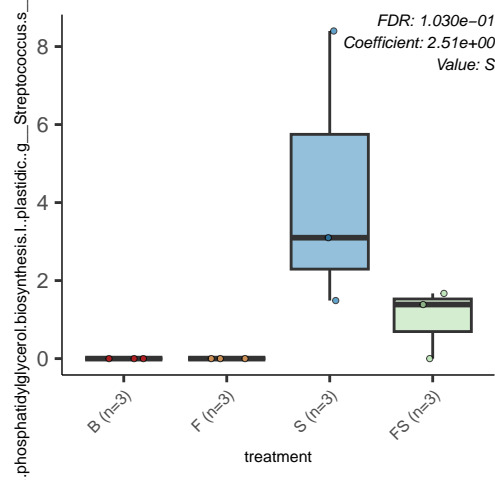
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Coefficient: 1.25e+00
Value: F

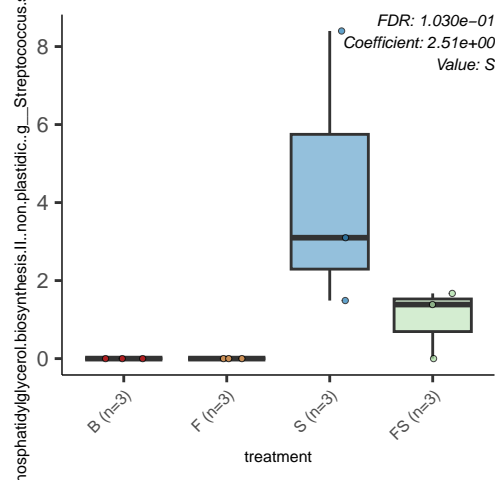




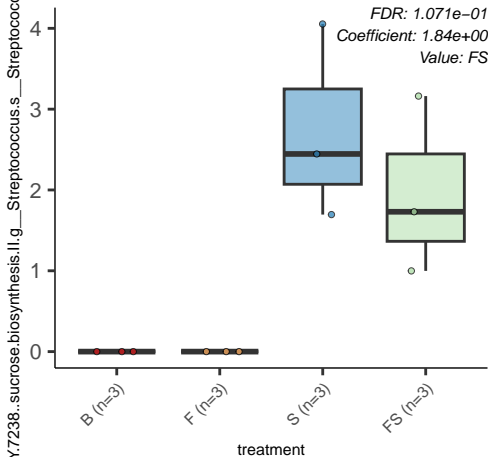






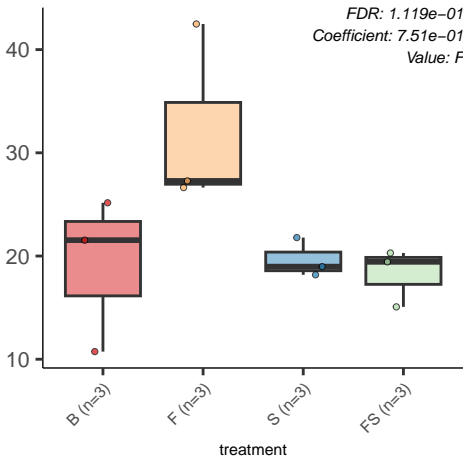


WY.7238..sucrose.biosynthesis.ll.g__Streptococcus.s__Streptococcus



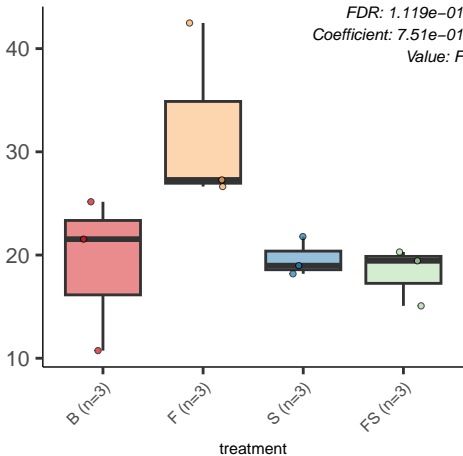
uvate.fermentation.to.acetate.and...S..lactate.l.g__Bifidobacterium.s

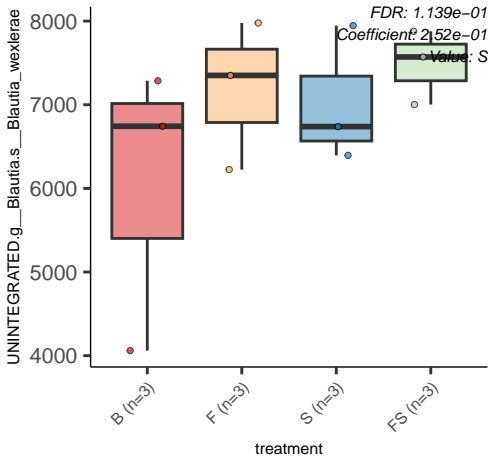
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Coefficient: 7.51e-01
Value: F

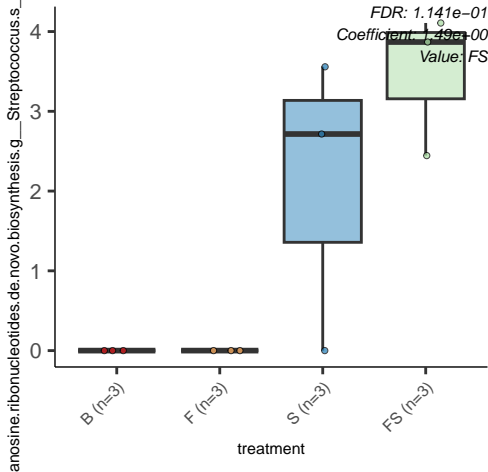


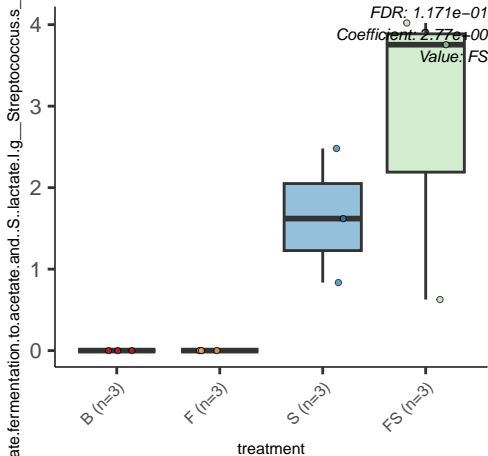
pyruvate,fermentation.to.acetate.and.lactate.11.g__Bifidobacterium.s

