

Competence.in.Streptococci

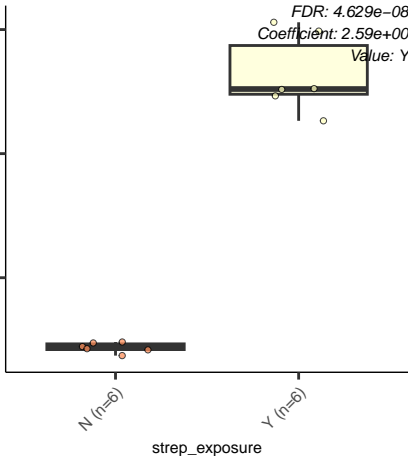
0.06  
0.04  
0.02

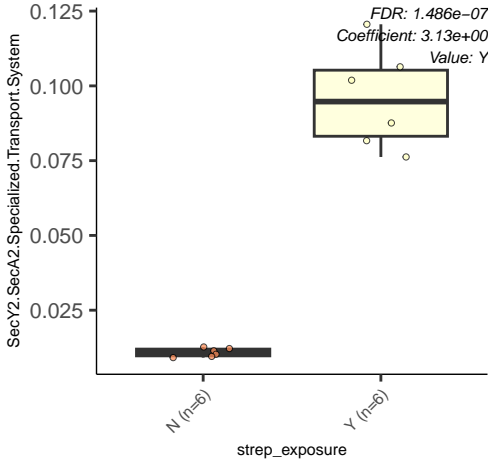
N (n=6)

Y (n=6)

strep\_exposure

FDR:  $4.629 \times 10^{-8}$   
Coefficient:  $2.59 \times 10^0$   
Value: Y





Late.competence

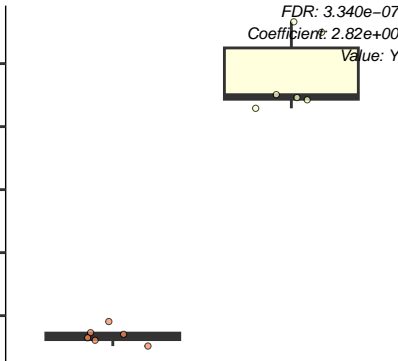
0.05  
0.04  
0.03  
0.02  
0.01

N (n=6)

Y (n=6)

strep\_exposure

FDR:  $3.340 \times 10^{-7}$   
Coefficient:  $2.82 \times 10^0$   
Value: Y



Sucrose.specific.PTS

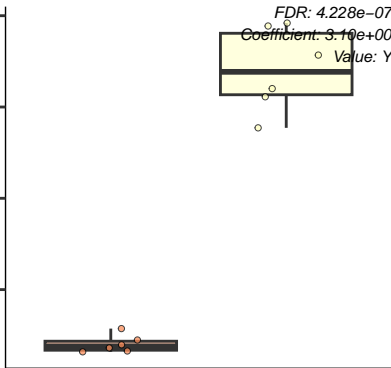
0.012  
0.009  
0.006  
0.003

N (n=6)

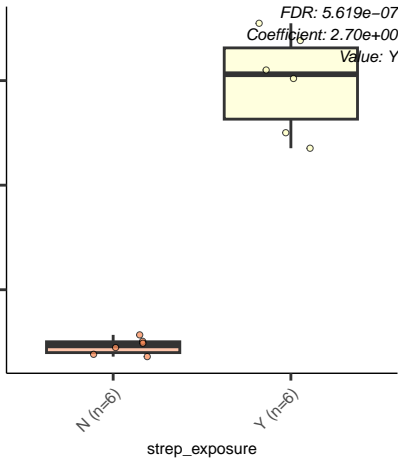
Y (n=6)

strep\_exposure

FDR: 4.228e-07  
Coefficient: 3.10e+00  
Value: Y



Beta.lactamase.cluster.in.Streptococcus



Urea.decomposition

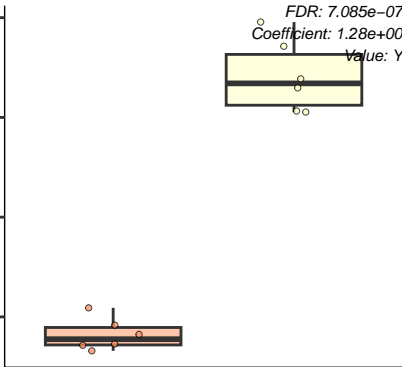
0.05  
0.04  
0.03  
0.02

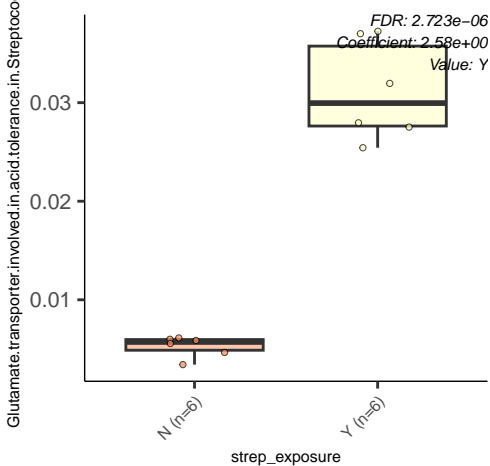
N (n=6)

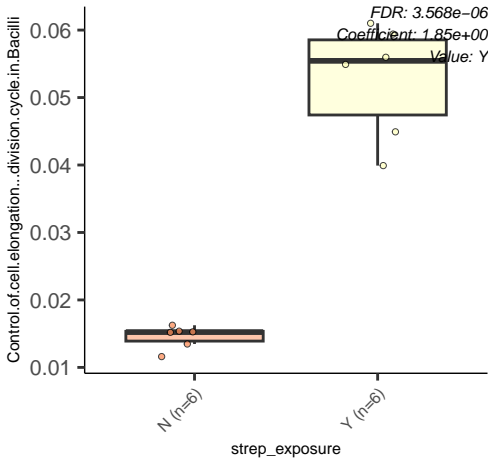
Y (n=6)

strep\_exposure

FDR: 7.085e-07  
Coefficient: 1.28e+00  
Value: Y

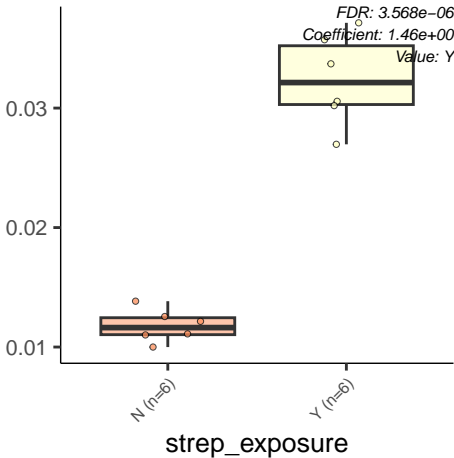








Urease.subunits



Gram.Positive.Competence

0.06

0.04

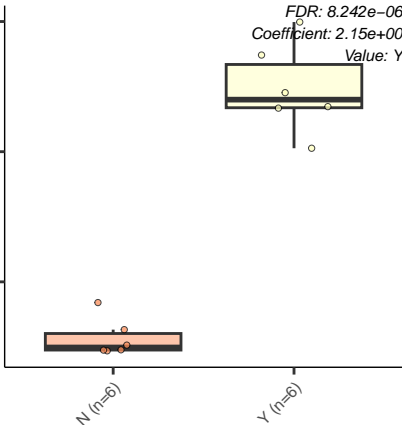
0.02

N (n=6)

Y (n=6)

strep\_exposure

FDR: 8.242e-06  
Coefficient: 2.15e+00  
Value: Y



HtrA.and.Sec.secretion

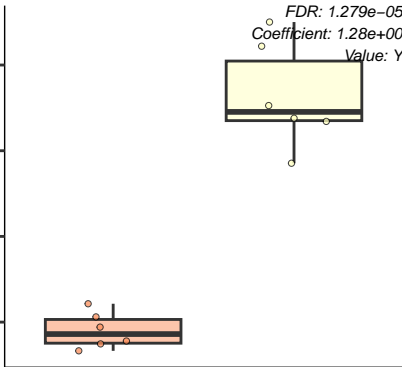
0.05  
0.04  
0.03  
0.02

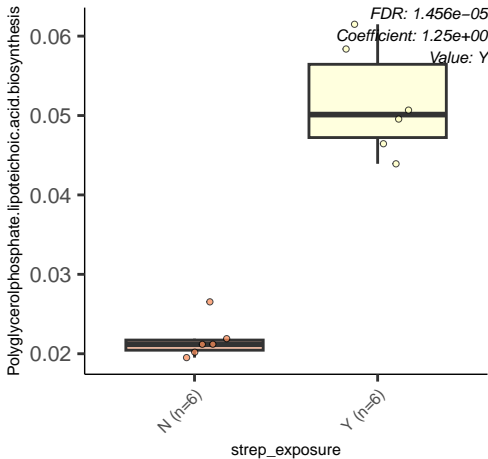
N (n=6)

Y (n=6)

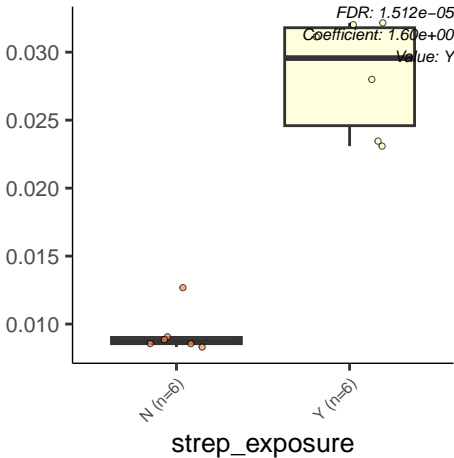
strep\_exposure

FDR: 1.279e-05  
Coefficient: 1.28e+00  
Value: Y

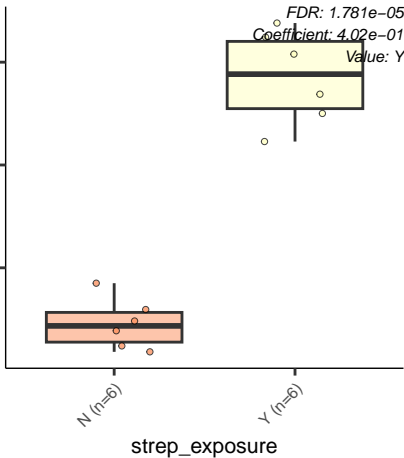




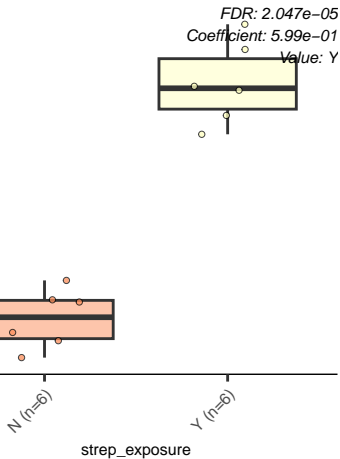
Archaeal.lipids

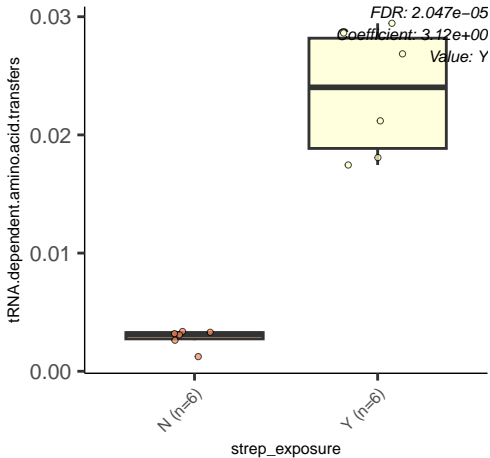


pyrimidine.conversions



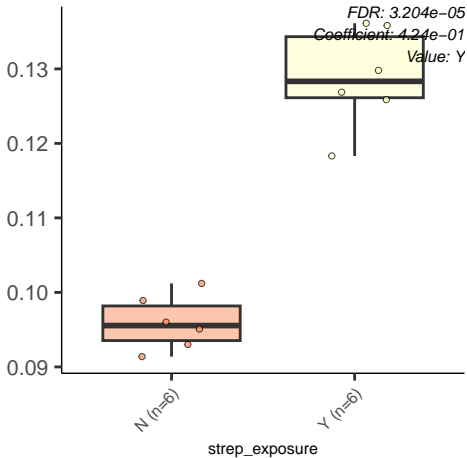
Conserved.gene.cluster.possibly.involved.in.RNA.metabolism







positive.cluster.that.relates.ribosomal.protein.L28P.to.a.set.of.uncha



At4g10620.At3g57180.At3g47450

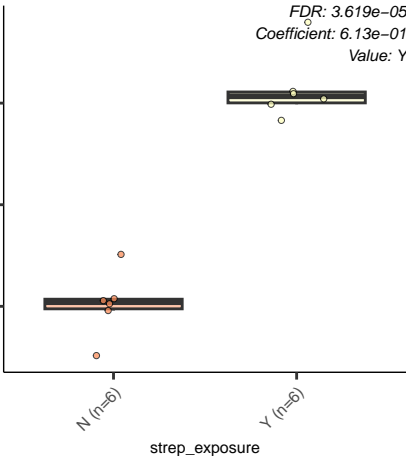
*FDR: 3.619e-05*  
*Coefficient: 6.13e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure

0.06  
0.05  
0.04



Streptococcus.agalactiae.virulome

0.006

0.004

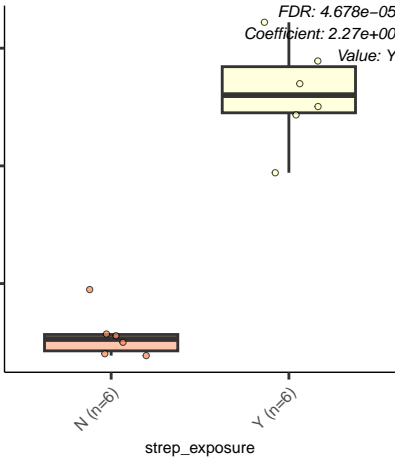
0.002

N (n=6)

Y (n=6)

strep\_exposure

FDR: 4.678e-05  
Coefficient: 2.27e+00  
Value: Y



Acetoin..butanediol.metabolism

0.14  
0.13  
0.12  
0.11  
0.10  
0.09

N (n=6)

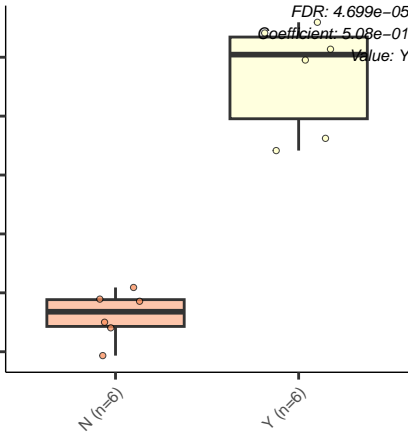
Y (n=6)

strep\_exposure

FDR: 4.699e-05

Coefficient: 5.08e-01

Value: Y



Cell.Division.Cluster

0.08  
0.07  
0.06  
0.05

N (n=6)

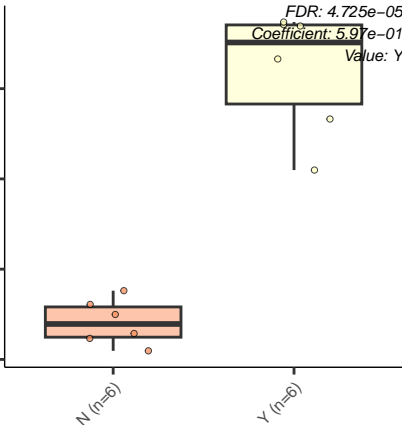
Y (n=6)

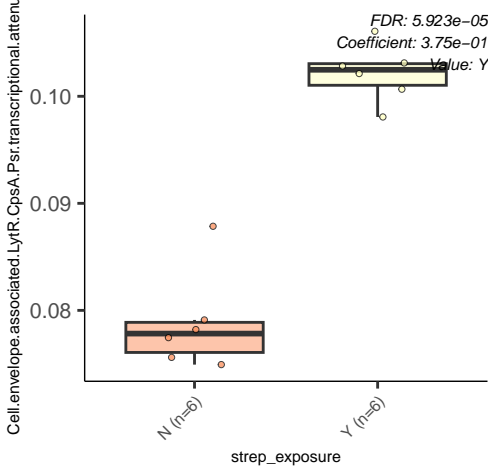
strep\_exposure

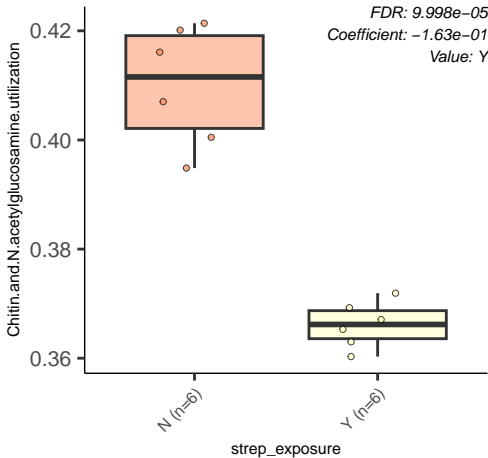
FDR: 4.725e-05

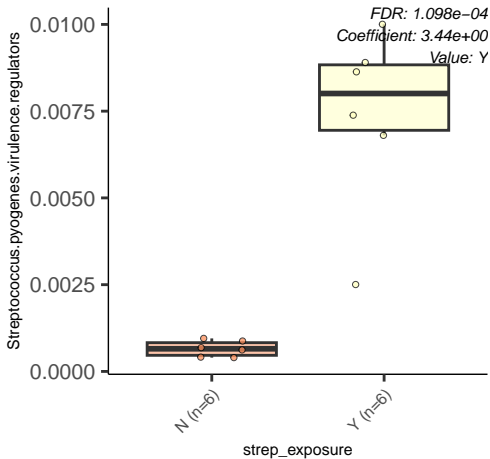
Coefficient: 5.97e-01

Value: Y











CBSS.262719.3.peg.410

0.13

0.12

0.11

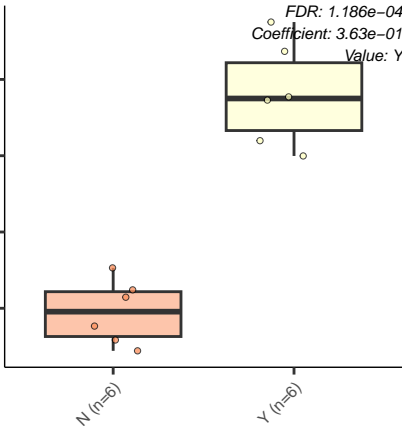
0.10

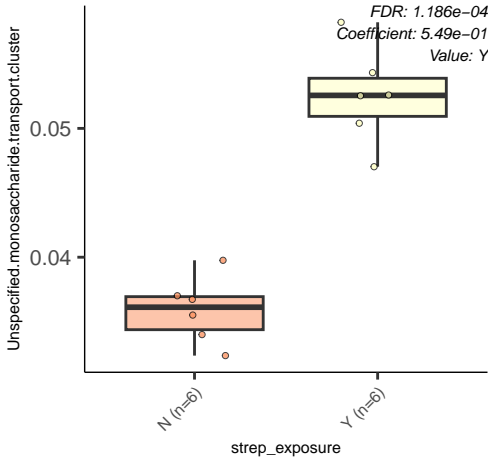
N (n=6)

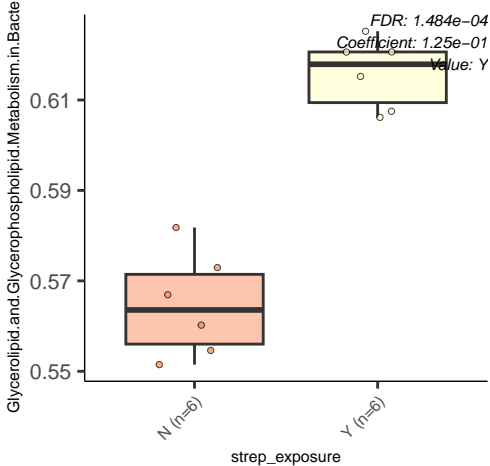
Y (n=6)

strep\_exposure

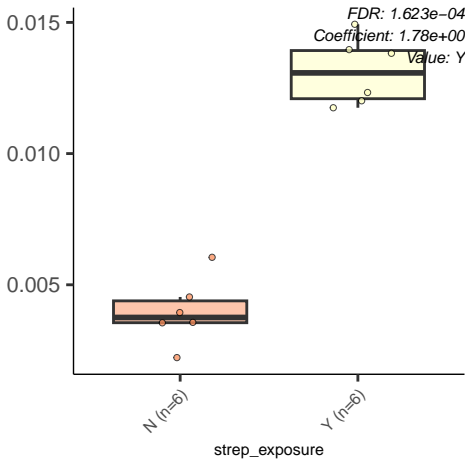
FDR: 1.186e-04  
Coefficient: 3.63e-01  
Value: Y







Single.Rhodanese.domain.proteins



Streptococcus.pyogenes.Virulome

0.015

0.010

0.005

N (n=6)

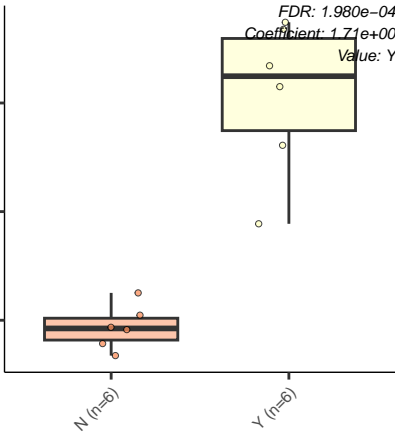
Y (n=6)

strep\_exposure

FDR: 1.980e-04

Coefficient: 1.71e+00

Value: Y



ATP.dependent.Nuclease

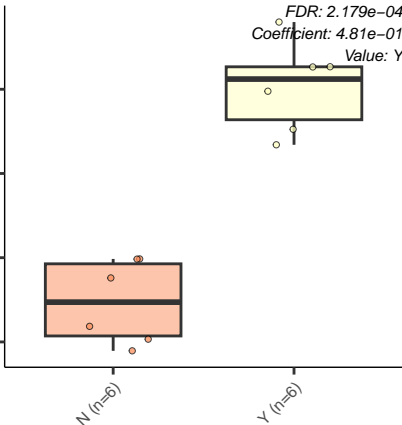
FDR: 2.179e-04  
Coefficient: 4.81e-01  
Value: Y

0.18  
0.16  
0.14  
0.12

N (n=6)

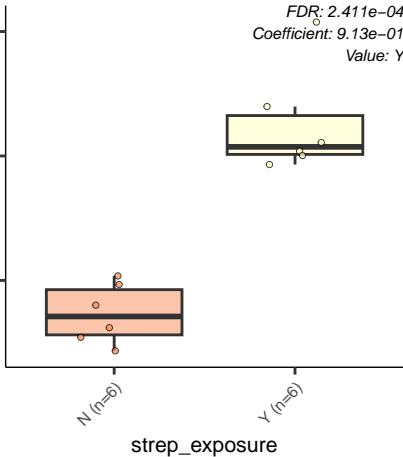
Y (n=6)

strep\_exposure



CBSS.222523.1.peg.1311

*FDR: 2.411e-04*  
*Coefficient: 9.13e-01*  
*Value: Y*



L.Arabinose.utilization

*FDR: 2.891e-04*  
*Coefficient: -1.84e-01*  
*Value: Y*

0.68

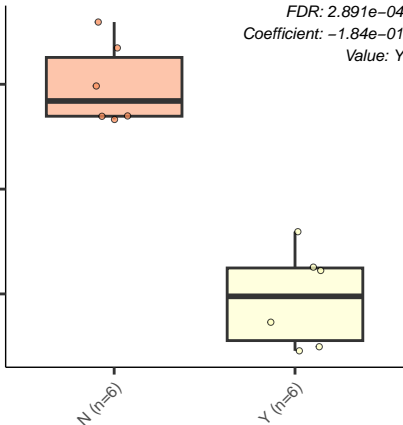
0.64

0.60

N (n=6)

Y (n=6)

strep\_exposure





Omega.amidase

0.008

0.006

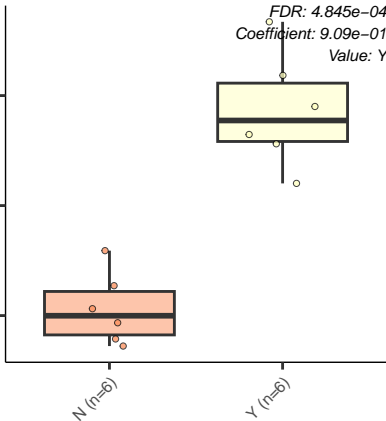
0.004

N (n=6)

Y (n=6)

strep\_exposure

FDR: 4.845e-04  
Coefficient: 9.09e-01  
Value: Y



CBSS.261594.1.peg.788

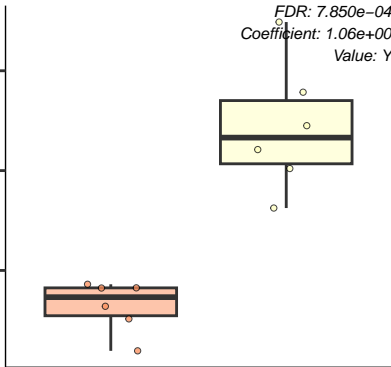
*FDR: 7.850e-04*  
*Coefficient: 1.06e+00*  
*Value: Y*

0.016  
0.012  
0.008

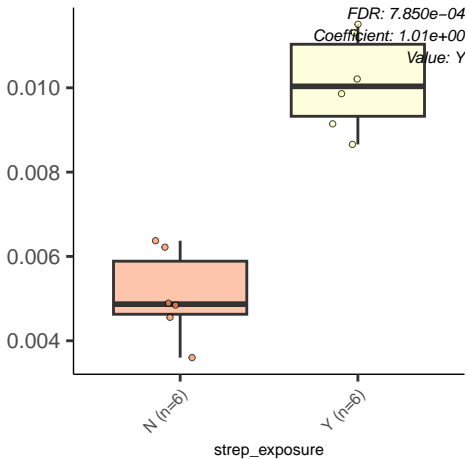
*N (n=6)*

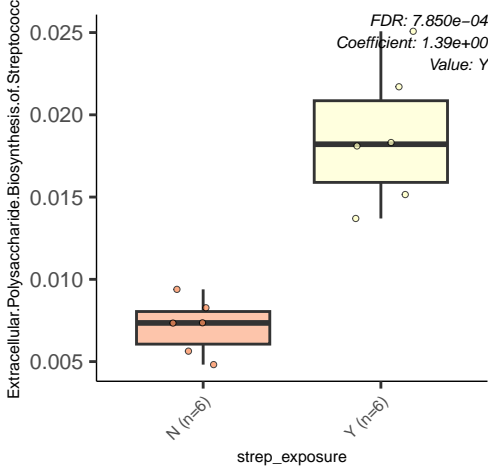
*Y (n=6)*

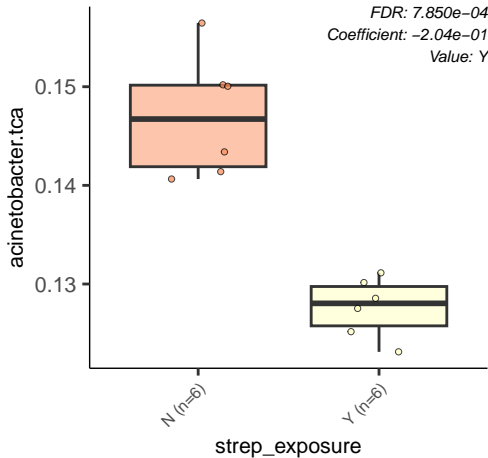
strep\_exposure



D.Alanyl.Lipoteichoic.Acid.Biosynthesis







RNA.pseudouridine.syntheses

0.080

0.075

0.070

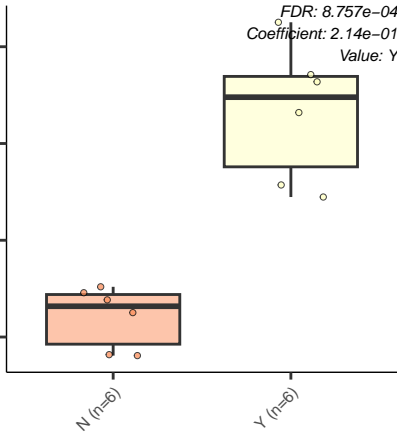
0.065

N (n=6)

Y (n=6)

strep\_exposure

FDR:  $8.757e-04$   
Coefficient:  $2.14e-01$   
Value: Y



Copper.homeostasis

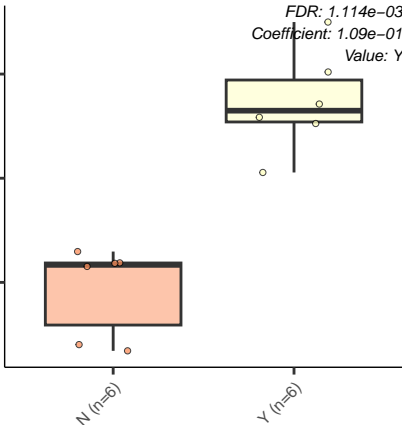
0.50  
0.48  
0.46

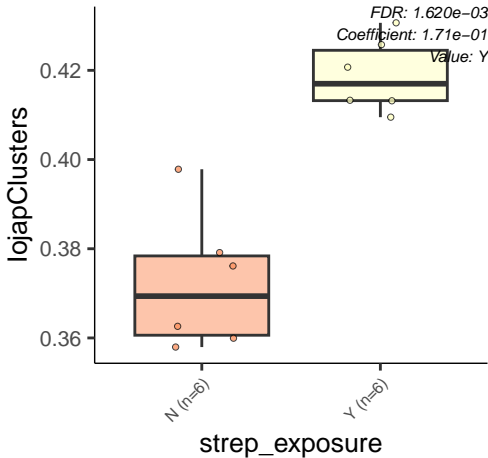
N (n=6)

Y (n=6)

strep\_exposure

FDR: 1.114e-03  
Coefficient: 1.09e-01  
Value: Y







Methionine.Biosynthesis

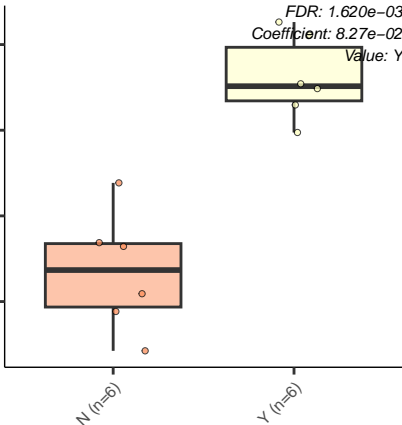
0.82  
0.80  
0.78  
0.76

N (n=6)

Y (n=6)

strep\_exposure

FDR: 1.620e-03  
Coefficient: 8.27e-02  
Value: Y



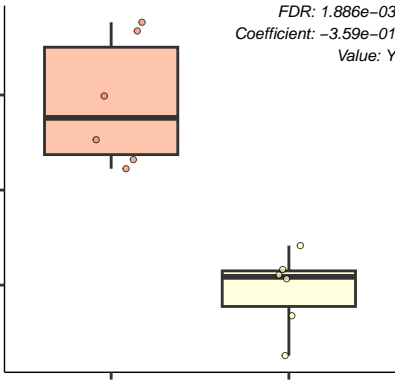
Glycerol.fermentation.to.1.3.propanediol

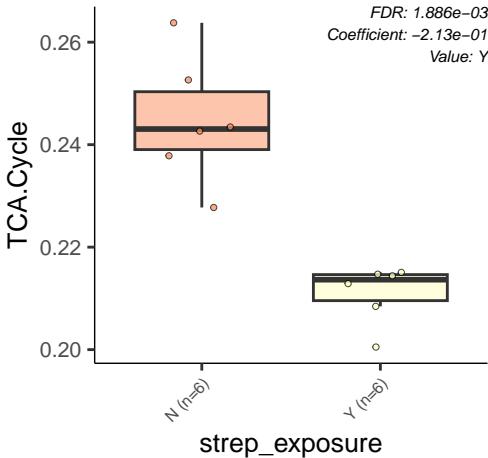
*FDR: 1.886e-03*  
*Coefficient: -3.59e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure





Streptococcal.Mga.Regulon

0.010

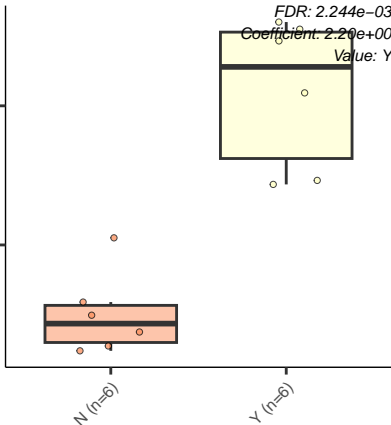
0.005

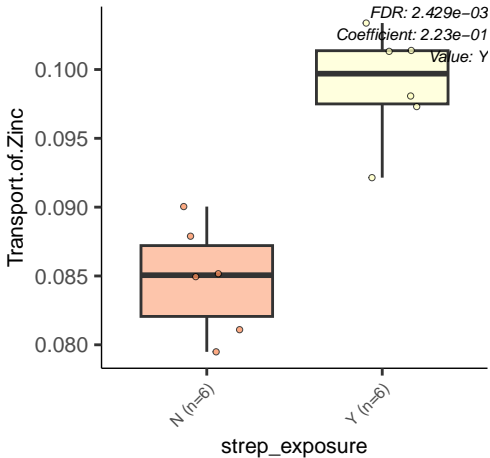
N (n=6)

Y (n=6)

strep\_exposure

FDR: 2.244e-03  
Coefficient: 2.26e+00  
Value: Y





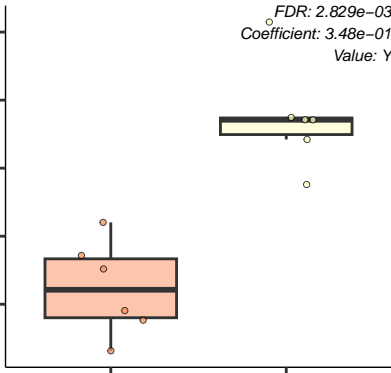
CBSS.257314.1.peg.676

*FDR: 2.829e-03*  
*Coefficient: 3.48e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



Dehydrogenase.complexes

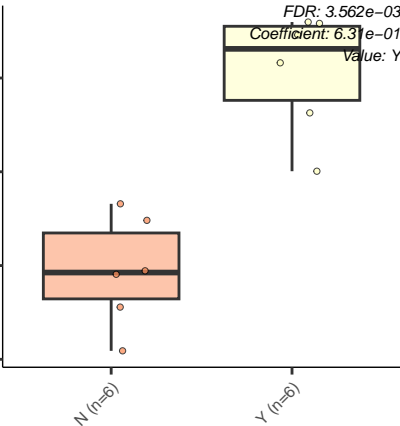
0.06  
0.05  
0.04  
0.03

N (n=6)

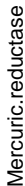
Y (n=6)

strep\_exposure

FDR:  $3.562 \times 10^{-3}$   
Coefficient:  $6.31 \times 10^{-1}$   
Value: Y

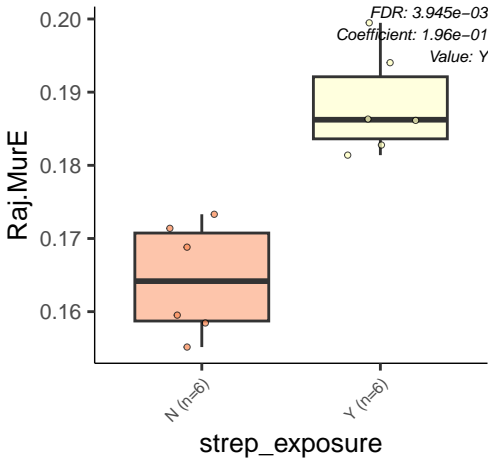


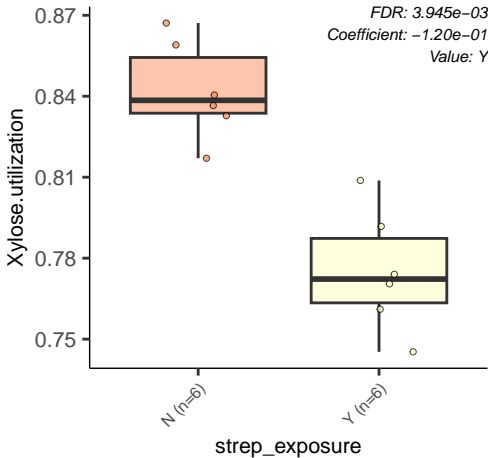
FDR: 3.562e-03  
Coefficient: 5.64e-01  
Value: Y

 $N(n=6)$  $\gamma (n=6)$ 

strep\_exposure







Adhesion.of.Campylobacter

0.036

0.032

0.028

0.024

N (n=6)

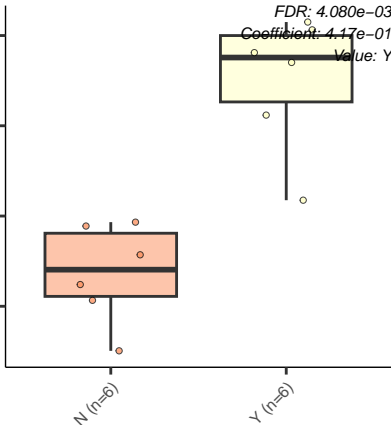
Y (n=6)

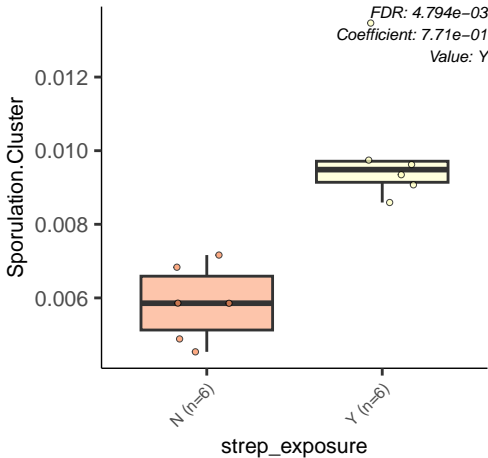
strep\_exposure

FDR: 4.080e-03

Coefficient: 4.17e-01

Value: Y





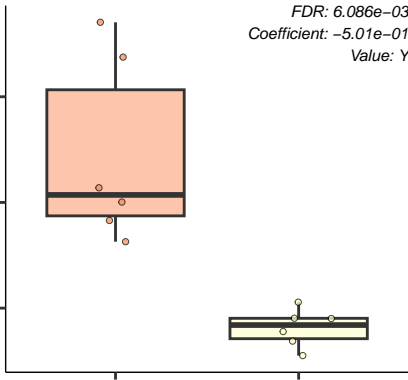
Threonine.anaerobic.catabolism.gene.cluster

*FDR: 6.086e-03*  
*Coefficient: -5.01e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



Alpha.acetolactate.operon

0.008

0.006

0.004

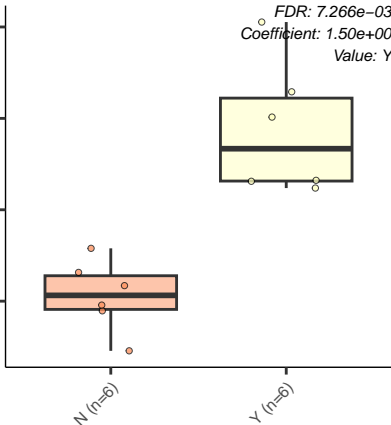
0.002

N (n=6)

Y (n=6)

strep\_exposure

FDR: 7.266e-03  
Coefficient: 1.50e+00  
Value: Y



Mercury.resistance.operon

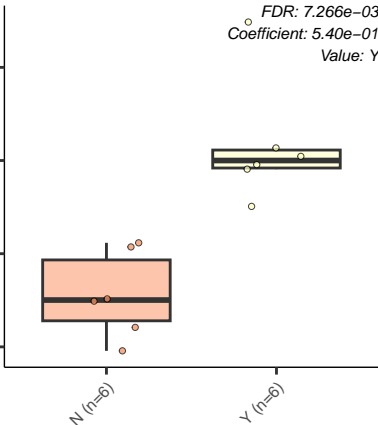
*FDR: 7.266e-03*  
*Coefficient: 5.40e-01*  
*Value: Y*

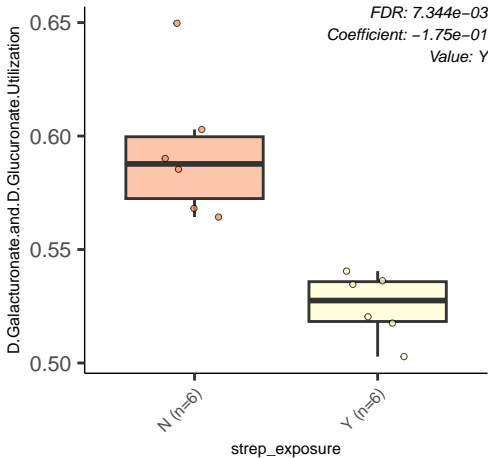
0.0150  
0.0125  
0.0100  
0.0075

N (n=6)

Y (n=6)

strep\_exposure







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

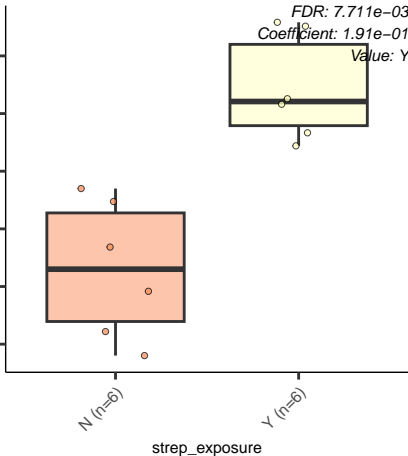
0.26  
0.25  
0.24  
0.23  
0.22  
0.21

N (n=6)

Y (n=6)

strep\_exposure

FDR: 7.711e-03  
Coefficient: 1.91e-01  
Value: Y



Prophage.lysogenic.conversion.modules

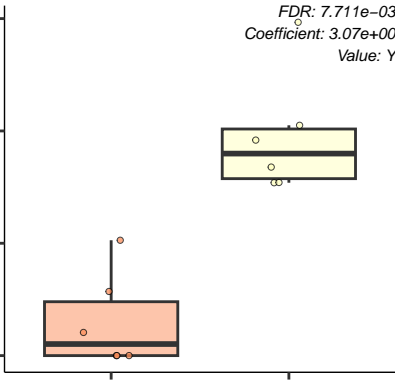
*FDR: 7.711e-03*  
*Coefficient: 3.07e+00*  
*Value: Y*

