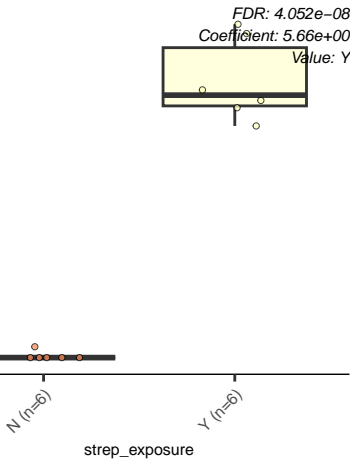
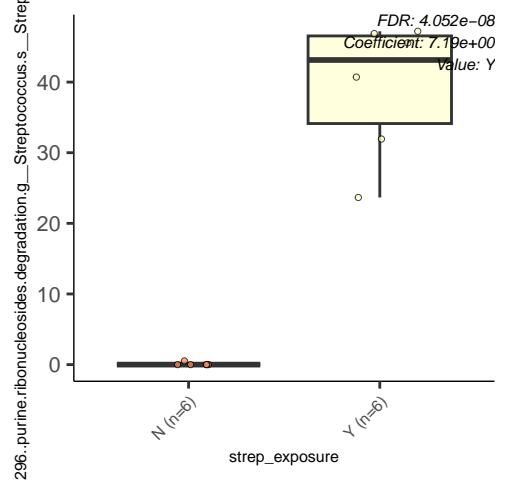
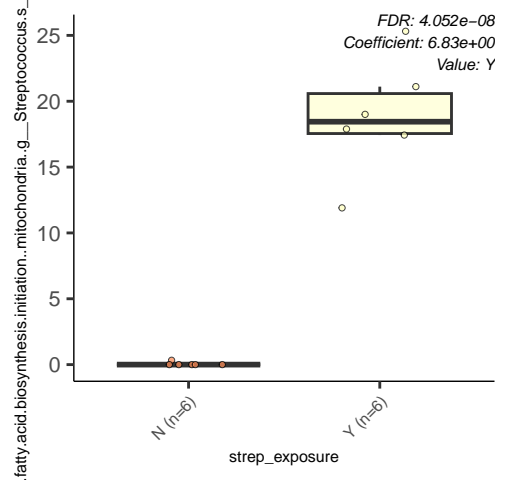
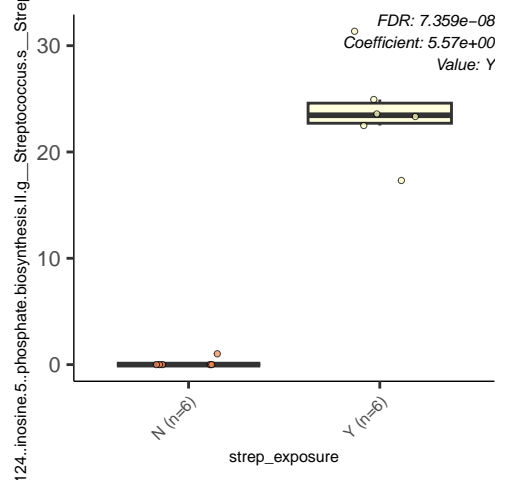


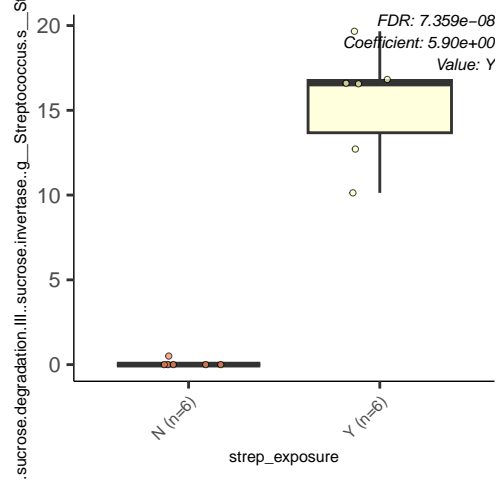
WY.7238..sucrose.biosynthesis.ll.g\_\_Streptococcus

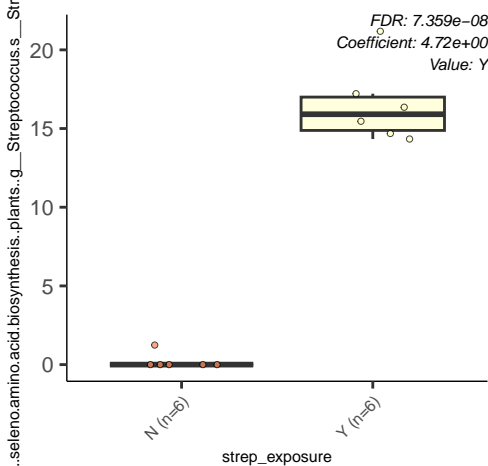




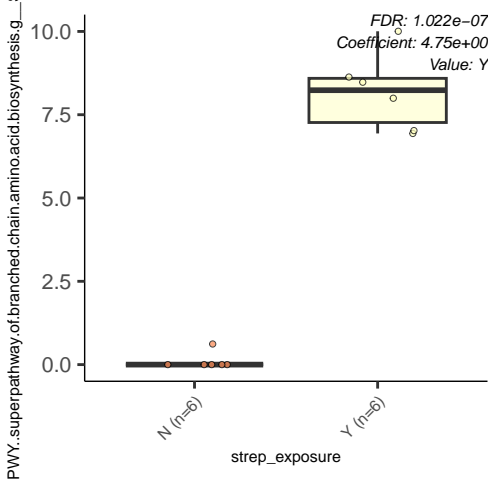


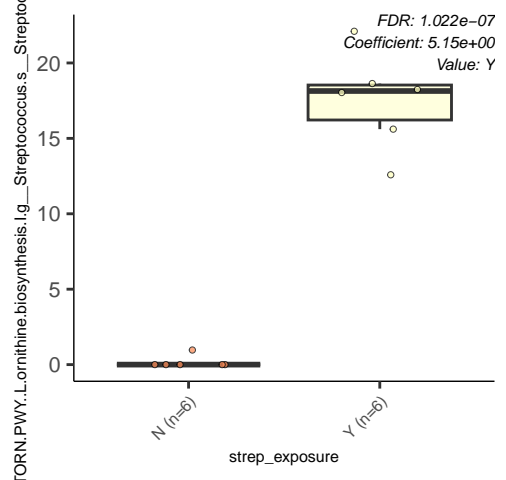


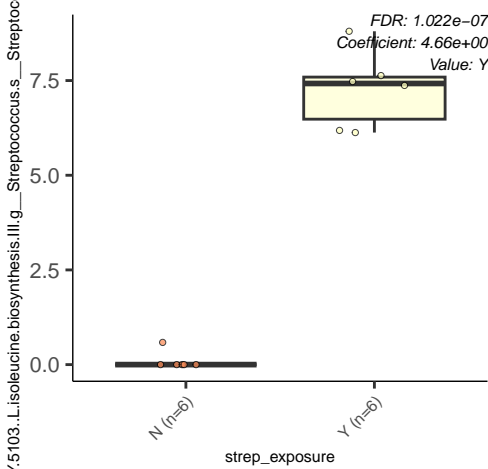


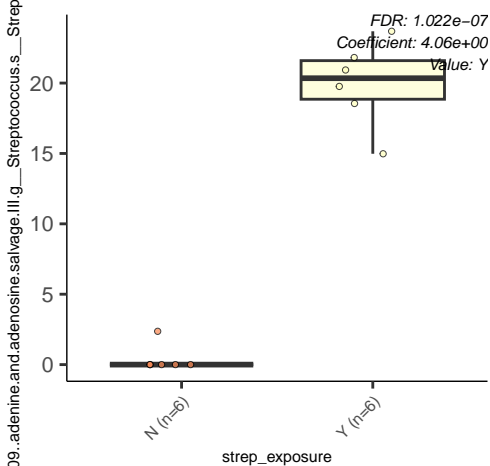


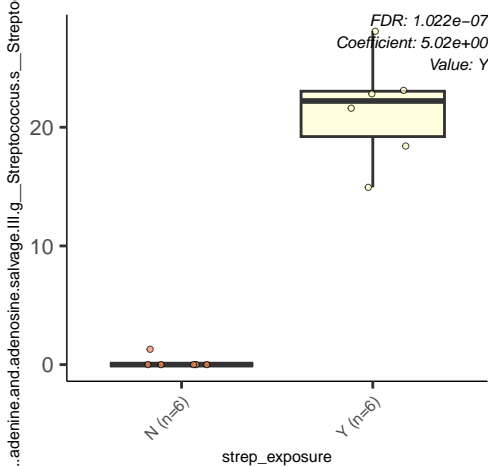


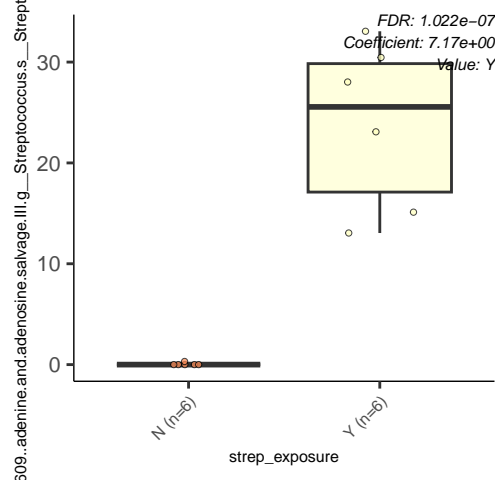


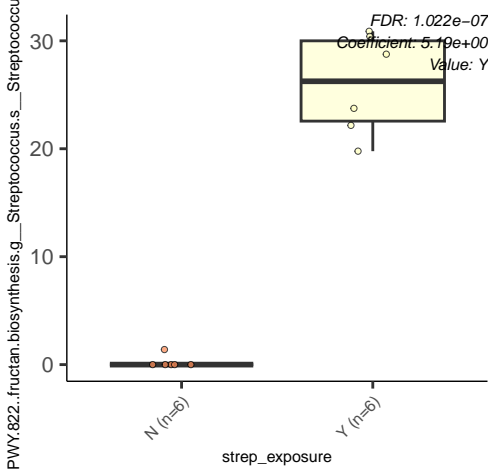


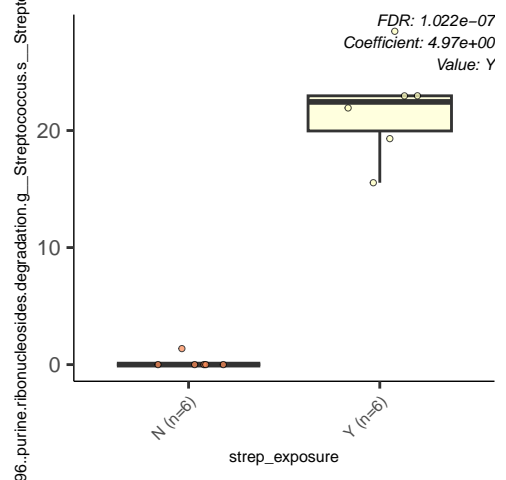




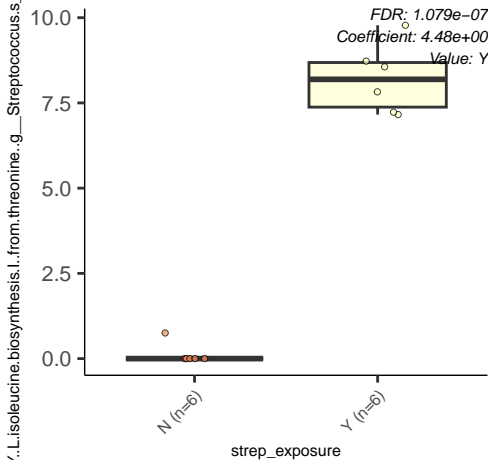




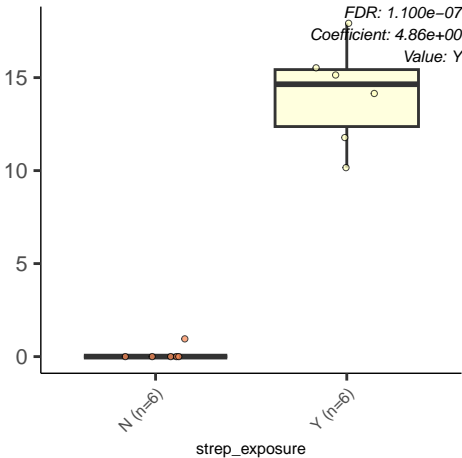


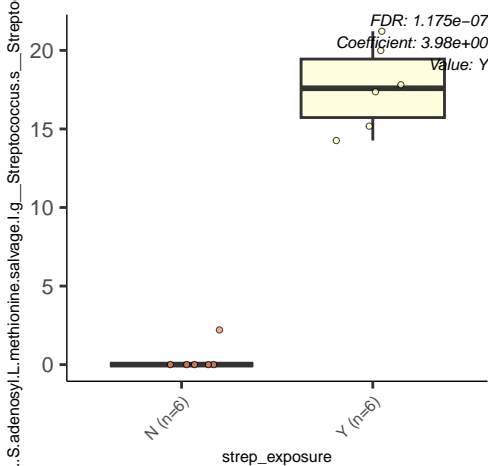


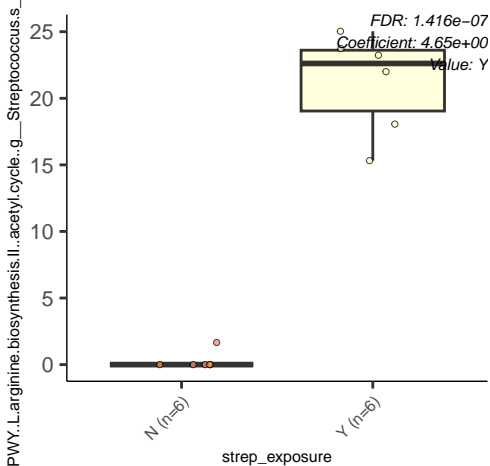




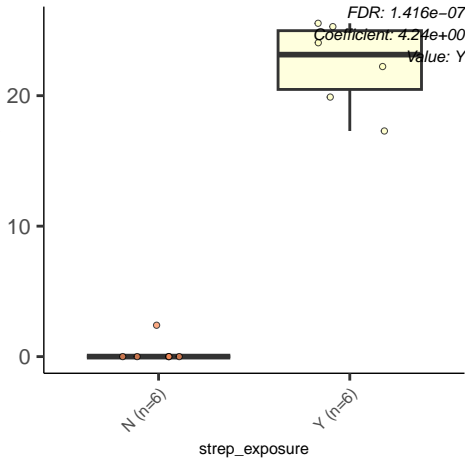
PWY.822...fructan.biosynthesis.g\_\_Streptococcus.s\_\_Streptococcus

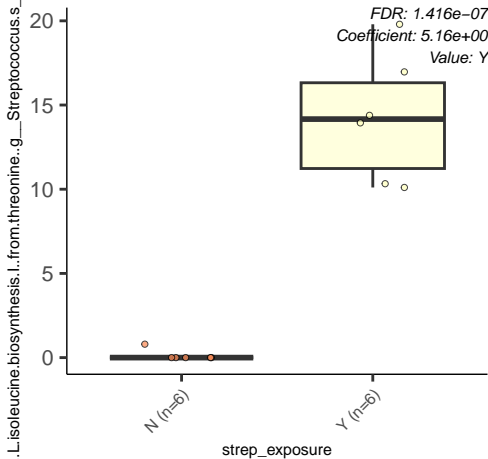


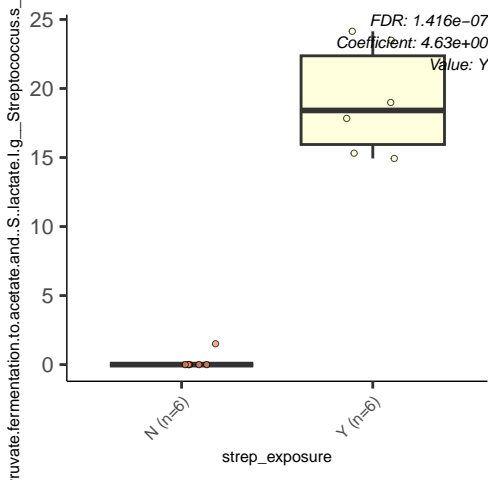


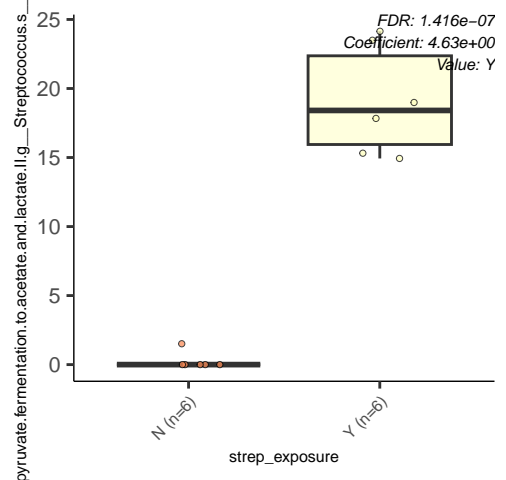


YN.PWY..dTDP..beta..L.rhamnose.biosynthesis.g\_\_Streptococcus.s

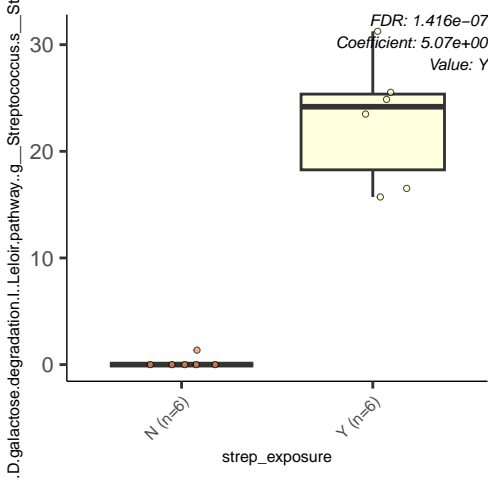




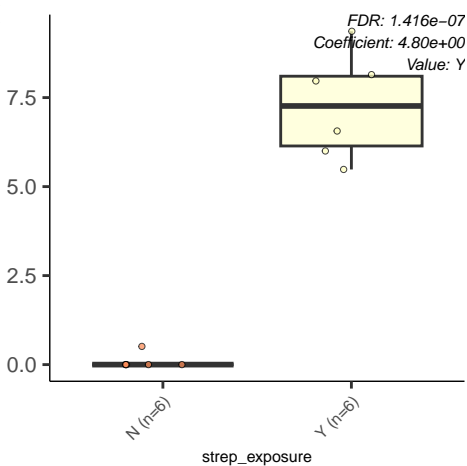




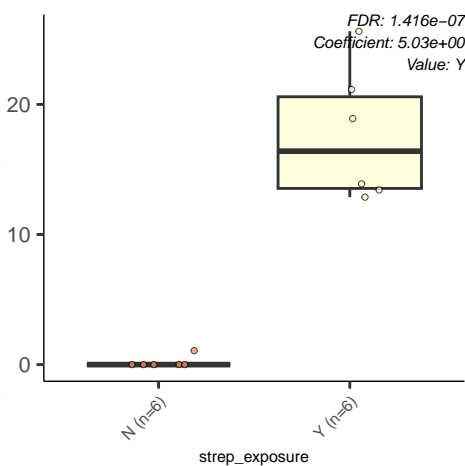




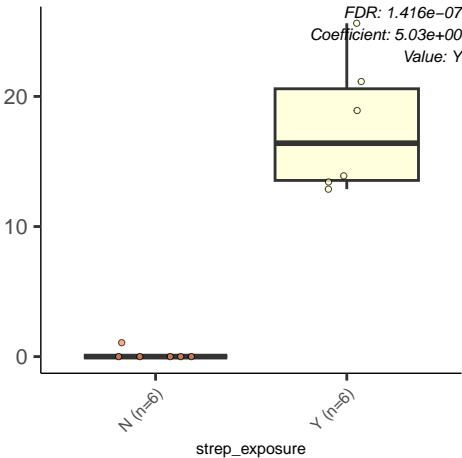
oyl.pentapeptide.biosynthesis.l..meso.diaminopimelate.containing.g

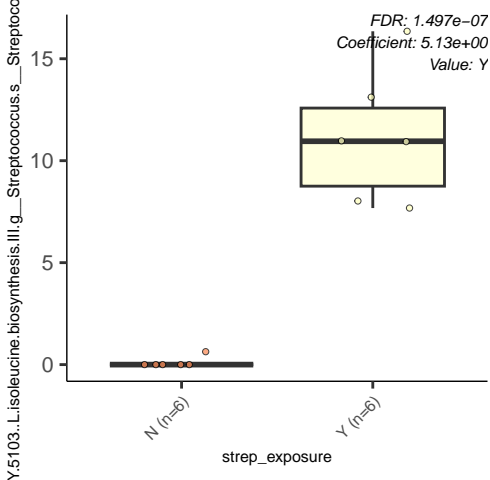


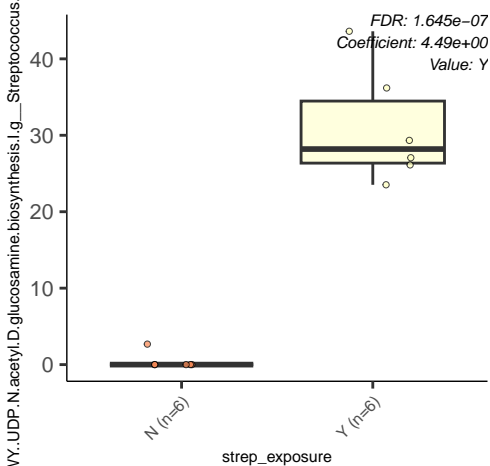
phosphatidylglycerol.biosynthesis.l.plastidic..g\_\_Streptococcus.s\_\_S

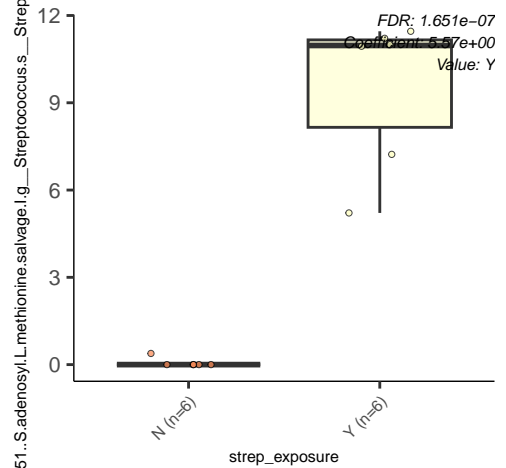


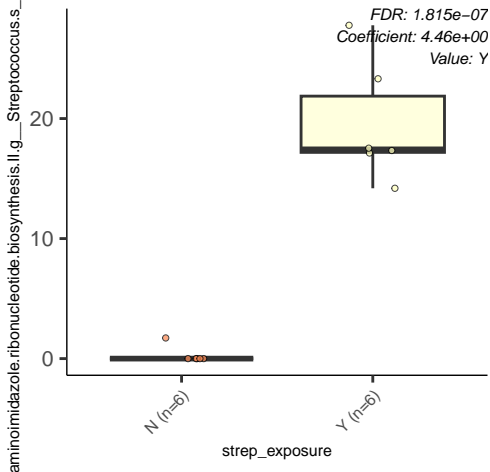
sphatidylglycerol.biosynthesis.11..non.plasticidic..g\_\_Streptococcus.s





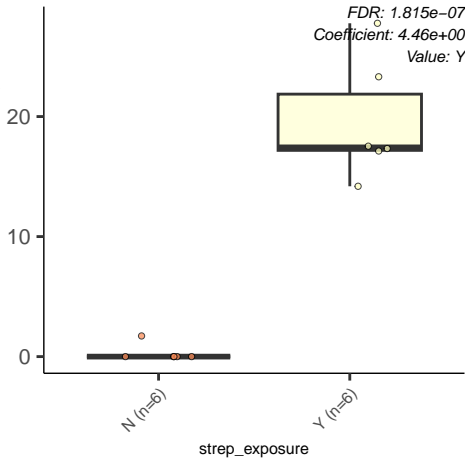




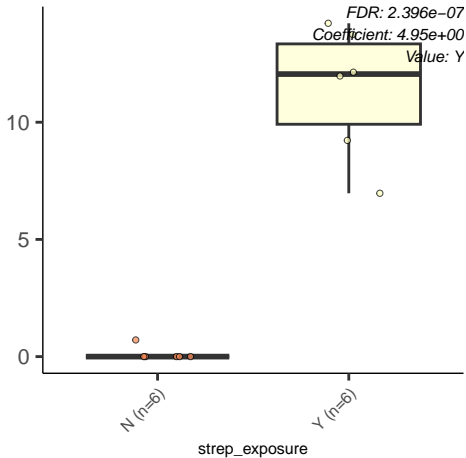


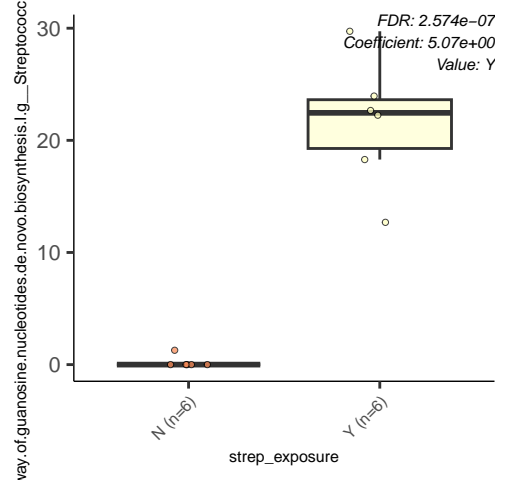


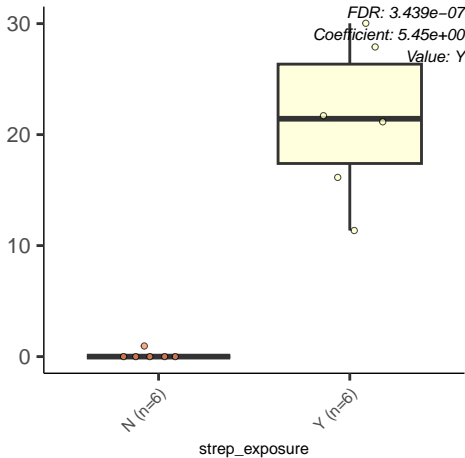
pathway.of.5.aminoimidazole.ribonucleotide.biosynthesis.g\_\_Streptococcus



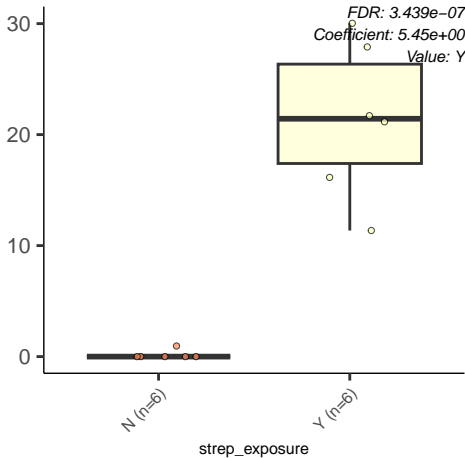
JB.PWY..L.arginine.biosynthesis.II..acetyl.cycle..g\_\_Streptococcus.s