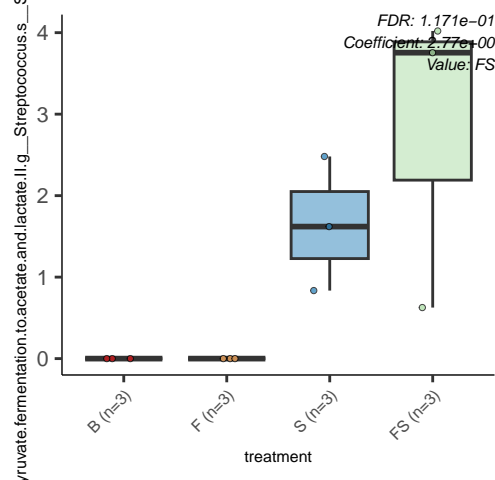
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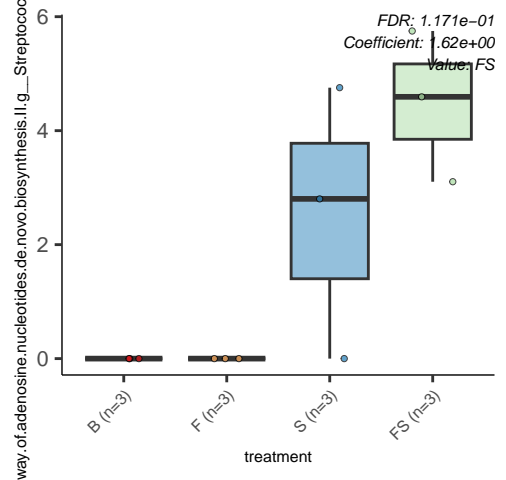




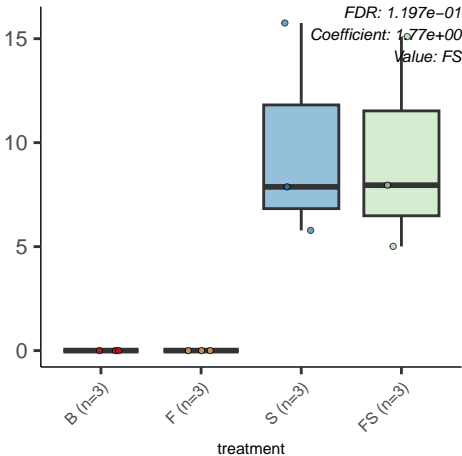


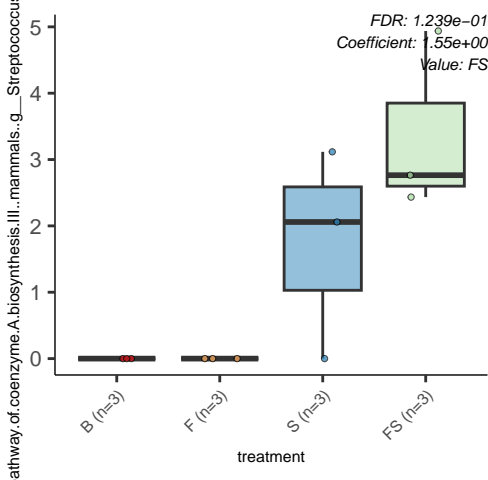




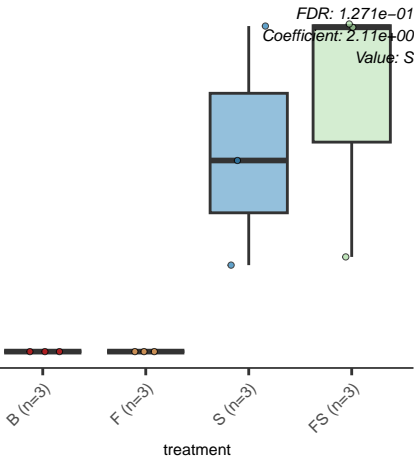


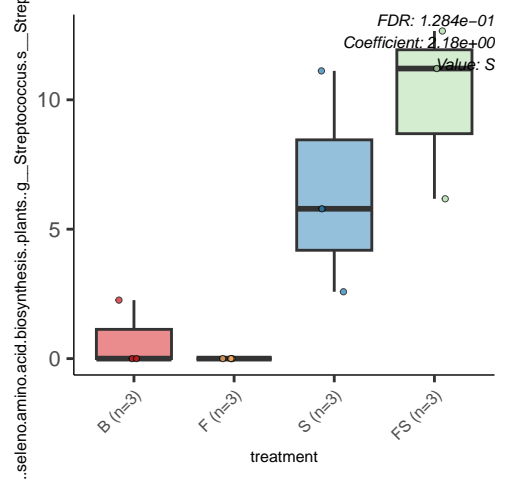
700..queuosine.biosynthesis.l..de.novo.g__Streptococcus.s__Strep



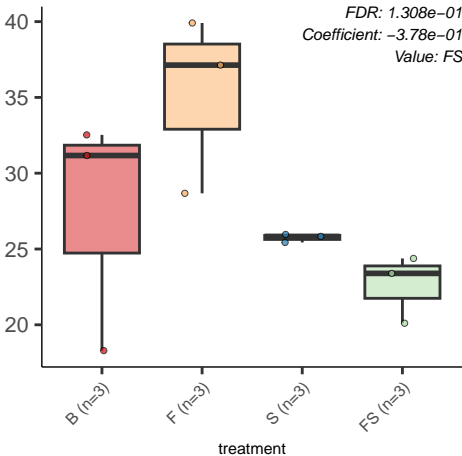


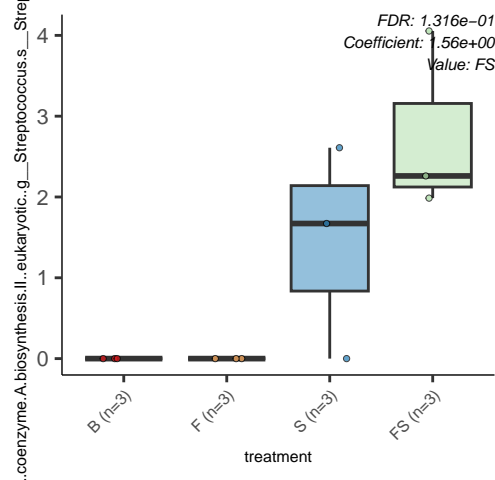
guanosine.ribonucleotides.de.novo.biosynthesis.g__Streptococcus.s