0.003  
0.002  
0.001  
0.000

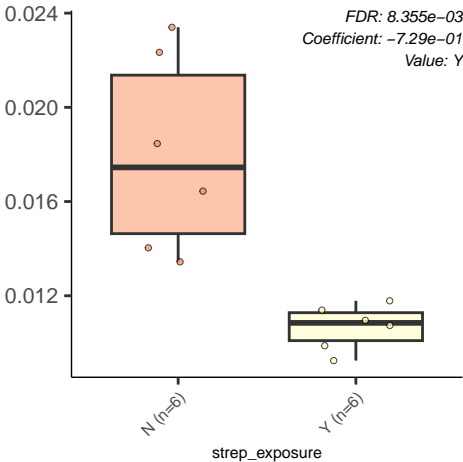
N (n=6)

Y (n=6)

strep\_exposure



Capsular.surface.virulence.antigen.loci



Heat.shock.dnaK.gene.cluster.extended

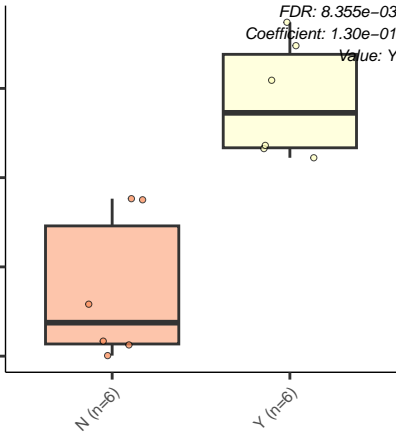
0.625  
0.600  
0.575  
0.550

N (n=6)

Y (n=6)

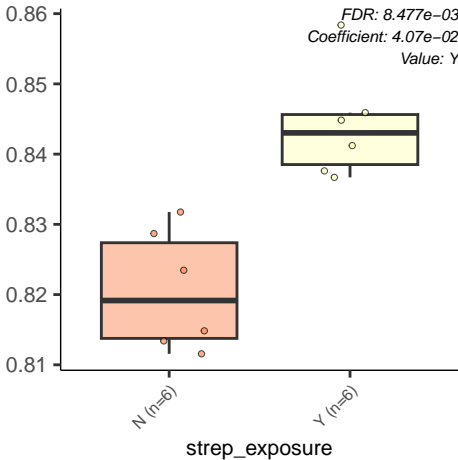
strep\_exposure

FDR:  $8.355e-03$   
Coefficient:  $1.30e-01$   
Value: Y



DNA.repair..bacterial

*FDR: 8.477e-03*  
*Coefficient: 4.07e-02*  
*Value: Y*



Glutathione..Redox.cycle

0.05

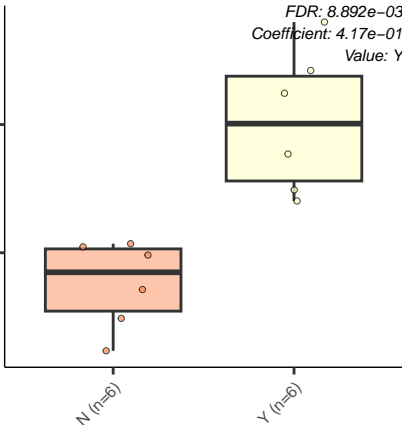
0.04

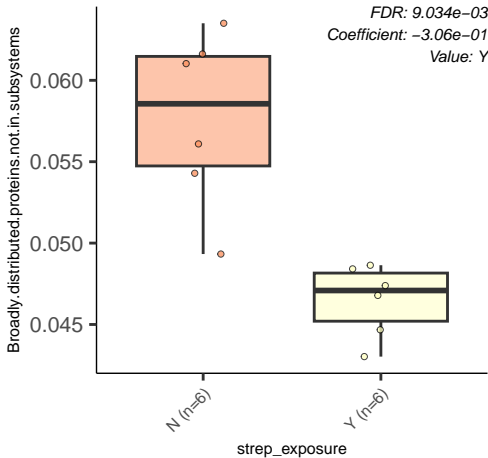
N (n=6)

Y (n=6)

strep\_exposure

FDR:  $8.892e-03$   
Coefficient:  $4.17e-01$   
Value: Y





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

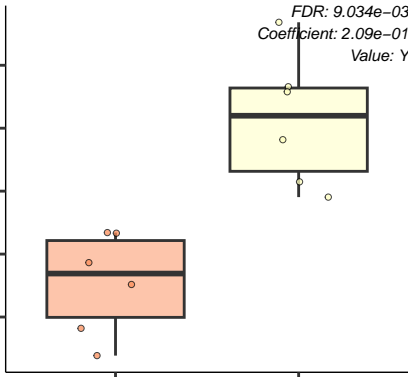
0.20  
0.19  
0.18  
0.17  
0.16

*FDR: 9.034e-03*  
*Coefficient: 2.09e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure





Monika.MRSA

*FDR: 9.034e-03*  
*Coefficient: 2.51e-01*  
*Value: Y*

0.044

0.040

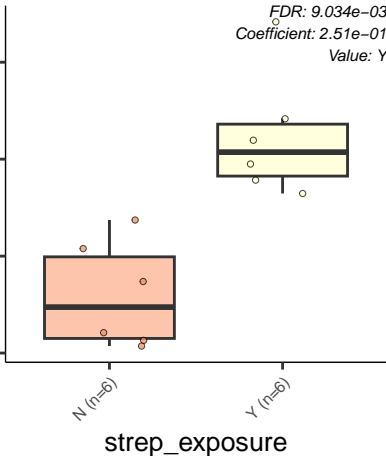
0.036

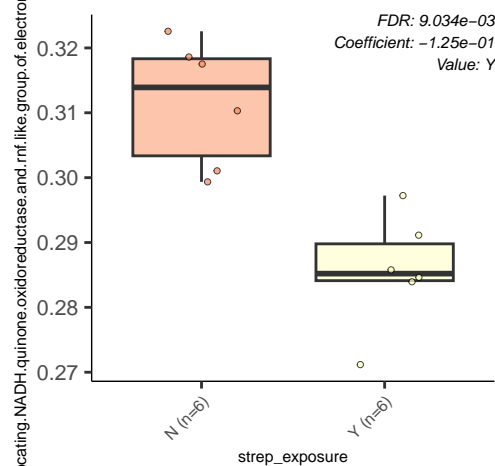
0.032

N (n=6)

Y (n=6)

strep\_exposure





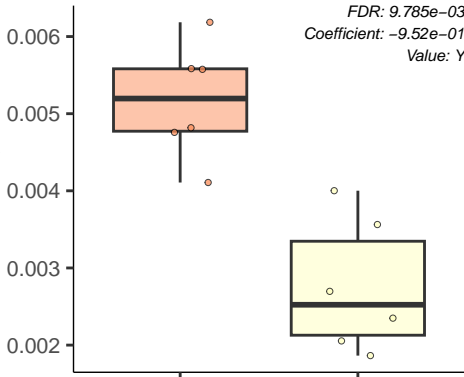
Unknown.carbohydrate.utilization.containing.Fructose.bisphosphat

FDR:  $9.785e-03$   
Coefficient:  $-9.52e-01$   
Value: Y

N (n=6)

Y (n=6)

strep\_exposure



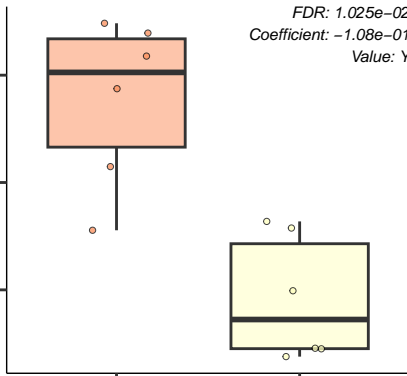
Fructooligosaccharides.FOS..and.Raffinose.Utilization

*FDR: 1.025e-02*  
*Coefficient: -1.08e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



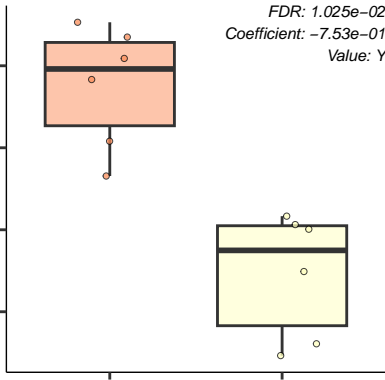
Two.partner.secretion..TPS.

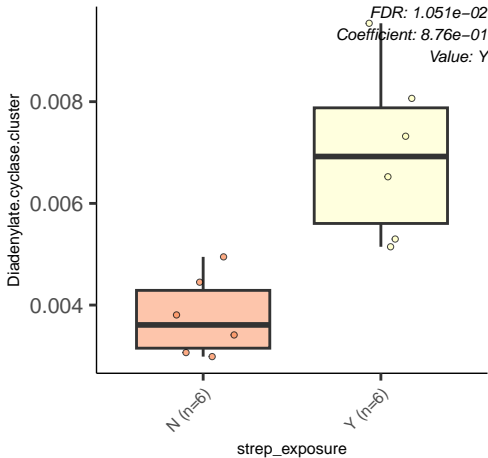
*FDR: 1.025e-02*  
*Coefficient: -7.53e-01*  
*Value: Y*

N (n=6)

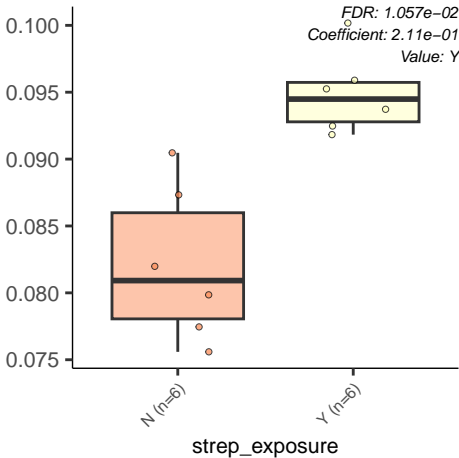
Y (n=6)

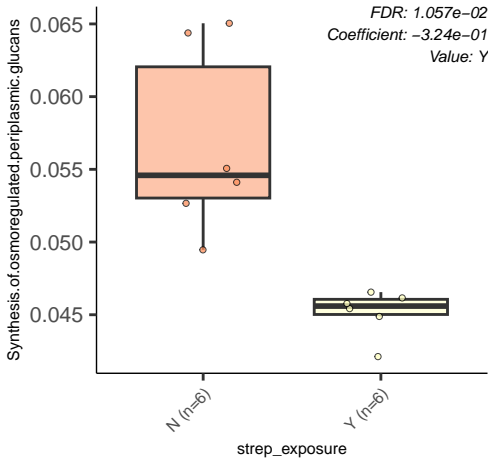
strep\_exposure



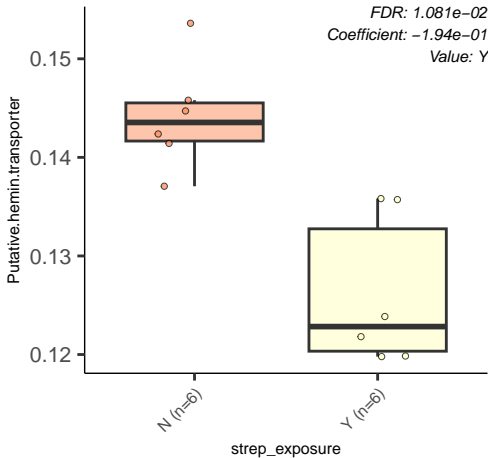


CBSS.84588.1.peg.1247









Outer.membrane

FDR: 1.134e-02

Coefficient: -3.38e-01

Value: Y

0.045

0.040

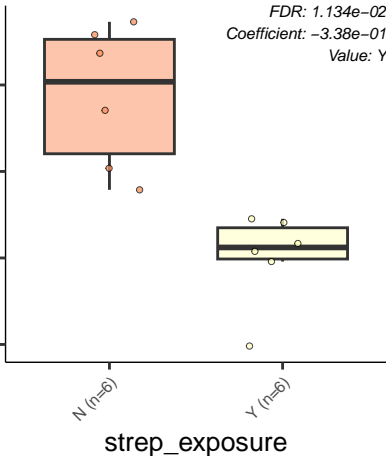
0.035

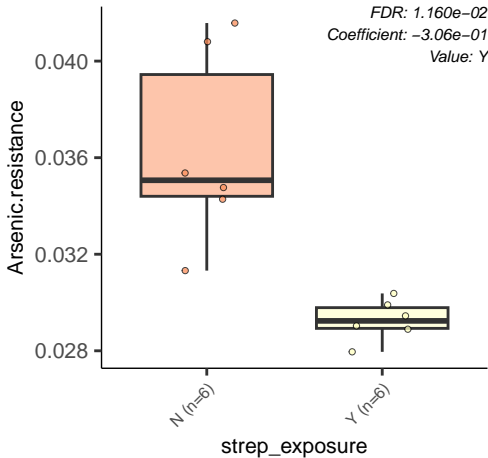
0.030

N (n=6)

Y (n=6)

strep\_exposure





CBSS.393130.3.pcg.794

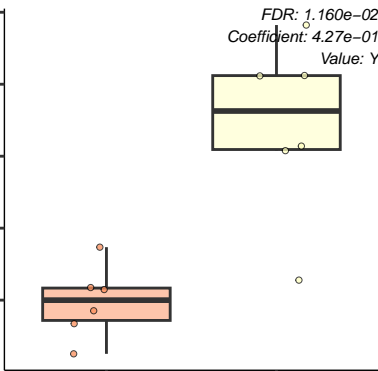
0.0275  
0.0250  
0.0225  
0.0200  
0.0175

N (n=6)

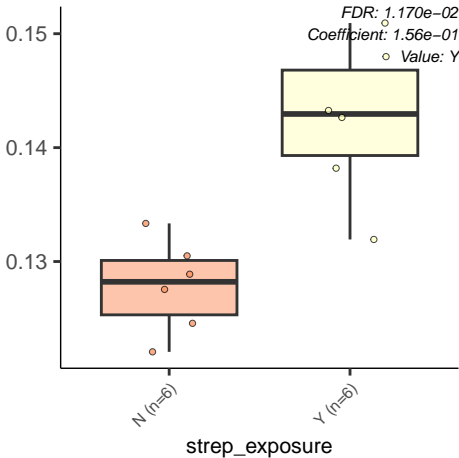
Y (n=6)

strep\_exposure

FDR: 1.160e-02  
Coefficient: 4.27e-01  
Value: Y



Fe.S.cluster.assembly



LMPTP.YwIE.cluster

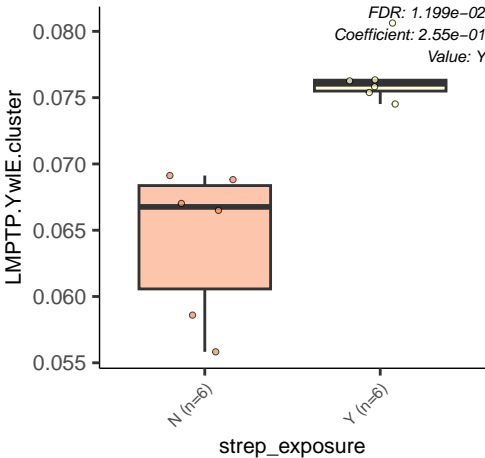
*FDR: 1.199e-02*  
*Coefficient: 2.55e-01*  
*Value: Y*

0.080  
0.075  
0.070  
0.065  
0.060  
0.055

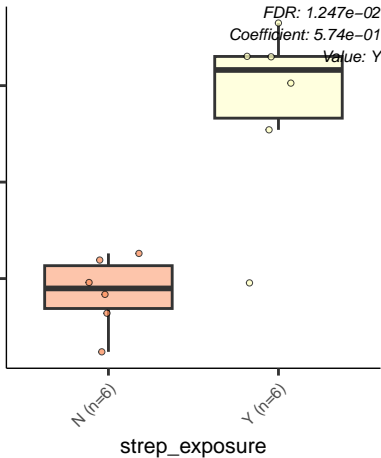
N (n=6)

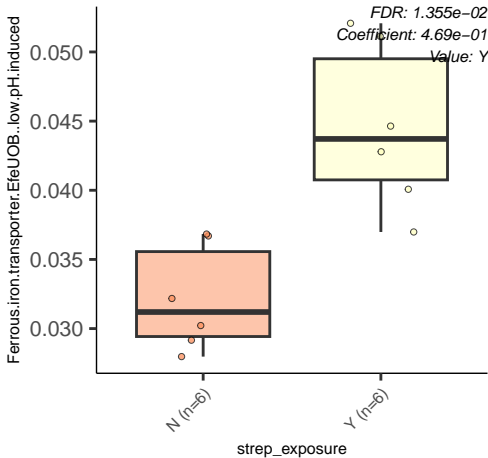
Y (n=6)

strep\_exposure



CBSS.279010.5.peg.3195







Histidine.Biosynthesis

0.575

0.550

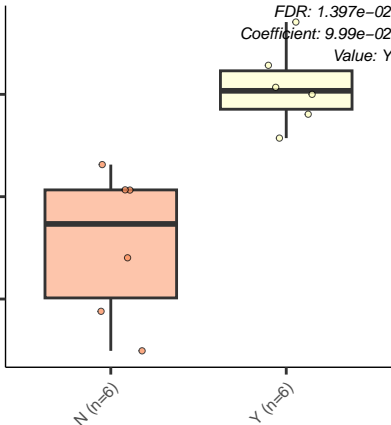
0.525

N (n=6)

Y (n=6)

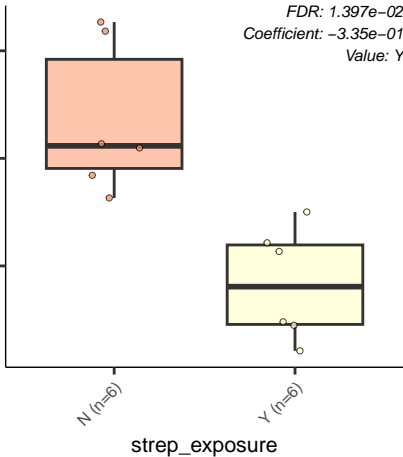
strep\_exposure

FDR: 1.397e-02  
Coefficient: 9.99e-02  
Value: Y



Phage.tail.proteins.2

FDR:  $1.397e-02$   
Coefficient:  $-3.35e-01$   
Value: Y



KDO2.Lipid.A.biosynthesis

FDR:  $1.410\text{e-}02$   
Coefficient:  $-1.75\text{e-}01$   
Value: Y

0.28

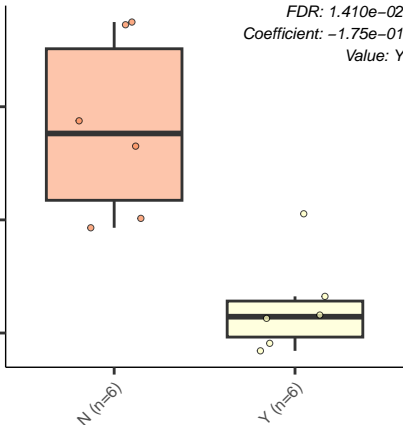
0.26

0.24

N (n=6)

Y (n=6)

strep\_exposure



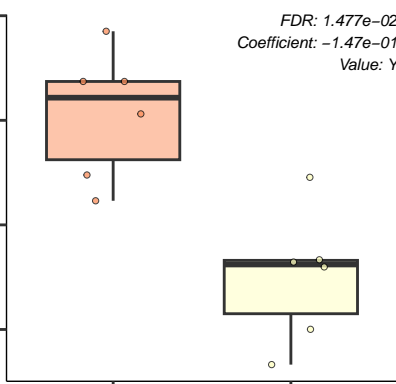
Menaquinone.biosynthesis.from.chorismate.via.1.4.dihydroxy.2.na

FDR: 1.477e-02  
Coefficient: -1.47e-01  
Value: Y

N (n=6)

Y (n=6)

strep\_exposure



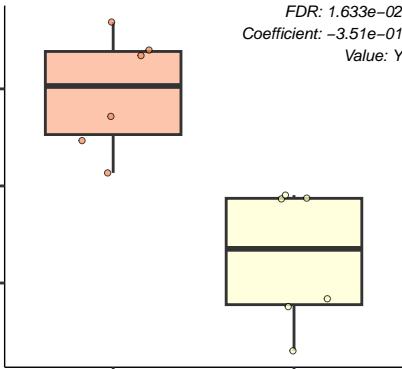
Hemin.transport.system

FDR: 1.633e-02  
Coefficient: -3.51e-01  
Value: Y

N (n=6)

Y (n=6)

strep\_exposure



Transport.of.Manganese

0.070

0.065

0.060

0.055

0.050

0.045

N (n=6)

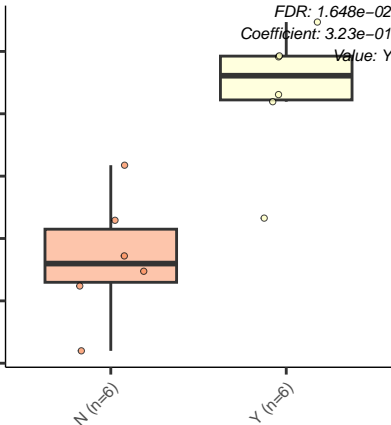
Y (n=6)

strep\_exposure

FDR: 1.648e-02

Coefficient: 3.23e-01

Value: Y



BOX..RUP.and.SPRITE.repeats.in.Streptococcus.pneumoni

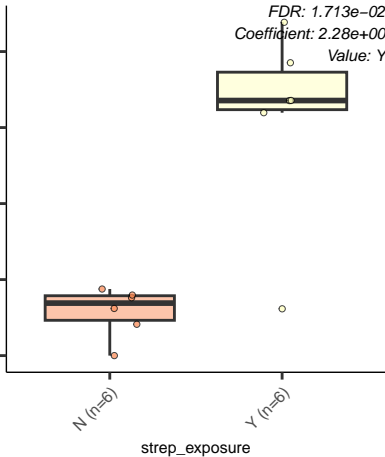
0.0020  
0.0015  
0.0010  
0.0005  
0.0000

N (n=6)

Y (n=6)

strep\_exposure

FDR: 1.713e-02  
Coefficient: 2.28e+00  
Value: Y



CBSS.243265.1.peg.198

0.030

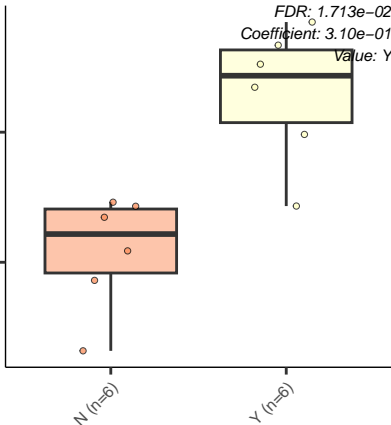
0.025

N (n=6)

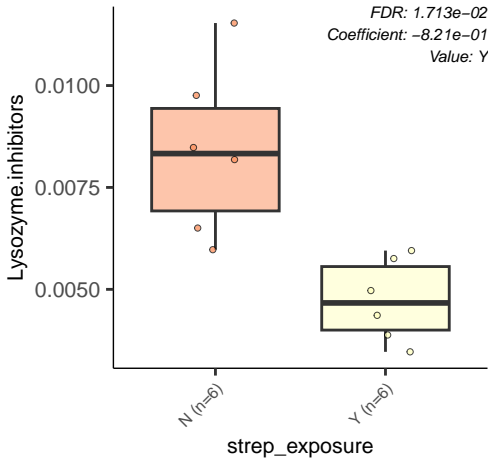
Y (n=6)

strep\_exposure

FDR: 1.713e-02  
Coefficient: 3.10e-01  
Value: Y







Murein.Hydrolases

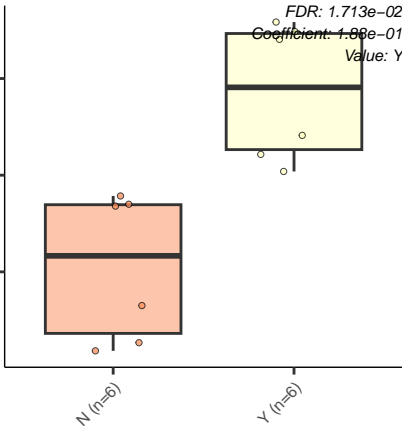
0.15  
0.14  
0.13

N (n=6)

Y (n=6)

strep\_exposure

FDR: 1.713e-02  
Coefficient: 1.88e-01  
Value: Y



Carbon.Starvation

*FDR: 1.894e-02*  
*Coefficient: -1.73e-01*  
*Value: Y*

0.15

0.14

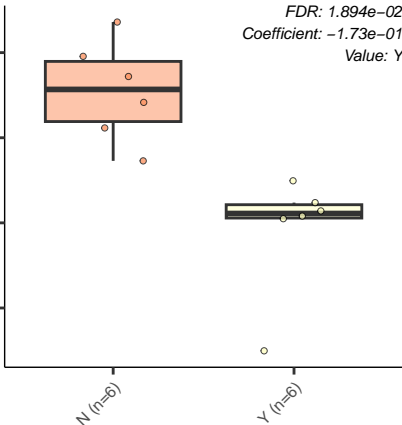
0.13

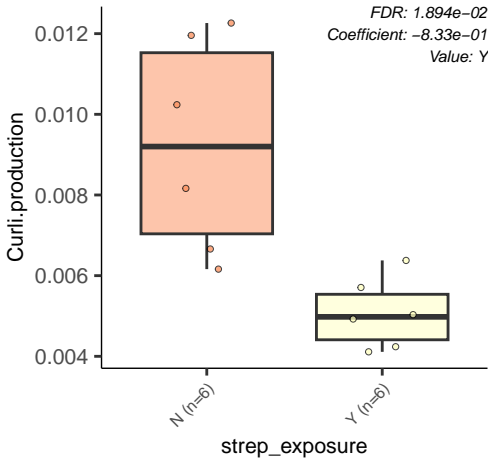
0.12

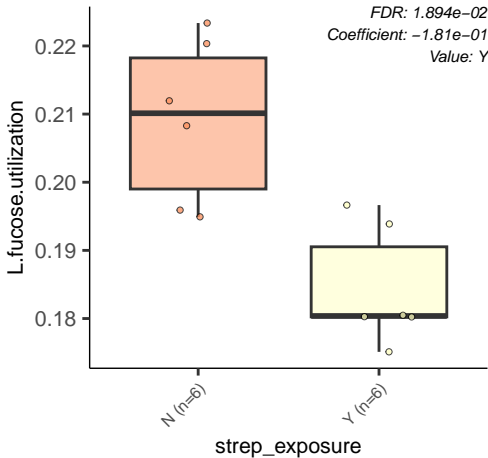
N (n=6)

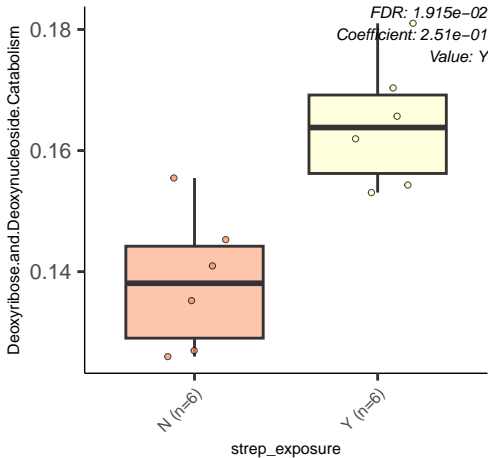
Y (n=6)

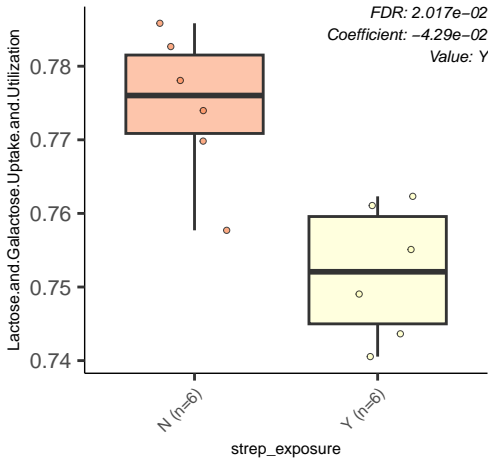
strep\_exposure











Glutaredoxins

*FDR: 2.040e-02*  
*Coefficient: -6.91e-02*  
*Value: Y*

0.225

0.220

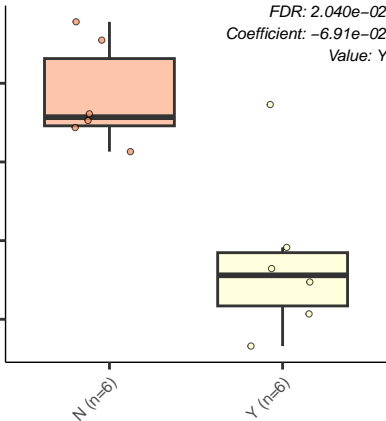
0.215

0.210

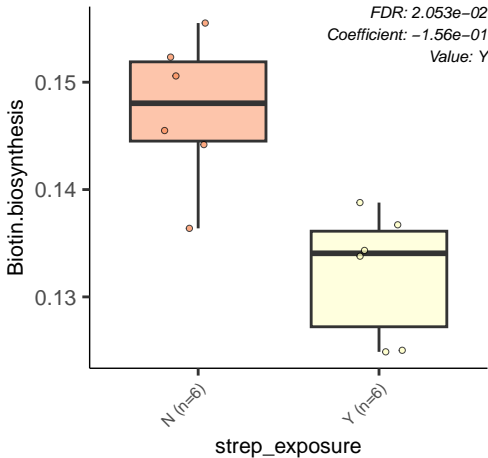
N (n=6)

Y (n=6)

strep\_exposure







CBSS.393121.3.peg.2760

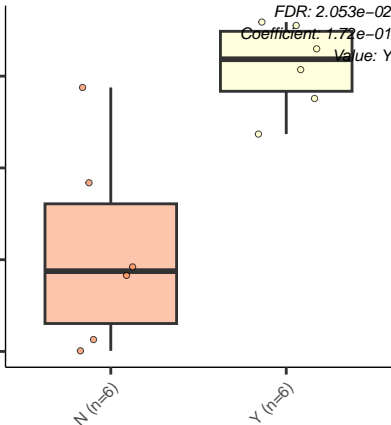
0.450  
0.425  
0.400  
0.375

N (n=6)

Y (n=6)

strep\_exposure

FDR: 2.053e-02  
Coefficient: 1.72e-01  
Value: Y



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

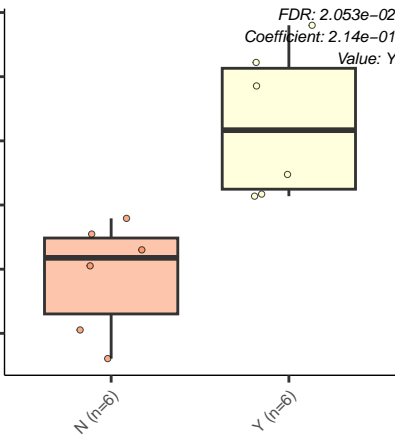
0.095  
0.090  
0.085  
0.080  
0.075  
0.070

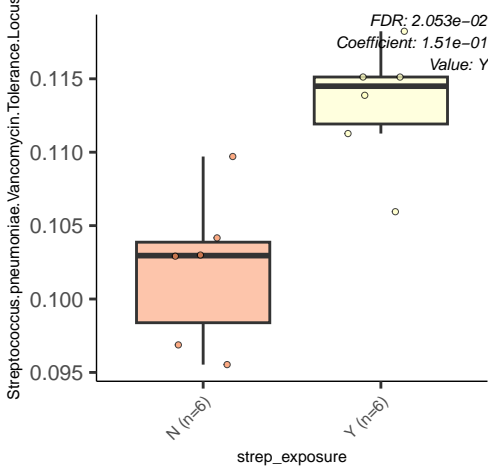
N (n=6)

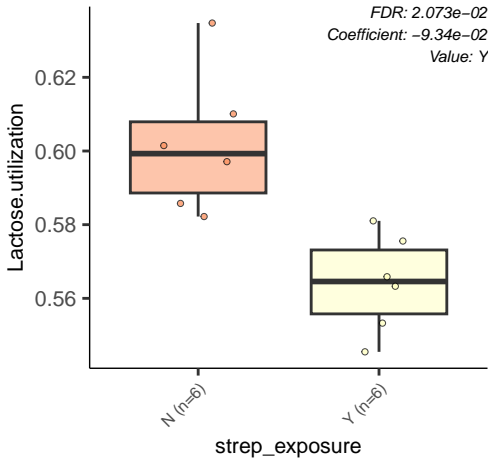
Y (n=6)

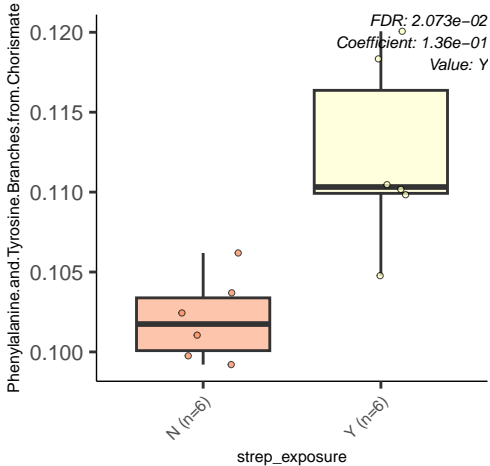
strep\_exposure

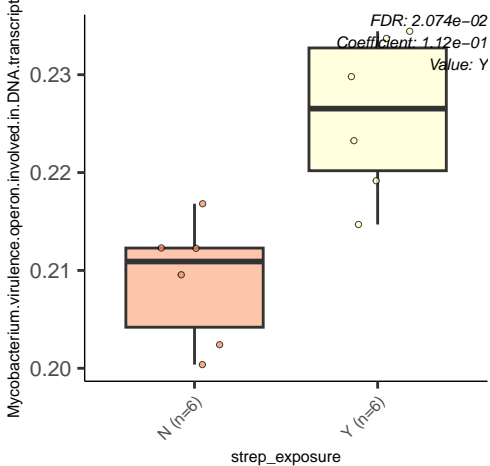
FDR: 2.053e-02  
Coefficient: 2.14e-01  
Value: Y











Alpha.Amylase.locus.in.Streptococcus

0.08

0.07

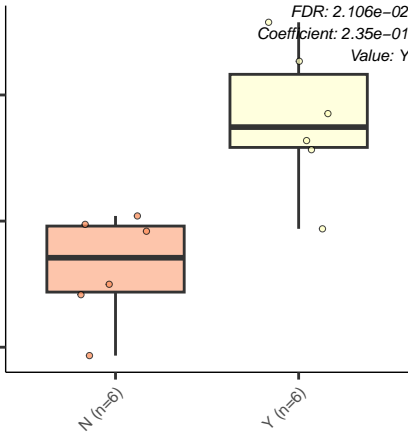
0.06

N (n=6)

Y (n=6)

strep\_exposure

FDR: 2.106e-02  
Coefficient: 2.35e-01  
Value: Y





cell.division.cluster.containing.FtsQ

*FDR: 2.236e-02*  
*Coefficient: 3.18e-01*  
*Value: Y*

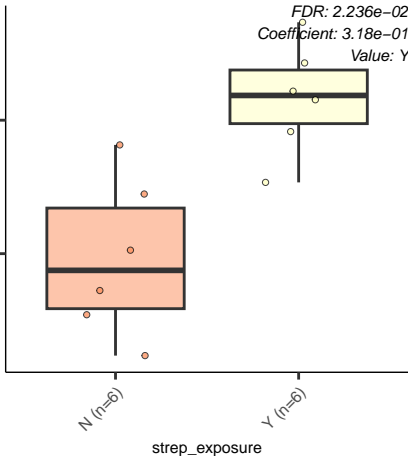
0.06

0.05

*N (n=6)*

*Y (n=6)*

strep\_exposure



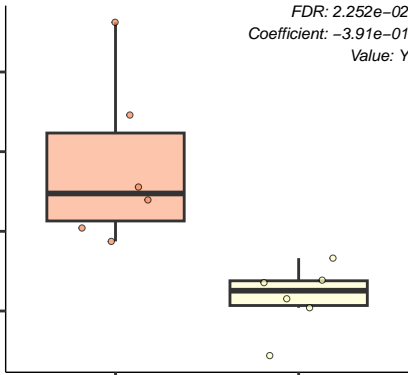
Phd.Doc.. YdcE. YdcD.toxin.antitoxin.. programmed.cell.death..s

FDR: 2.252e-02  
Coefficient: -3.91e-01  
Value: Y

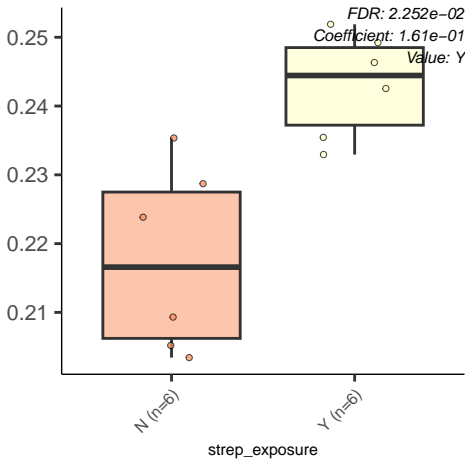
N (n=6)

Y (n=6)

strep\_exposure



tRNA.aminoacylation...Asp.and.Asn



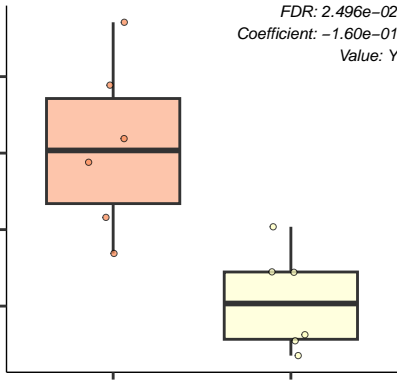
Glycolate..glyoxylate.interconversions

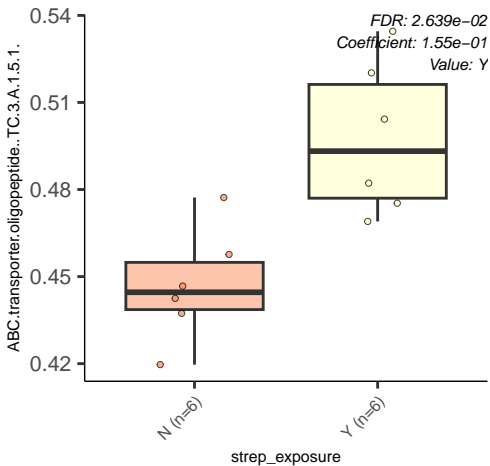
*FDR: 2.496e-02*  
*Coefficient: -1.60e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure





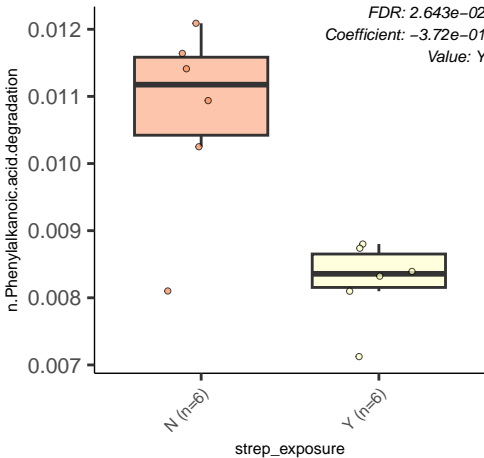
n.Phenylalkanoic.acid.degradation

*FDR: 2.643e-02*  
*Coefficient: -3.72e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



Cell.Division.Subsystem.including.YidCD

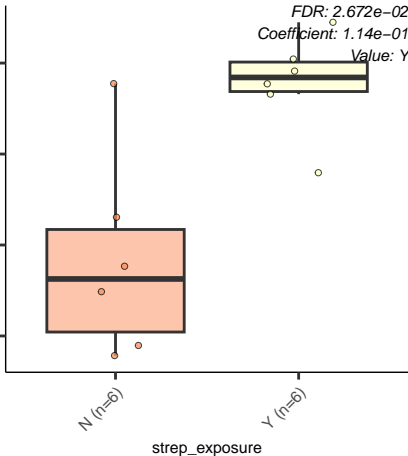
0.26  
0.25  
0.24  
0.23

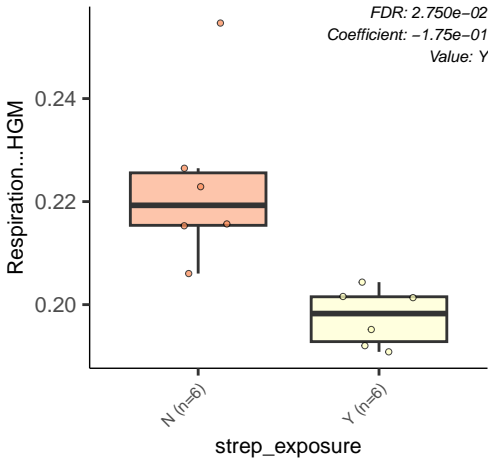
N (n=6)

Y (n=6)

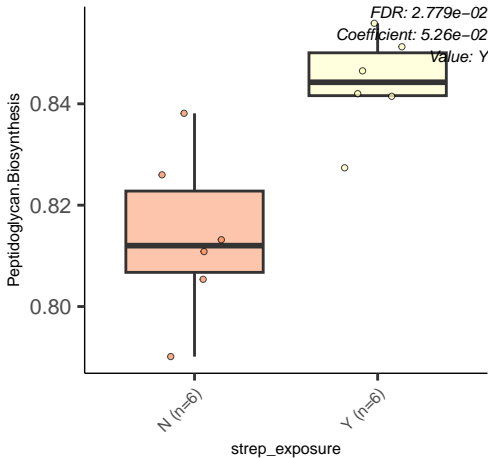
strep\_exposure

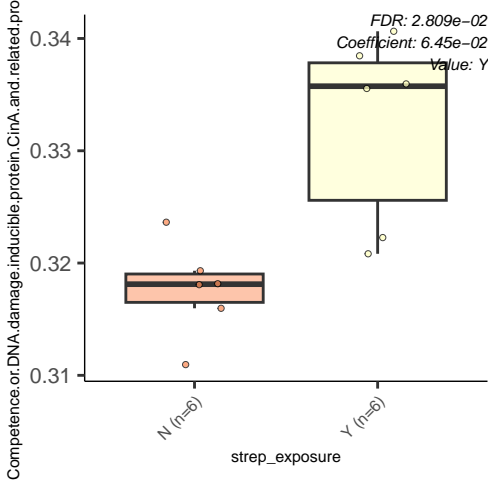
FDR: 2.672e-02  
Coefficient: 1.14e-01  
Value: Y