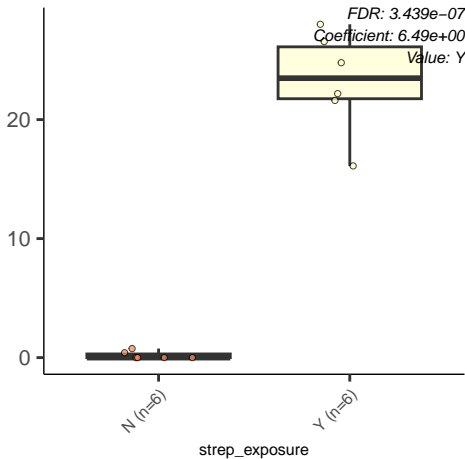


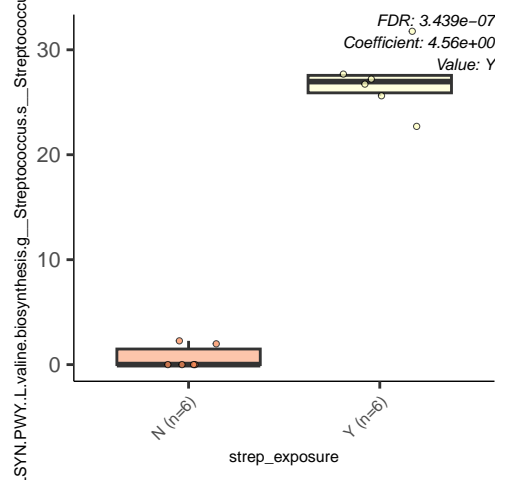


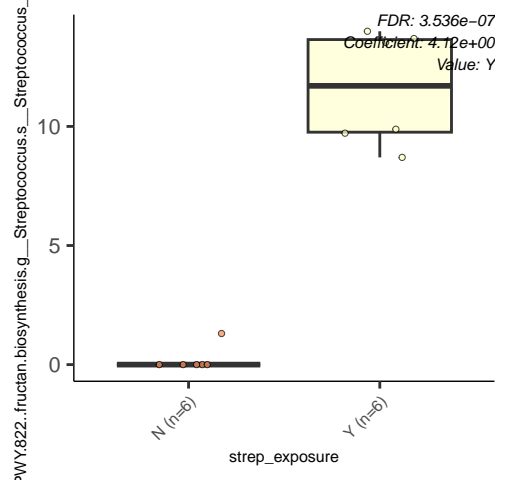
ine.deoxyribonucleotides.de.novo.biosynthesis.ll.g\_\_Streptococcus.s



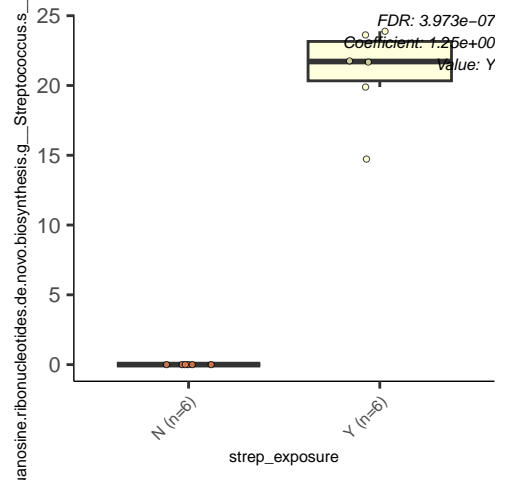
WY..superpathway.of.L.threonine.biosynthesis.g\_\_Streptococcus.s

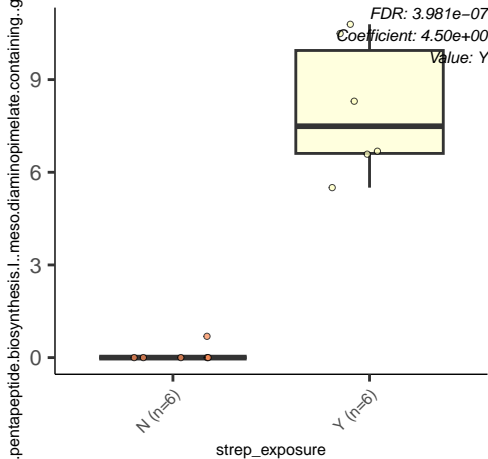


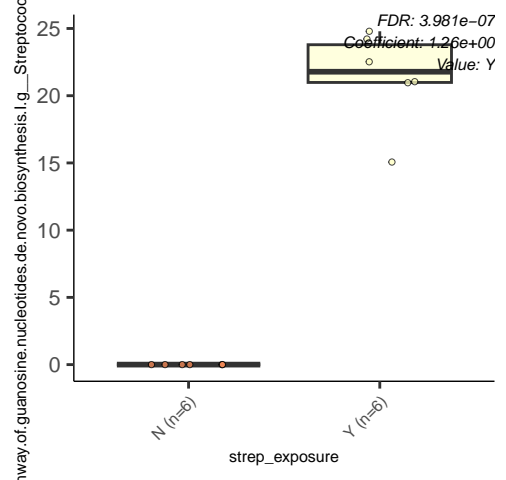


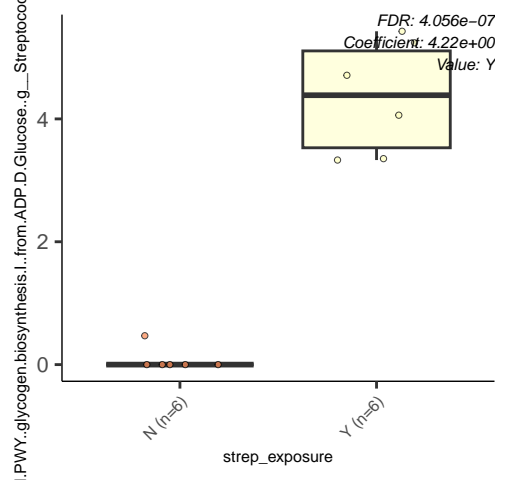


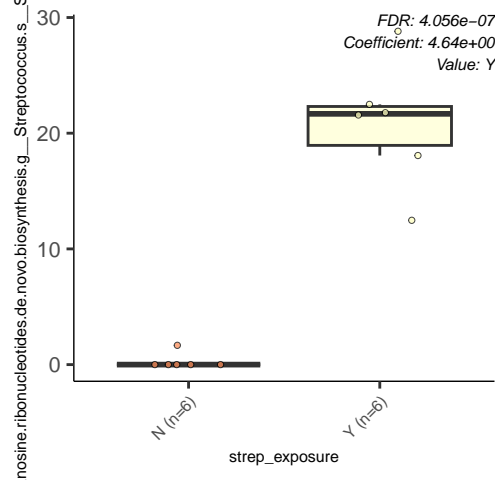


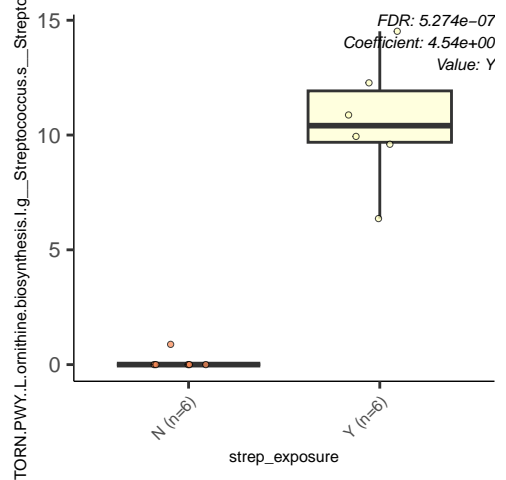


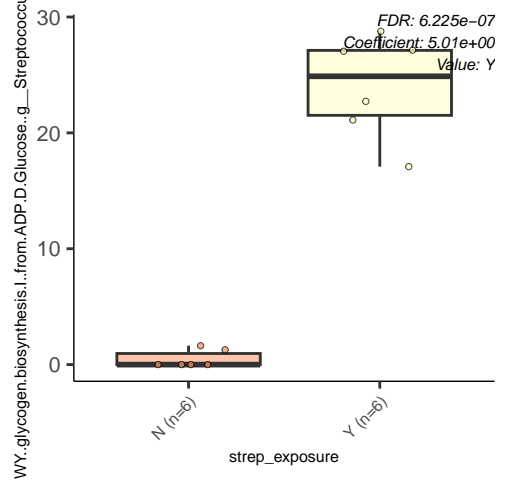


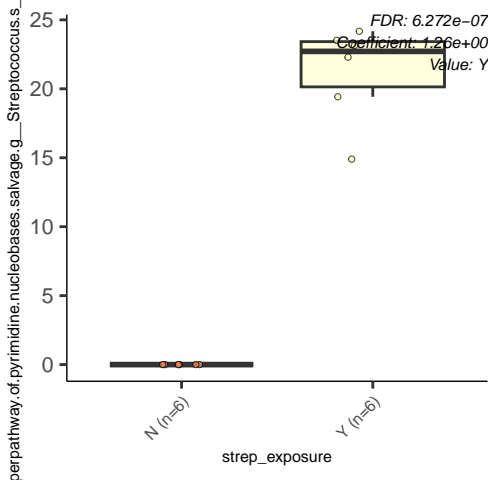




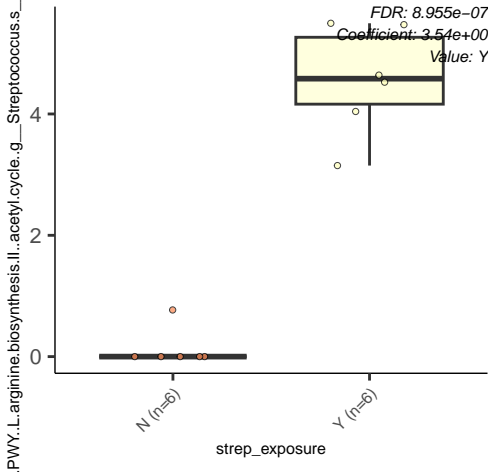












667..CDP.diacylglycerol.biosynthesis.l.g\_\_Streptococcus.s\_\_Strept

FDR:  $8.955e-07$   
Coefficient:  $4.98e+00$   
Value: Y

10

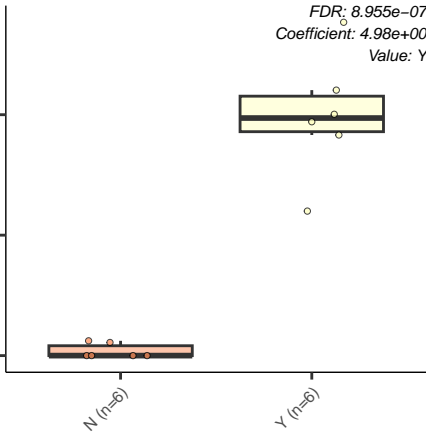
5

0

N (n=6)

Y (n=6)

strep\_exposure



319..CDP..diacylglycerol.biosynthesis.II.g\_\_Streptococcus.s\_\_Strep

*FDR: 8.955e-07*  
*Coefficient: 4.98e+00*  
*Value: Y*

10

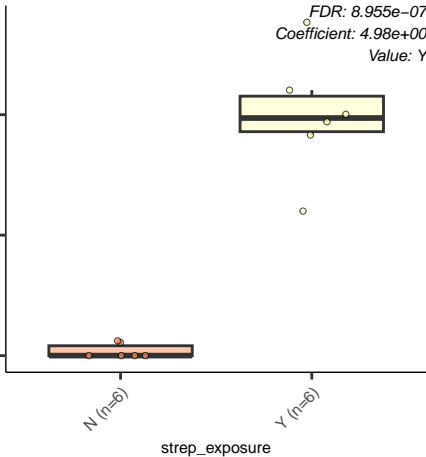
5

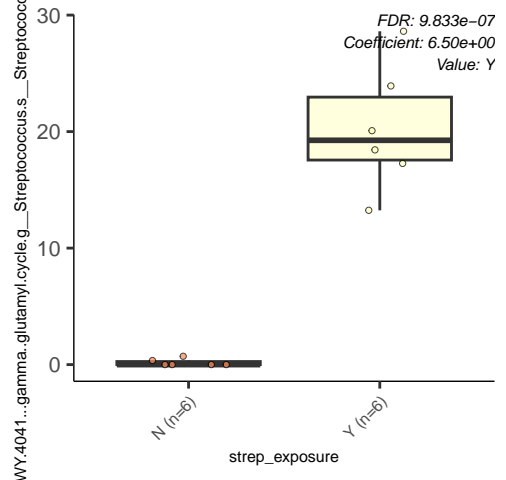
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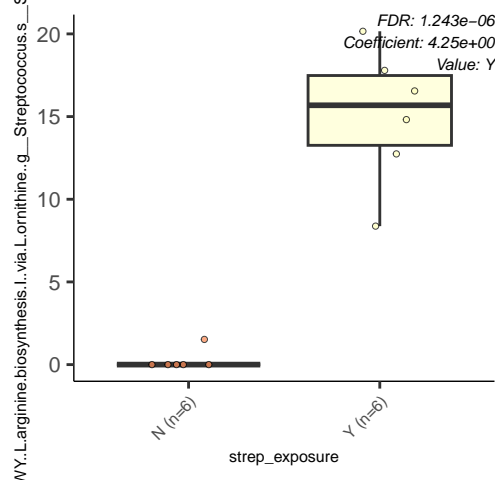
N (n=6)

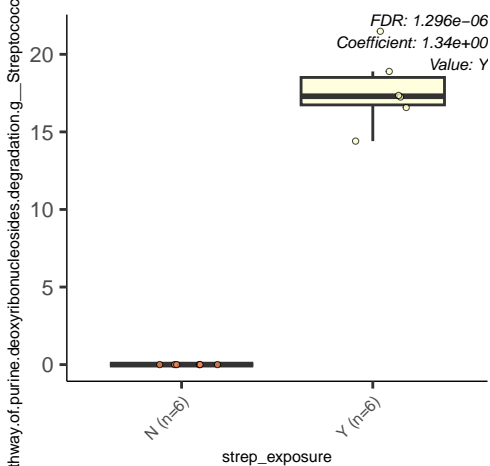
Y (n=6)

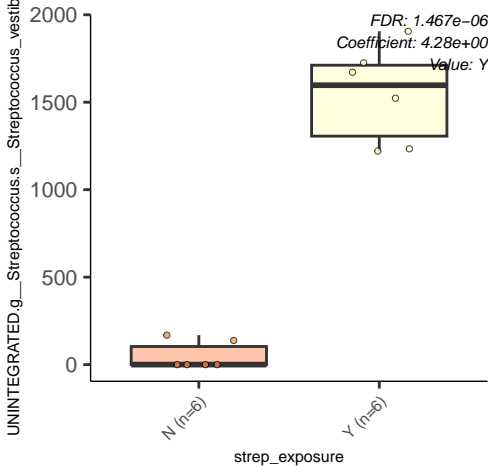
strep\_exposure

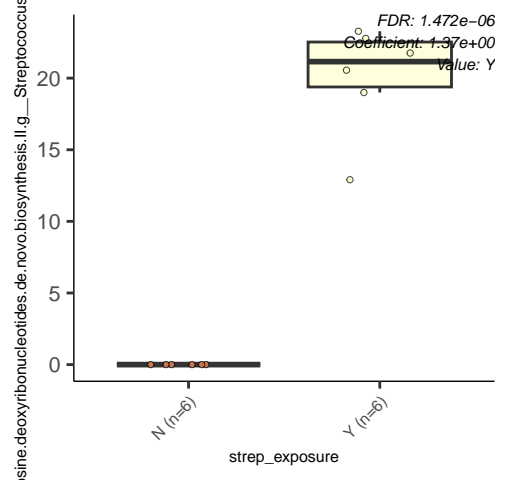






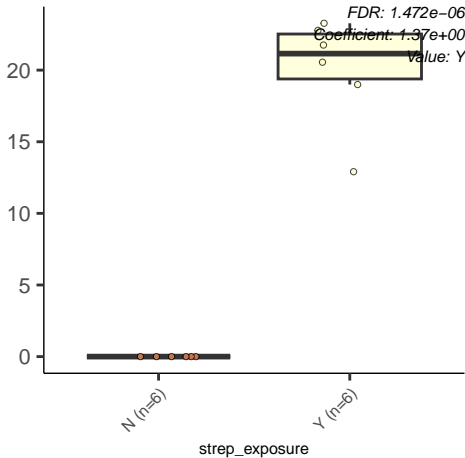


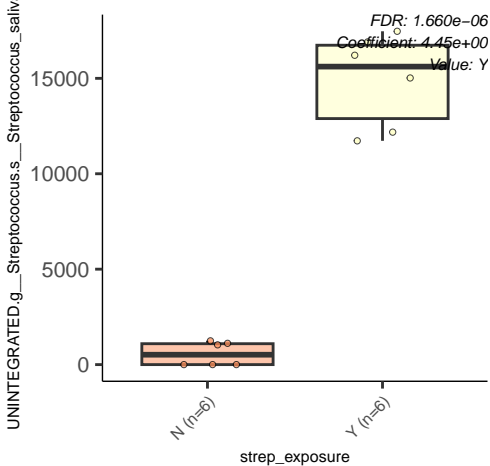


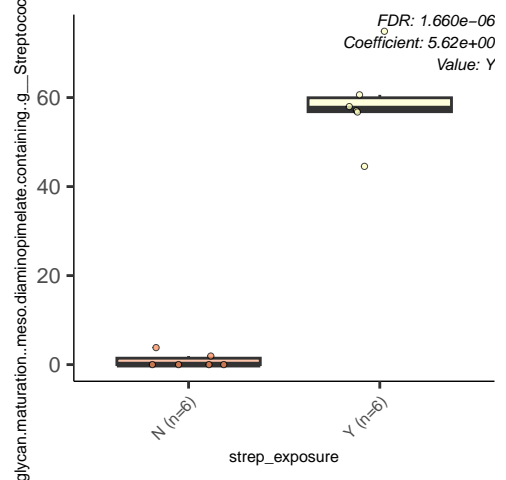


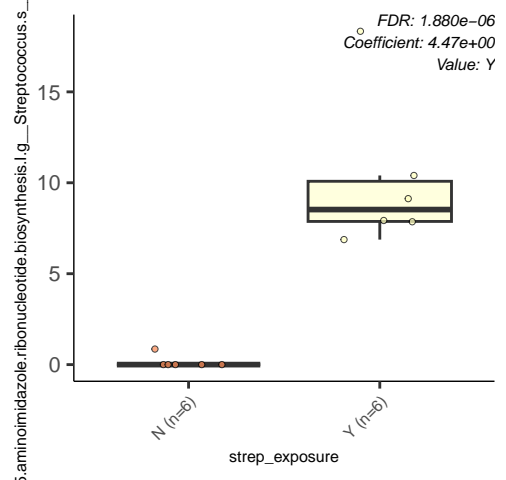


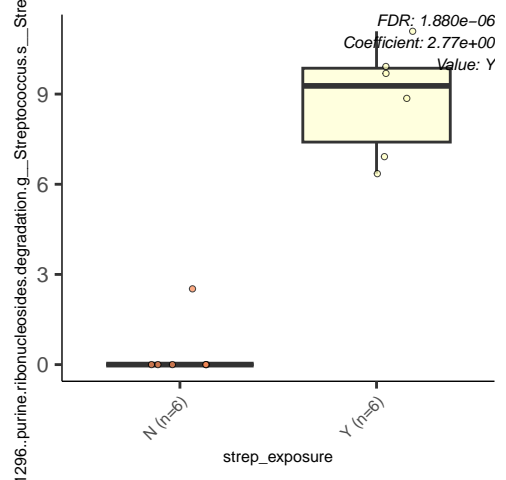
isine.deoxyribonucleotides.de.novo.biosynthesis.II.g\_\_Streptococcus



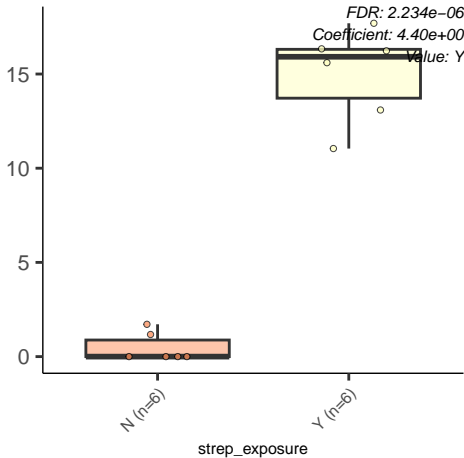


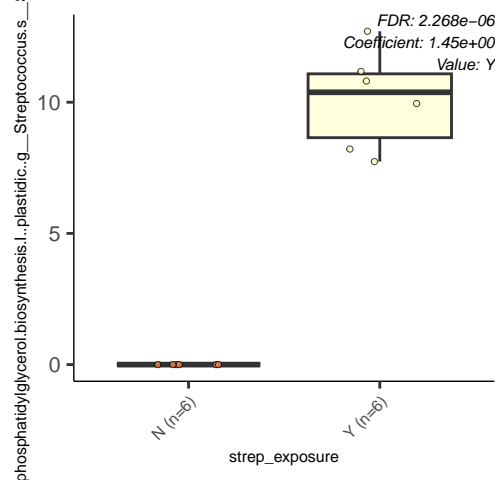




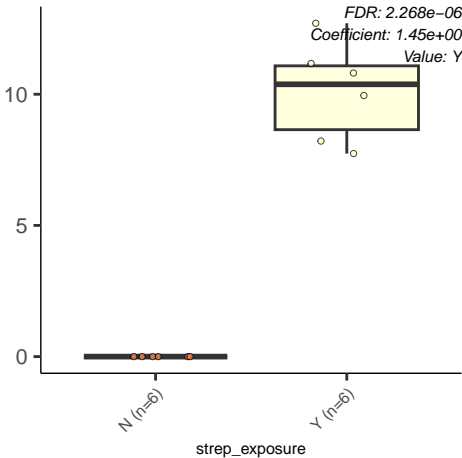


L.pentapeptide.biosynthesis.l...meso.diaminopimelate.containing..g

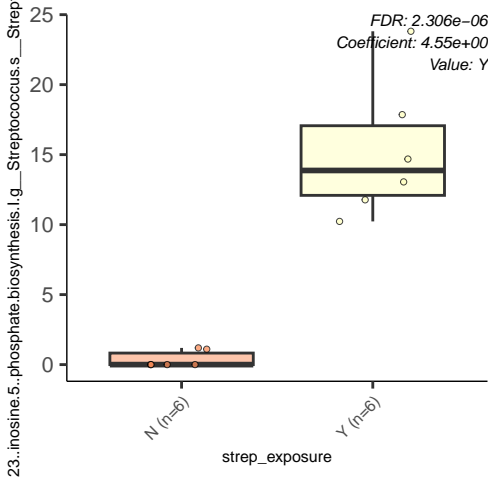




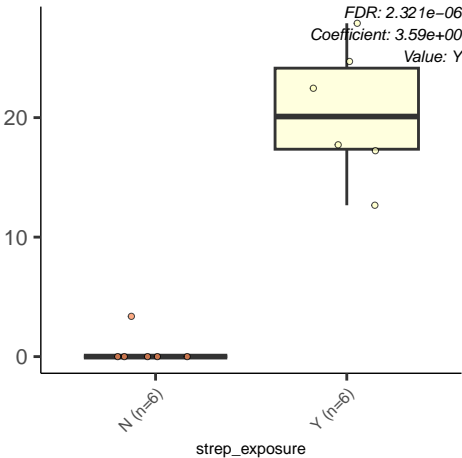
phosphatidylglycerol.biosynthesis.II...non.plastidic..g\_\_Streptococcus.s

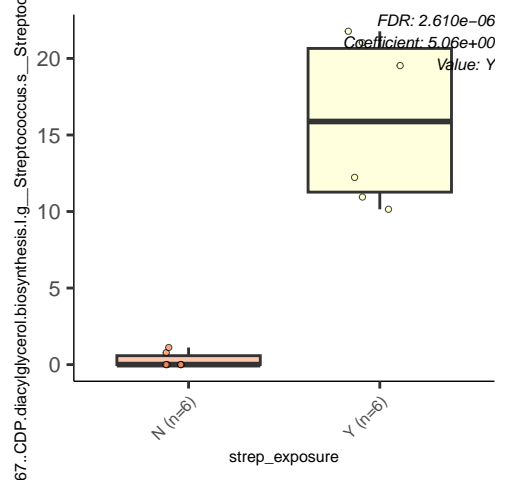


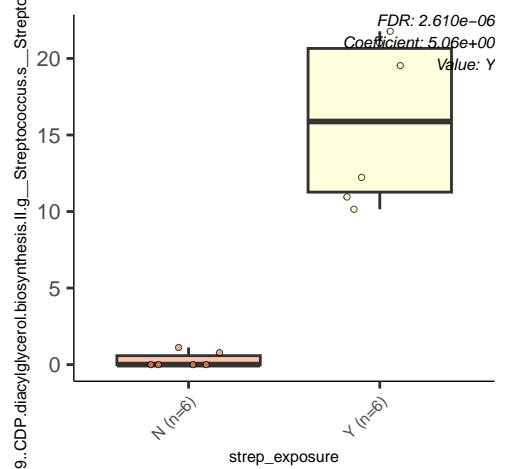


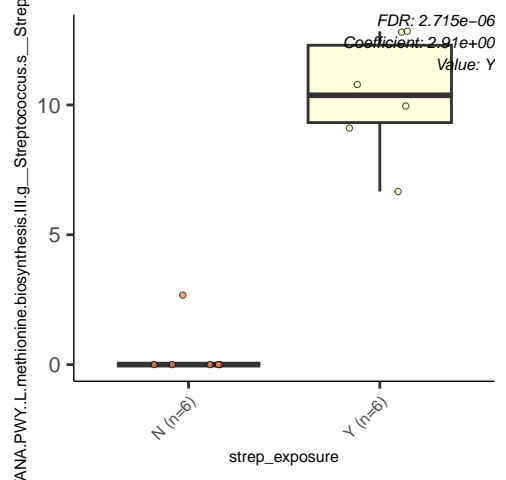


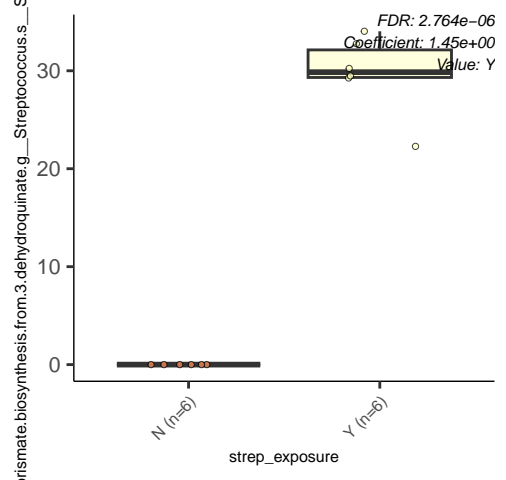
341..folate.transformations.II..plants..g\_\_Streptococcus

