

Competence.in.Streptococci

0.06

0.04

0.02

FDR: 4.629e-08

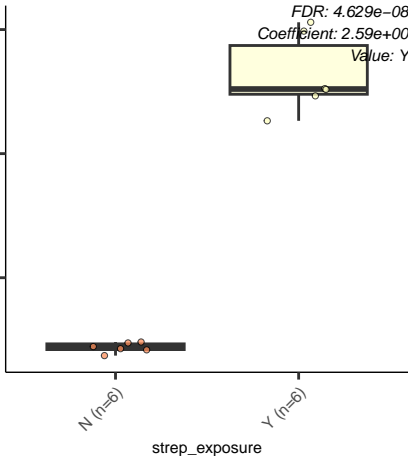
Coefficient: 2.59e+00

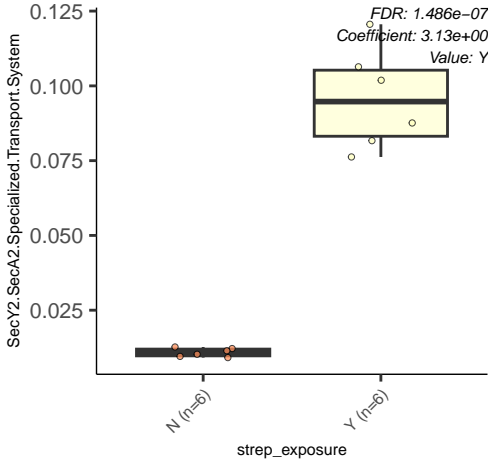
Value: Y

N (n=6)

Y (n=6)

strep_exposure





Late.competence

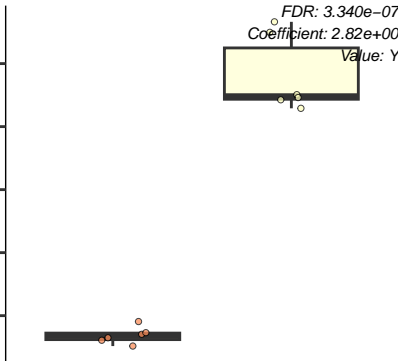
0.05
0.04
0.03
0.02
0.01

N (n=6)

Y (n=6)

strep_exposure

FDR: 3.340×10^{-7}
Coefficient: 2.82×10^0
Value: Y



Sucrose.specific.PTS

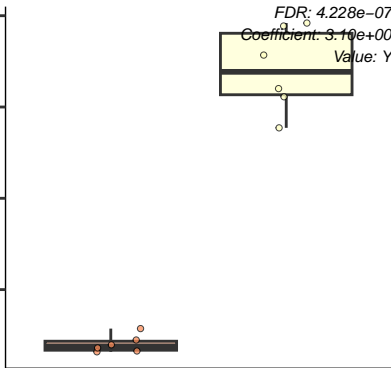
0.012
0.009
0.006
0.003

N (n=6)

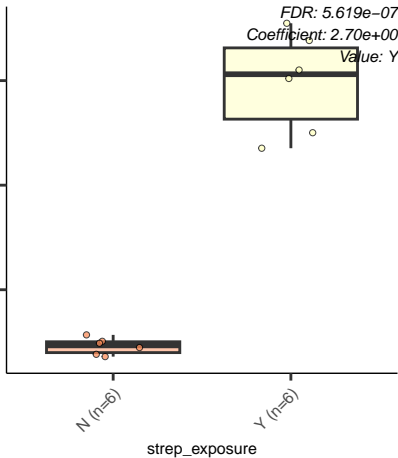
Y (n=6)

strep_exposure

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



Beta.lactamase.cluster.in.Streptococcus



Urea.decomposition

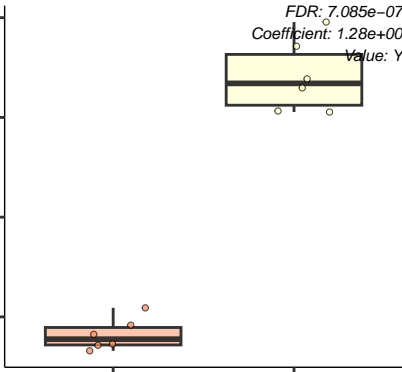
0.05
0.04
0.03
0.02

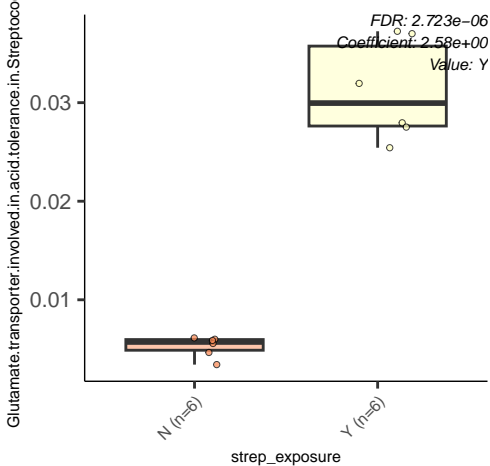
N (n=6)

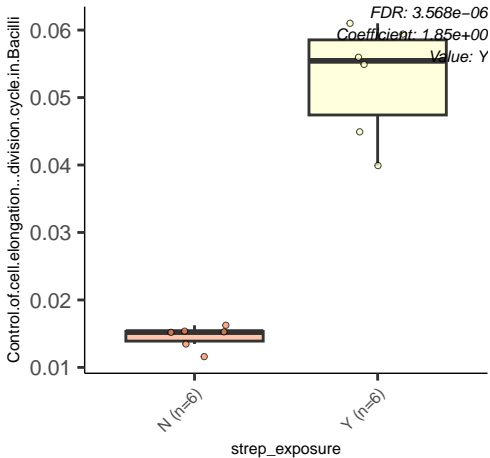
Y (n=6)

strep_exposure

FDR: 7.085×10^{-7}
Coefficient: 1.28×10^0
Value: Y







Urease.subunits

0.03

0.02

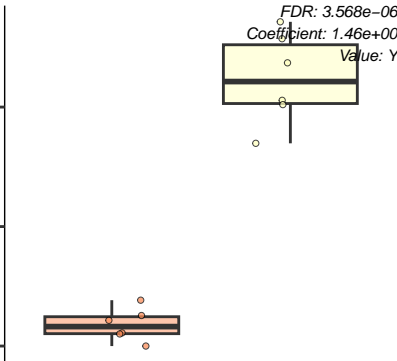
0.01

N (n=6)

Y (n=6)

strep_exposure

FDR: 3.568e-06
Coefficient: 1.46e+00
Value: Y



Gram.Positive.Competence

0.06

0.04

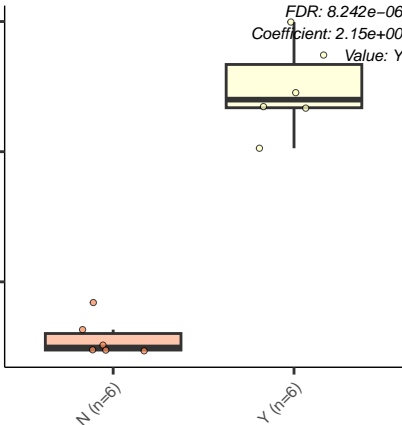
0.02

N (n=6)

Y (n=6)

strep_exposure

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



HtrA.and.Sec.secretion

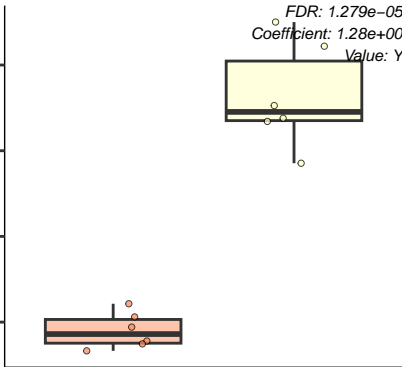
0.05
0.04
0.03
0.02

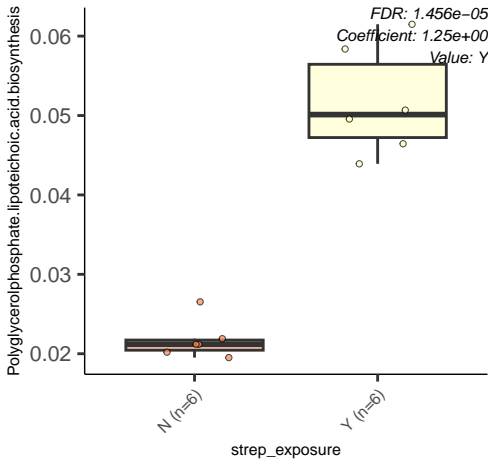
N (n=6)

Y (n=6)

strep_exposure

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





Archaeal.lipids

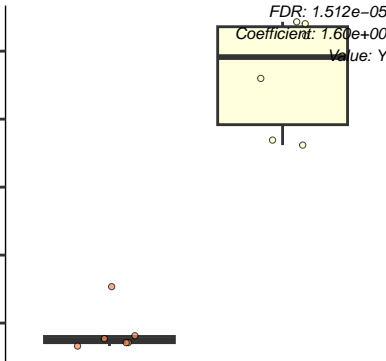
0.030
0.025
0.020
0.015
0.010

N (n=6)

Y (n=6)

strep_exposure

FDR: 1.512e-05
Coefficient: 1.60e+00
Value: Y



pyrimidine.conversions

0.50

0.45

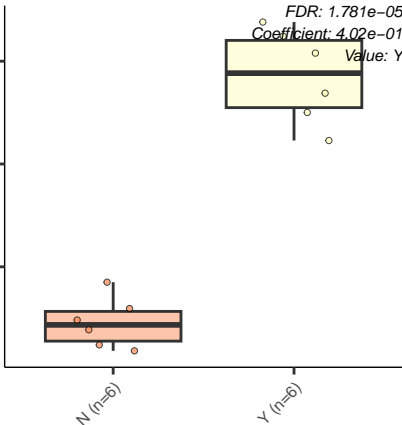
0.40

N (n=6)

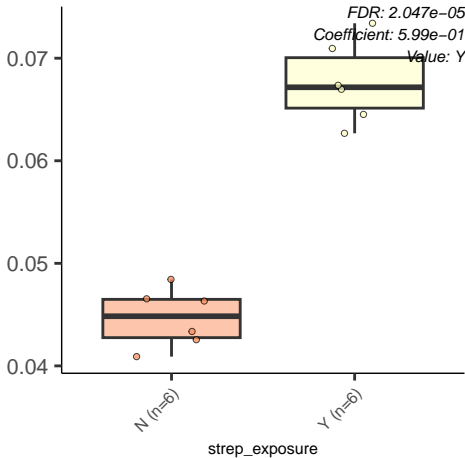
Y (n=6)

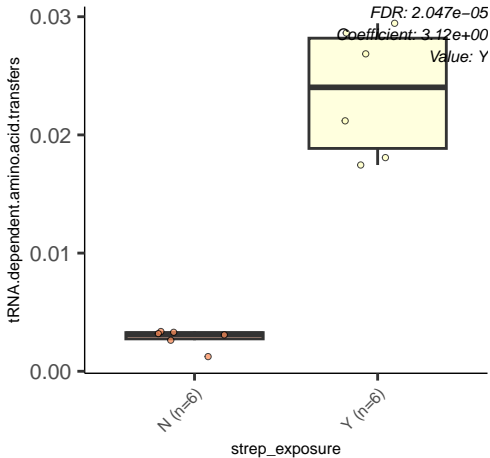
strep_exposure

FDR: 1.781e-05
Coefficient: 4.02e-01
Value: Y

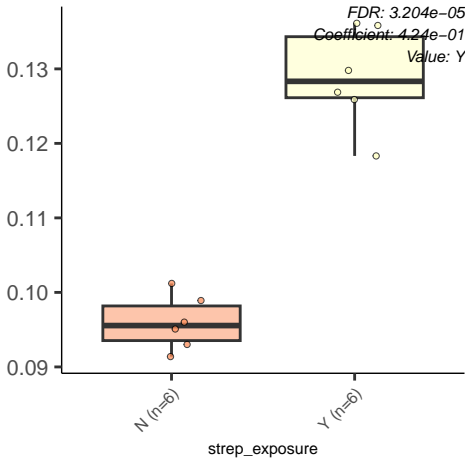


Conserved.gene.cluster.possibly.involved.in.RNA.metabolism





positive cluster that relates ribosomal protein L28P to a set of unchanged



At4g10620.At3g57180.At3g47450

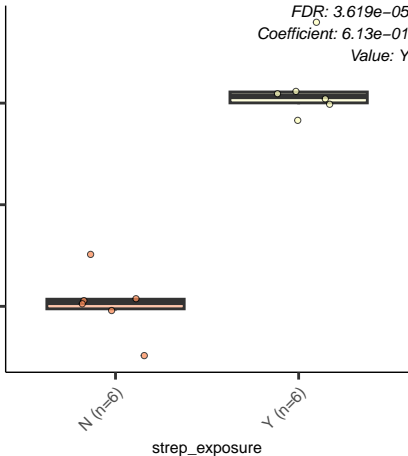
FDR: 3.619e-05
Coefficient: 6.13e-01
Value: Y

0.06
0.05
0.04

N (n=6)

Y (n=6)

strep_exposure



Streptococcus.agalactiae.virulome

0.006

0.004

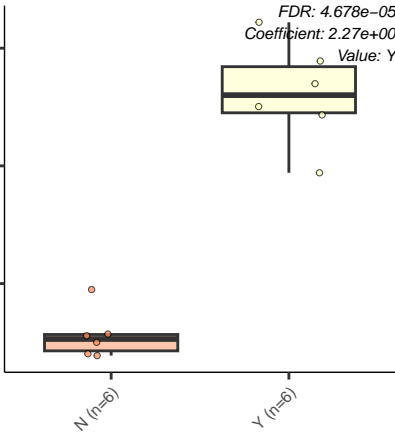
0.002

N (n=6)

Y (n=6)

strep_exposure

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



Acetoin..butanediol.metabolism

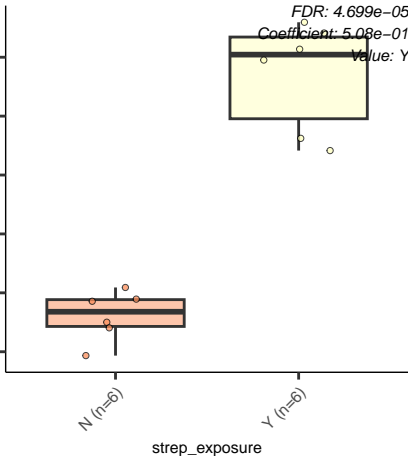
0.14
0.13
0.12
0.11
0.10
0.09

N (n=6)

Y (n=6)

strep_exposure

FDR: 4.699e-05
Coefficient: 5.08e-01
Value: Y



Cell.Division.Cluster

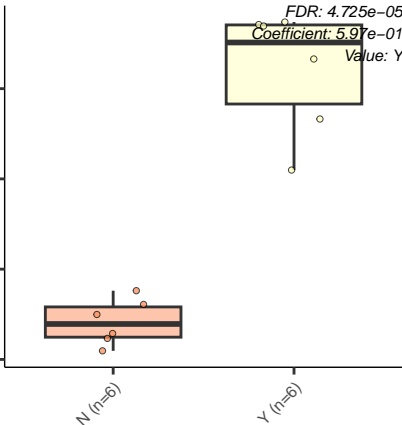
0.08
0.07
0.06
0.05

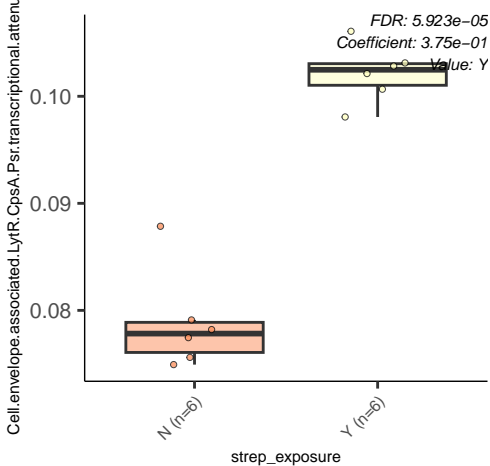
N (n=6)

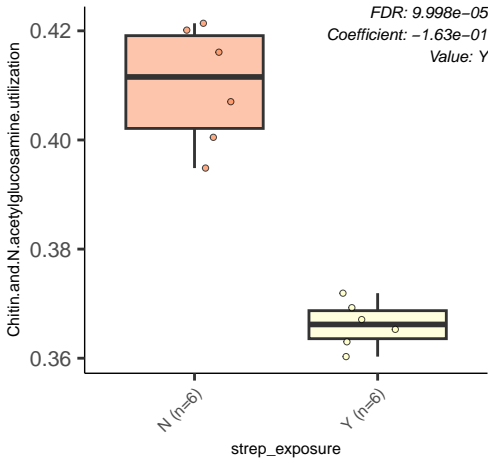
Y (n=6)

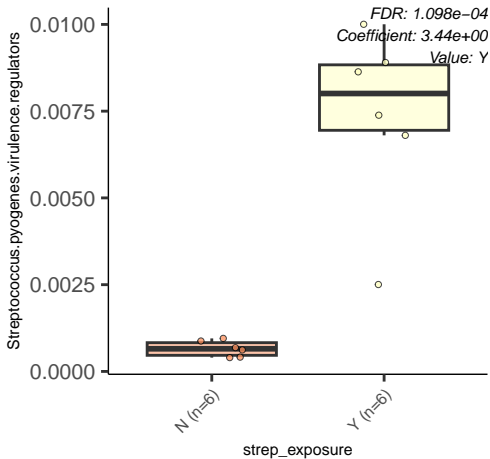
strep_exposure

FDR: 4.725×10^{-5}
Coefficient: 5.97×10^{-1}
Value: Y









CBSS.262719.3.pcg.410

0.13

0.12

0.11

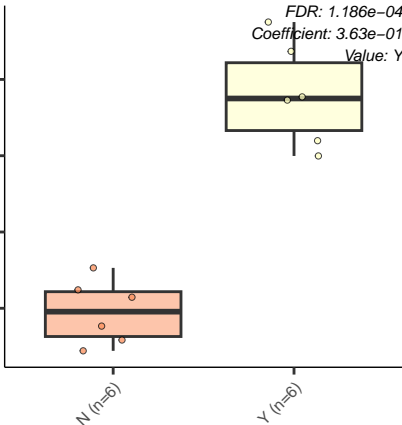
0.10

N (n=6)

Y (n=6)

strep_exposure

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



Unspecified.monosaccharide.transport.cluster

0.05

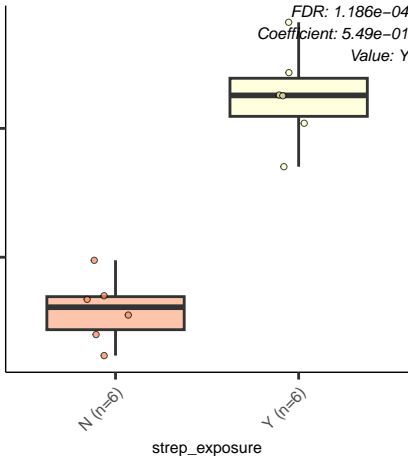
0.04

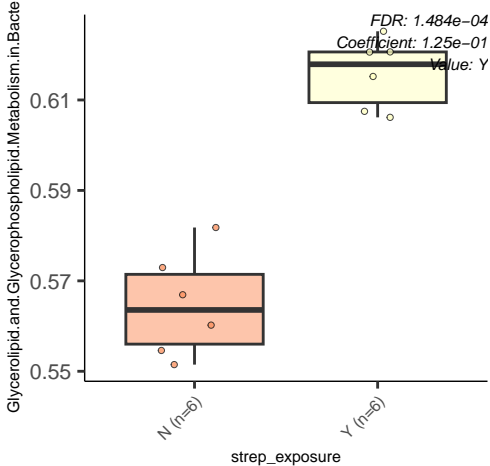
N (n=6)

Y (n=6)

strep_exposure

FDR: 1.186e-04
Coefficient: 5.49e-01
Value: Y





Single.Rhodanese.domain.proteins

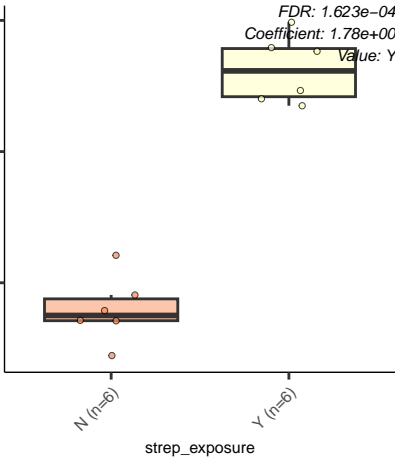
0.015
0.010
0.005

N (n=6)

Y (n=6)

strep_exposure

FDR: 1.623e-04
Coefficient: 1.78e+00
Value: Y



Streptococcus.pyogenes.Virulome

0.015

0.010

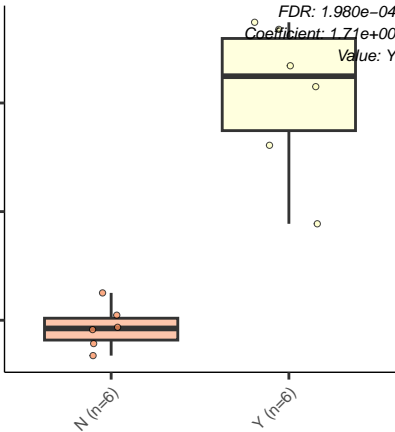
0.005

N (n=6)

Y (n=6)

strep_exposure

FDR: 1.980e-04
Coefficient: 1.71e+00
Value: Y



ATP.dependent.Nuclease

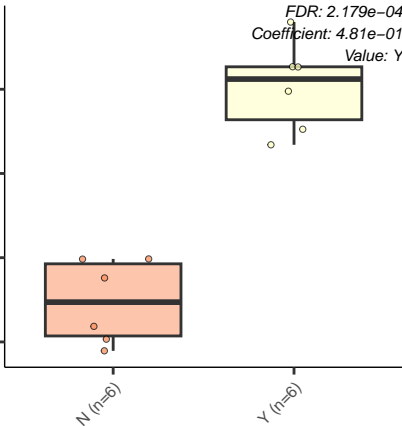
FDR: 2.179e-04
Coefficient: 4.81e-01
Value: Y

0.18
0.16
0.14
0.12

N (n=6)

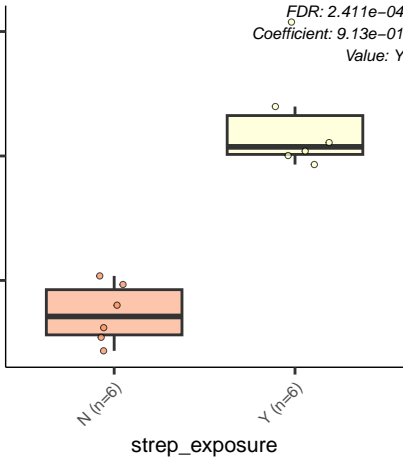
Y (n=6)

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

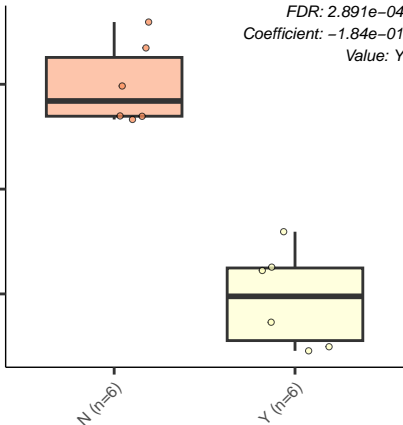
0.64

0.60

N (n=6)

Y (n=6)

strep_exposure



Omega.amidase

0.008

0.006

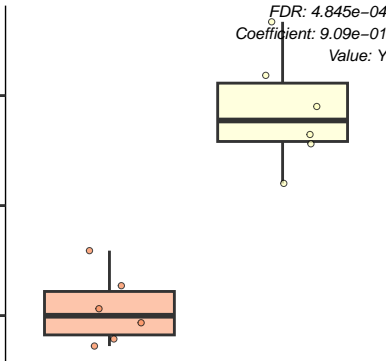
0.004

N (n=6)

Y (n=6)

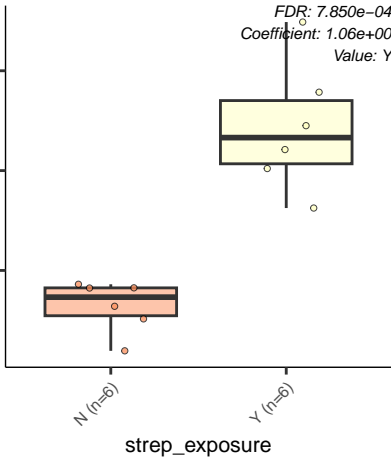
strep_exposure

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

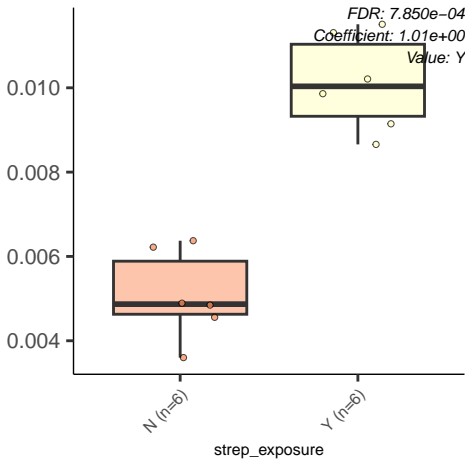


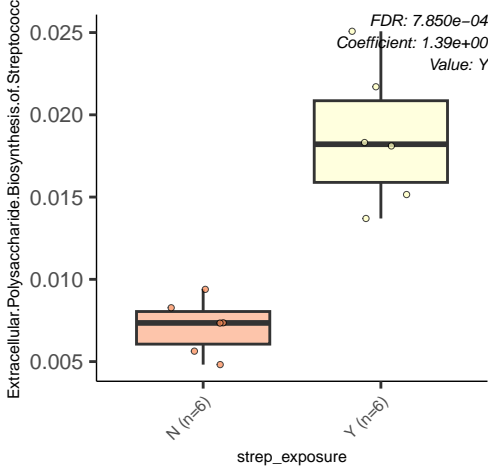
CBSS.261594.1.peg.788

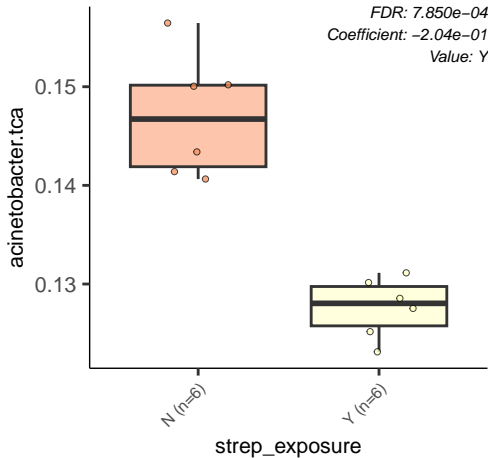
FDR: 7.850e-04
Coefficient: 1.06e+00
Value: Y



D.Alanyl.Lipoteichoic.Acid.Biosynthesis







RNA.pseudouridine.syntheses

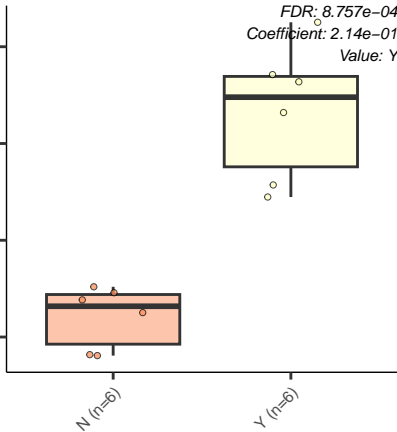
0.080
0.075
0.070
0.065

N (n=6)

Y (n=6)

strep_exposure

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



Copper.homeostasis

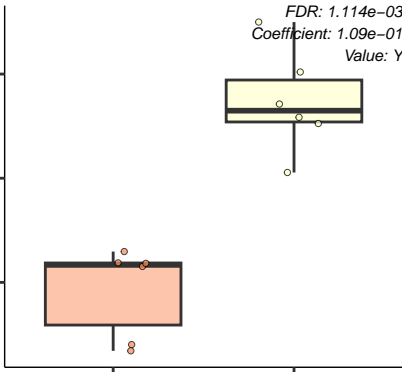
0.50
0.48
0.46

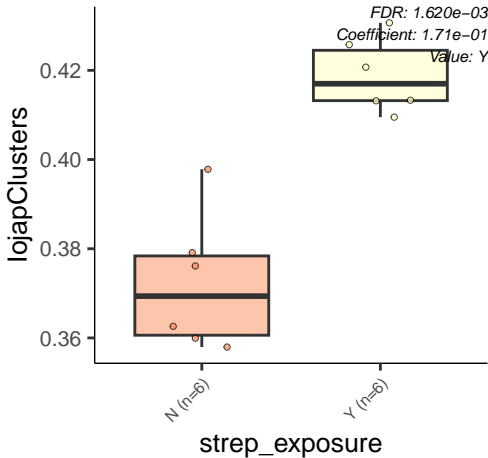
N (n=6)

Y (n=6)

strep_exposure

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





Methionine.Biosynthesis

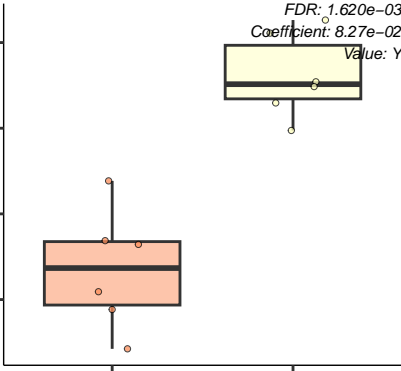
0.82
0.80
0.78
0.76

N (n=6)

Y (n=6)

strep_exposure

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



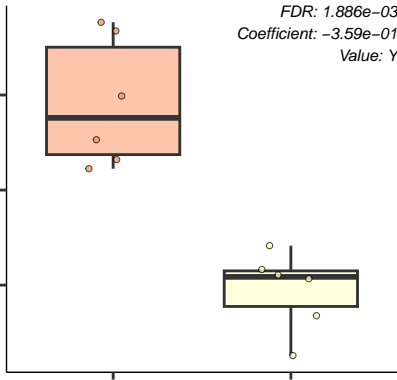
Glycerol.fermentation.to.1.3.propanediol