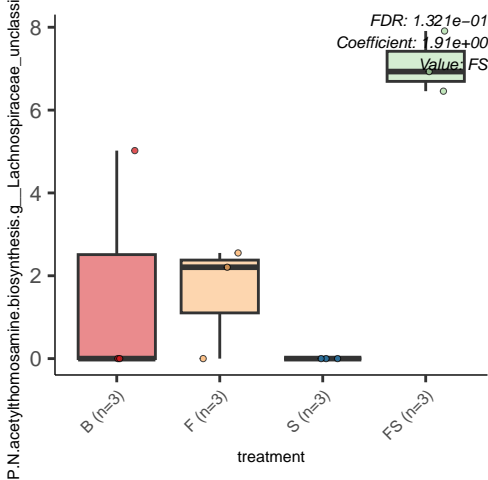




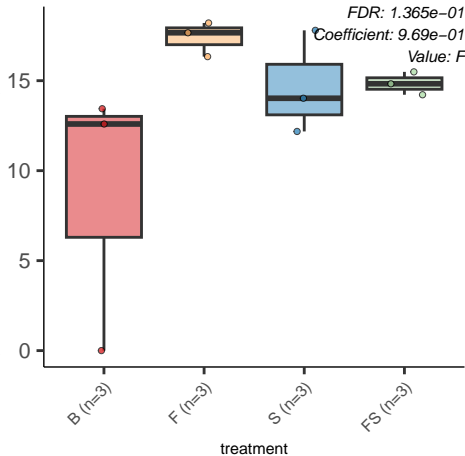
ALSYN.PWY..L.valine.biosynthesis.g__Bifidobacterium.s__Bifidobac



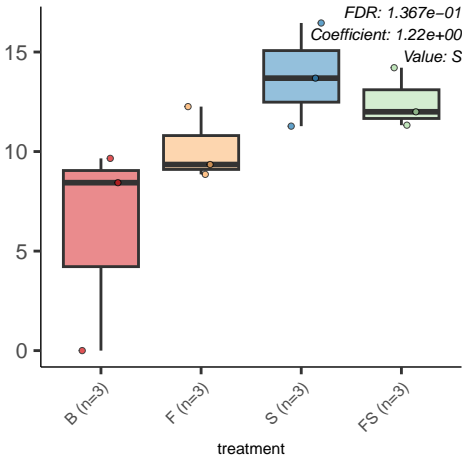


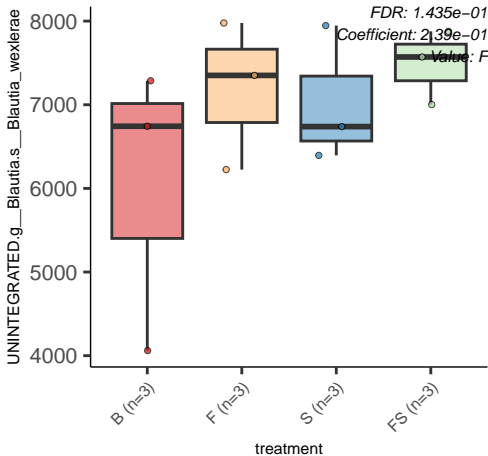


gSYN.PWY..L-arginine.biosynthesis.l.via.L-ornithine..g_Blaustia.s

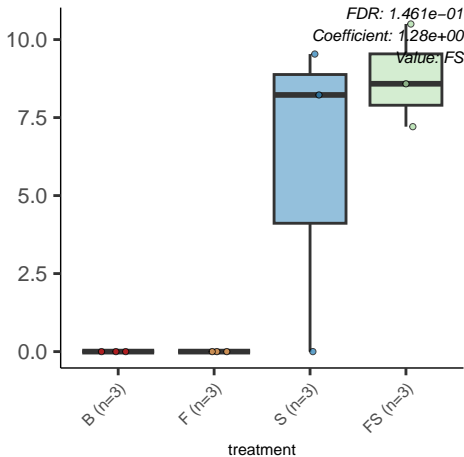


PWY.6123..inosine.5..phosphate.biosynthesis.l.g__Blautia.s__Blau

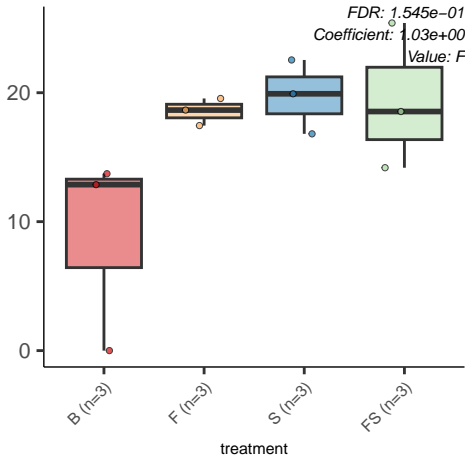


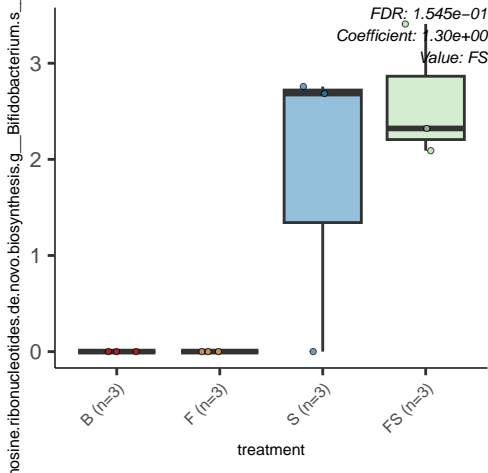


pathway.of.purine.deoxyribonucleosides.degradation.g__Streptococcus



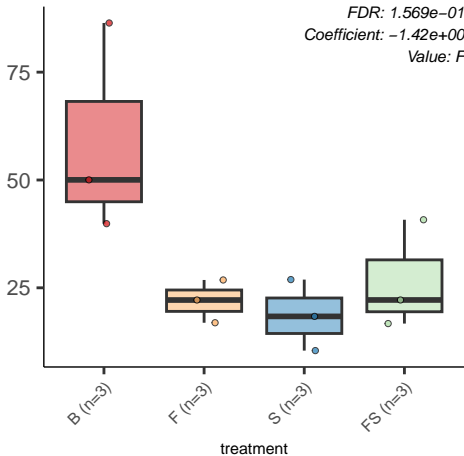
LACTOSECAT.PWY..lactose.and.galactose.degradation..l.uncle



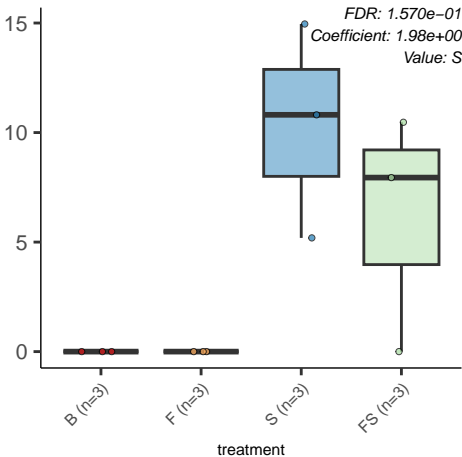


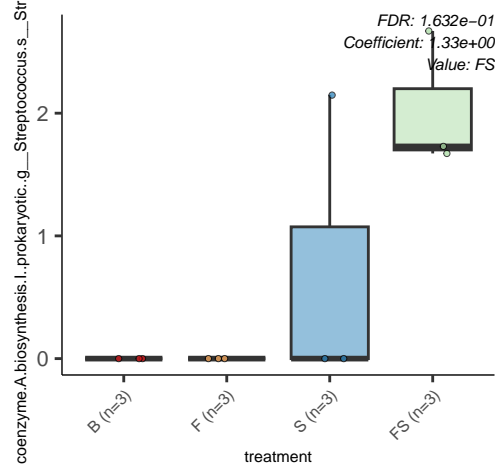
VALSYN.PWY..L.valine.biosynthesis.g_Escherichia.s_Escher