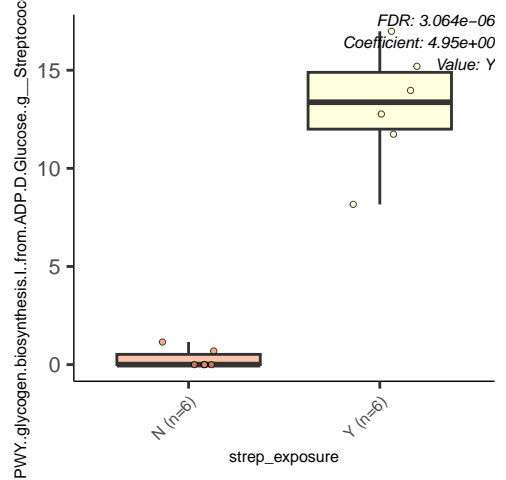


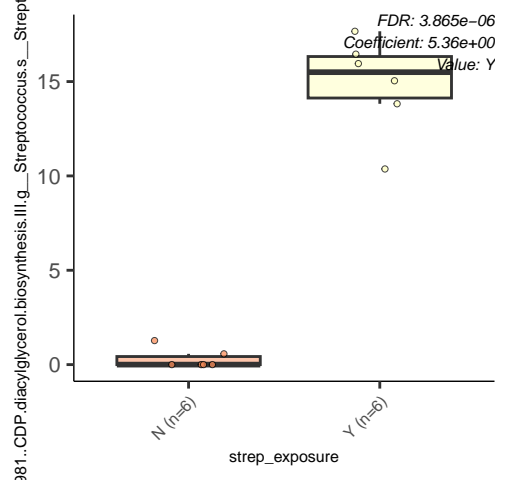






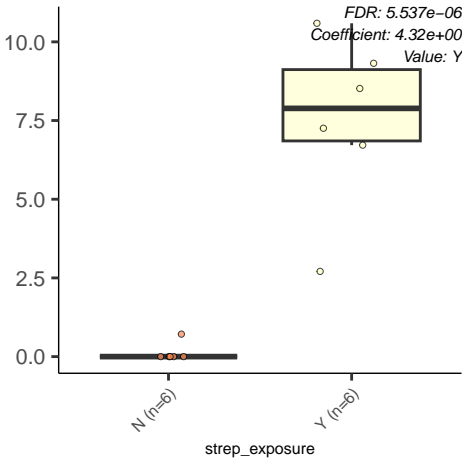


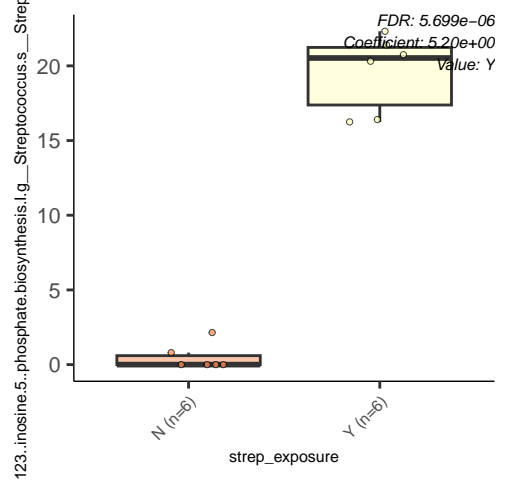


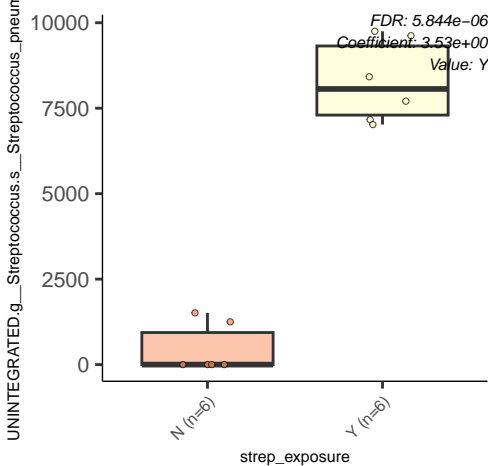


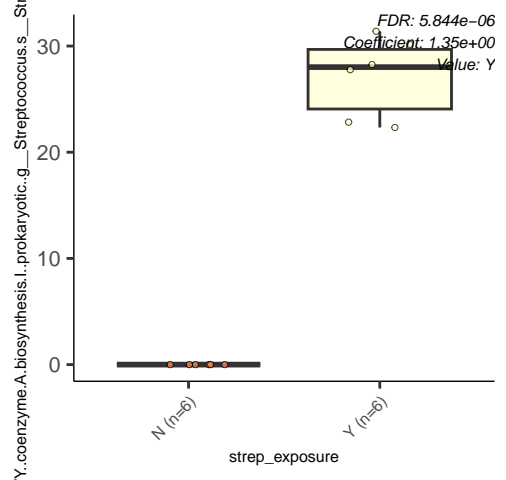


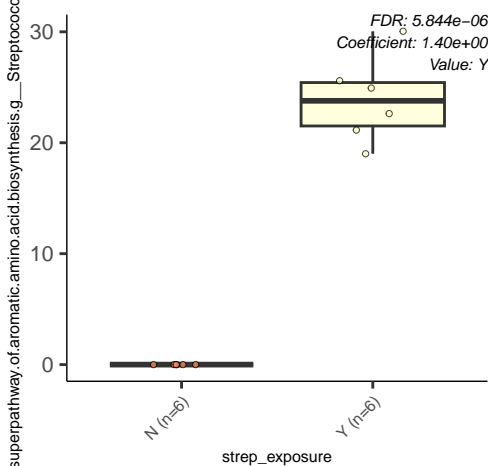
WY.702..L.methionine.biosynthesis.II.g\_\_Streptococcus

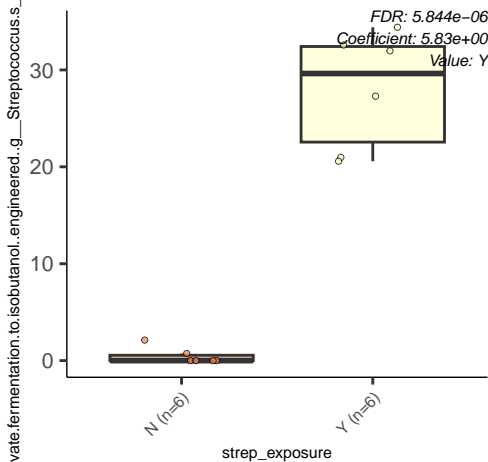












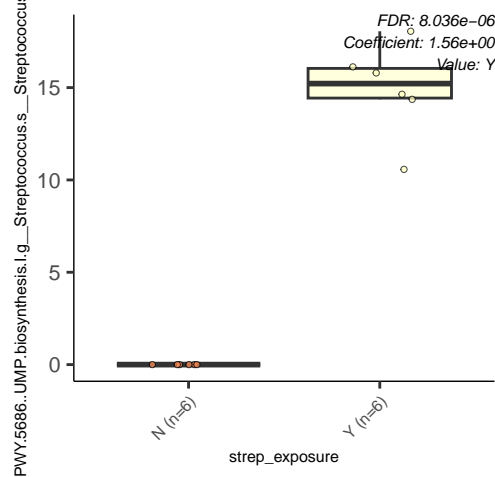
PWY.5686..UMP.biosynthesis.l.g\_\_Streptococcus.s\_\_Streptococcus

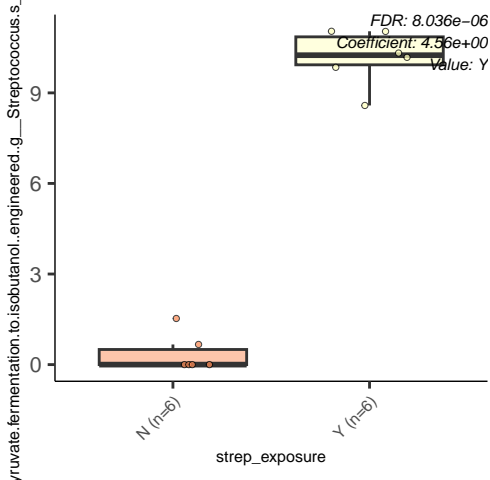
N (n=6)

Y (n=6)

strep\_exposure

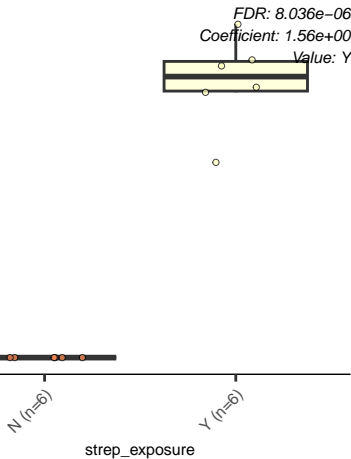
FDR:  $8.036e-06$   
Coefficient:  $1.56e+00$   
Value: Y



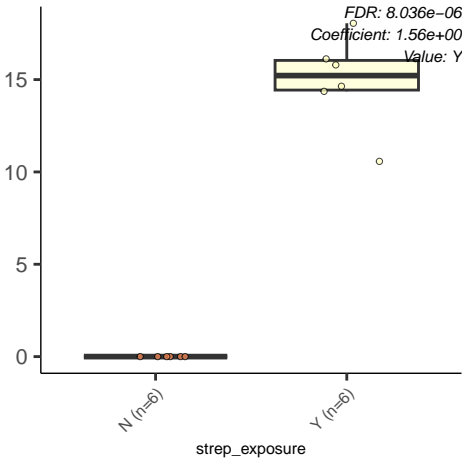


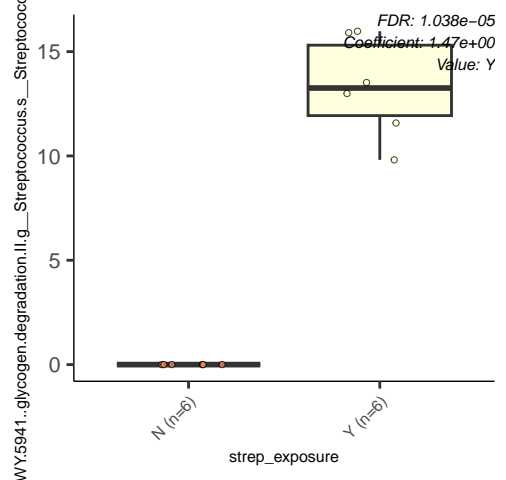


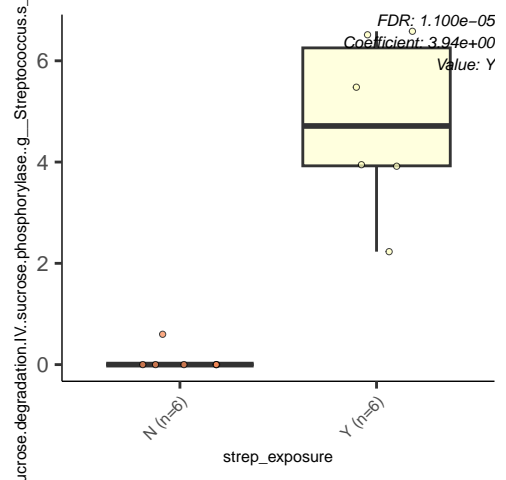
PWY.7790..UMP.biosynthesis.ll.g\_\_Streptococcus.s\_\_Streptococcus

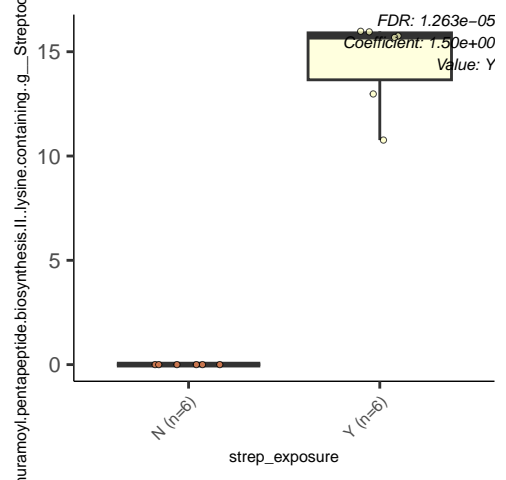


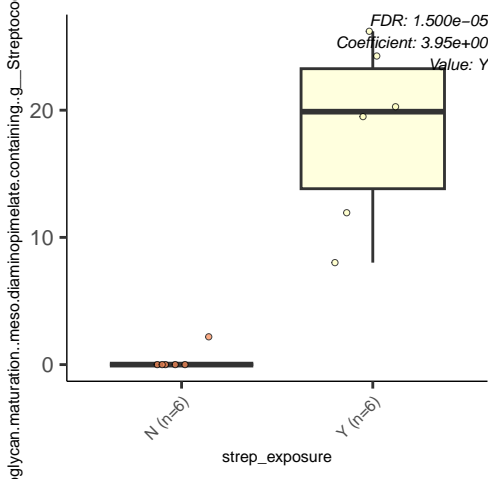
PWY.7791..UMP.biosynthesis.III.g\_\_Streptococcus.s\_\_Streptococcus

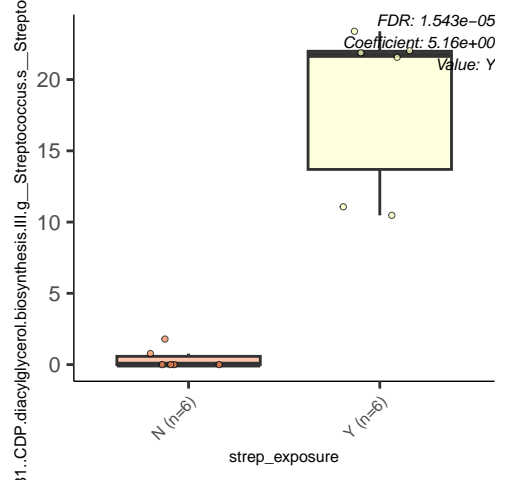


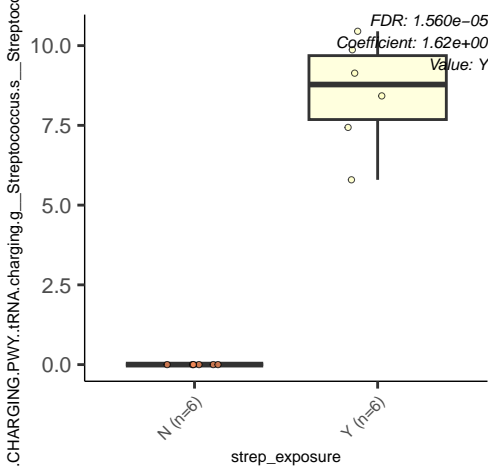




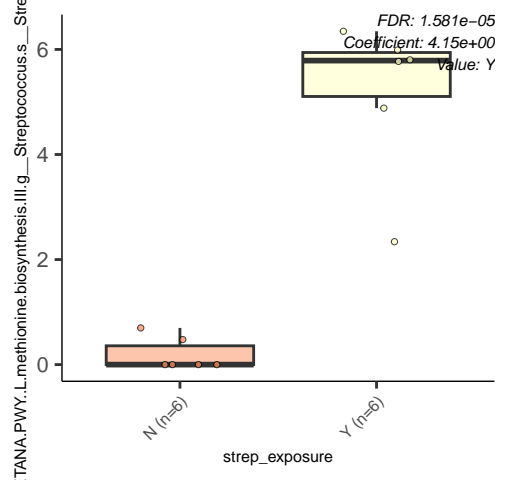




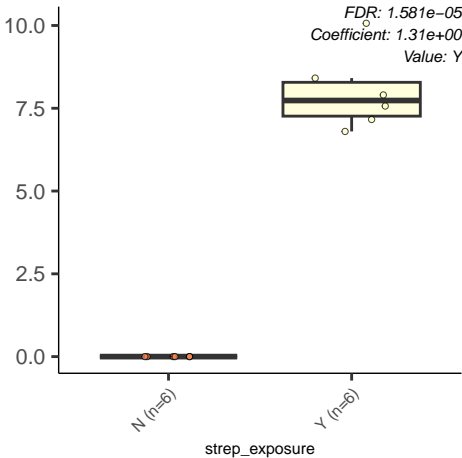




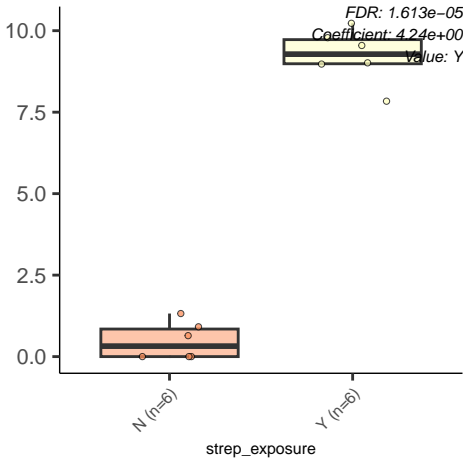




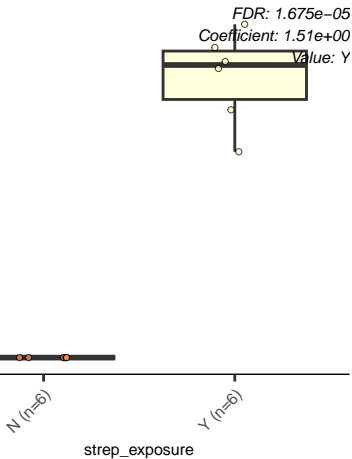
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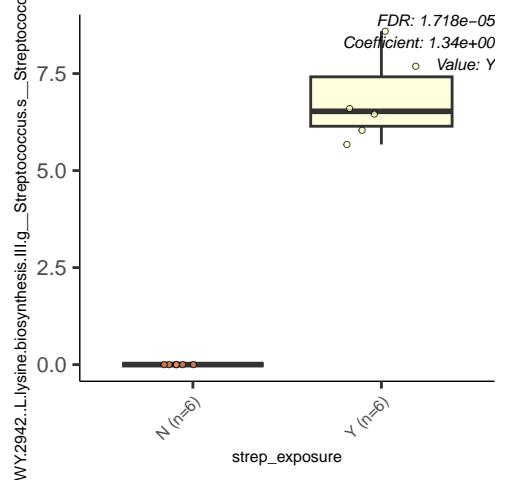


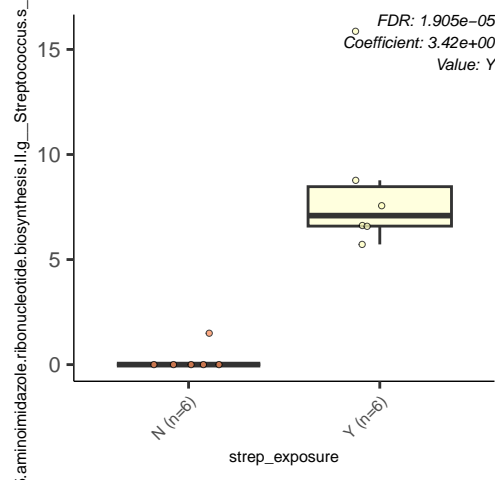
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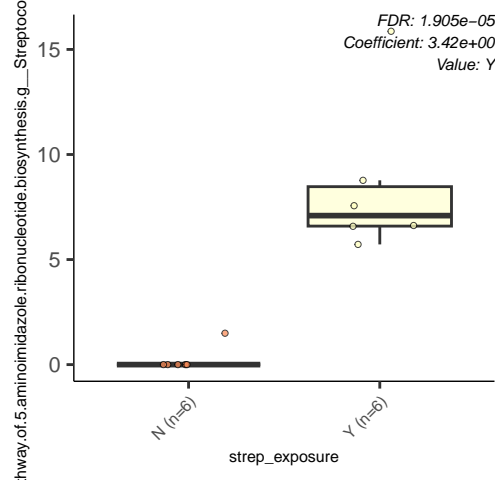


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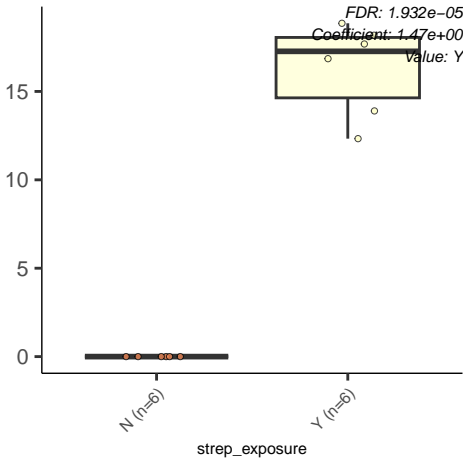






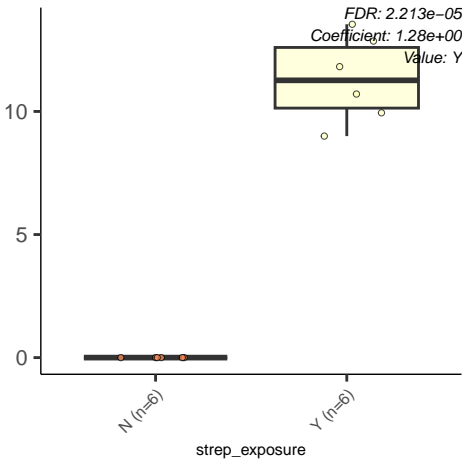


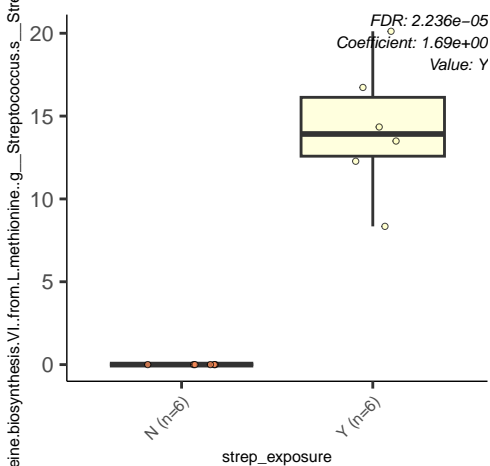
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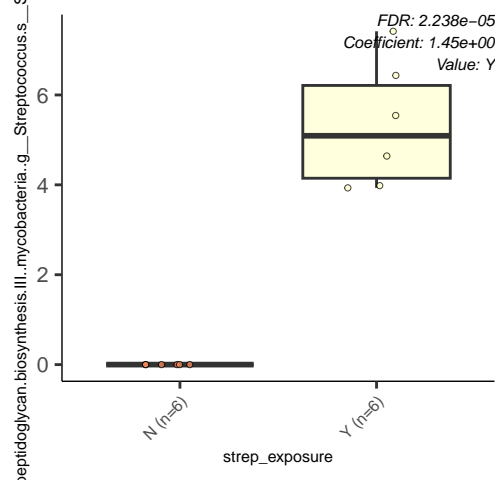


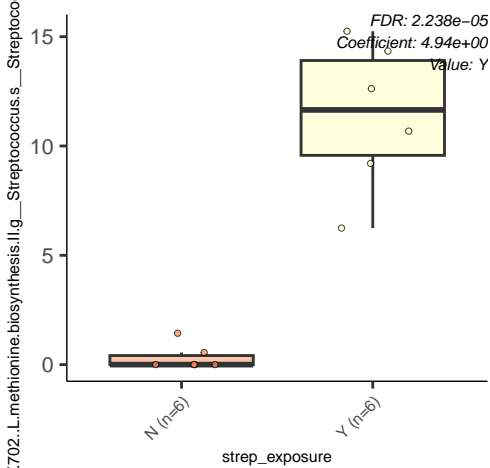


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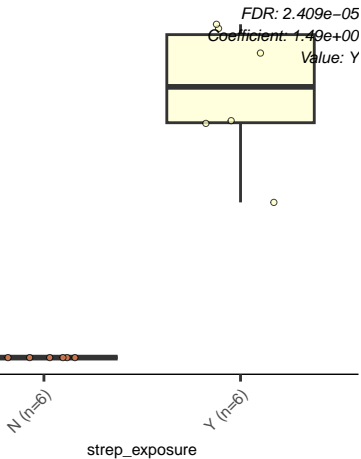


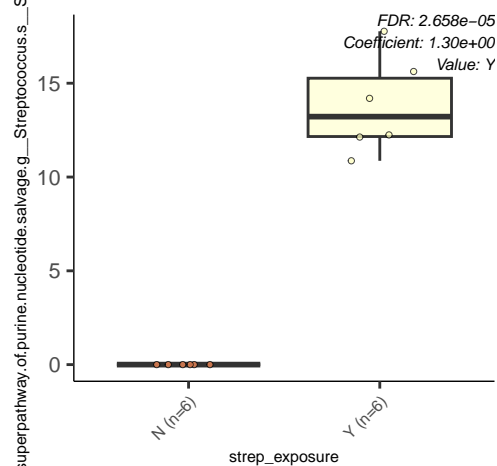


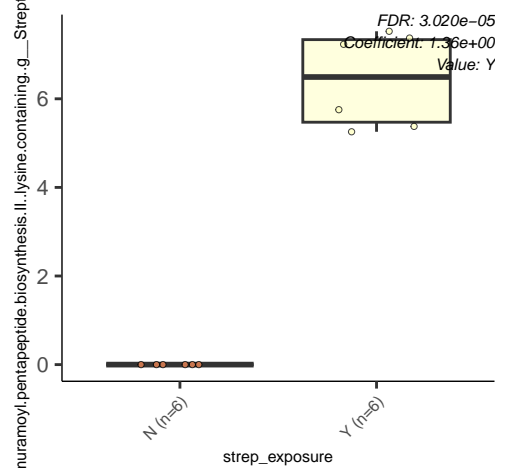


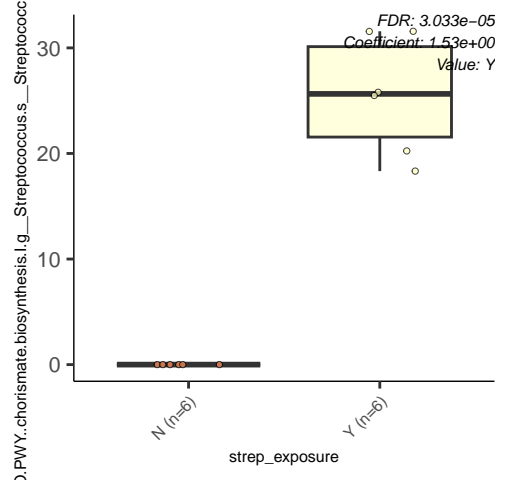


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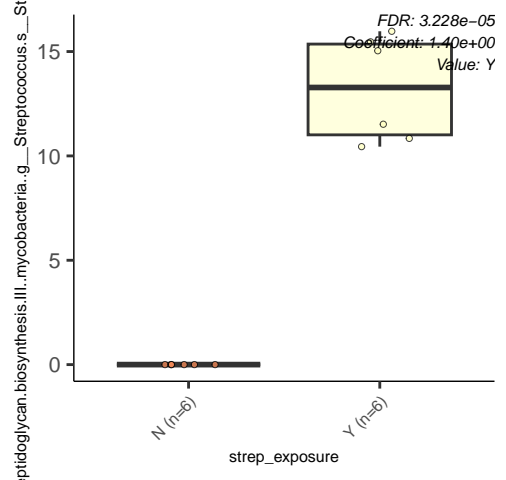