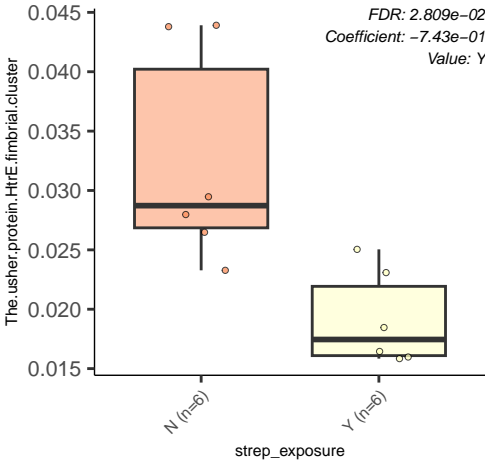
The.usher.protein.HtrE.fimbral.cluster

FDR: 2.809e-02  
Coefficient: -7.43e-01  
Value: Y

N (n=6)

Y (n=6)

strep\_exposure



Calvin.Benson.cycle

0.20

0.19

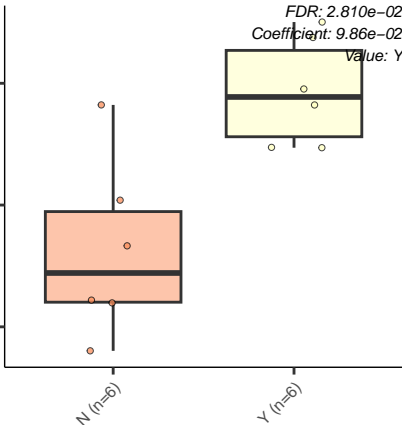
0.18

N (n=6)

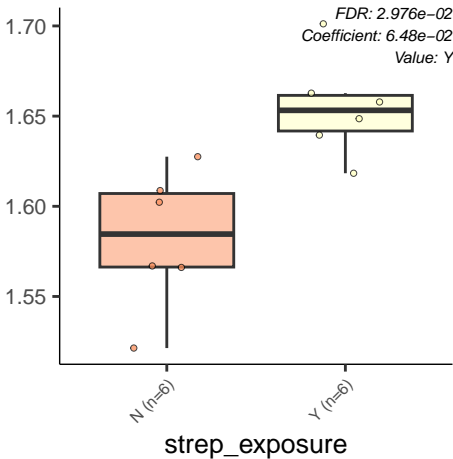
Y (n=6)

strep\_exposure

FDR: 2.810e-02  
Coefficient: 9.86e-02  
Value: Y



DNA.replication



CBSS.176299.4.peg.1292

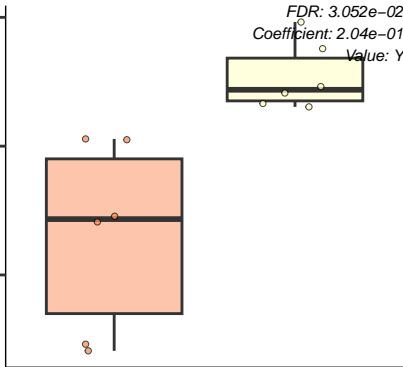
0.10  
0.09  
0.08

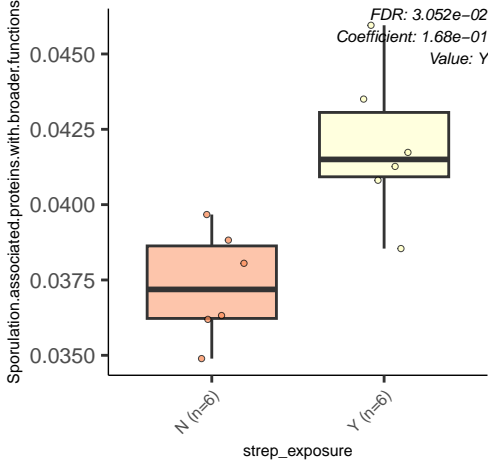
N (n=6)

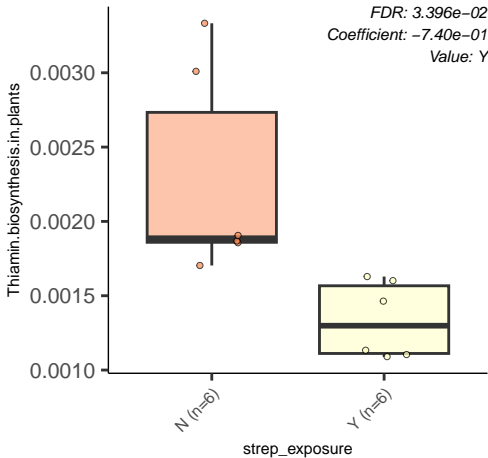
Y (n=6)

strep\_exposure

FDR: 3.052e-02  
Coefficient: 2.04e-01  
Value: Y

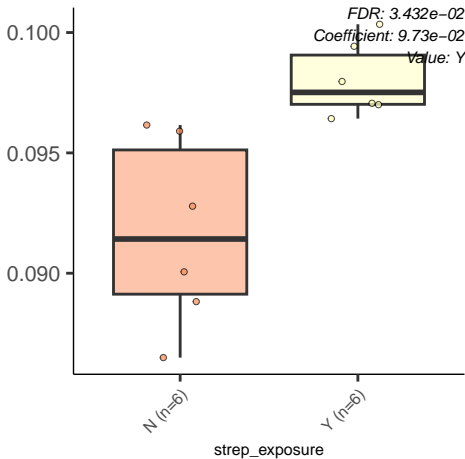








RuvABC.plus.a.hypothetical



Arginine.and.Ornithine.Degradation

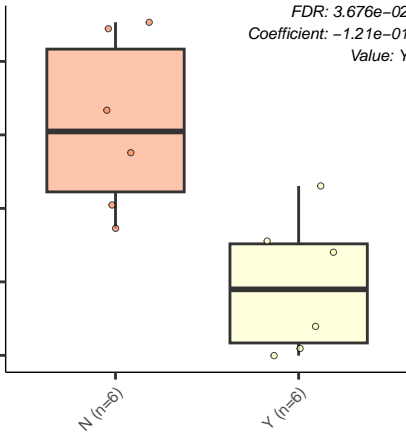
*FDR: 3.676e-02*  
*Coefficient: -1.21e-01*  
*Value: Y*

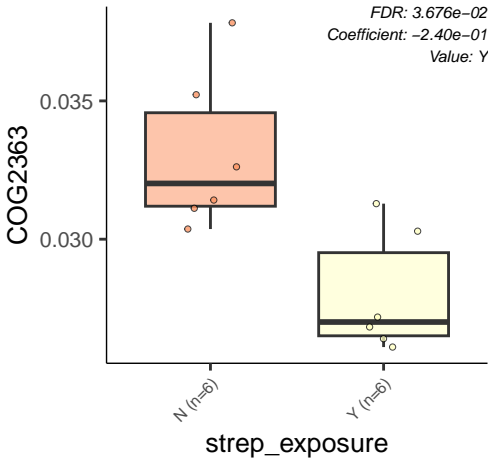
0.28  
0.27  
0.26  
0.25  
0.24

N (n=6)

Y (n=6)

strep\_exposure





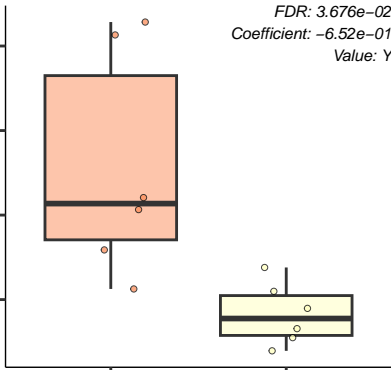
Cinnamic.Acid.Degradation

*FDR: 3.676e-02*  
*Coefficient: -6.52e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



Hydantoin.metabolism

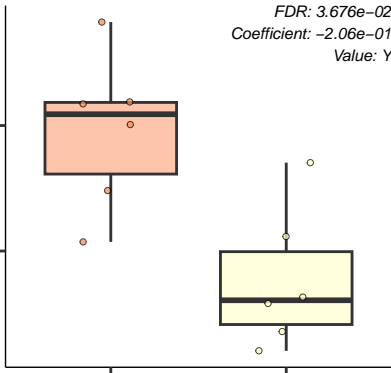
*FDR: 3.676e-02*  
*Coefficient: -2.06e-01*  
*Value: Y*

0.045  
0.040

N (n=6)

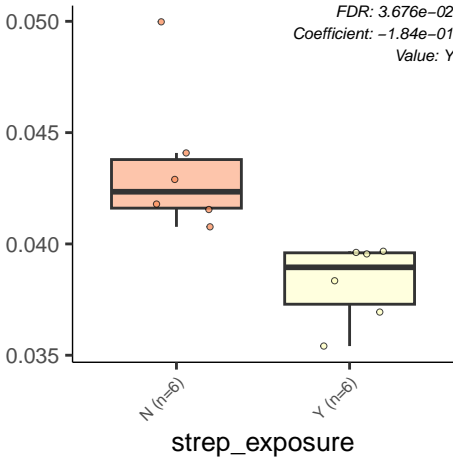
Y (n=6)

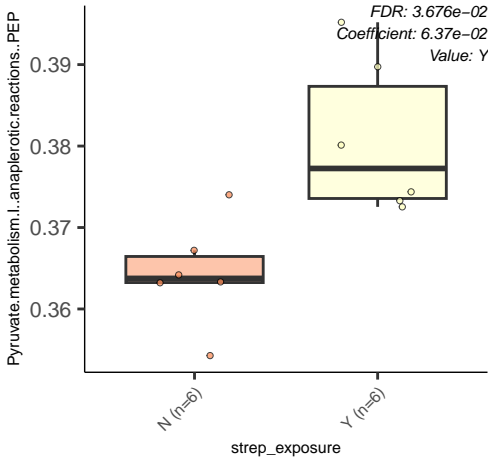
strep\_exposure



Osmoregulation

*FDR: 3.676e-02*  
*Coefficient: -1.84e-01*  
*Value: Y*





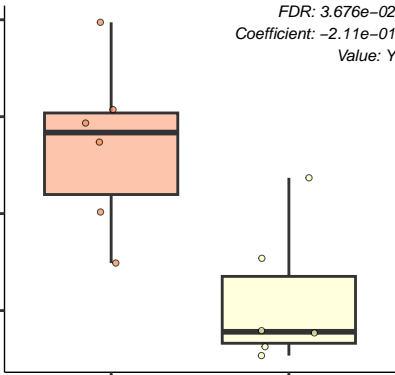
Uptake.of.selenate.and.selenite

*FDR: 3.676e-02*  
*Coefficient: -2.11e-01*  
*Value: Y*

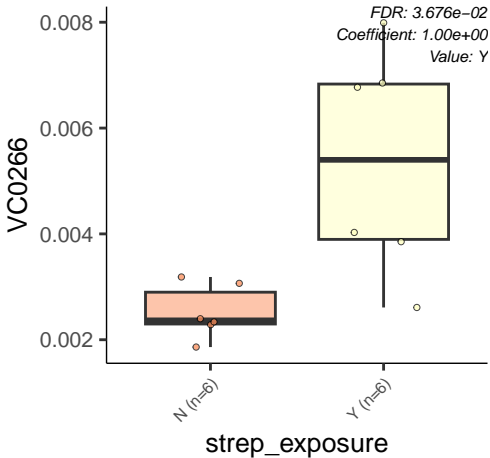
N (n=6)

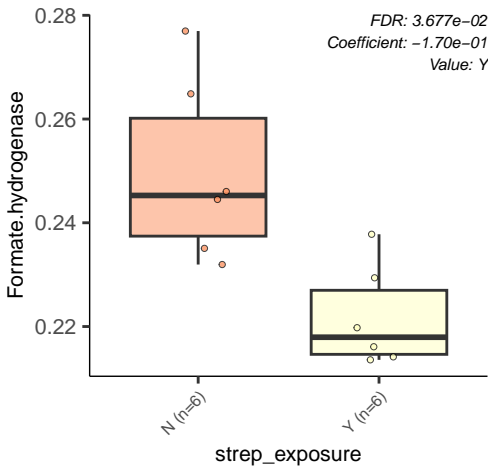
Y (n=6)

strep\_exposure

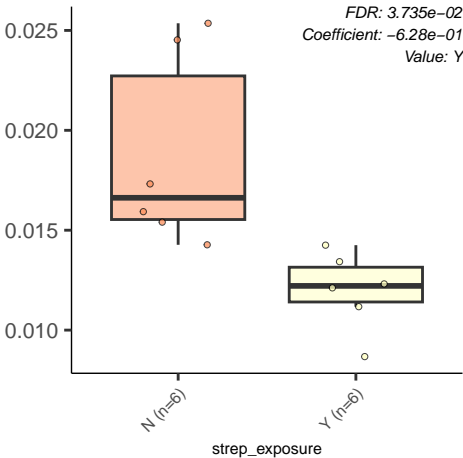








Accessory.colonization.factor



GroEL.GroES

0.115

0.110

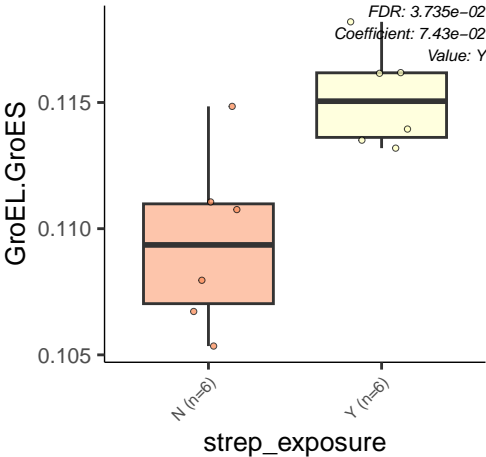
0.105

N (n=6)

Y (n=6)

strep\_exposure

FDR:  $3.735e-02$   
Coefficient:  $7.43e-02$   
Value: Y



ECF.class.transporters

0.32

0.30

0.28

0.26

N (n=6)

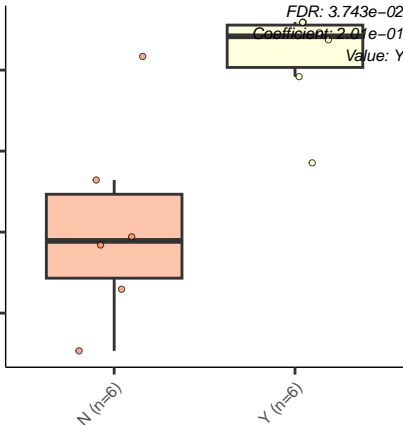
Y (n=6)

strep\_exposure

FDR: 3.743e-02

Coefficient: 2.01e-01

Value: Y



CbiZ.Main

FDR: 3.844e-02

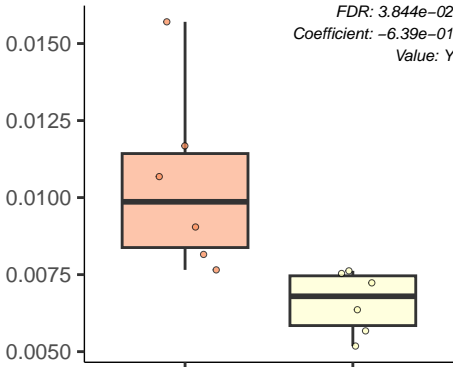
Coefficient: -6.39e-01

Value: Y

N (n=6)

Y (n=6)

strep\_exposure



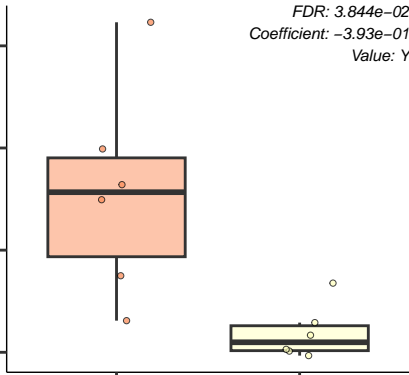
DNA.binding.regulatory.proteins..strays

*FDR: 3.844e-02*  
*Coefficient: -3.93e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



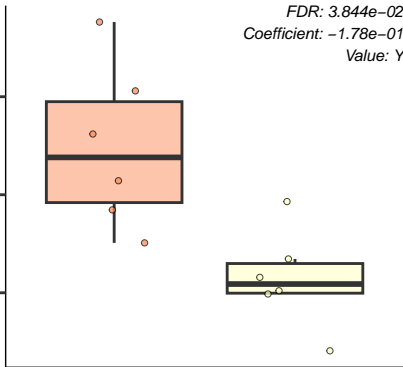
L.rhamnose.utilization

FDR:  $3.844e-02$   
Coefficient:  $-1.78e-01$   
Value: Y

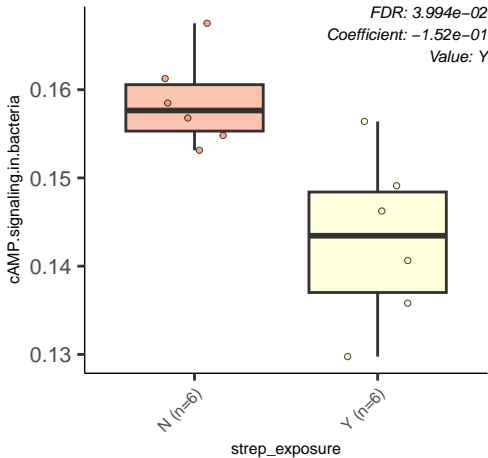
N (n=6)

Y (n=6)

strep\_exposure







HPr.catabolite.repression.system

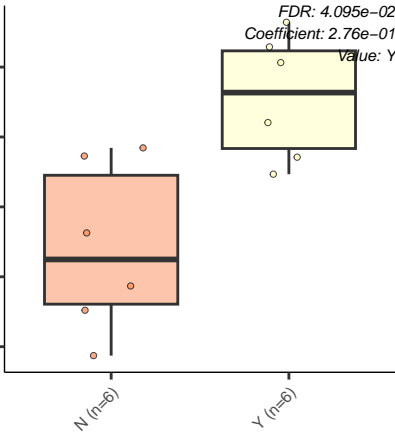
0.065  
0.060  
0.055  
0.050  
0.045

N (n=6)

Y (n=6)

strep\_exposure

FDR:  $4.095e-02$   
Coefficient:  $2.76e-01$   
Value: Y



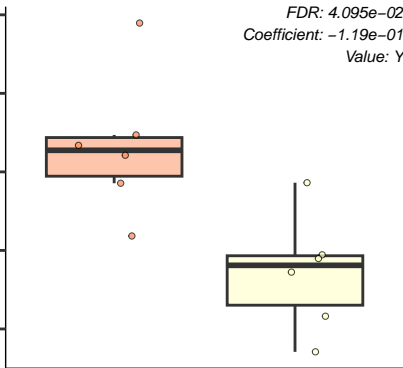
Trehalose.Biosynthesis

*FDR: 4.095e-02*  
*Coefficient: -1.19e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



Siderophore.Enterobactin

FDR: 4.128e-02

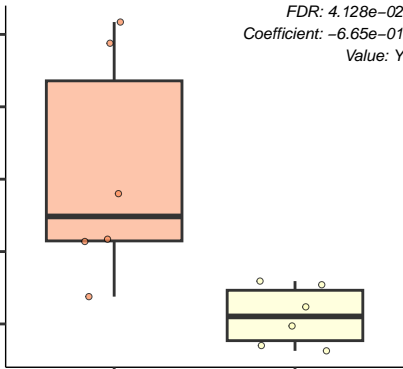
Coefficient: -6.65e-01

Value: Y

N (n=6)

Y (n=6)

strep\_exposure



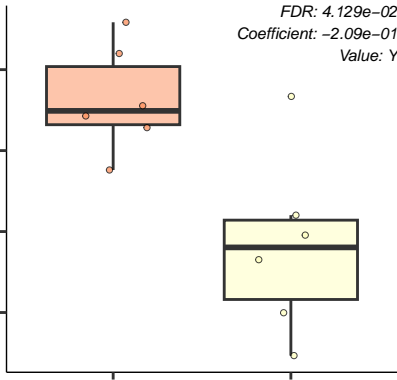
D. Tagatose.and. Galactitol.Utilization

*FDR: 4.129e-02*  
*Coefficient: -2.09e-01*  
*Value: Y*

N (n=6)

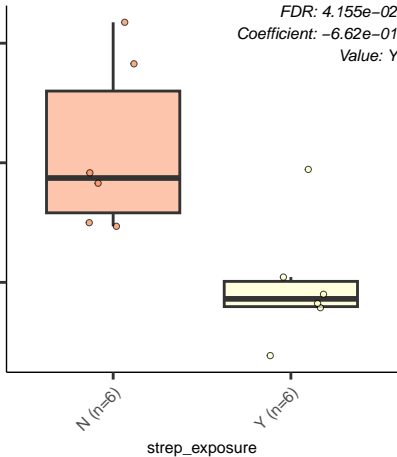
Y (n=6)

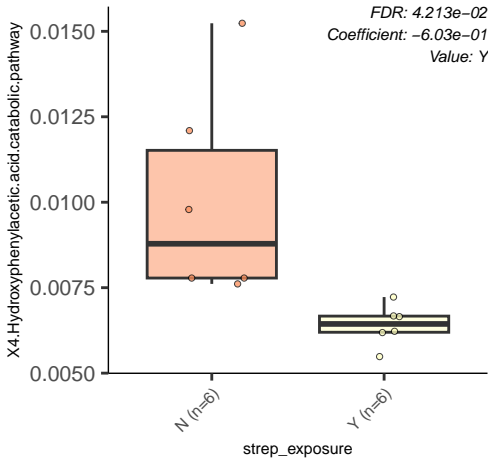
strep\_exposure

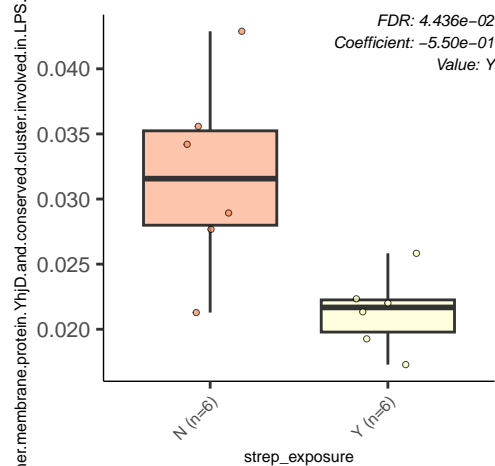


Siderophore.Yersiniabactin.Biosynthesis

*FDR: 4.155e-02*  
*Coefficient: -6.62e-01*  
*Value: Y*









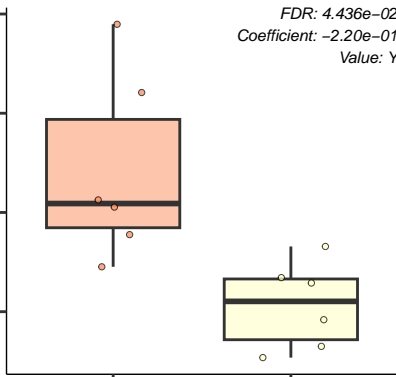
Propionyl.CoA.to.Succinyl.CoA.Module

*FDR: 4.436e-02*  
*Coefficient: -2.20e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



Terminal.cytochrome.d.ubiquinol.oxidases

FDR:  $4.436e-02$   
Coefficient:  $-1.29e-01$   
Value: Y

0.125

0.120

0.115

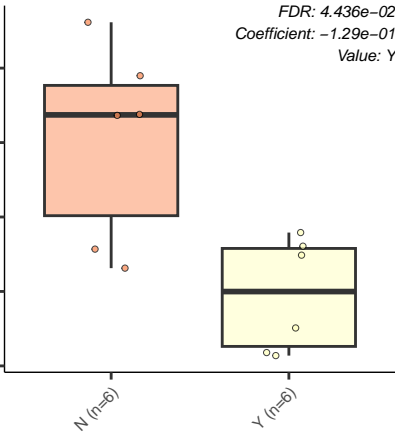
0.110

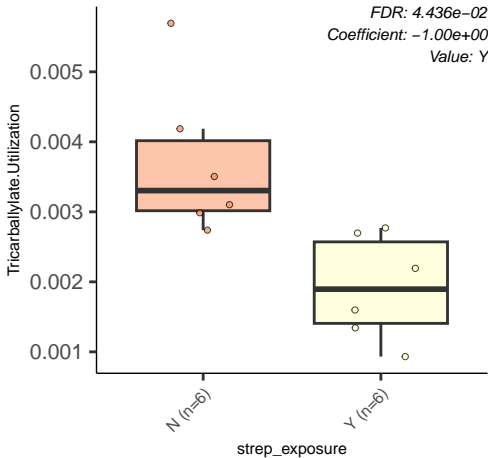
0.105

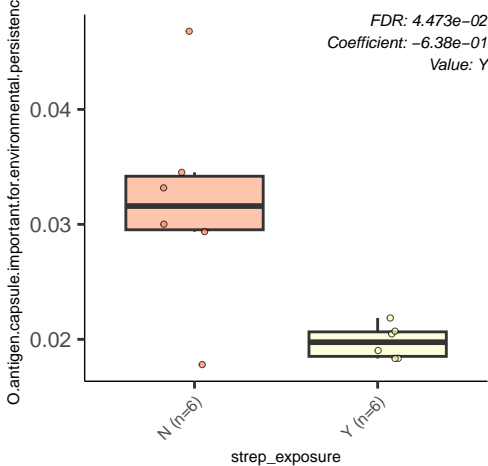
N (n=6)

Y (n=6)

strep\_exposure







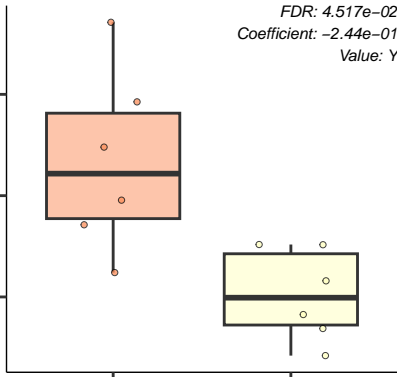
D.galactarate..D.glucarate.and.D.glycerate.catabolism

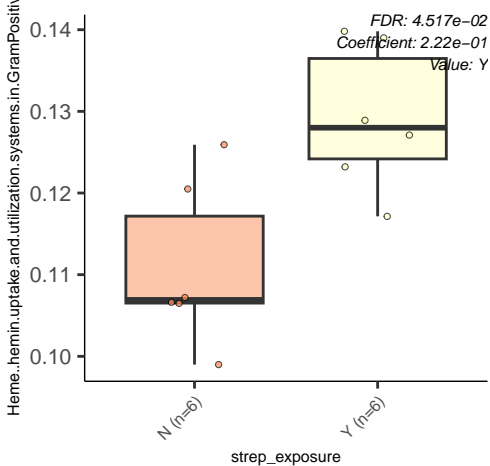
FDR:  $4.517e-02$   
Coefficient:  $-2.44e-01$   
Value: Y

N (n=6)

Y (n=6)

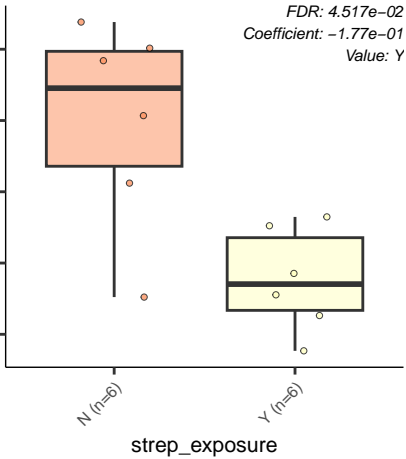
strep\_exposure





Respiratory.Complex.I

FDR: 4.517e-02  
Coefficient: -1.77e-01  
Value: Y

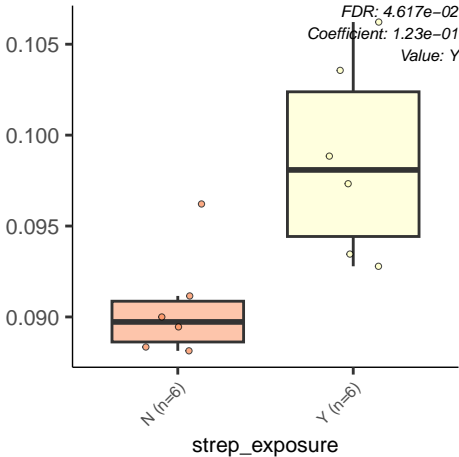


N (n=6)

Y (n=6)

strep\_exposure

Alanine.biosynthesis





Glycine.Biosynthesis

*FDR: 4.665e-02*

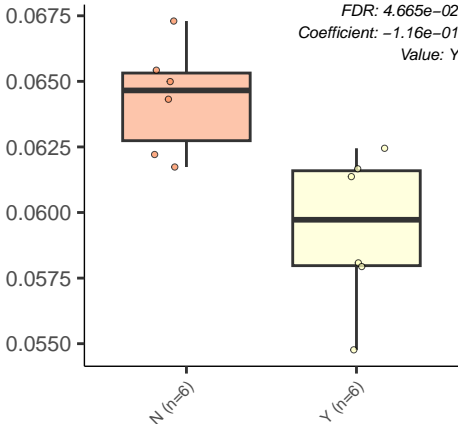
*Coefficient: -1.16e-01*

*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



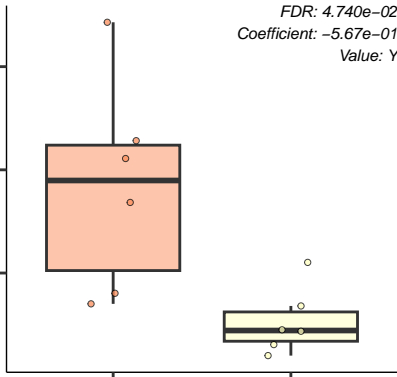
Acetone.Butanol.Ethanol.Synthesis

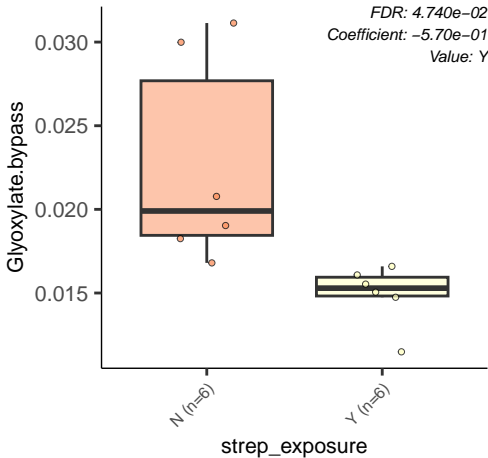
*FDR: 4.740e-02*  
*Coefficient: -5.67e-01*  
*Value: Y*

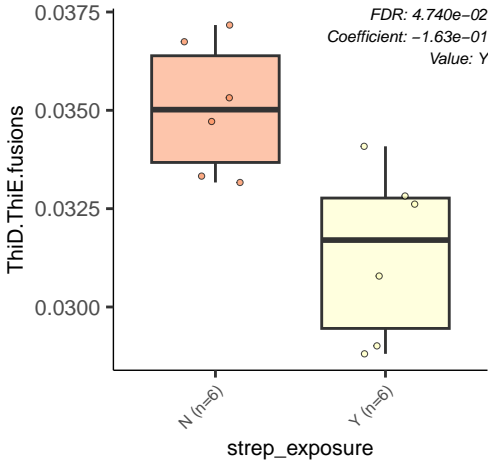
N (n=6)

Y (n=6)

strep\_exposure







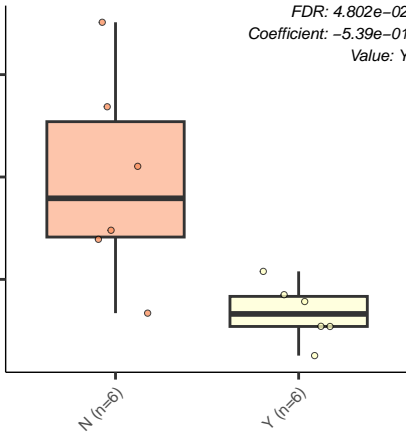
Carnitine.Metabolism.in.Microorganisms

*FDR: 4.802e-02*  
*Coefficient: -5.39e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



Hexose.Phosphate.Uptake.System

FDR:  $4.825e-02$   
Coefficient:  $-5.14e-01$   
Value: Y

0.024

0.020

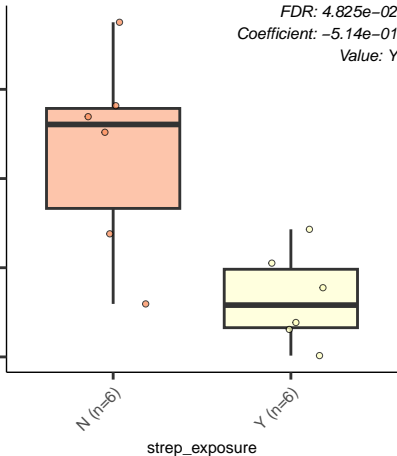
0.016

0.012

N (n=6)

Y (n=6)

strep\_exposure



Pyrroloquinoline.Quinone.biosynthesis

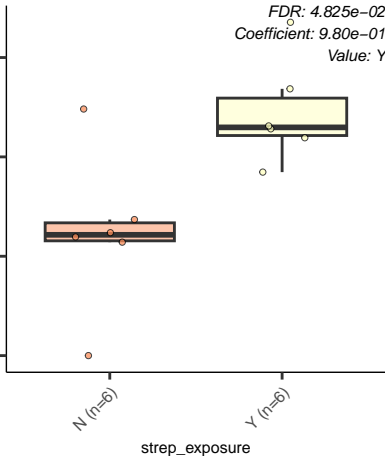
*FDR: 4.825e-02*  
*Coefficient: 9.80e-01*  
*Value: Y*

0.0015  
0.0010  
0.0005  
0.0000

N (n=6)

Y (n=6)

strep\_exposure



t.6.A.synthesis.in.bacteria

0.030

0.028

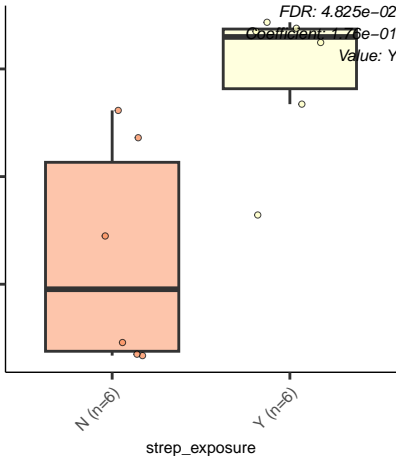
0.026

N (n=6)

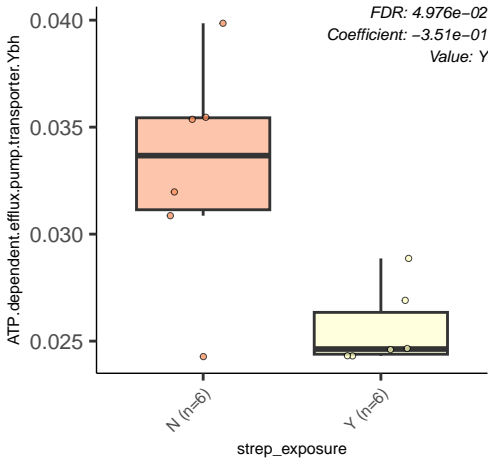
Y (n=6)

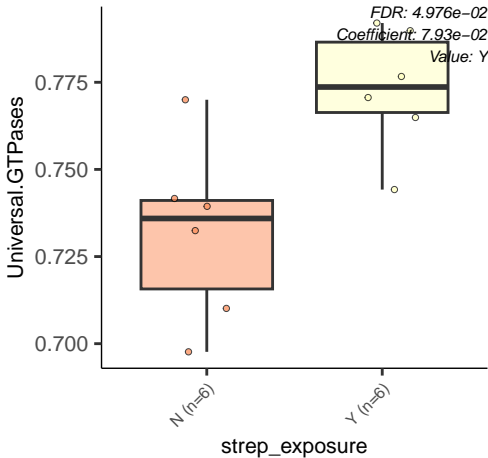
strep\_exposure

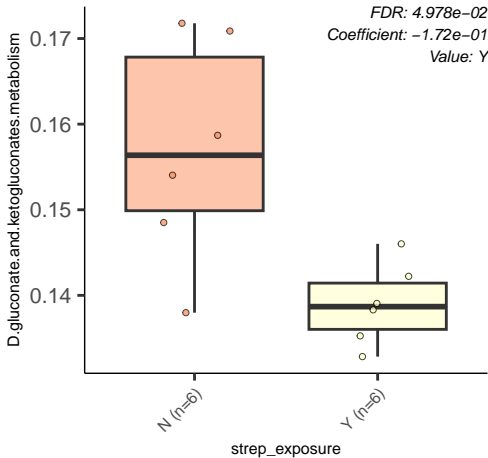
FDR:  $4.825e-02$   
Coefficient:  $1.76e-01$   
Value: Y











Menaquinone.Biosynthesis.via.Futalosine

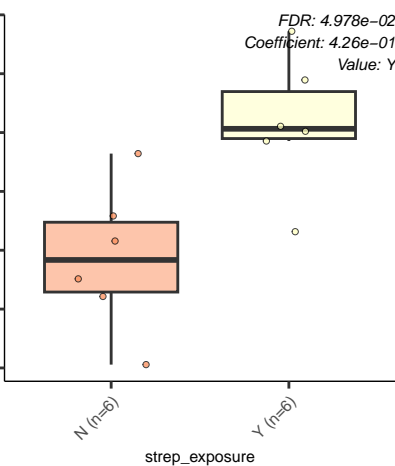
0.011  
0.010  
0.009  
0.008  
0.007  
0.006  
0.005

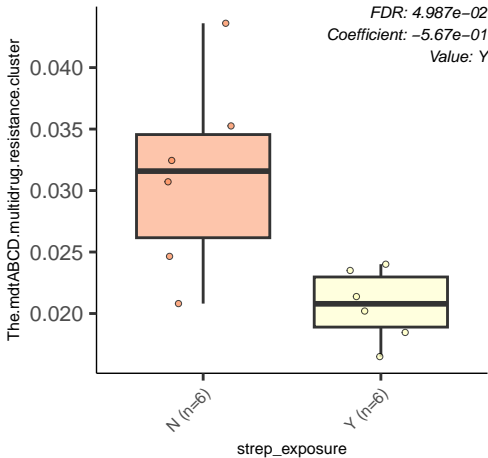
N (n=6)

Y (n=6)

strep\_exposure

FDR: 4.978e-02  
Coefficient: 4.26e-01  
Value: Y





ATP.dependent.RNA.helicases..bacterial

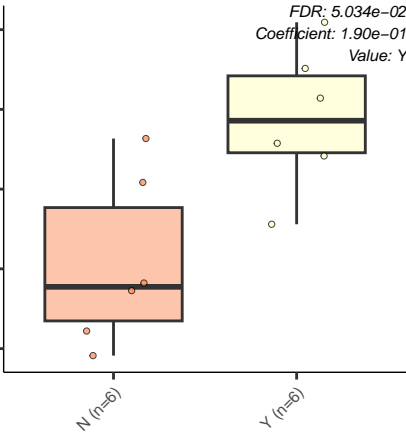
0.16  
0.15  
0.14  
0.13  
0.12

N (n=6)

Y (n=6)

strep\_exposure

FDR: 5.034e-02  
Coefficient: 1.90e-01  
Value: Y



At3g21300

FDR:  $5.034e-02$   
Coefficient:  $1.52e-01$   
Value: Y

0.15

0.14

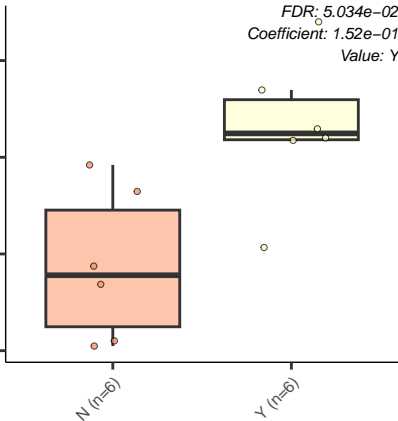
0.13

0.12

N (n=6)

Y (n=6)

strep\_exposure



CBSS.211586.1.pcg.3133

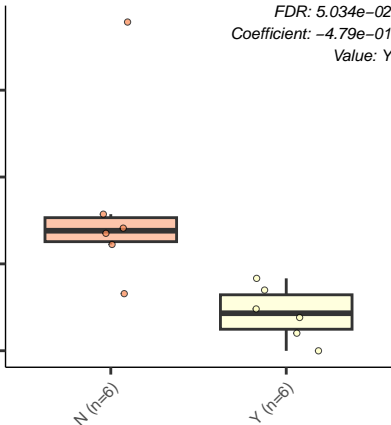
*FDR: 5.034e-02*  
*Coefficient: -4.79e-01*  
*Value: Y*

N (n=6)

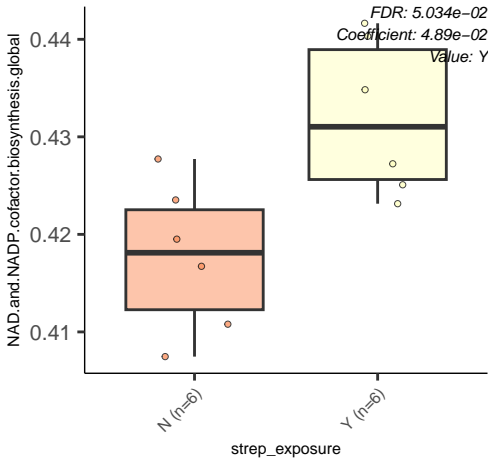
Y (n=6)

strep\_exposure

0.011  
0.009  
0.007  
0.005

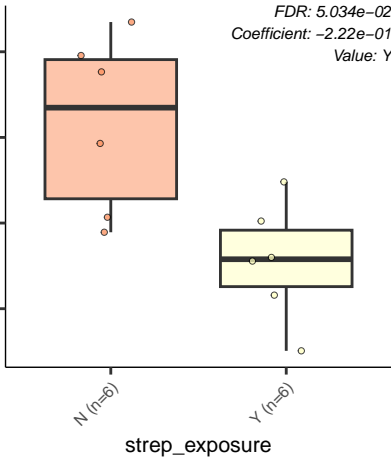


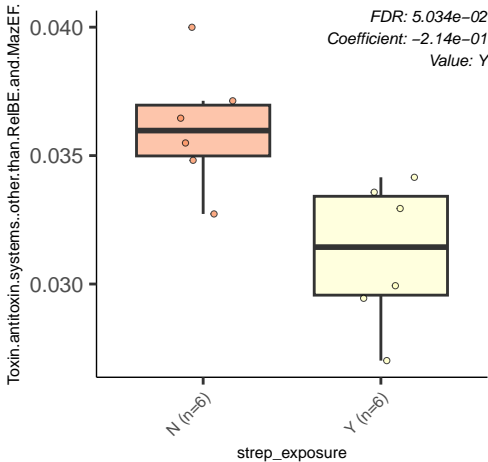




Phage.packaging.machinery

*FDR: 5.034e-02*  
*Coefficient: -2.22e-01*  
*Value: Y*





A.Gammaproteobacteria.Cluster.Relating.to.Translation

*FDR: 5.114e-02*  
*Coefficient: -4.91e-01*  
*Value: Y*

N (n=6)

Y (n=6)

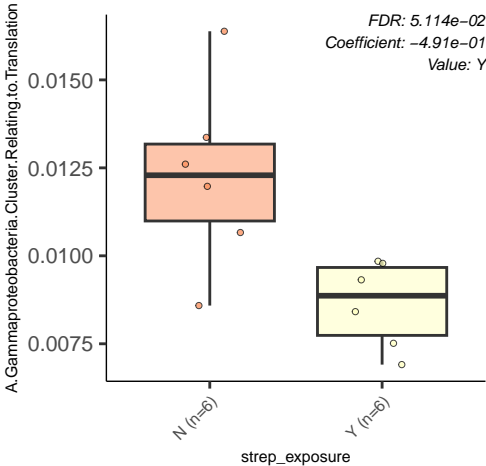
strep\_exposure

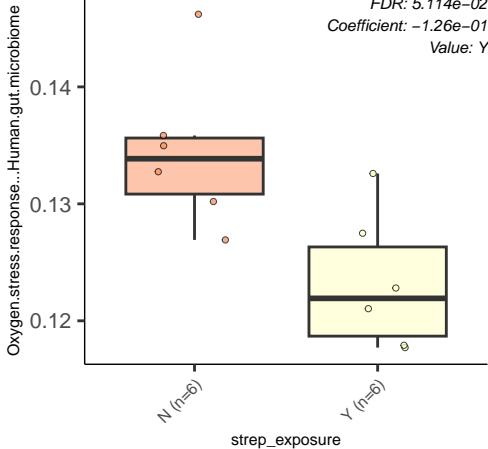
0.0150

0.0125

0.0100

0.0075





At1g69340.At2g40600

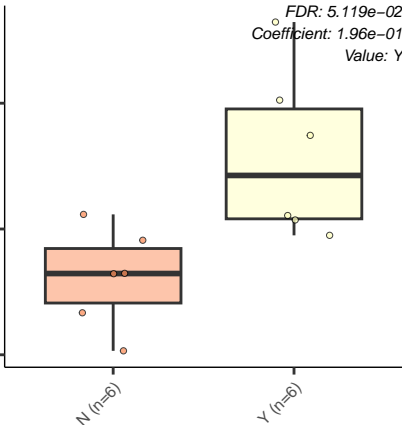
0.08  
0.07  
0.06

N (n=6)

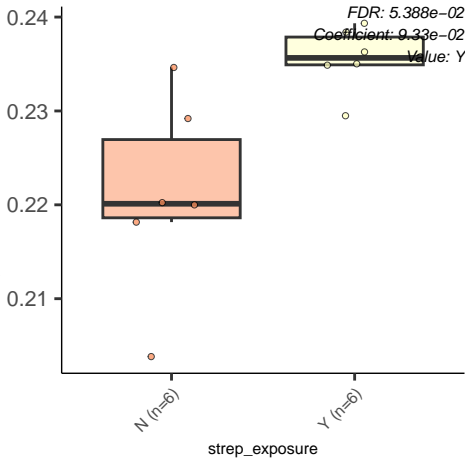
Y (n=6)

strep\_exposure

FDR: 5.119e-02  
Coefficient: 1.96e-01  
Value: Y



At5g37530..CsdL.protein.family.