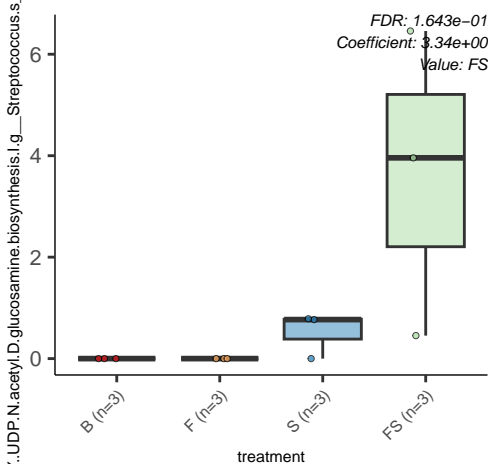
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Coefficient: -1.42e+00
Value: F

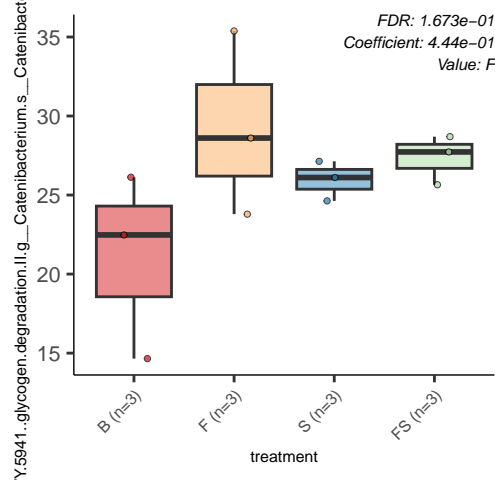


VY..superpathway.of.aromatic.amino.acid.biosynthesis.g__Streptococcus



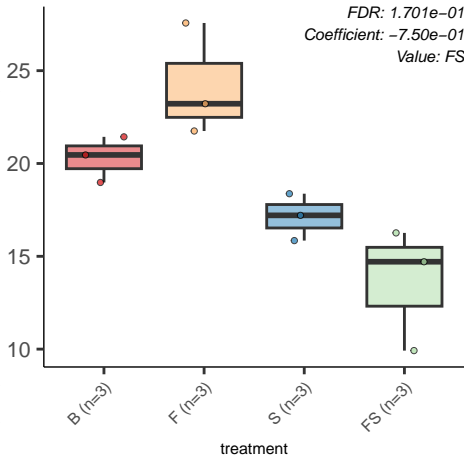


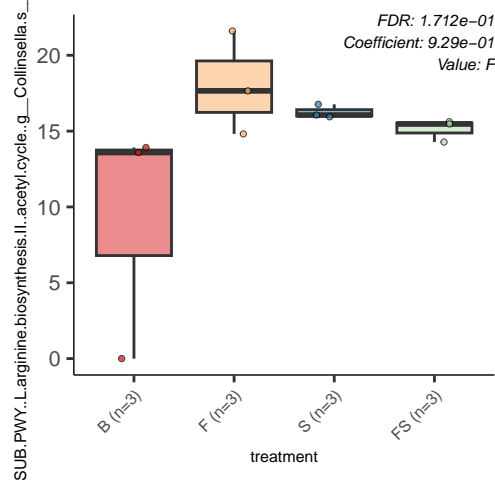




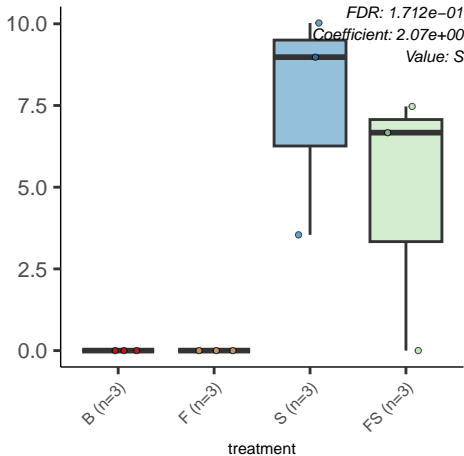
.PWY..glycogen.biosynthesis.l..from.ADP.D.Glucose.g__Bifidobacte

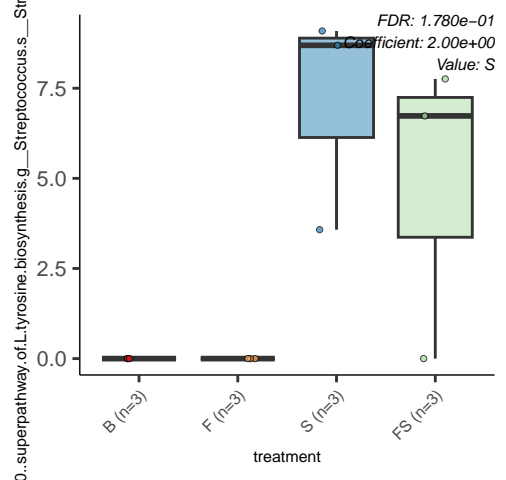
FDR: 1.701e-01
Coefficient: -7.50e-01
Value: FS

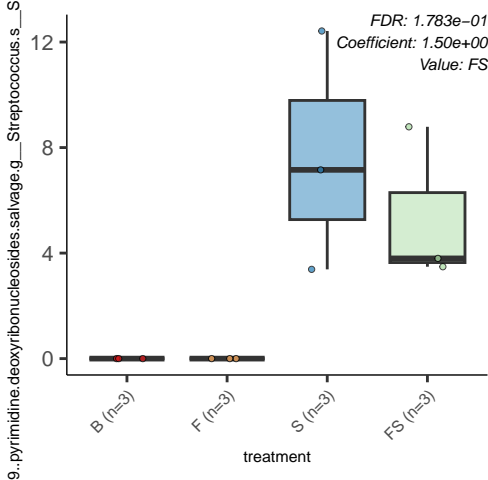




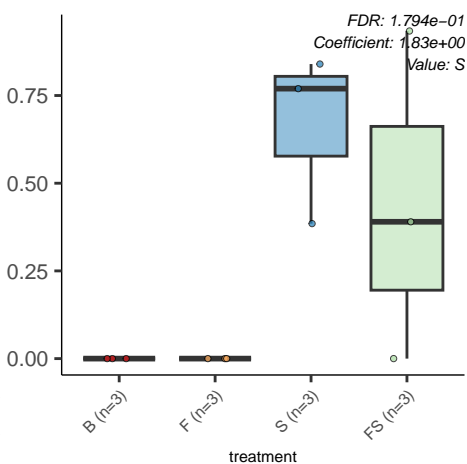
superpathway.of.L.phenylalanine.biosynthesis.g__Streptococcus.s