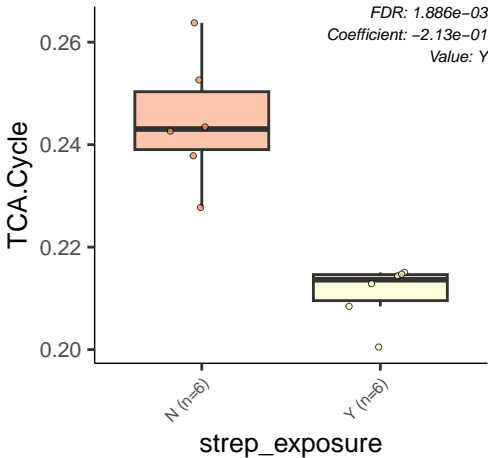
FDR: 1.886e-03
Coefficient: -3.59e-01
Value: Y

N (n=6)

Y (n=6)

strep_exposure





Streptococcal.Mga.Regulon

0.010

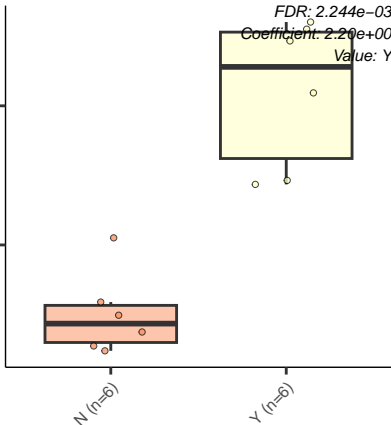
0.005

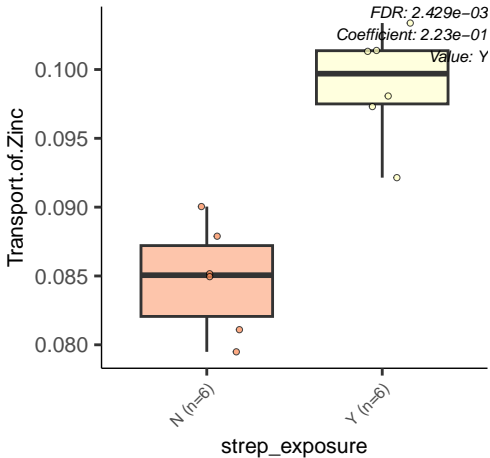
N (n=6)

Y (n=6)

strep_exposure

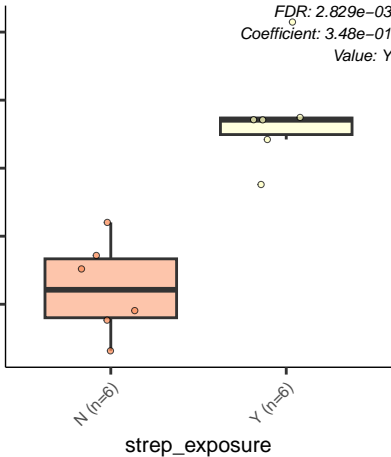
FDR: 2.244e-03
Coefficient: 2.26e+00
Value: Y





CBSS.257314.1.peg.676

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



Dehydrogenase.complexes

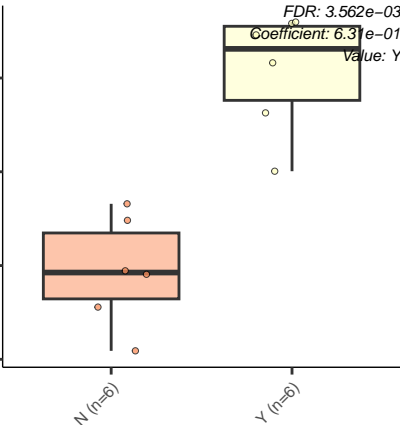
0.06
0.05
0.04
0.03

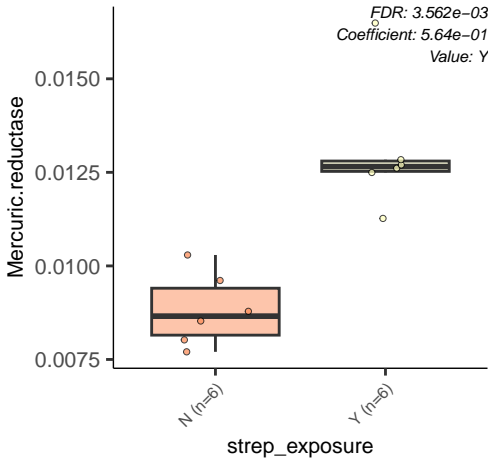
N (n=6)

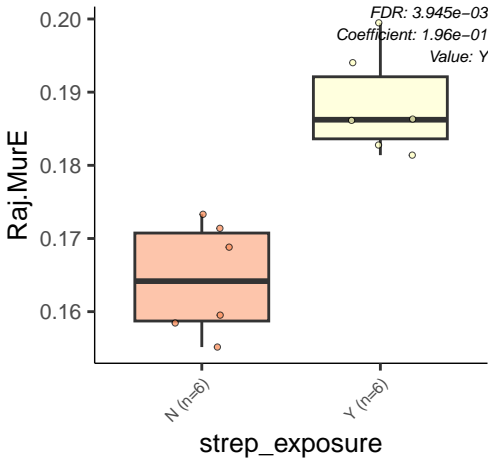
Y (n=6)

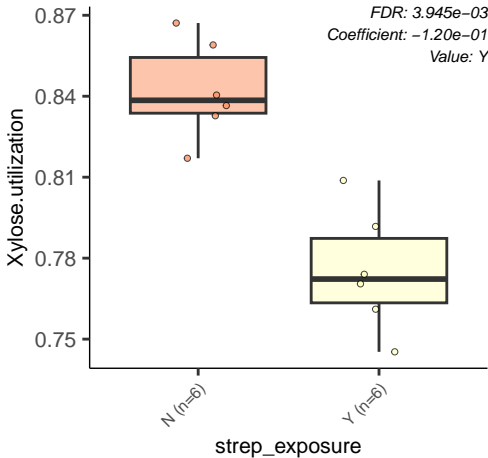
strep_exposure

FDR: 3.562e-03
Coefficient: 6.31e-01
Value: Y

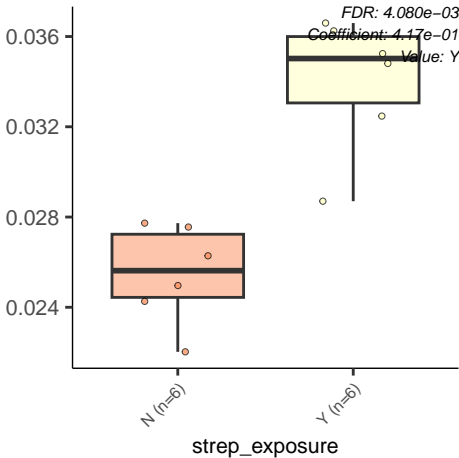


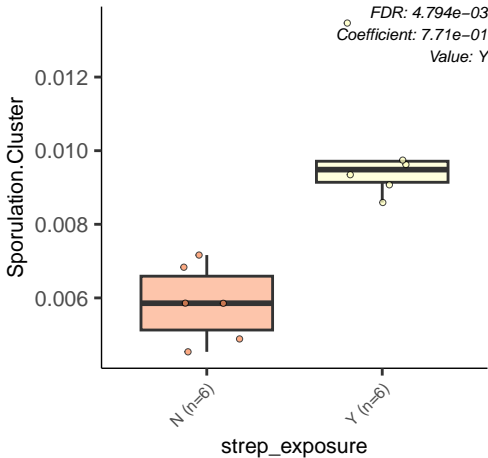






Adhesion.of.Campylobacter





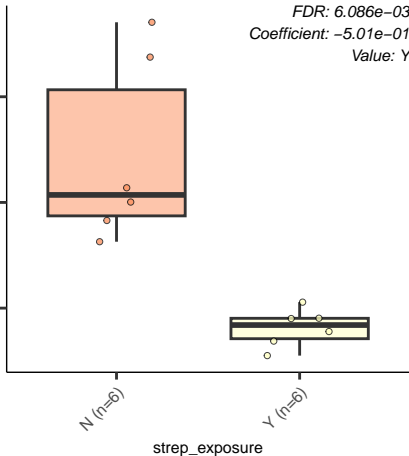
Threonine.anaerobic.catabolism.gene.cluster

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

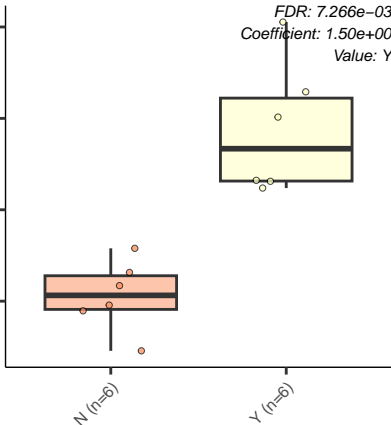
0.002

N (n=6)

Y (n=6)

strep_exposure

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



Mercury.resistance.operon

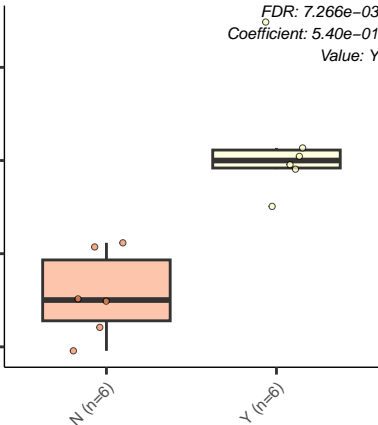
FDR: $7.266e-03$
Coefficient: $5.40e-01$
Value: Y

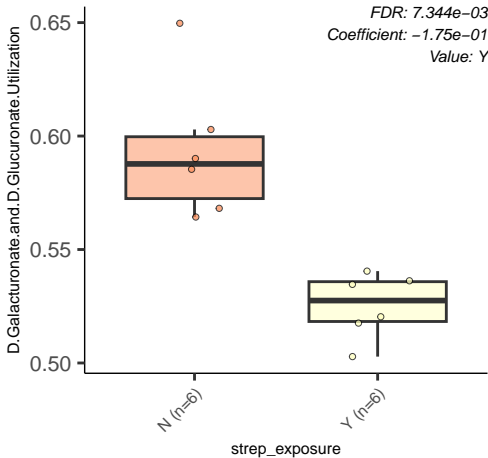
0.0150
0.0125
0.0100
0.0075

N (n=6)

Y (n=6)

strep_exposure





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

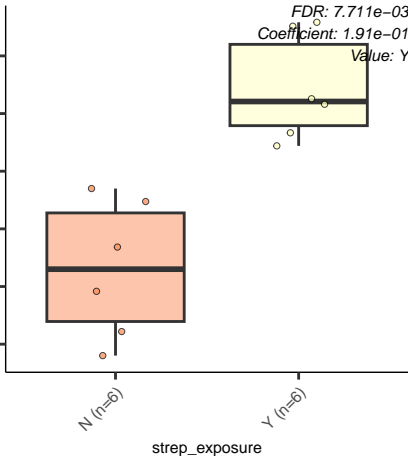
0.26
0.25
0.24
0.23
0.22
0.21

N (n=6)

Y (n=6)

strep_exposure

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



Prophage.lysogenic.conversion.modules

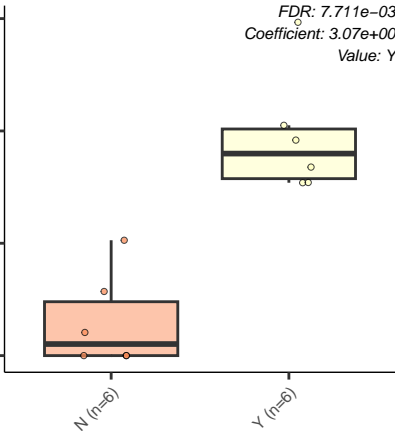
FDR: 7.711e-03
Coefficient: 3.07e+00
Value: Y

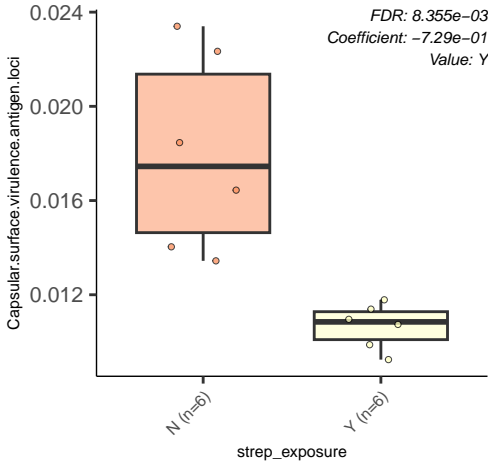
0.003
0.002
0.001
0.000

N (n=6)

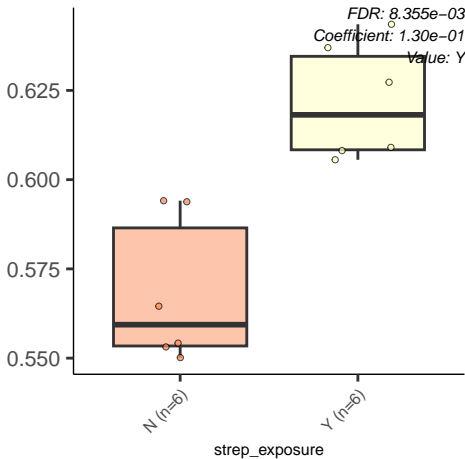
Y (n=6)

strep_exposure



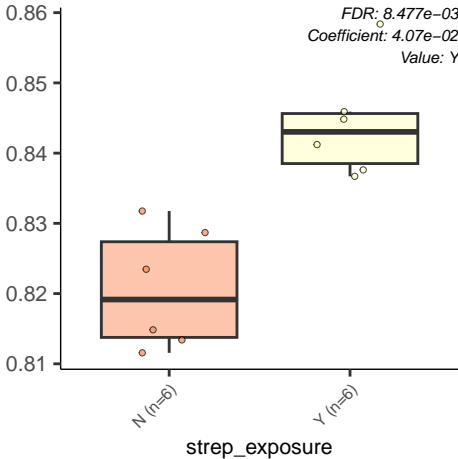


Heat.shock.dnaK.gene.cluster.extended



DNA.repair..bacterial

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



Glutathione..Redox.cycle

0.05

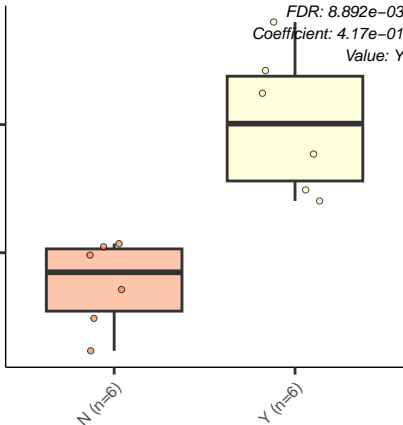
0.04

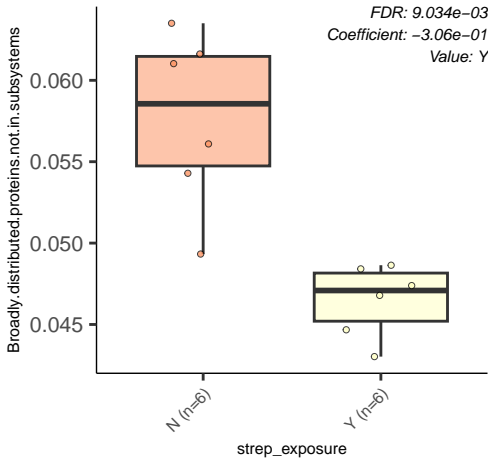
N (n=6)

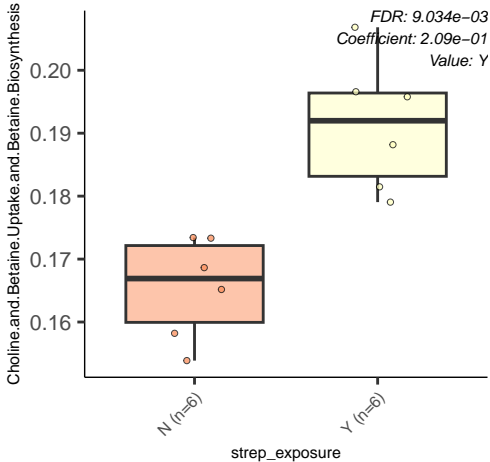
Y (n=6)

strep_exposure

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







Monika.MRSA

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

0.044

0.040

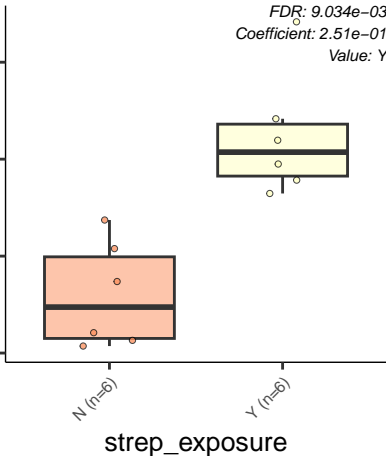
0.036

0.032

N (n=6)

Y (n=6)

strep_exposure



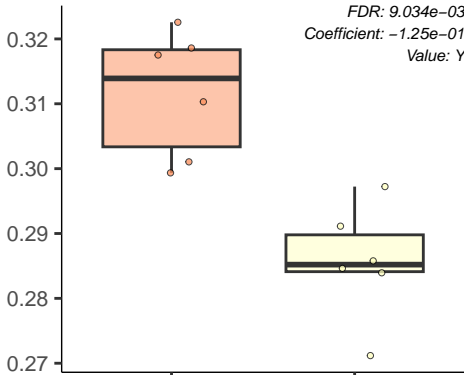
islocating.NADH.quinone.oxidoreductase.and.rnf.like.group.of.electro

FDR: 9.034e-03
Coefficient: -1.25e-01
Value: Y

N (n=6)

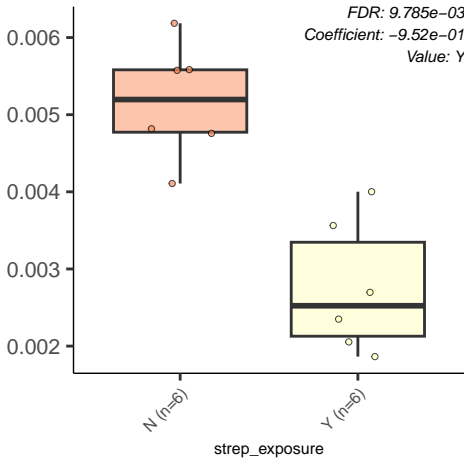
Y (n=6)

strep_exposure



Unknown.carbohydrate.utilization.containing.Fructose.bisphosphat

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



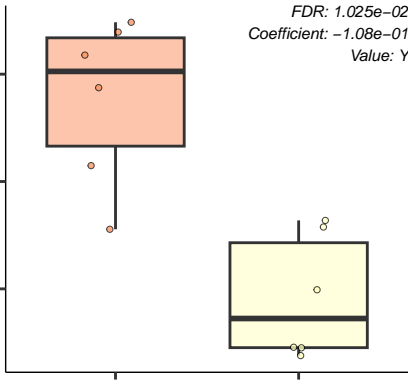
Fructooligosaccharides.FOS..and.Raffinose.Utilization

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

N (n=6)

Y (n=6)

strep_exposure



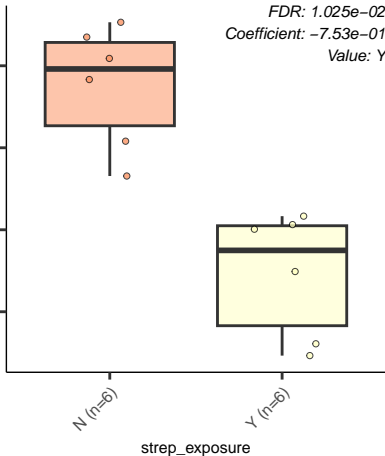
Two.partner.secretion..TPS.

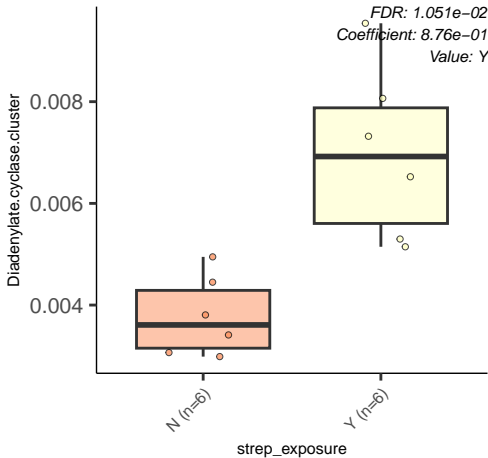
FDR: 1.025e-02
Coefficient: -7.53e-01
Value: Y

N (n=6)

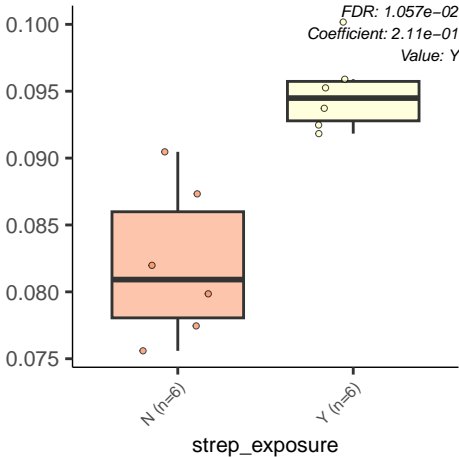
Y (n=6)

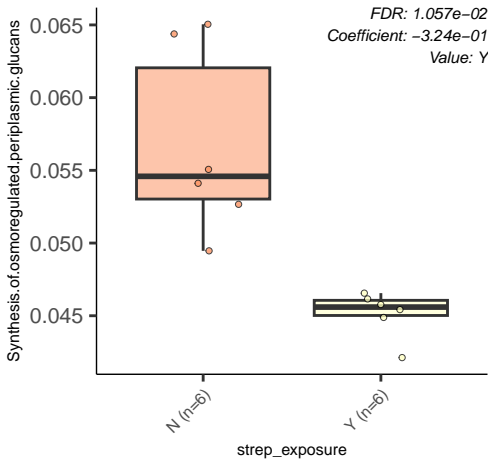
strep_exposure

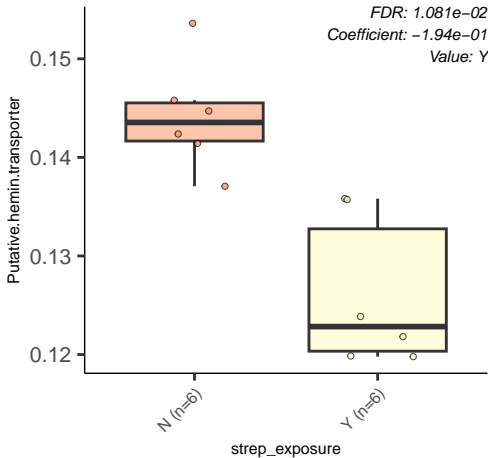




CBSS.84588.1.peg.1247







Outer.membrane

FDR: 1.134e-02

Coefficient: -3.38e-01

Value: Y

0.045

0.040

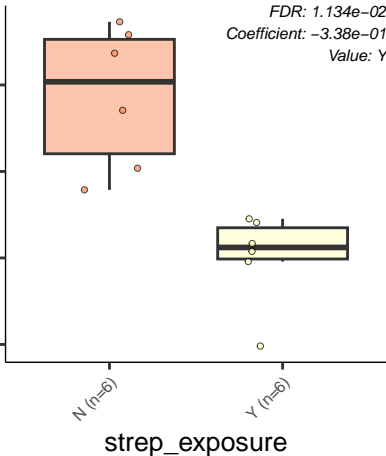
0.035

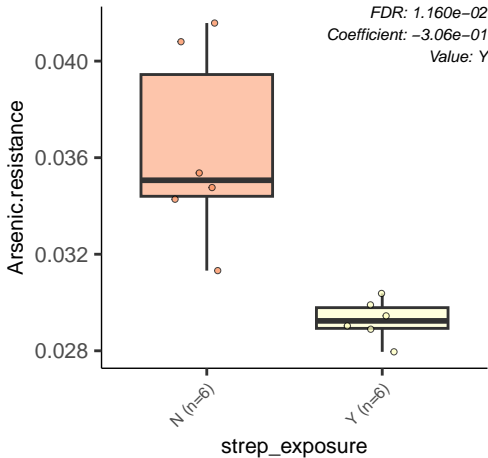
0.030

N (n=6)

Y (n=6)

strep_exposure





CBSS.393130.3.pcg.794

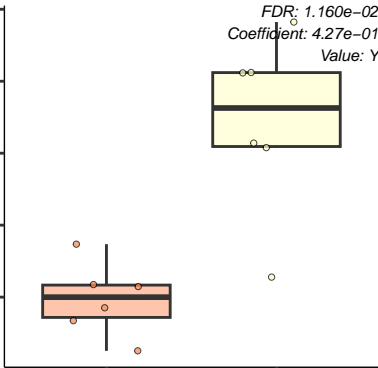
0.0275
0.0250
0.0225
0.0200
0.0175

N (n=6)

Y (n=6)

strep_exposure

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



Fe.S.cluster.assembly

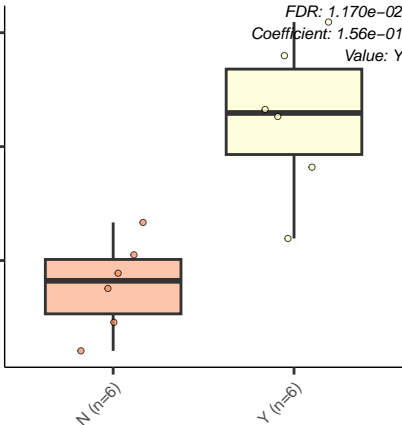
0.15
0.14
0.13

N (n=6)

Y (n=6)

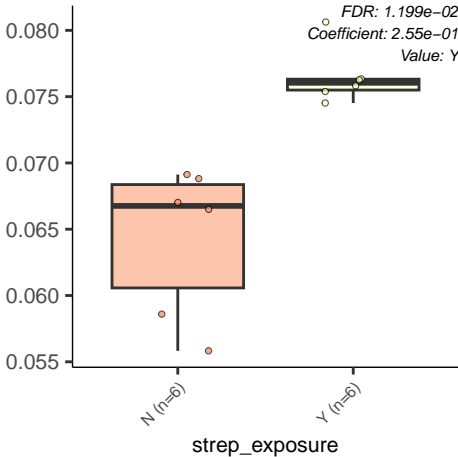
strep_exposure

FDR: 1.170e-02
Coefficient: 1.56e-01
Value: Y

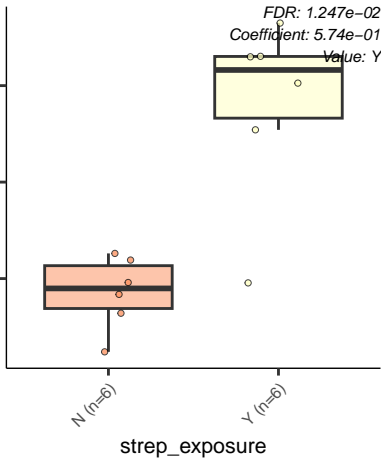


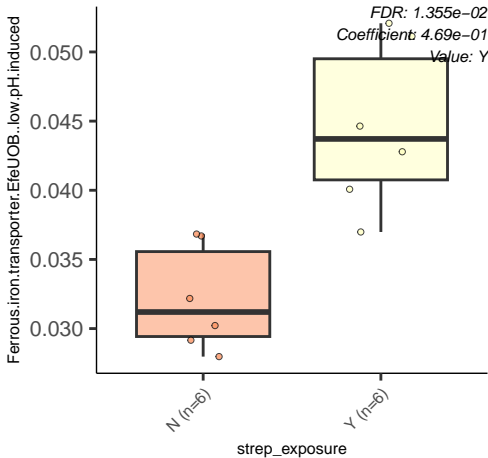
LMPTP.YwIE.cluster

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



CBSS.279010.5.peg.3195





Histidine.Biosynthesis

0.575

0.550

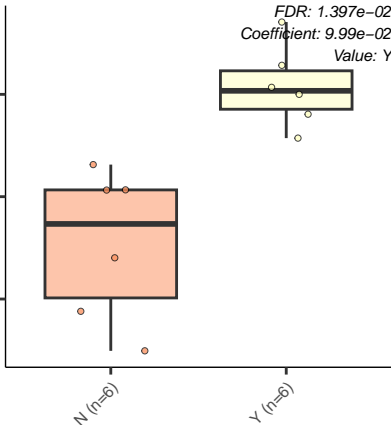
0.525

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

0.08

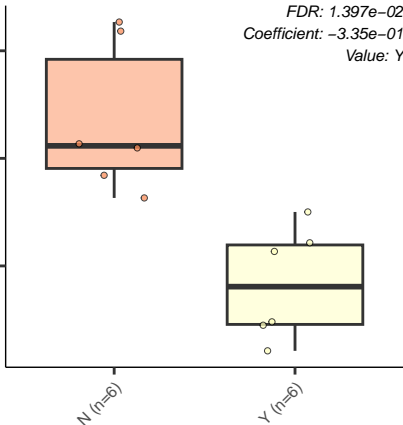
0.07

0.06

N (n=6)

Y (n=6)

strep_exposure



KDO2.Lipid.A.biosynthesis

FDR: 1.410e-02
Coefficient: -1.75e-01
Value: Y

0.28

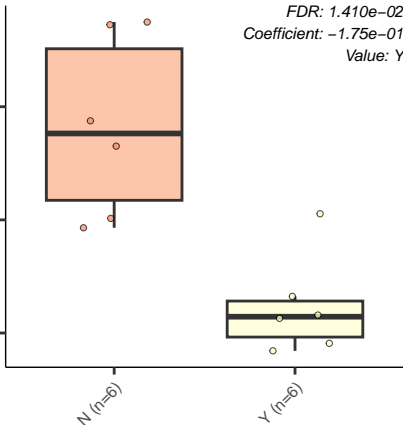
0.26

0.24

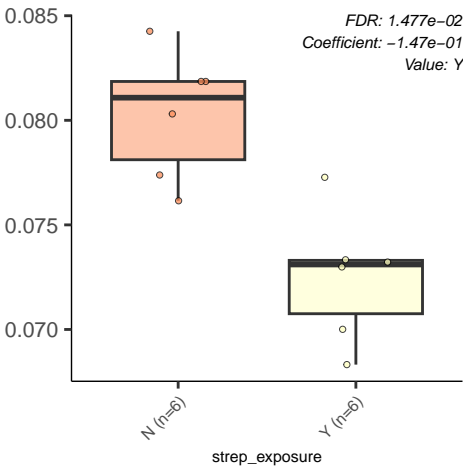
N (n=6)

Y (n=6)

strep_exposure



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



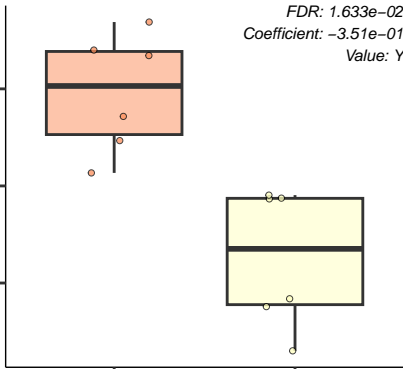
Hemin.transport.system

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

N (n=6)