ABC.transporter.branched.chain.amino.acid..TC.3.A.1.4.1

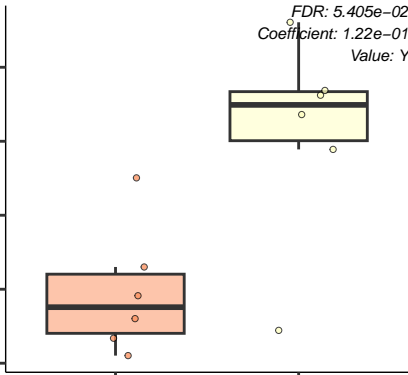
0.27  
0.26  
0.25  
0.24  
0.23

N (n=6)

Y (n=6)

strep\_exposure

FDR: 5.405e-02  
Coefficient: 1.22e-01  
Value: Y





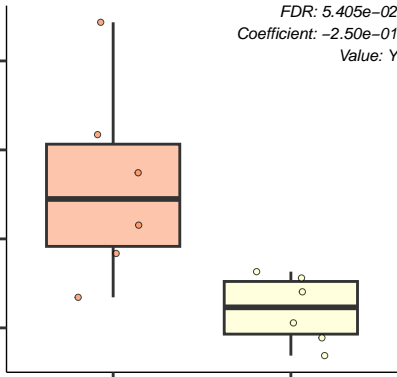
D.galactarate..D.glucarate.and.D.glycerate.catabolism...g

FDR:  $5.405e-02$   
Coefficient:  $-2.50e-01$   
Value: Y

N (n=6)

Y (n=6)

strep\_exposure



Galactosylceramide.and.Sulfatide.metabolism

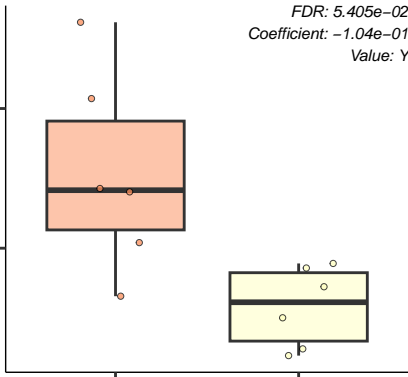
*FDR: 5.405e-02*  
*Coefficient: -1.04e-01*  
*Value: Y*

0.70  
0.65

N (n=6)

Y (n=6)

strep\_exposure



Methionine.Degradation

0.38

0.37

0.36

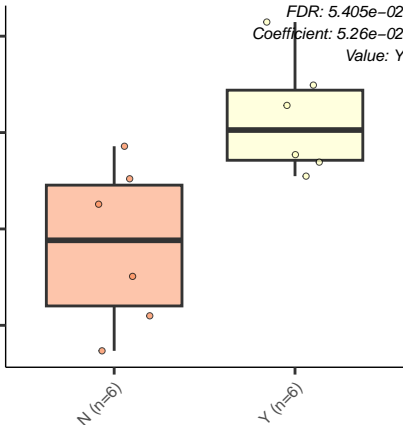
0.35

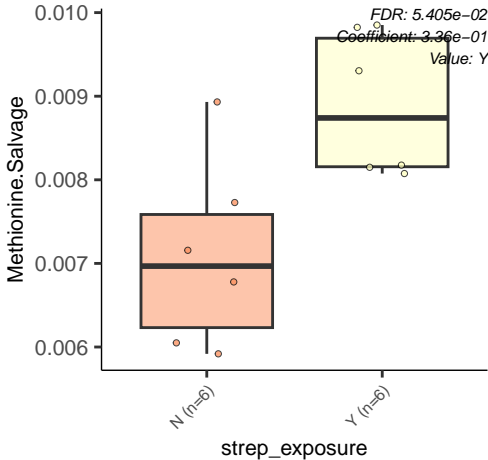
N (n=6)

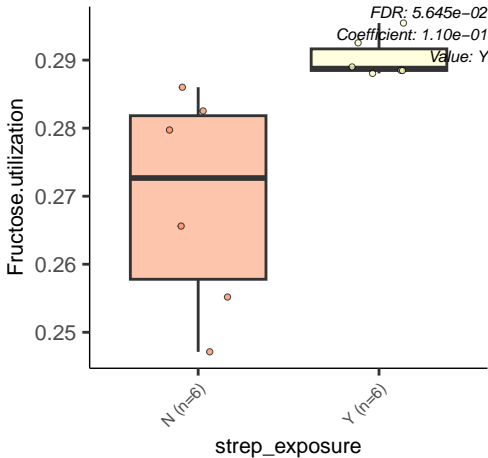
Y (n=6)

strep\_exposure

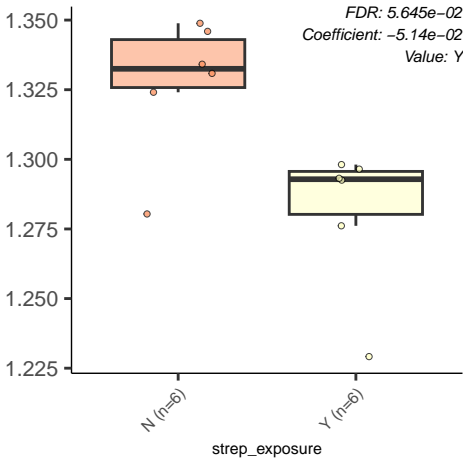
FDR: 5.405e-02  
Coefficient: 5.26e-02  
Value: Y







Maltose.and.Maltodextrin.Utilization



General.Secretion.Pathway

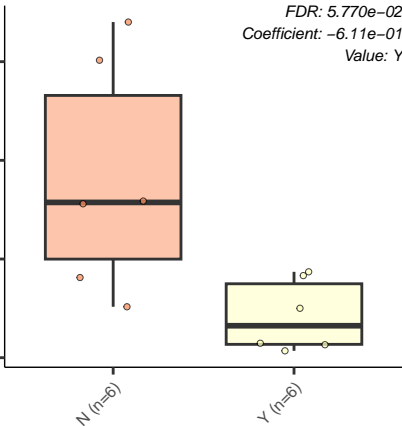
FDR: 5.770e-02  
Coefficient: -6.11e-01  
Value: Y

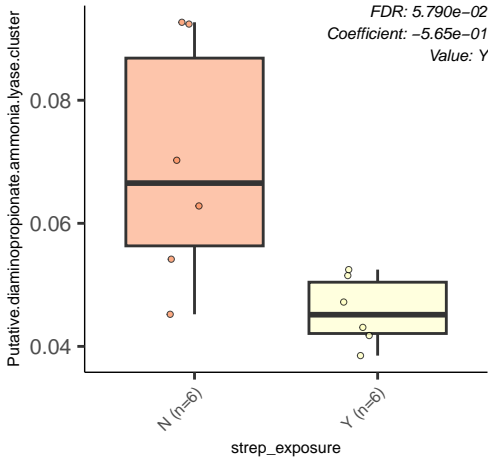
0.10  
0.08  
0.06  
0.04

N (n=6)

Y (n=6)

strep\_exposure

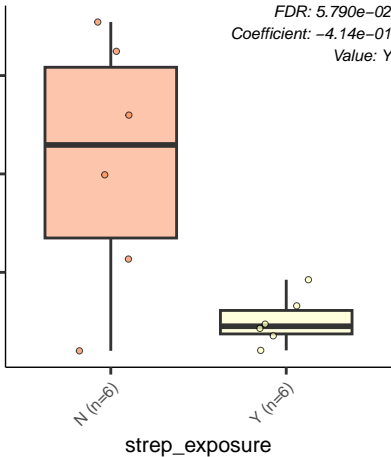


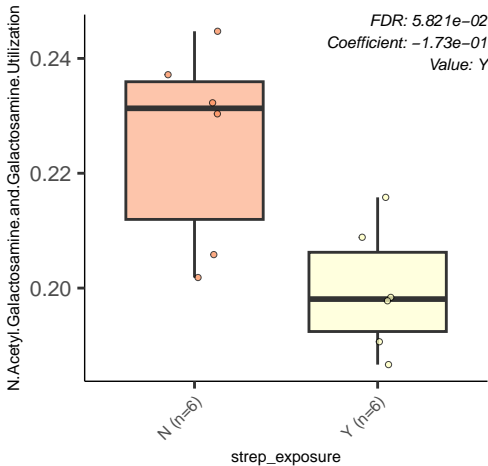




Transposase.in.entrics

FDR: 5.790e-02  
Coefficient: -4.14e-01  
Value: Y





Rhamnose.containing.glycans

0.62

0.60

0.58

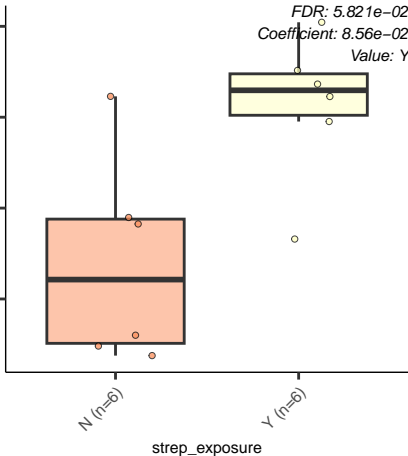
0.56

N (n=6)

Y (n=6)

strep\_exposure

FDR:  $5.821 \times 10^{-2}$   
Coefficient:  $8.56 \times 10^{-2}$   
Value: Y



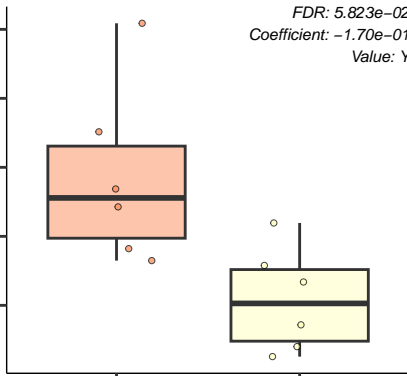
Respiration...Human.gut.microbiome

*FDR: 5.823e-02*  
*Coefficient: -1.70e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



Homogenisate.pathway.of.aromatic.compound.degradatio

FDR: 5.904e-02  
Coefficient: -2.35e-01  
Value: Y

0.048

0.044

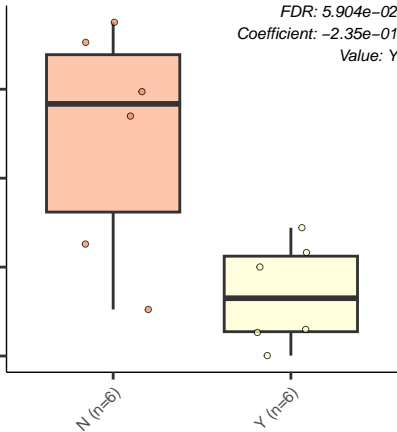
0.040

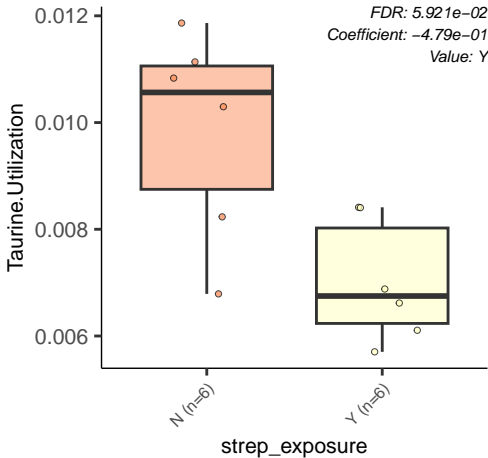
0.036

N (n=6)

Y (n=6)

strep\_exposure





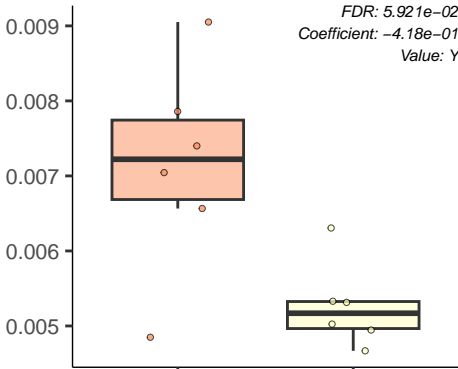
Transport.of.Molybdenum

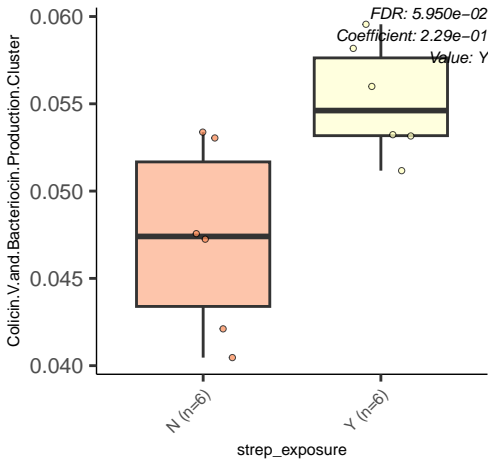
*FDR: 5.921e-02*  
*Coefficient: -4.18e-01*  
*Value: Y*

N (n=6)

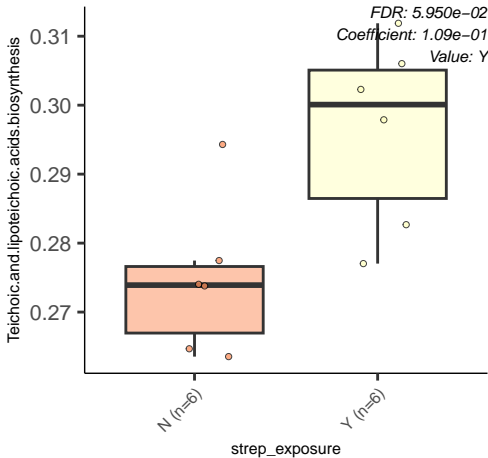
Y (n=6)

strep\_exposure



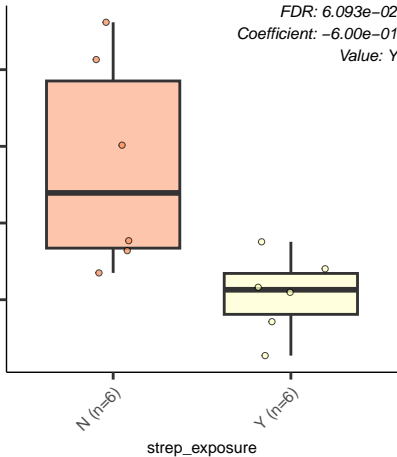






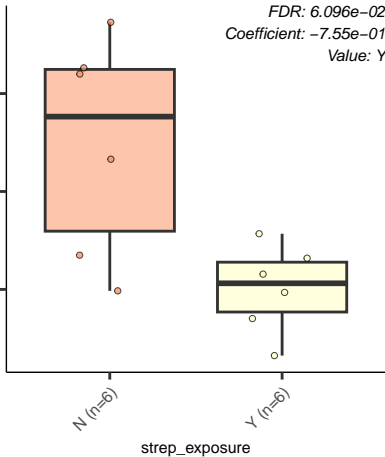
Molybdopterin.cytosine.dinucleotide

*FDR: 6.093e-02*  
*Coefficient: -6.00e-01*  
*Value: Y*



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

FDR: 6.096e-02  
Coefficient: -7.55e-01  
Value: Y



Dihydroxyacetone.kinases

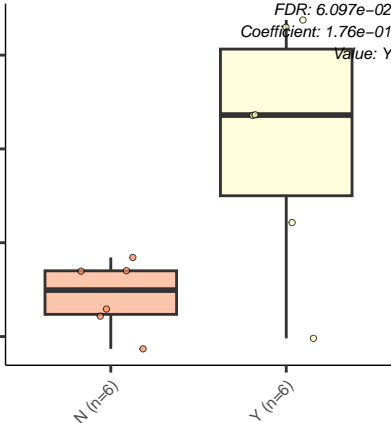
0.075  
0.070  
0.065  
0.060

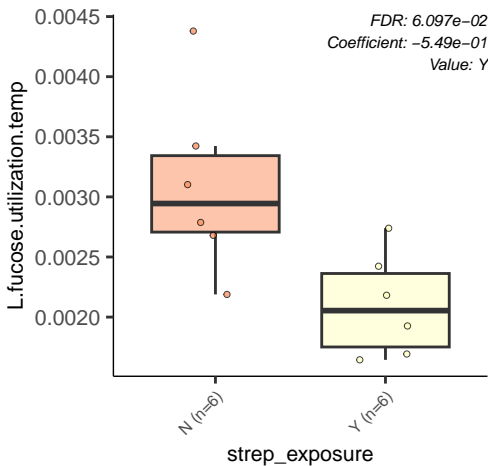
N (n=6)

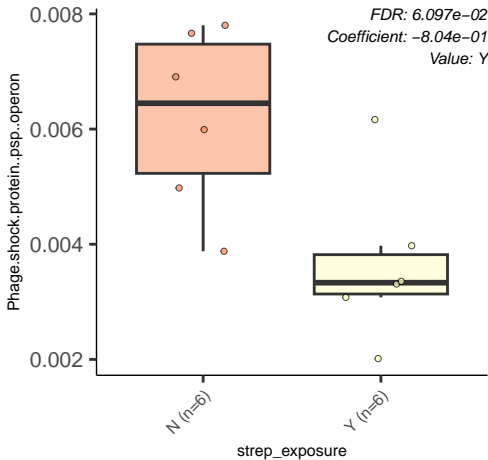
Y (n=6)

strep\_exposure

FDR: 6.097e-02  
Coefficient: 1.76e-01  
Value: Y







Polysaccharide.deacetylases

0.06

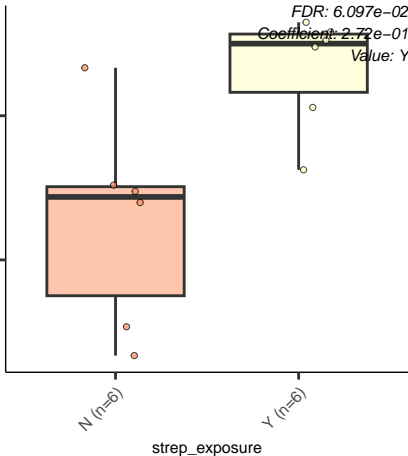
0.05

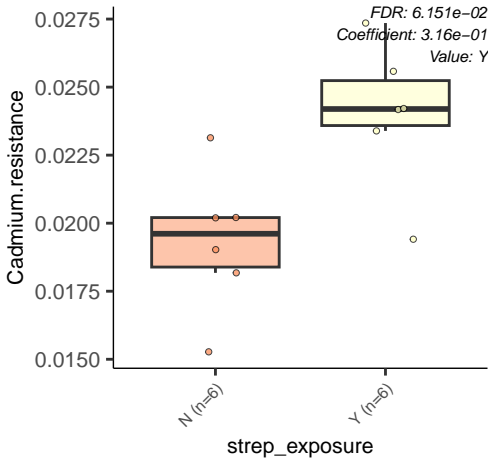
N (n=6)

Y (n=6)

strep\_exposure

FDR:  $6.097 \times 10^{-2}$   
Coefficient:  $2.72 \times 10^{-1}$   
Value: Y







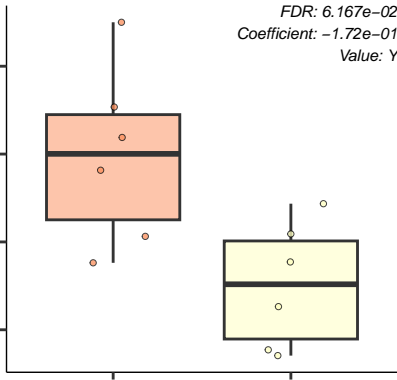
Acetyl.CoA.fermentation.to.Butyrate

FDR: 6.167e-02  
Coefficient: -1.72e-01  
Value: Y

N (n=6)

Y (n=6)

strep\_exposure



Peptidoglycan.biosynthesis..gjo

0.23

0.22

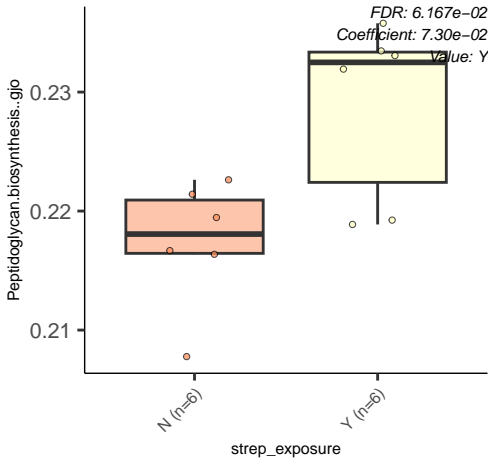
0.21

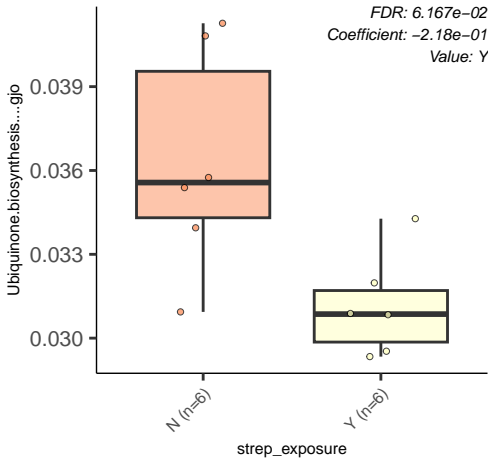
N (n=6)

Y (n=6)

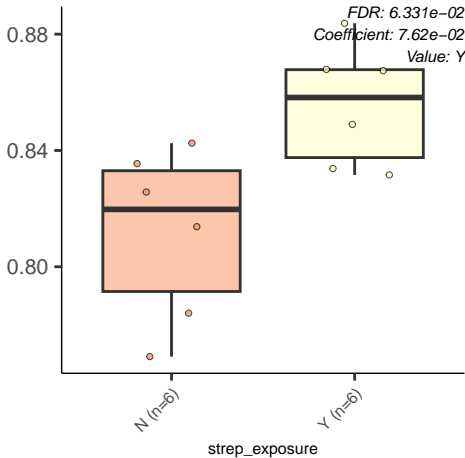
strep\_exposure

FDR:  $6.167 \times 10^{-2}$   
Coefficient:  $7.30 \times 10^{-2}$   
Value: Y





De.Novo.Purine.Biosynthesis



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

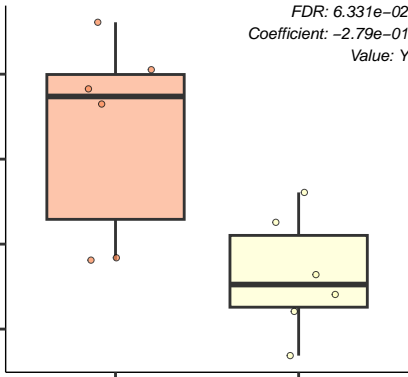
FDR: 6.331e-02  
Coefficient: -2.79e-01  
Value: Y

N (n=6)

Y (n=6)

strep\_exposure

0.10  
0.09  
0.08  
0.07



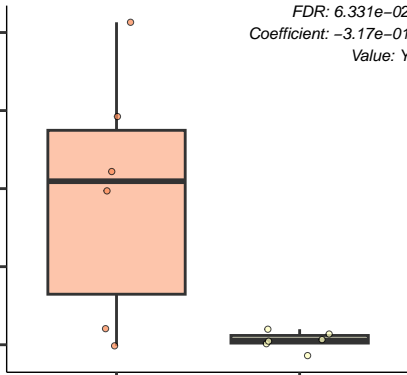
Nitrate.and.nitrite.ammonification

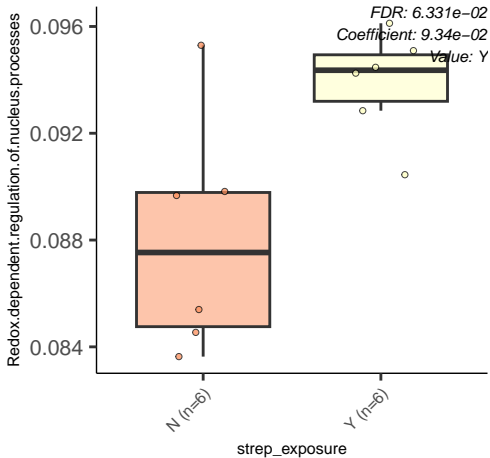
*FDR: 6.331e-02*  
*Coefficient: -3.17e-01*  
*Value: Y*

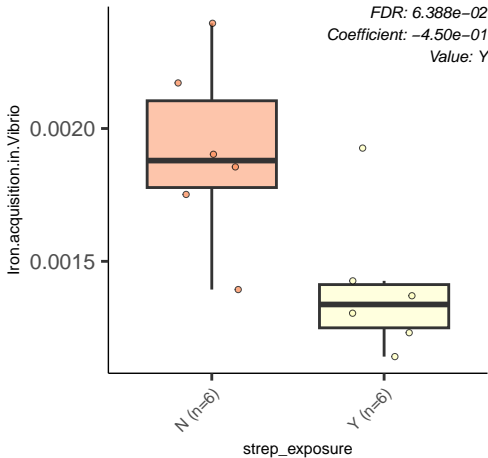
N (n=6)

Y (n=6)

strep\_exposure









Tryptophan.synthesis

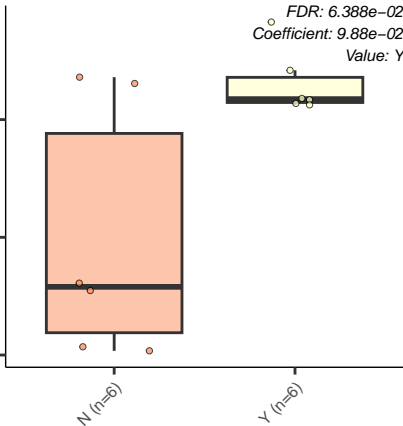
*FDR: 6.388e-02*  
*Coefficient: 9.88e-02*  
*Value: Y*

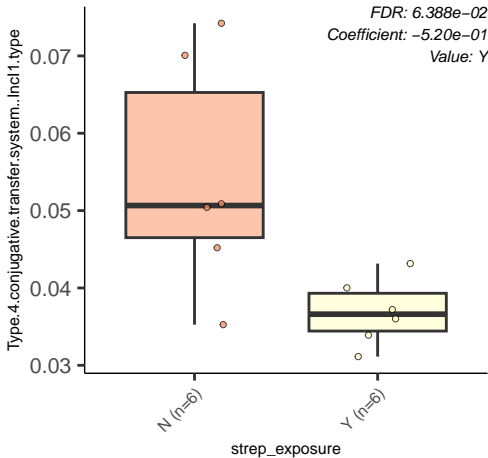
0.40  
0.38  
0.36

N (n=6)

Y (n=6)

strep\_exposure





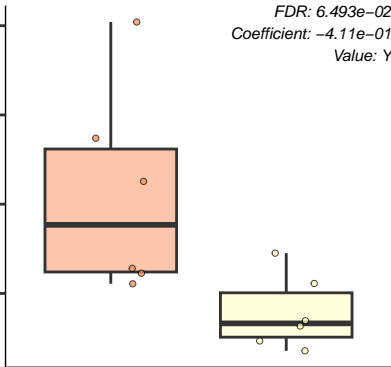
At2g33980.At1g28960

FDR:  $6.493e-02$   
Coefficient:  $-4.11e-01$   
Value: Y

N (n=6)

Y (n=6)

strep\_exposure



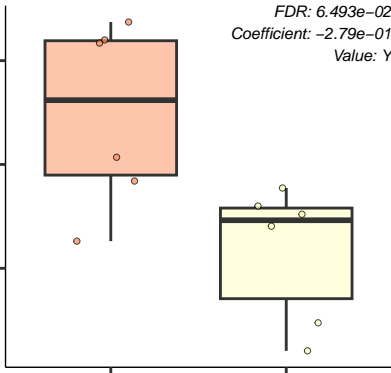
CBSS.320372.3.peg.6046

*FDR: 6.493e-02*  
*Coefficient: -2.79e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



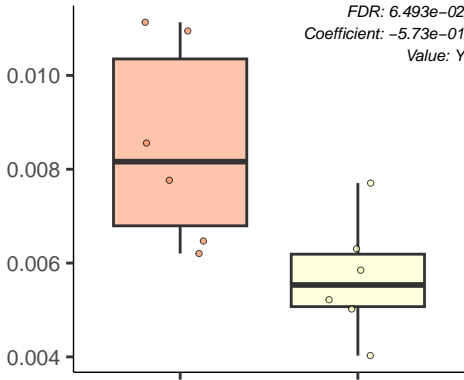
Osmoprotectant.ABC.transporter.YehZYXW.of.Enterobacter

FDR:  $6.493e-02$   
Coefficient:  $-5.73e-01$   
Value: Y

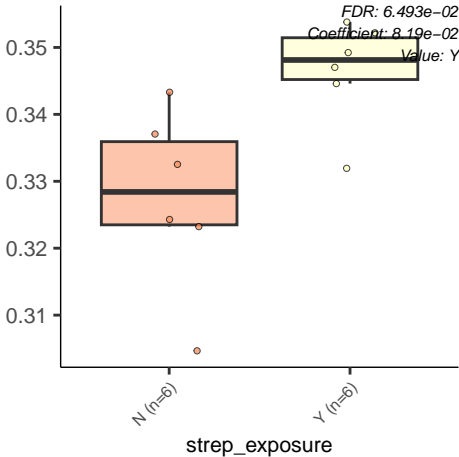
N (n=6)

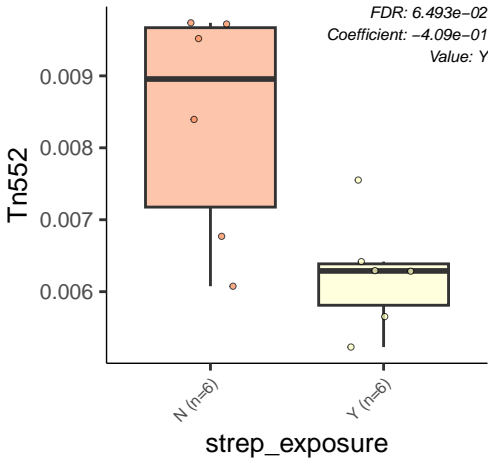
Y (n=6)

strep\_exposure



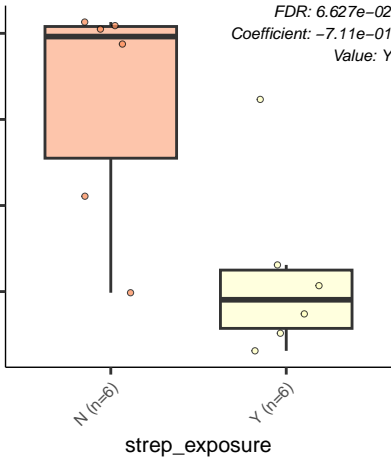
Ribosome.SSU.bacterial



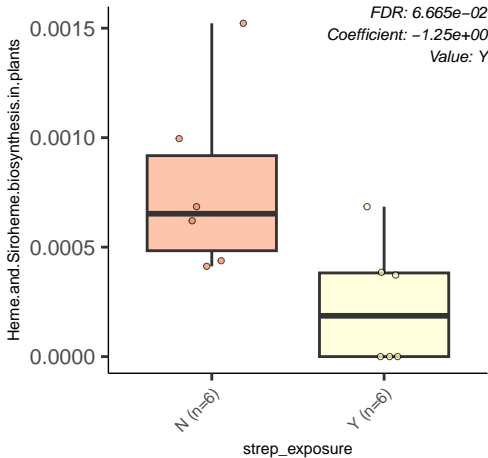


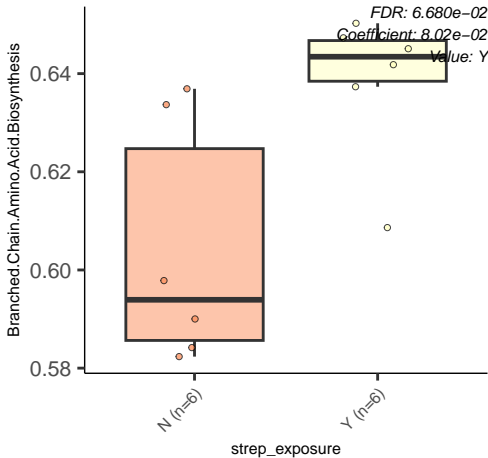
CBSS.502800.3.pcg.2785

FDR:  $6.627e-02$   
Coefficient:  $-7.11e-01$   
Value: Y









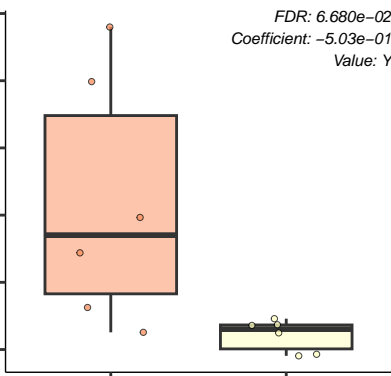
Siderophore.assembly.kit

FDR:  $6.680e-02$   
Coefficient:  $-5.03e-01$   
Value: Y

N (n=6)

Y (n=6)

strep\_exposure



Periplasmic.disulfide.interchange

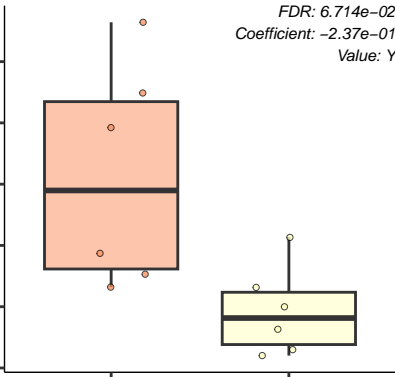
FDR: 6.714e-02  
Coefficient: -2.37e-01  
Value: Y

0.032  
0.030  
0.028  
0.026  
0.024  
0.022

N (n=6)

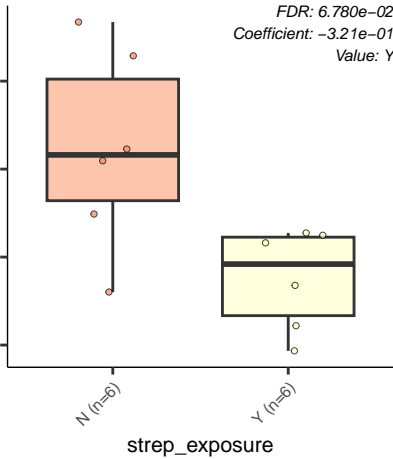
Y (n=6)

strep\_exposure



Phage.head.and.packaging

FDR: 6.780e-02  
Coefficient: -3.21e-01  
Value: Y



strep\_exposure

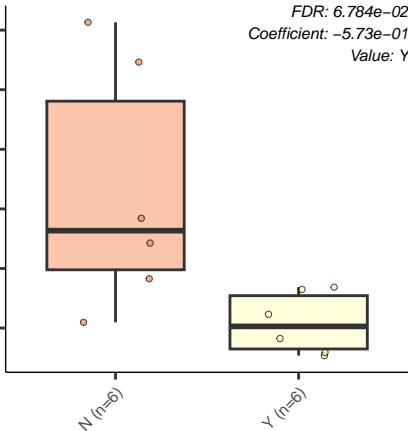
Type.1.pili.\_mannose.sensitive.fimbriae.