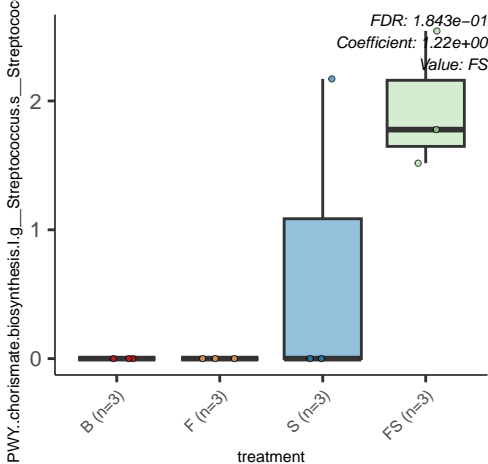




PWY..glycogen.biosynthesis.l..from.ADP.D.Glucose..g__Streptococ

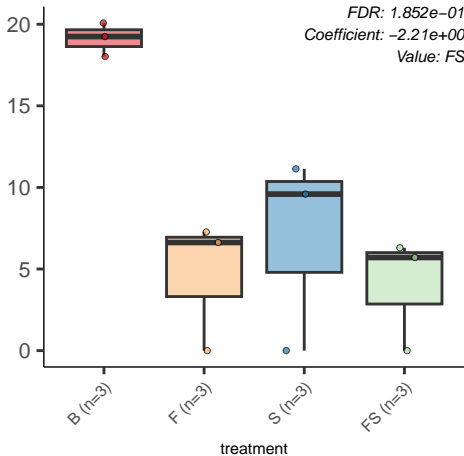


O.PWY..chorismate.biosynthesis.l.g__Streptococcus



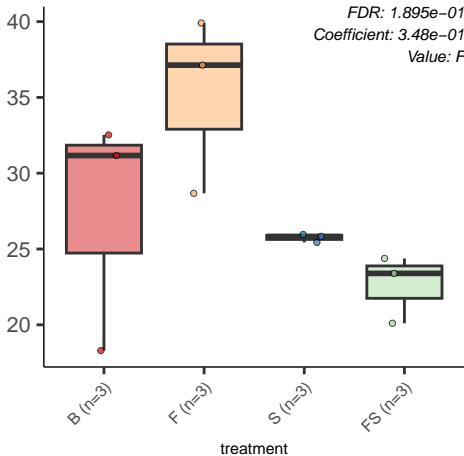
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FDR: 1.852e-01
Coefficient: -2.21e+00
Value: FS

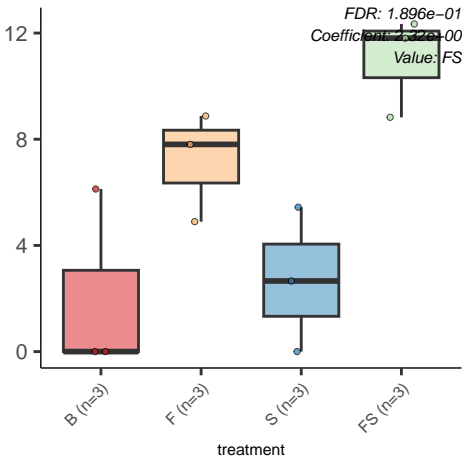


ALSYN.PWY..L.valine.biosynthesis.g__Bifidobacterium.s__Bifidoba

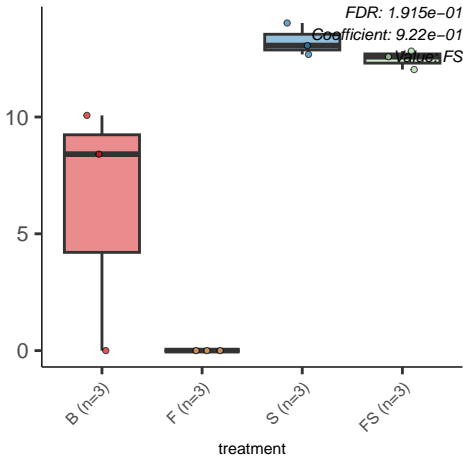
FDR: 1.895e-01
Coefficient: 3.48e-01
Value: F



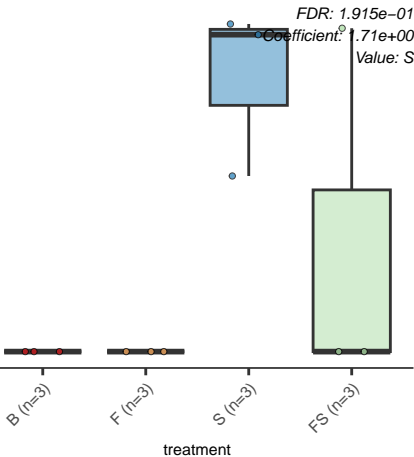
PWY.7761..NAD.salvage.pathway.II..PNC.IV.cycle..unclass



hway.of.adenosylcobalamin.salvage.from.cobinamide.l.g__Faecalib

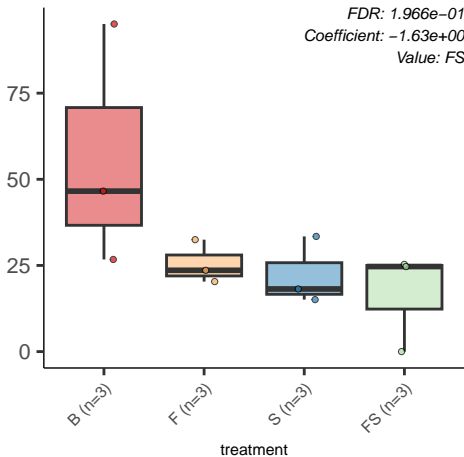


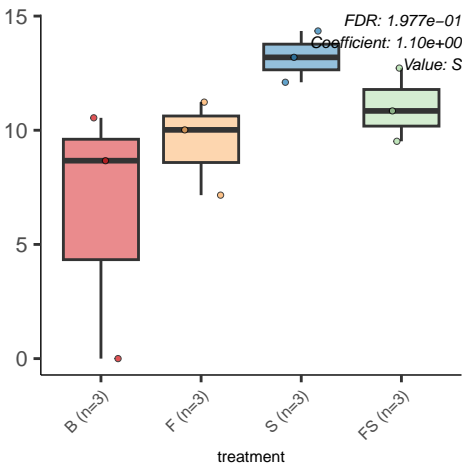
P164.PWY..purine.nucleobases.degradation.l...anaerobic...uncia