Y (n=6)

strep_exposure



Transport.of.Manganese

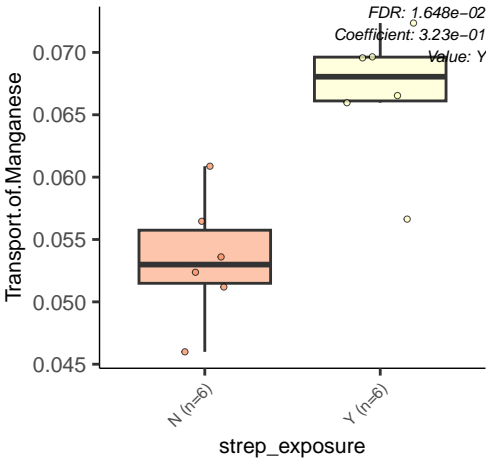
0.070
0.065
0.060
0.055
0.050
0.045

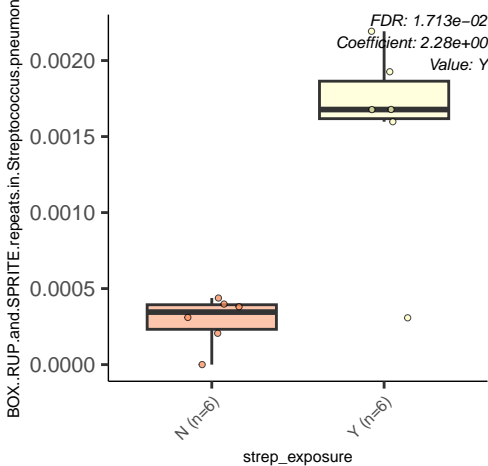
N (n=6)

Y (n=6)

strep_exposure

FDR: 1.648e-02
Coefficient: 3.23e-01
Value: Y





CBSS.243265.1.peg.198

0.030

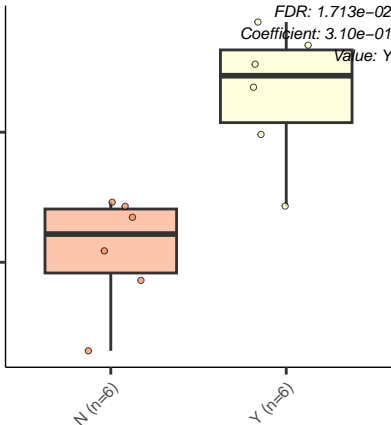
0.025

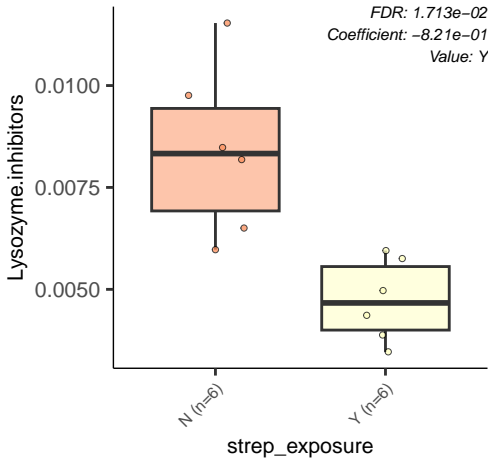
N (n=6)

Y (n=6)

strep_exposure

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





Murein.Hydrolases

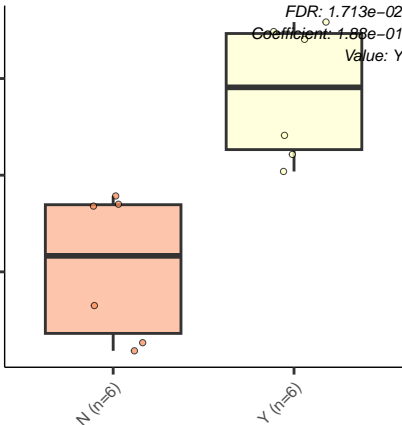
0.15
0.14
0.13

N (n=6)

Y (n=6)

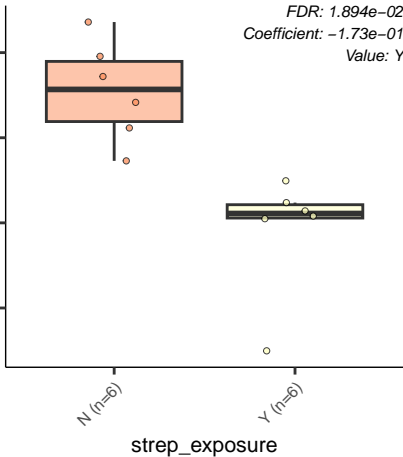
strep_exposure

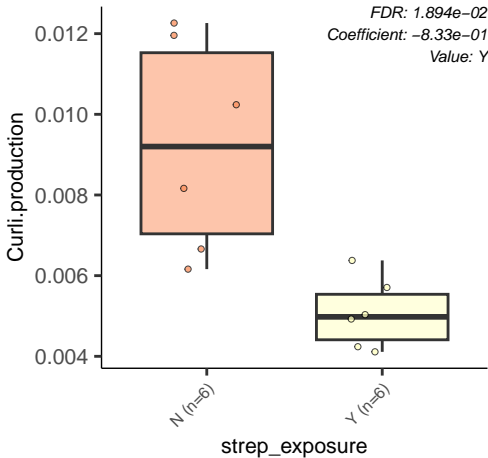
FDR: 1.713e-02
Coefficient: 1.88e-01
Value: Y

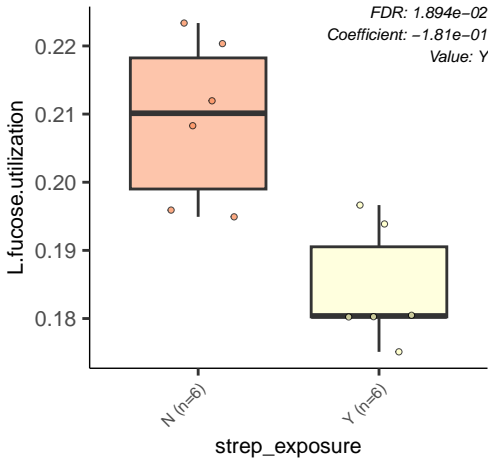


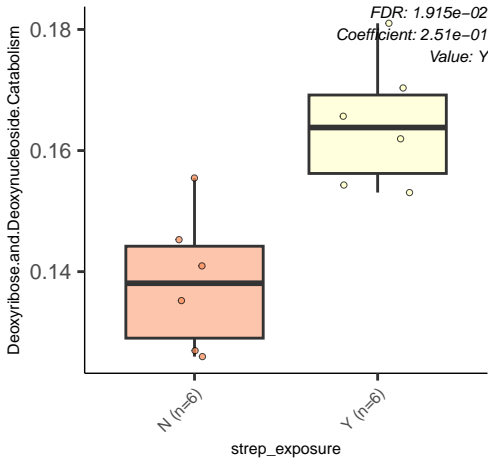
Carbon.Starvation

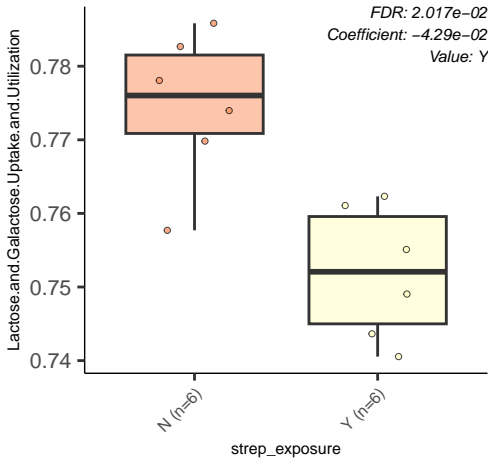
FDR: $1.894\text{e-}02$
Coefficient: $-1.73\text{e-}01$
Value: Y











Glutaredoxins

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

0.225

0.220

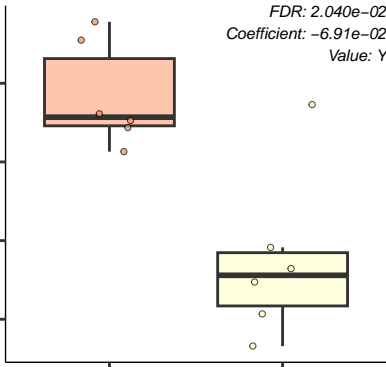
0.215

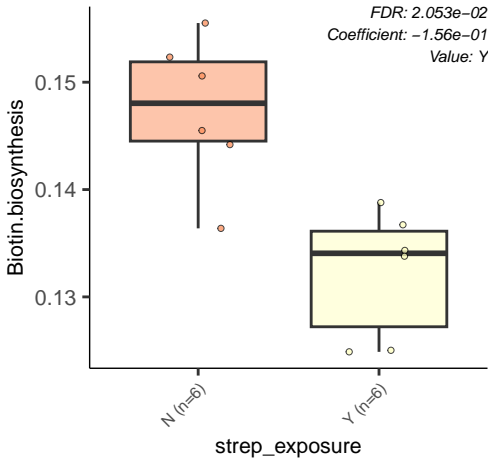
0.210

N (n=6)

Y (n=6)

strep_exposure





CBSS.393121.3.pcg.2760

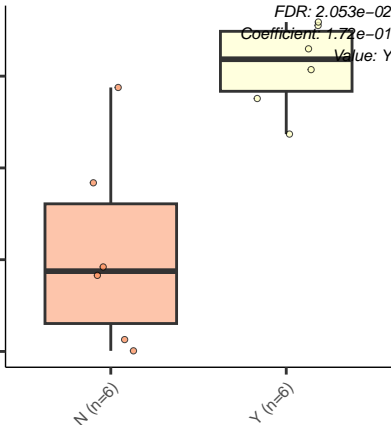
0.450
0.425
0.400
0.375

N (n=6)

Y (n=6)

strep_exposure

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



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

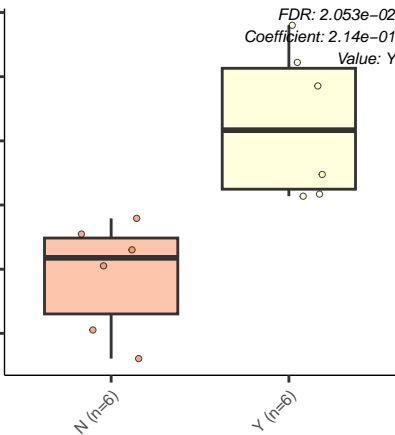
0.095
0.090
0.085
0.080
0.075
0.070

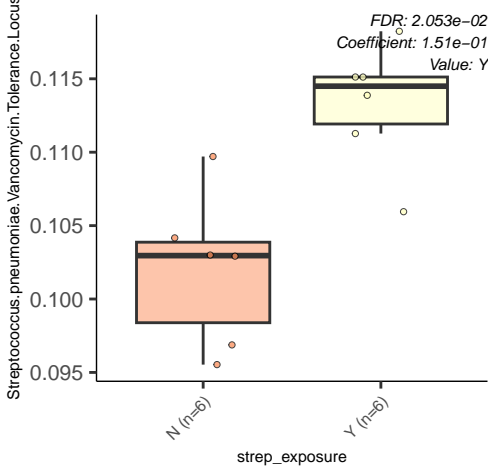
N (n=6)

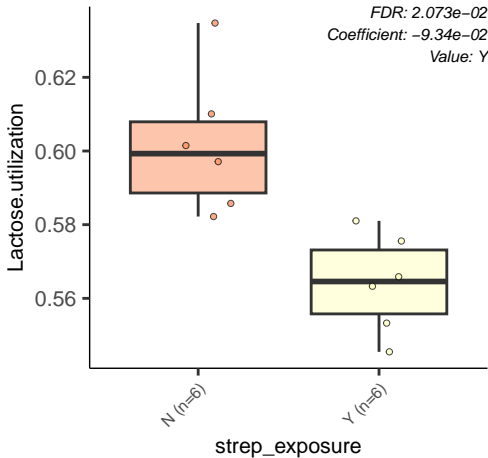
Y (n=6)

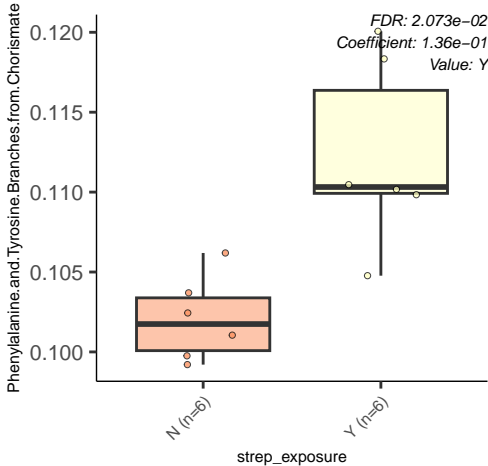
strep_exposure

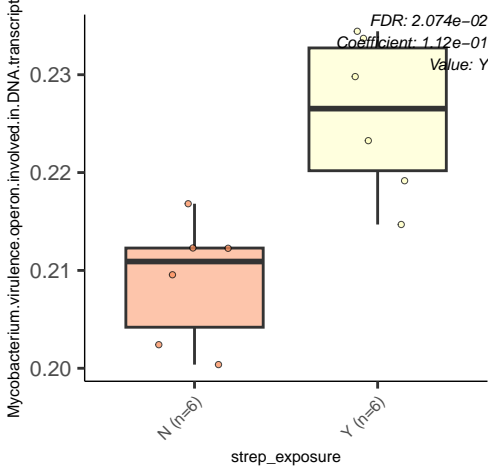
FDR: 2.053e-02
Coefficient: 2.14e-01
Value: Y











Alpha.Amylase.locus.in.Streptococcus

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

0.08

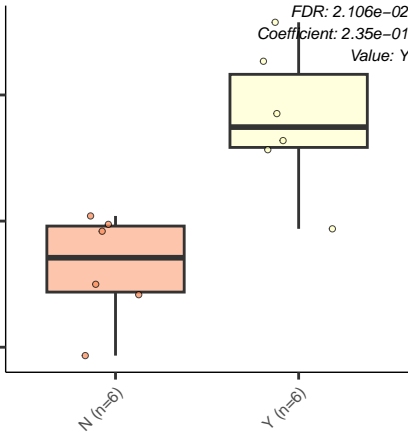
0.07

0.06

N (n=6)

Y (n=6)

strep_exposure



cell.division.cluster.containing.FtsQ

0.06

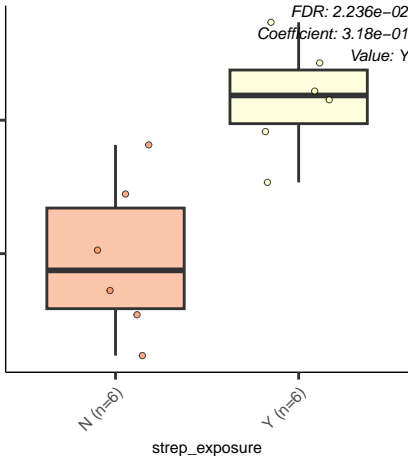
0.05

N (n=6)

Y (n=6)

strep_exposure

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



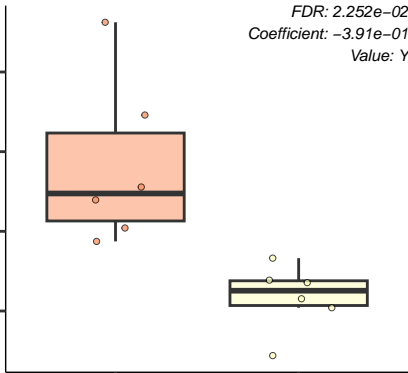
Phd.Doc., YdcE, YdcD, toxin, antitoxin, programmed, cell, death, s

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

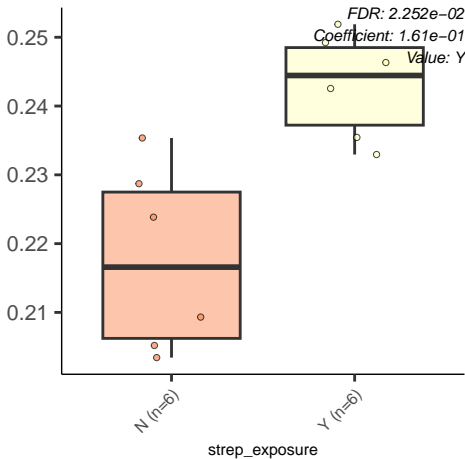
N (n=6)

Y (n=6)

strep_exposure



tRNA.aminoacylation...Asp.and.Asn



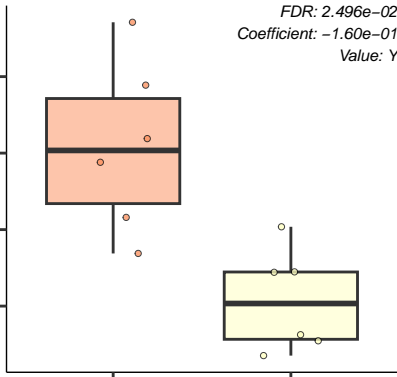
Glycolate..glyoxylate.interconversions

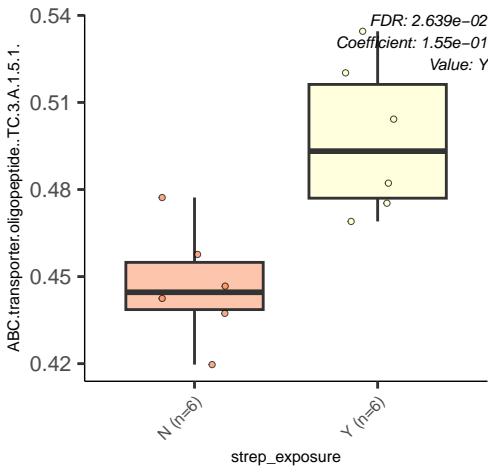
FDR: 2.496e-02
Coefficient: -1.60e-01
Value: Y

N (n=6)

Y (n=6)

strep_exposure





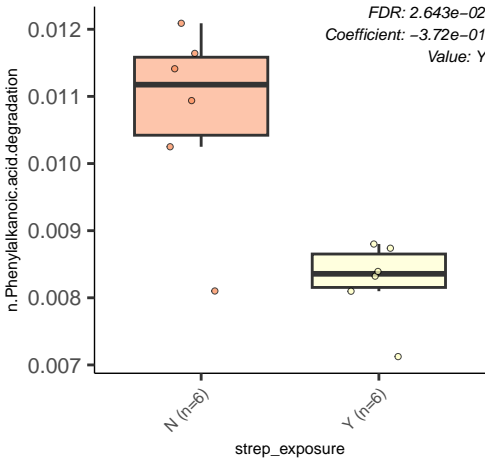
n.Phenylalkanoic.acid.degradation

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

N (n=6)

Y (n=6)

strep_exposure



Cell.Division.Subsystem.including.YidCD

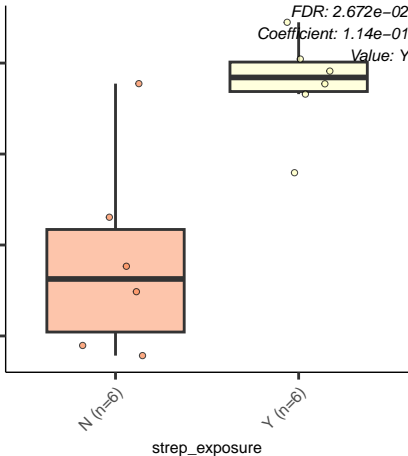
FDR: 2.672e-02
Coefficient: 1.14e-01
Value: Y

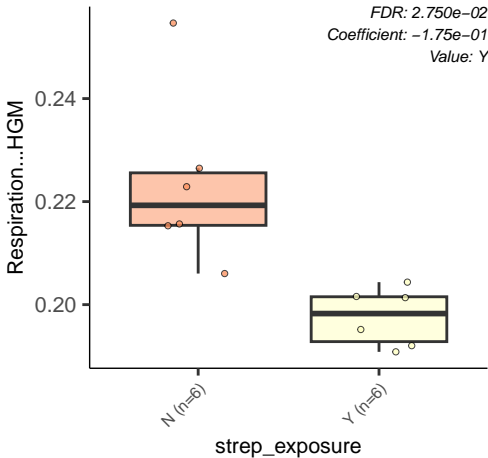
0.26
0.25
0.24
0.23

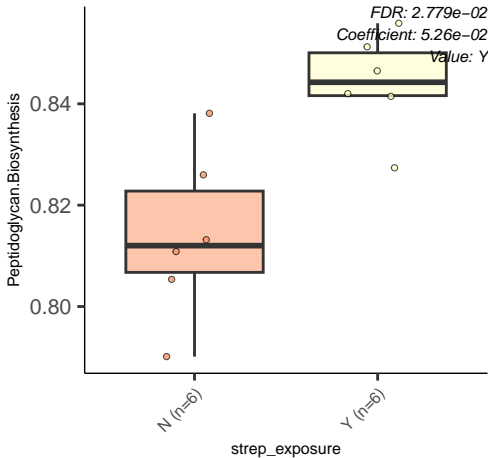
N (n=6)

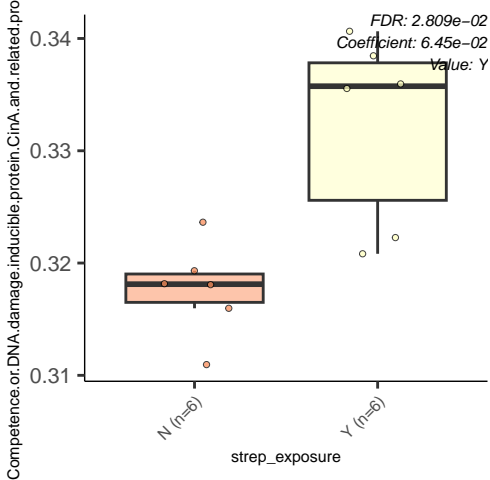
Y (n=6)

strep_exposure









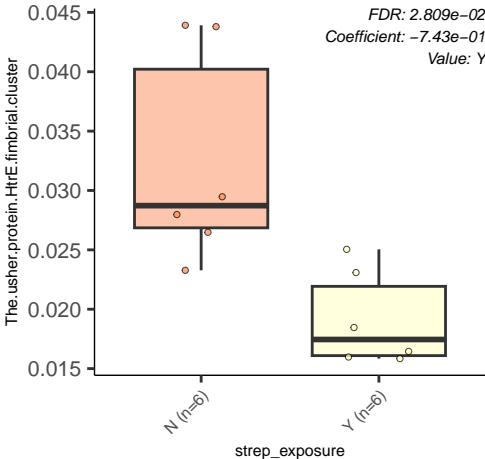
The.usher.protein.HtrE.fimbral.cluster

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

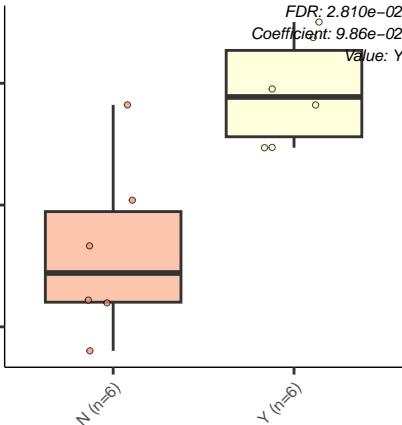
0.18

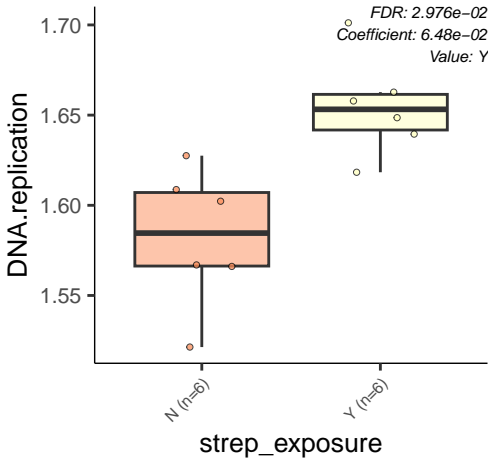
N (n=6)

Y (n=6)

strep_exposure

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





CBSS.176299.4.peg.1292

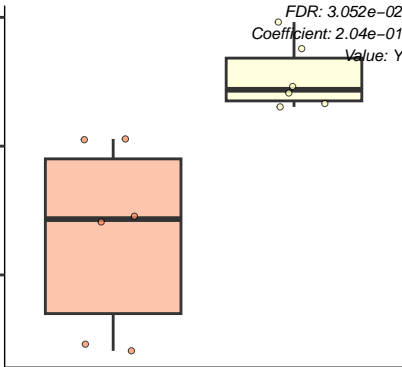
0.10
0.09
0.08

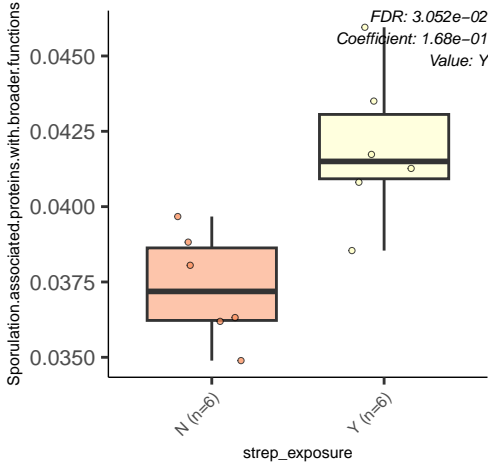
N (n=6)

Y (n=6)

strep_exposure

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





Thiamin.biosynthesis.in.plants

FDR: $3.396e-02$
Coefficient: $-7.40e-01$
Value: Y

0.0030

0.0025

0.0020

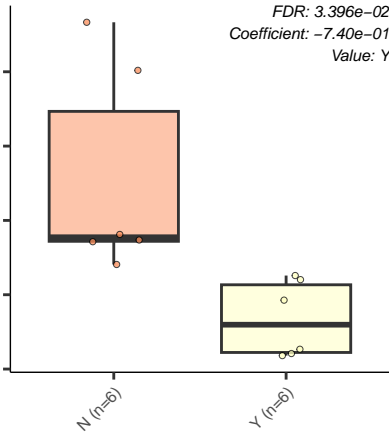
0.0015

0.0010

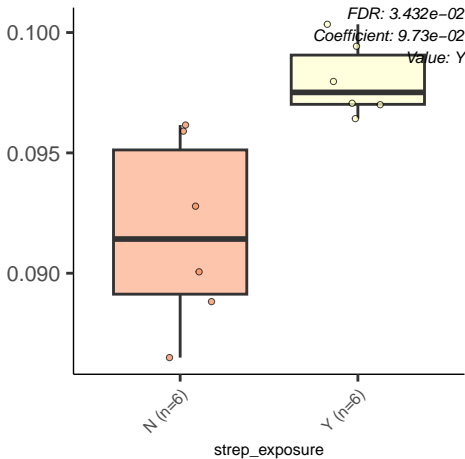
N (n=6)

Y (n=6)

strep_exposure



RuvABC.plus.a.hypothetical



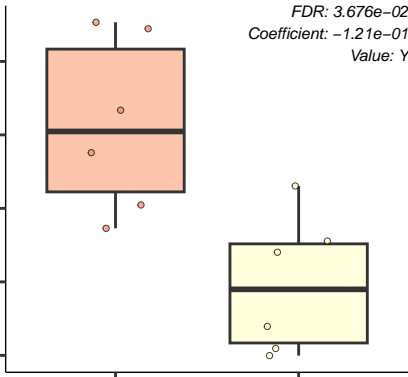
Arginine.and.Ornithine.Degradation

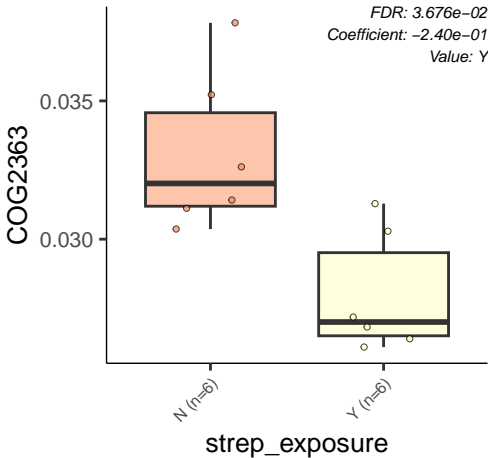
FDR: 3.676e-02
Coefficient: -1.21e-01
Value: Y

N (n=6)

Y (n=6)

strep_exposure





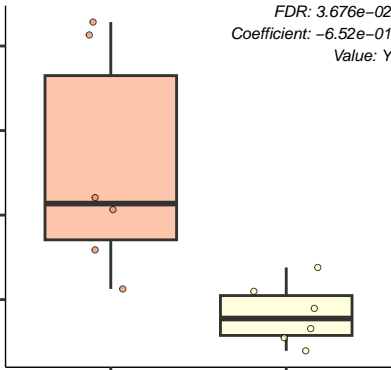
Cinnamic.Acid.Degradation

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

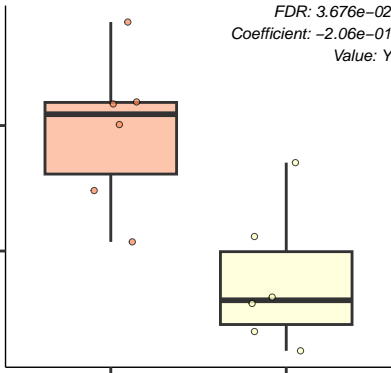
0.045

0.040

N (n=6)

Y (n=6)

strep_exposure



Osmoregulation

FDR: 3.676e-02

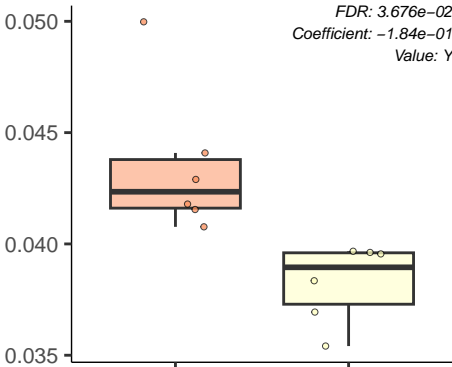
Coefficient: -1.84e-01

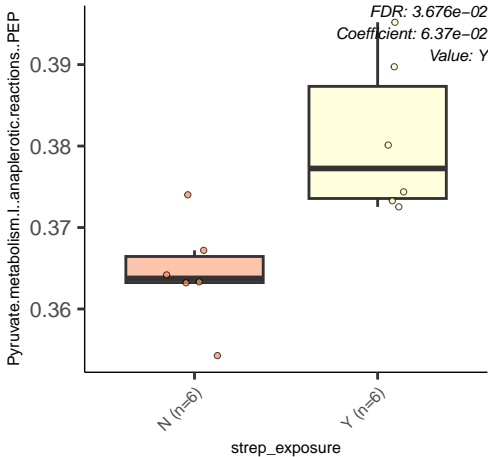
Value: Y

N (n=6)