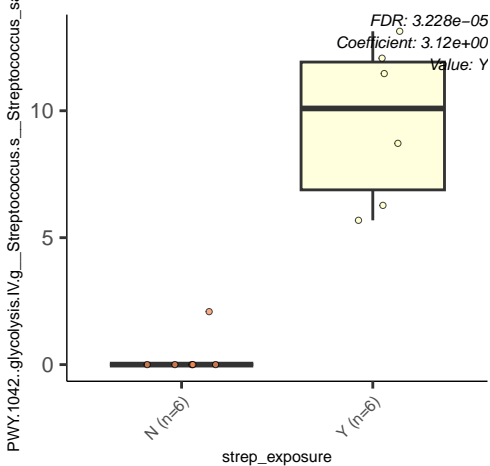


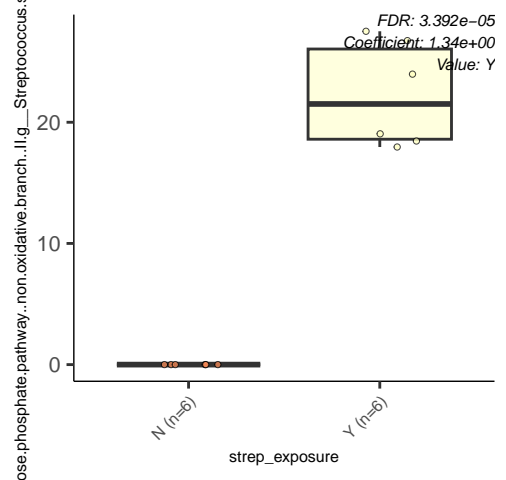


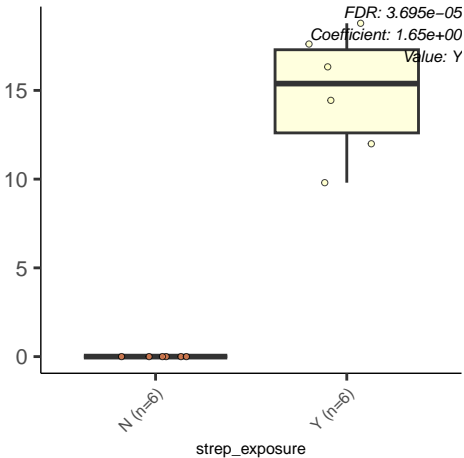




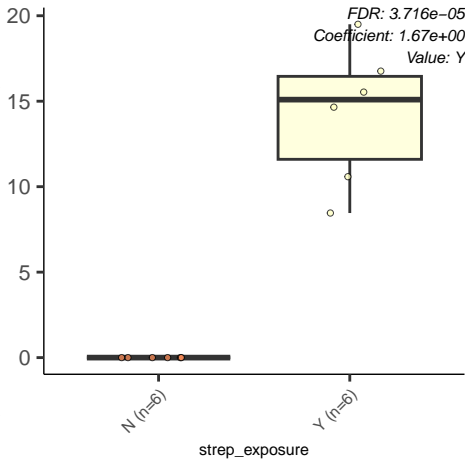


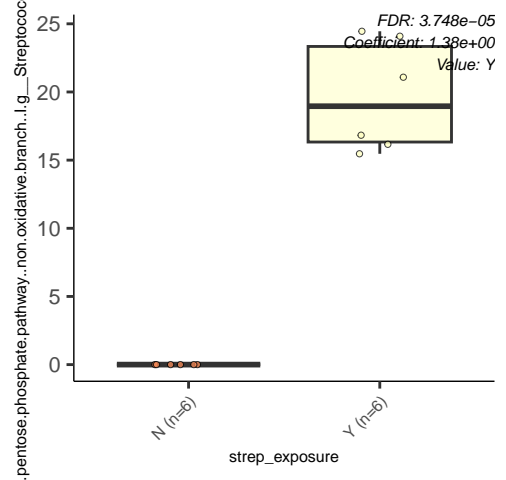


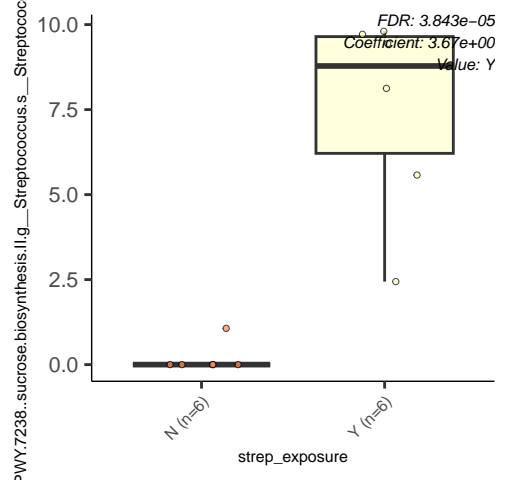




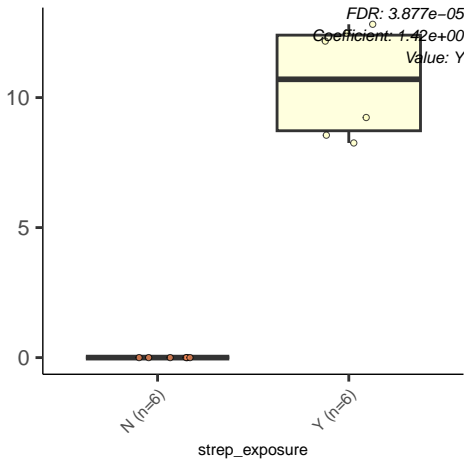
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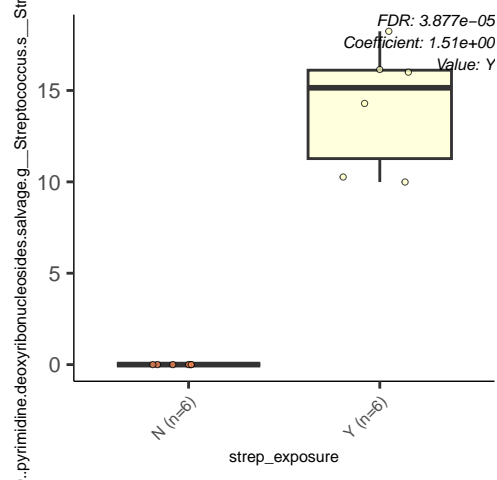




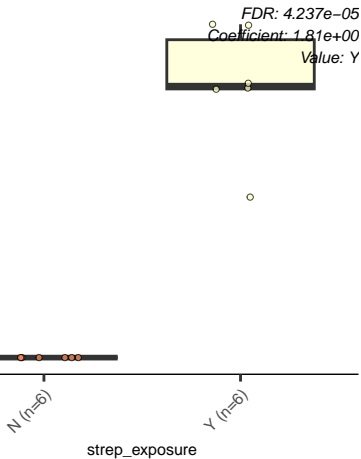
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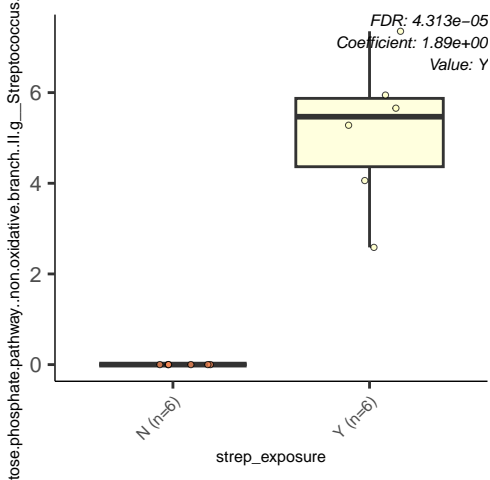


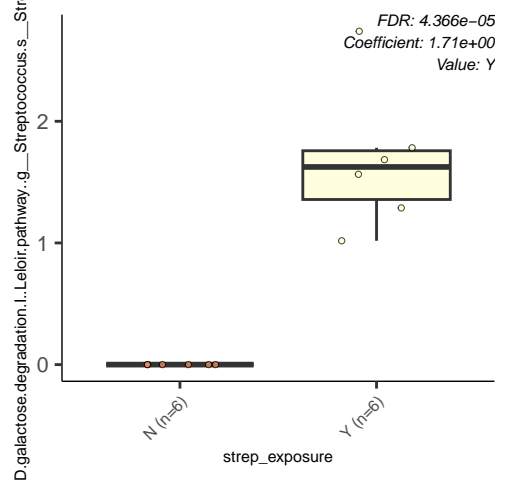


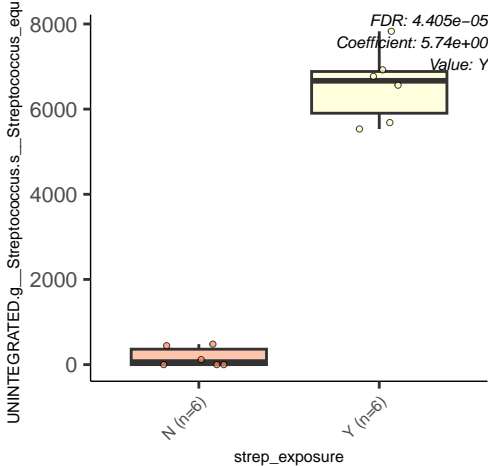


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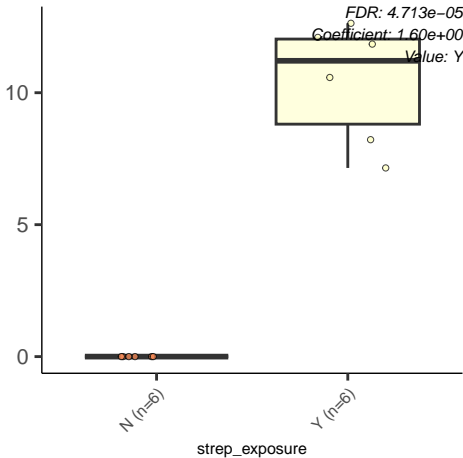


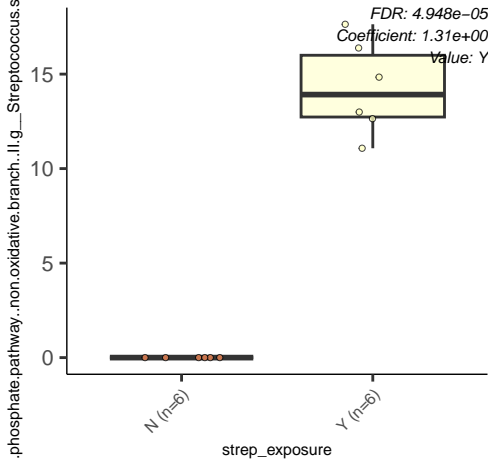




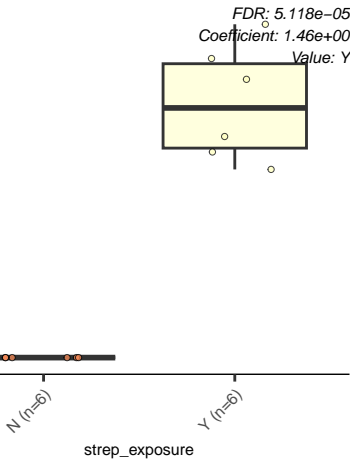


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PWY.6703..preQ0.biosynthesis.g\_\_Streptococcus.s\_\_Streptococcus





midline.deoxyribonucleotide.phosphorylation.g\_\_Streptococcus.s\_\_s

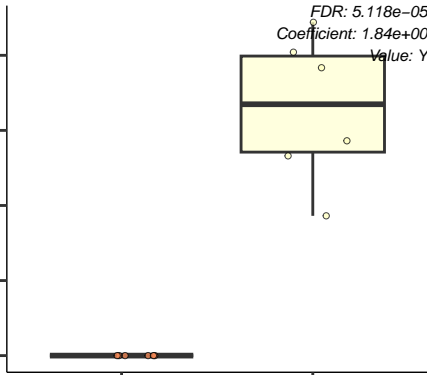
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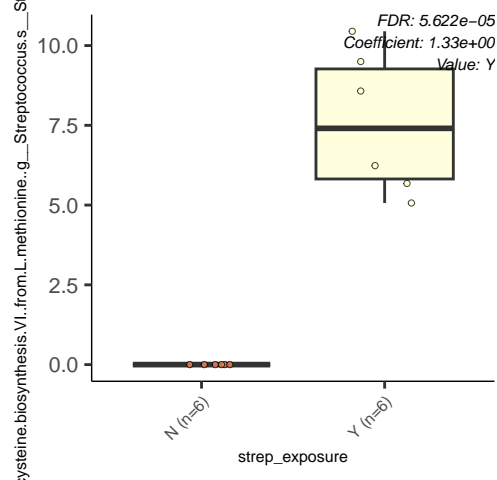
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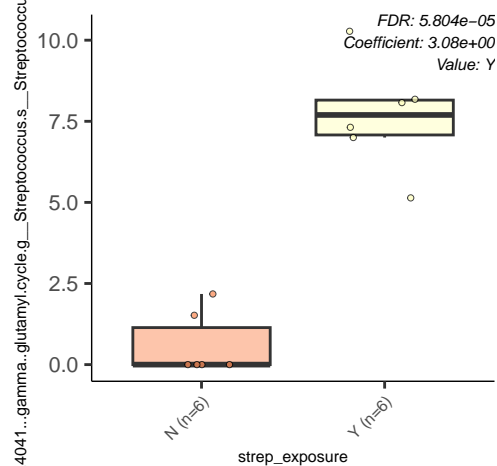
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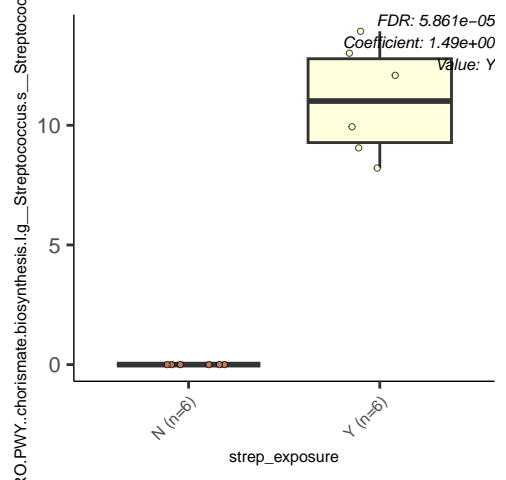
strep\_exposure

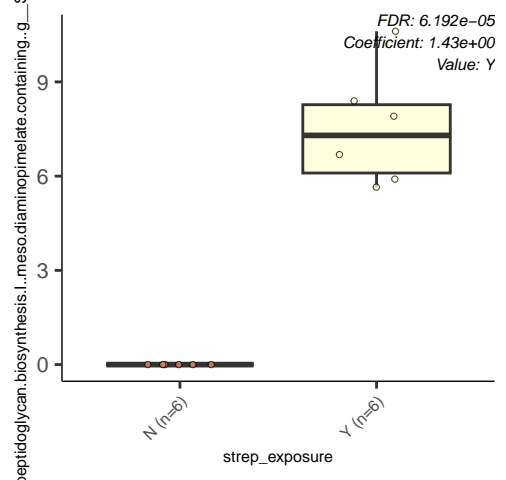
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Value: Y

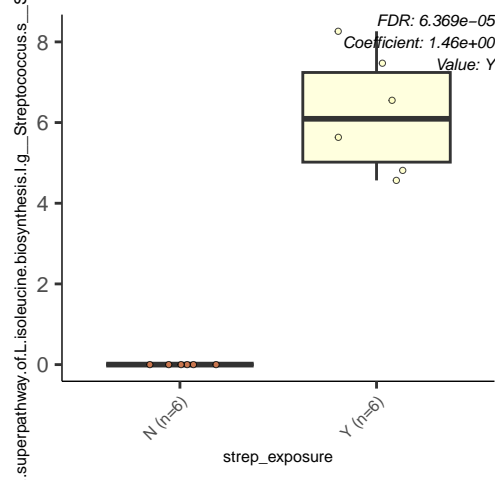


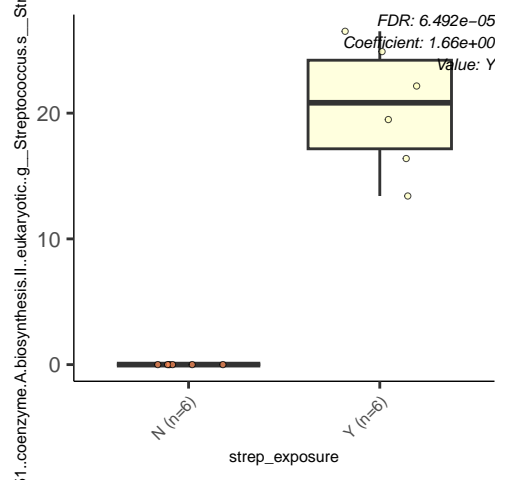


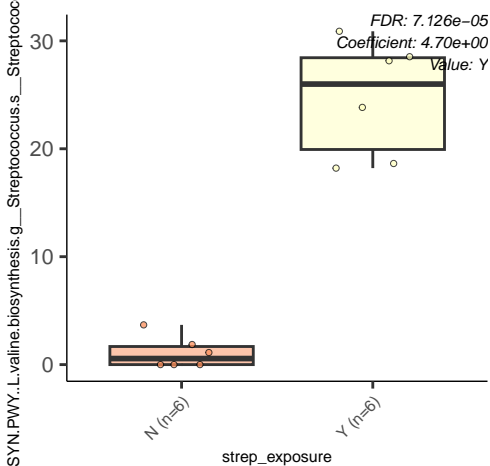






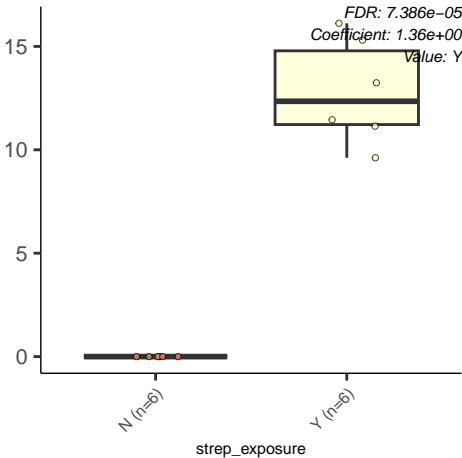


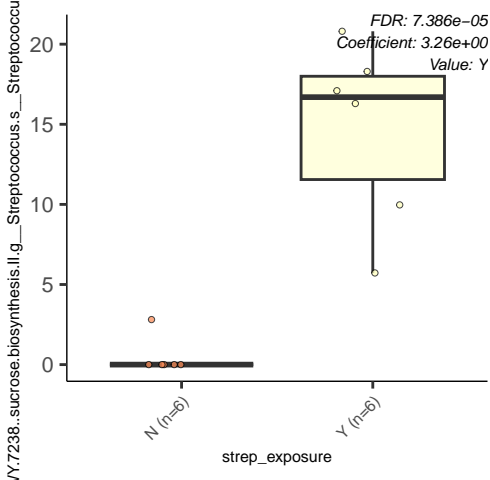


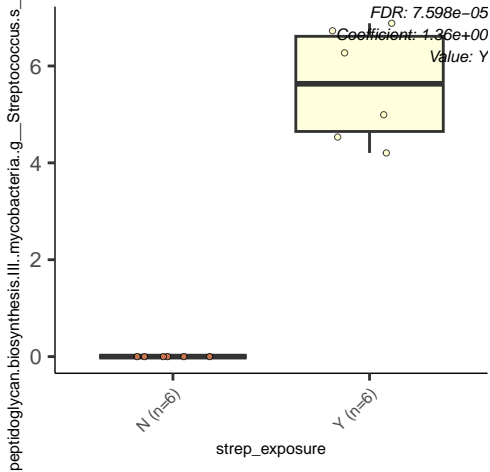


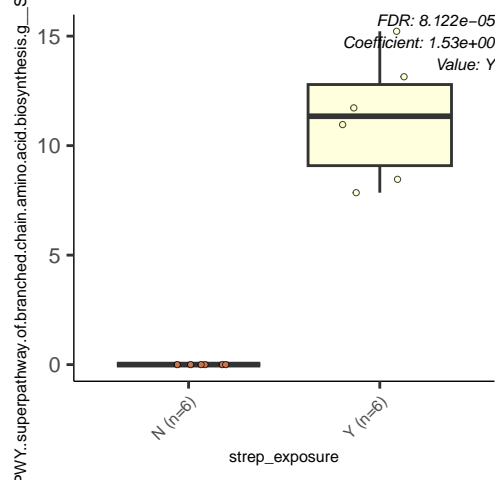


entose.phosphate.pathway..non.oxidative.branch..l.g\_\_Streptococcus

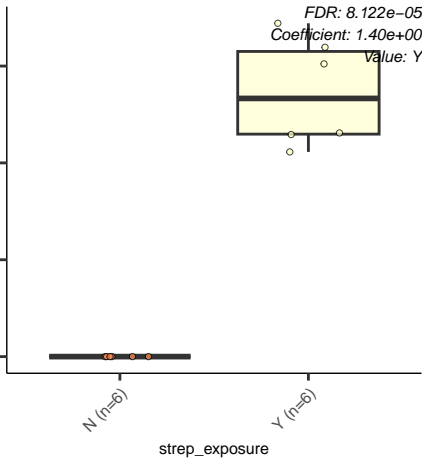


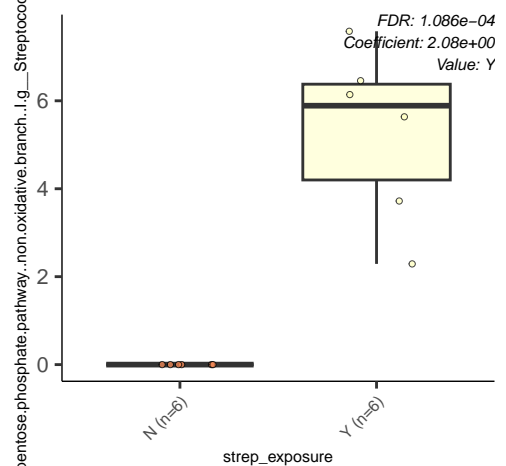


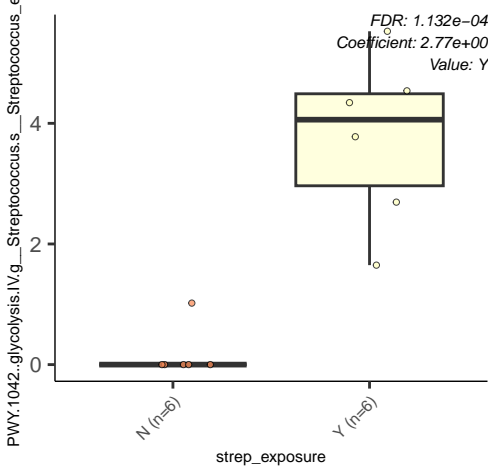


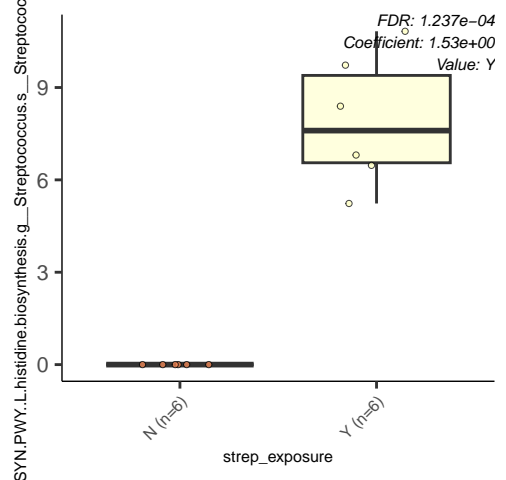


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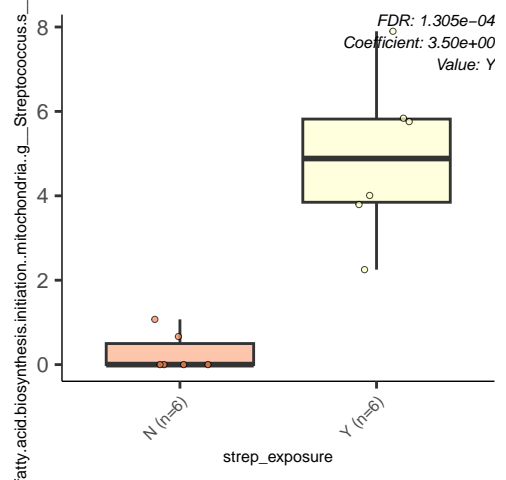