WY.7663..gondate.biosynthesis..anaerobic..g__Escherichia.s__Es

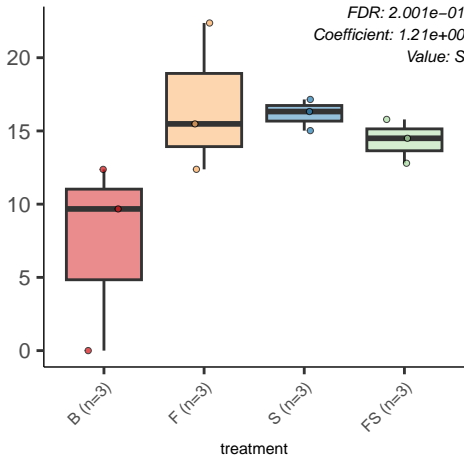
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Coefficient: -1.63e+00
Value: FS



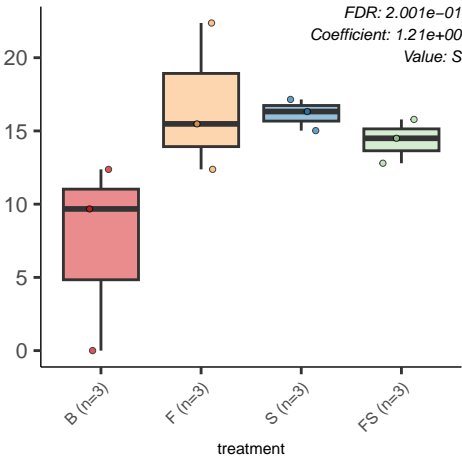


PWY.5686..UMP.biosynthesis.l.g__Collinsella.s__Collinsella_ae

FDR: 2.001e-01
Coefficient: 1.21e+00
Value: S

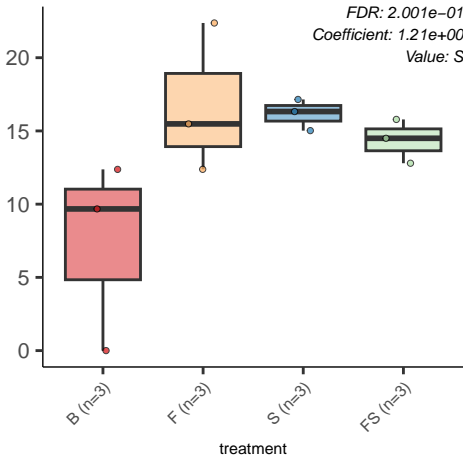


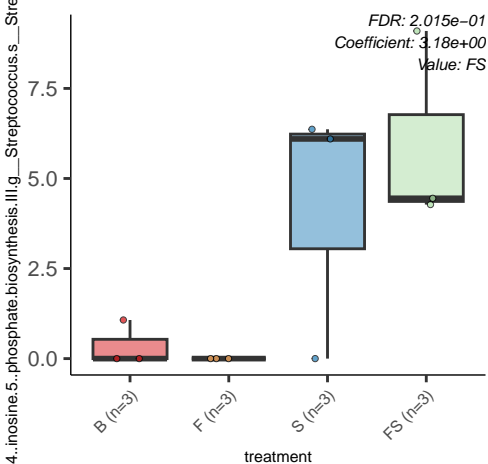
PWY.7790..UMP.biosynthesis.ll.g__Collinsella.s__Collinsella_ae



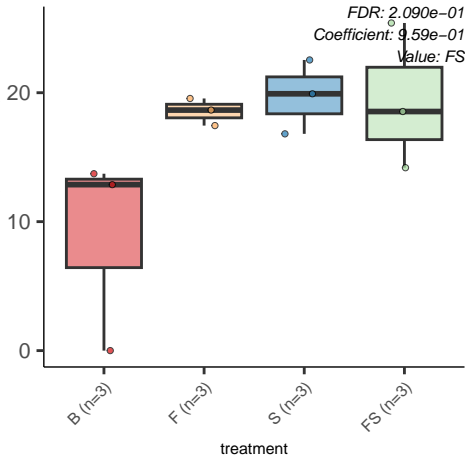
PWY.7791..UMP.biosynthesis.III.g_Collinsella.s_Collinsella_ae

FDR: 2.001e-01
Coefficient: 1.21e+00
Value: S



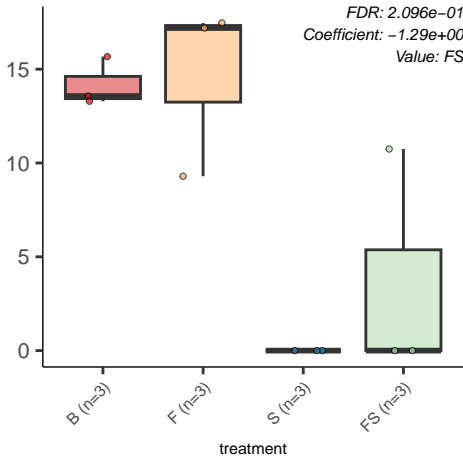


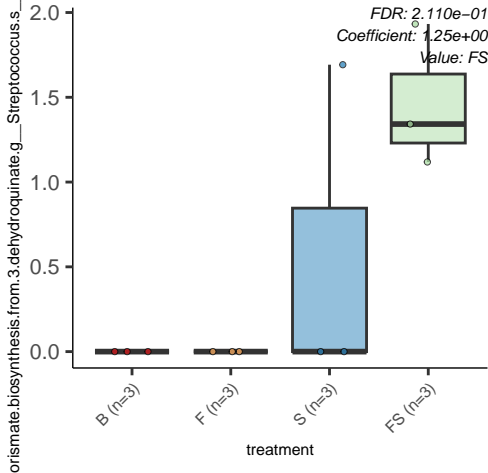
LACTOSECAT.PWY..lactose.and.galactose.degradation..l.uncle



PWY.7234..inosine.5..phosphate.biosynthesis.III.unclassified

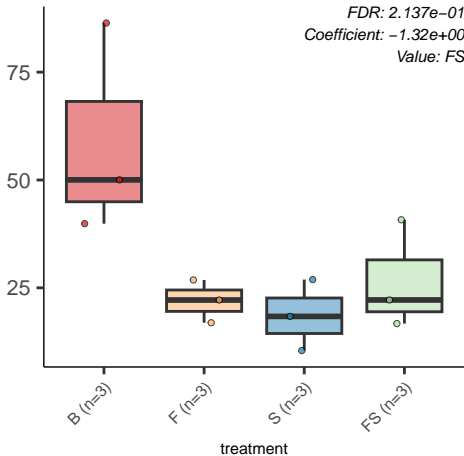
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Coefficient: -1.29e+00
Value: FS