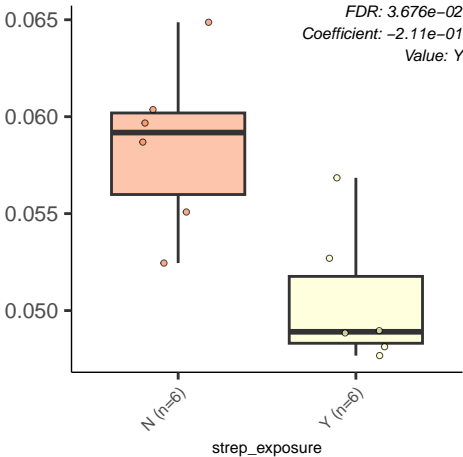
Y (n=6)

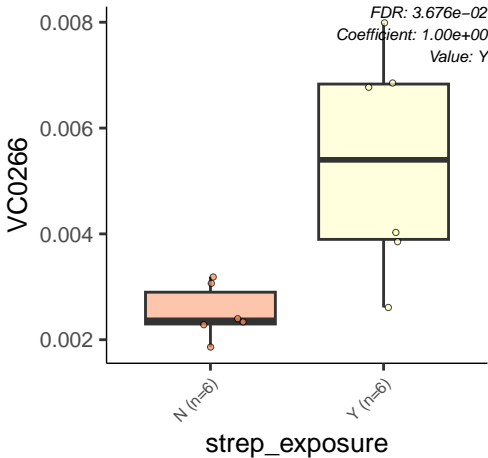
strep_exposure

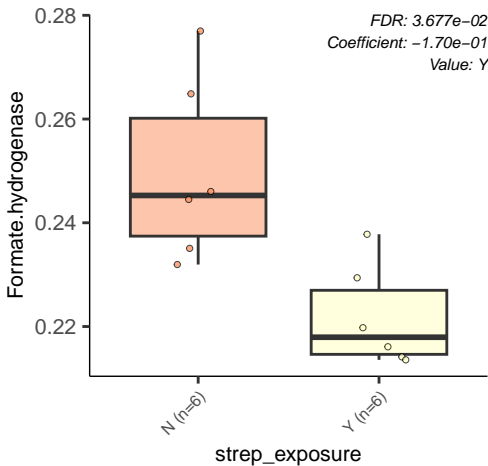




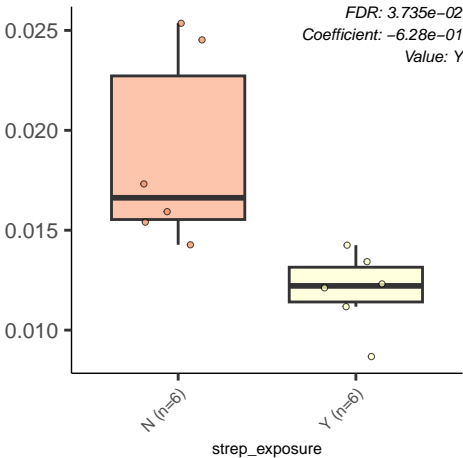
Uptake.of.selenate.and.selenite



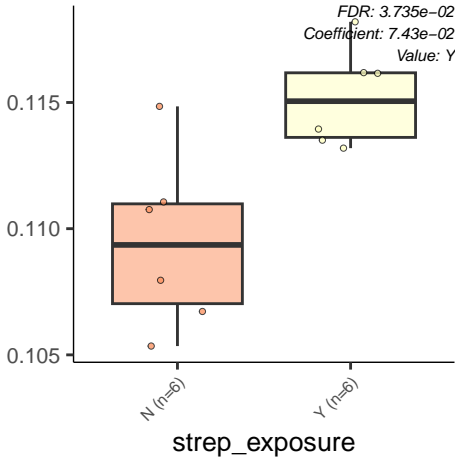




Accessory.colonization.factor



GroEL.GroES



ECF.class.transporters

0.32

0.30

0.28

0.26

N (n=6)

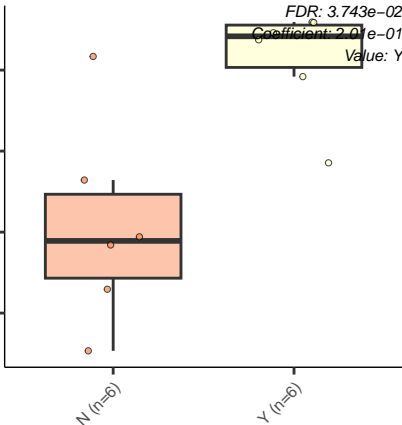
Y (n=6)

strep_exposure

FDR: 3.743e-02

Coefficient: 2.01e-01

Value: Y



CbiZ.Main

FDR: 3.844e-02

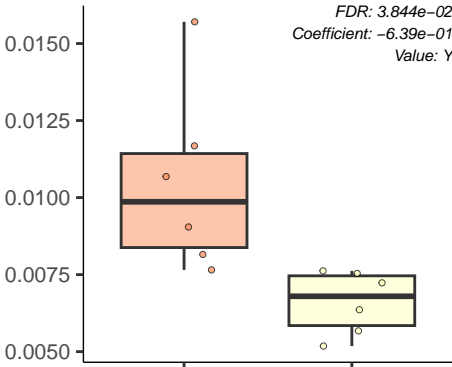
Coefficient: -6.39e-01

Value: Y

N (n=6)

Y (n=6)

strep_exposure



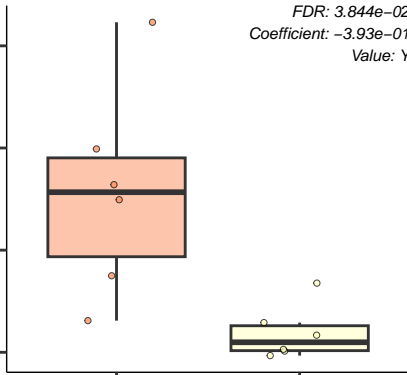
DNA.binding.regulatory.proteins..strays

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

N (n=6)

Y (n=6)

strep_exposure



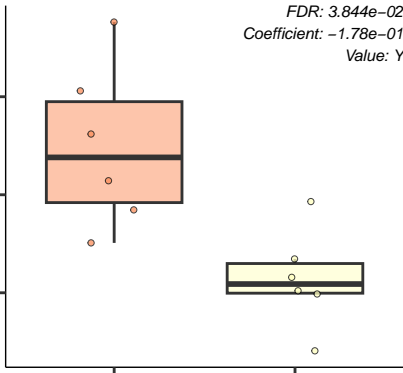
L.rhamnose.utilization

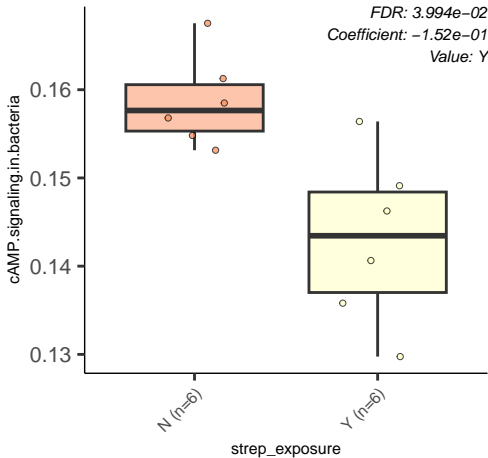
FDR: $3.844e-02$
Coefficient: $-1.78e-01$
Value: Y

N (n=6)

Y (n=6)

strep_exposure





HPr.catabolite.repression.system

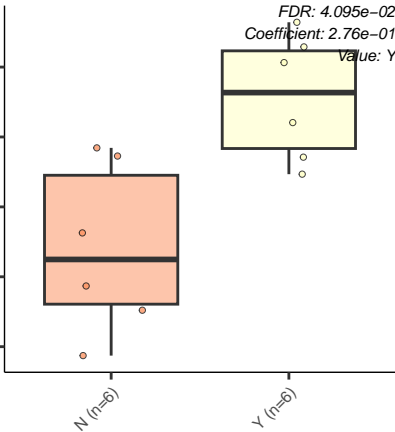
0.065
0.060
0.055
0.050
0.045

N (n=6)

Y (n=6)

strep_exposure

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



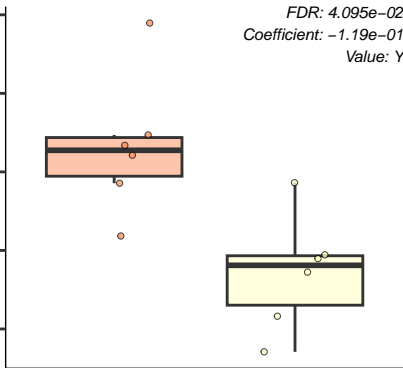
Trehalose.Biosynthesis

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

N (n=6)

Y (n=6)

strep_exposure



Siderophore.Enterobactin

FDR: 4.128e-02

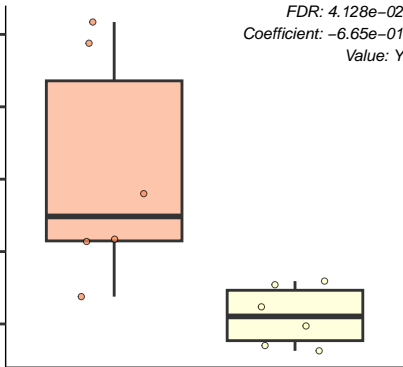
Coefficient: -6.65e-01

Value: Y

N (n=6)

Y (n=6)

strep_exposure



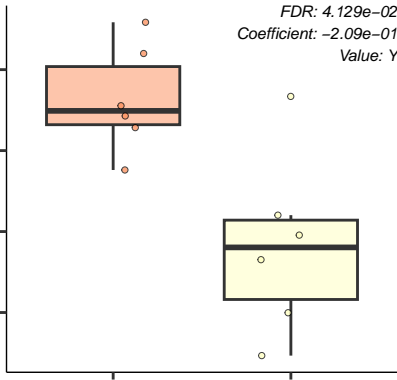
D. Tagatose.and. Galactitol.Utilization

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

N (n=6)

Y (n=6)

strep_exposure



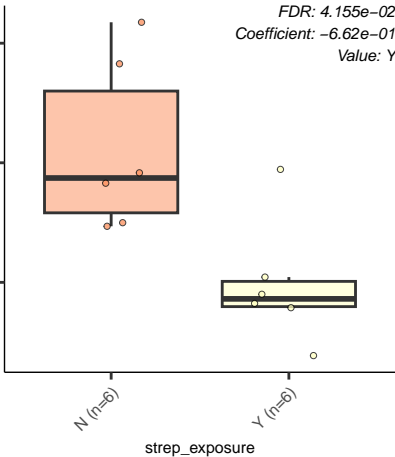
Siderophore.Yersiniabactin.Biosynthesis

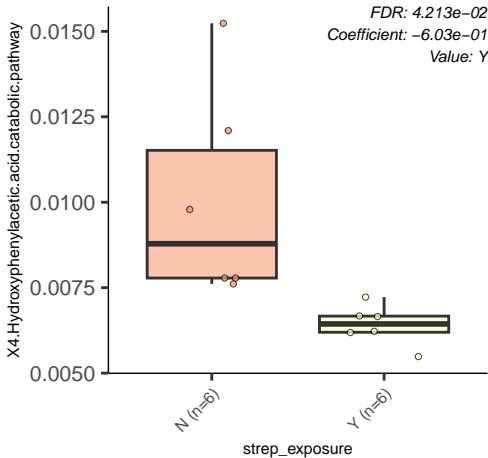
FDR: 4.155e-02
Coefficient: -6.62e-01
Value: Y

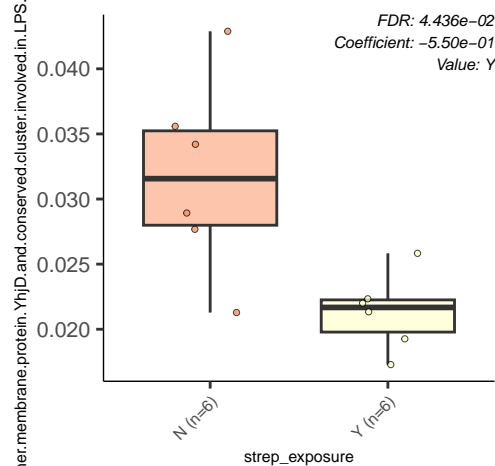
N (n=6)

Y (n=6)

strep_exposure







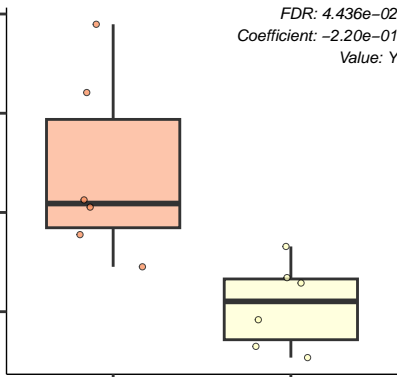
Propionyl.CoA.to.Succinyl.CoA.Module

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

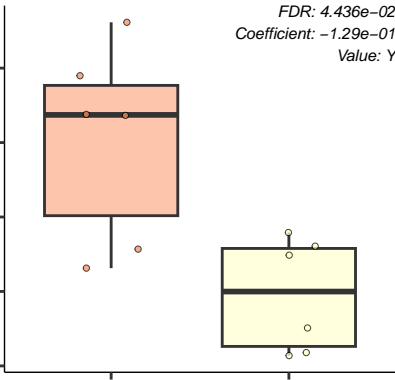
0.110

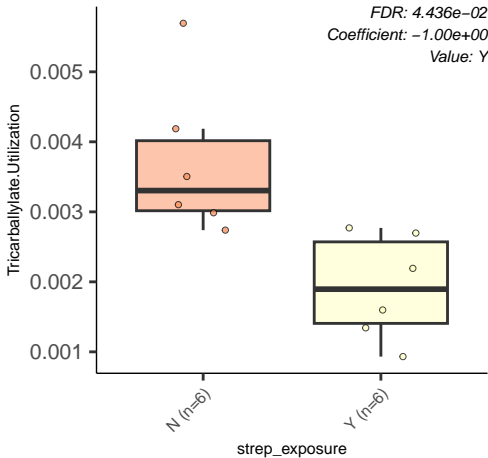
0.105

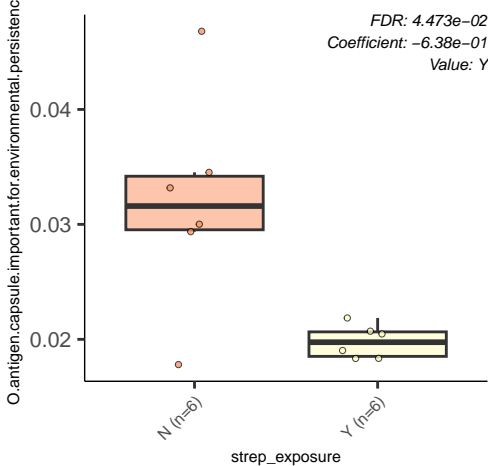
N (n=6)

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)

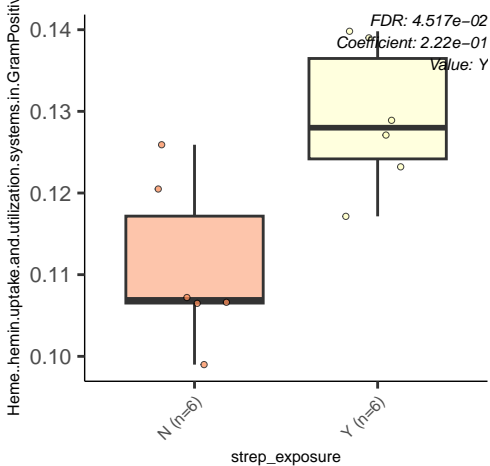
Y (n=6)

strep_exposure

0.045

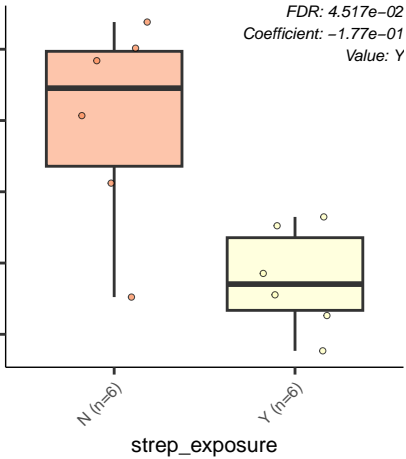
0.040

0.035



Respiratory.Complex.I

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



strep_exposure

Alanine.biosynthesis

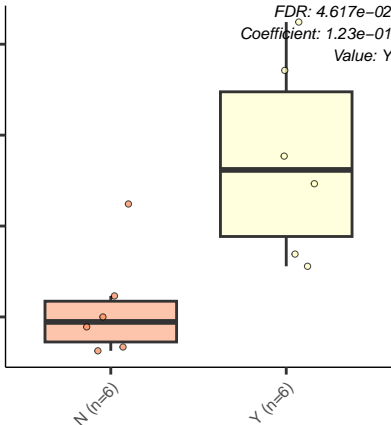
0.105
0.100
0.095
0.090

N (n=6)

Y (n=6)

strep_exposure

FDR: 4.617e-02
Coefficient: 1.23e-01
Value: Y



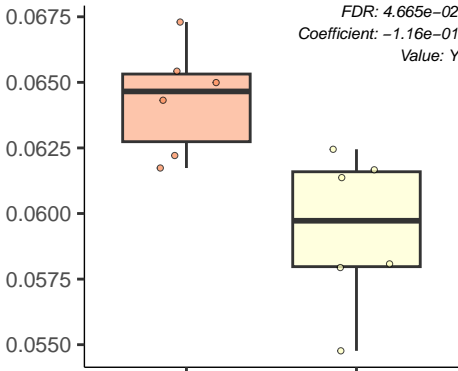
Glycine.Biosynthesis

FDR: 4.665e-02
Coefficient: -1.16e-01
Value: Y

N (n=6)

Y (n=6)

strep_exposure



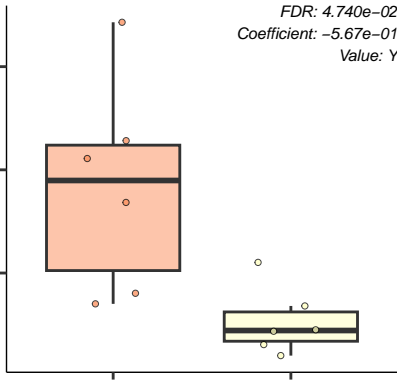
Acetone.Butanol.Ethanol.Synthesis

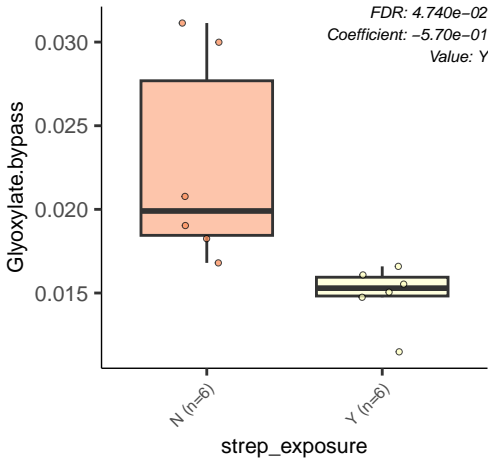
FDR: 4.740e-02
Coefficient: -5.67e-01
Value: Y

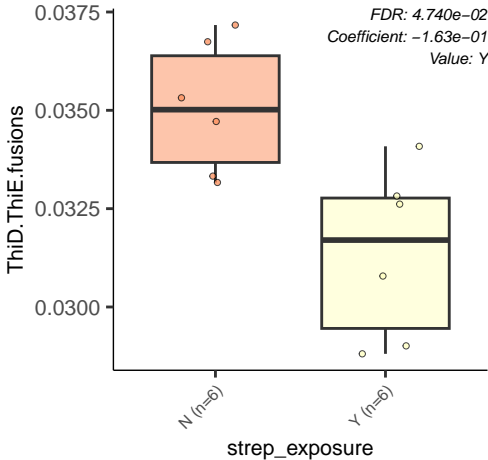
N (n=6)

Y (n=6)

strep_exposure







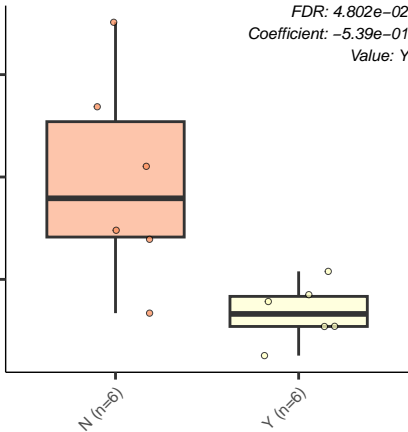
Carnitine.Metabolism.in.Microorganisms

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

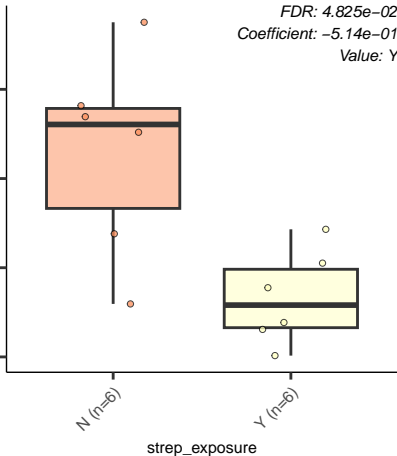
0.016

0.012

N (n=6)

Y (n=6)

strep_exposure



Pyrroloquinoline.Quinone.biosynthesis

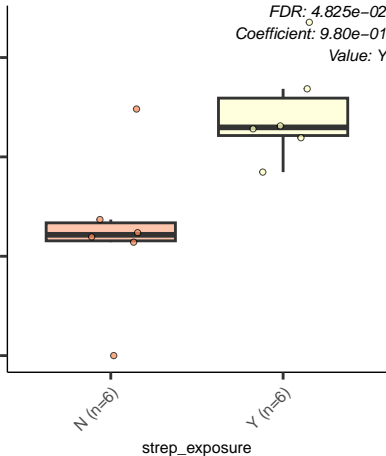
FDR: 4.825e-02
Coefficient: 9.80e-01
Value: Y

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)

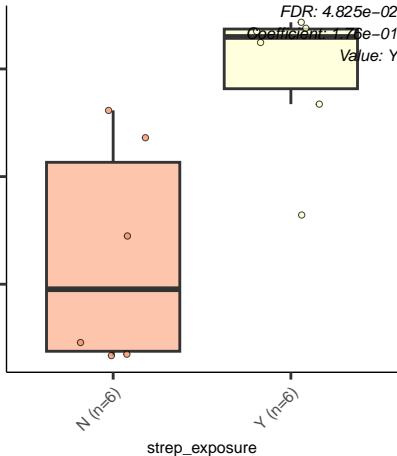
Y (n=6)

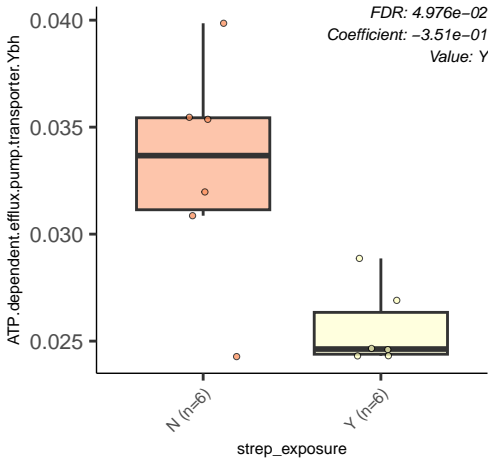
strep_exposure

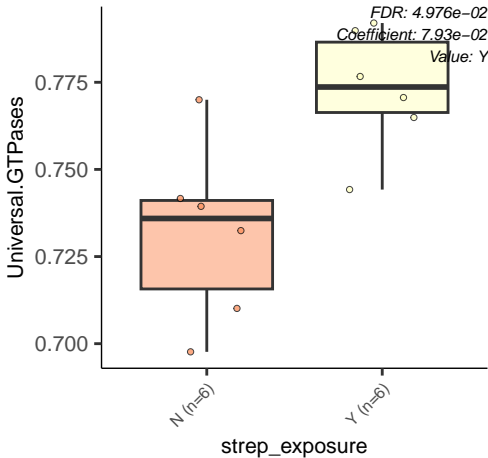
FDR: 4.825e-02

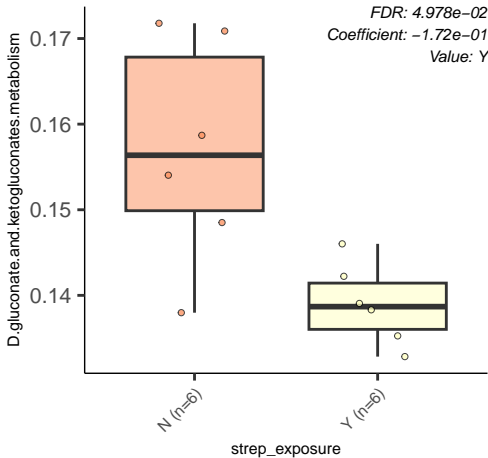
Coefficient: 1.76e-01

Value: Y

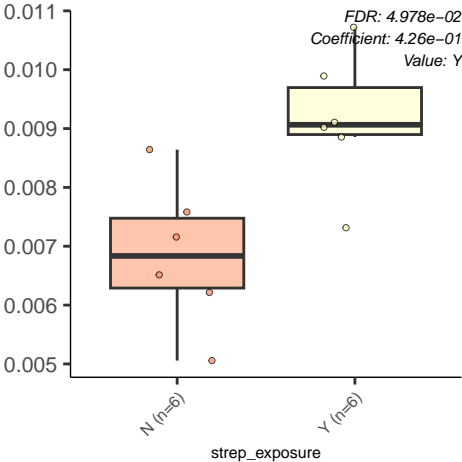


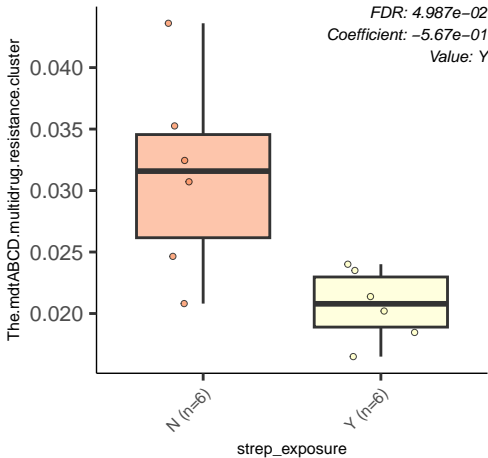






Menaquinone.Biosynthesis.via.Futalosine





ATP.dependent.RNA.helicases..bacterial

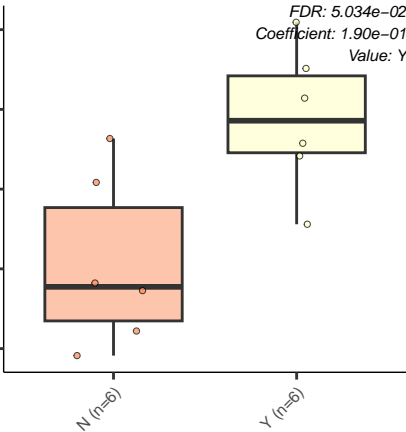
0.16
0.15
0.14
0.13
0.12

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

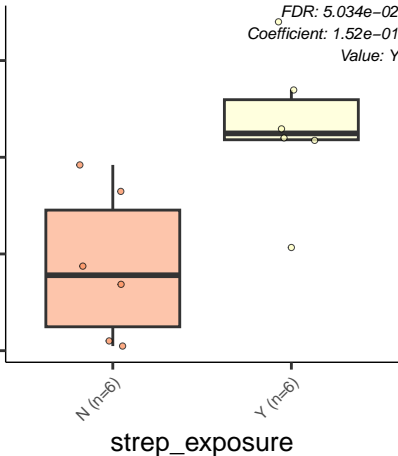
0.13

0.12

N (n=6)

Y (n=6)

strep_exposure



CBSS.211586.1.pcg.3133

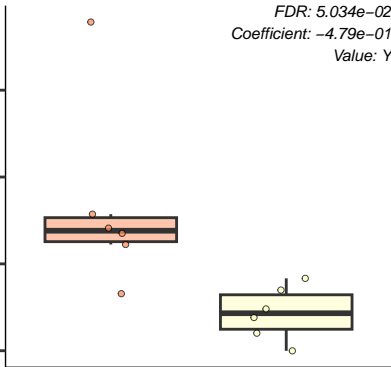
FDR: $5.034e-02$
Coefficient: $-4.79e-01$
Value: Y

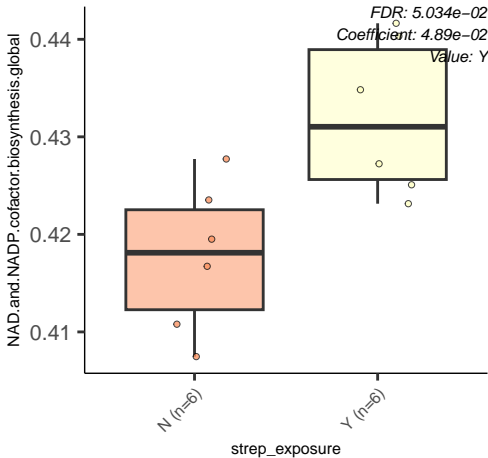
0.011
0.009
0.007
0.005

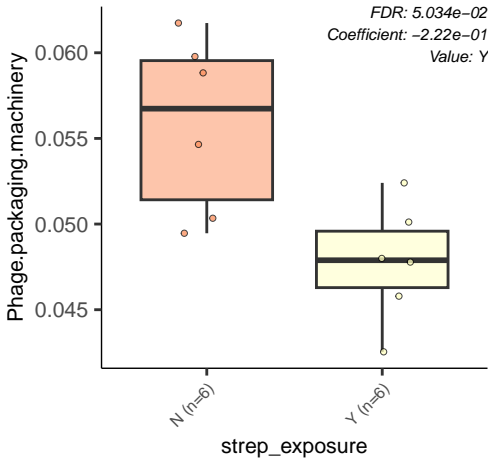
N (n=6)

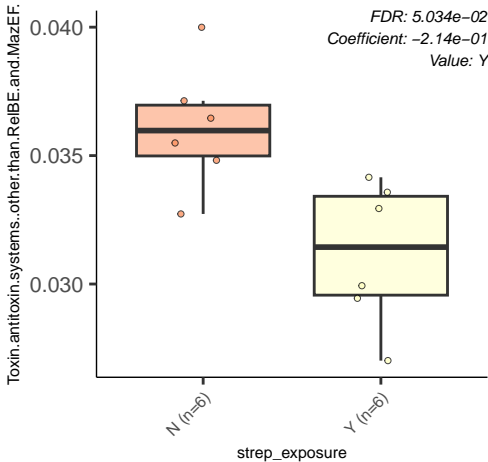
Y (n=6)

strep_exposure









A.Gammaproteobacteria.Cluster.Relating.to.Translation

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

0.0150

0.0125

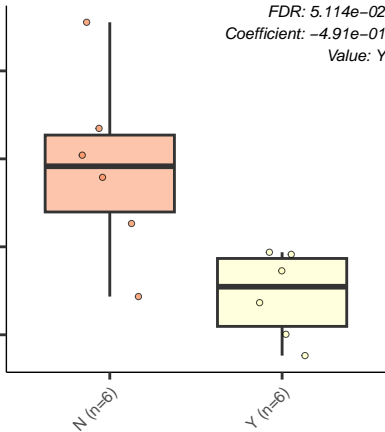
0.0100

0.0075

N (n=6)

Y (n=6)

strep_exposure



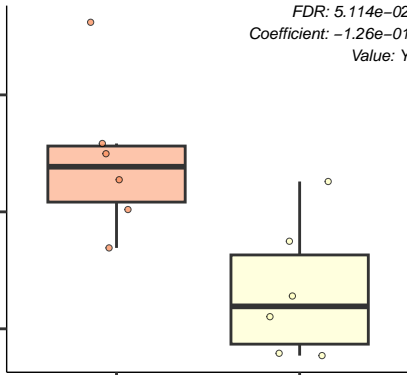
Oxygen.stress.response...Human.gut.microbiome

FDR: $5.114e-02$
Coefficient: $-1.26e-01$
Value: Y

N (n=6)

Y (n=6)

strep_exposure



At1g69340.At2g40600

FDR: 5.119×10^{-2}
Coefficient: 1.96×10^{-1}
Value: Y

0.08

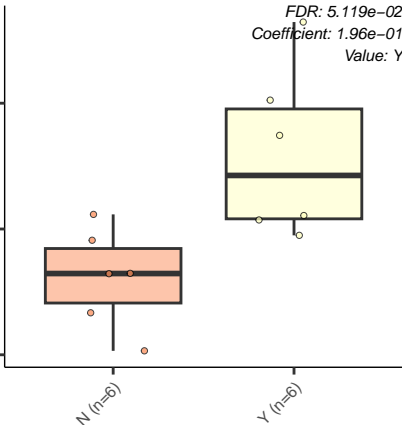
0.07

0.06

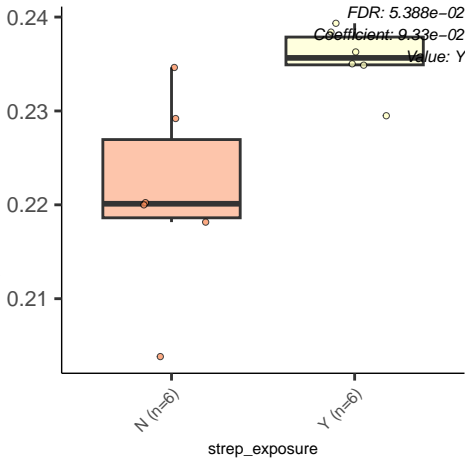
N (n=6)

Y (n=6)

strep_exposure



At5g37530..CsdL.protein.family.