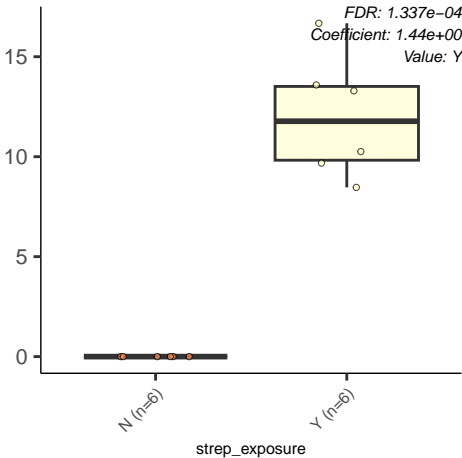


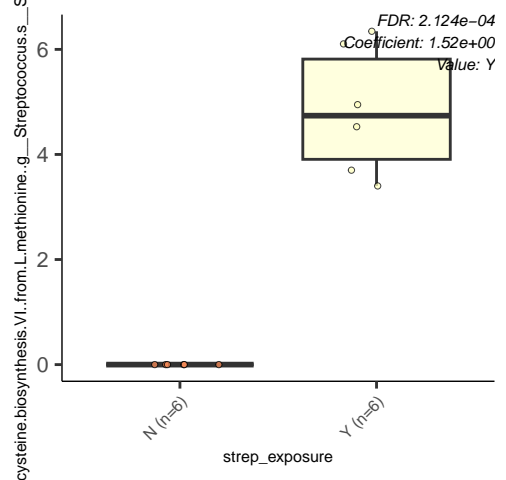


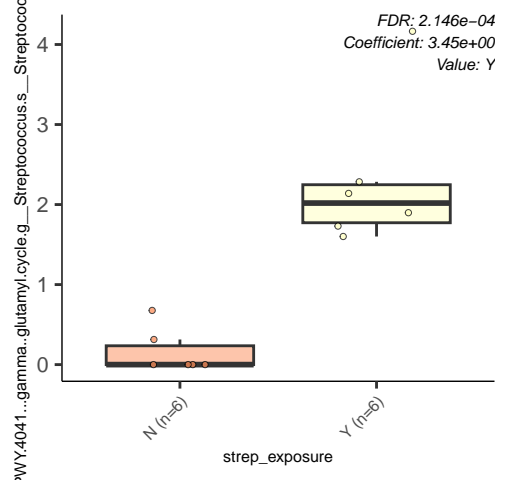


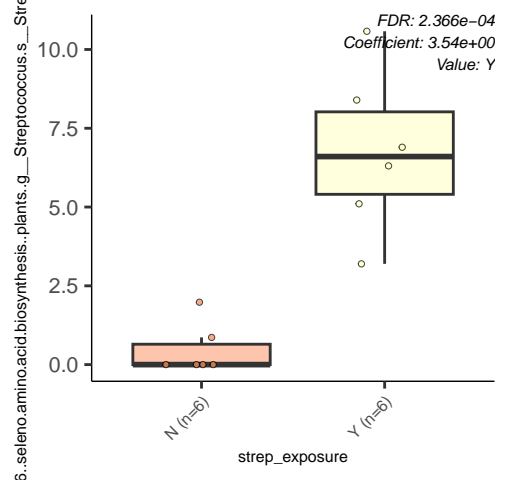


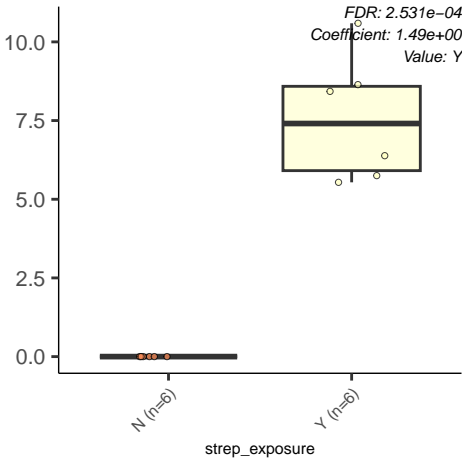


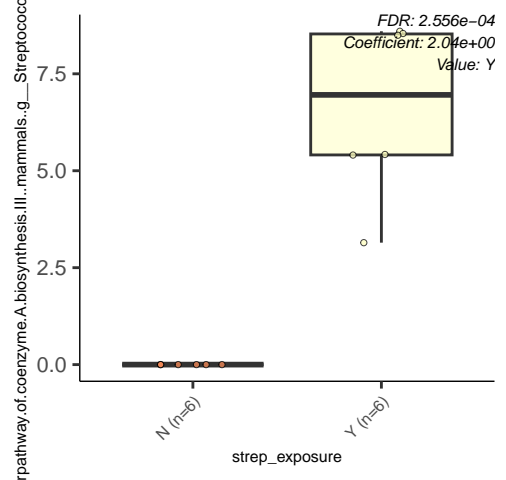


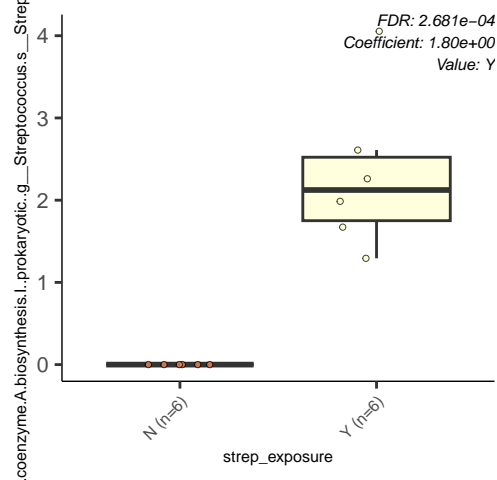




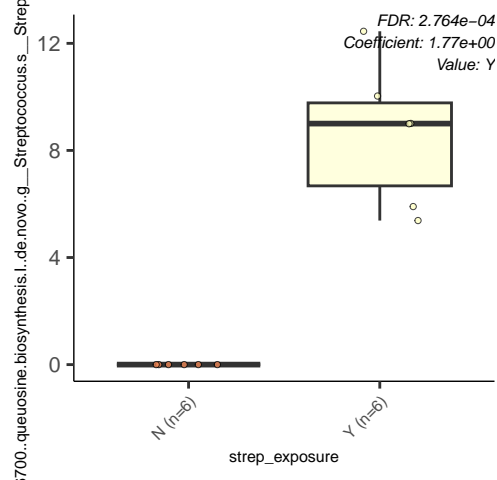


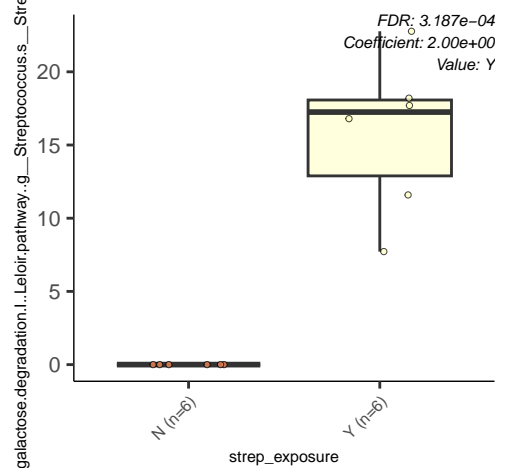


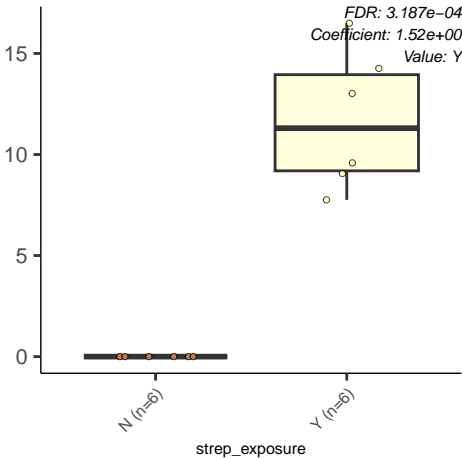


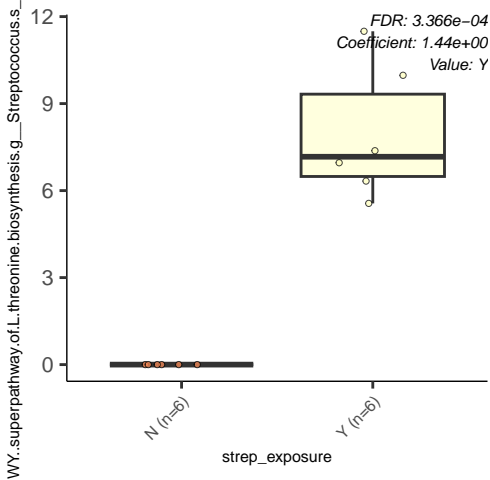


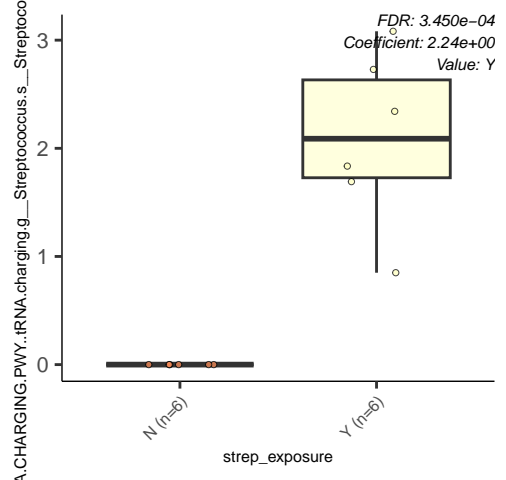


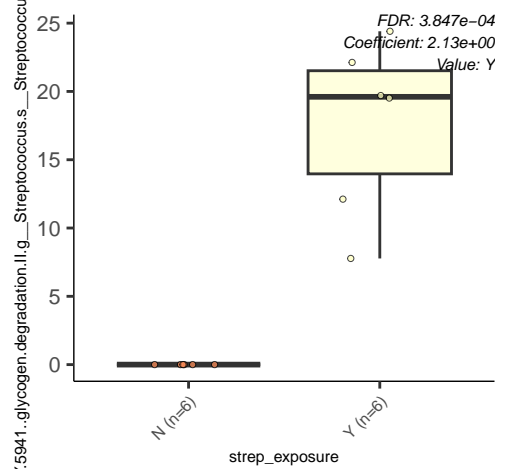


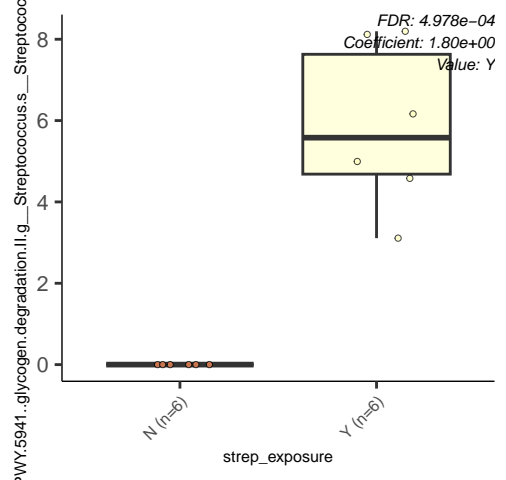


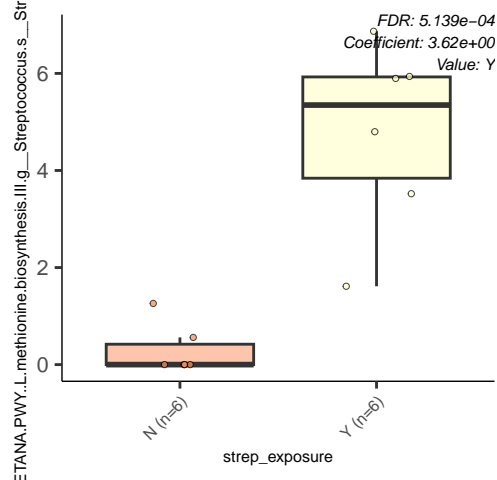




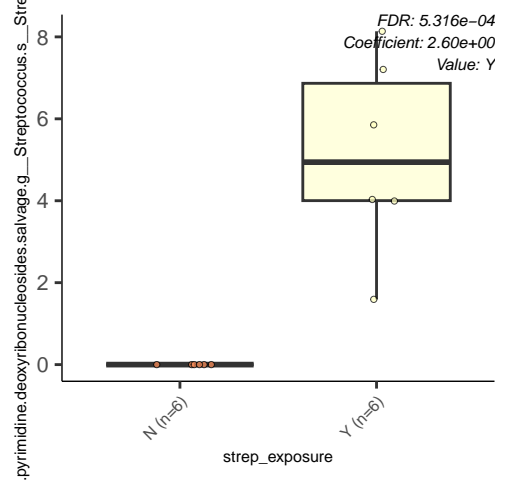


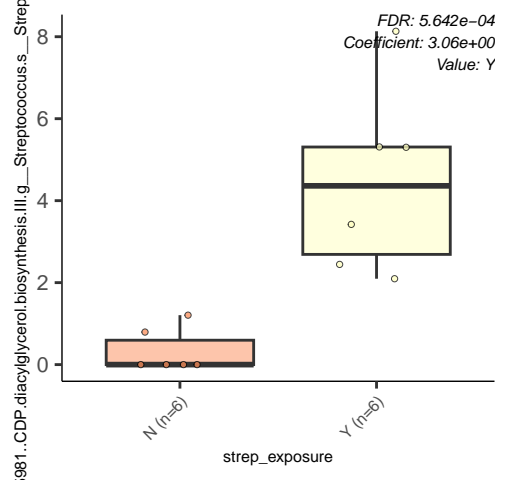


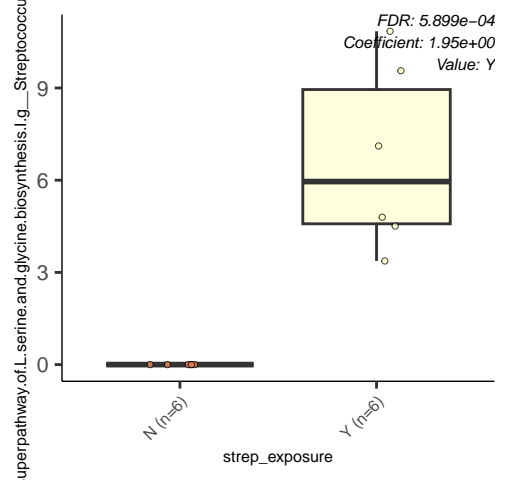


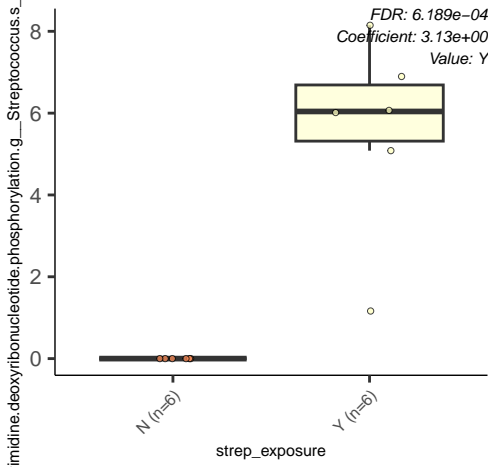


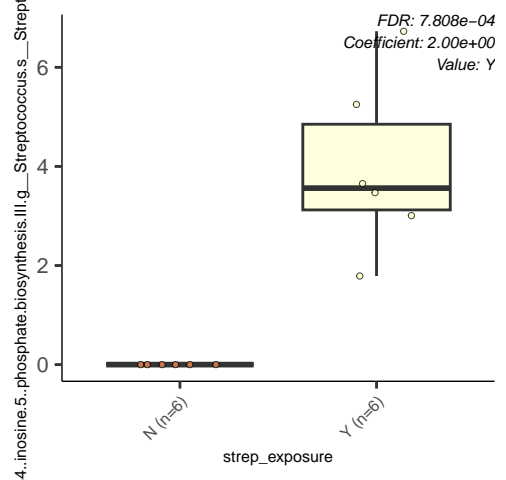


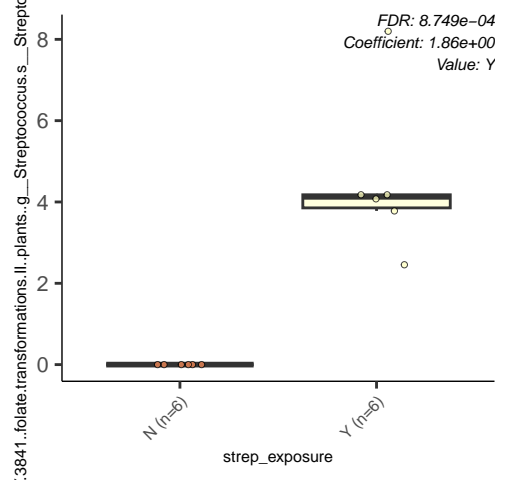






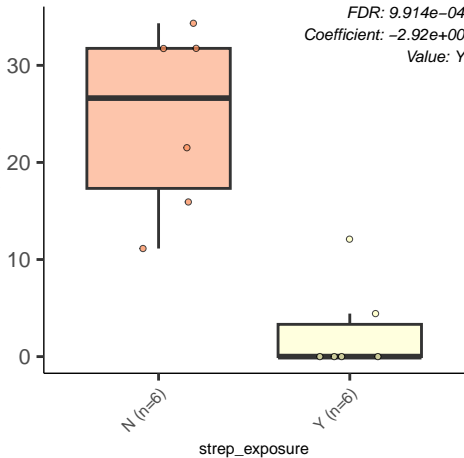


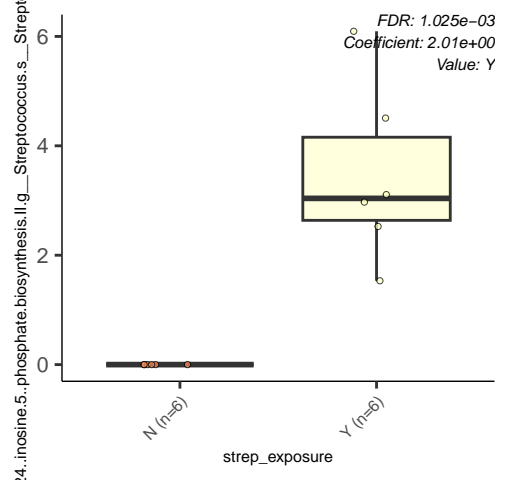




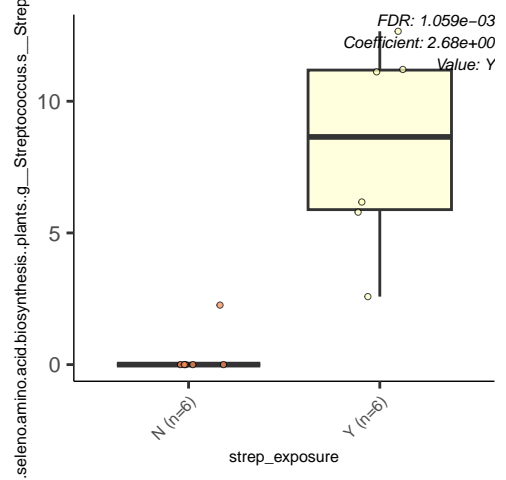
WY.6609..adenine.and.adenosine.salvage.Ill.g\_\_Escherichia.s\_\_Es

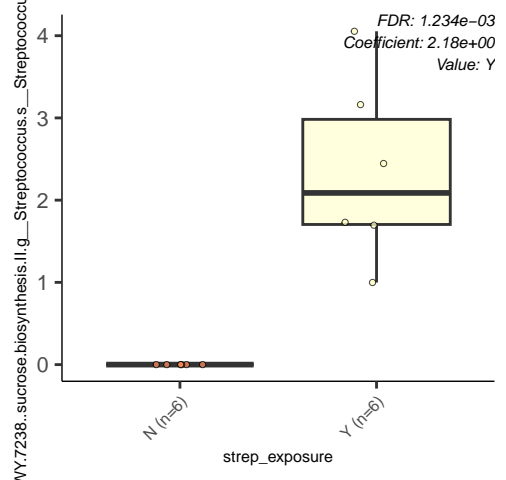
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*Value: Y*

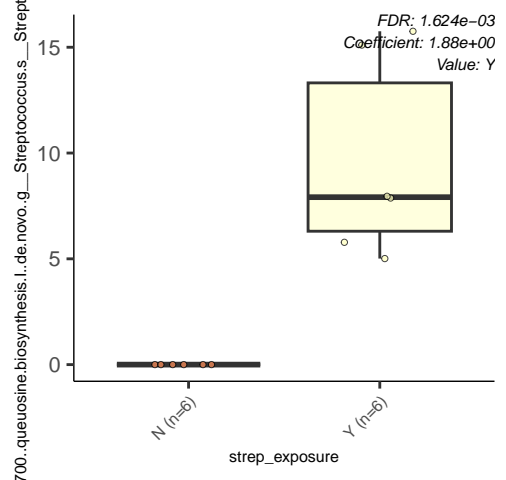


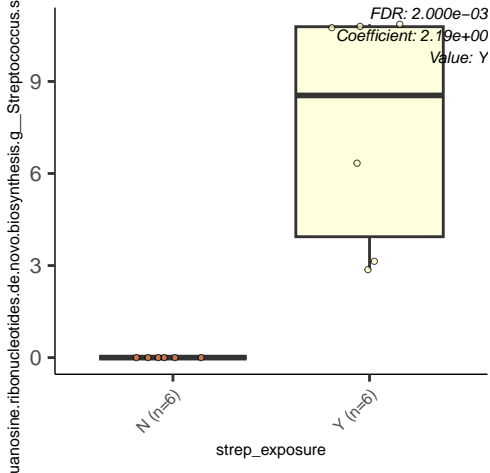


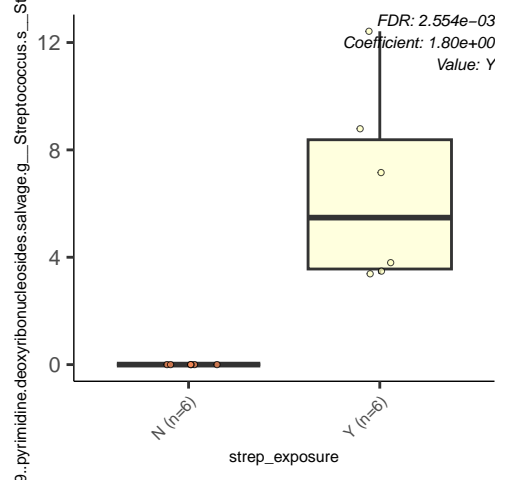




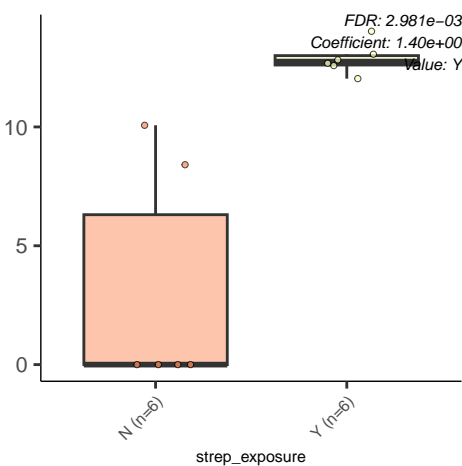


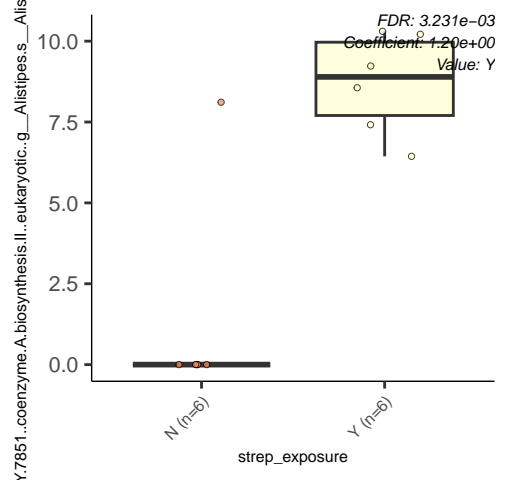






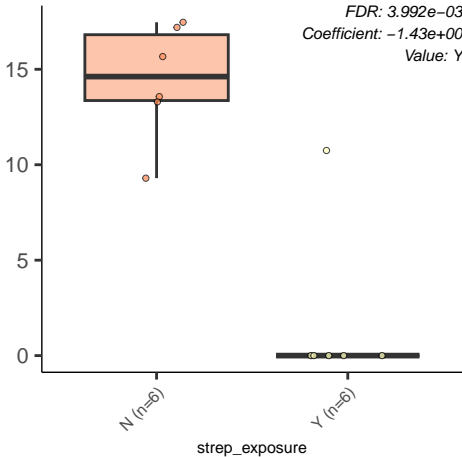
way.of.adenosylcobalamin.salvage.from.cobinamide.l.g\_\_Faecalib



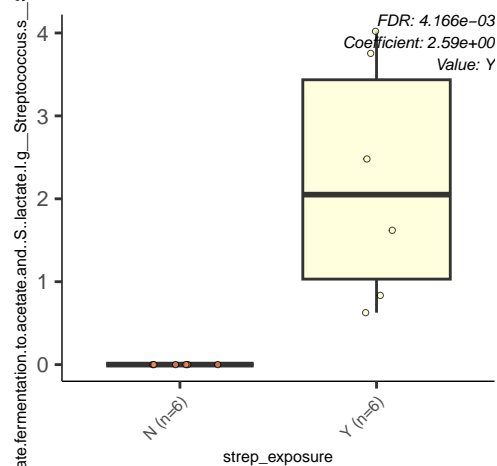


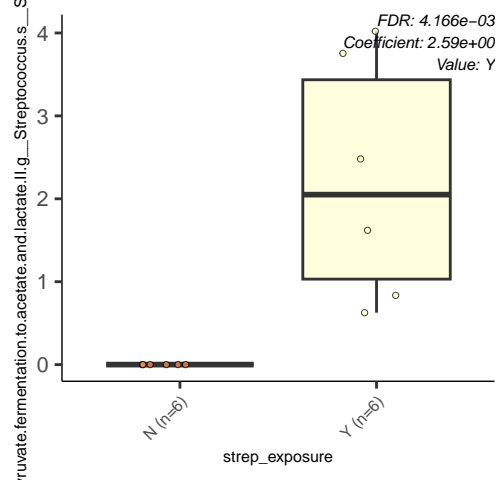
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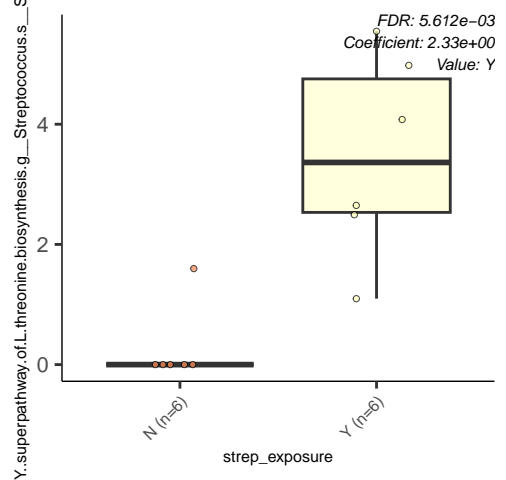
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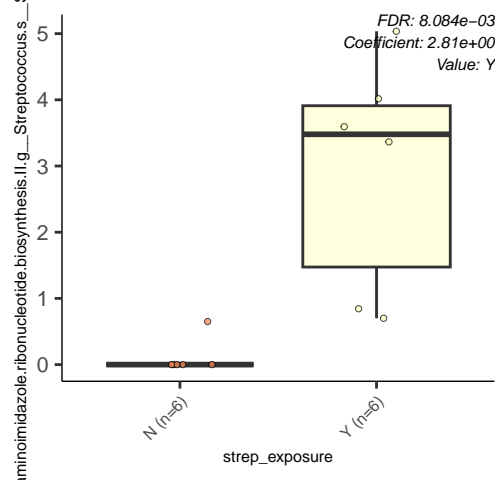