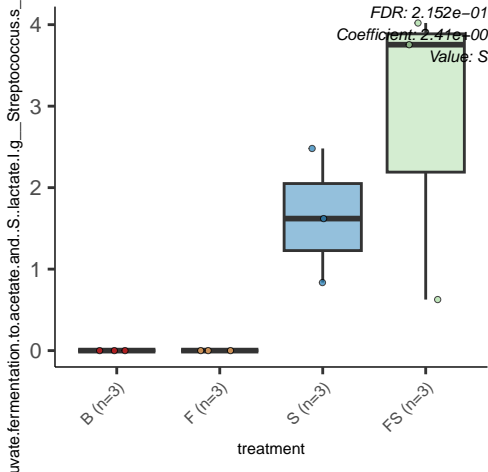


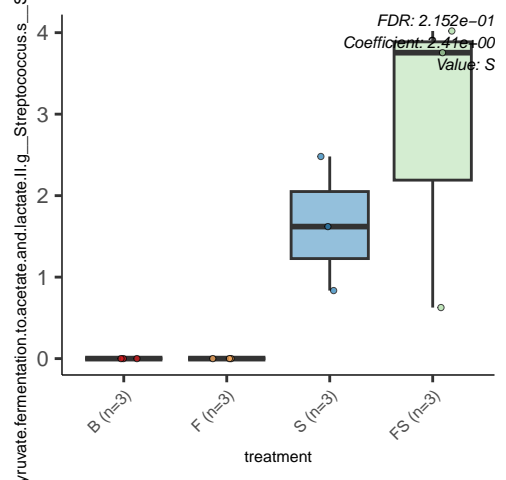


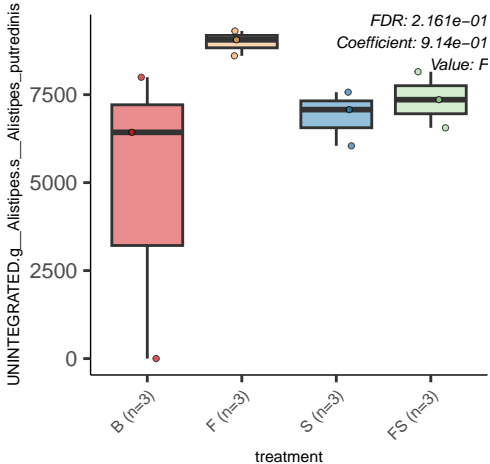
VALSYN.PWY..L.valine.biosynthesis.g_Escherichia.s_Escher

FDR: $2.137e-01$
Coefficient: $-1.32e+00$
Value: FS



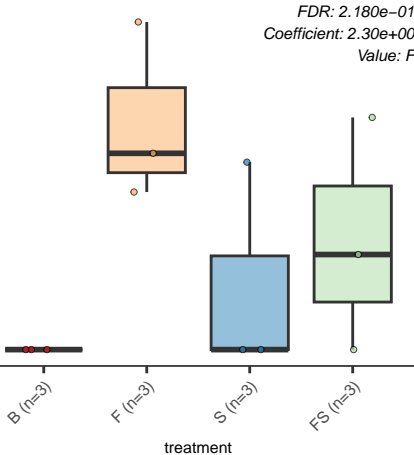




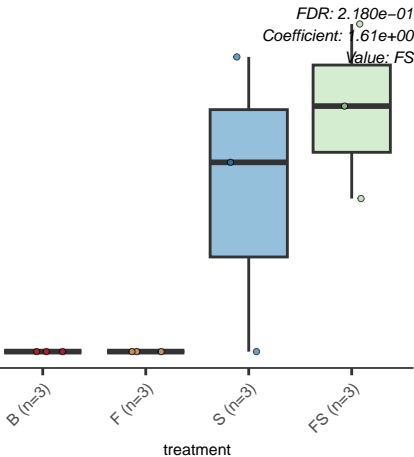


WY.5667..CDP.diacylglycerol.biosynthesis.l.g__Bacteroides.s__Bac

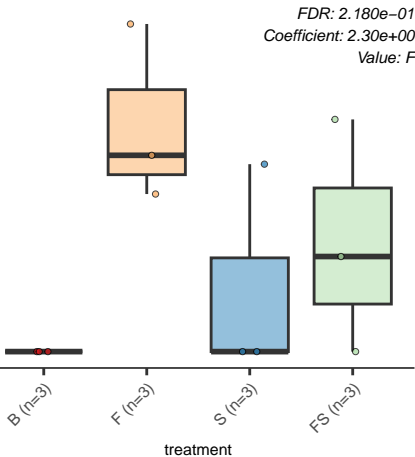
FDR: 2.180e-01
Coefficient: 2.30e+00
Value: F



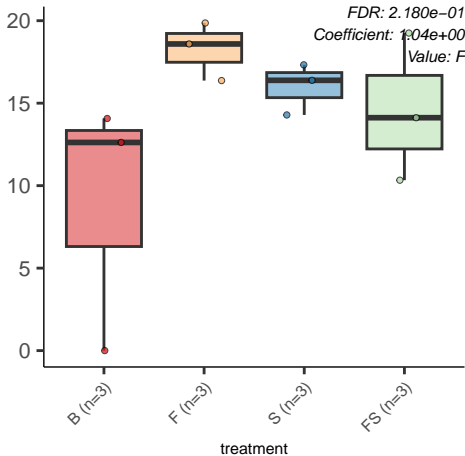
way.of.guanosine.nucleotides.de.novo.biosynthesis.l.g__Streptococ

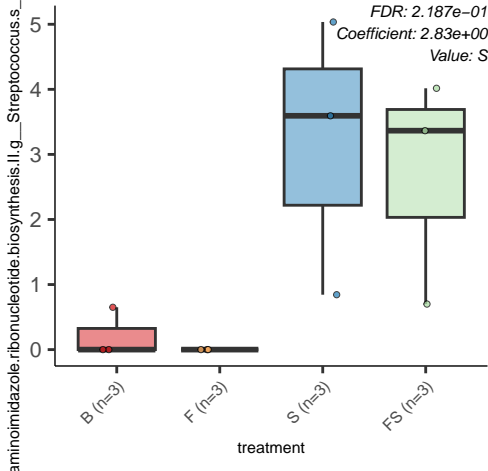


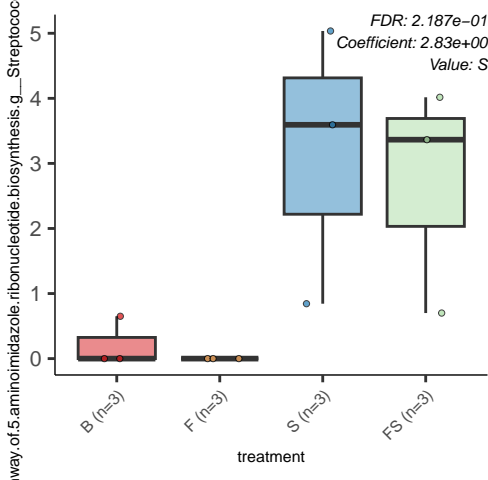
VY0.1319..CDP.diacylglycerol.biosynthesis.II.g__Bacteroides.s__Ba