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

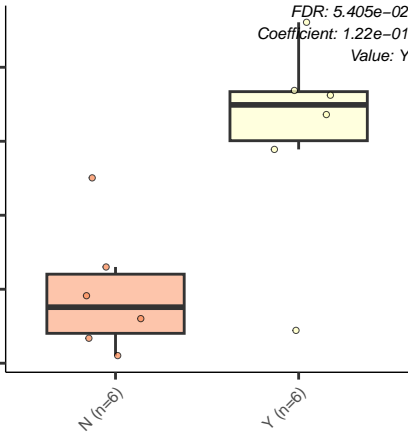
0.27
0.26
0.25
0.24
0.23

N (n=6)

Y (n=6)

strep_exposure

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



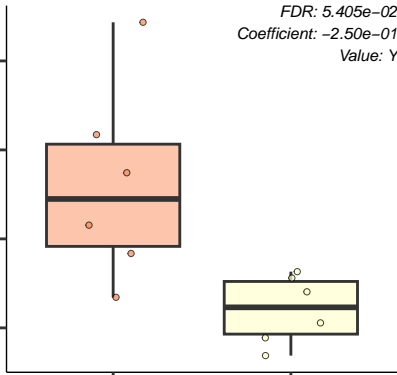
D.galactarate..D.glucarate.and.D.glycerate.catabolism...g

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

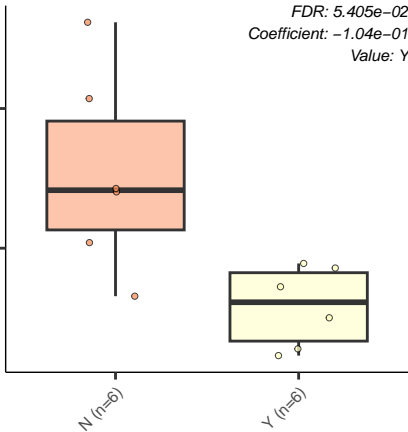
0.70

0.65

N (n=6)

Y (n=6)

strep_exposure



Methionine.Degradation

0.38

0.37

0.36

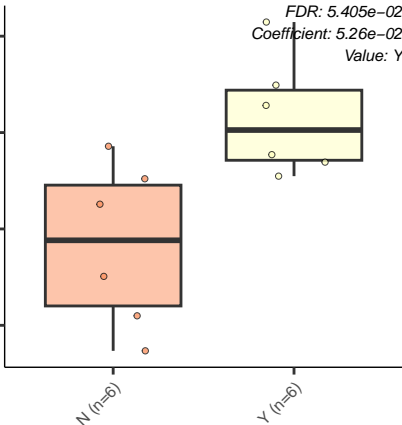
0.35

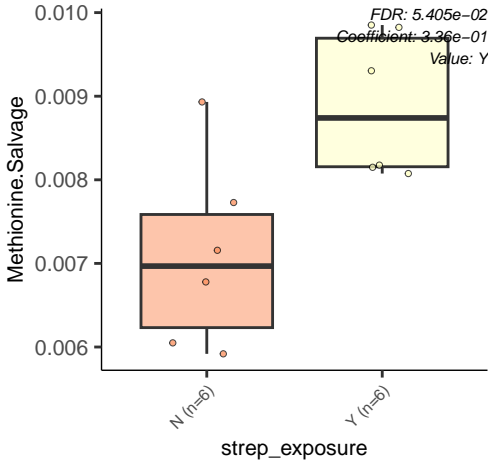
N (n=6)

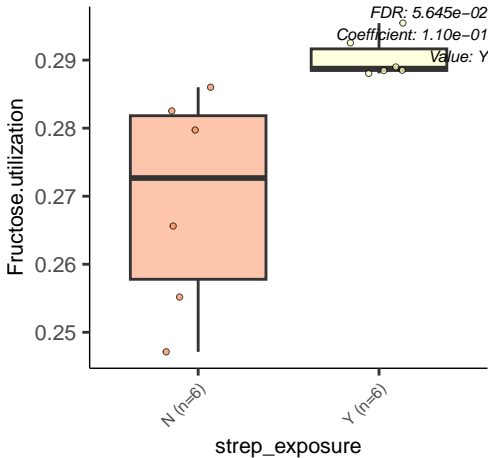
Y (n=6)

strep_exposure

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







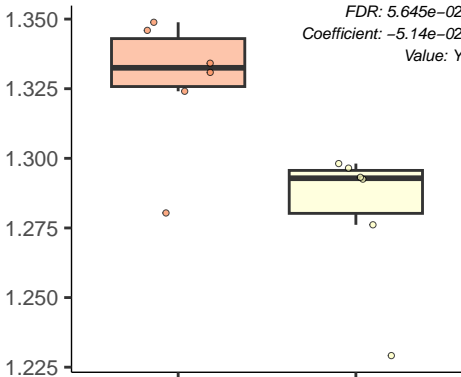
Maltose.and.Maltodextrin.Utilization

FDR: 5.645e-02
Coefficient: -5.14e-02
Value: Y

N (n=6)

Y (n=6)

strep_exposure



General.Secretion.Pathway

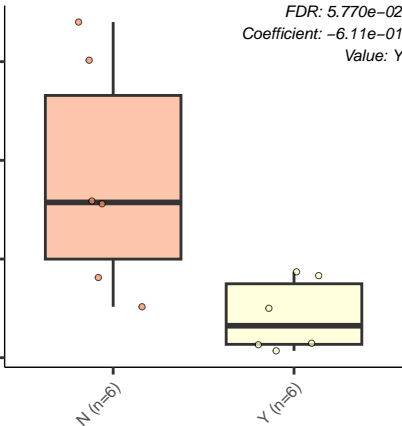
FDR: $5.770e-02$
Coefficient: $-6.11e-01$
Value: Y

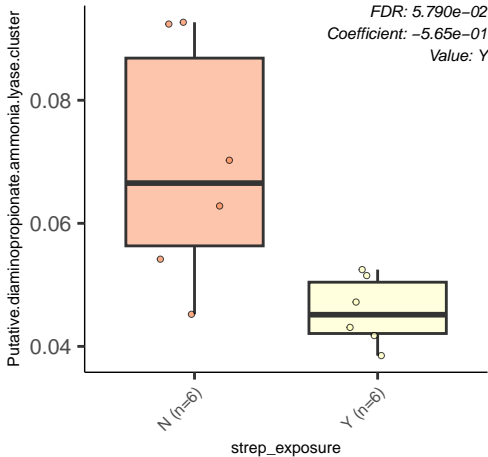
0.10
0.08
0.06
0.04

N (n=6)

Y (n=6)

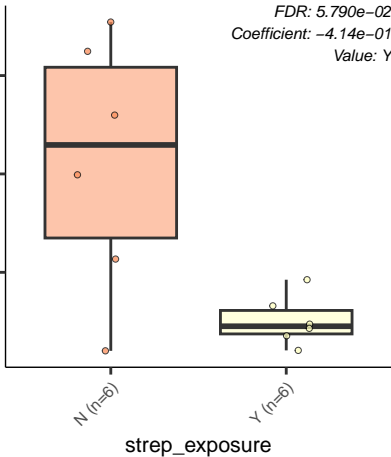
strep_exposure

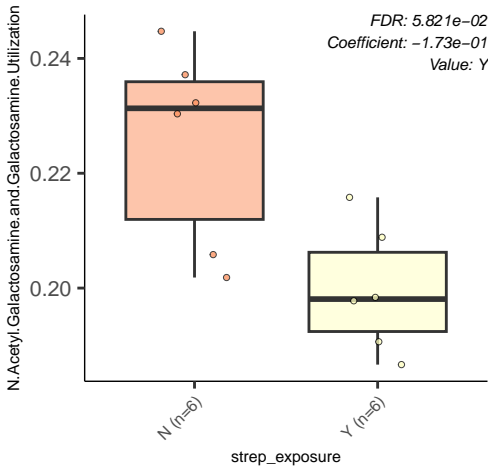




Transposase.in.enterics

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





Rhamnose.containing.glycans

0.62

0.60

0.58

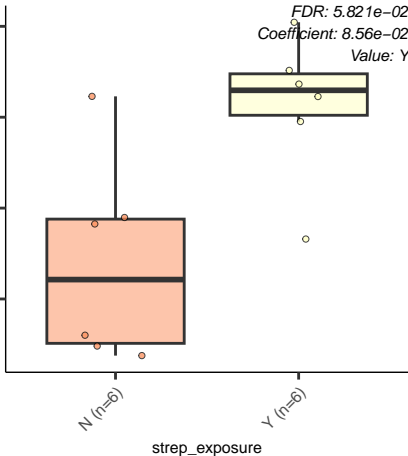
0.56

N (n=6)

Y (n=6)

strep_exposure

FDR: 5.821e-02
Coefficient: 8.56e-02
Value: Y



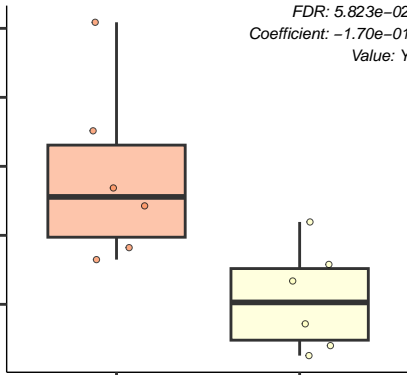
Respiration...Human.gut.microbiome

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

N (n=6)

Y (n=6)

strep_exposure



Homogenitise.pathway.of.aromatic.compound.degradatio

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

0.048

0.044

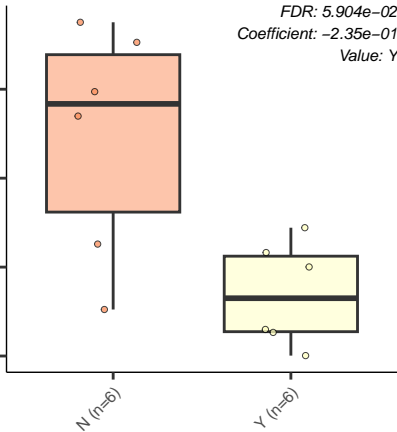
0.040

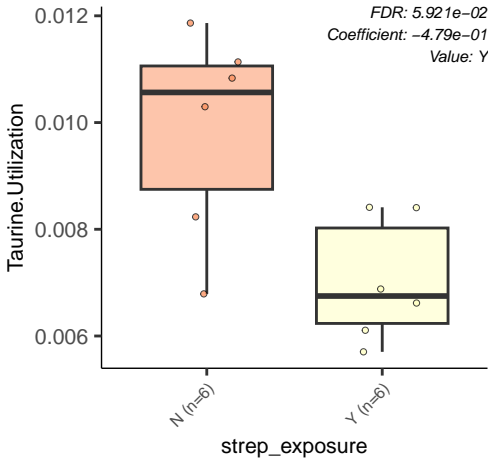
0.036

N (n=6)

Y (n=6)

strep_exposure





Transport.of.Molybdenum

FDR: $5.921e-02$

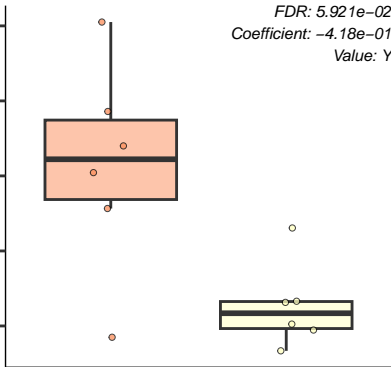
Coefficient: $-4.18e-01$

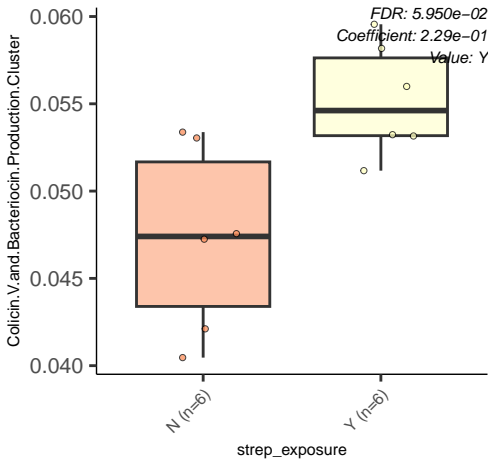
Value: Y

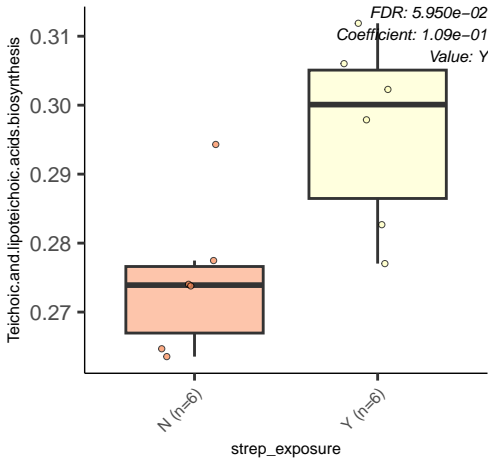
N (n=6)

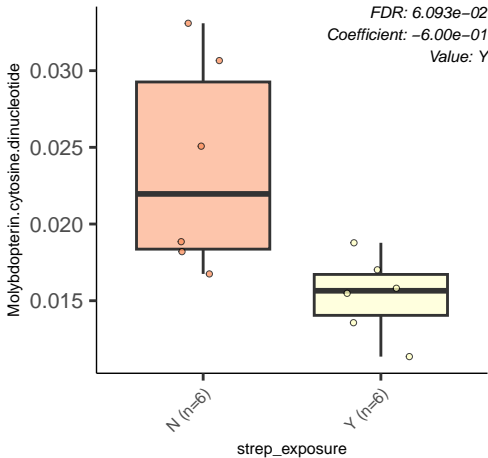
Y (n=6)

strep_exposure



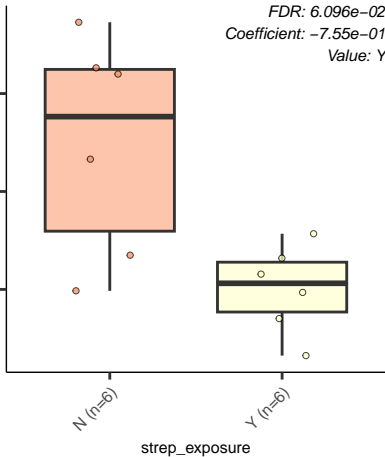






Iron.III..dicitrate.transport.system.Fec

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



Dihydroxyacetone.kinases

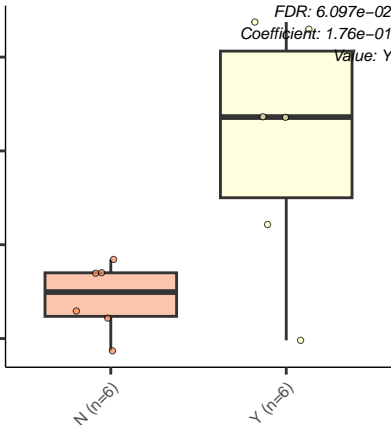
0.075
0.070
0.065
0.060

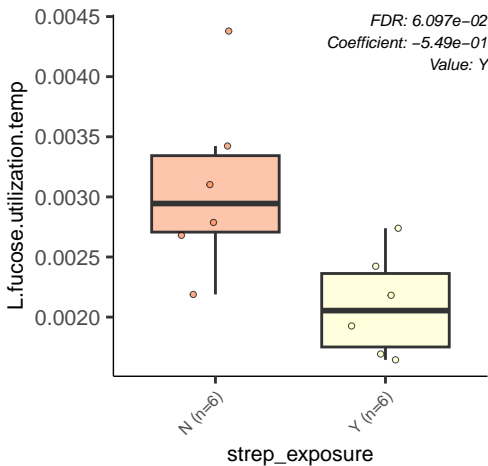
N (n=6)

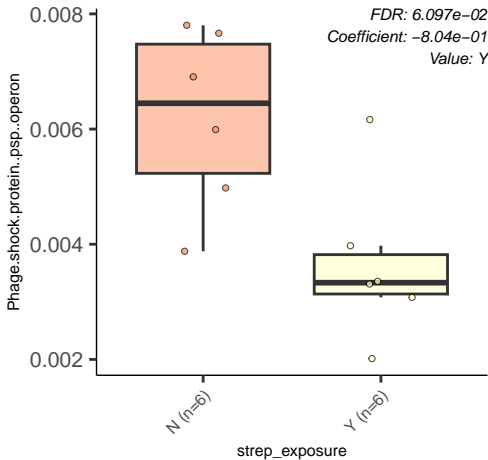
Y (n=6)

strep_exposure

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







Polysaccharide.deacetylases

0.06

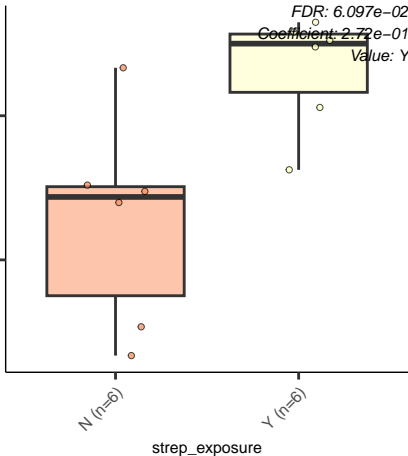
0.05

N (n=6)

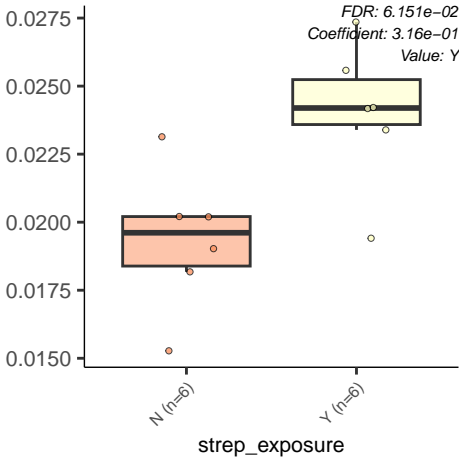
Y (n=6)

strep_exposure

FDR: 6.097e-02
Coefficient: 2.72e-01
Value: Y



Cadmium.resistance



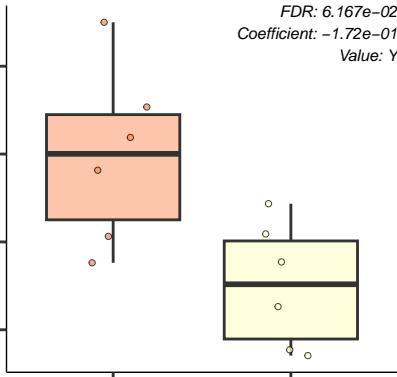
Acetyl-CoA fermentation.to. Butyrate

FDR: 6.167×10^{-2}
Coefficient: -1.72×10^{-1}
Value: Y

N (n=6)

Y (n=6)

strep_exposure



Peptidoglycan.biosynthesis..gjo

0.23

0.22

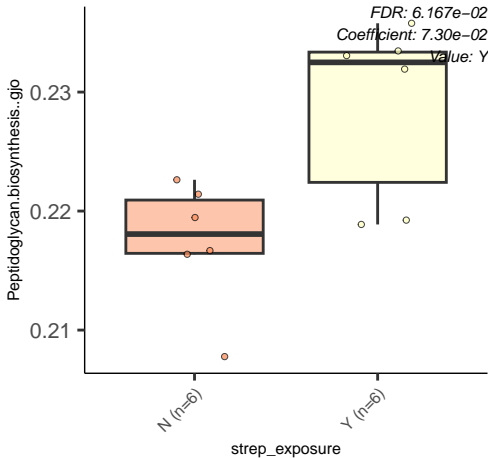
0.21

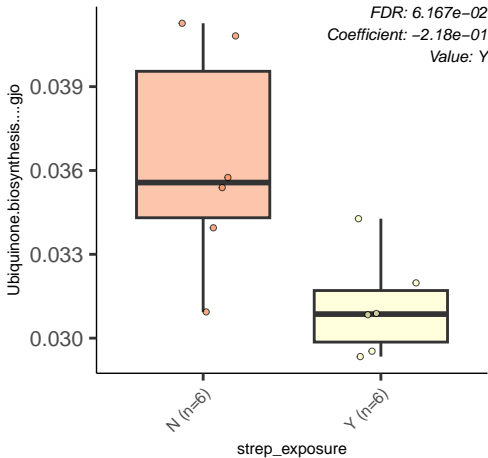
N (n=6)

Y (n=6)

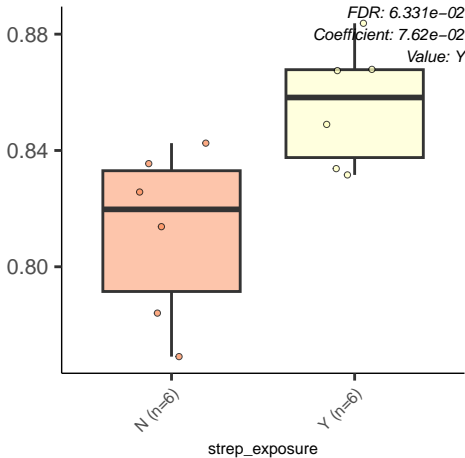
strep_exposure

FDR: 6.167×10^{-2}
Coefficient: 7.30×10^{-2}
Value: Y





De.Novo.Purine.Biosynthesis



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

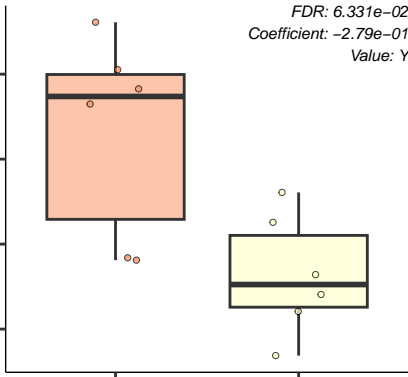
FDR: 6.331e-02
Coefficient: -2.79e-01
Value: Y

N (n=6)

Y (n=6)

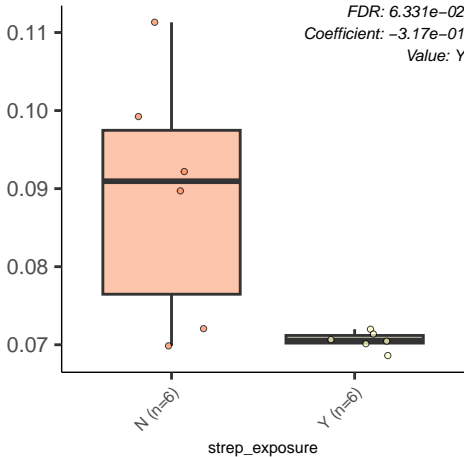
strep_exposure

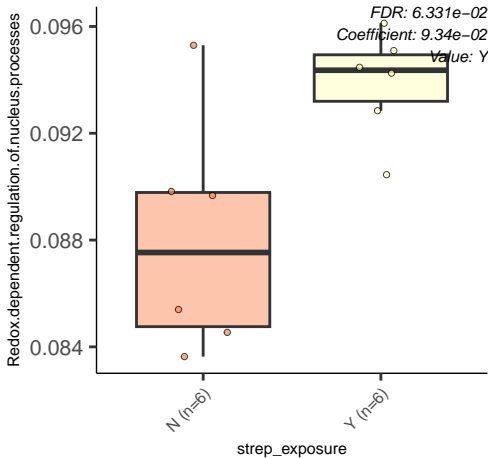
0.10
0.09
0.08
0.07

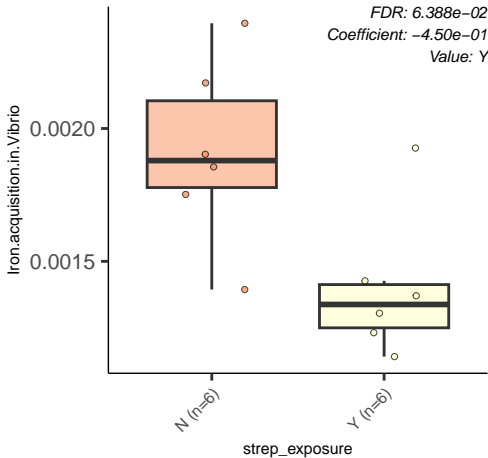


Nitrate.and.nitrite.ammonification

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







Tryptophan.synthesis

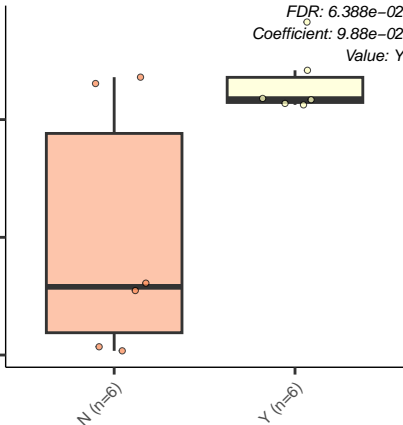
FDR: 6.388e-02
Coefficient: 9.88e-02
Value: Y

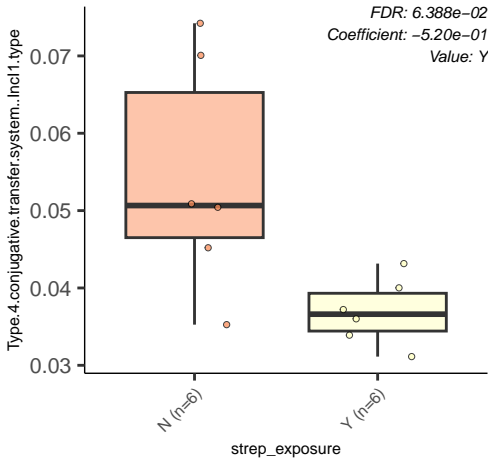
0.40
0.38
0.36

N (n=6)

Y (n=6)

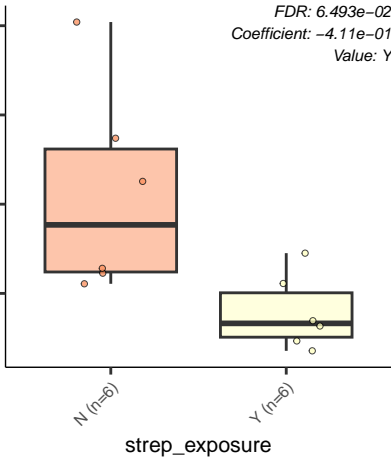
strep_exposure





At2g33980.At1g28960

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



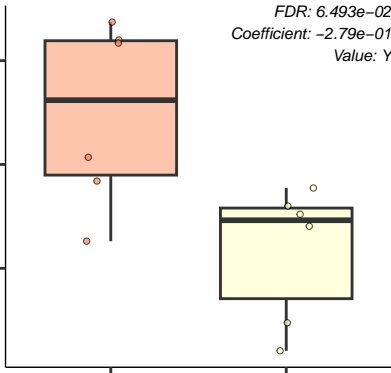
CBSS.320372.3.peg.6046

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

N (n=6)

Y (n=6)

strep_exposure



Osmoprotectant.ABC.transporter.YehZYXW.of.Enterobacter

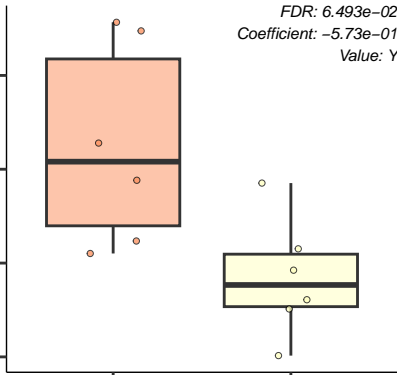
FDR: $6.493e-02$
Coefficient: $-5.73e-01$
Value: Y

N (n=6)