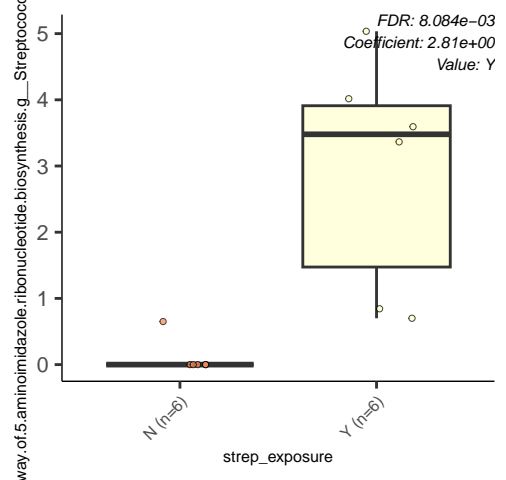


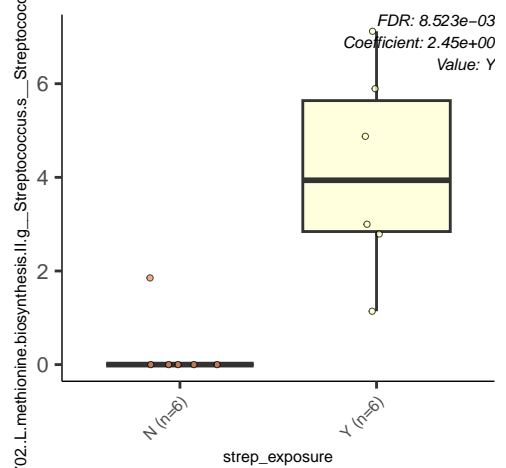


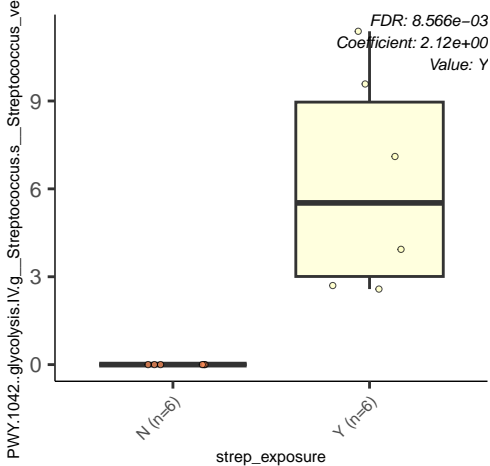


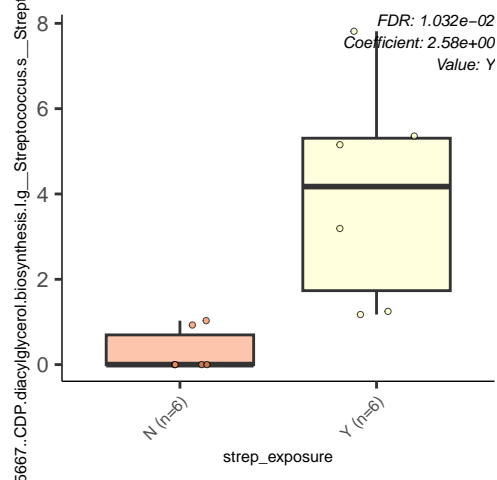




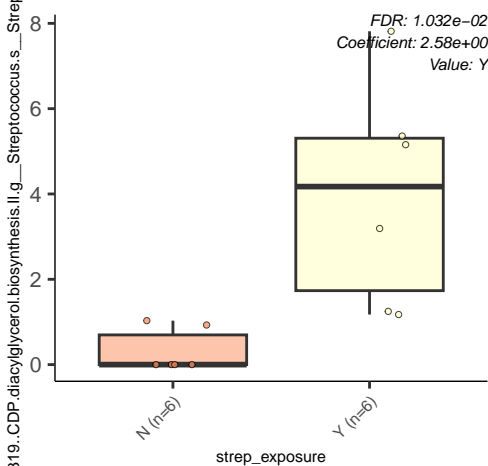


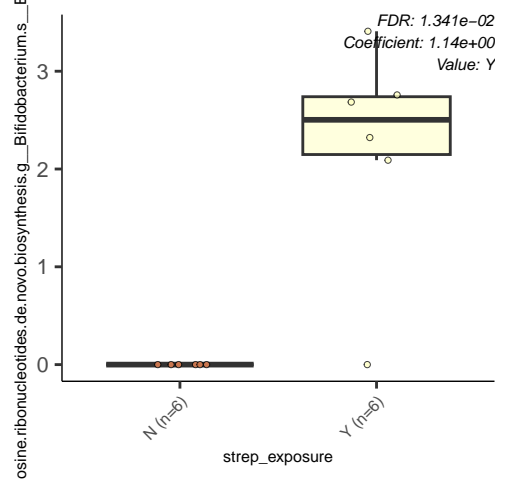


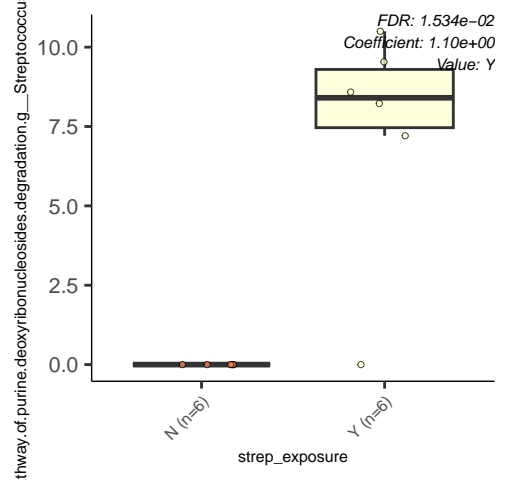


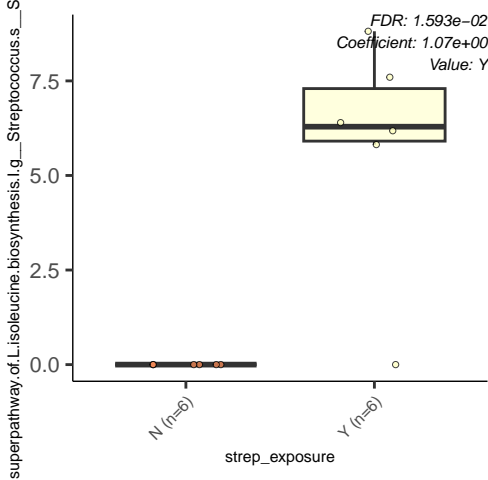


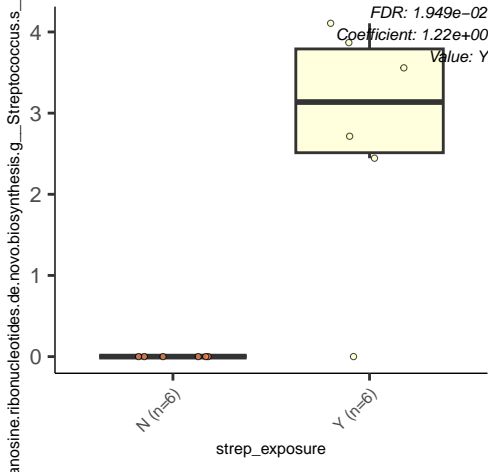


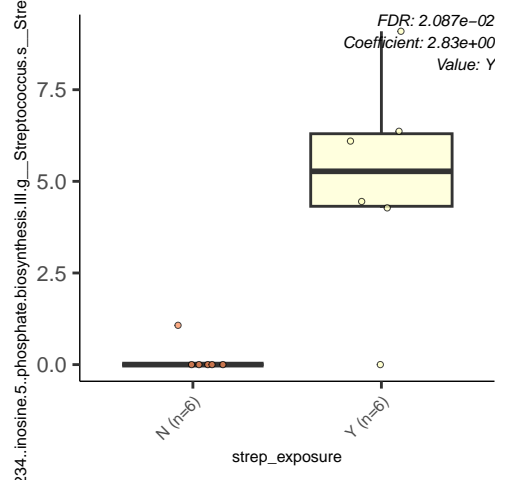


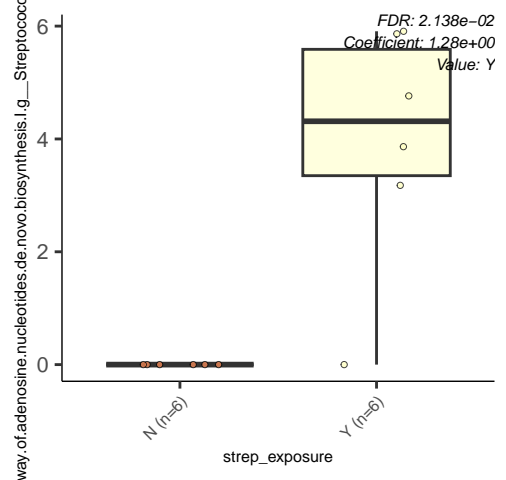


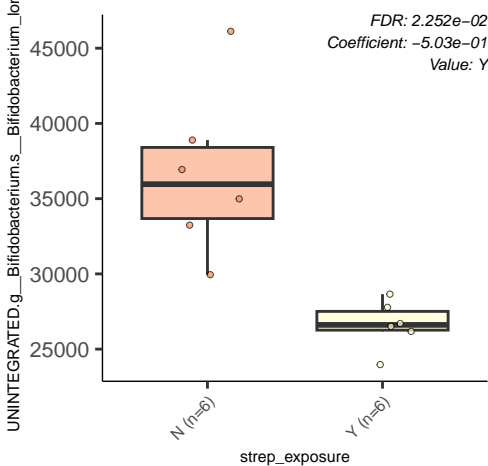














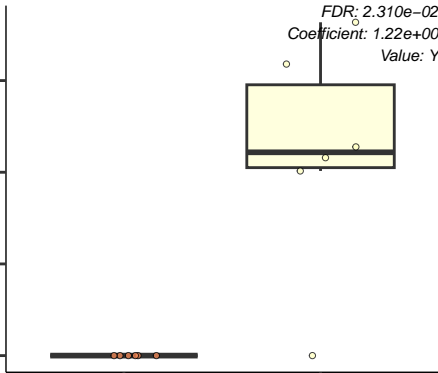
P108.PWY..pyruvate.fermentation.to.propanoate.l.unclassified

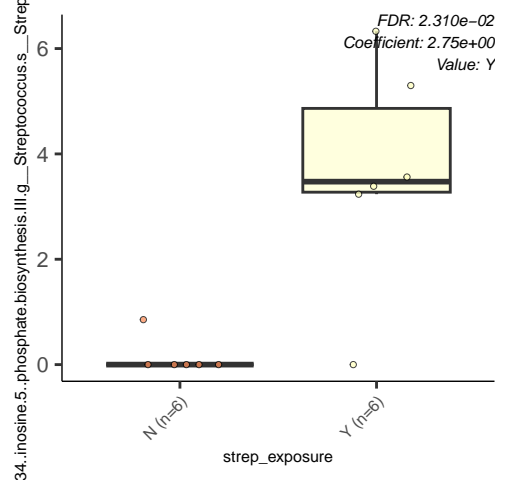
N (n=6)

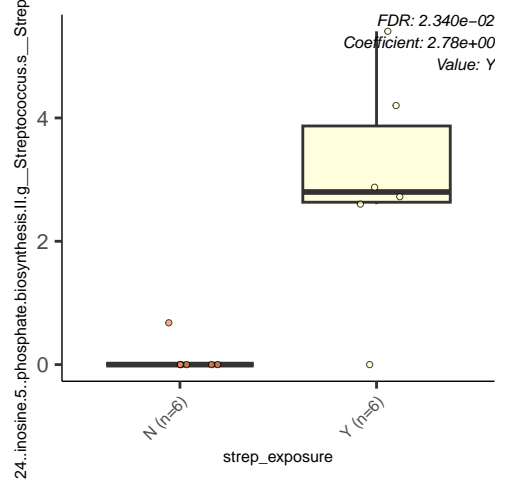
Y (n=6)

strep\_exposure

FDR: 2.310e-02  
Coefficient: 1.22e+00  
Value: Y

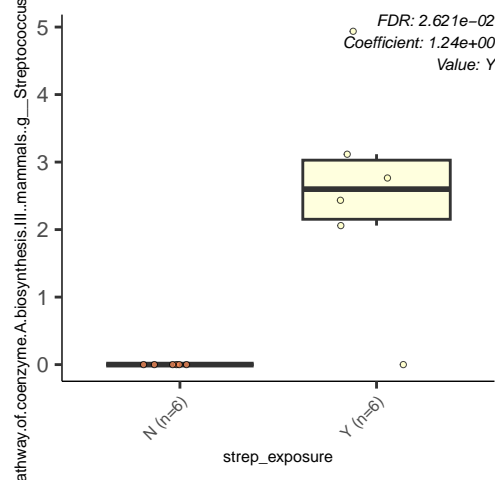


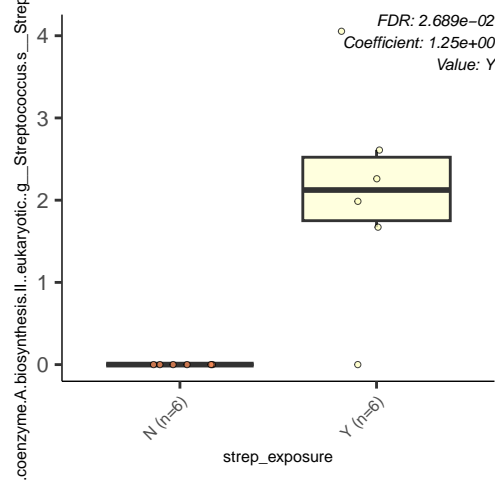




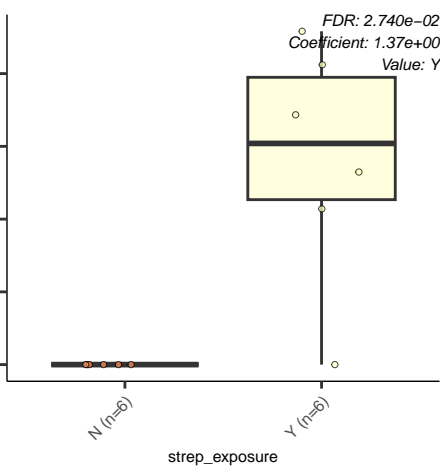
VY.5941..glycogen.degradation.ll.g\_\_Streptococcus.s\_\_Streptococcus

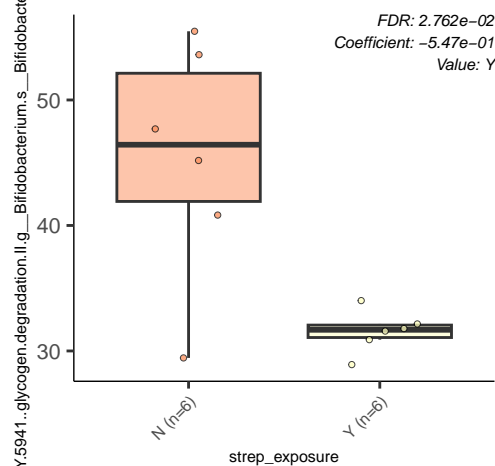




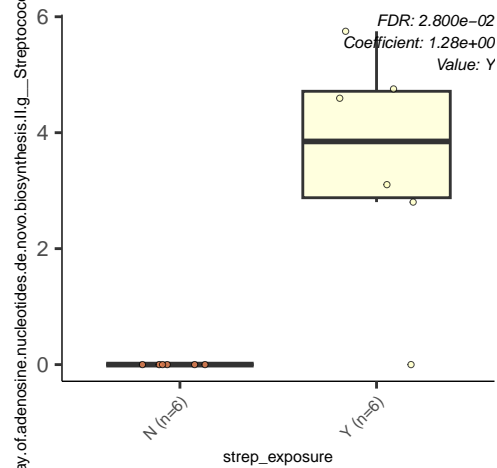


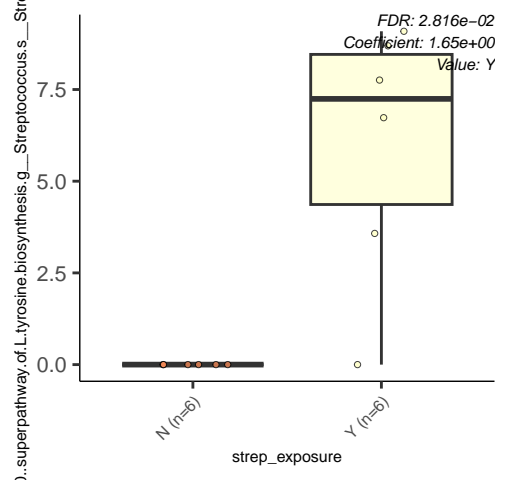
way.of.guanosine.nucleotides.de.novo.biosynthesis.l.g\_\_Streptococcus

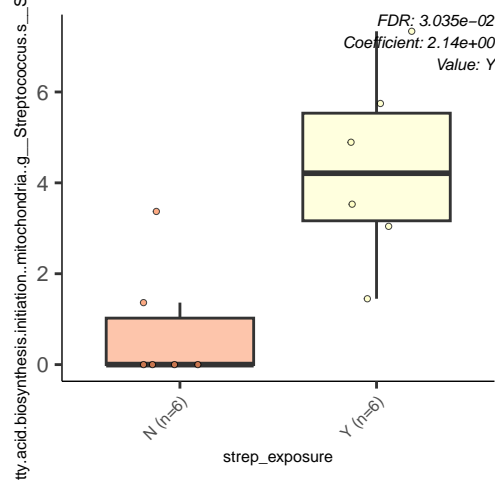


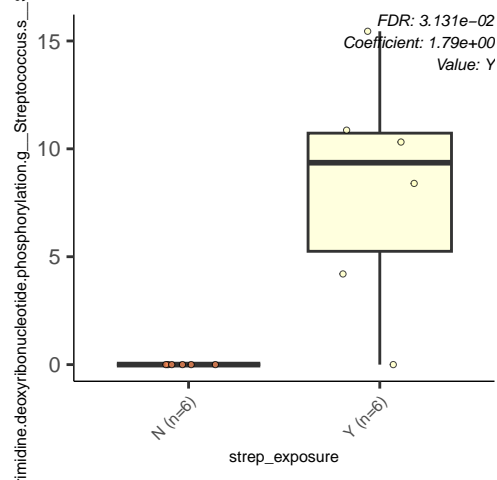


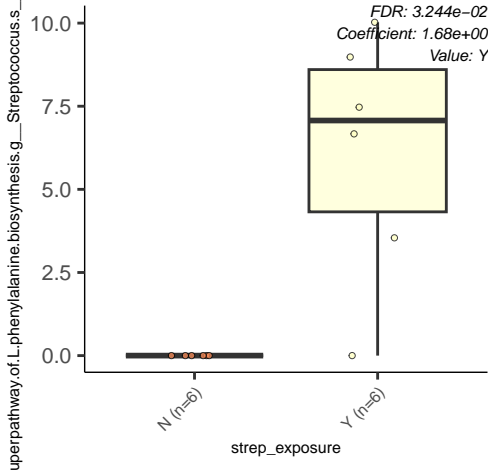


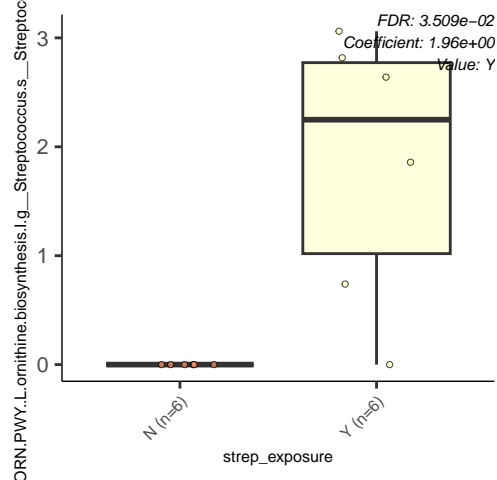


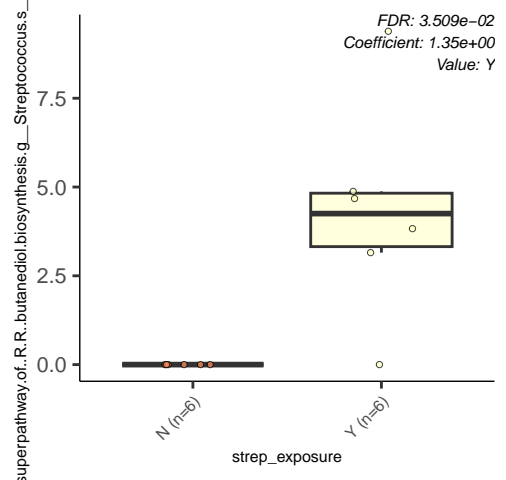




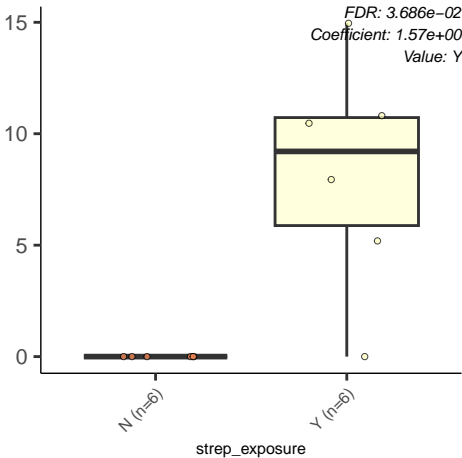




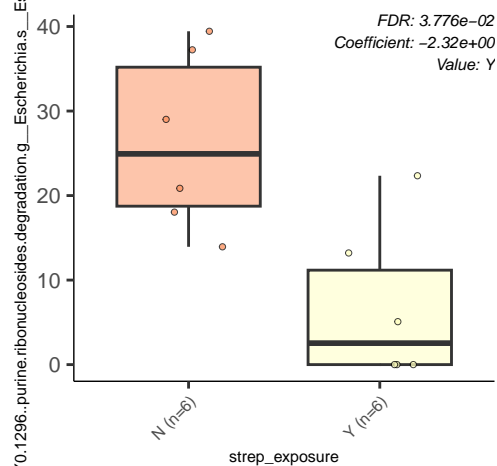


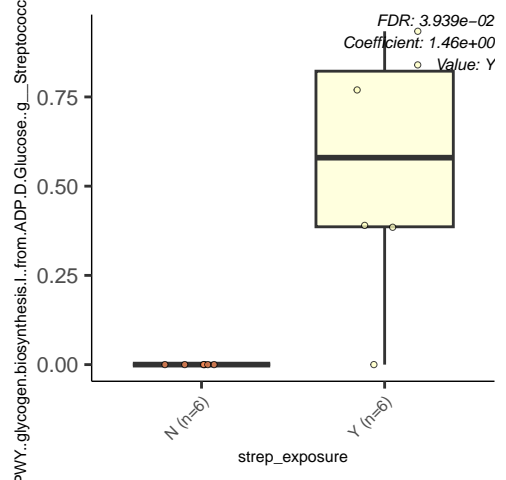


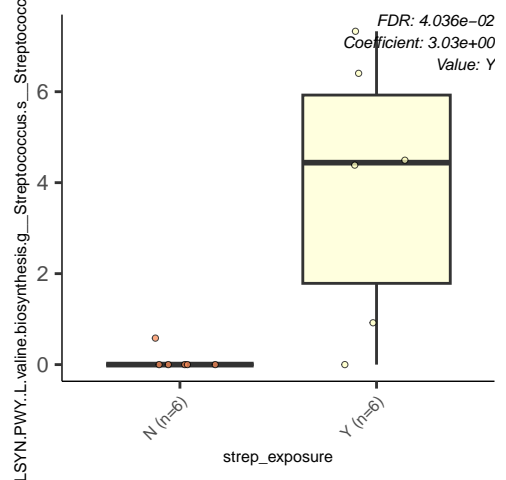
Y..superpathway.of.aromatic.amino.acid.biosynthesis.g\_\_Streptococcus

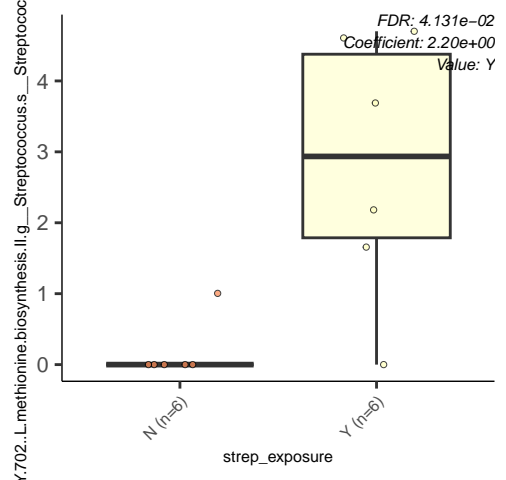


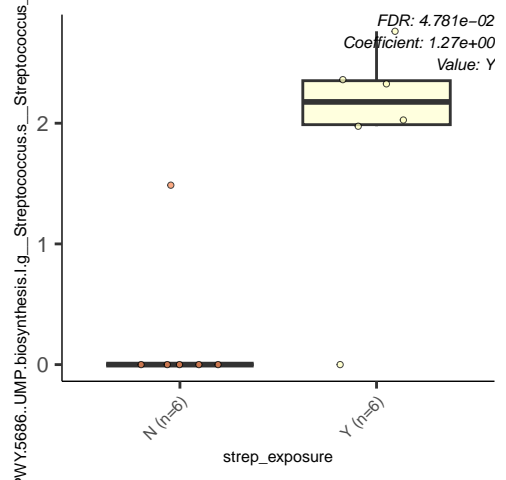


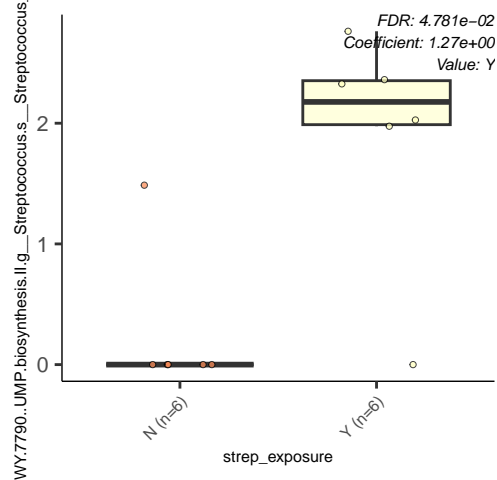


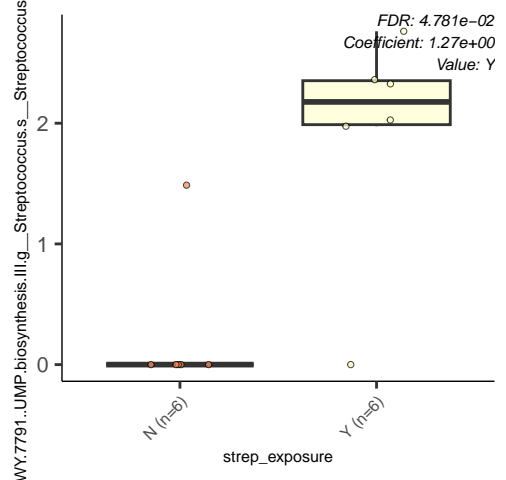






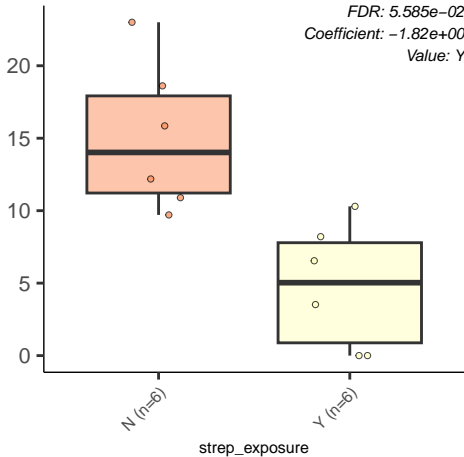




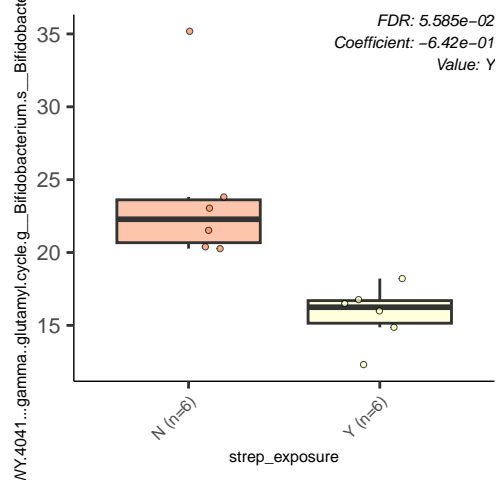


AMSYN.PWY..dTDP..beta...L..rhamnose.biosynthesis.g\_\_Escherichia

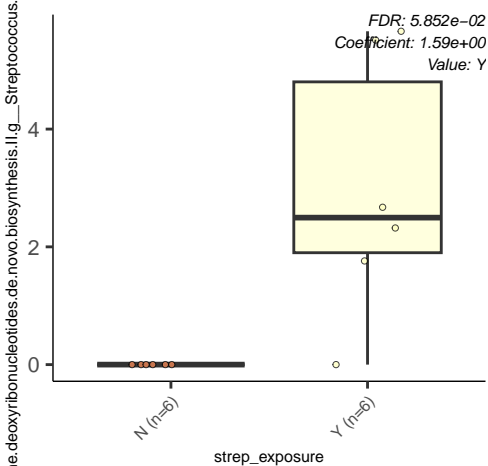
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Coefficient: -1.82e+00  
Value: Y



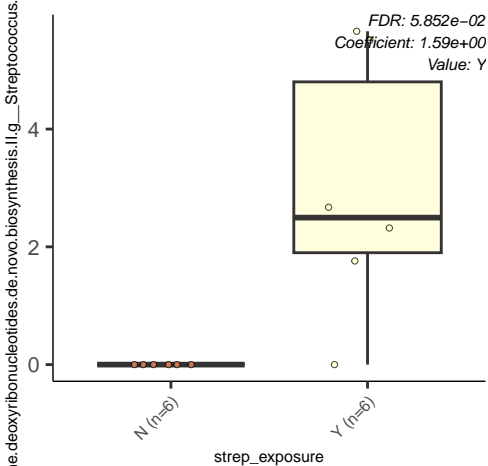


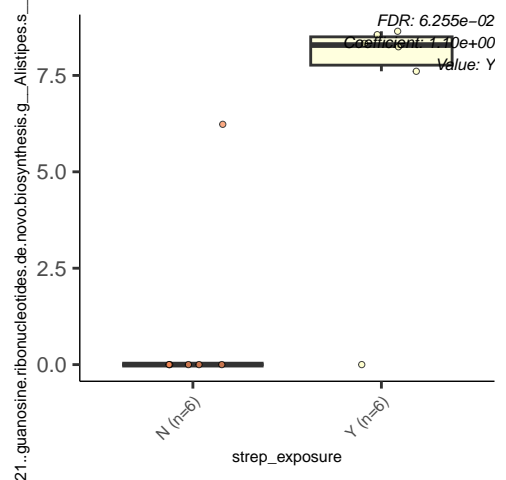


sine.deoxyribonucleotides.de.novo.biosynthesis.ll.g\_\_Streptococcus.