J.P.WY..superpathway.of.L.threonine.biosynthesis.g_Collinsella.s

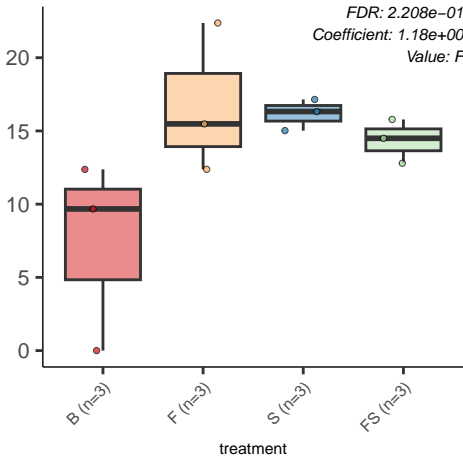






PWY.5686..UMP.biosynthesis.l.g__Collinsella.s__Collinsella_ae

FDR: 2.208e-01
Coefficient: 1.18e+00
Value: F



PWY.7790..UMP.biosynthesis.ll.g__Collinsella.s__Collinsella_ae

20
15
10
5
0

B (n=3)

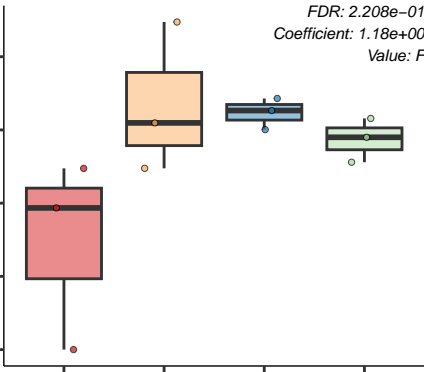
F (n=3)

S (n=3)

FS (n=3)

treatment

FDR: 2.208e-01
Coefficient: 1.18e+00
Value: F



PWY.7791..UMP.biosynthesis.III.g__Collinsella.s__Collinsella_ae

20
15
10
5
0

FDR: 2.208e-01
Coefficient: 1.18e+00
Value: F

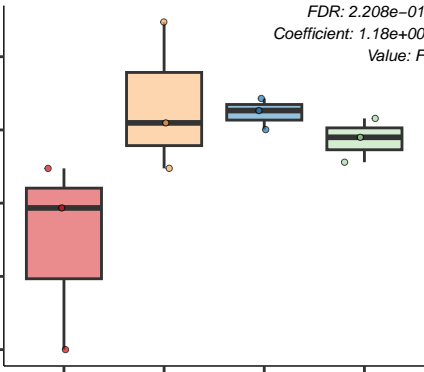
B (n=3)

F (n=3)

S (n=3)

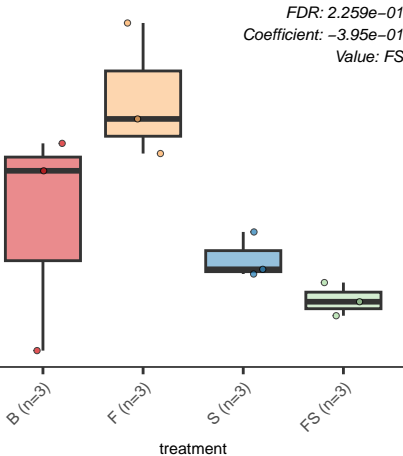
FS (n=3)

treatment



icrose.degradation.IV..sucrose.phosphorylase.g__Bifidobacterium.s

FDR: 2.259e-01
Coefficient: -3.95e-01
Value: FS



YY.702...L.methionine.biosynthesis.ll.g__Bifidobacterium.s__Bifidoba

FDR: 2.264e-01
Coefficient: -8.50e-01
Value: FS

17.5
15.0
12.5
10.0

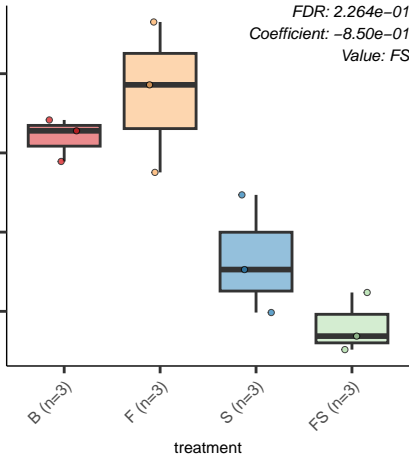
B (n=3)

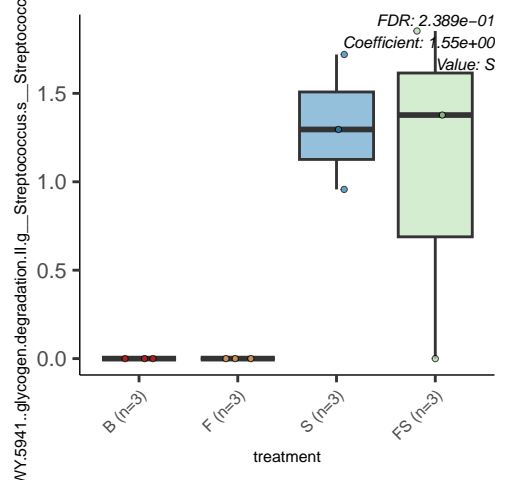
F (n=3)

S (n=3)

FS (n=3)

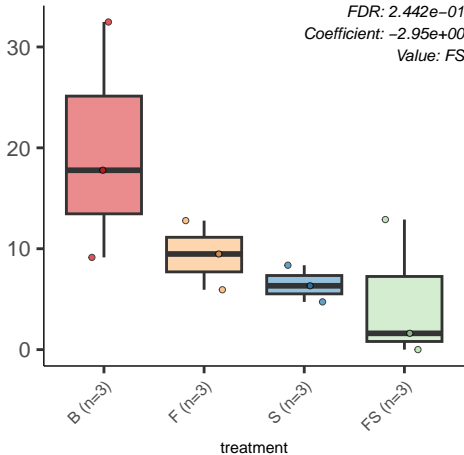
treatment





PWY.5973..cis.vaccenate.biosynthesis.g_Escherichia.s_Esche

FDR: 2.442e-01
Coefficient: -2.95e+00
Value: FS



FDR: $2.496e-01$
Coefficient: $-1.96e+00$
Value: S