FDR:  $6.784e-02$   
Coefficient:  $-5.73e-01$   
Value: Y

N (n=6)

Y (n=6)

strep\_exposure



CBSS.216592.1.peg.3534

FDR:  $6.795e-02$   
Coefficient:  $-2.75e-01$   
Value: Y

0.018

0.016

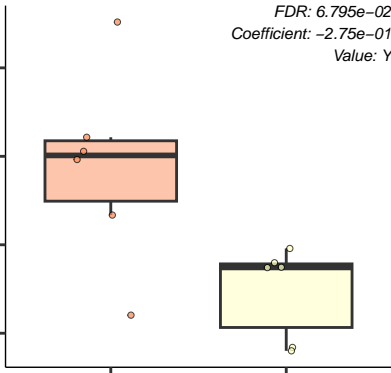
0.014

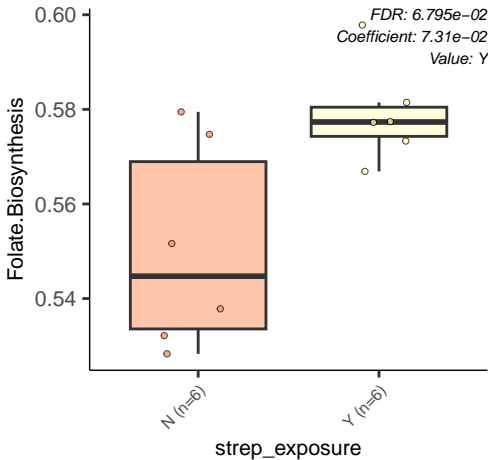
0.012

N (n=6)

Y (n=6)

strep\_exposure







Proteolysis.in.bacteria..ATP.dependent

0.54

0.52

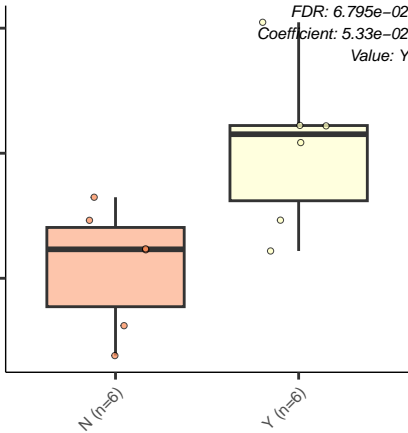
0.50

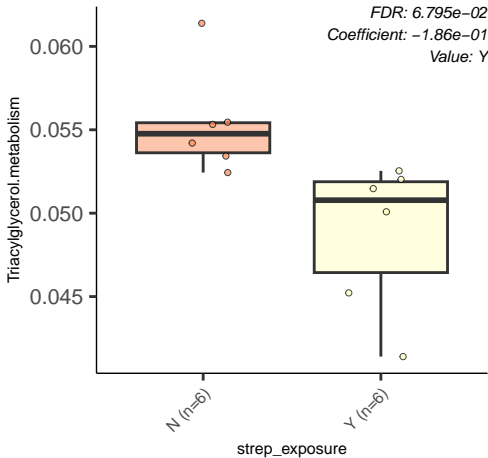
N (n=6)

Y (n=6)

strep\_exposure

FDR:  $6.795e-02$   
Coefficient:  $5.33e-02$   
Value: Y





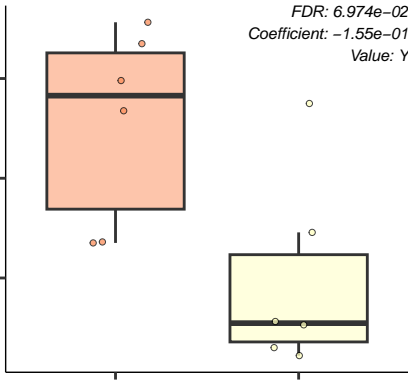
Proline,.4.hydroxyproline.uptake.and.utilization

*FDR: 6.974e-02*  
*Coefficient: -1.55e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



CoenzymeM.Archaea

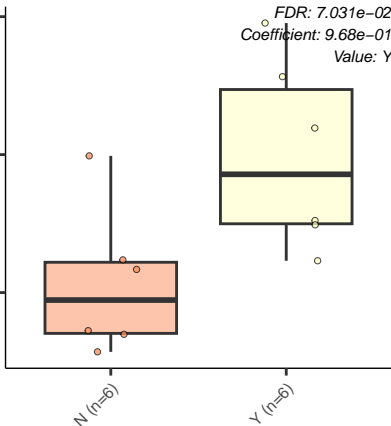
0.003  
0.002  
0.001

N (n=6)

Y (n=6)

strep\_exposure

FDR: 7.031e-02  
Coefficient: 9.68e-01  
Value: Y



COG0277

0.023

0.021

0.019

0.017

N (n=6)

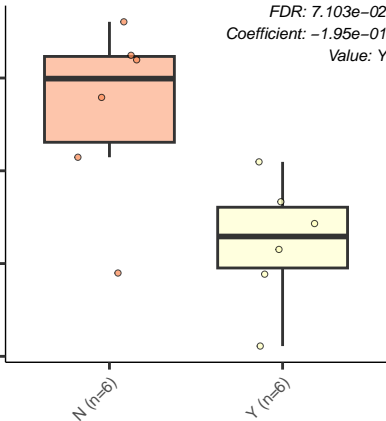
Y (n=6)

strep\_exposure

*FDR: 7.103e-02*

*Coefficient: -1.95e-01*

*Value: Y*



DNA.Repair.Base.Excision

FDR:  $7.123e-02$   
Coefficient:  $5.21e-02$   
Value: Y

0.44

0.43

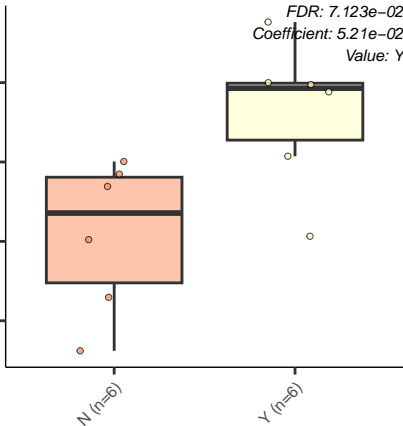
0.42

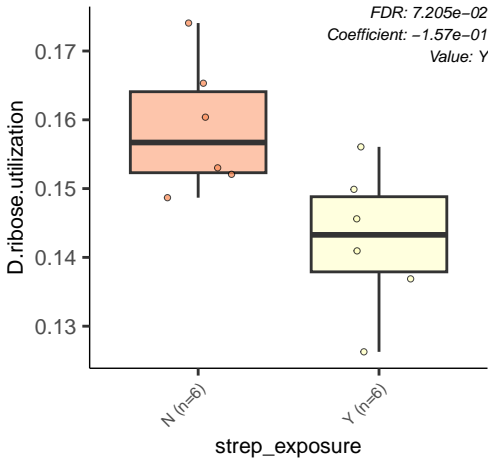
0.41

N (n=6)

Y (n=6)

strep\_exposure





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

FDR:  $7.342e-02$   
Coefficient:  $-2.38e-01$   
Value: Y

0.050

0.045

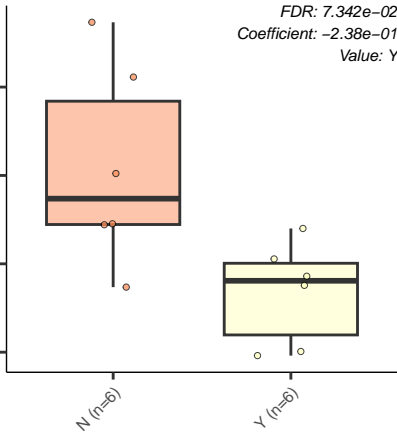
0.040

0.035

N (n=6)

Y (n=6)

strep\_exposure





Cyanate.hydrolysis

0.040

0.035

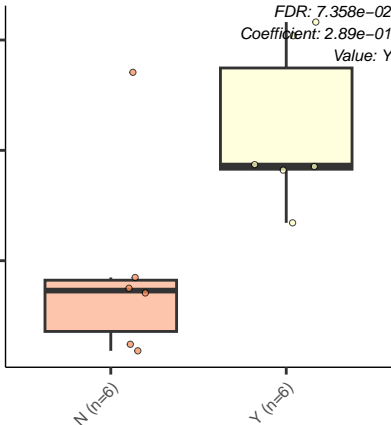
0.030

N (n=6)

Y (n=6)

strep\_exposure

FDR:  $7.358 \times 10^{-2}$   
Coefficient:  $2.89 \times 10^{-1}$   
Value: Y





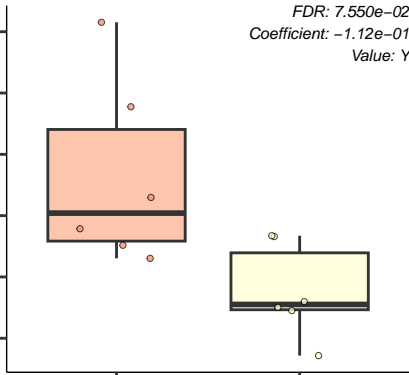
Lacto.N.Biose.l.and.Galacto.N.Biose.Metabolic.Pathway

FDR: 7.550e-02  
Coefficient: -1.12e-01  
Value: Y

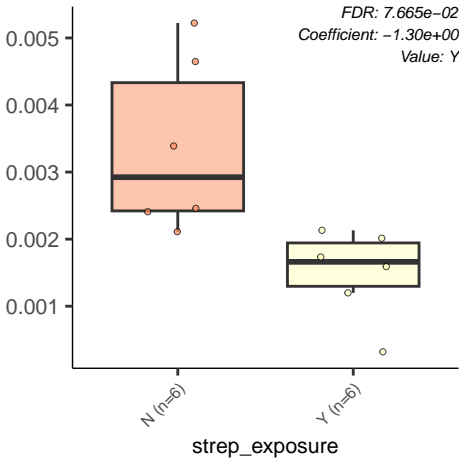
N (n=6)

Y (n=6)

strep\_exposure

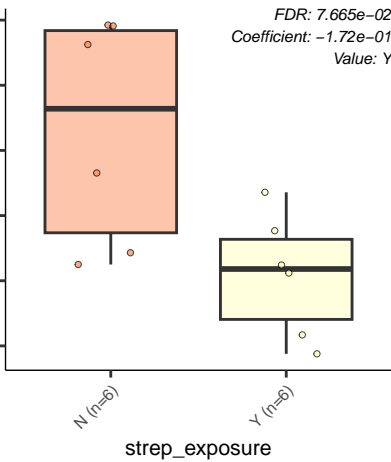


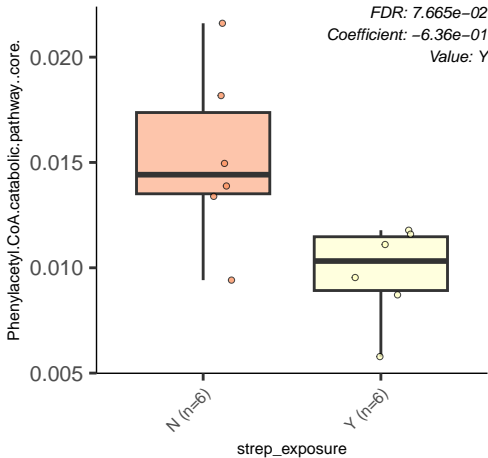
X..945..Fimbriae

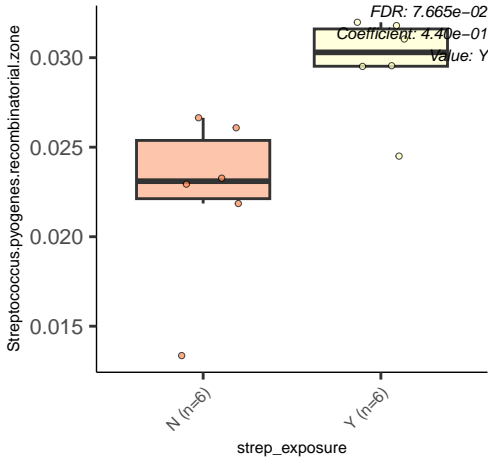


Ethanolamine.utilization

FDR: 7.665e-02  
Coefficient: -1.72e-01  
Value: Y







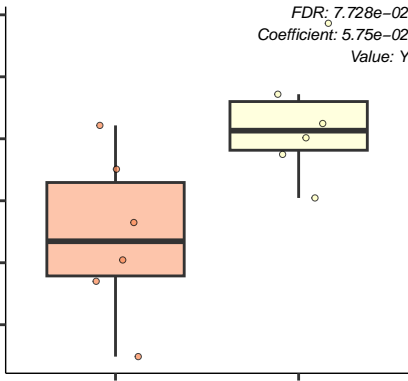
Threonine.and.Homoserine.Biosynthesis

*FDR: 7.728e-02*  
*Coefficient: 5.75e-02*  
*Value: Y*

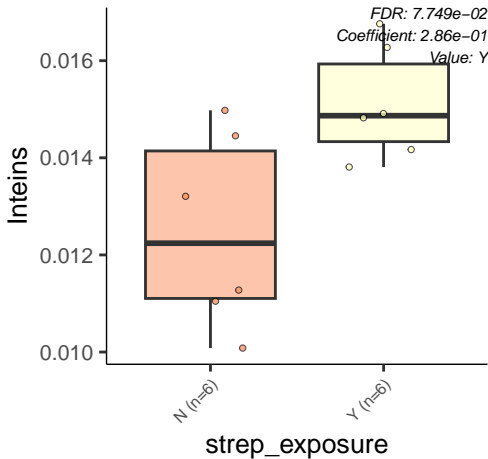
N (n=6)

Y (n=6)

strep\_exposure







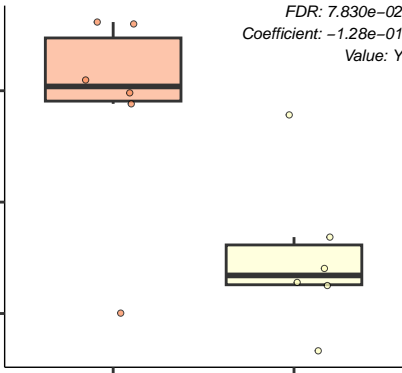
Bacterial.Chemotaxis

*FDR: 7.830e-02*  
*Coefficient: -1.28e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



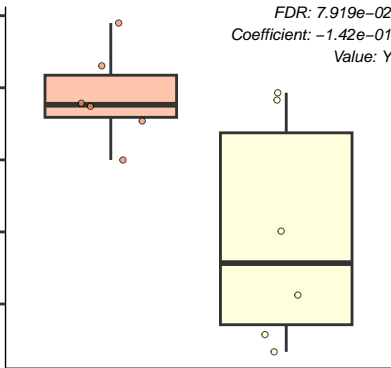
Heme.biosynthesis.orphans

*FDR: 7.919e-02*  
*Coefficient: -1.42e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



Glycine.and.Serine.Utilization

*FDR: 8.014e-02*  
*Coefficient: -7.56e-02*  
*Value: Y*

0.23

0.22

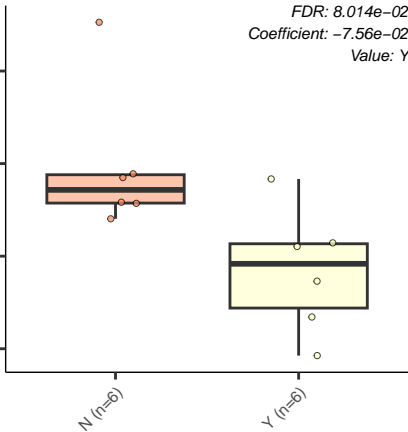
0.21

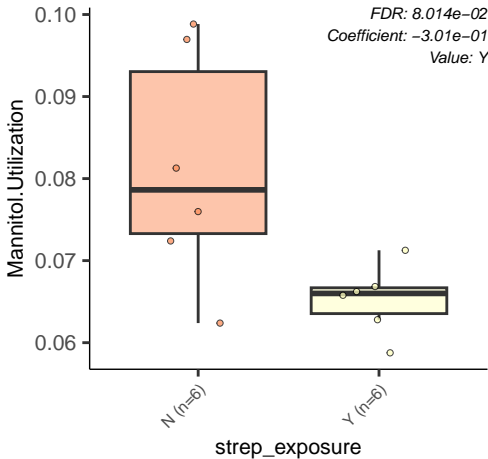
0.20

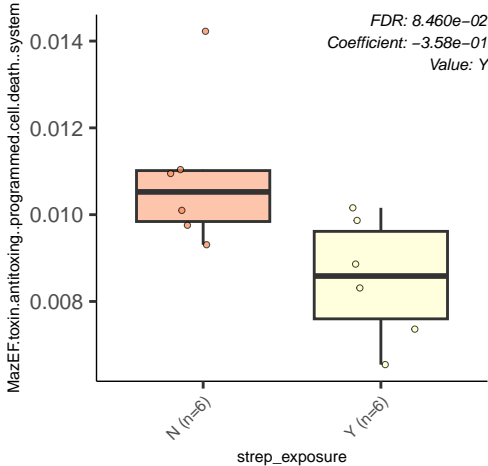
N (n=6)

Y (n=6)

strep\_exposure







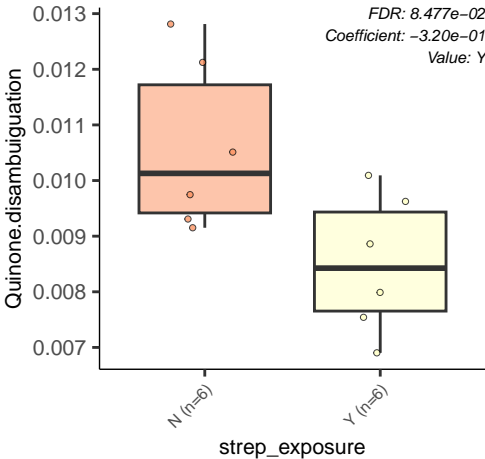
Quinone.disambuigation

*FDR: 8.477e-02*  
*Coefficient: -3.20e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



DNA.phosphorothioation

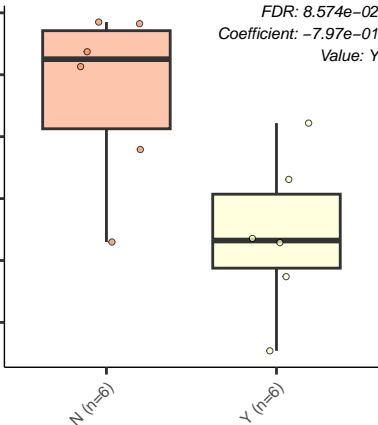
0.0035  
0.0030  
0.0025  
0.0020  
0.0015  
0.0010

N (n=6)

Y (n=6)

strep\_exposure

*FDR: 8.574e-02*  
*Coefficient: -7.97e-01*  
*Value: Y*





Fatty Acid Biosynthesis.FASII

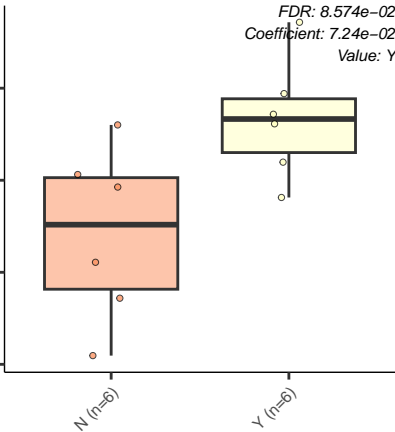
*FDR: 8.574e-02*  
*Coefficient: 7.24e-02*  
*Value: Y*

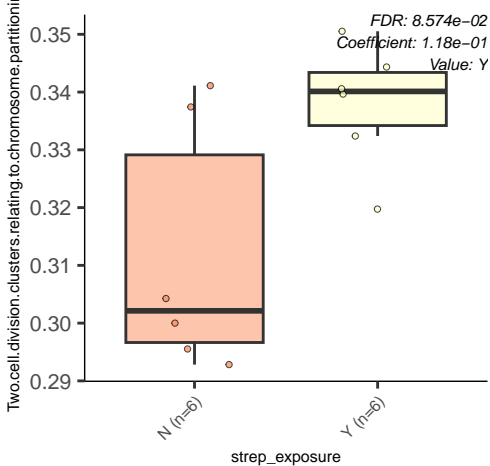
0.650  
0.625  
0.600  
0.575

N (n=6)

Y (n=6)

strep\_exposure





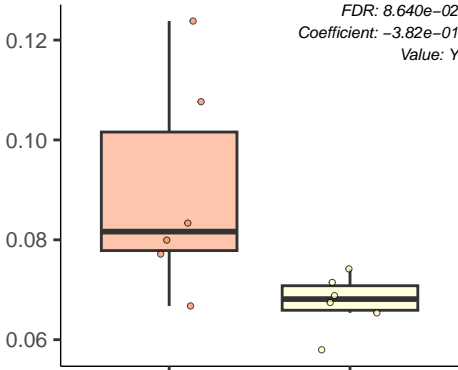
Type.VI.secretion.systems

FDR:  $8.640e-02$   
Coefficient:  $-3.82e-01$   
Value: Y

N (n=6)

Y (n=6)

strep\_exposure



CBSS.257314.1.peg.488

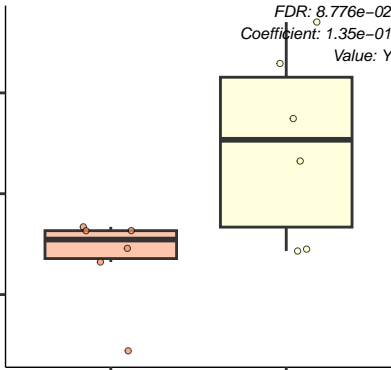
0.065  
0.060  
0.055

N (n=6)

Y (n=6)

strep\_exposure

FDR:  $8.776e-02$   
Coefficient:  $1.35e-01$   
Value: Y



CBSS.342610.3.peg.1536

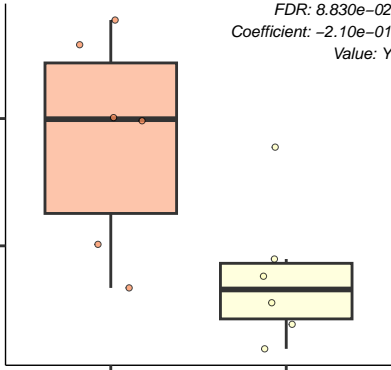
*FDR: 8.830e-02*  
*Coefficient: -2.10e-01*  
*Value: Y*

0.040  
0.035

N (n=6)

Y (n=6)

strep\_exposure



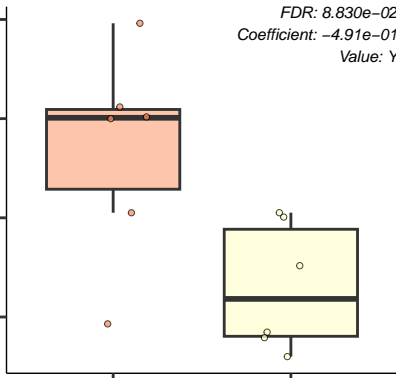
Pterin.carbinolamine.dehydratase

*FDR: 8.830e-02*  
*Coefficient: -4.91e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



Colanic.acid.biosynthesis

*FDR: 8.874e-02*  
*Coefficient: -2.16e-01*  
*Value: Y*

0.11

0.10

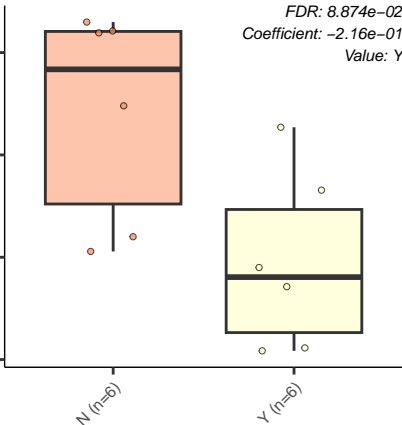
0.09

0.08

N (n=6)

Y (n=6)

strep\_exposure



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

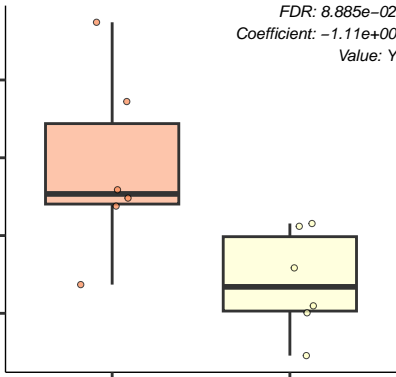
FDR:  $8.885e-02$   
Coefficient:  $-1.11e+00$   
Value: Y

0.004  
0.003  
0.002  
0.001

N (n=6)

Y (n=6)

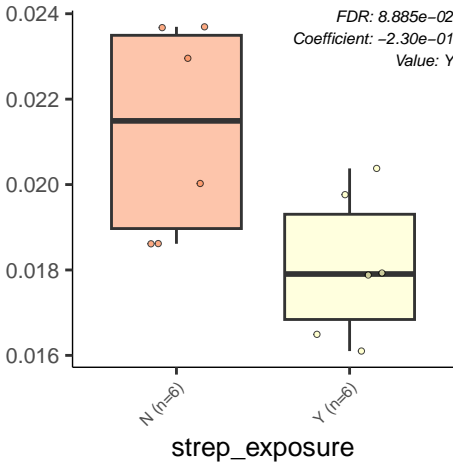
strep\_exposure





At1g14345

*FDR: 8.885e-02*  
*Coefficient: -2.30e-01*  
*Value: Y*



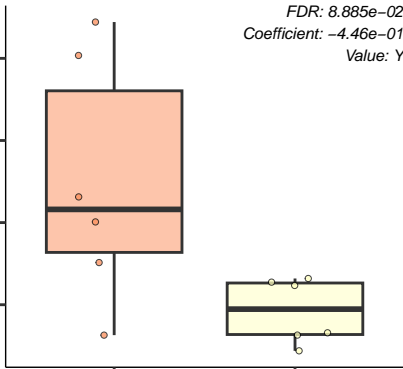
CBSS.216592.1.peg.3937

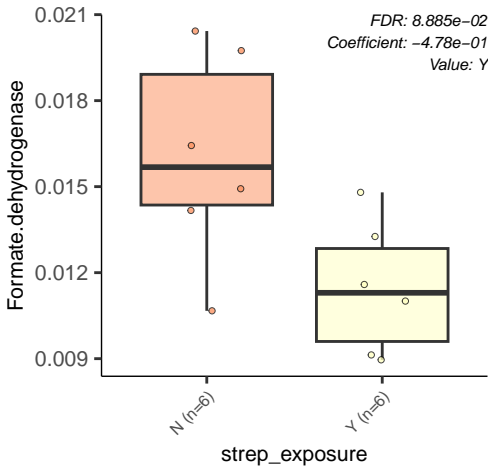
FDR:  $8.885e-02$   
Coefficient:  $-4.46e-01$   
Value: Y

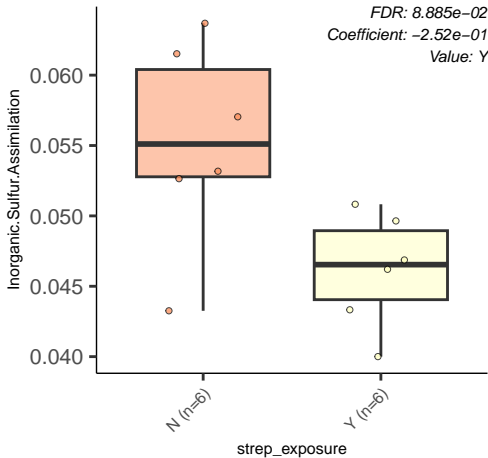
N (n=6)

Y (n=6)

strep\_exposure







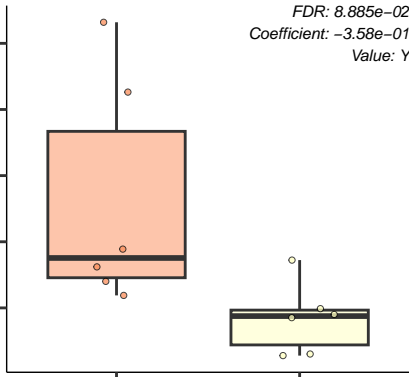
L.ascorbate.utilization..and.related.gene.clusters.

*FDR: 8.885e-02*  
*Coefficient: -3.58e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



Polyadenylation.bacterial

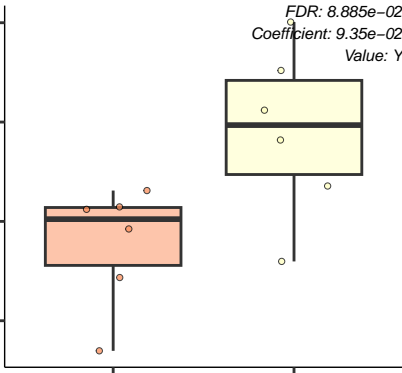
0.19  
0.18  
0.17  
0.16

*FDR: 8.885e-02*  
*Coefficient: 9.35e-02*  
*Value: Y*

*N (n=6)*

*Y (n=6)*

strep\_exposure



Putative.oxidase.COG2907

0.025

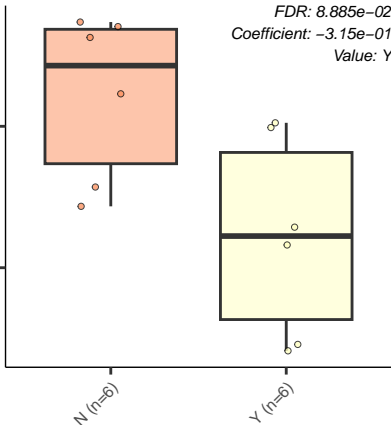
0.020

N (n=6)

Y (n=6)

strep\_exposure

FDR:  $8.885e-02$   
Coefficient:  $-3.15e-01$   
Value: Y



Teichuronic.acid.biosynthesis

FDR:  $8.885e-02$   
Coefficient:  $-2.00e-01$   
Value: Y

0.045

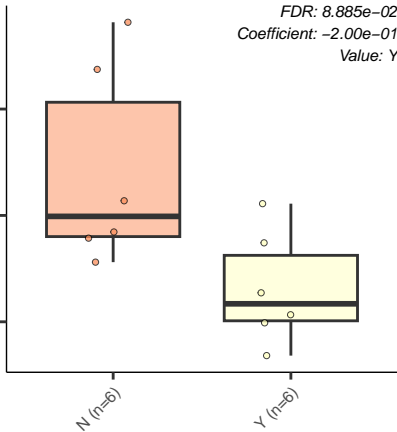
0.040

0.035

N (n=6)

Y (n=6)

strep\_exposure





Siderophore.Aerobactin

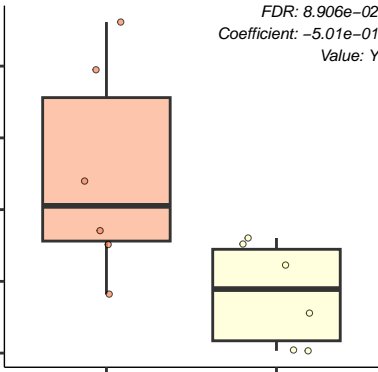
*FDR: 8.906e-02*  
*Coefficient: -5.01e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure

0.0175  
0.0150  
0.0125  
0.0100  
0.0075



High.affinity.phosphate.transporter.and.control.of.PHO.regu

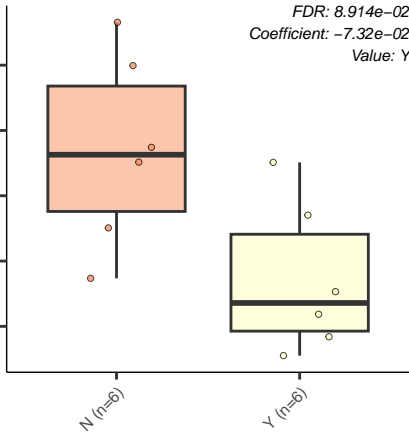
FDR:  $8.914e-02$   
Coefficient:  $-7.32e-02$   
Value: Y

N (n=6)

Y (n=6)

strep\_exposure

0.37  
0.38  
0.39  
0.40  
0.41



Isoprenoid.Biosynthesis

*FDR: 8.914e-02*  
*Coefficient: 5.67e-02*  
*Value: Y*

0.205

0.200

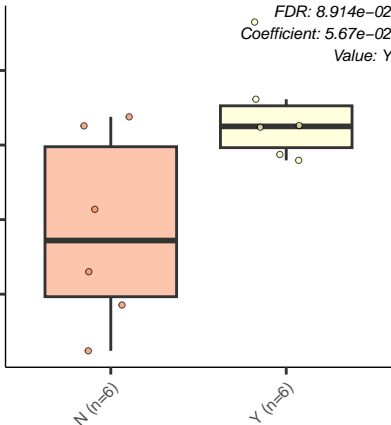
0.195

0.190

N (n=6)

Y (n=6)

strep\_exposure



Bacterial.Cytoskeleton

0.50

0.48

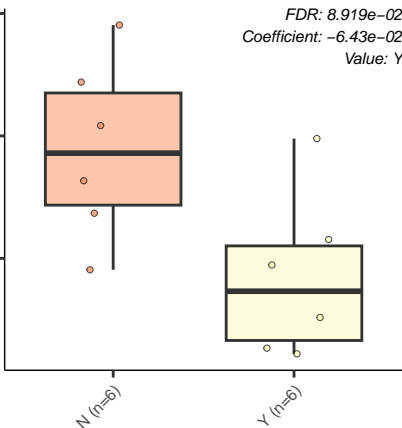
0.46

N (n=6)

Y (n=6)

strep\_exposure

FDR:  $8.919e-02$   
Coefficient:  $-6.43e-02$   
Value: Y



Synechocystis.experimental

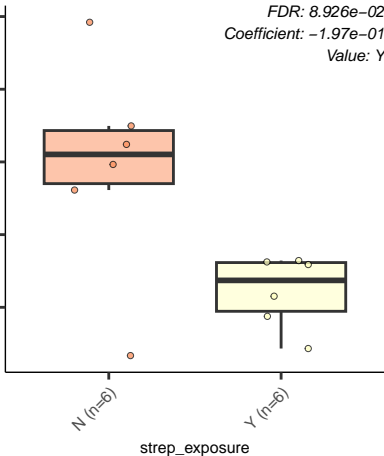
0.0375  
0.0350  
0.0325  
0.0300  
0.0275

*FDR: 8.926e-02*  
*Coefficient: -1.97e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



N.linked.Glycosylation.in.Bacteria

FDR:  $8.968e-02$   
Coefficient:  $-8.85e-02$   
Value: Y

N (n=6)

Y (n=6)

strep\_exposure

0.13

0.12

p.Hydroxybenzoate.degradation

0.0030

0.0025

0.0020

0.0015

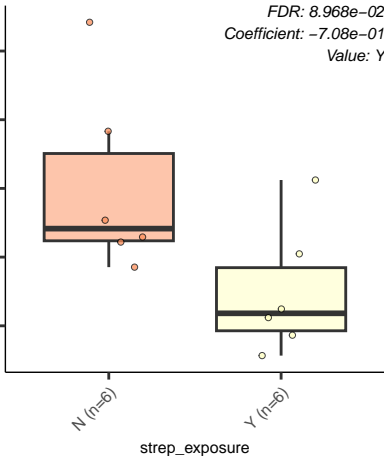
0.0010

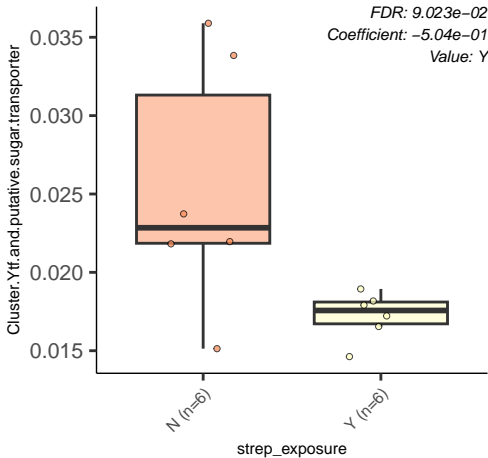
N (n=6)

Y (n=6)

strep\_exposure

FDR: 8.968e-02  
Coefficient: -7.08e-01  
Value: Y







tRNA.aminoacylation..Arg

0.16

0.15

0.14

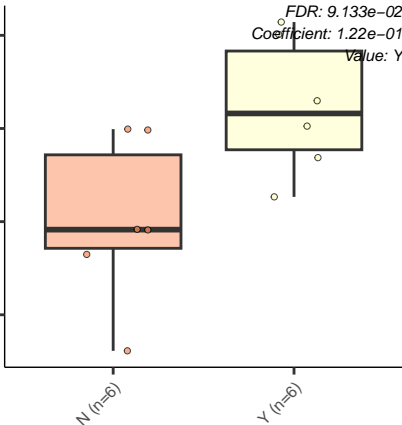
0.13

N (n=6)

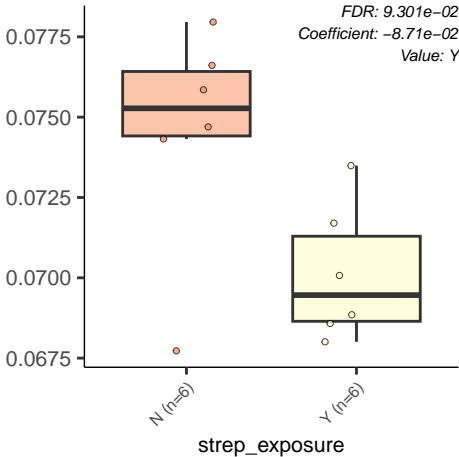
Y (n=6)

strep\_exposure

FDR: 9.133e-02  
Coefficient: 1.22e-01  
Value: Y



Butanol.Biosynthesis



Nitric.oxide.synthase

0.003

0.002

0.001

N (n=6)

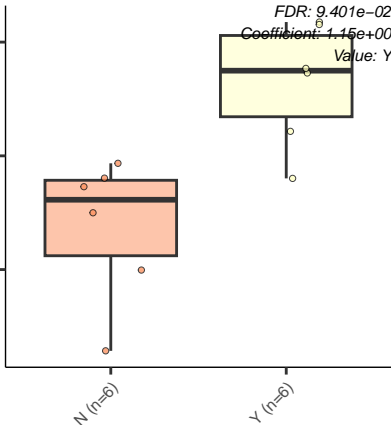
Y (n=6)

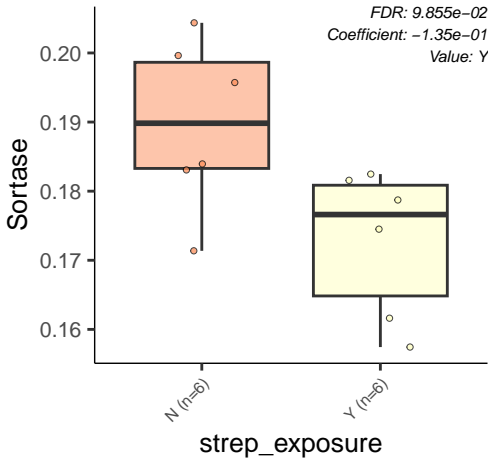
strep\_exposure

FDR:  $9.401e-02$

Coefficient:  $1.15e+00$

Value: Y





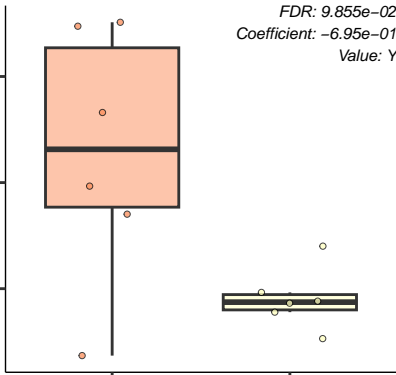
YjbEFGH.Locus.Involved.in.Exopolysaccharide.Production

FDR:  $9.855e-02$   
Coefficient:  $-6.95e-01$   
Value: Y

N (n=6)

Y (n=6)

strep\_exposure



tRNA.aminoacylation..Thr

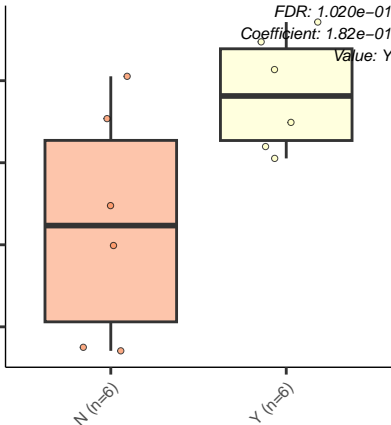
0.070  
0.065  
0.060  
0.055

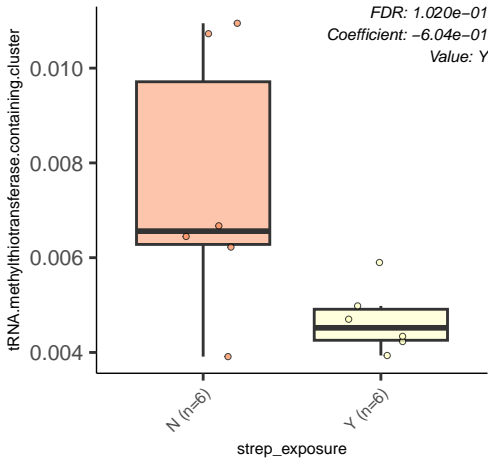
N (n=6)

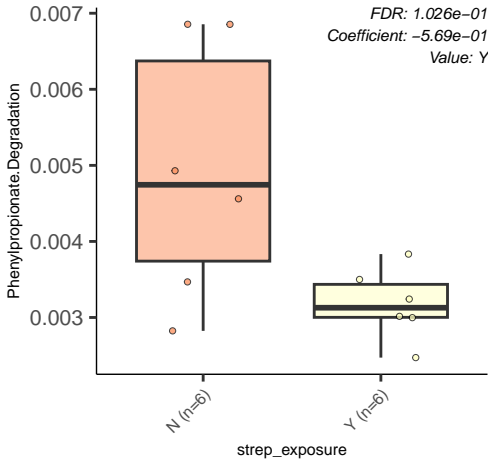
Y (n=6)

strep\_exposure

FDR: 1.020e-01  
Coefficient: 1.82e-01  
Value: Y









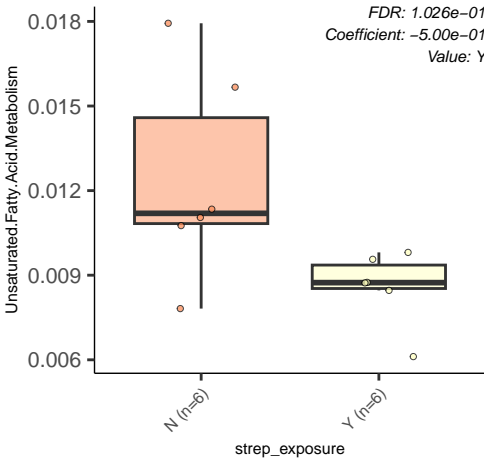
Unsaturated.Fatty.Acid.Metabolism

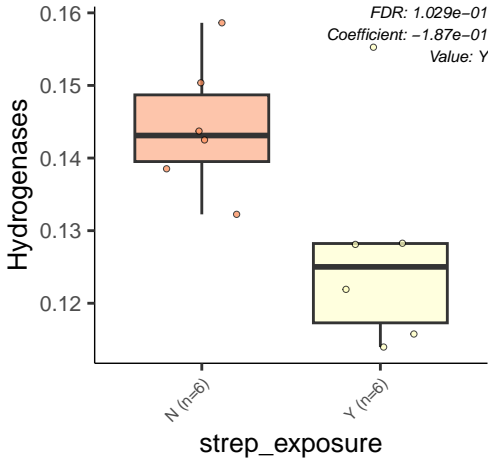
FDR: 1.026e-01  
Coefficient: -5.00e-01  
Value: Y

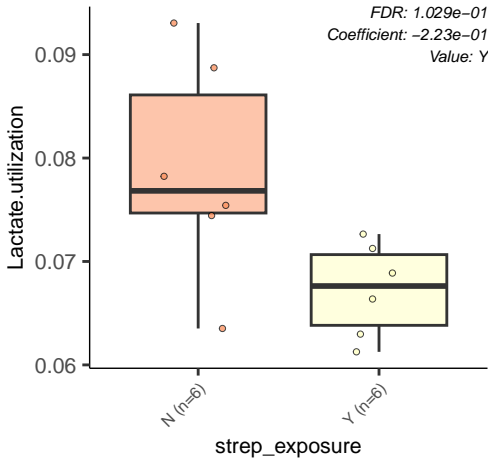
N (n=6)