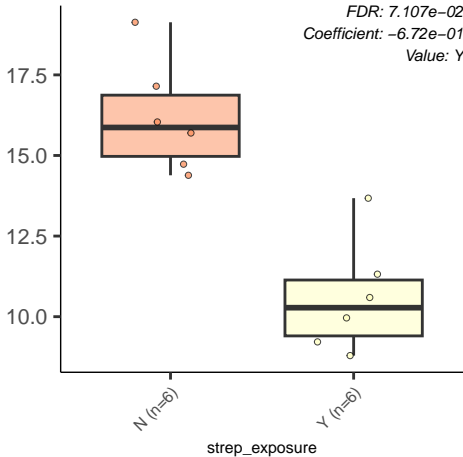
sine.deoxyribonucleotides.de.novo.biosynthesis.II.g\_\_Streptococcus.



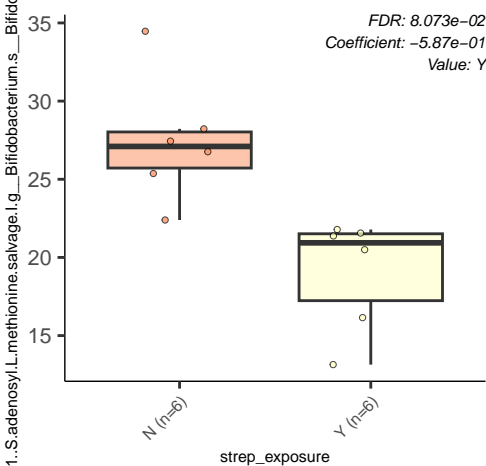


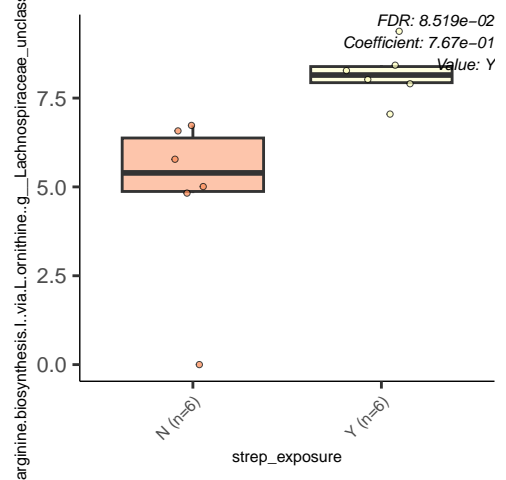
Y.702..L.methionine.biosynthesis.II.g\_\_Bifidobacterium.s\_\_Bifidobac

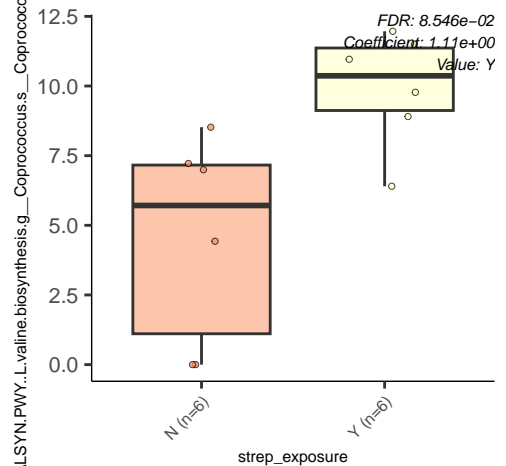
FDR:  $7.107e-02$   
Coefficient:  $-6.72e-01$   
Value: Y



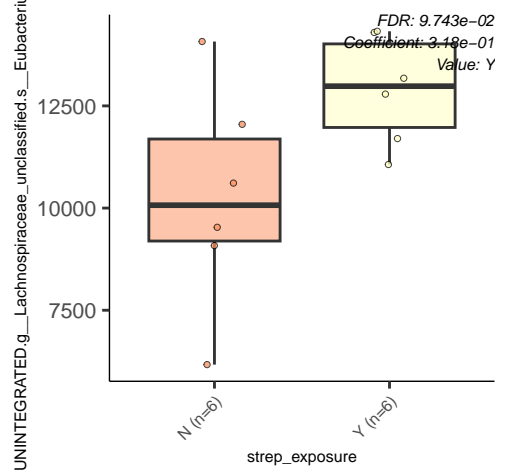
Value: Y

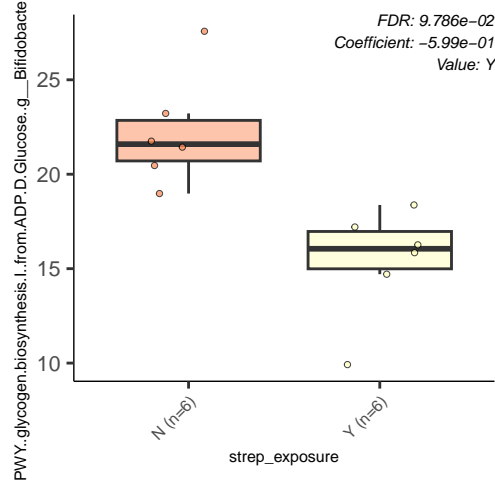


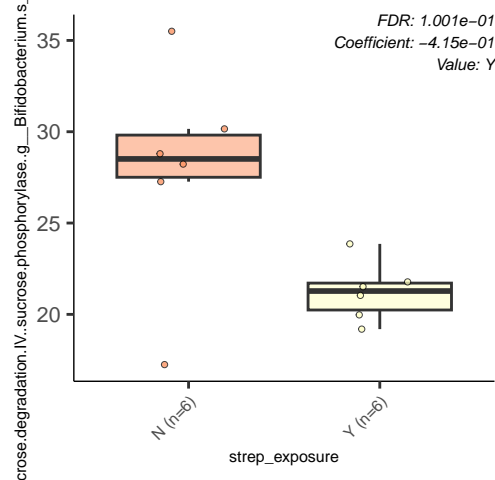


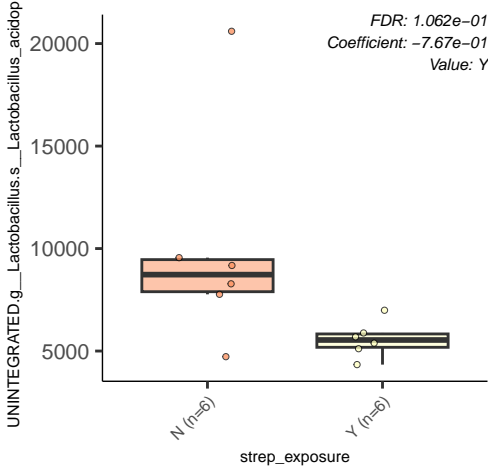






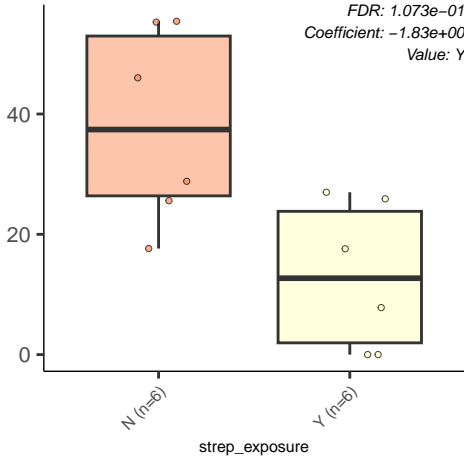


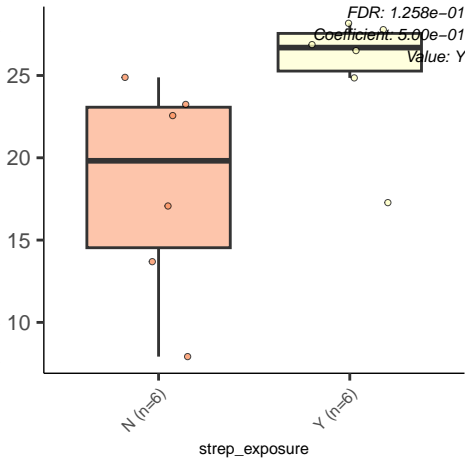




Y.6608..guanine.nucleotides.degradation.III.g\_Escherichia.s\_E

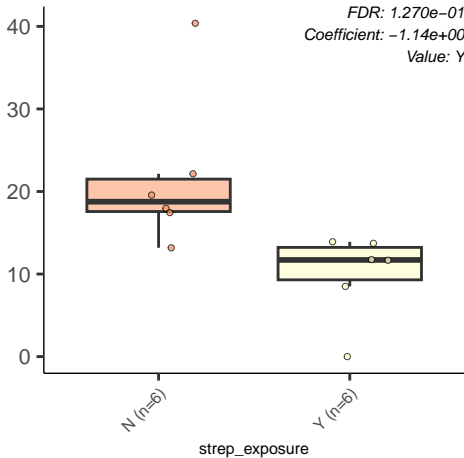
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Coefficient: -1.83e+00  
Value: Y

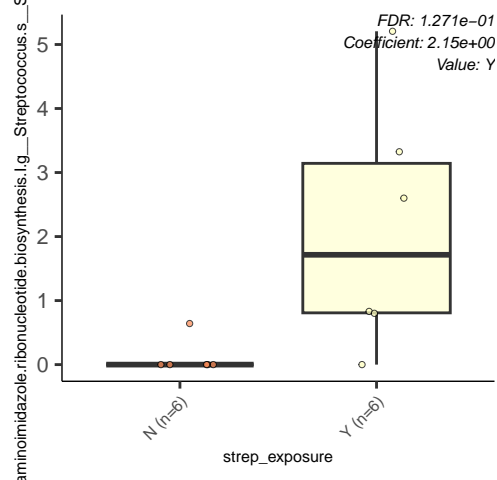




WY..UDP.N.acetyl.D.glucosamine.biosynthesis.l.g\_\_Lactobacillus.s

FDR: 1.270e-01  
Coefficient: -1.14e+00  
Value: Y

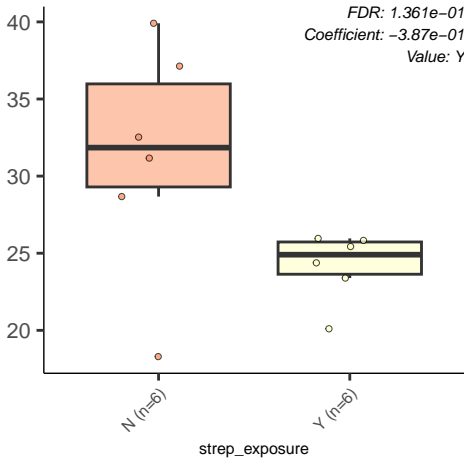


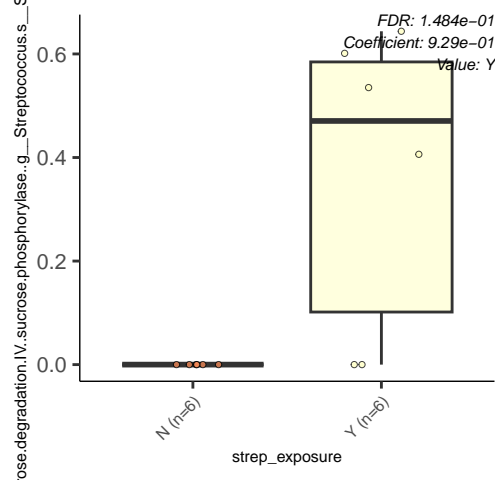


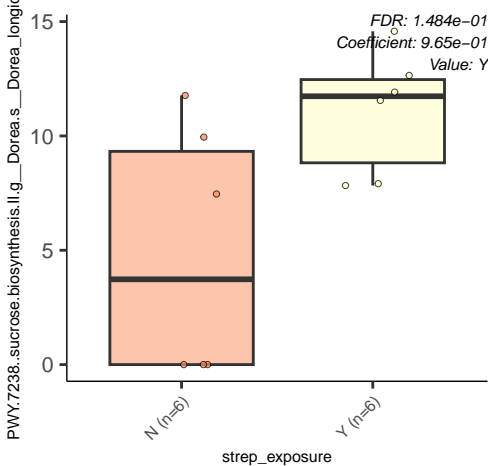


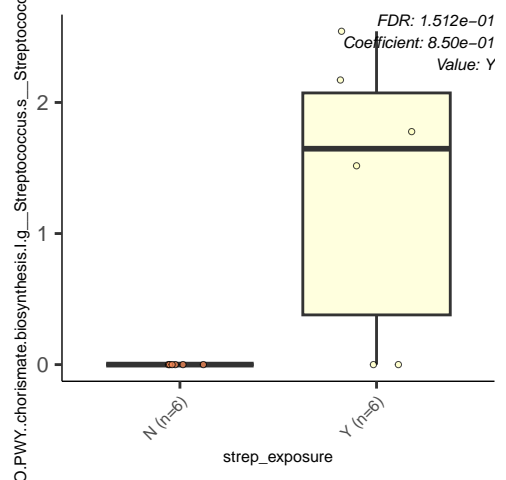
LSYN.PWY..L\_valine.biosynthesis.g\_\_Bifidobacterium.s\_\_Bifidobact

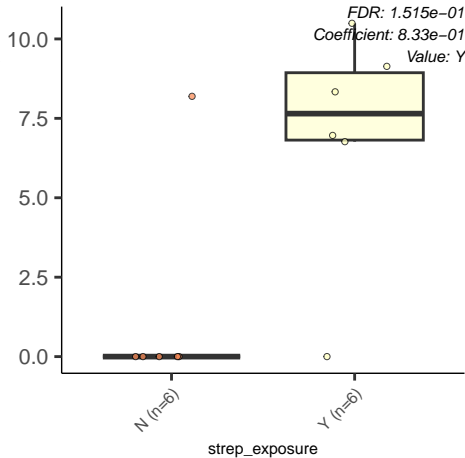
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Coefficient: -3.87e-01  
Value: Y

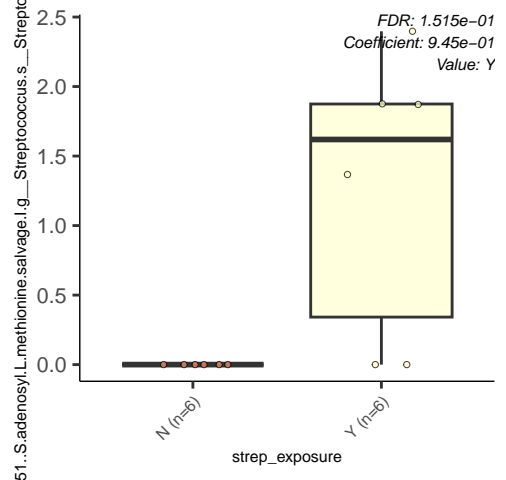






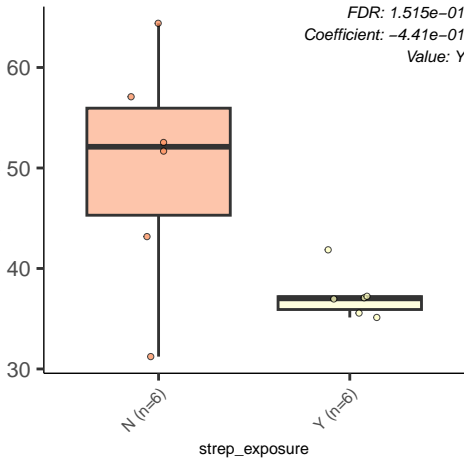


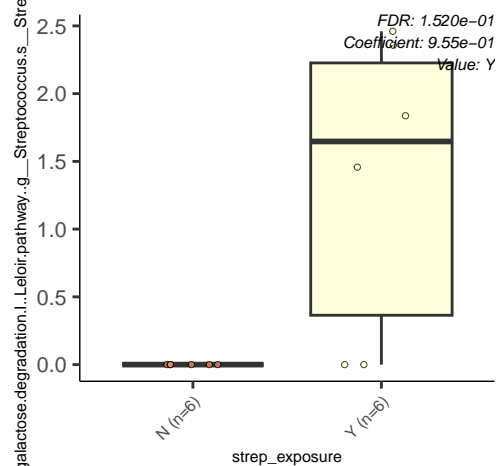




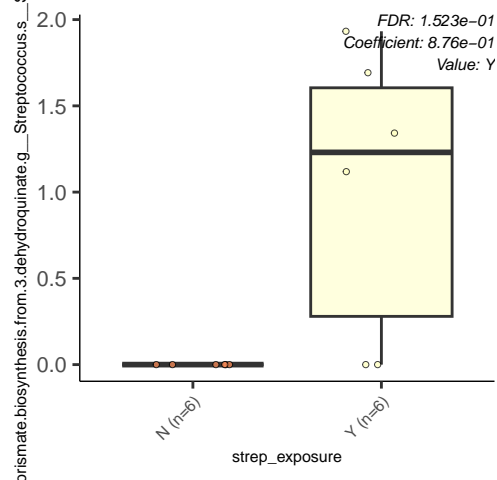
WY.7238..sucrose.biosynthesis.ll.g\_\_Bifidobacterium.s\_\_Bifidobacte

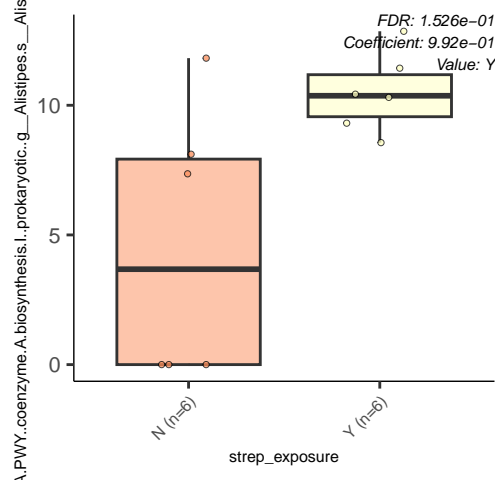
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Coefficient: -4.41e-01  
Value: Y

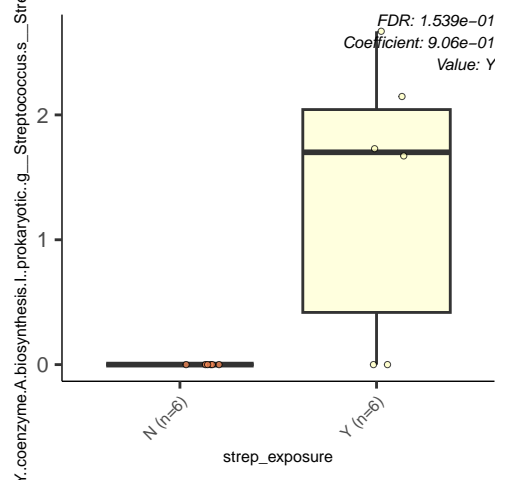


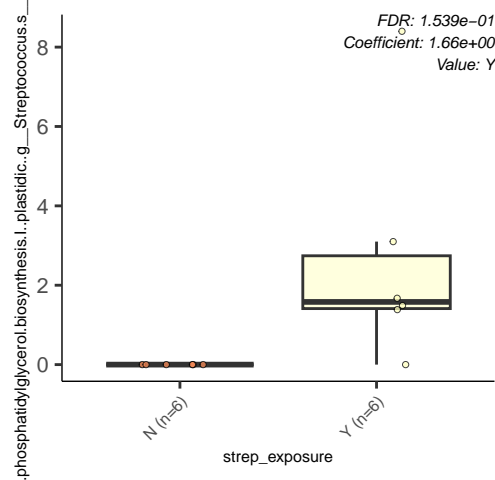


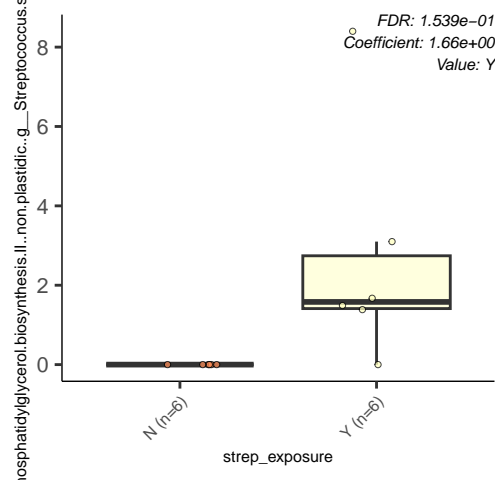


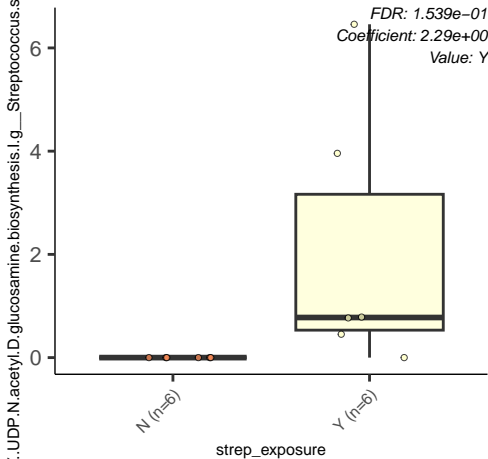


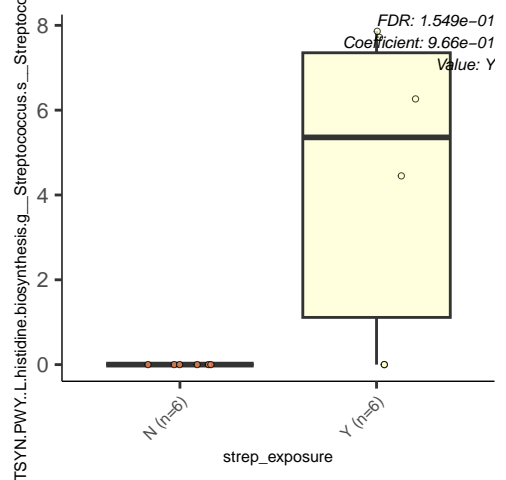


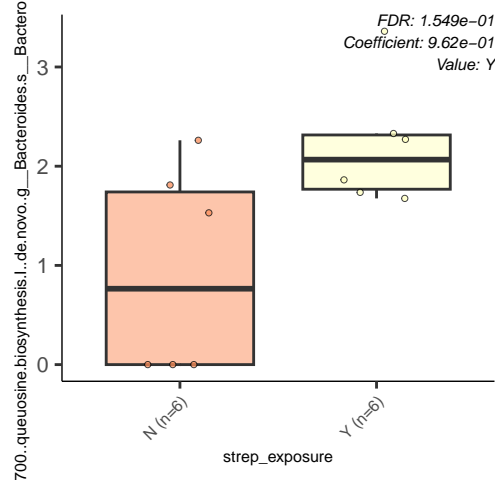




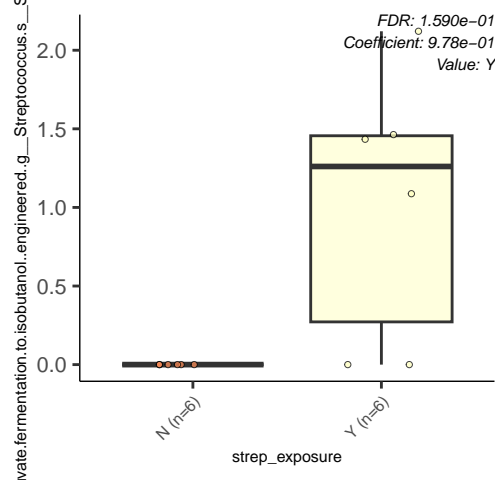


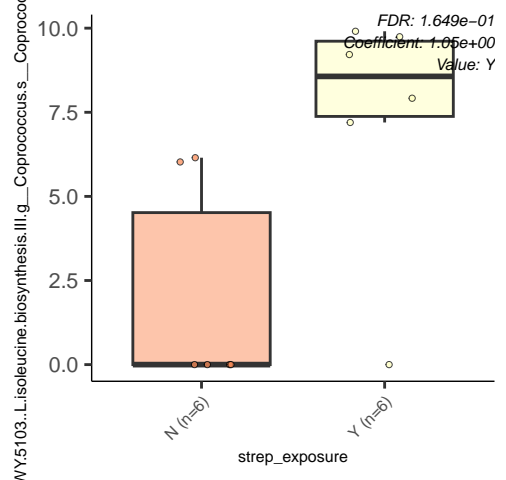


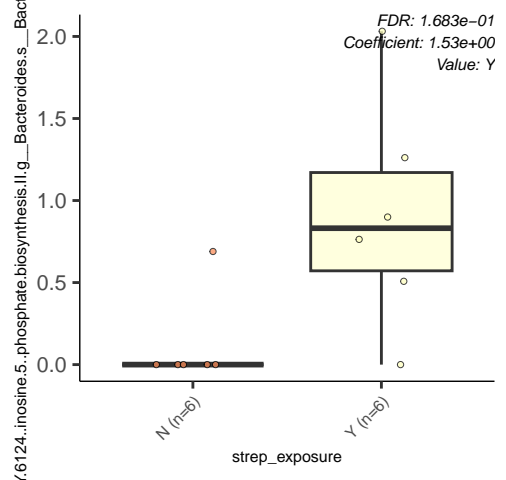




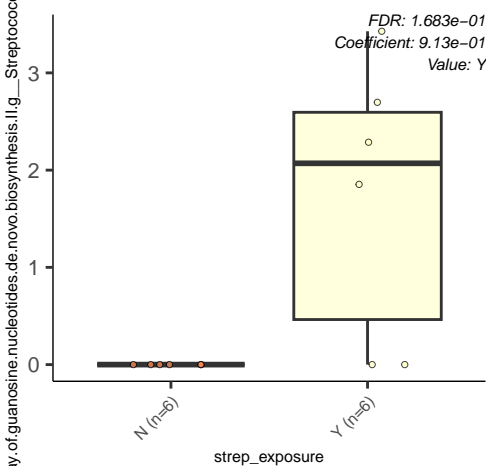


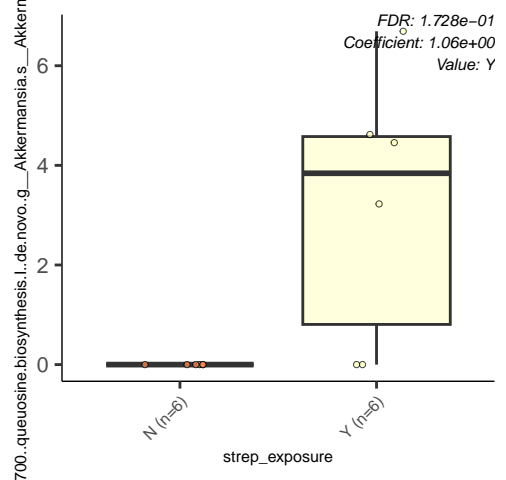




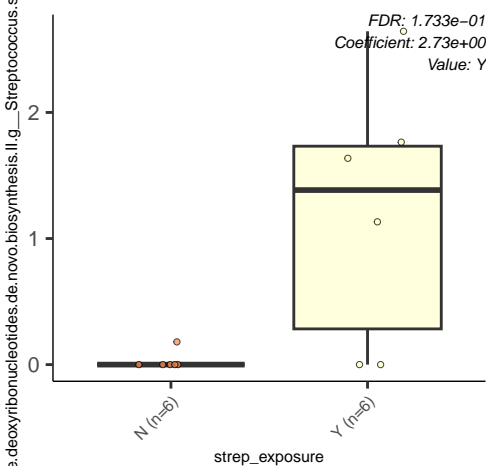


way.of.guanosine.nucleotides.de.novo.biosynthesis.II.g\_\_Streptococ

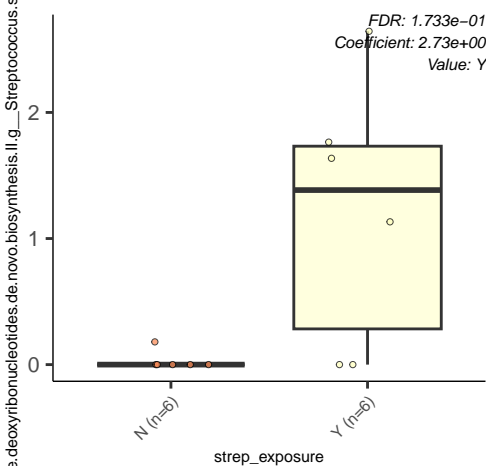


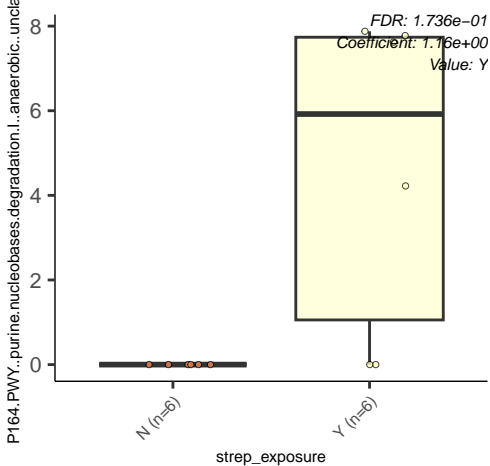


ne.deoxyribonucleotides.de.novo.biosynthesis.ll.g\_\_Streptococcus

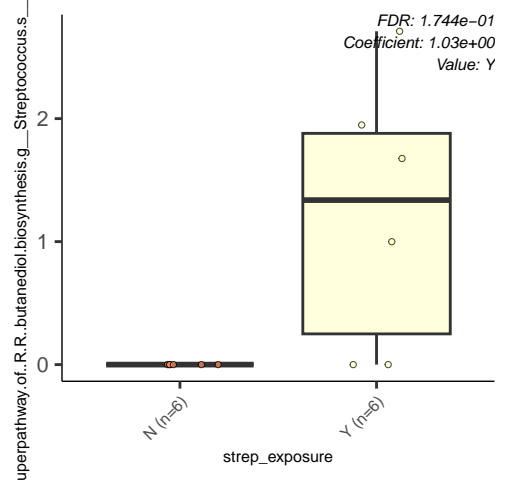


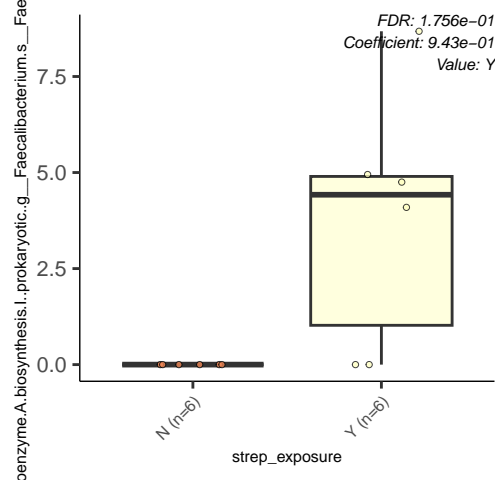
ne.deoxyribonucleotides.de.novo.biosynthesis.ll.g\_\_Streptococcus