Y (n=6)

strep_exposure

0.010
0.008
0.006
0.004



Ribosome.SSU.bacterial

FDR: $6.493e-02$

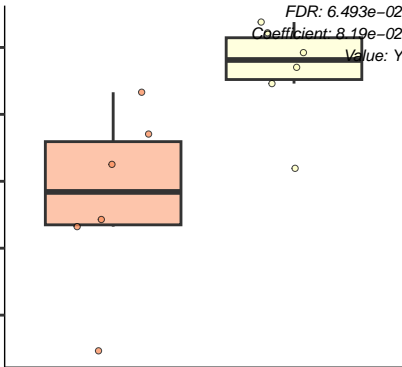
Coefficient: $8.19e-02$

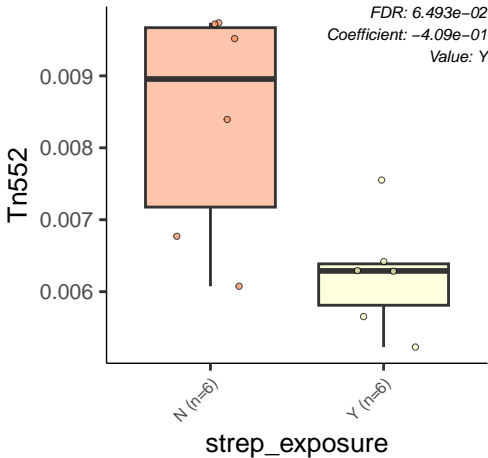
Value: Y

N (n=6)

Y (n=6)

strep_exposure





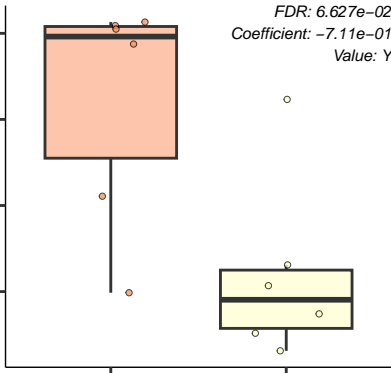
CBSS.502800.3.pcg.2785

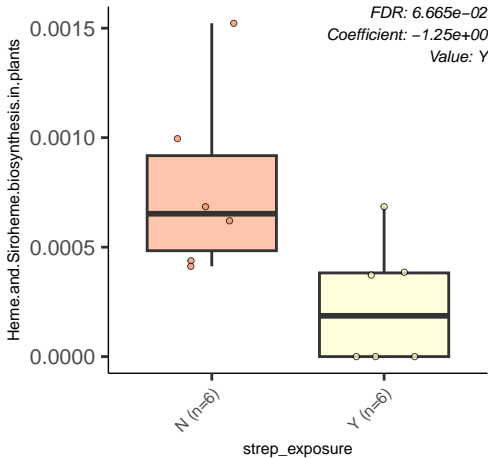
FDR: 6.627e-02
Coefficient: -7.11e-01
Value: Y

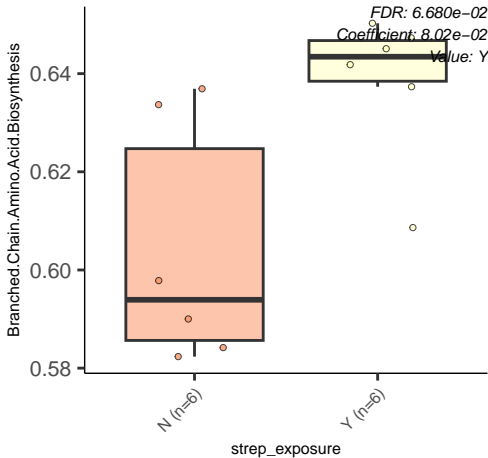
N (n=6)

Y (n=6)

strep_exposure







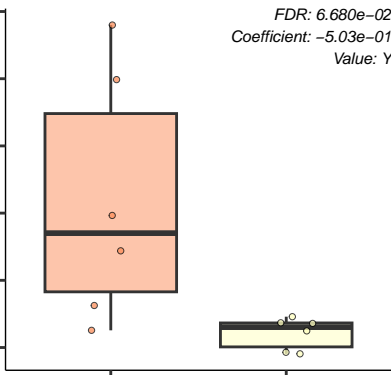
Siderophore.assembly.kit

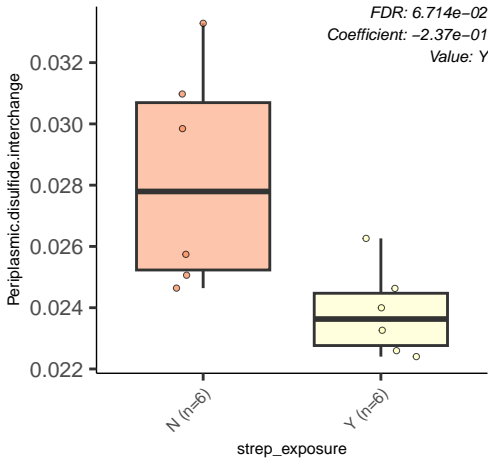
FDR: 6.680e-02
Coefficient: -5.03e-01
Value: Y

N (n=6)

Y (n=6)

strep_exposure





Phage.head.and.packaging

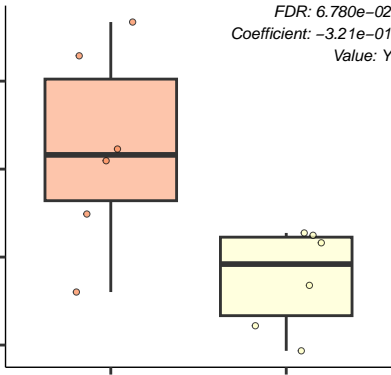
FDR: 6.780e-02
Coefficient: -3.21e-01
Value: Y

0.040
0.035
0.030
0.025

N (n=6)

Y (n=6)

strep_exposure



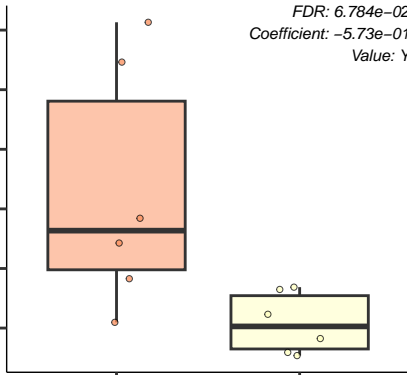
Type.1.pili..mannose.sensitive.fimbriae.

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

N (n=6)

Y (n=6)

strep_exposure



CBSS.216592.1.peg.3534

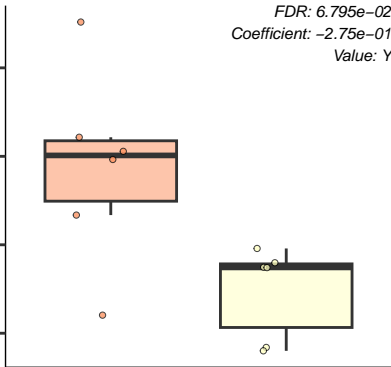
FDR: $6.795e-02$
Coefficient: $-2.75e-01$
Value: Y

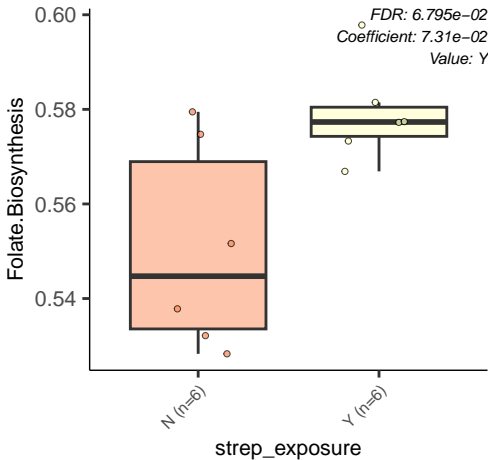
0.018
0.016
0.014
0.012

N (n=6)

Y (n=6)

strep_exposure





Proteolysis.in.bacteria..ATP.dependent

0.54

0.52

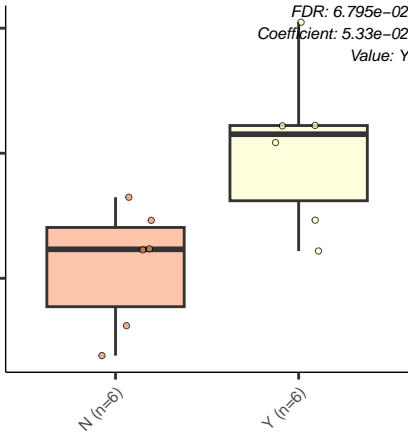
0.50

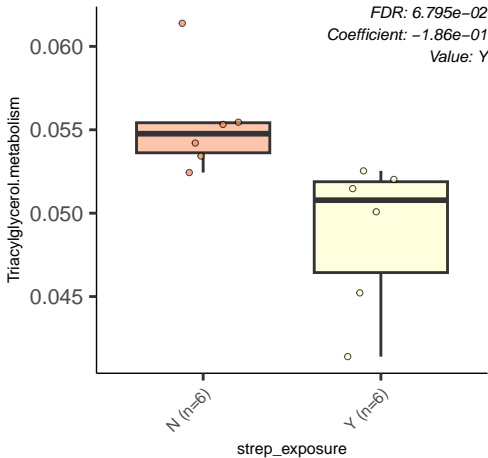
N (n=6)

Y (n=6)

strep_exposure

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





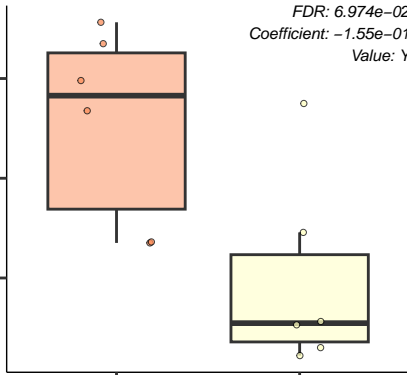
Proline..4.hydroxyproline.uptake.and.utilization

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

N (n=6)

Y (n=6)

strep_exposure



CoenzymeM.Archaea

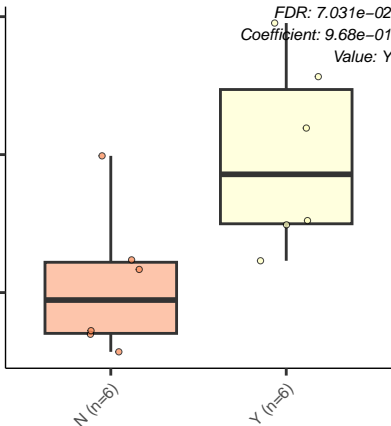
0.003
0.002
0.001

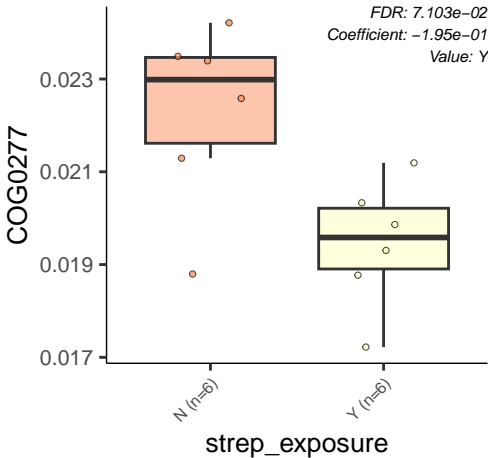
N (n=6)

Y (n=6)

strep_exposure

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





DNA.Repair.Base.Excision

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

0.44

0.43

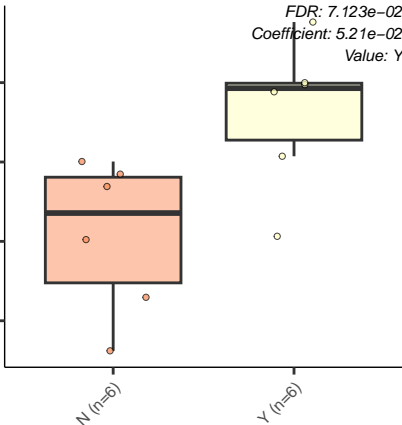
0.42

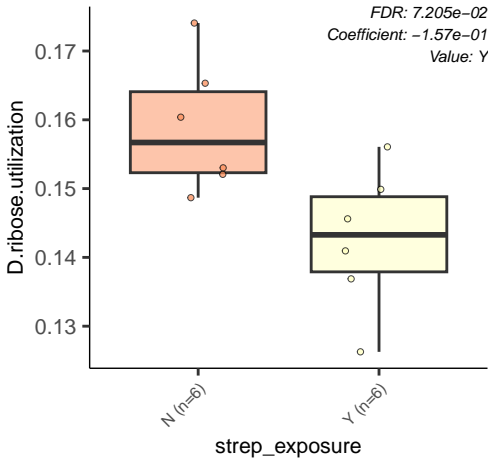
0.41

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

N (n=6)

Y (n=6)

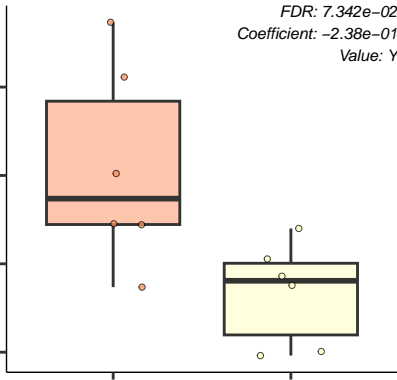
strep_exposure

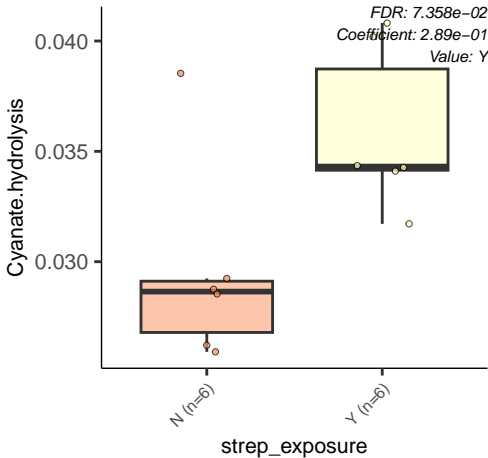
0.050

0.045

0.040

0.035





CLO.thiaminPP.biosynthesis

0.069

0.066

0.063

0.060

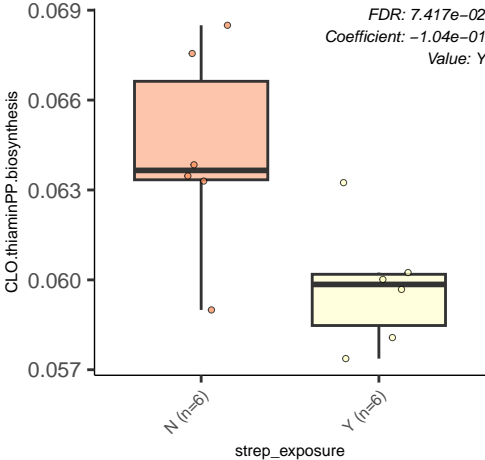
0.057

N (n=6)

Y (n=6)

strep_exposure

FDR: $7.417e-02$
Coefficient: $-1.04e-01$
Value: Y



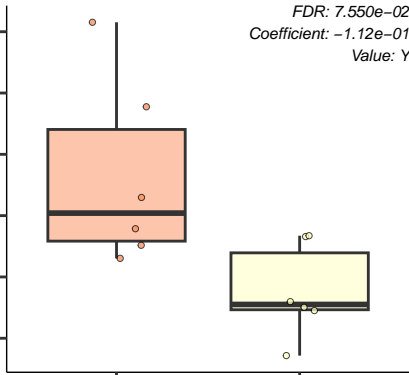
Lacto.N.Biose.l.and.Galacto.N.Biose.Metabolic.Pathway

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

N (n=6)

Y (n=6)

strep_exposure

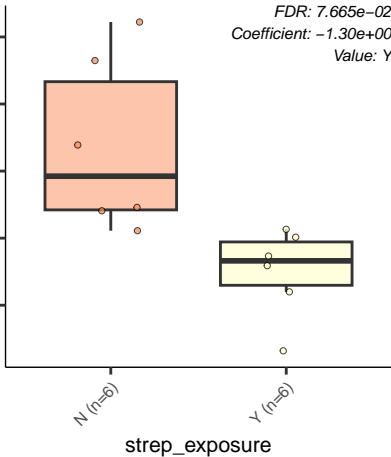


X..945..Fimbriae

FDR: 7.665e-02

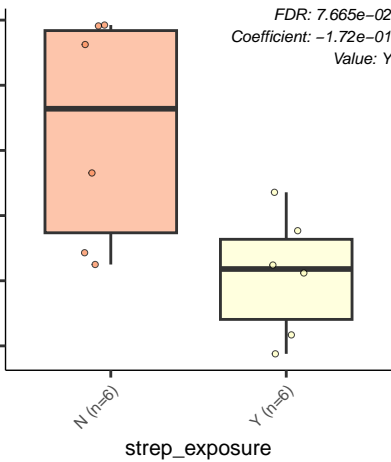
Coefficient: -1.30e+00

Value: Y

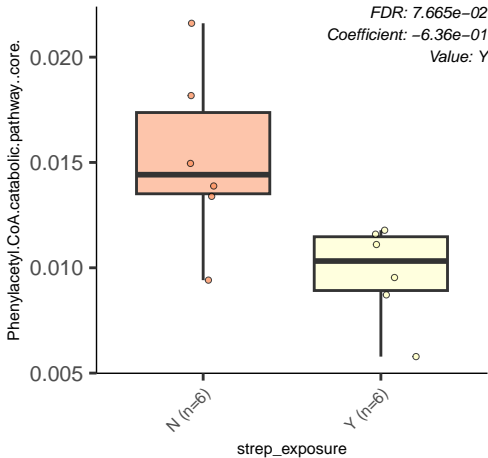


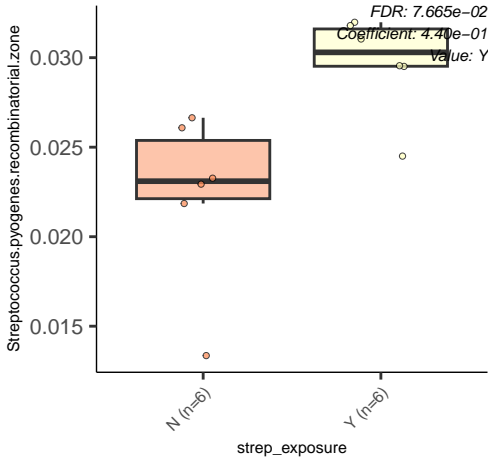
Ethanolamine.utilization

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



strep_exposure





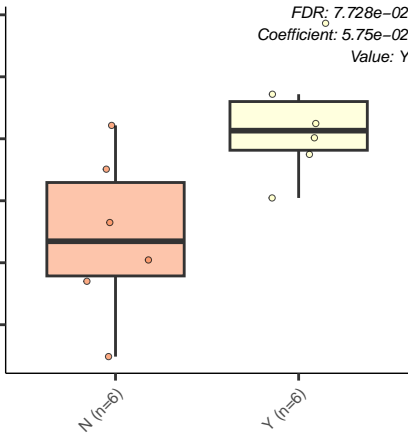
Threonine.and.Homoserine.Biosynthesis

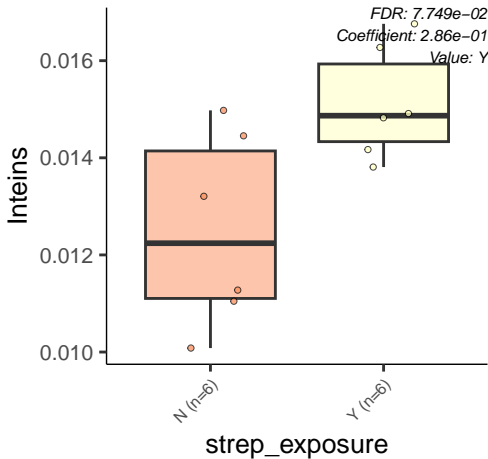
FDR: 7.728e-02
Coefficient: 5.75e-02
Value: Y

N (n=6)

Y (n=6)

strep_exposure





Bacterial.Chemotaxis

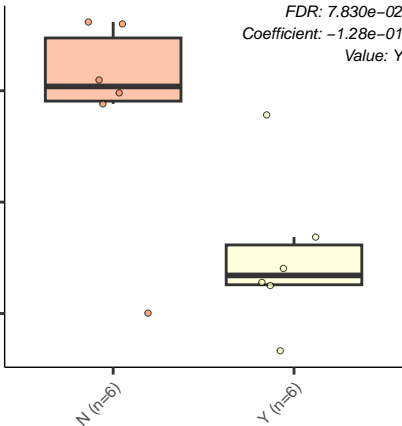
FDR: $7.830e-02$
Coefficient: $-1.28e-01$
Value: Y

0.16
0.15
0.14

N (n=6)

Y (n=6)

strep_exposure



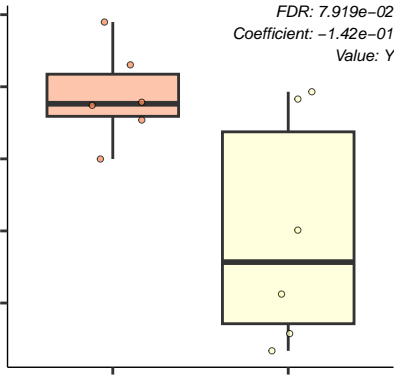
Heme.biosynthesis.orphans

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

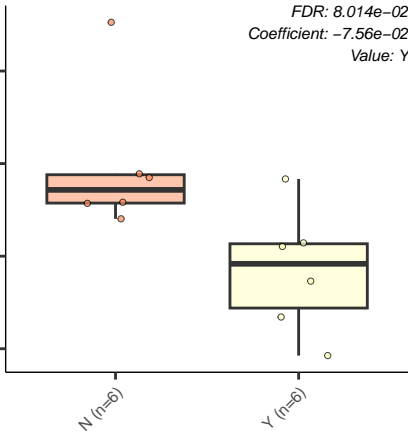
0.21

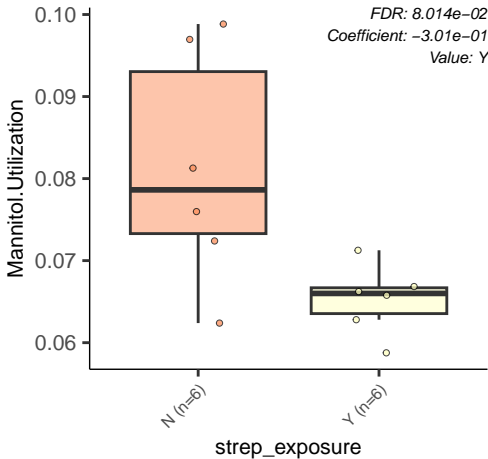
0.20

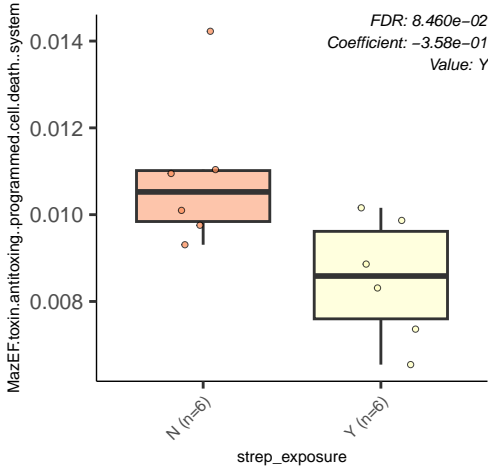
N (n=6)

Y (n=6)

strep_exposure







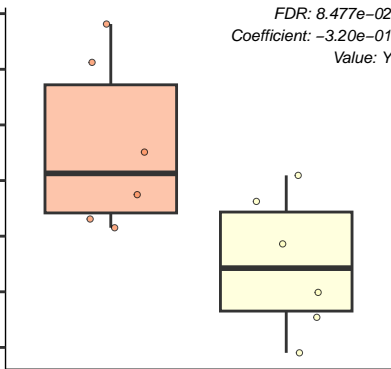
Quinone.disambuigation

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

N (n=6)

Y (n=6)

strep_exposure



DNA.phosphorothioation

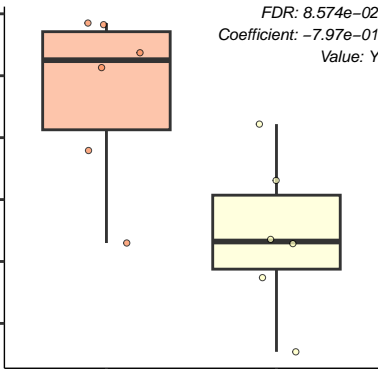
0.0035
0.0030
0.0025
0.0020
0.0015
0.0010

N (n=6)

Y (n=6)

strep_exposure

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



Fatty Acid Biosynthesis.FASII

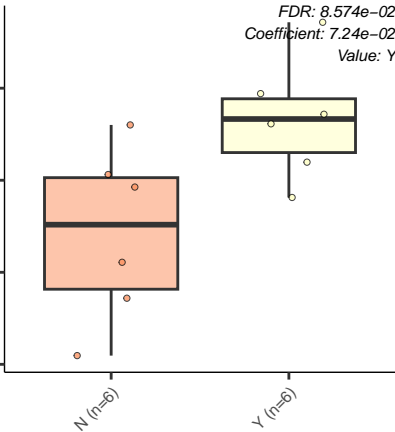
FDR: 8.574e-02
Coefficient: 7.24e-02
Value: Y

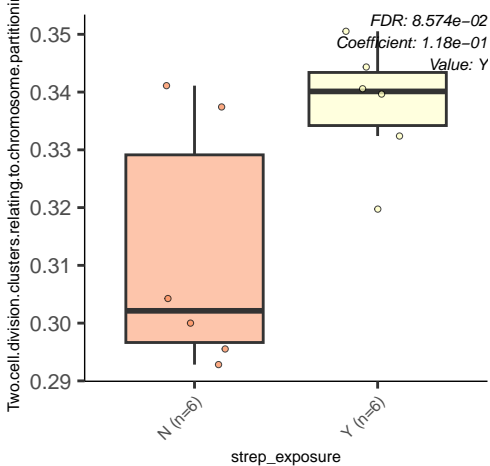
0.650
0.625
0.600
0.575

N (n=6)

Y (n=6)

strep_exposure





Type.VI.secretion.systems

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

0.12

0.10

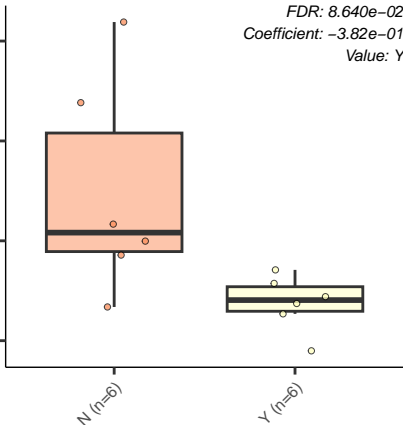
0.08

0.06

N (n=6)

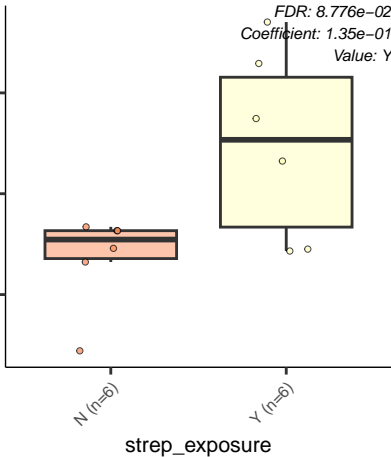
Y (n=6)

strep_exposure



CBSS.257314.1.peg.488

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



CBSS.342610.3.peg.1536

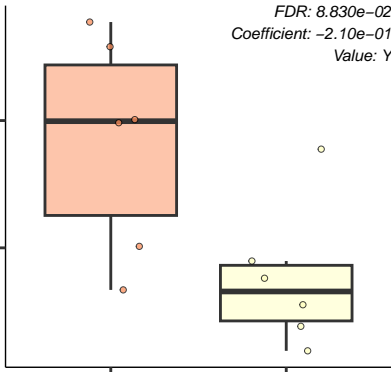
FDR: 8.830e-02
Coefficient: -2.10e-01
Value: Y

0.040
0.035

N (n=6)

Y (n=6)

strep_exposure



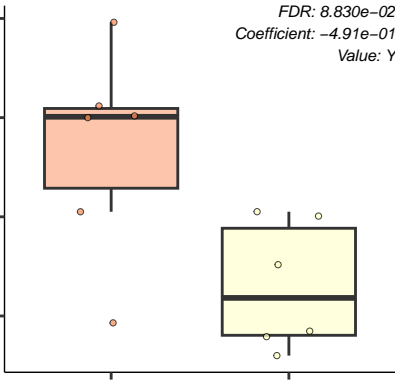
Pterin.carbinolamine.dehydratase

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

N (n=6)

Y (n=6)

strep_exposure



Colanic.acid.biosynthesis

0.11

0.10

0.09

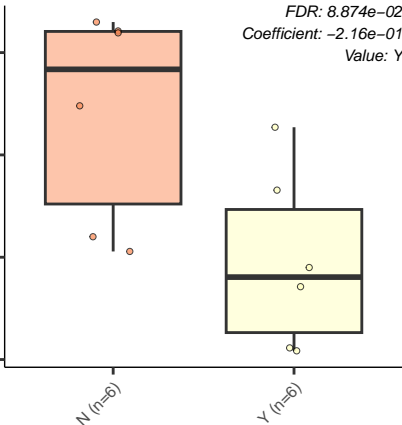
0.08

N (n=6)

Y (n=6)

strep_exposure

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



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

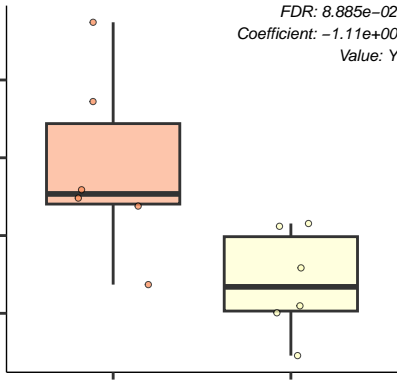
FDR: $8.885e-02$
Coefficient: $-1.11e+00$
Value: Y

0.004
0.003
0.002
0.001

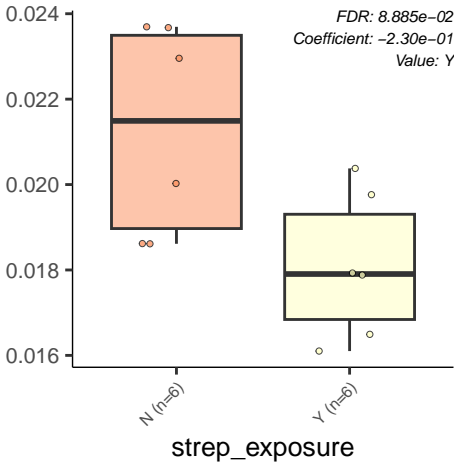
N (n=6)

Y (n=6)

strep_exposure

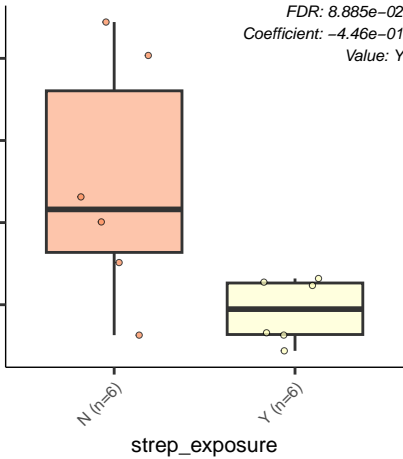


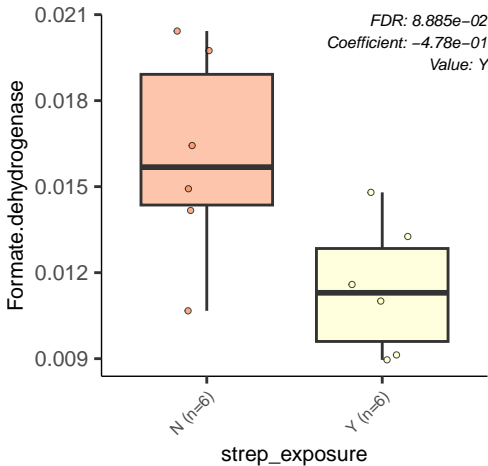
At1g14345



CBSS.216592.1.peg.3937

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





Inorganic.Sulfur.Assimilation

FDR: 8.885e-02
Coefficient: -2.52e-01
Value: Y

0.060

0.055

0.050

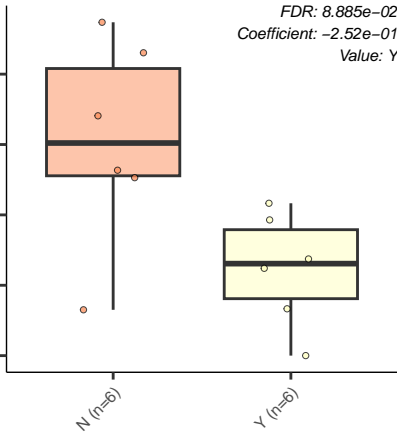
0.045

0.040

N (n=6)

Y (n=6)

strep_exposure



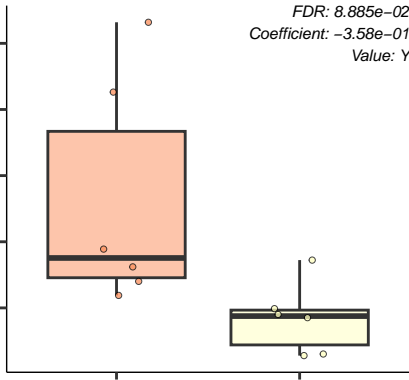
L.ascorbate.utilization..and.related.gene.clusters.