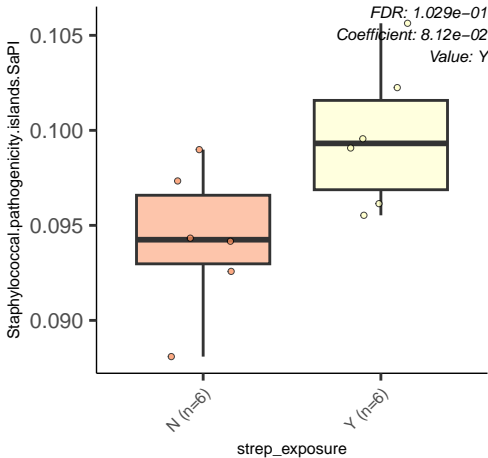
Y (n=6)

strep\_exposure



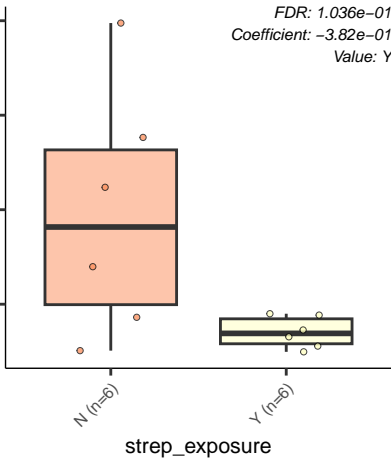


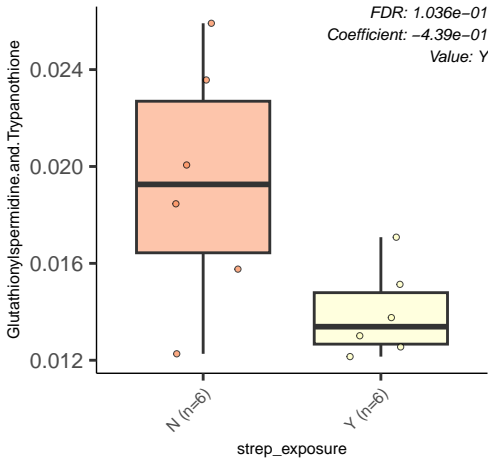


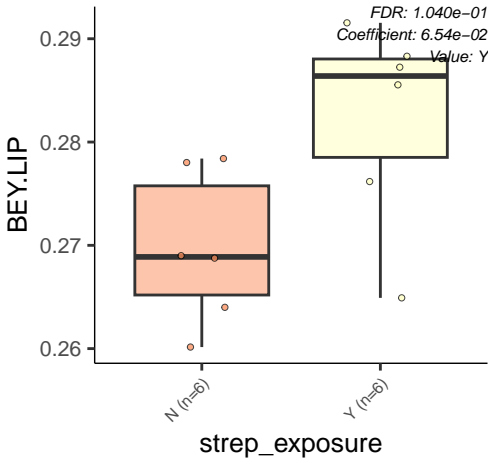


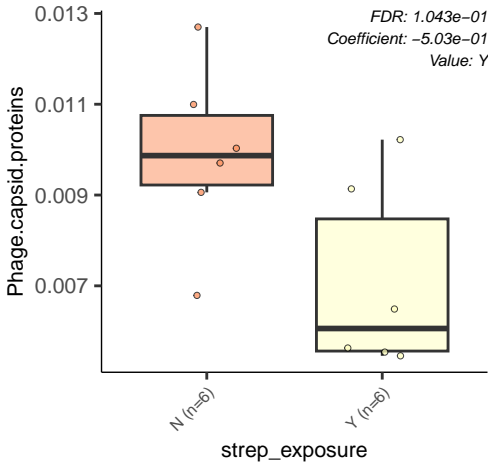
CBSS.316407.3.pcg.1371

*FDR: 1.036e-01*  
*Coefficient: -3.82e-01*  
*Value: Y*











Fatty.acid.degradation.regulons

0.040

0.035

0.030

0.025

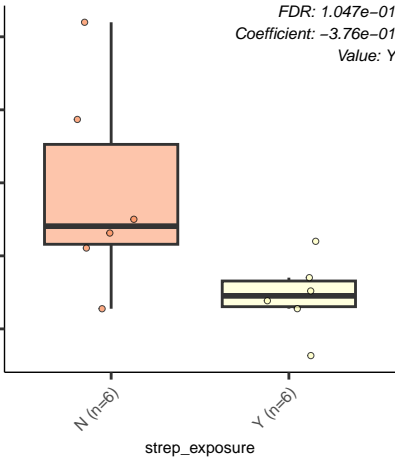
0.020

N (n=6)

Y (n=6)

strep\_exposure

FDR: 1.047e-01  
Coefficient: -3.76e-01  
Value: Y



Proton.dependent.Peptide.Transporters

0.070

0.065

0.060

0.055

0.050

N (n=6)

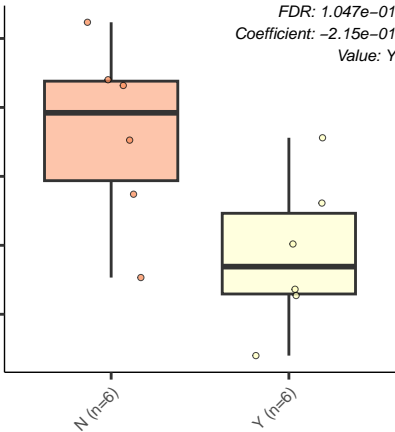
Y (n=6)

strep\_exposure

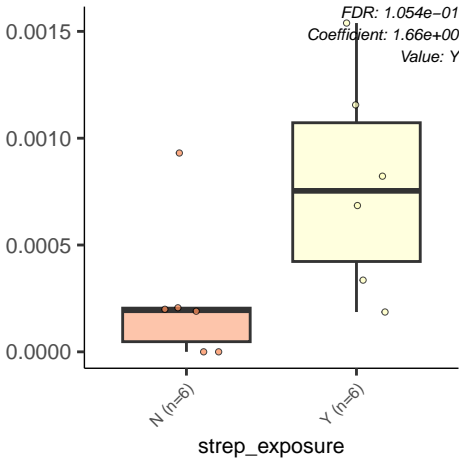
FDR: 1.047e-01

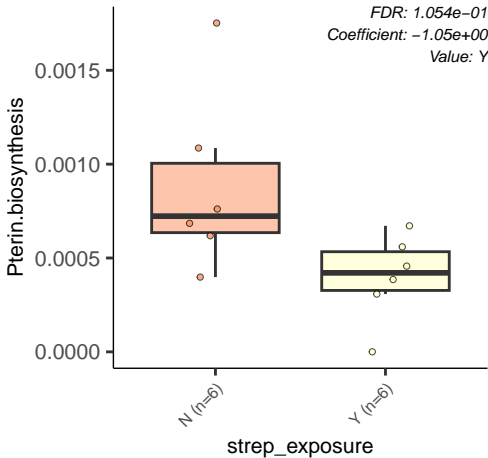
Coefficient: -2.15e-01

Value: Y

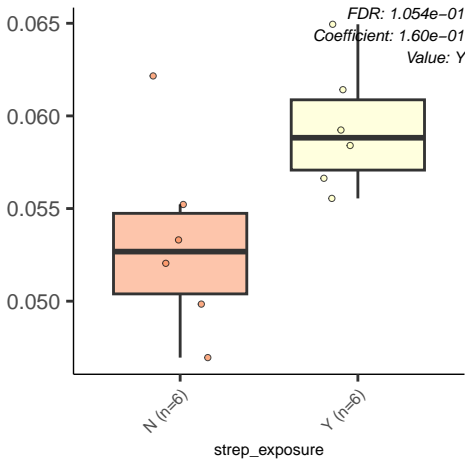


Phenazine.biosynthesis



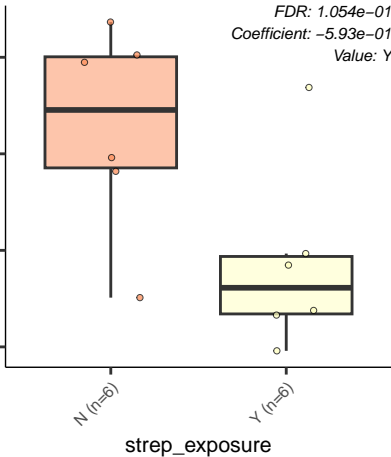


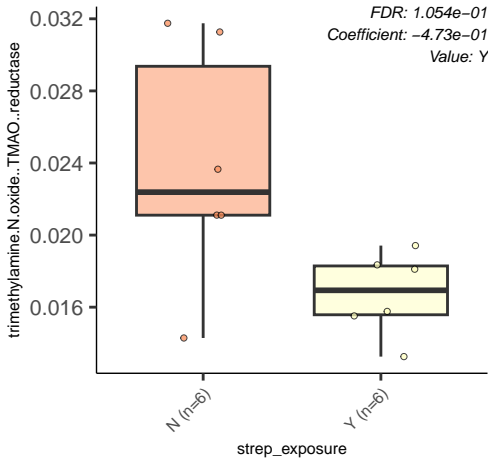
Transport of Nickel and Cobalt



rRNA.modification.Archaea

*FDR: 1.054e-01*  
*Coefficient: -5.93e-01*  
*Value: Y*





tRNA.aminoacylation..Val

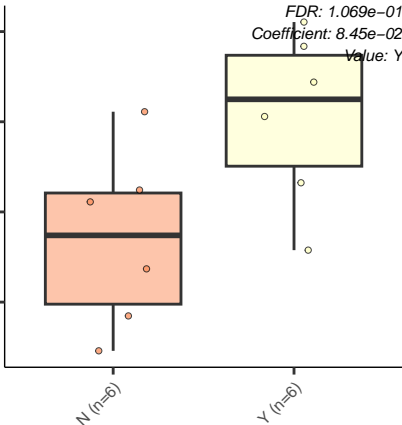
0.25  
0.24  
0.23  
0.22

N (n=6)

Y (n=6)

strep\_exposure

FDR: 1.069e-01  
Coefficient: 8.45e-02  
Value: Y





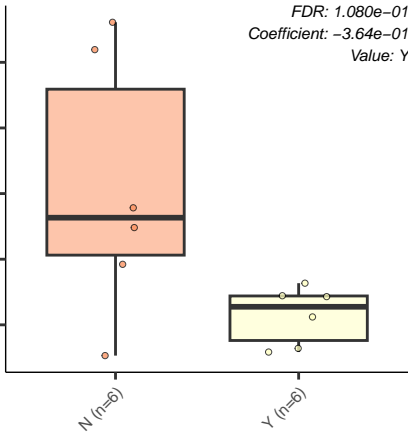
Lipopolysaccharide.assembly

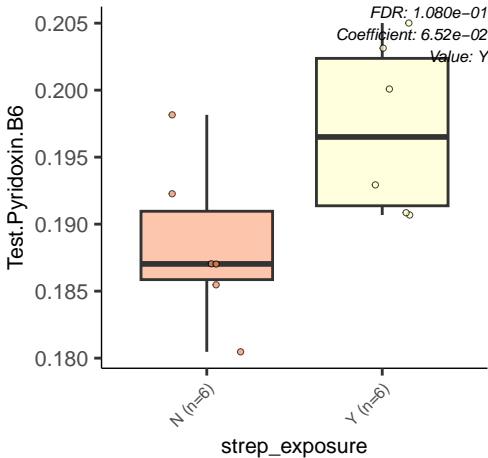
FDR: 1.080e-01  
Coefficient: -3.64e-01  
Value: Y

N (n=6)

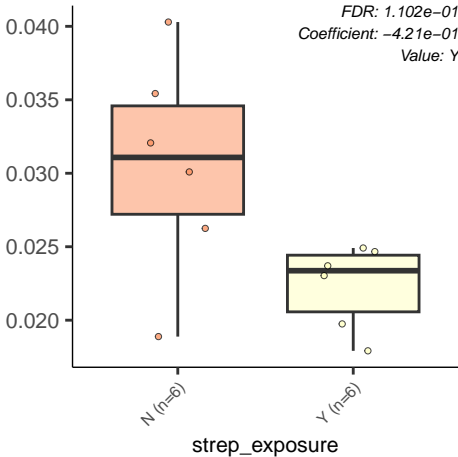
Y (n=6)

strep\_exposure





Pyrimidine.utilization



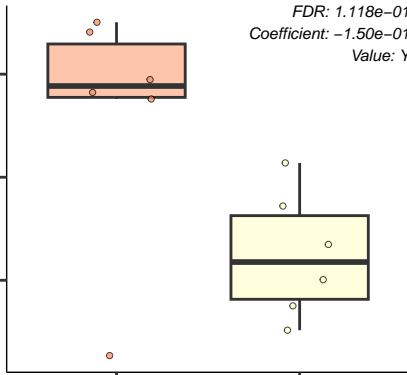
ABC.transporter.dipeptide..TC.3.A.1.5.2.

FDR: 1.118e-01  
Coefficient: -1.50e-01  
Value: Y

N (n=6)

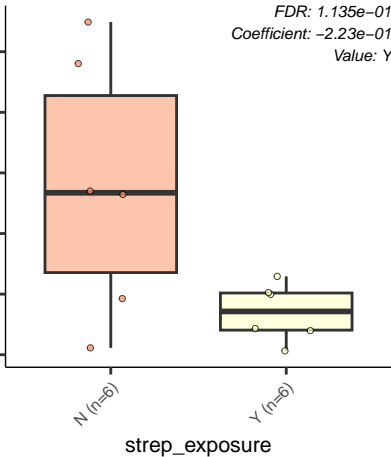
Y (n=6)

strep\_exposure



CBSS.326442.4.peg.1852

FDR: 1.135e-01  
Coefficient: -2.23e-01  
Value: Y



Glycolysis.test

*FDR: 1.135e-01*  
*Coefficient: -4.60e-01*  
*Value: Y*

0.025

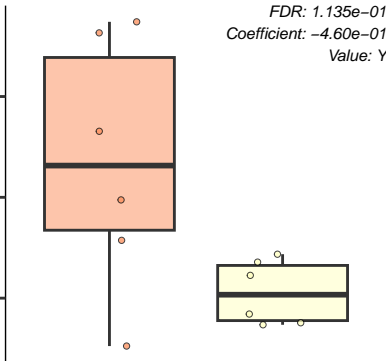
0.020

0.015

*N (n=6)*

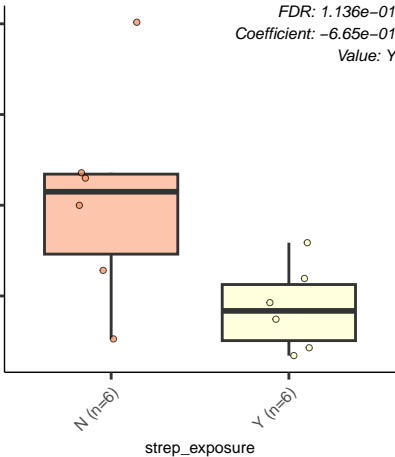
*Y (n=6)*

strep\_exposure



Multiple.Antibiotic.Resistance.MAR.locus

*FDR: 1.136e-01*  
*Coefficient: -6.65e-01*  
*Value: Y*



Phage.tail.fiber.proteins

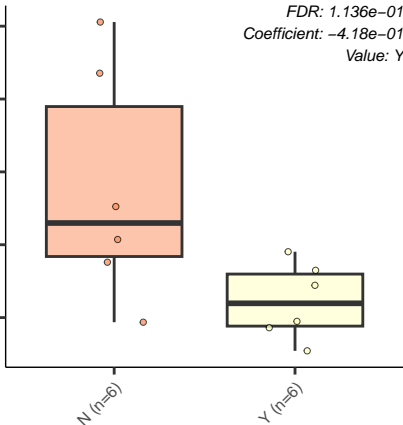
*FDR: 1.136e-01*  
*Coefficient: -4.18e-01*  
*Value: Y*

0.08  
0.07  
0.06  
0.05  
0.04

N (n=6)

Y (n=6)

strep\_exposure





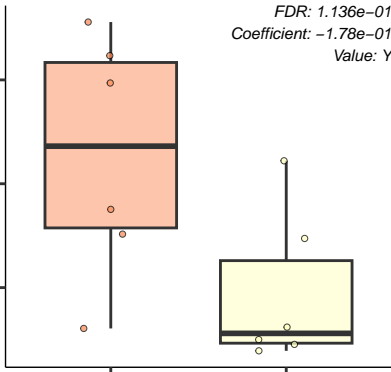
Amino.acid.racemase

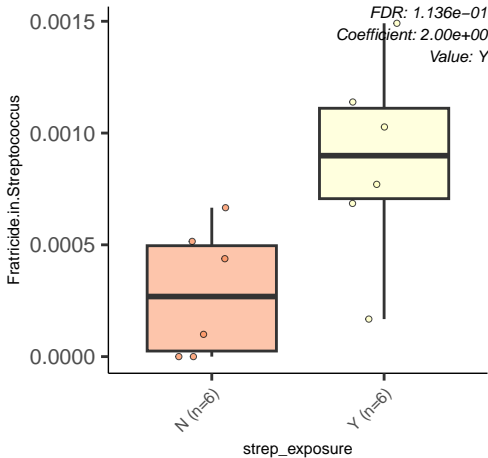
*FDR: 1.136e-01*  
*Coefficient: -1.78e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure





Methicillin.resistance.in.Staphylococci

*FDR: 1.145e-01*  
*Coefficient: 1.13e-01*  
*Value: Y*

0.0475

0.0450

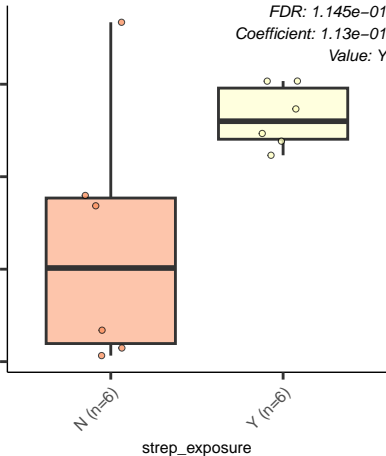
0.0425

0.0400

N (n=6)

Y (n=6)

strep\_exposure



CBSS.211586.1.peg.2357

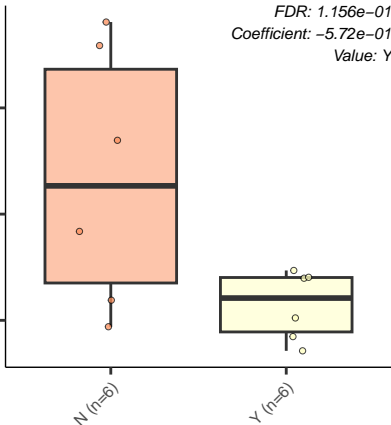
*FDR: 1.156e-01*  
*Coefficient: -5.72e-01*  
*Value: Y*

0.008  
0.006  
0.004

N (n=6)

Y (n=6)

strep\_exposure



Citrate.Metabolism.KE2

*FDR: 1.160e-01*  
*Coefficient: -6.01e-01*  
*Value: Y*

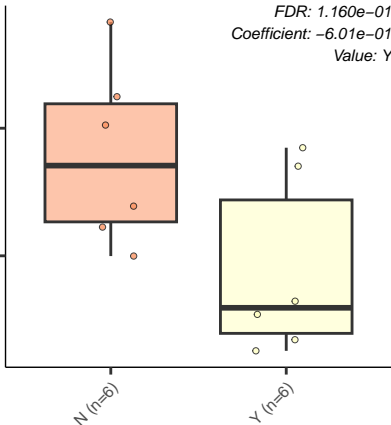
0.003

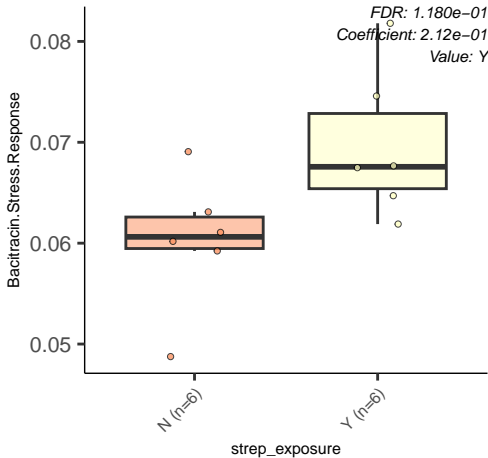
0.002

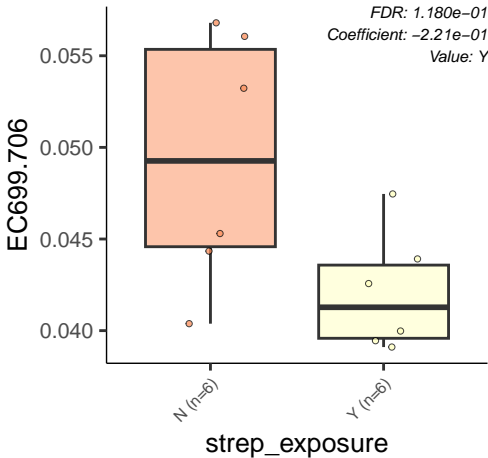
N (n=6)

Y (n=6)

strep\_exposure







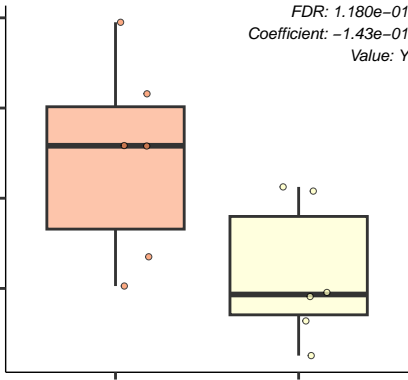
Lipid.A.Ara4N.pathway...Polymyxin.resistance..

FDR: 1.180e-01  
Coefficient: -1.43e-01  
Value: Y

N (n=6)

Y (n=6)

strep\_exposure





Biofilm.Adhesin.Biosynthesis

0.025

0.020

0.015

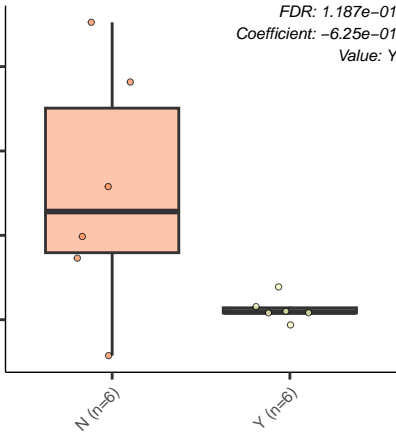
0.010

N (n=6)

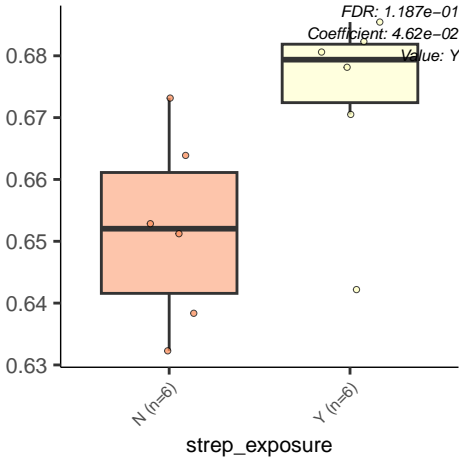
Y (n=6)

strep\_exposure

FDR: 1.187e-01  
Coefficient: -6.25e-01  
Value: Y



Beta.Glucoside.Metabolism



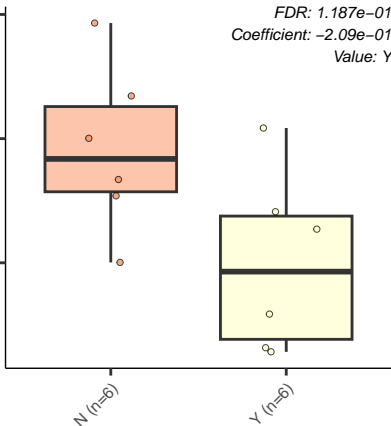
Propanediol.utilization

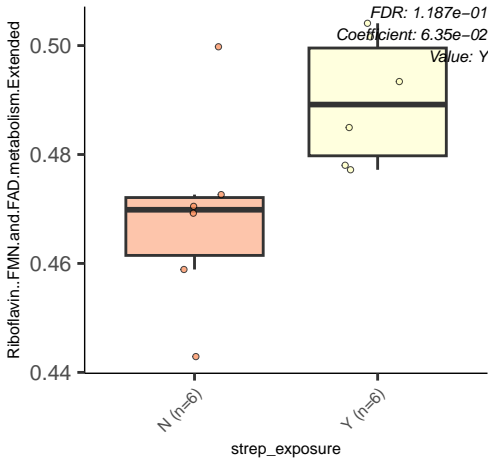
FDR: 1.187e-01  
Coefficient: -2.09e-01  
Value: Y

N (n=6)

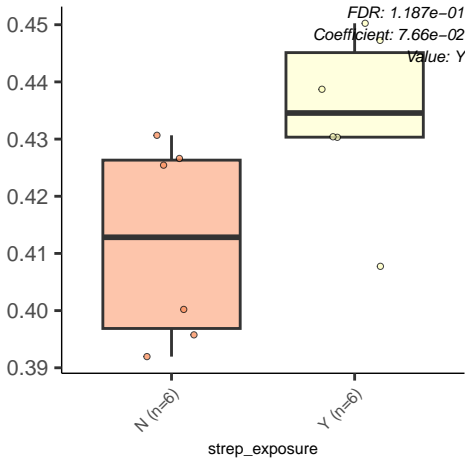
Y (n=6)

strep\_exposure

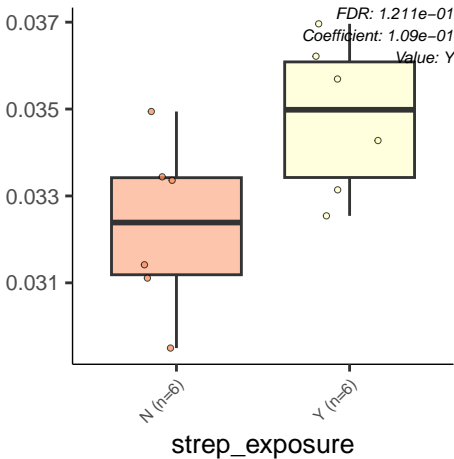


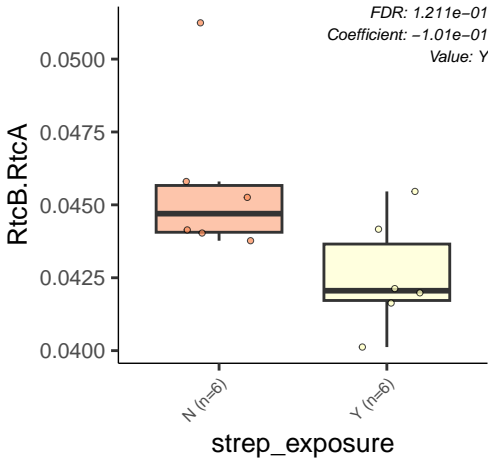


Ribosome.biogenesis.bacterial



At1g21350





TenI.like.tautomerase

FDR: 1.211e-01  
Coefficient: -7.27e-02  
Value: Y

0.130

0.125

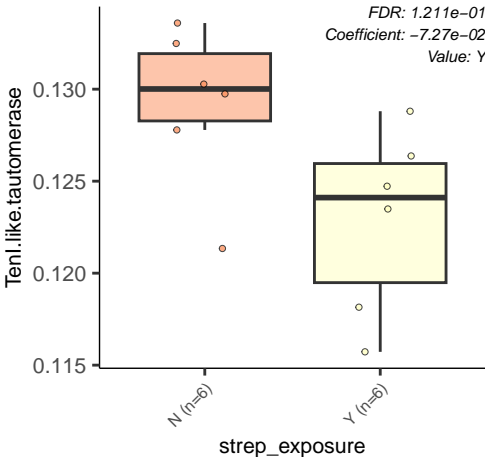
0.120

0.115

N (n=6)

Y (n=6)

strep\_exposure





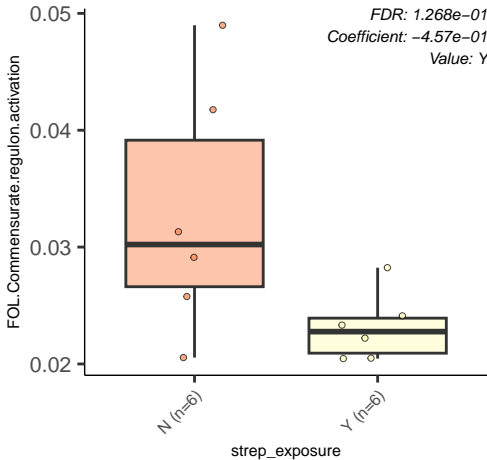
FOL.Commensurate.regulon.activation

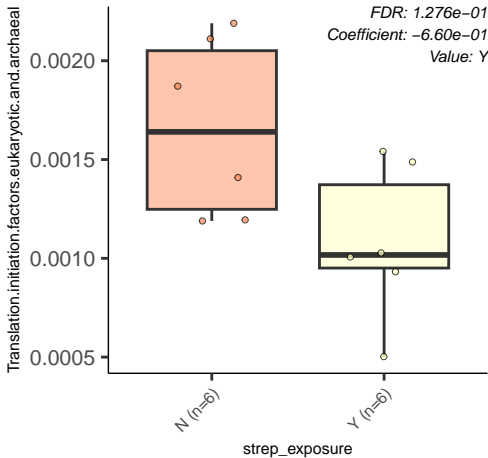
*FDR: 1.268e-01*  
*Coefficient: -4.57e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure





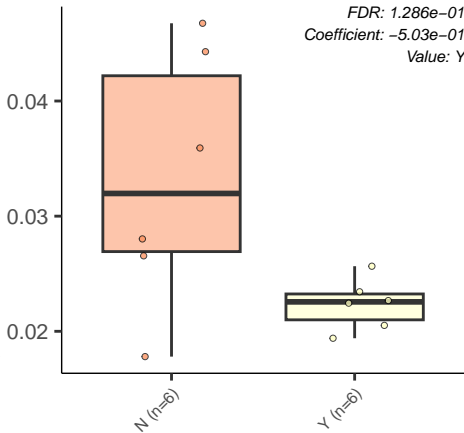
Multidrug.efflux.pump.in.Campylobacter.jejuni..CmeABC.op

FDR: 1.286e-01  
Coefficient: -5.03e-01  
Value: Y

N (n=6)

Y (n=6)

strep\_exposure



Galactose.inducible.PTS

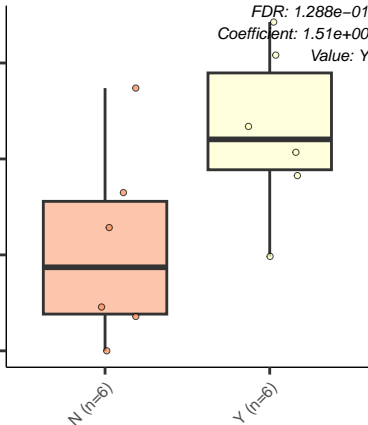
0.00075  
0.00050  
0.00025  
0.00000

N (n=6)

Y (n=6)

strep\_exposure

FDR: 1.288e-01  
Coefficient: 1.51e+00  
Value: Y



Selenocysteine.metabolism

*FDR: 1.288e-01*  
*Coefficient: -1.58e-01*  
*Value: Y*

0.08

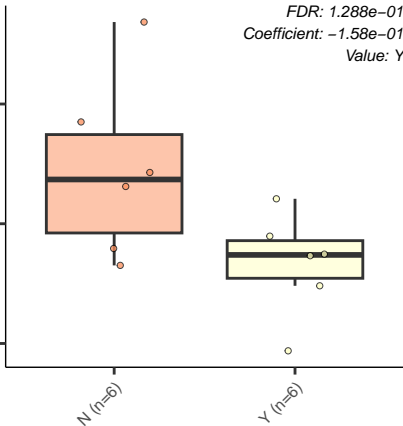
0.07

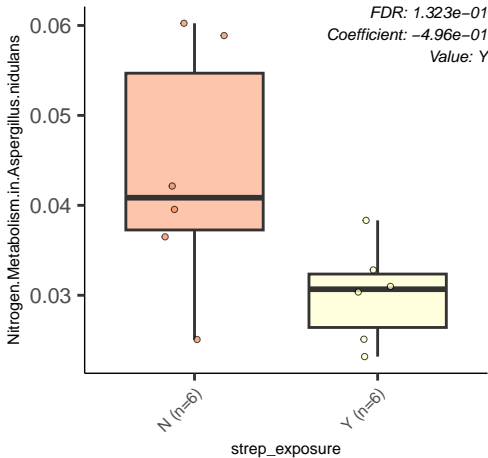
0.06

N (n=6)

Y (n=6)

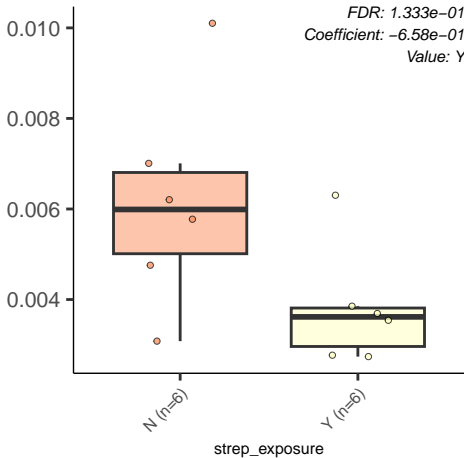
strep\_exposure





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

FDR: 1.333e-01  
Coefficient: -6.58e-01  
Value: Y



At2g23840

FDR: 1.333e-01  
Coefficient: -8.24e-02  
Value: Y

0.0625

0.0600

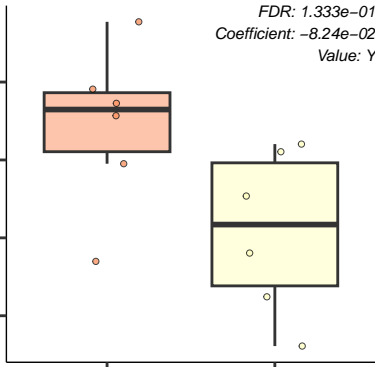
0.0575

0.0550

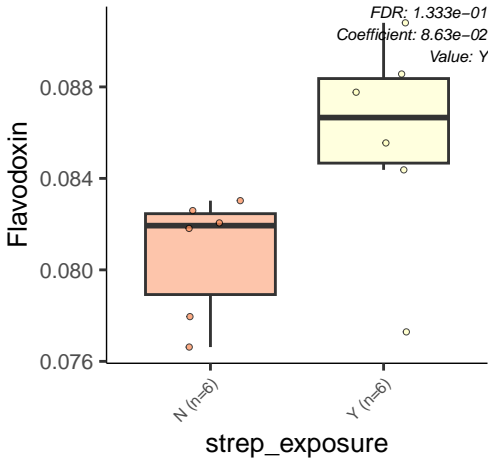
N (n=6)

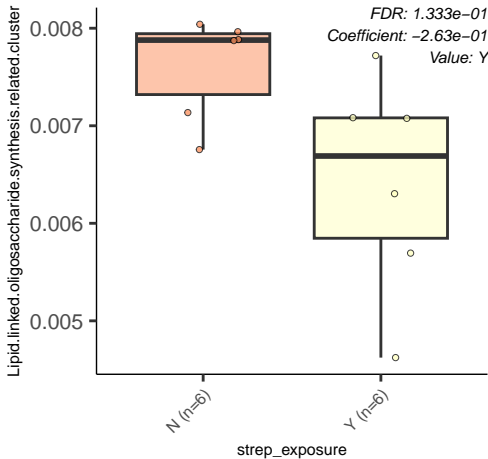
Y (n=6)

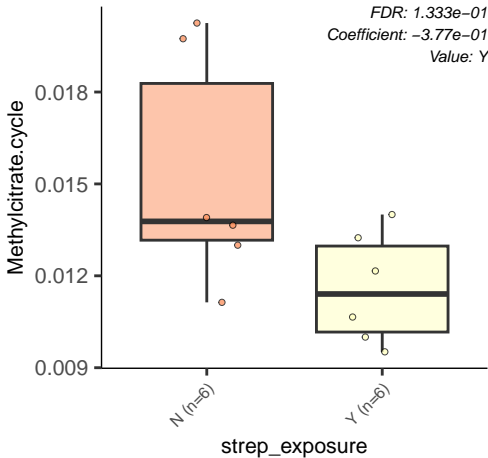
strep\_exposure

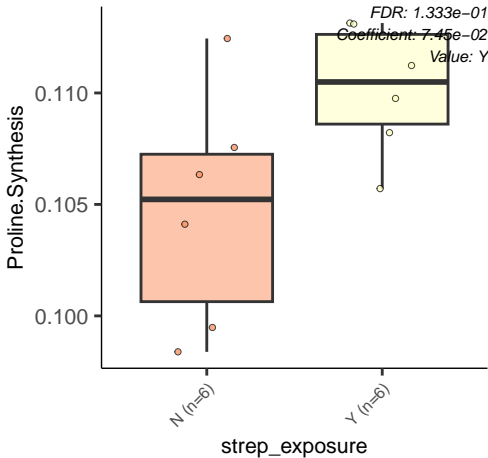


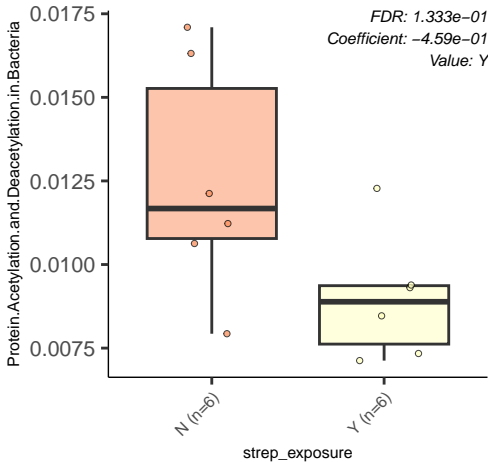












tRNA.aminoacylation..Leu

FDR: 1.333e-01

Coefficient: 6.75e-02

Value: Y

0.200

0.195

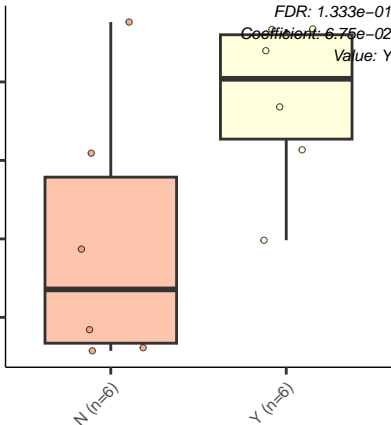
0.190

0.185

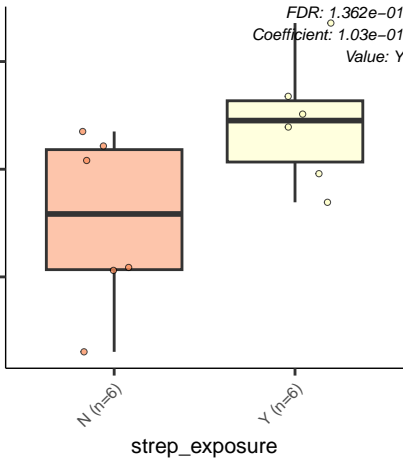
N (n=6)

Y (n=6)

strep\_exposure



tRNA.aminoacylation..Gly



Trehalose.Uptake.and.Utilization

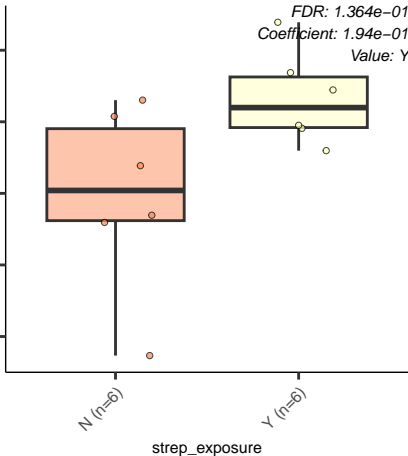
0.12  
0.11  
0.10  
0.09  
0.08

N (n=6)

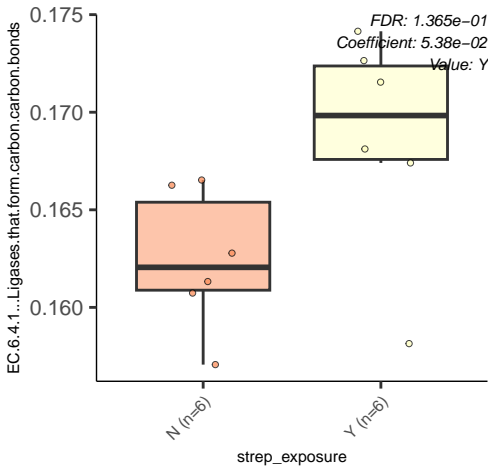
Y (n=6)

strep\_exposure

FDR: 1.364e-01  
Coefficient: 1.94e-01  
Value: Y







Alkylphosphate.utilization

FDR: 1.370e-01  
Coefficient: -3.25e-01  
Value: Y

0.045

0.040

0.035

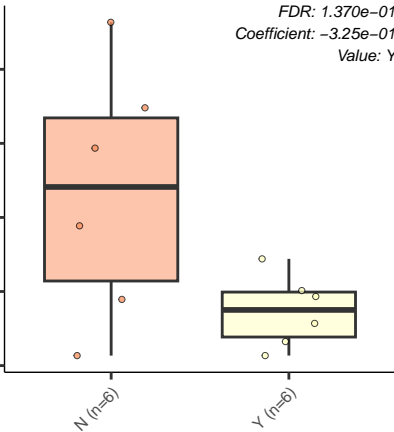
0.030

0.025

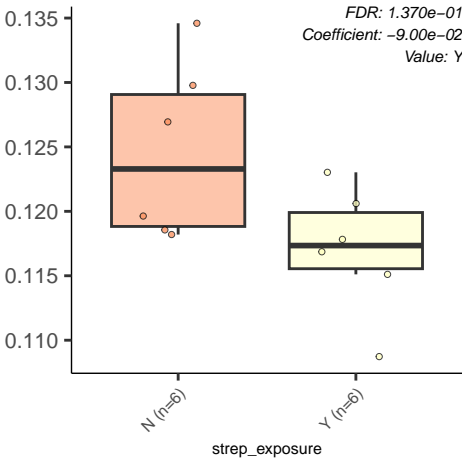
N (n=6)

Y (n=6)

strep\_exposure



ium.virulence.operon.involved.in.an.unknown.function.with.a.Jag.Pro



D.galactonate.catabolism

FDR:  $1.388e-01$   
Coefficient:  $-4.52e-01$   
Value: Y

0.04

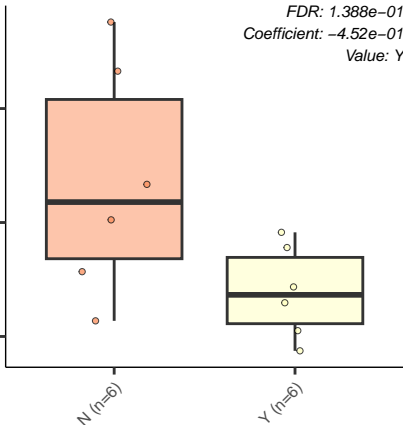
0.03

0.02

N (n=6)

Y (n=6)

strep\_exposure



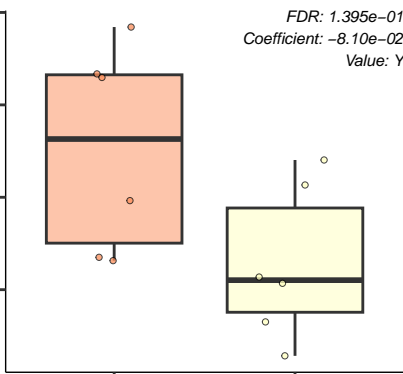
tRNA.aminoacylation..Ile

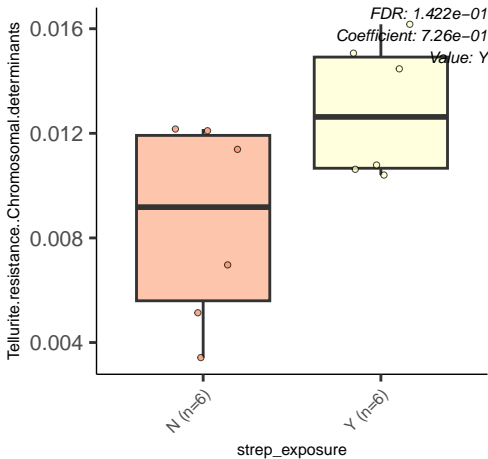
FDR: 1.395e-01  
Coefficient: -8.10e-02  
Value: Y

N (n=6)