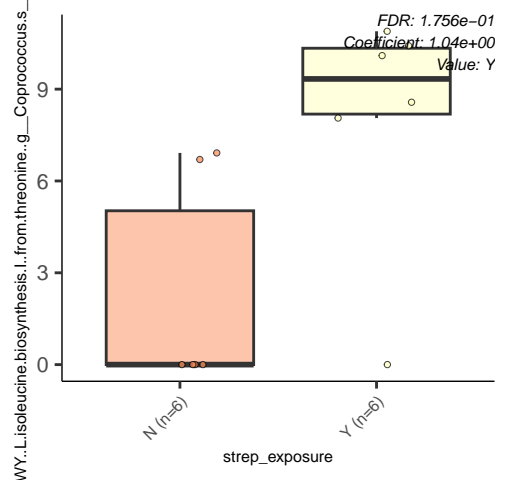






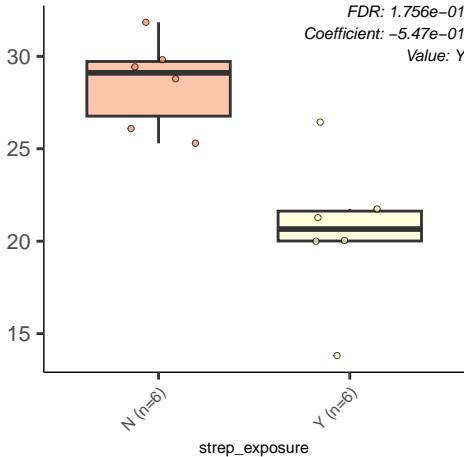




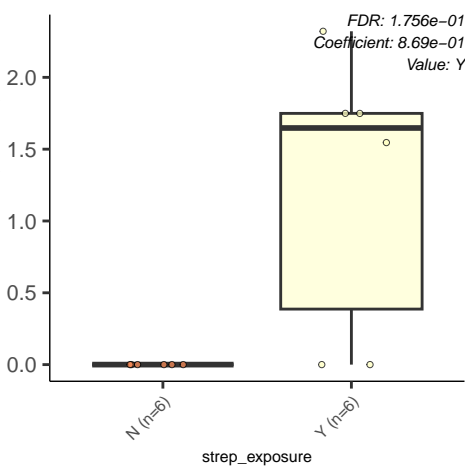


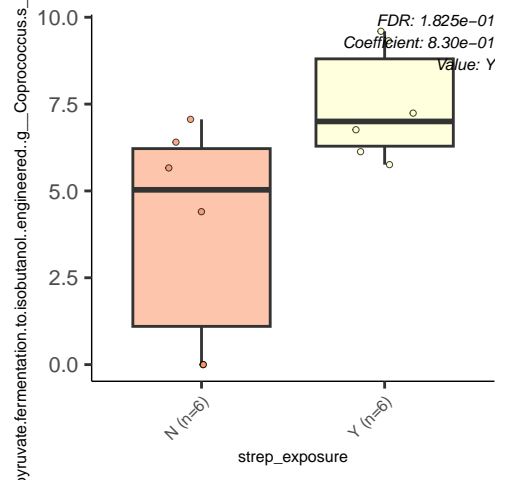
ysole.biosynthesis.VI..from.L.methionine..g\_\_Bifidobacterium.s\_\_E

FDR: 1.756e-01  
Coefficient: -5.47e-01  
Value: Y

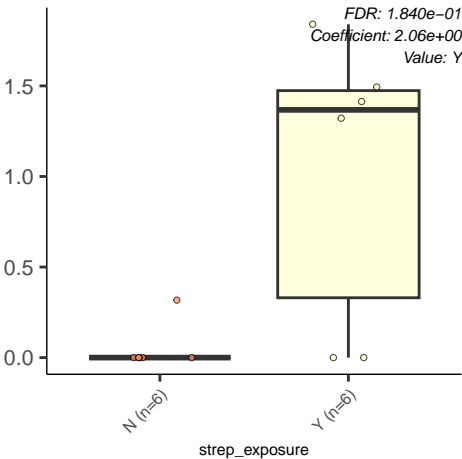


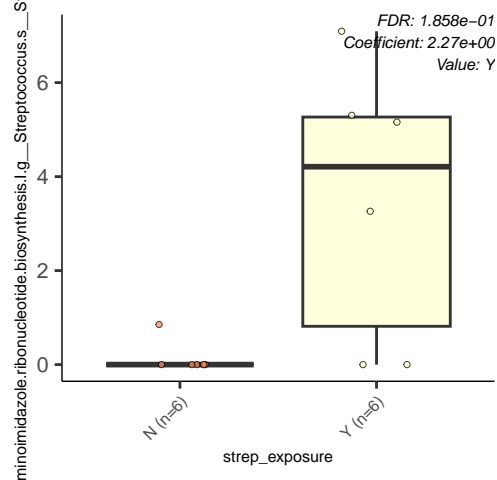
pathway.of.purine.deoxyribonucleosides.degradation.g\_\_Streptococ



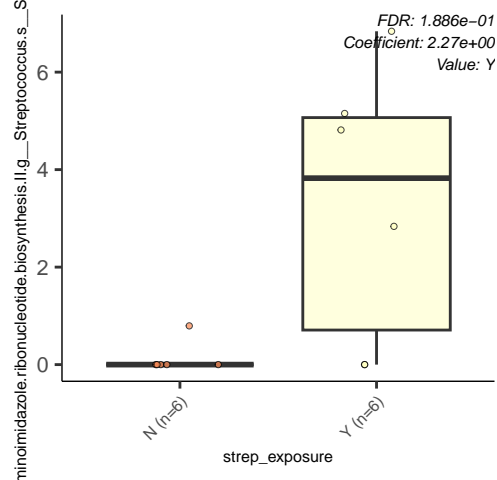


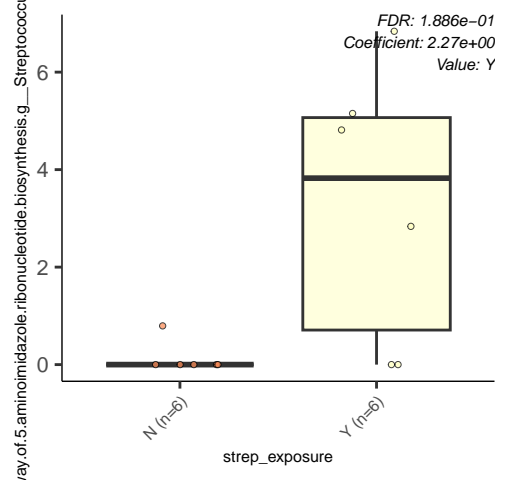
SYN.PWY.L.valine.biosynthesis.g\_\_Streptococcus.s\_\_Streptococcus

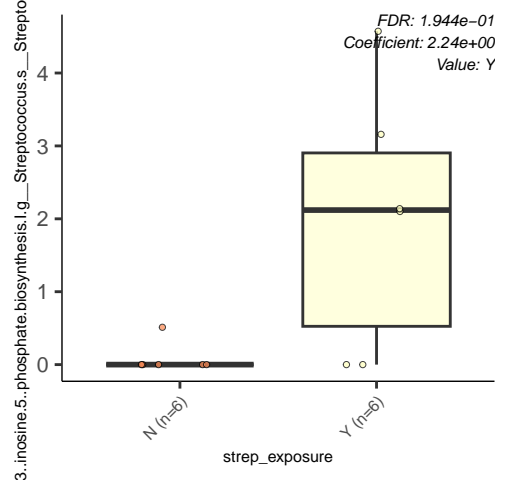


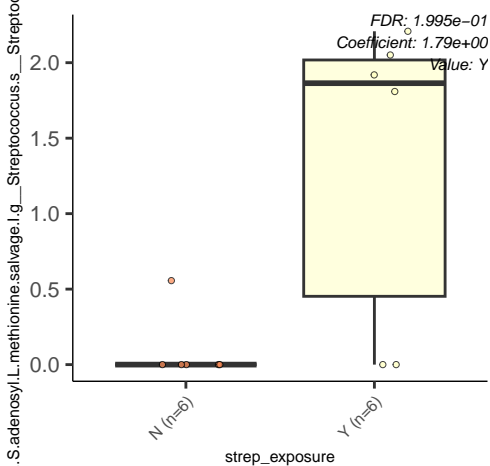




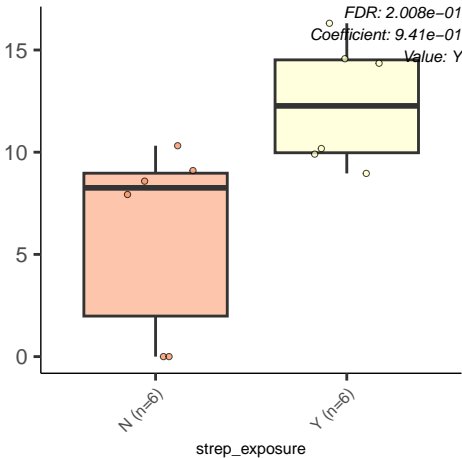




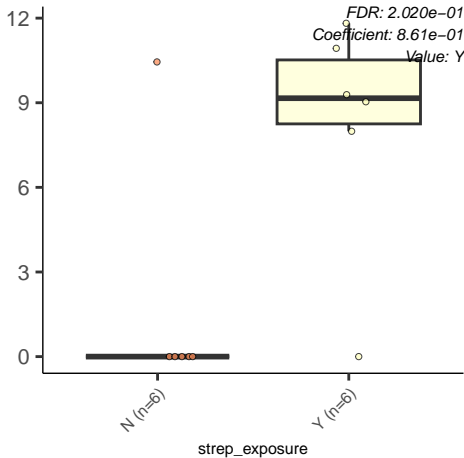


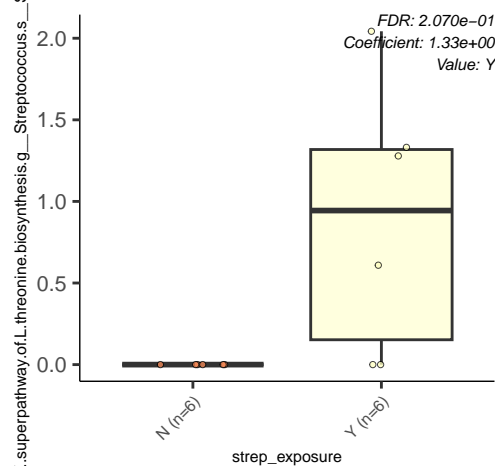


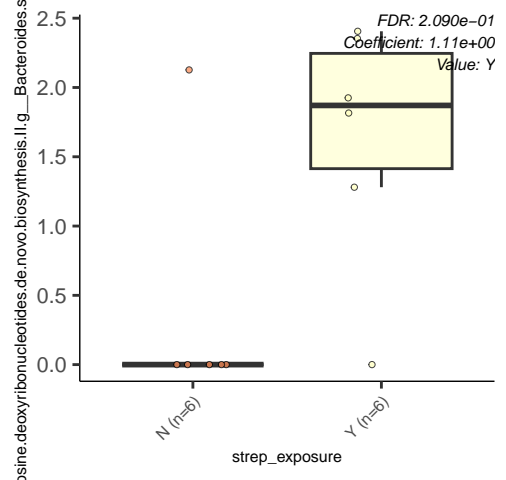
uperpathway.of.L.aspartate.and.L.asparagine.biosynthesis.g\_Blaut



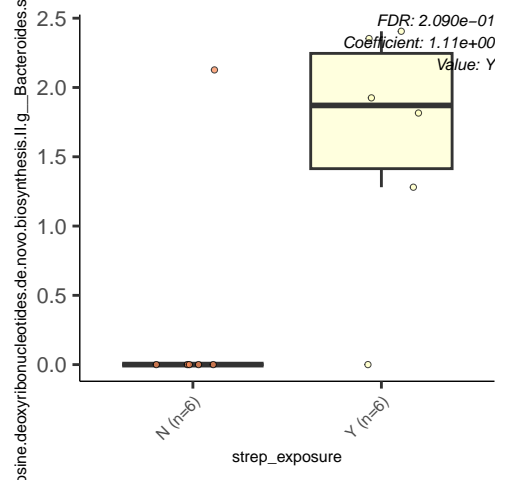
PWY.7238..sucrose.biosynthesis.II.g\_\_Coprococcus.s\_\_Coprococcus



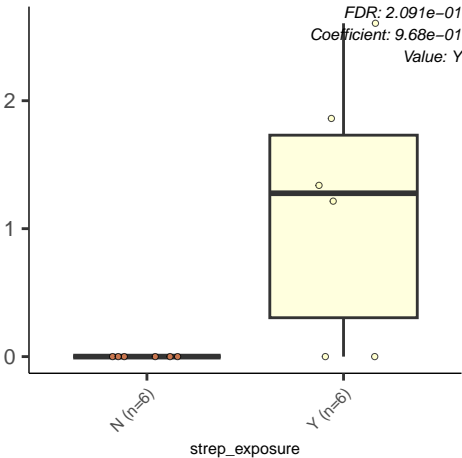


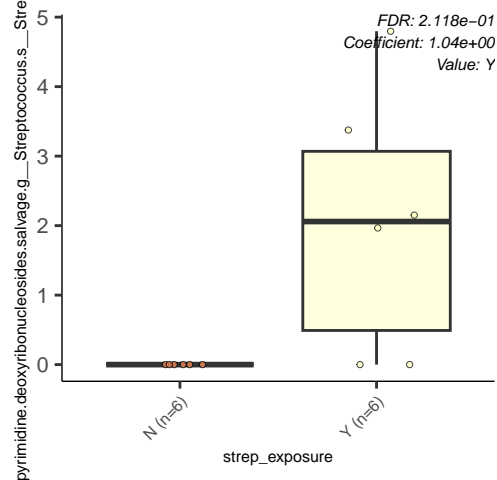






TANA.PWY..L.methionine.biosynthesis.III.g\_\_Streptococcus.s\_\_Stre





PWY.6527..stachyose.degradation.g\_\_Blautia.s\_\_Ruminococcus

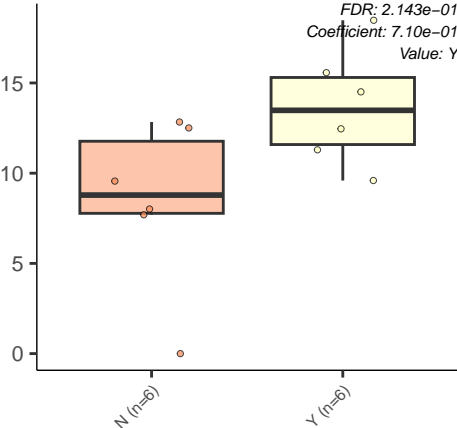
*FDR: 2.143e-01*  
*Coefficient: 7.10e-01*  
*Value: Y*

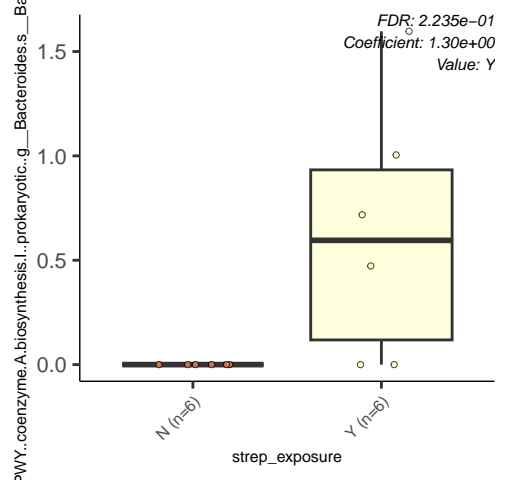
15  
10  
5  
0

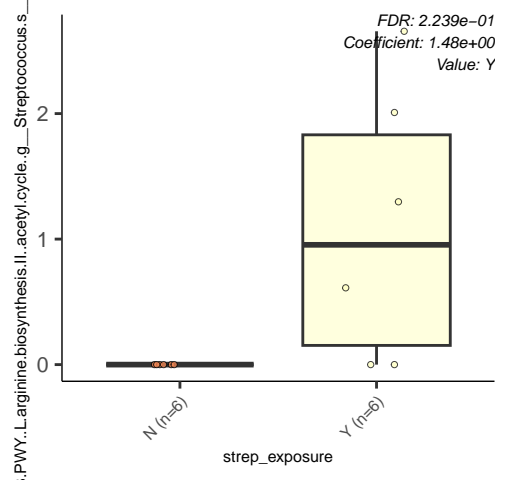
N (n=6)

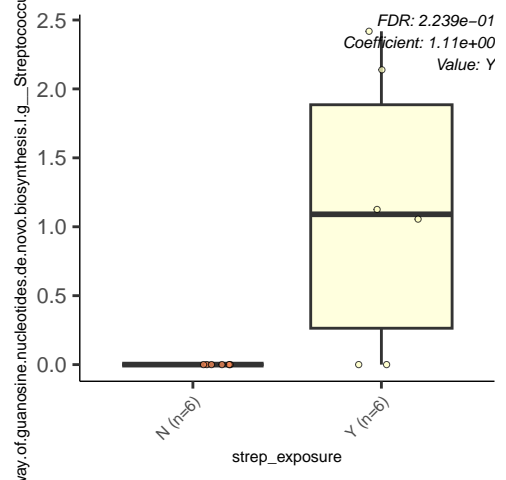
Y (n=6)

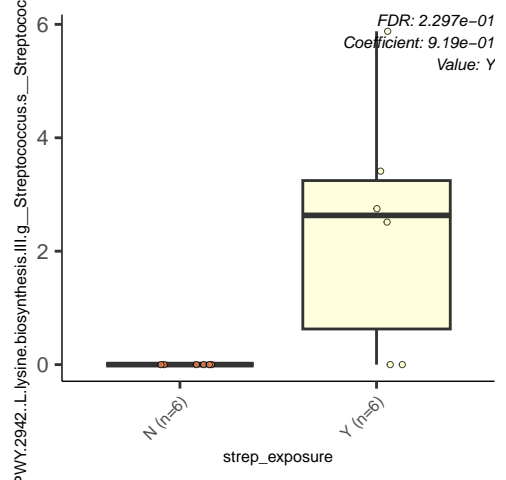
strep\_exposure



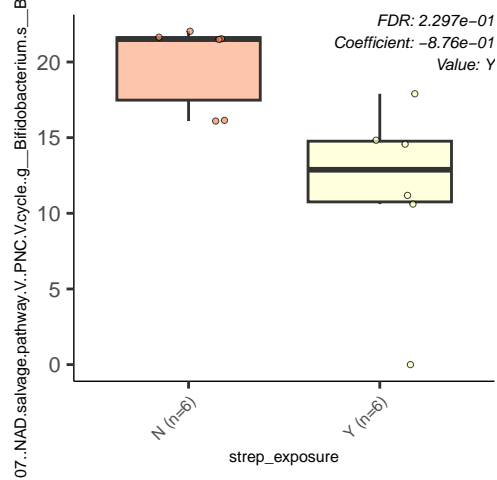


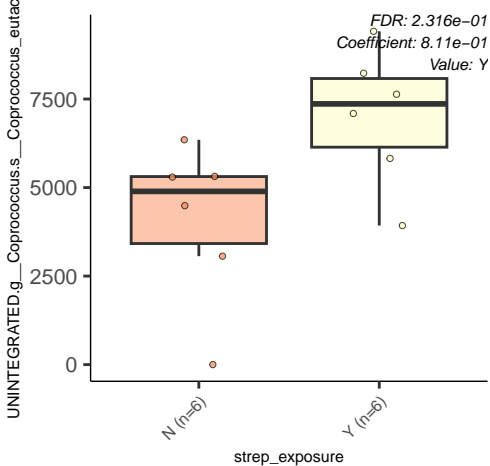




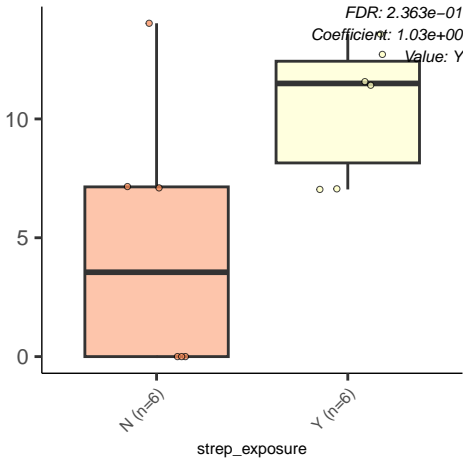




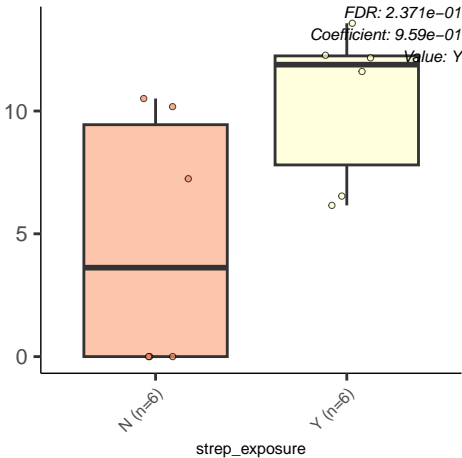




PWY.6700..queuosine.biosynthesis.l..de.novo.g\_\_Blautia.s\_\_Blau

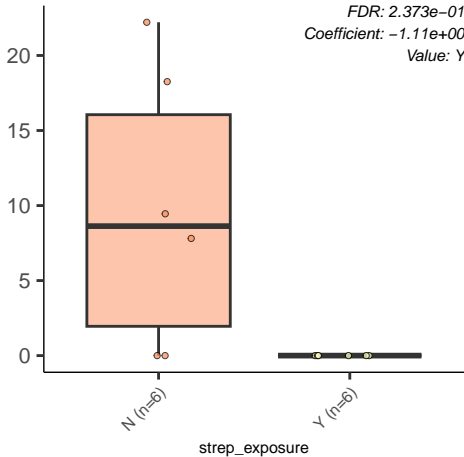


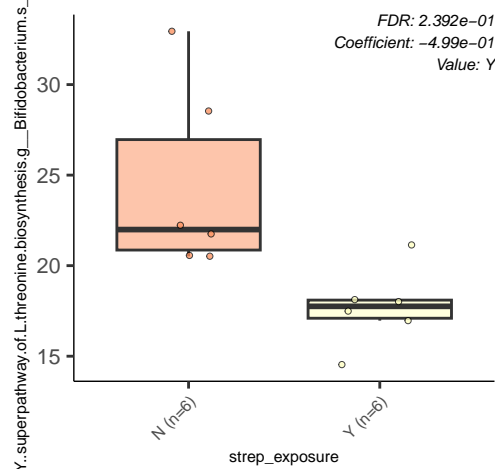
PWY5941..glycogen.degradation.ll.g\_\_Dorea.s\_\_Dorea\_longi

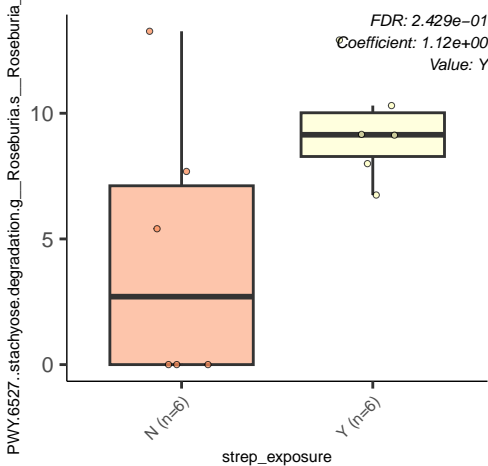


formaldehyde.assimilation.II...assimilatory.RuMP.Cycle..g\_\_Escherichia

FDR: 2.373e-01  
Coefficient: -1.11e+00  
Value: Y







UNINTEGRATED.g\_\_Bifidobacterium.s\_\_Bifidobacterium\_bif

FDR: 2.439e-01  
Coefficient: -2.84e-01  
Value: Y

30000

25000

N (n=6)

Y (n=6)

strep\_exposure