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

N (n=6)

Y (n=6)

strep_exposure



Polyadenylation.bacterial

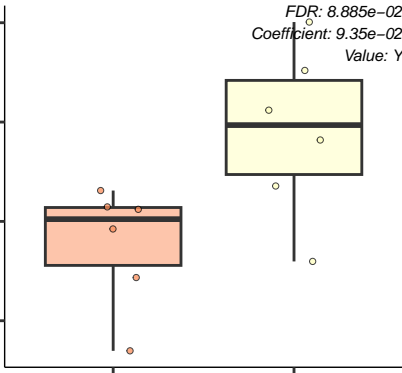
0.19
0.18
0.17
0.16

N (n=6)

Y (n=6)

strep_exposure

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



Putative.oxidase.COG2907

0.025

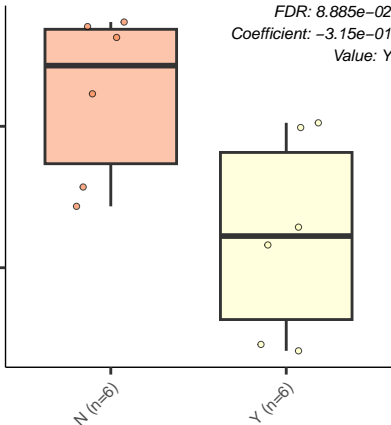
0.020

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

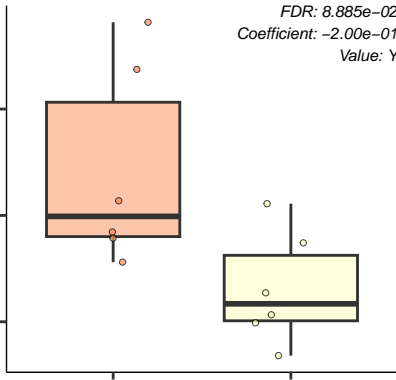
0.040

0.035

N (n=6)

Y (n=6)

strep_exposure



Siderophore.Aerobactin

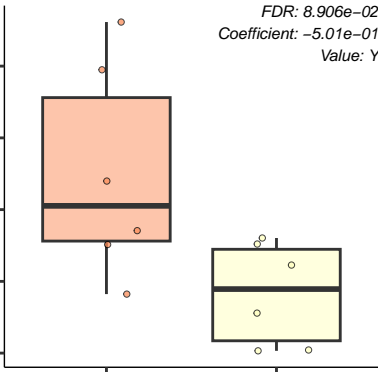
FDR: 8.906e-02
Coefficient: -5.01e-01
Value: Y

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

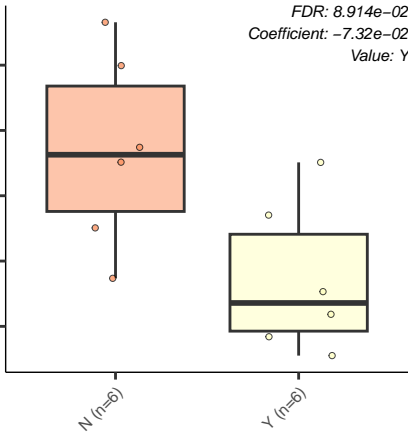
FDR: $8.914e-02$
Coefficient: $-7.32e-02$
Value: Y

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

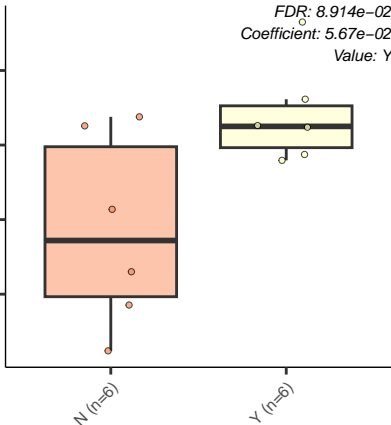
0.195

0.190

N (n=6)

Y (n=6)

strep_exposure



Bacterial.Cytoskeleton

0.50

0.48

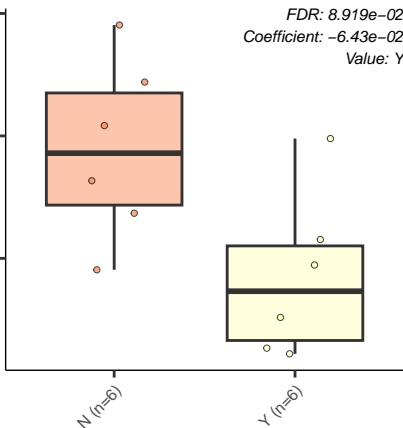
0.46

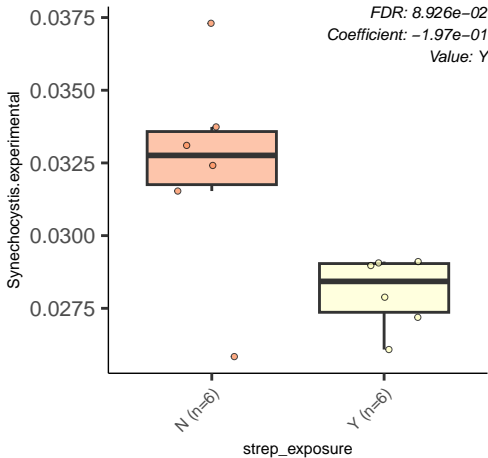
N (n=6)

Y (n=6)

strep_exposure

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





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

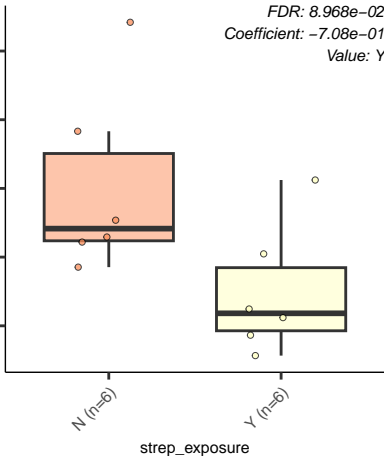
0.0010

N (n=6)

Y (n=6)

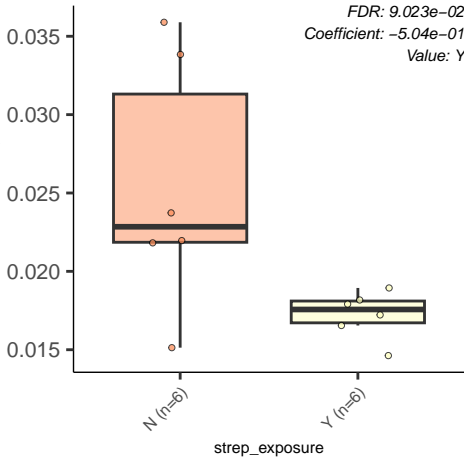
strep_exposure

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

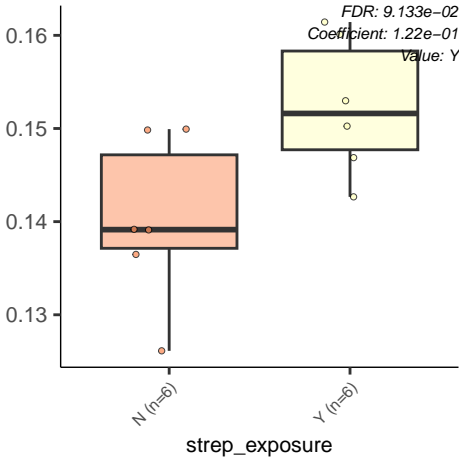


Cluster.Ytf.and.putative.sugar.transporter

FDR: $9.023e-02$
Coefficient: $-5.04e-01$
Value: Y



tRNA.aminoacylation..Arg

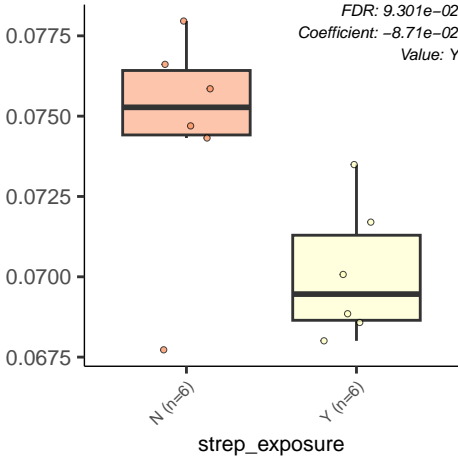


Butanol.Biosynthesis

FDR: $9.301e-02$

Coefficient: $-8.71e-02$

Value: Y



Nitric.oxide.synthase

0.003

0.002

0.001

N (n=6)

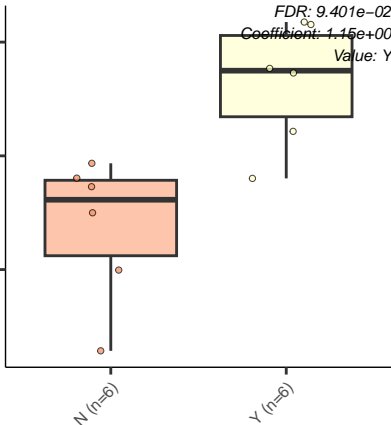
Y (n=6)

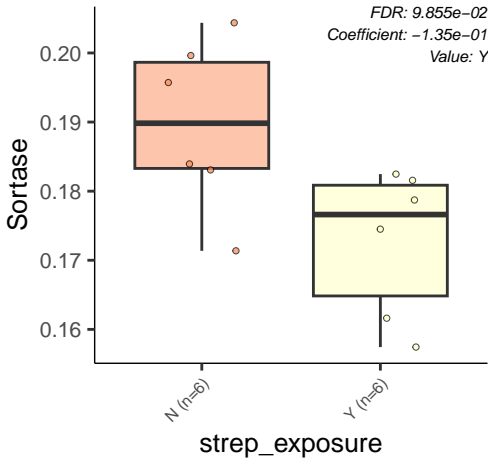
strep_exposure

FDR: $9.401e-02$

Coefficient: $1.15e+00$

Value: Y





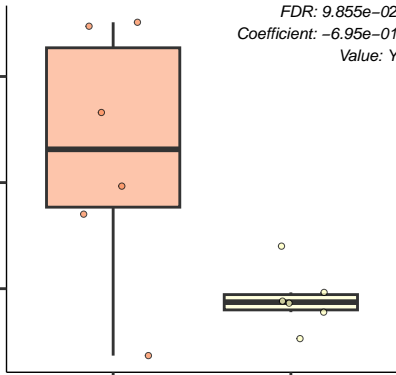
YjbEFGH.Locus.Involved.in.Exopolysaccharide.Production

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

N (n=6)

Y (n=6)

strep_exposure



tRNA.aminoacylation..Thr

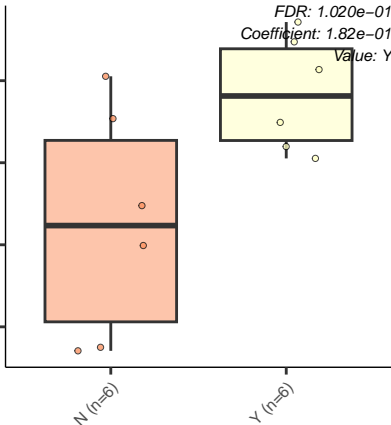
0.070
0.065
0.060
0.055

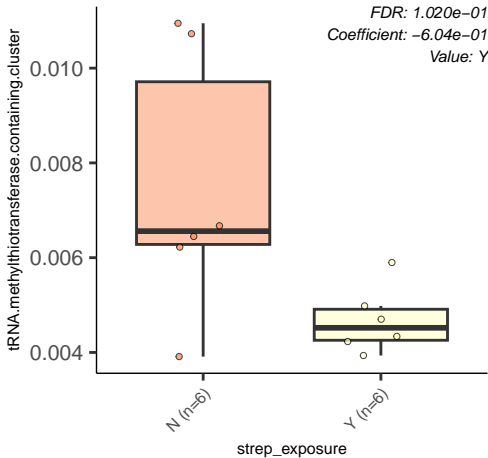
N (n=6)

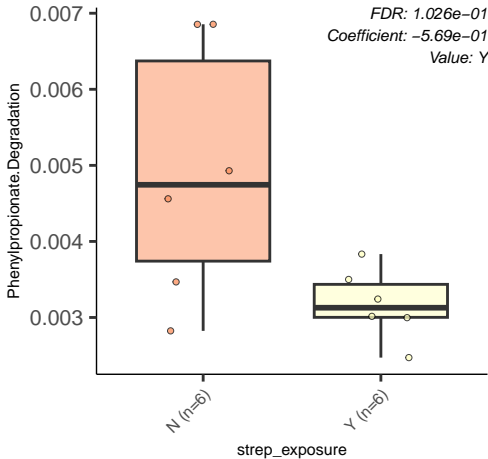
Y (n=6)

strep_exposure

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







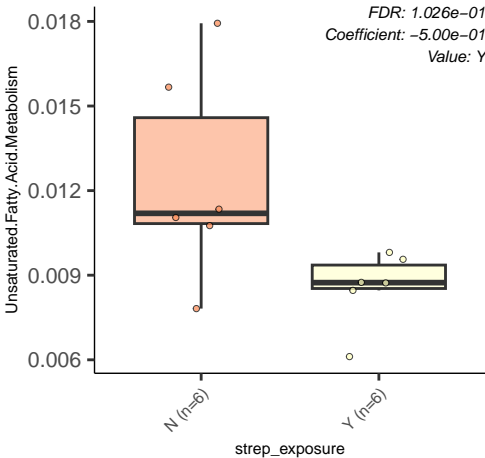
Unsaturated.Fatty.Acid.Metabolism

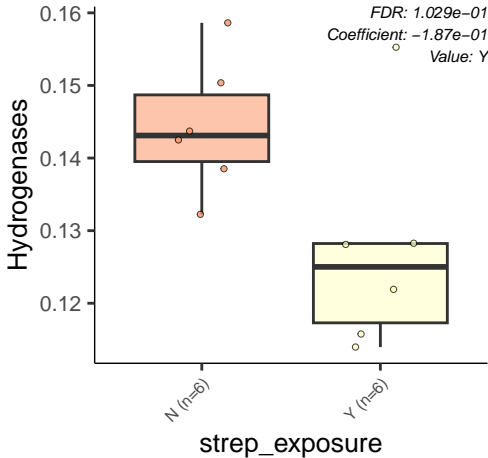
FDR: 1.026e-01
Coefficient: -5.00e-01
Value: Y

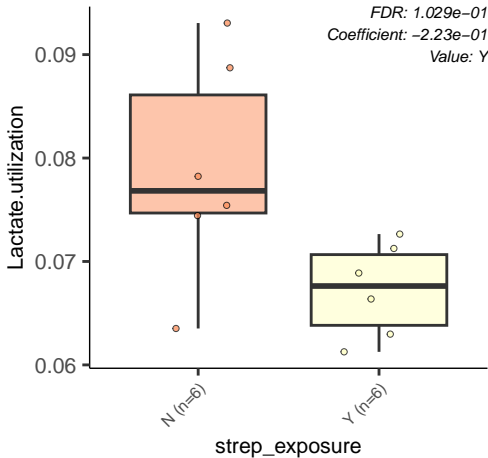
N (n=6)

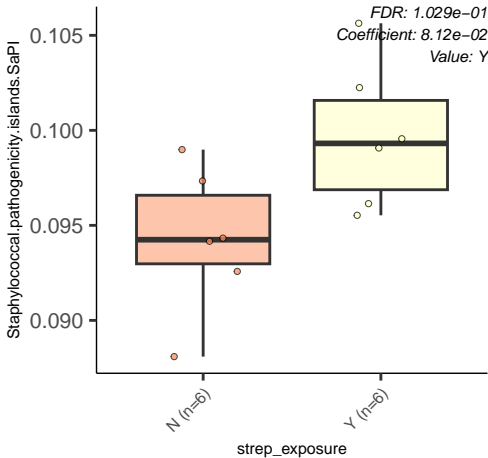
Y (n=6)

strep_exposure



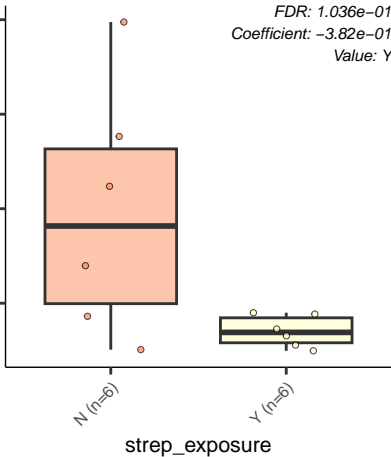


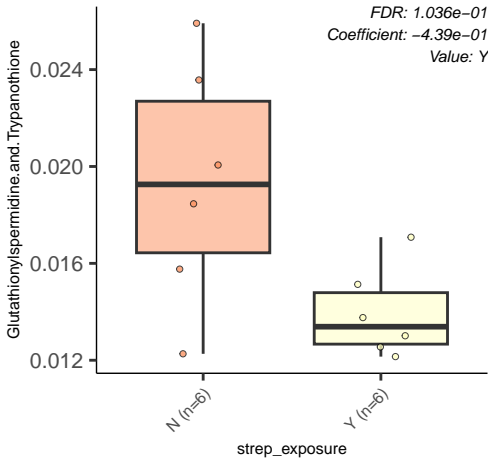


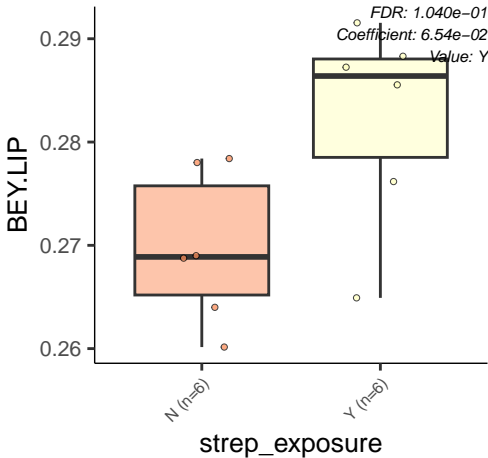


CBSS.316407.3.peg.1371

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







Phage.capsid.proteins

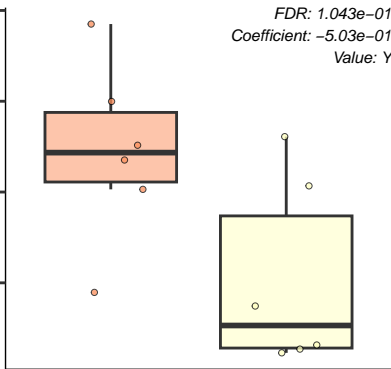
0.013
0.011
0.009
0.007

FDR: 1.043e-01
Coefficient: -5.03e-01
Value: Y

N (n=6)

Y (n=6)

strep_exposure



Fatty acid.degradation.regulons

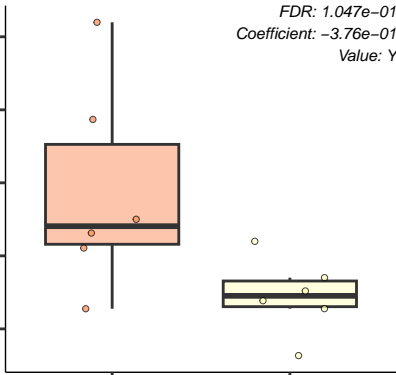
0.040
0.035
0.030
0.025
0.020

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

N (n=6)

Y (n=6)

strep_exposure



Proton.dependent.Peptide.Transporters

0.070

0.065

0.060

0.055

0.050

N (n=6)

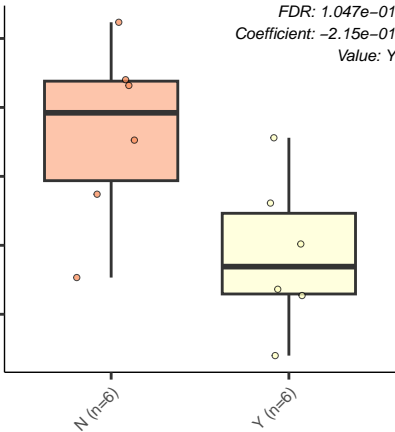
Y (n=6)

strep_exposure

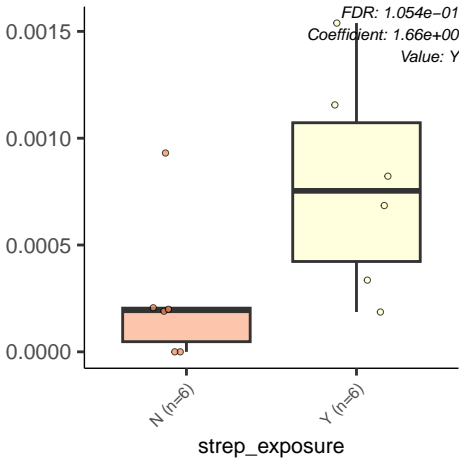
FDR: 1.047e-01

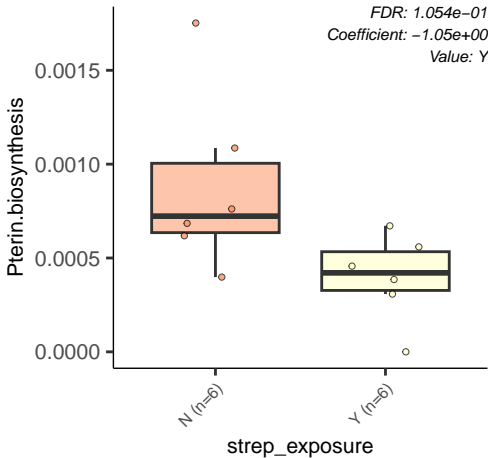
Coefficient: -2.15e-01

Value: Y

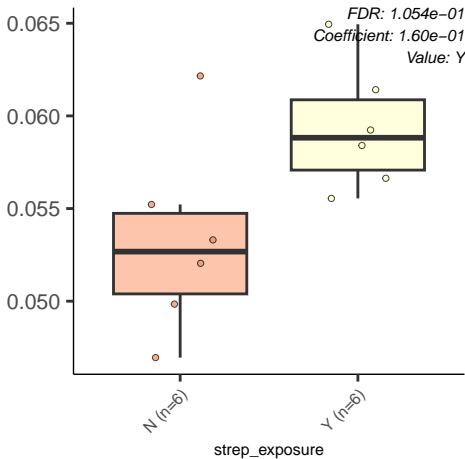


Phenazine.biosynthesis



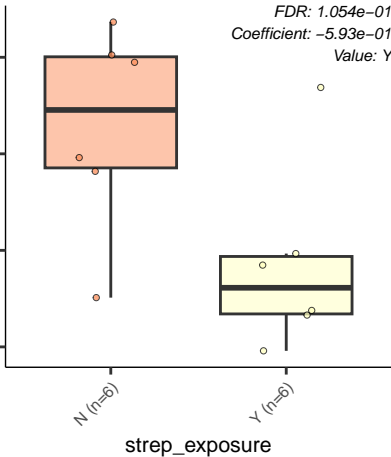


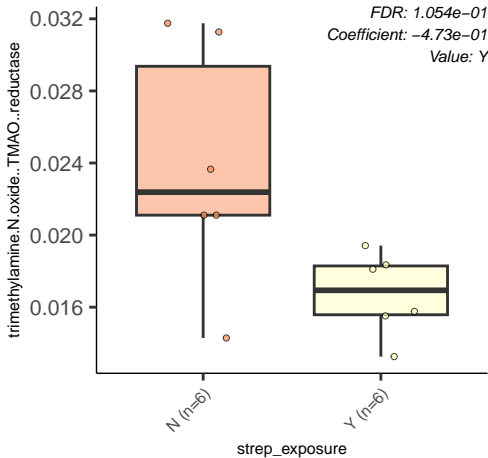
Transport of Nickel and Cobalt



rRNA.modification.Archaea

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





tRNA.aminoacylation..Val

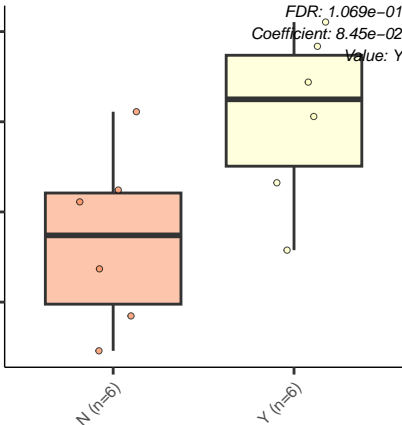
0.25
0.24
0.23
0.22

N (n=6)

Y (n=6)

strep_exposure

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



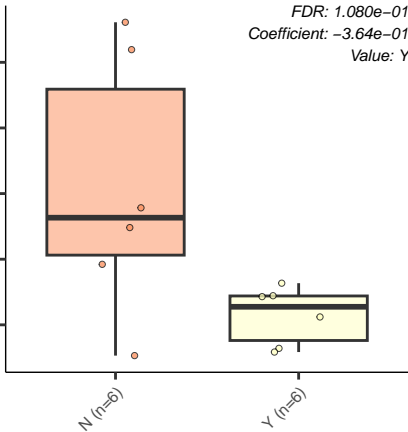
Lipopolysaccharide.assembly

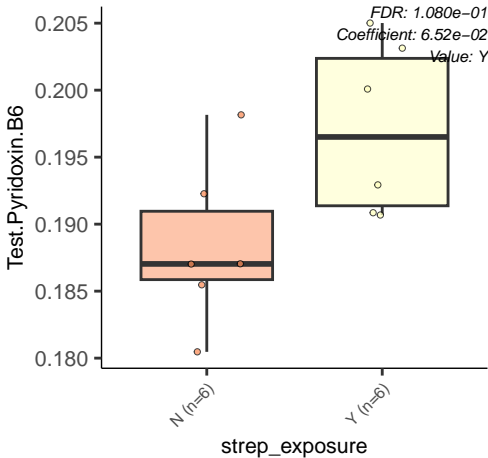
FDR: 1.080e-01
Coefficient: -3.64e-01
Value: Y

N (n=6)

Y (n=6)

strep_exposure





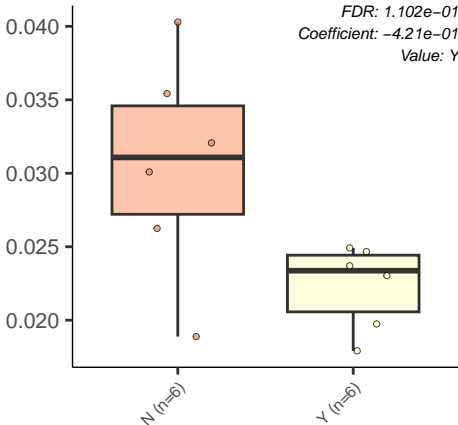
Pyrimidine.utilization

FDR: 1.102e-01
Coefficient: -4.21e-01
Value: Y

N (n=6)

Y (n=6)

strep_exposure



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

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

N (n=6)

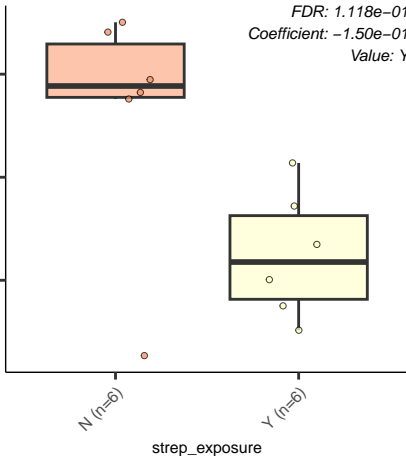
Y (n=6)

strep_exposure

0.28

0.26

0.24



CBSS.326442.4.peg.1852

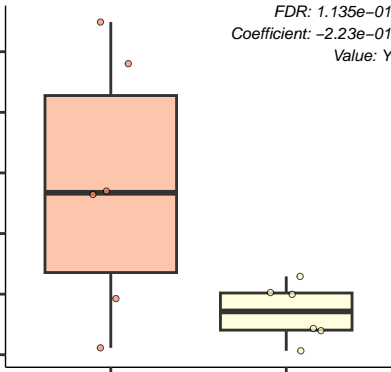
FDR: 1.135e-01
Coefficient: -2.23e-01
Value: Y