Y (n=6)

strep\_exposure





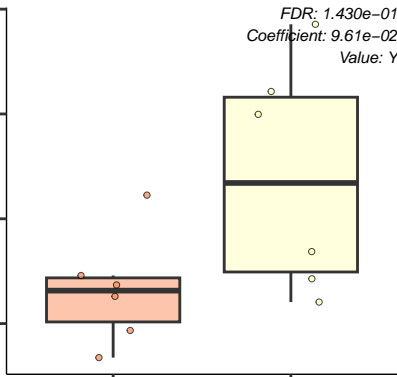
Hyperosmotic.potassium.uptake

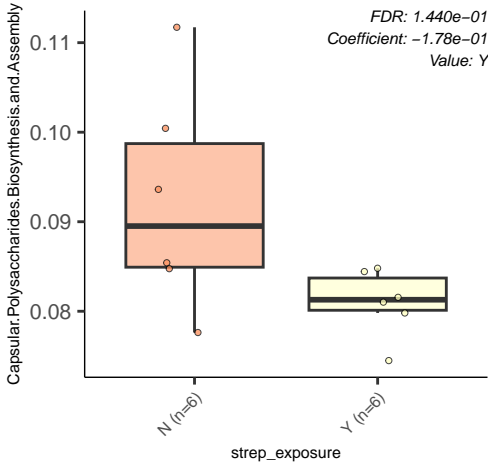
*FDR: 1.430e-01*  
*Coefficient: 9.61e-02*  
*Value: Y*

N (n=6)

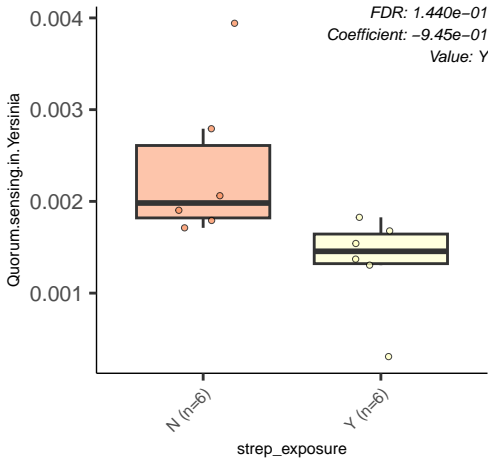
Y (n=6)

strep\_exposure









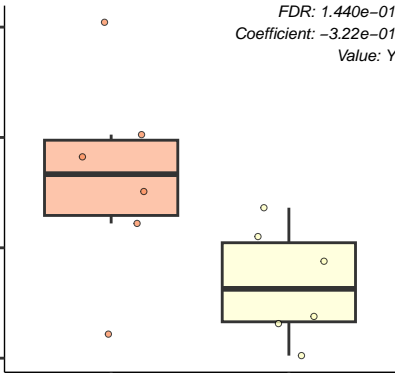
p.Aminobenzoyl.Glutamate.Utilization

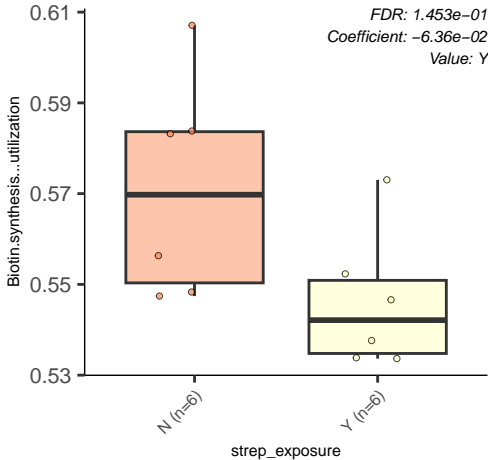
*FDR: 1.440e-01*  
*Coefficient: -3.22e-01*  
*Value: Y*

N (n=6)

Y (n=6)

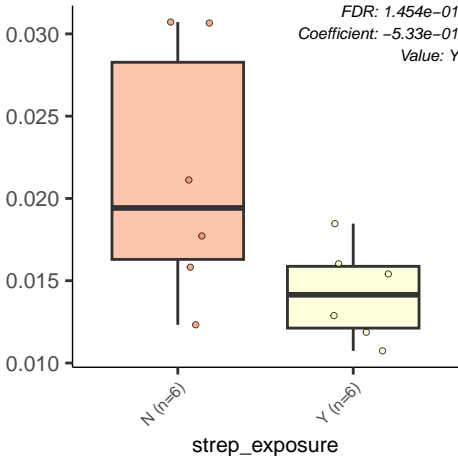
strep\_exposure





The.fimbrial.Stf.cluster

*FDR: 1.454e-01*  
*Coefficient: -5.33e-01*  
*Value: Y*



Glycogen.metabolism

1.00

0.96

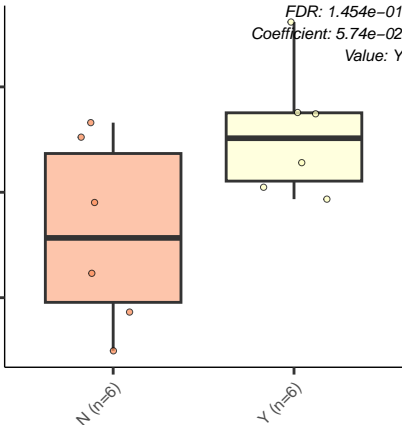
0.92

N (n=6)

Y (n=6)

strep\_exposure

FDR: 1.454e-01  
Coefficient: 5.74e-02  
Value: Y



CBSS.584.1.peg.841

FDR: 1.464e-01

Coefficient: -4.70e-01

Value: Y

0.010

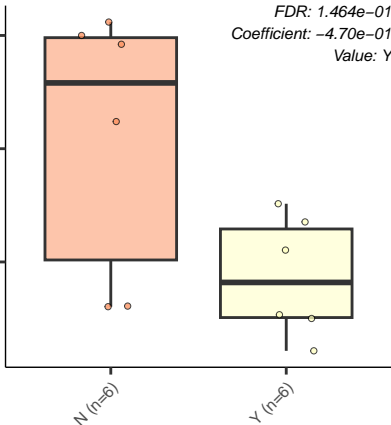
0.008

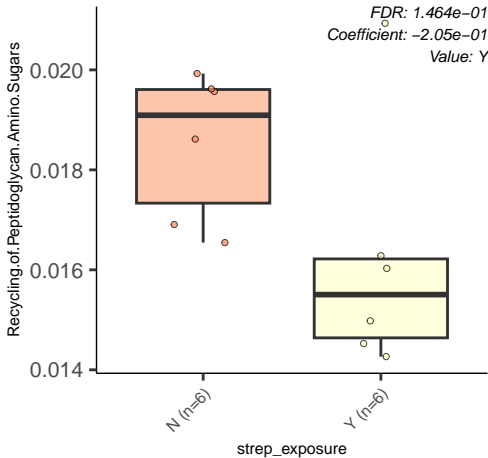
0.006

N (n=6)

Y (n=6)

strep\_exposure





DNA.repair..bacterial.RecBCD.pathway

*FDR: 1.465e-01*  
*Coefficient: -6.45e-02*  
*Value: Y*

0.40

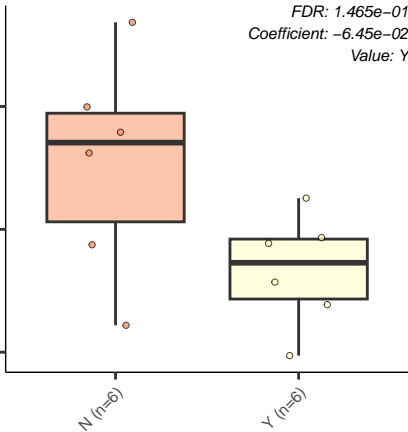
0.38

0.36

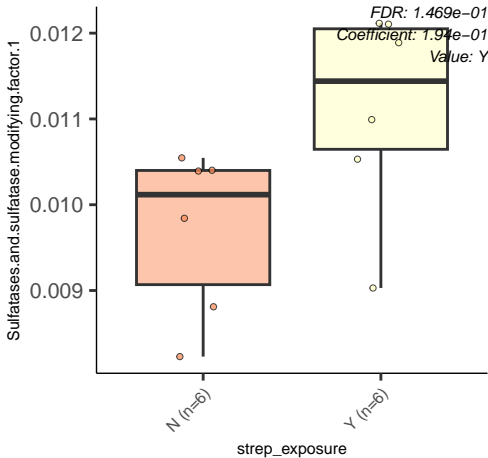
N (n=6)

Y (n=6)

strep\_exposure







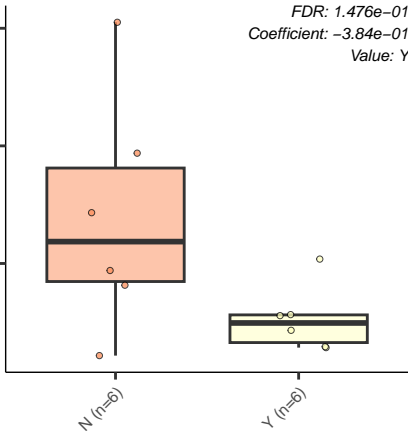
Major.Outer.Membrane.Proteins

*FDR: 1.476e-01*  
*Coefficient: -3.84e-01*  
*Value: Y*

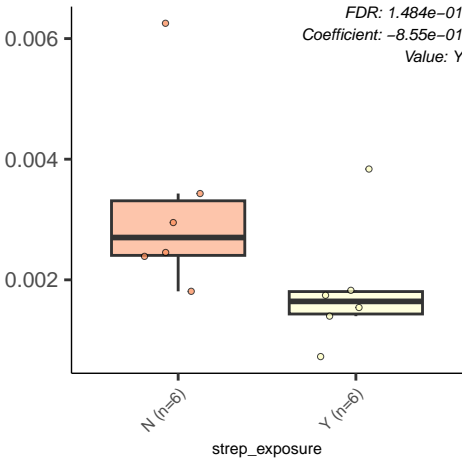
N (n=6)

Y (n=6)

strep\_exposure



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



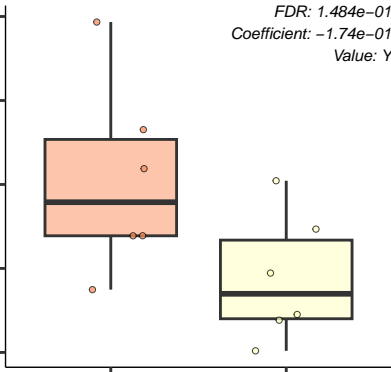
CBSS.246196.1.peg.364

*FDR: 1.484e-01*  
*Coefficient: -1.74e-01*  
*Value: Y*

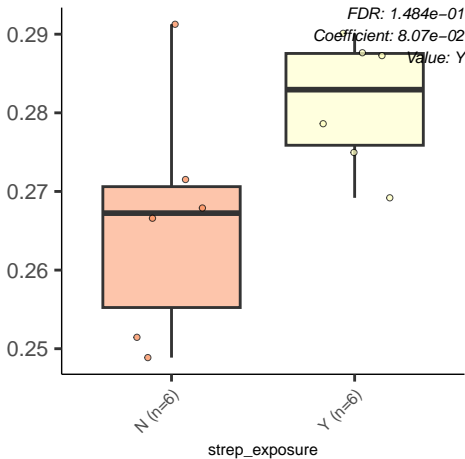
N (n=6)

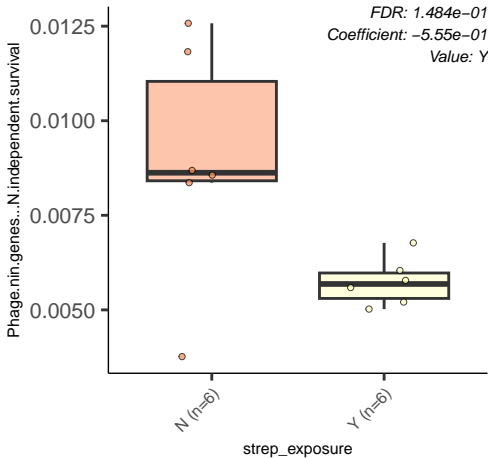
Y (n=6)

strep\_exposure



Exopolysaccharide.Biosynthesis





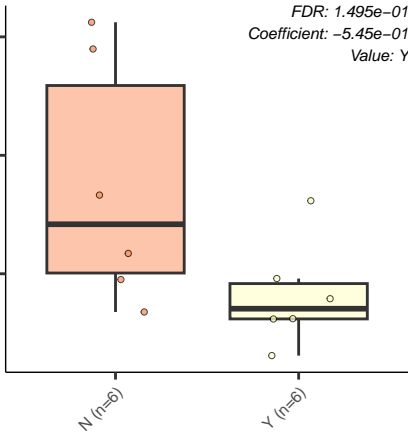
Peptide.ABC.transport.system.Sap

*FDR: 1.495e-01*  
*Coefficient: -5.45e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



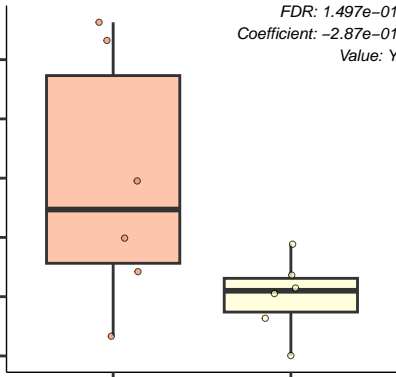
Aromatic.amino.acid.degradation

FDR: 1.497e-01  
Coefficient: -2.87e-01  
Value: Y

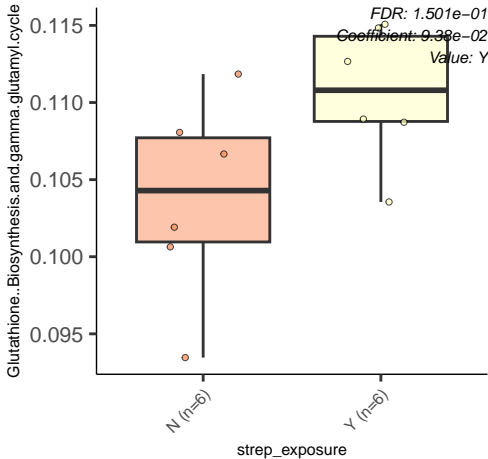
N (n=6)

Y (n=6)

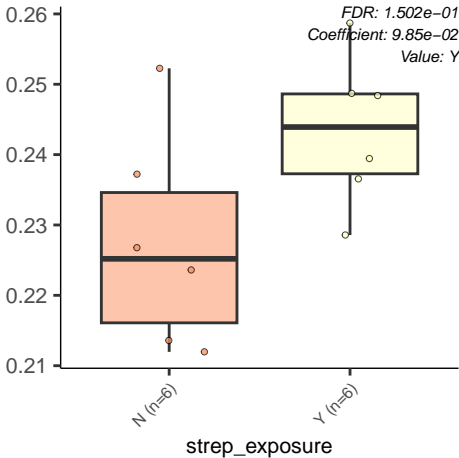
strep\_exposure







tRNA.aminoacylation..Phe



Rubrerythrin

*FDR: 1.510e-01*  
*Coefficient: -1.29e-01*  
*Value: Y*

0.060

0.056

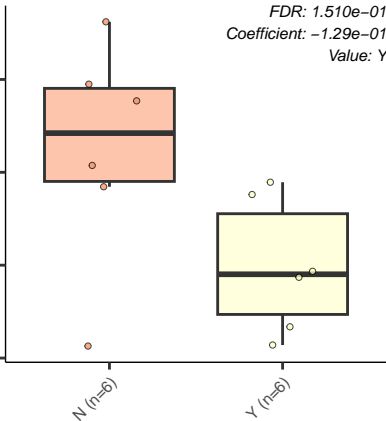
0.052

0.048

*N (n=6)*

*Y (n=6)*

strep\_exposure



Pyruvate.Alanine.Serine.Interconversions

FDR: 1.510e-01  
Coefficient: 6.72e-02  
Value: Y

0.140

0.135

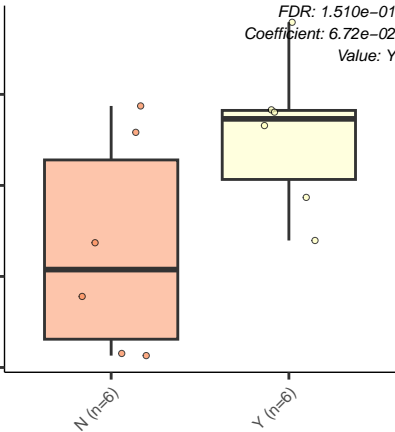
0.130

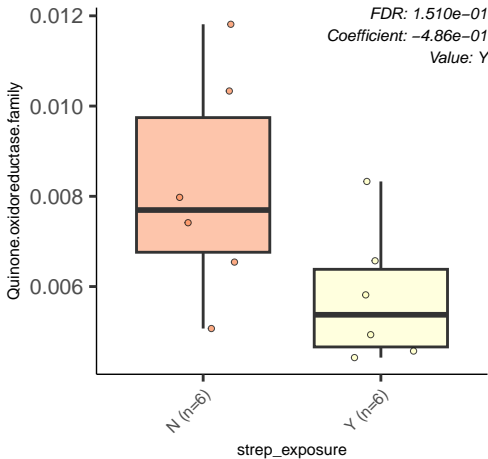
0.125

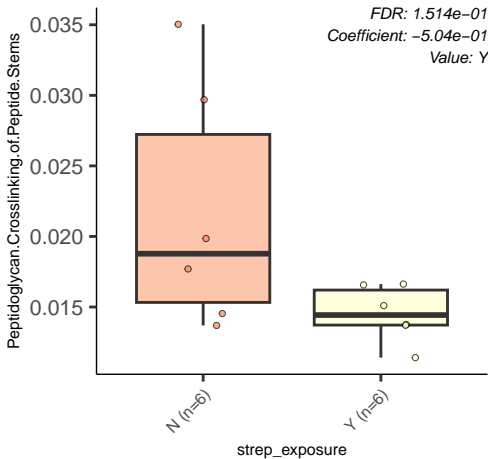
N (n=6)

Y (n=6)

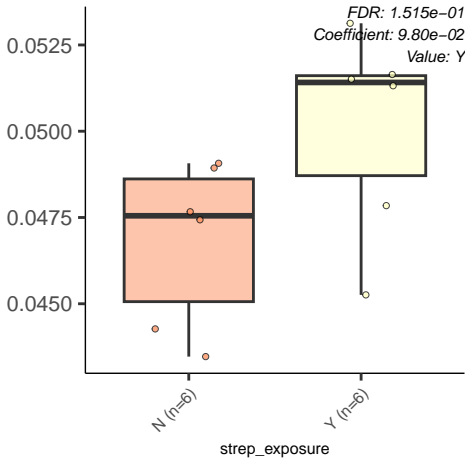
strep\_exposure

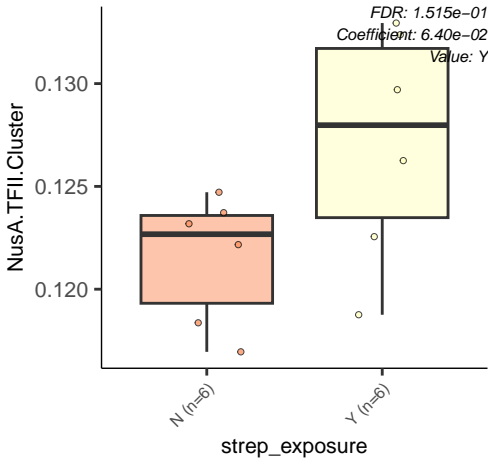






Glycine.reductase..sarcosine.reductase.and.betaine.reductase







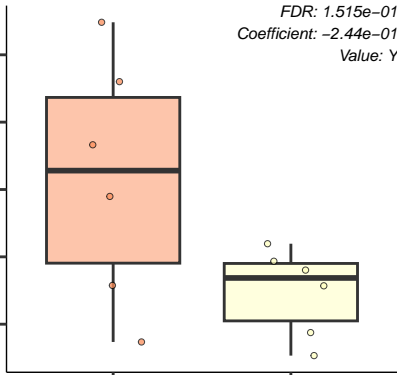
Unknown.sugar.utilization..cluster.yphABCDEFG.

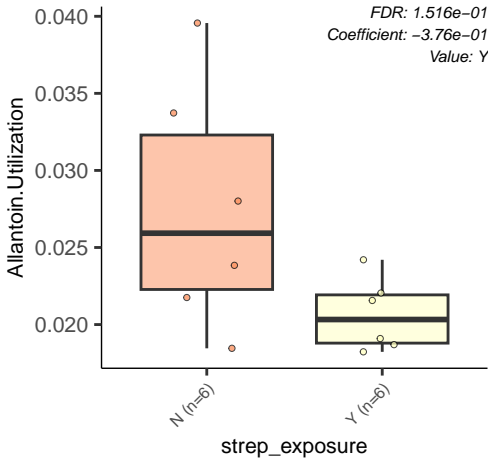
FDR: 1.515e-01  
Coefficient: -2.44e-01  
Value: Y

N (n=6)

Y (n=6)

strep\_exposure





CBSS.318161.14.peg.2599

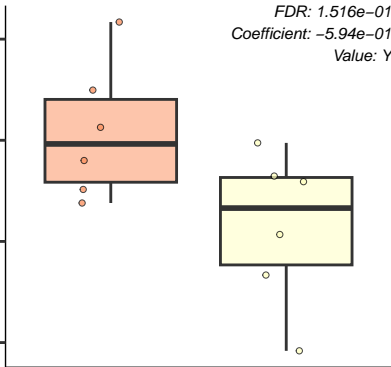
*FDR: 1.516e-01*  
*Coefficient: -5.94e-01*  
*Value: Y*

0.004  
0.003  
0.002  
0.001

N (n=6)

Y (n=6)

strep\_exposure



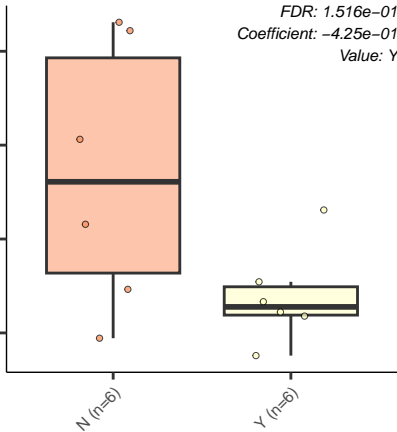
Colonization.factor.antigen.l.fimbriae

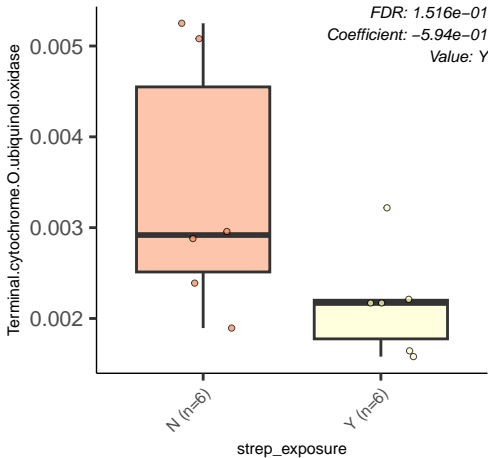
*FDR: 1.516e-01*  
*Coefficient: -4.25e-01*  
*Value: Y*

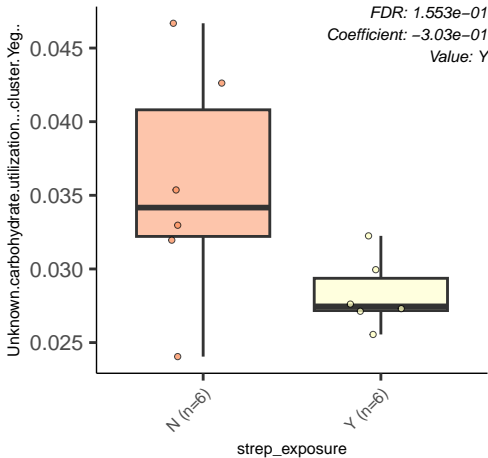
N (n=6)

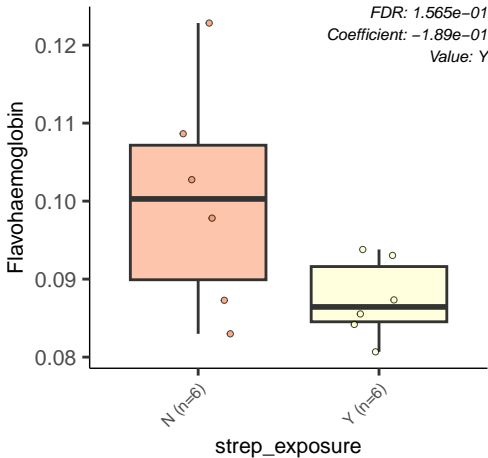
Y (n=6)

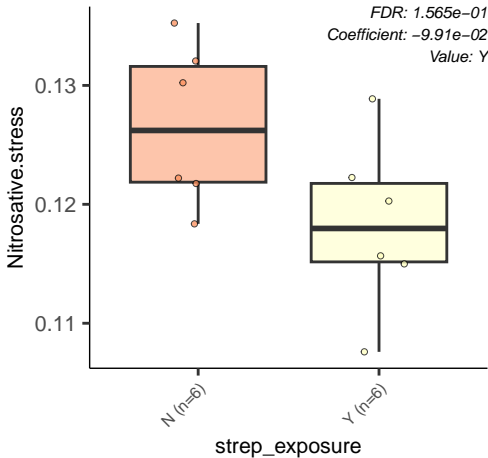
strep\_exposure













Queuosine,Archaeosine.Biosynthesis

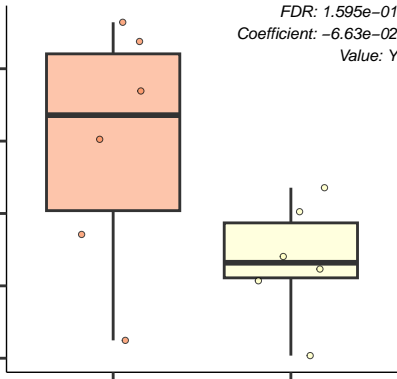
*FDR: 1.595e-01*  
*Coefficient: -6.63e-02*  
*Value: Y*

0.180  
0.175  
0.170  
0.165  
0.160

N (n=6)

Y (n=6)

strep\_exposure



Test...DHFR

*FDR: 1.606e-01*  
*Coefficient: 5.92e-02*  
*Value: Y*

0.30

0.29

0.28

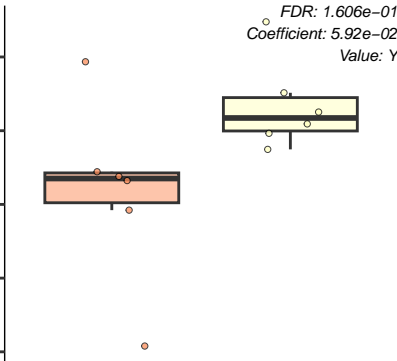
0.27

0.26

*N (n=6)*

*Y (n=6)*

strep\_exposure



Putative.TldE.TldD.proteolytic.complex

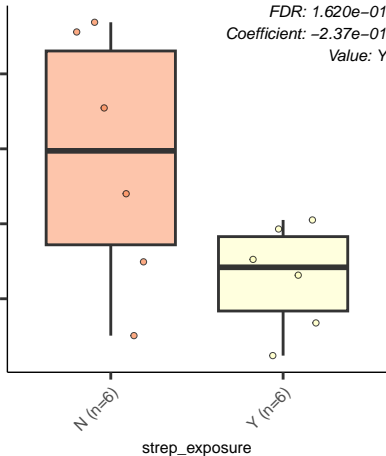
*FDR: 1.620e-01*  
*Coefficient: -2.37e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure

0.0275  
0.0250  
0.0225  
0.0200



CBSS.281090.3.peg.464

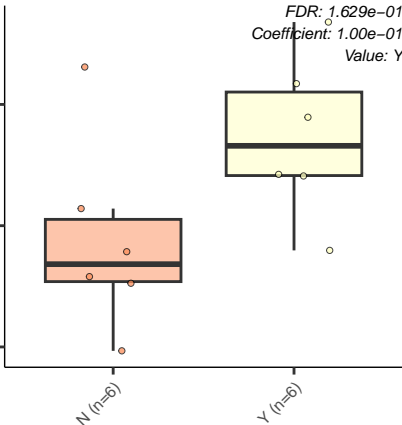
0.13  
0.12  
0.11

N (n=6)

Y (n=6)

strep\_exposure

FDR: 1.629e-01  
Coefficient: 1.00e-01  
Value: Y



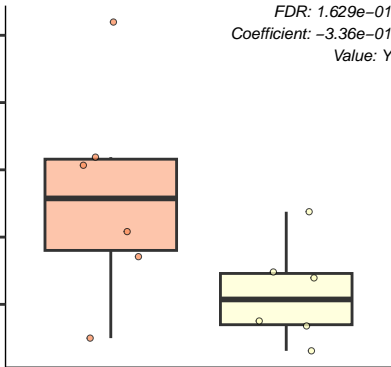
CBSS.52598.3.peg.2843

*FDR: 1.629e-01*  
*Coefficient: -3.36e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



Listeria.Pathogenicity.Island.LIPI.1.extended

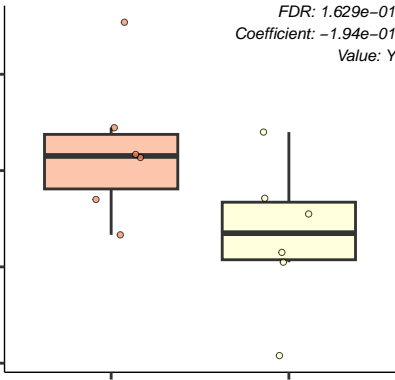
FDR: 1.629e-01  
Coefficient: -1.94e-01  
Value: Y

0.016  
0.014  
0.012  
0.010

N (n=6)

Y (n=6)

strep\_exposure



COG1836

0.0300

0.0275

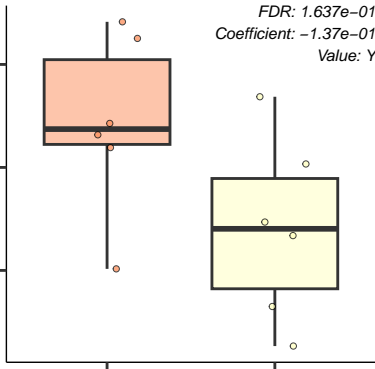
0.0250

N (n=6)

Y (n=6)

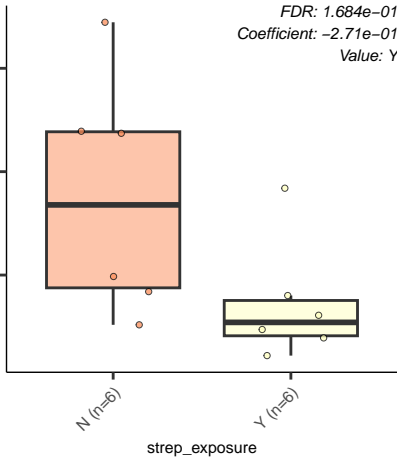
strep\_exposure

FDR: 1.637e-01  
Coefficient: -1.37e-01  
Value: Y



SeqA.and.Co.occuring.Genes

*FDR: 1.684e-01*  
*Coefficient: -2.71e-01*  
*Value: Y*





Streptothricin.resistance

*FDR: 1.692e-01*  
*Coefficient: -7.74e-01*  
*Value: Y*

0.003

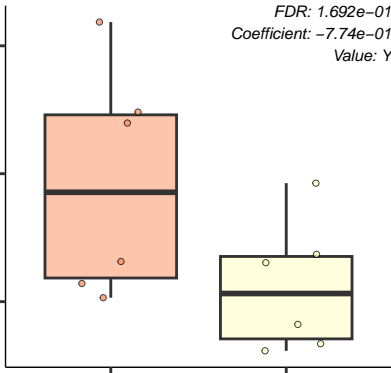
0.002

0.001

N (n=6)

Y (n=6)

strep\_exposure



Creatine.and.Creatinine.Degradation

0.035

0.030

0.025

N (n=6)

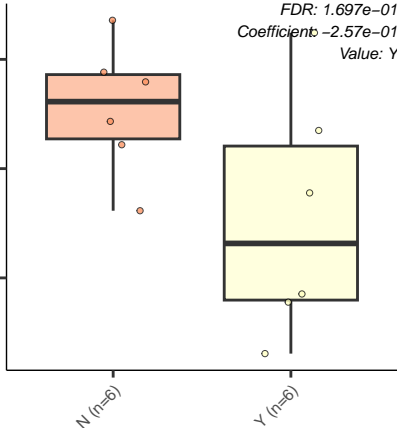
Y (n=6)

strep\_exposure

FDR: 1.697e-01

Coefficient: -2.57e-01

Value: Y



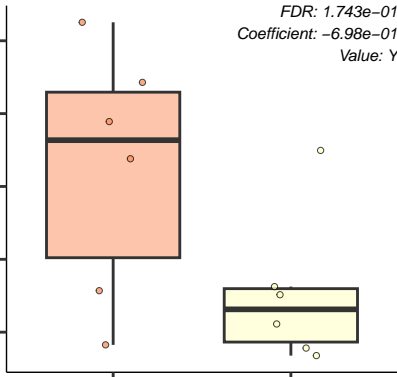
Biogenesis.of.cytochrome.c.oxidases

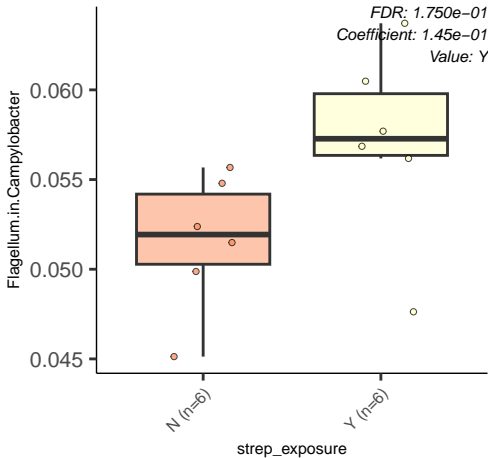
FDR: 1.743e-01  
Coefficient: -6.98e-01  
Value: Y

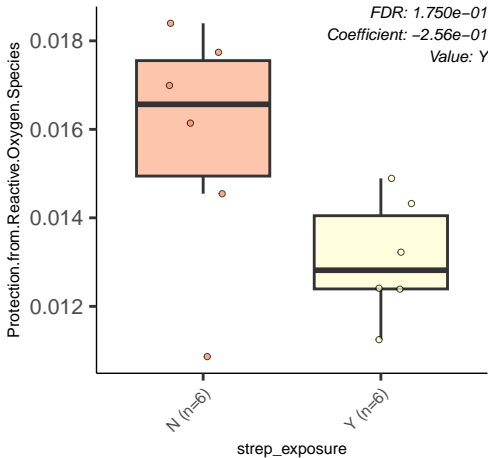
N (n=6)

Y (n=6)

strep\_exposure

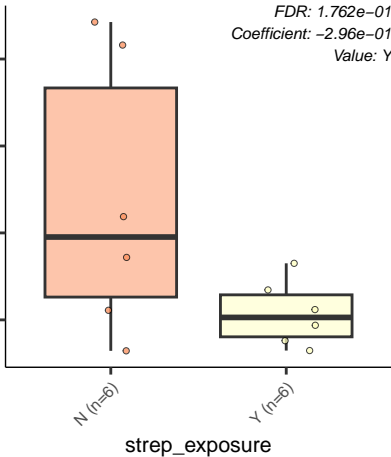






Bacterial.hemoglobins

FDR: 1.762e-01  
Coefficient: -2.96e-01  
Value: Y



Nonmevalonate.Branch.of.Isoprenoid.Biosynthesis

FDR: 1.767e-01  
Coefficient: -5.15e-02  
Value: Y

0.150

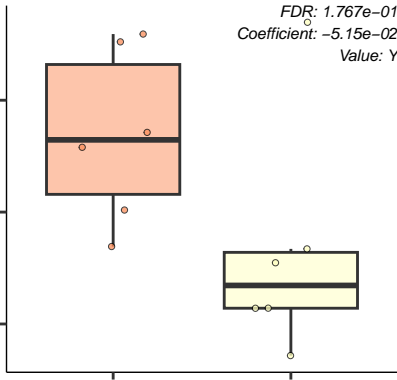
0.145

0.140

N (n=6)

Y (n=6)

strep\_exposure



Phage.integration.and.excision

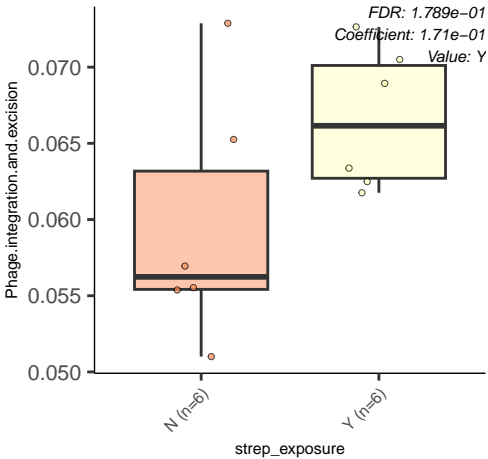
0.070  
0.065  
0.060  
0.055  
0.050

N (n=6)

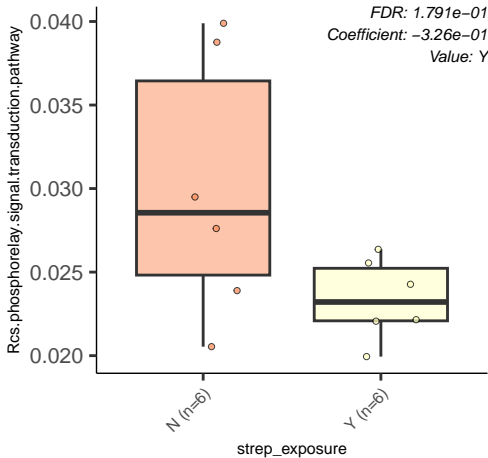
Y (n=6)

strep\_exposure

FDR: 1.789e-01  
Coefficient: 1.71e-01  
Value: Y







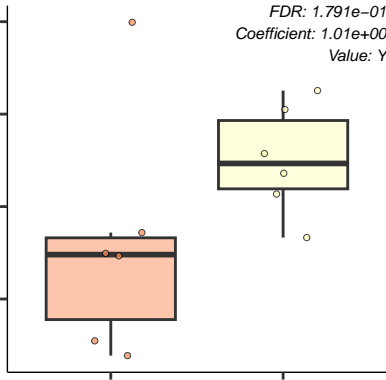
Terminal.cytochrome.C.oxidases

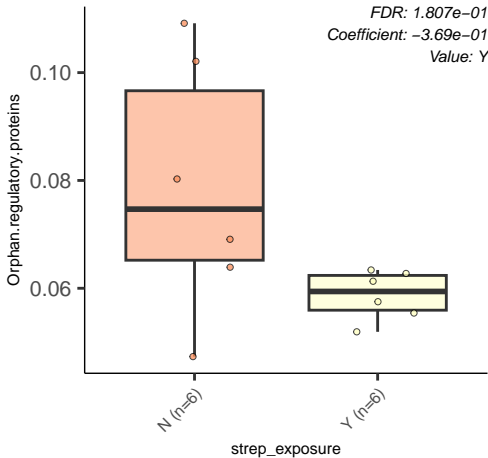
*FDR: 1.791e-01*  
*Coefficient: 1.01e+00*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure





Omega.amidase.KE2

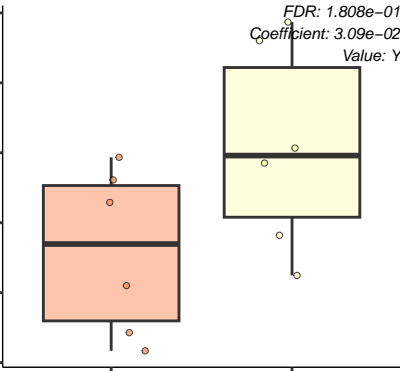
0.72  
0.71  
0.70  
0.69  
0.68  
0.67

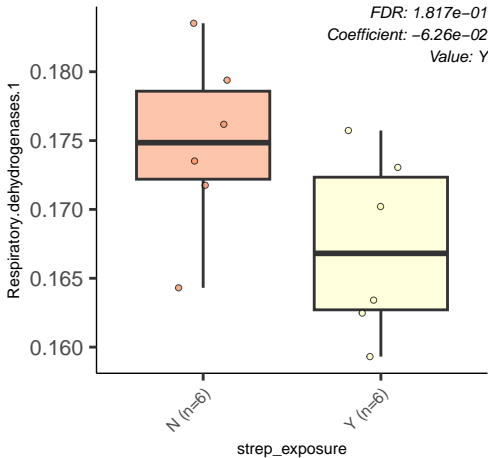
N (n=6)

Y (n=6)

strep\_exposure

FDR: 1.808e-01  
Coefficient: 3.09e-02  
Value: Y





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

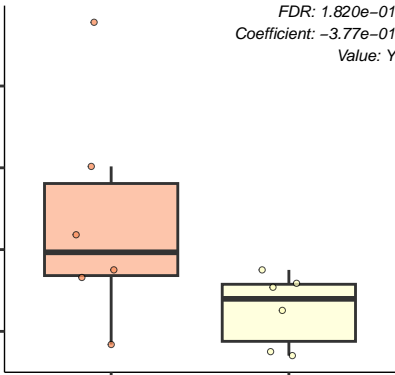
FDR: 1.820e-01  
Coefficient: -3.77e-01  
Value: Y

0.030  
0.025  
0.020  
0.015

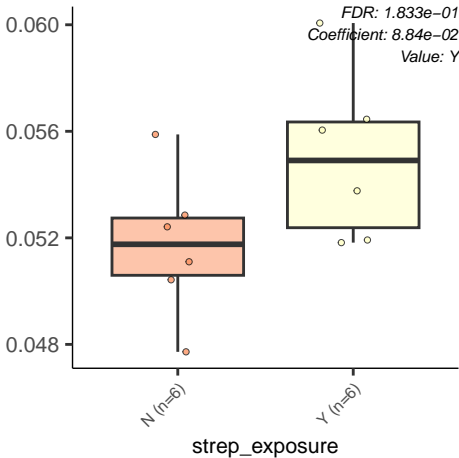
N (n=6)

Y (n=6)

strep\_exposure



t6A.synthesis.in.bacteria



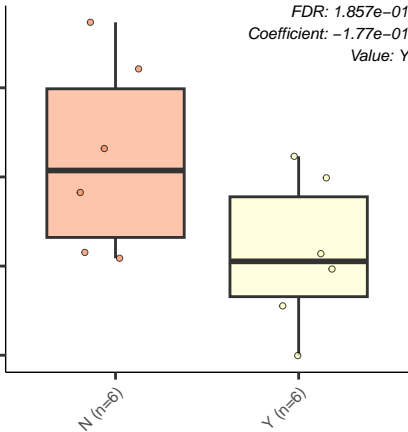
FDR:  $1.857e-01$   
Coefficient:  $-1.77e-01$   
Value: Y

0.10  
0.09  
0.08  
0.07

N (n=6)

Y (n=6)

strep\_exposure





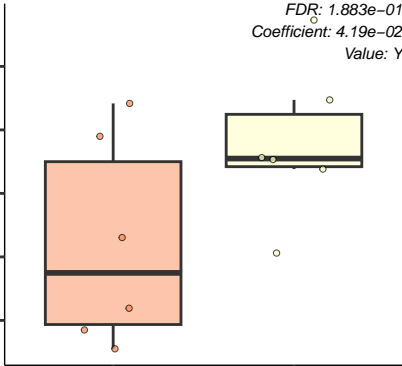
RNA.polymerase.bacterial

FDR: 1.883e-01  
Coefficient: 4.19e-02  
Value: Y

N (n=6)

Y (n=6)

strep\_exposure



Alkanesulfonates.Utilization

0.009

0.008

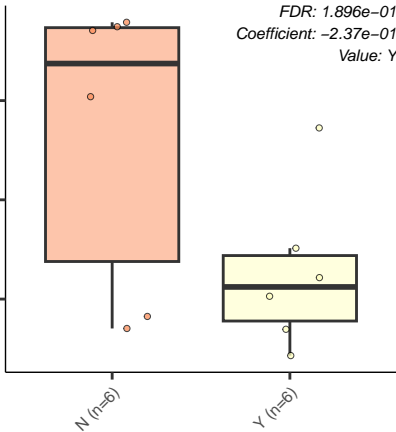
0.007

N (n=6)

Y (n=6)

strep\_exposure

FDR: 1.896e-01  
Coefficient: -2.37e-01  
Value: Y



Campylobacter.Iron.Metabolism

*FDR: 1.896e-01*  
*Coefficient: 3.90e-02*  
*Value: Y*

0.148

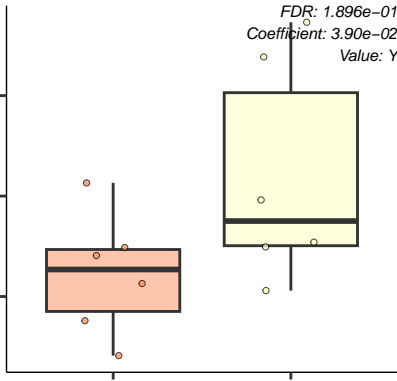
0.144

0.140

N (n=6)

Y (n=6)

strep\_exposure



Na..translocating.decarboxylases.and.related.biotin.dependent.e

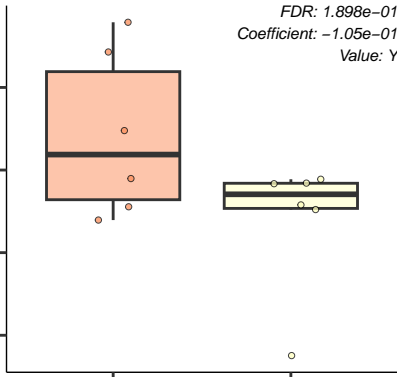
FDR: 1.898e-01  
Coefficient: -1.05e-01  
Value: Y

N (n=6)

Y (n=6)

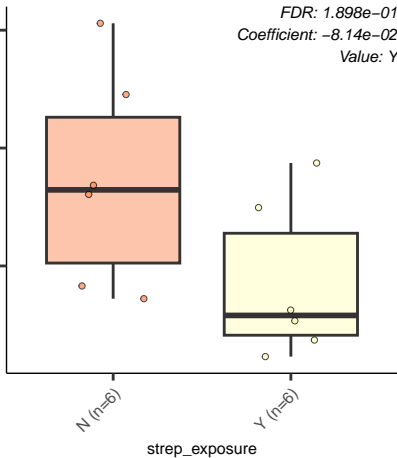
strep\_exposure

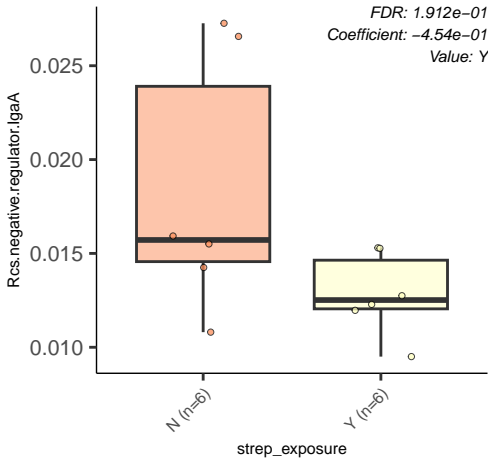
0.075  
0.070  
0.065  
0.060



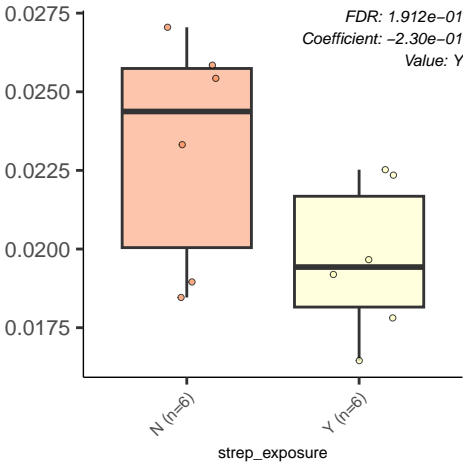
Terminal cytochrome oxidases

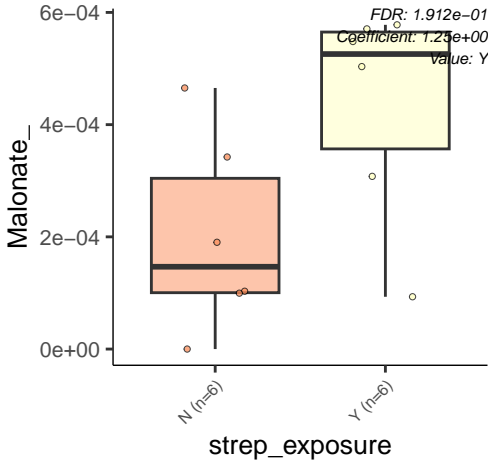
*FDR: 1.898e-01*  
*Coefficient: -8.14e-02*  
*Value: Y*





Khodge314.Isoleucine.Biosynthesis

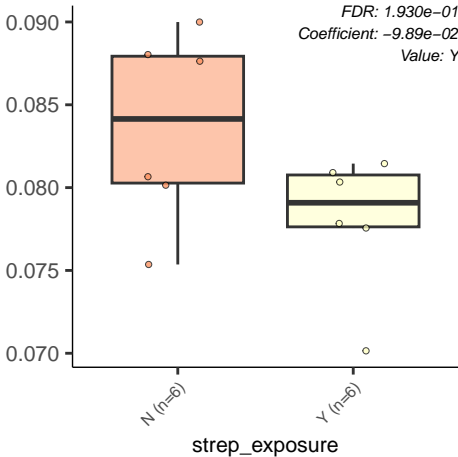




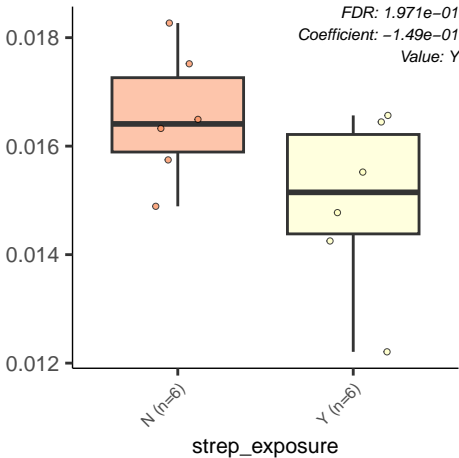


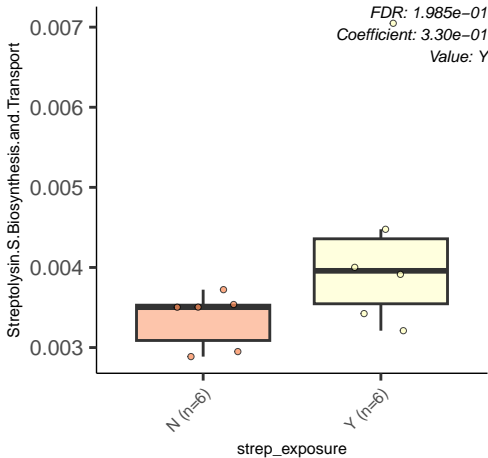
CBSS.498211.3.peg.1514

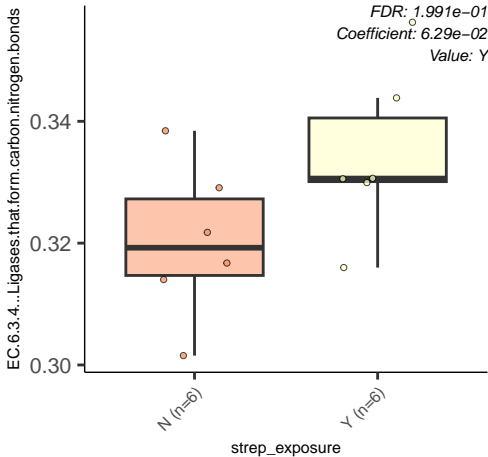
*FDR: 1.930e-01*  
*Coefficient: -9.89e-02*  
*Value: Y*



CBSS.316057.3.peg.659







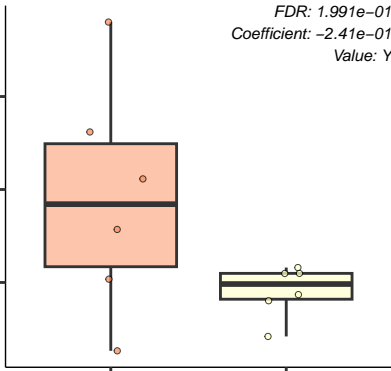
RpoS.Regulators.SG1

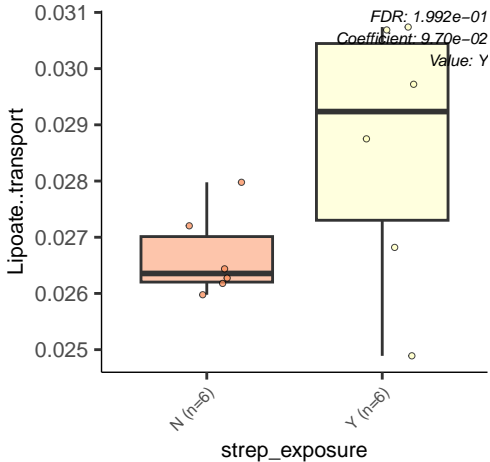
FDR: 1.991e-01  
Coefficient: -2.41e-01  
Value: Y

N (n=6)

Y (n=6)

strep\_exposure





At5g63290

0.46

0.44

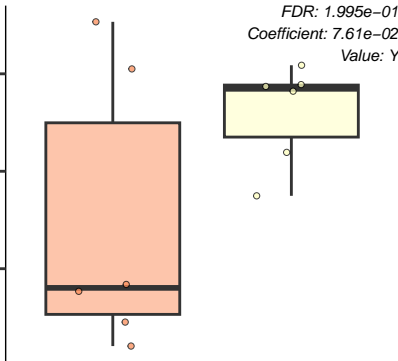
0.42

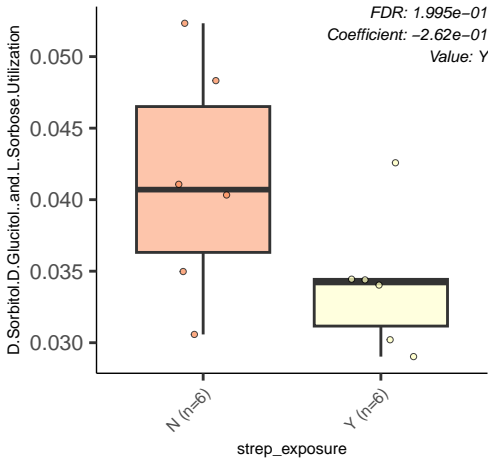
N (n=6)

Y (n=6)

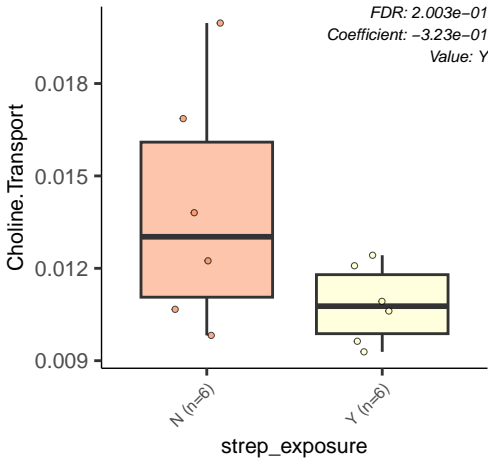
strep\_exposure

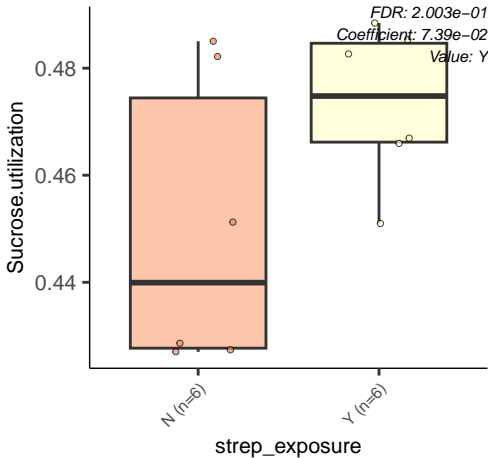
FDR: 1.995e-01  
Coefficient: 7.61e-02  
Value: Y



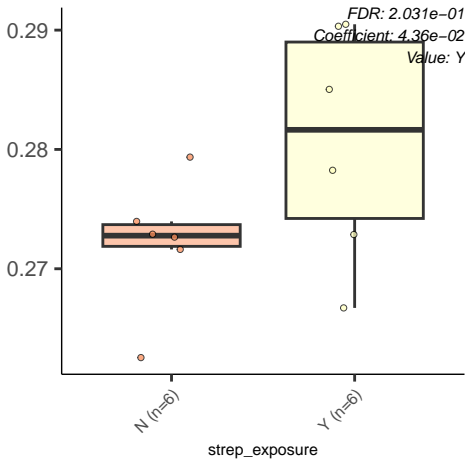






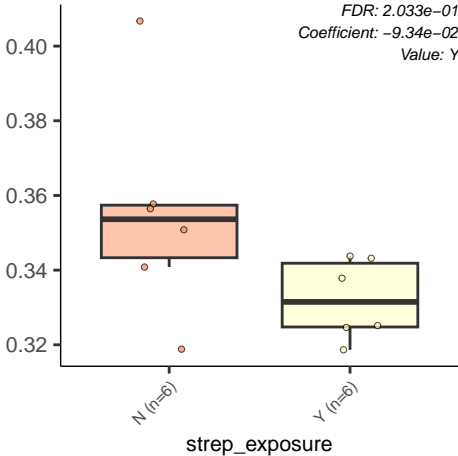


EC.3.4.11...Aminopeptidases



CBSS.258594.1.pcg.3339

FDR: 2.033e-01  
Coefficient: -9.34e-02  
Value: Y



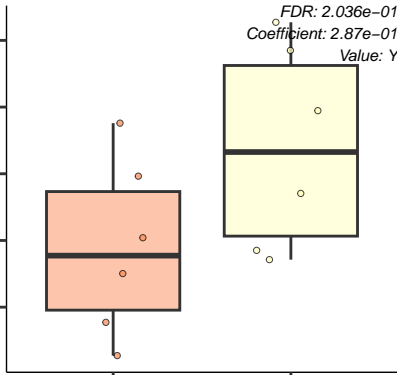
ESAT.6.proteins.secretion.system.in.Firmicutes

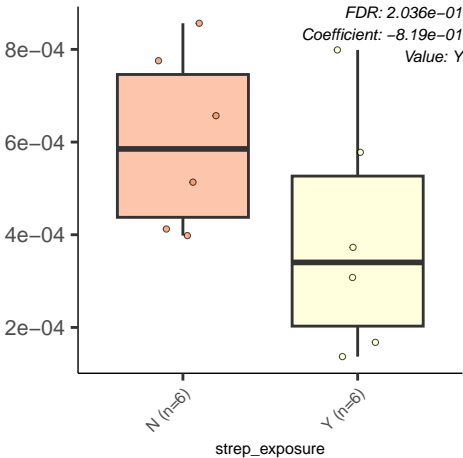
FDR: 2.036e-01  
Coefficient: 2.87e-01  
Value: Y

N (n=6)

Y (n=6)

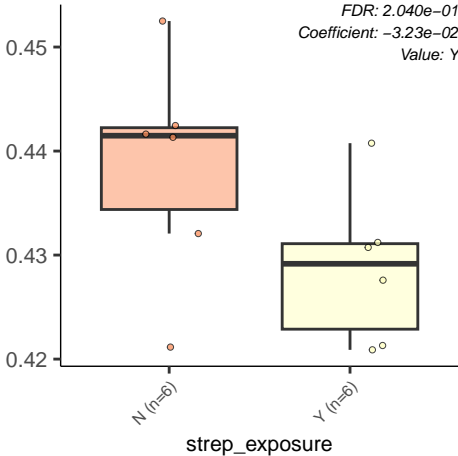
strep\_exposure





Polyamine.Metabolism

*FDR: 2.040e-01*  
*Coefficient: -3.23e-02*  
*Value: Y*

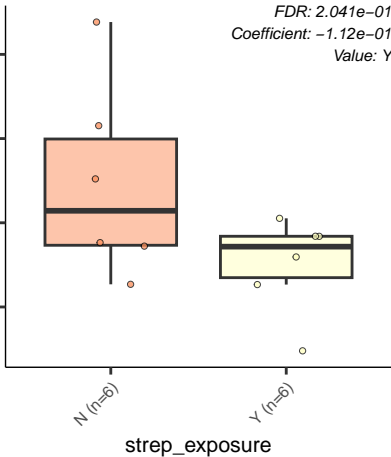


EC.3.4.13...Dipeptidases

*FDR: 2.041e-01*

*Coefficient: -1.12e-01*

*Value: Y*





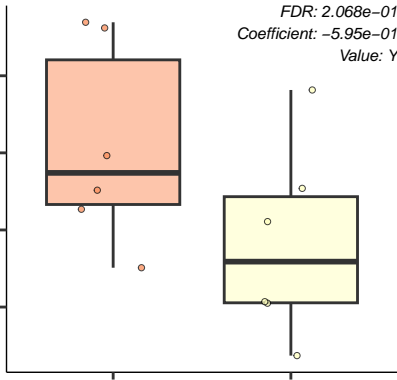
Commensurate.regulon.activation

*FDR: 2.068e-01*  
*Coefficient: -5.95e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure



Translation.termination.factors.bacterial

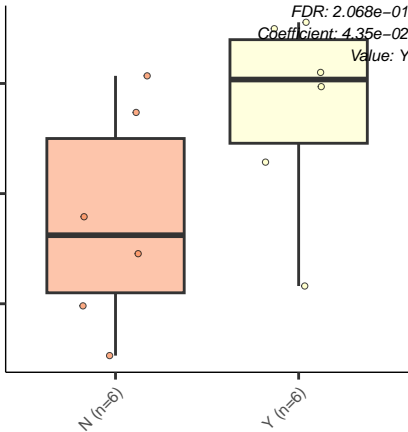
0.34  
0.33  
0.32

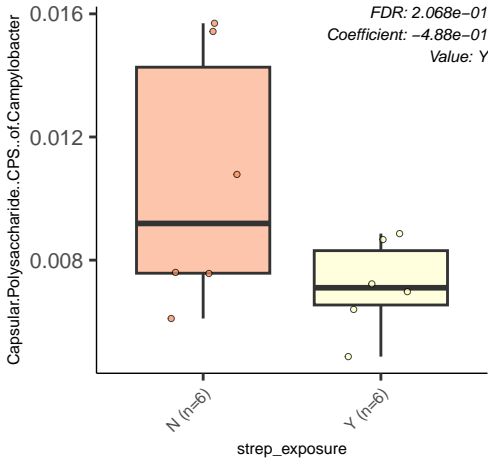
N (n=6)

Y (n=6)

strep\_exposure

FDR: 2.068e-01  
Coefficient: 4.35e-02  
Value: Y





Iron.Scavenging.cluster.in.Thermus

*FDR: 2.082e-01*  
*Coefficient: -1.10e+00*  
*Value: Y*

0.00075

0.00050

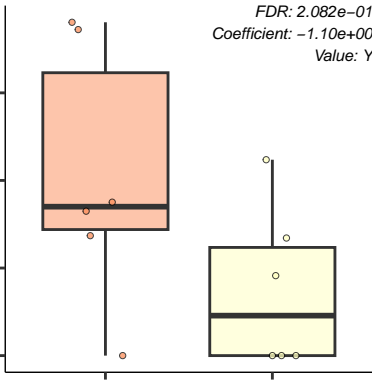
0.00025

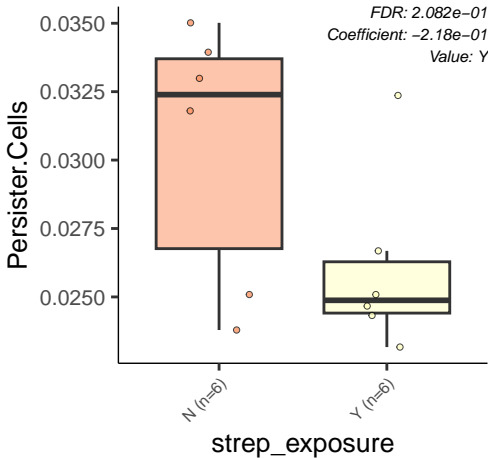
0.00000

N (n=6)

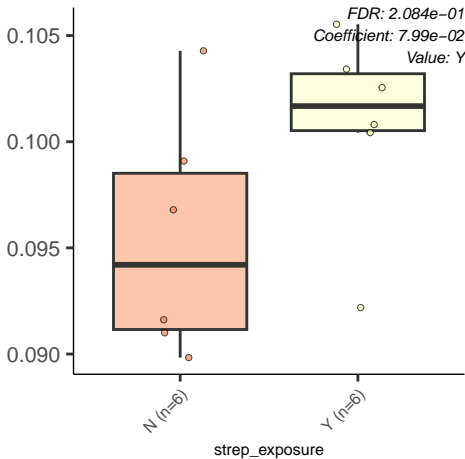
Y (n=6)

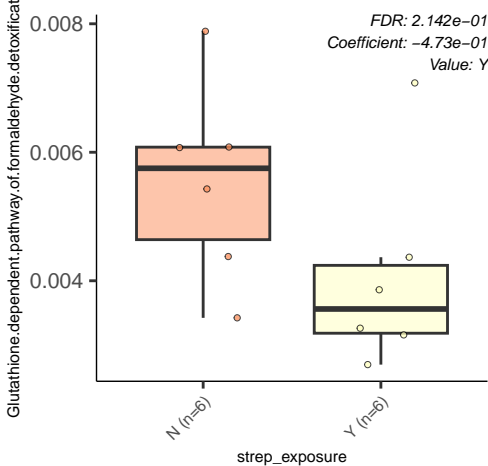
strep\_exposure





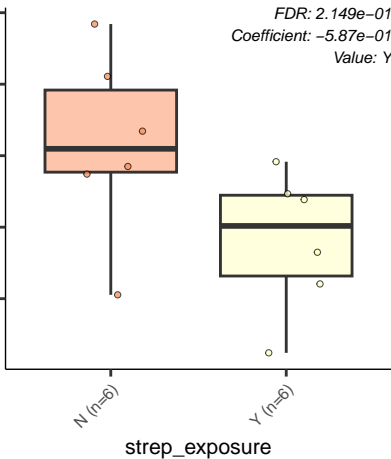
Thioredoxin.disulfide.reductase





CBSS.316275.9.peg.382

*FDR: 2.149e-01*  
*Coefficient: -5.87e-01*  
*Value: Y*





The.fimbral.Sfm.cluster

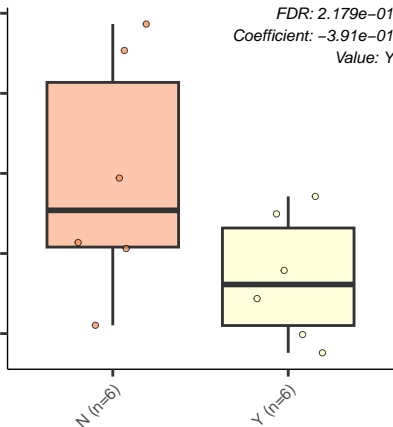
0.035  
0.030  
0.025  
0.020  
0.015

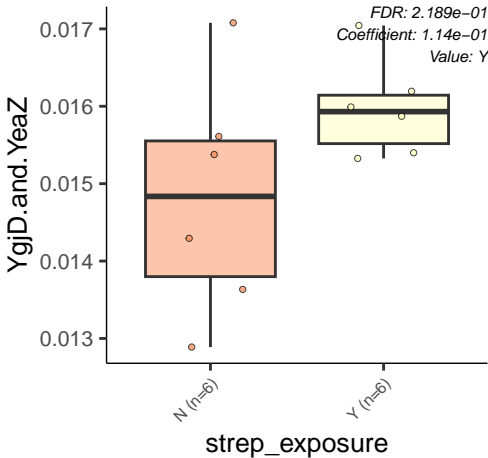
*FDR: 2.179e-01*  
*Coefficient: -3.91e-01*  
*Value: Y*

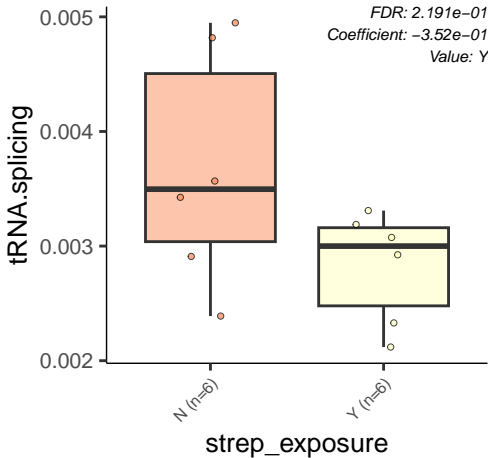
N (n=6)

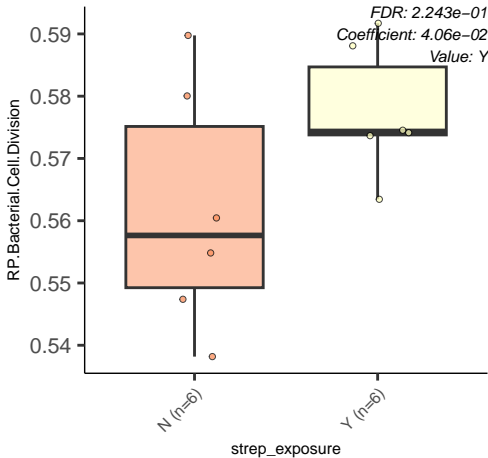
Y (n=6)

strep\_exposure









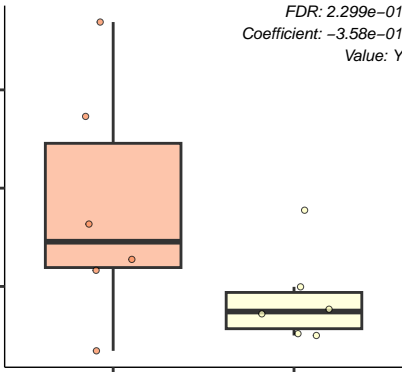
Lipid.A.modifications

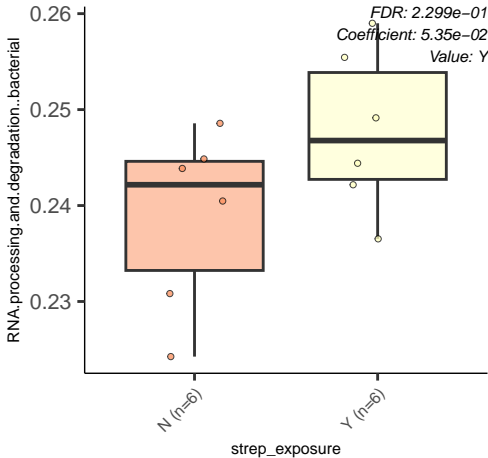
*FDR: 2.299e-01*  
*Coefficient: -3.58e-01*  
*Value: Y*

N (n=6)

Y (n=6)

strep\_exposure





A.DNA.integrity.scanning.protein.that.co.occurs.with.Rad

FDR: 2.314e-01  
Coefficient: -5.58e-01  
Value: Y

0.0020

0.0015

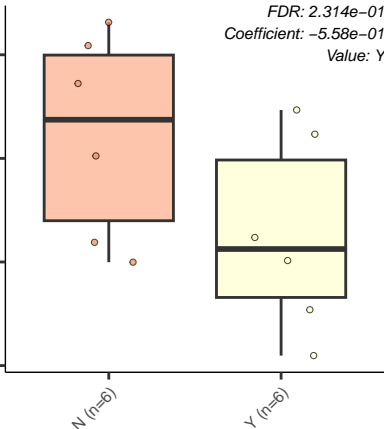
0.0010

0.0005

N (n=6)

Y (n=6)

strep\_exposure



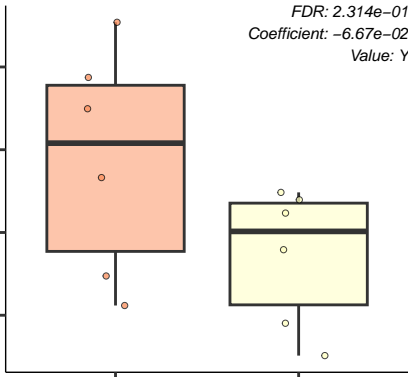
LOS.core.oligosaccharide.biosynthesis

FDR: 2.314e-01  
Coefficient: -6.67e-02  
Value: Y

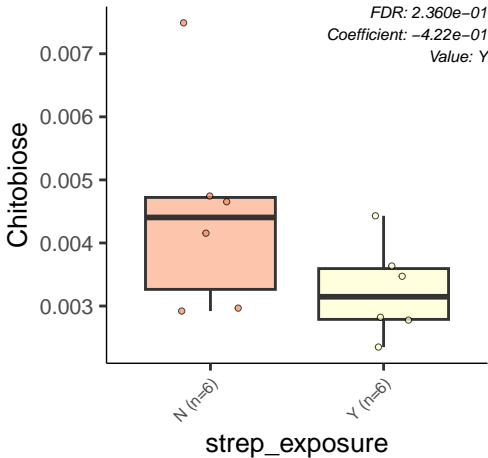
N (n=6)

Y (n=6)

strep\_exposure







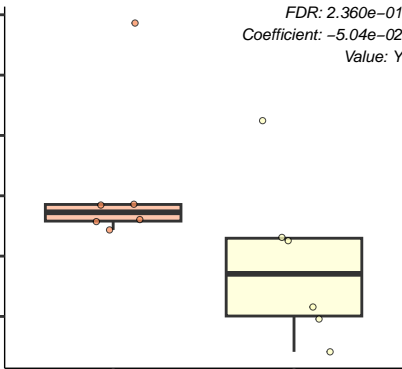
Entner.Doudoroff.Pathway

*FDR: 2.360e-01*  
*Coefficient: -5.04e-02*  
*Value: Y*

N (n=6)

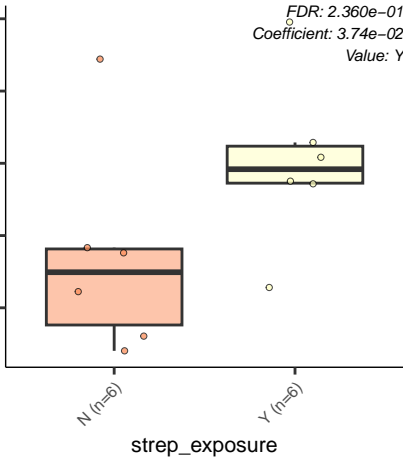
Y (n=6)

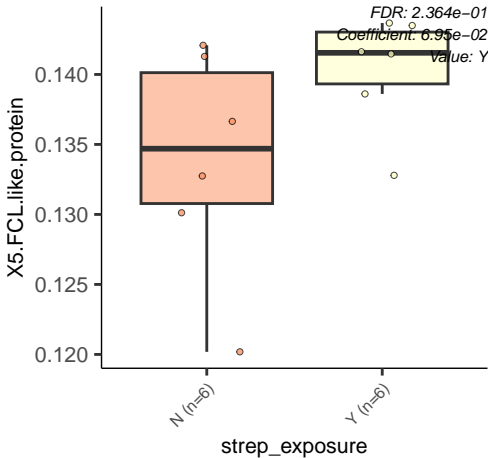
strep\_exposure



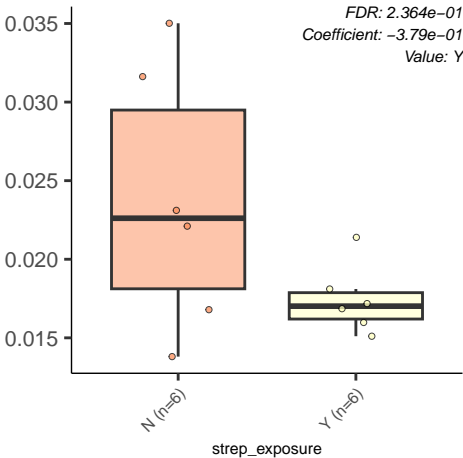
Fermentations..Mixed.acid

FDR: 2.360e-01  
Coefficient: 3.74e-02  
Value: Y



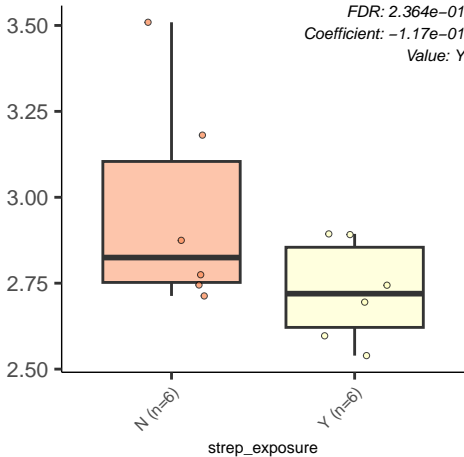


Putrescine.utilization.pathways



Ton.and.Tol.transport.systems

FDR: 2.364e-01  
Coefficient: -1.17e-01  
Value: Y



Alkanesulfonate.assimilation

*FDR: 2.366e-01*  
*Coefficient: -1.35e-01*  
*Value: Y*

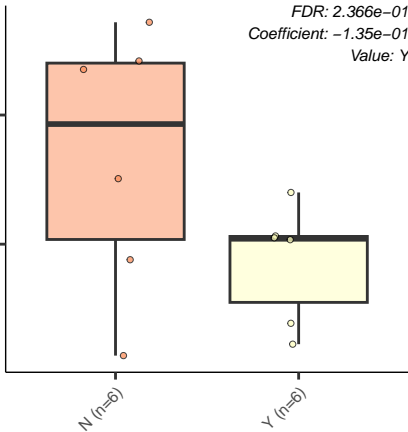
0.09

0.08

N (n=6)

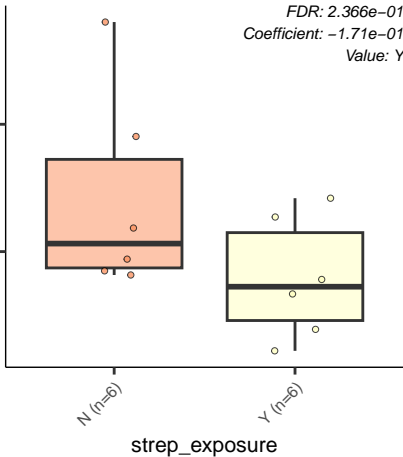
Y (n=6)

strep\_exposure

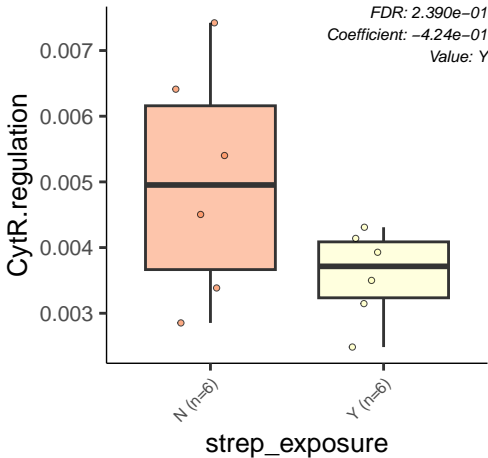


Ubiquinone.Biosynthesis

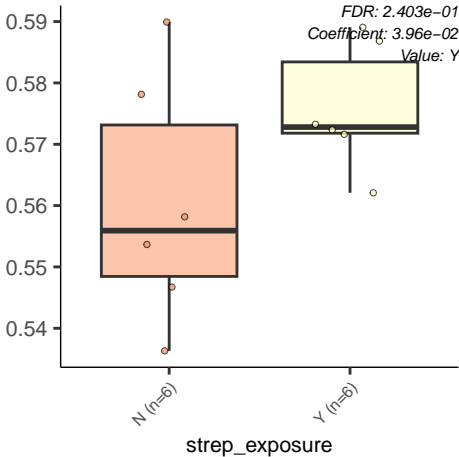
*FDR: 2.366e-01*  
*Coefficient: -1.71e-01*  
*Value: Y*

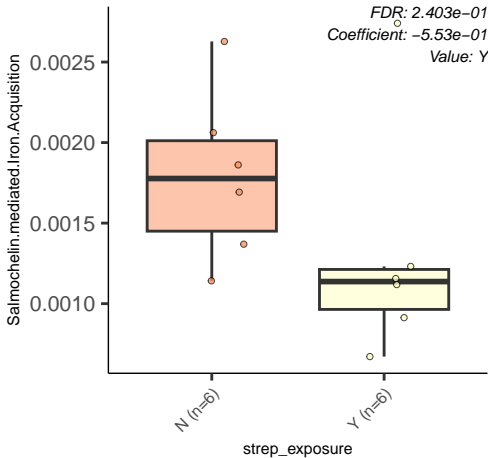






Bacterial.Cell.Division





EC.3.4.21...Serine.endopeptidase

0.015

0.013

0.011

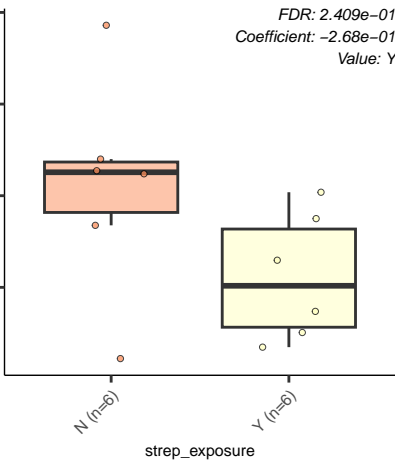
0.009

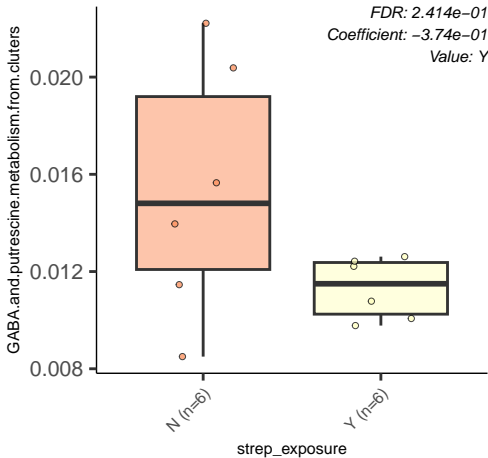
N (n=6)

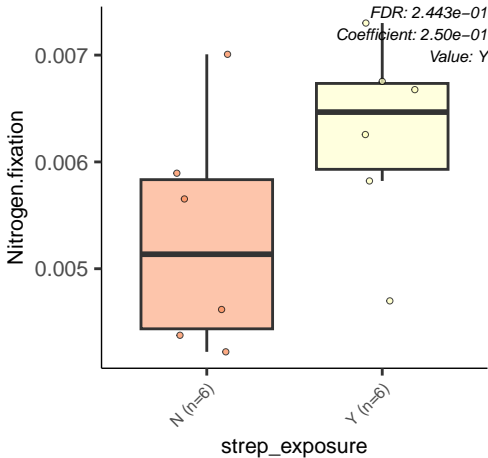
Y (n=6)

strep\_exposure

FDR: 2.409e-01  
Coefficient: -2.68e-01  
Value: Y







Cobalamin

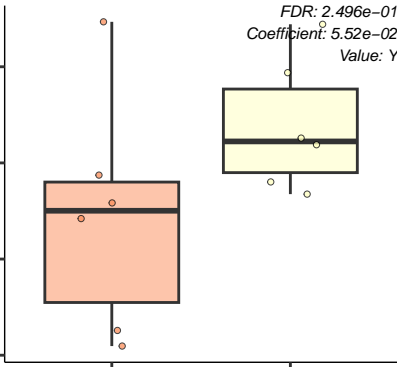
0.26  
0.25  
0.24  
0.23

N (n=6)

Y (n=6)

strep\_exposure

FDR: 2.496e-01  
Coefficient: 5.52e-02  
Value: Y



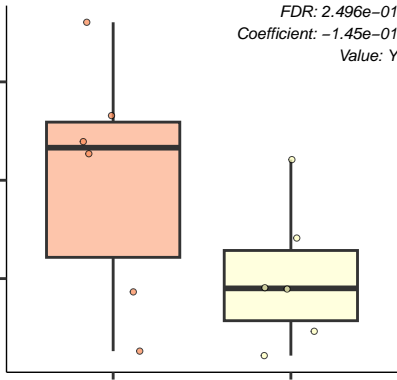
Small.acid.soluble.spore.proteins

*FDR: 2.496e-01*  
*Coefficient: -1.45e-01*  
*Value: Y*

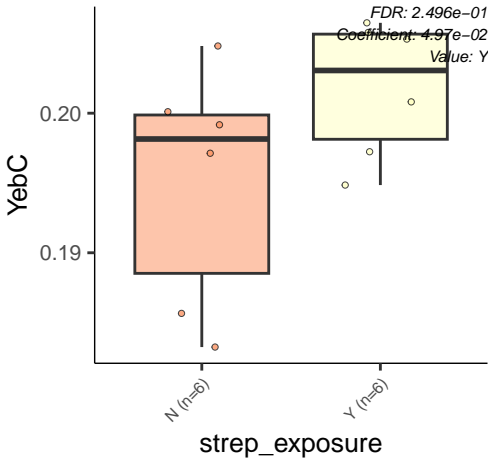
N (n=6)

Y (n=6)

strep\_exposure







tRNA.aminoacylation..Tyr

*FDR: 2.496e-01*  
*Coefficient: 7.20e-02*  
*Value: Y*