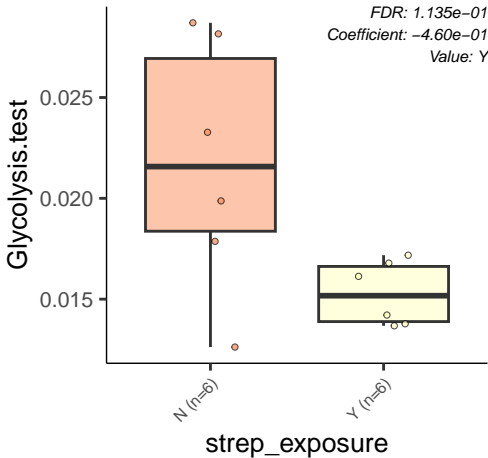
0.080
0.075
0.070
0.065
0.060
0.055

N (n=6)

Y (n=6)

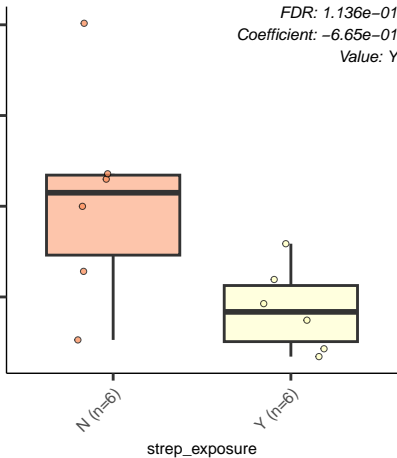
strep_exposure





Multiple.Antibiotic.Resistance.MAR.locus

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



Phage.tail.fiber.proteins

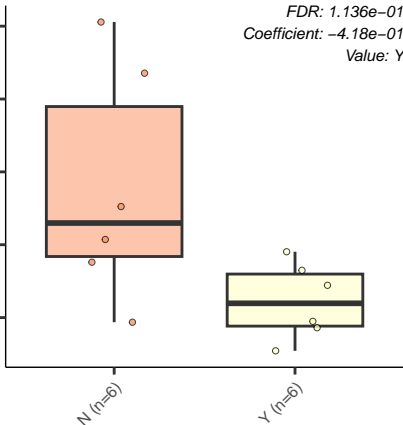
FDR: 1.136e-01
Coefficient: -4.18e-01
Value: Y

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

0.048

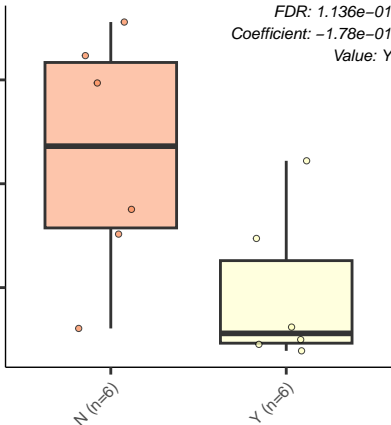
0.044

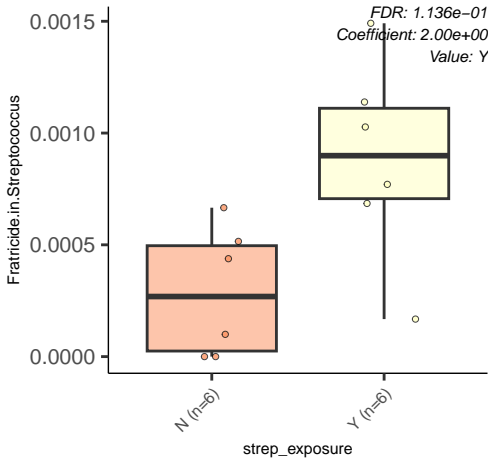
0.040

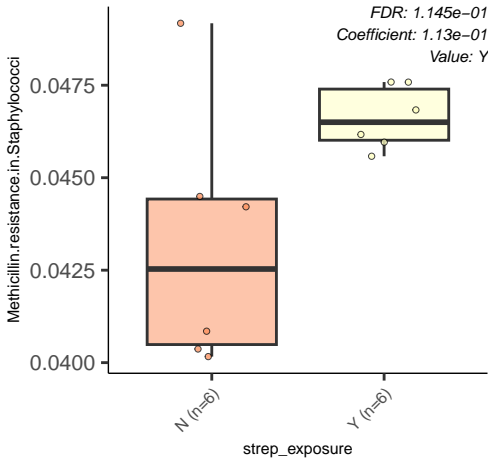
N (n=6)

Y (n=6)

strep_exposure







CBSS.211586.1.peg.2357

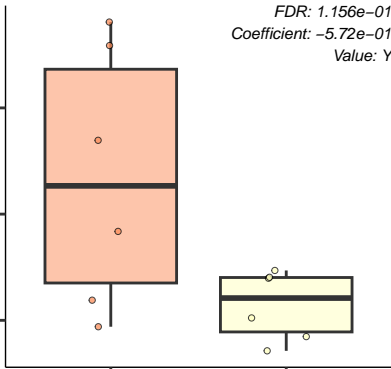
FDR: 1.156e-01
Coefficient: -5.72e-01
Value: Y

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

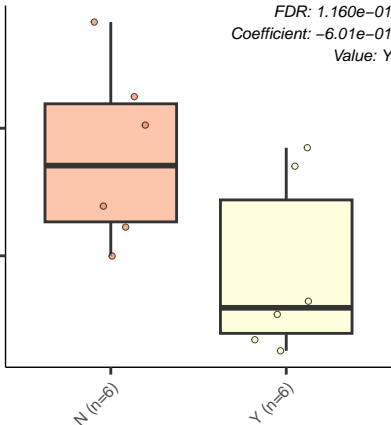
0.003

0.002

N (n=6)

Y (n=6)

strep_exposure



Bacitracin.Stress.Response

0.05

0.06

0.07

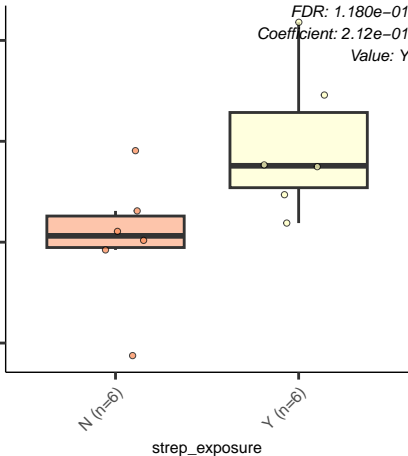
0.08

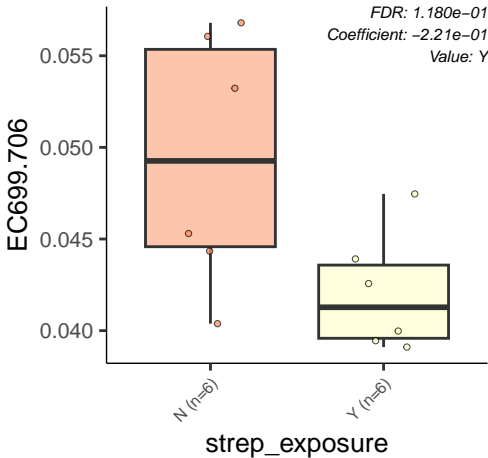
N (n=6)

Y (n=6)

strep_exposure

FDR: 1.180e-01
Coefficient: 2.12e-01
Value: Y





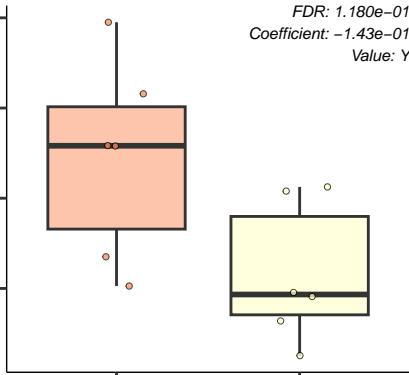
Lipid.A.Ara4N.pathway...Polymyxin.resistance..

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

N (n=6)

Y (n=6)

strep_exposure



Biofilm.Adhesin.Biosynthesis

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

0.025

0.020

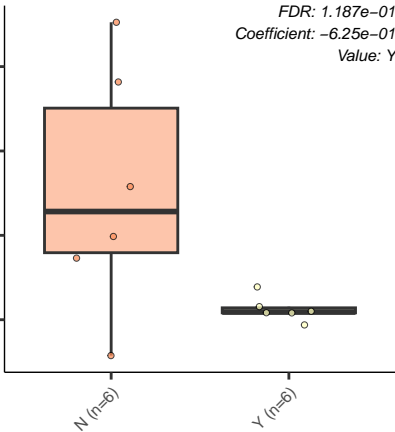
0.015

0.010

N (n=6)

Y (n=6)

strep_exposure



Beta.Glucoside.Metabolism

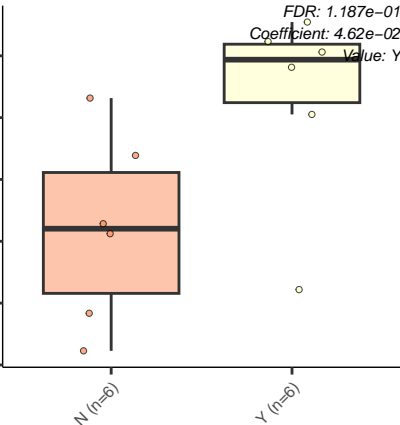
0.68
0.67
0.66
0.65
0.64
0.63

N (n=6)

Y (n=6)

strep_exposure

FDR: 1.187e-01
Coefficient: 4.62e-02
Value: Y



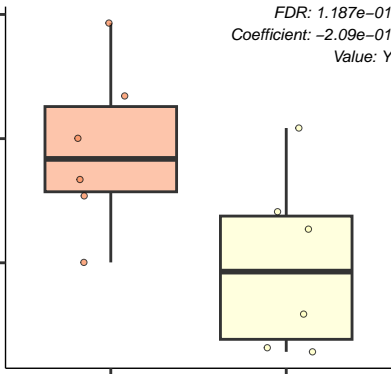
Propanediol.utilization

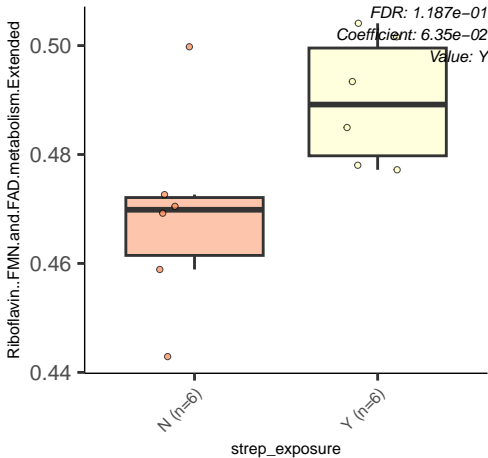
FDR: 1.187e-01
Coefficient: -2.09e-01
Value: Y

N (n=6)

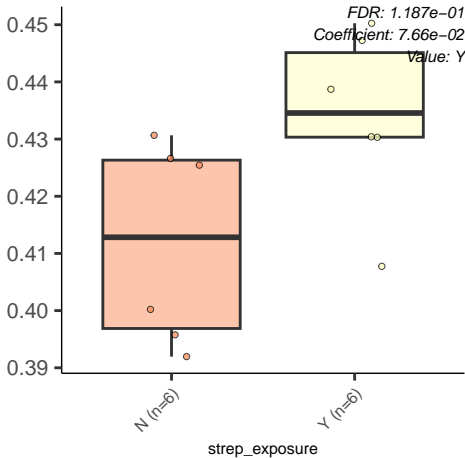
Y (n=6)

strep_exposure

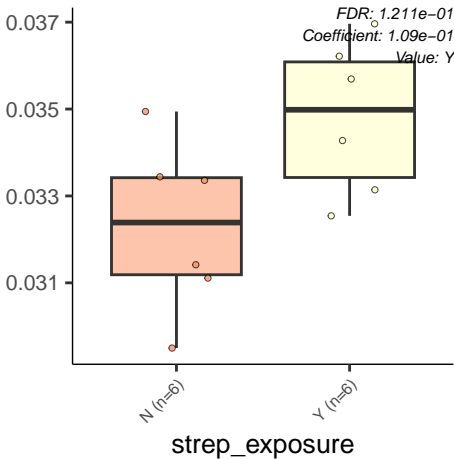


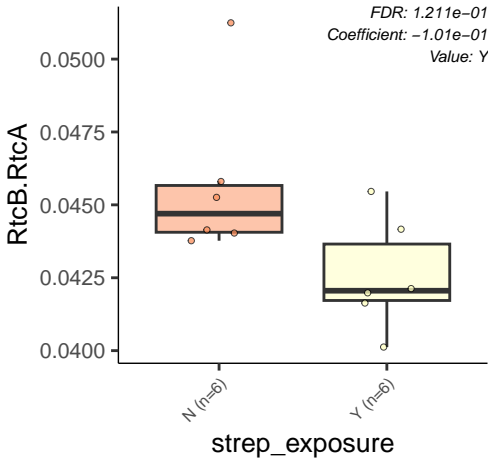


Ribosome.biogenesis.bacterial



At1g21350





TenI.like.tautomerase

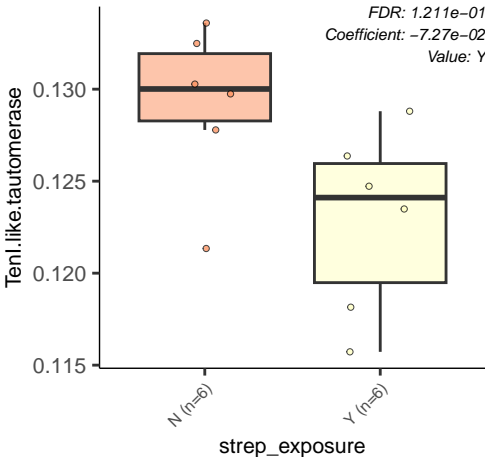
FDR: 1.211e-01
Coefficient: -7.27e-02
Value: Y

0.130
0.125
0.120
0.115

N (n=6)

Y (n=6)

strep_exposure



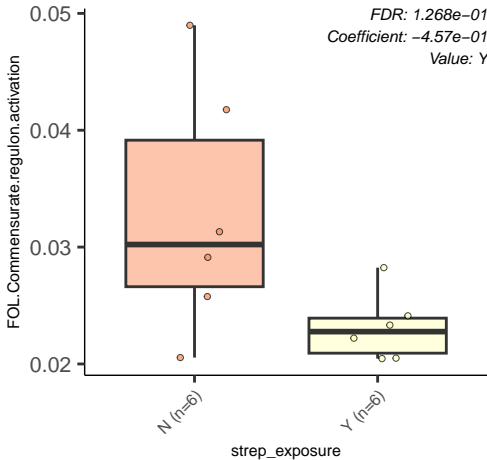
FOL.Commensurate.regulon.activation

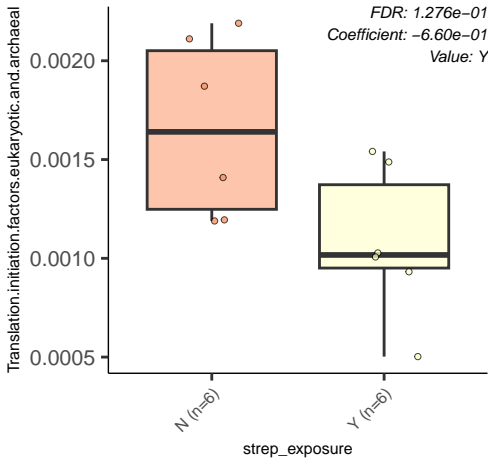
FDR: 1.268e-01
Coefficient: -4.57e-01
Value: Y

N (n=6)

Y (n=6)

strep_exposure





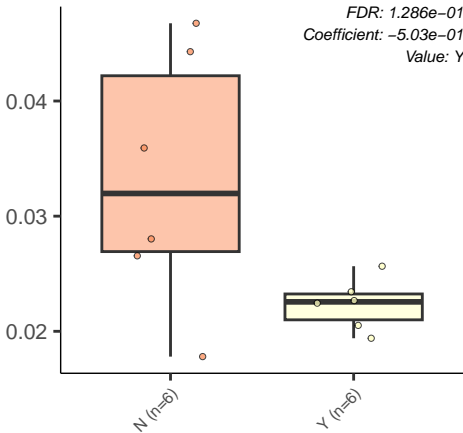
Multidrug.efflux.pump.in.Campylobacter.jejuni..CmeABC.op

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

N (n=6)

Y (n=6)

strep_exposure



Galactose.inducible.PTS

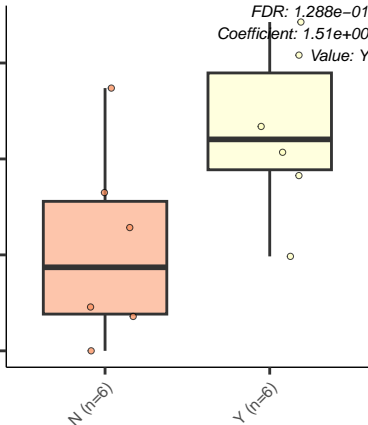
0.00075
0.00050
0.00025
0.00000

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

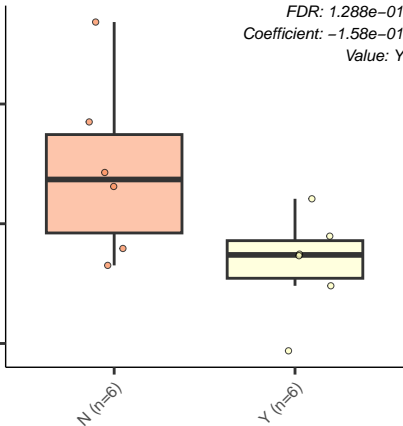
0.07

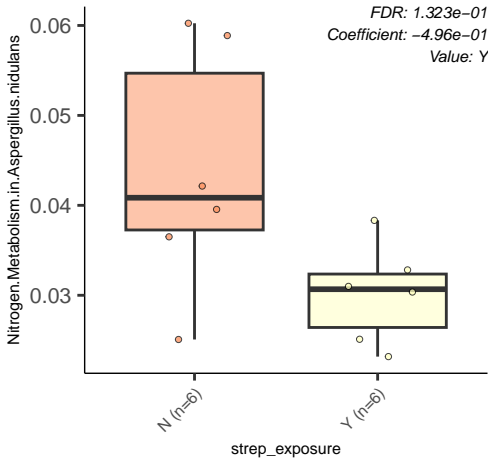
0.06

N (n=6)

Y (n=6)

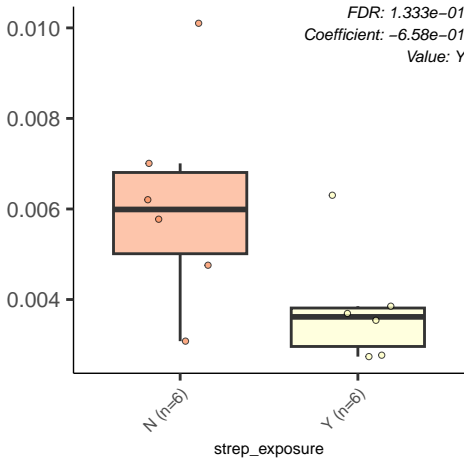
strep_exposure





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

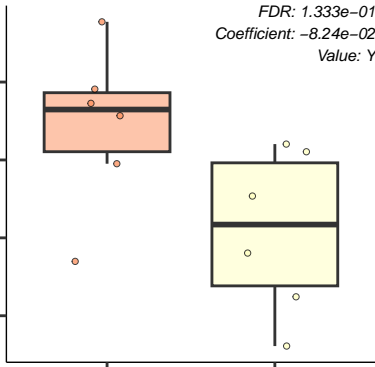
0.0575

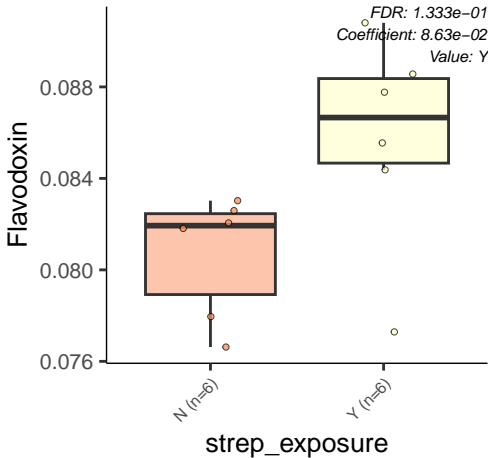
0.0550

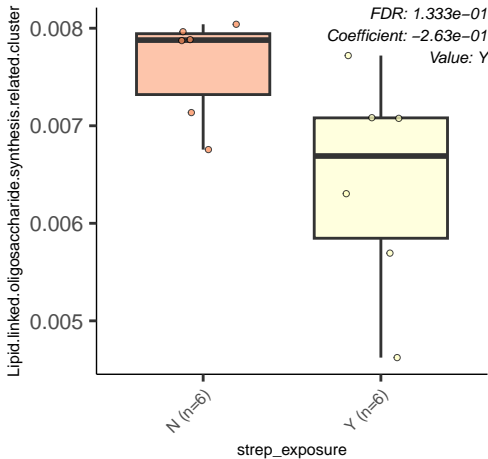
N (n=6)

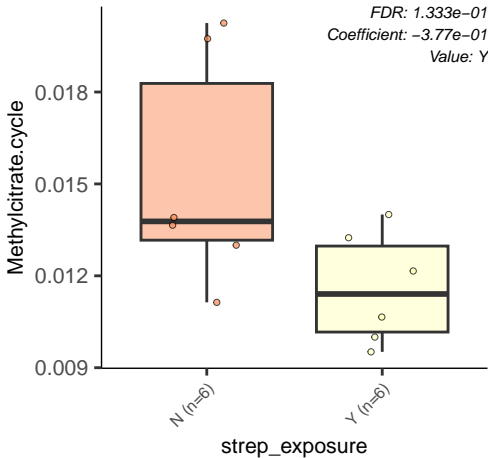
Y (n=6)

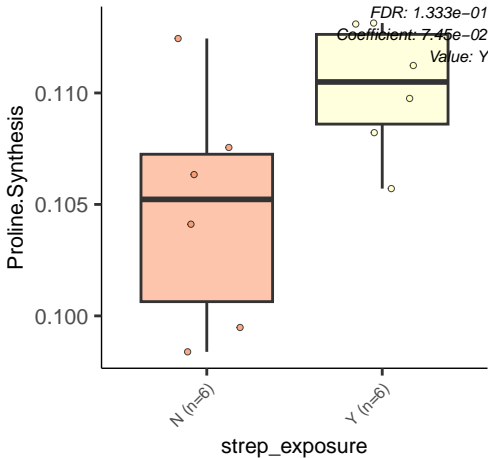
strep_exposure

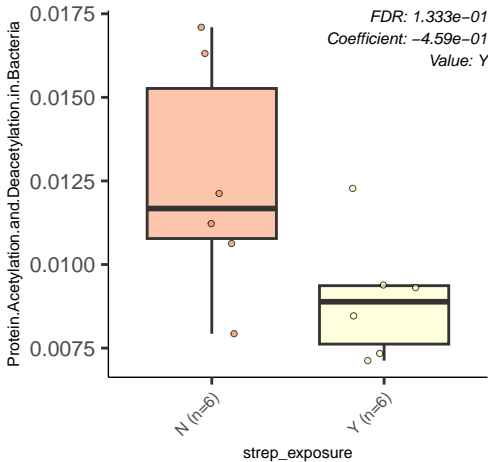












tRNA.aminoacylation..Leu

0.200

0.195

0.190

0.185

N (n=6)

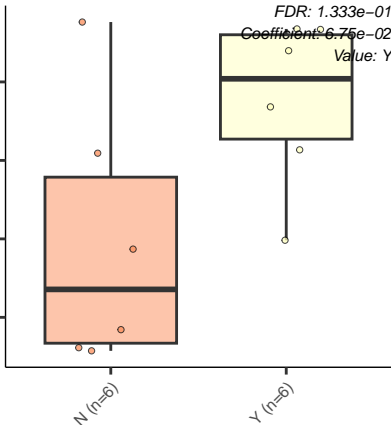
Y (n=6)

strep_exposure

FDR: 1.333e-01

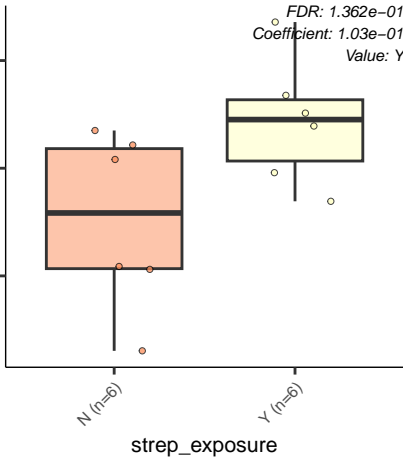
Coefficient: 6.75e-02

Value: Y



tRNA.aminoacylation..Gly

FDR: 1.362e-01
Coefficient: 1.03e-01
Value: Y



Trehalose.Uptake.and.Utilization

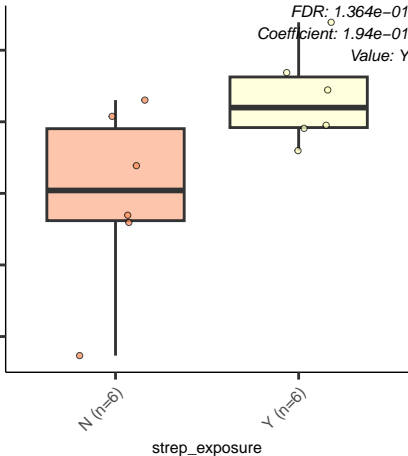
0.12
0.11
0.10
0.09
0.08

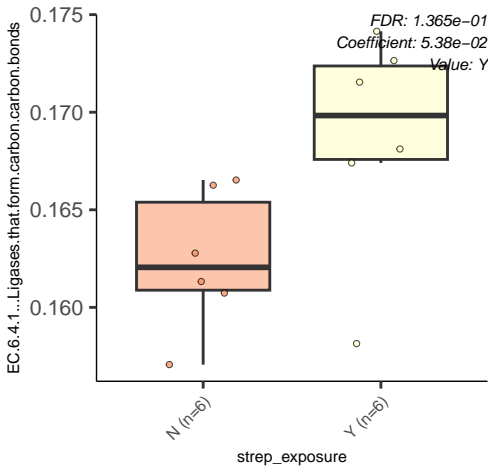
N (n=6)

Y (n=6)

strep_exposure

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





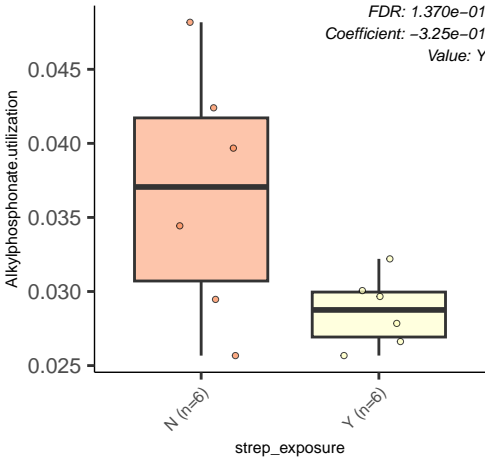
Alkylphosphate.utilization

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

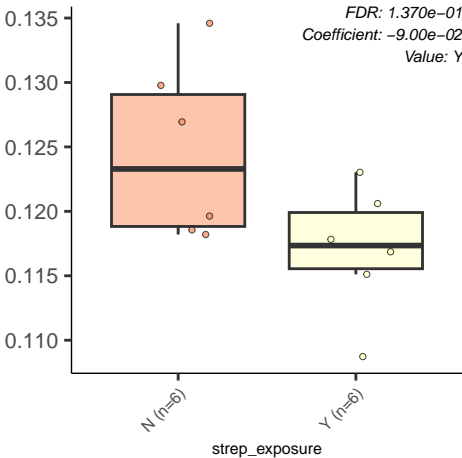
N (n=6)

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

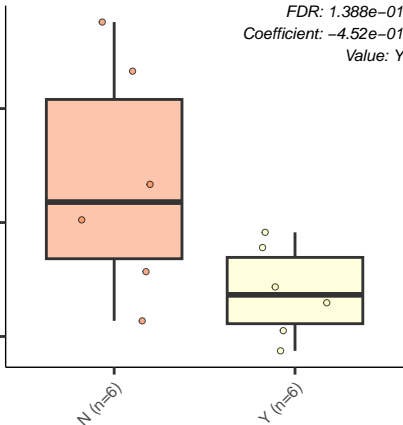
0.03

0.02

N (n=6)

Y (n=6)

strep_exposure



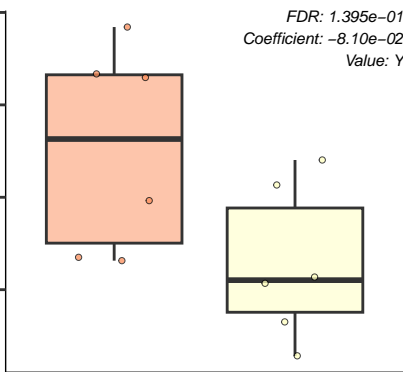
tRNA.aminoacylation..Ile

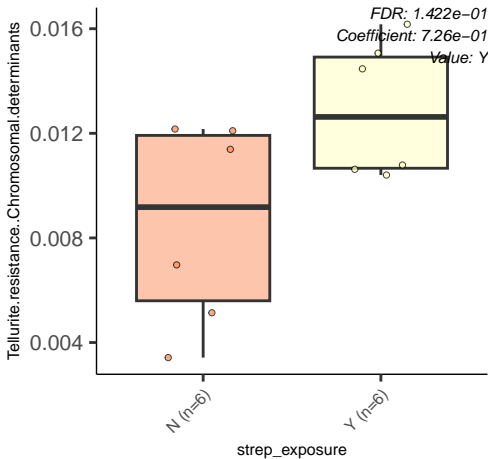
FDR: 1.395e-01
Coefficient: -8.10e-02
Value: Y

N (n=6)

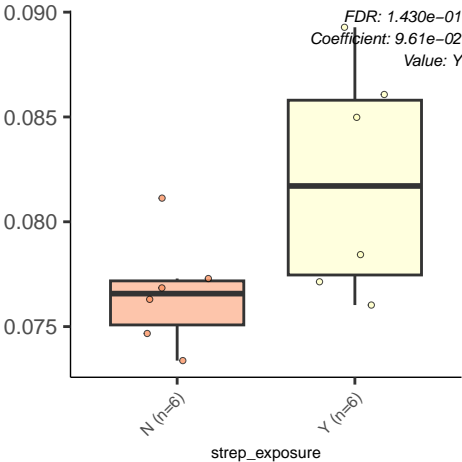
Y (n=6)

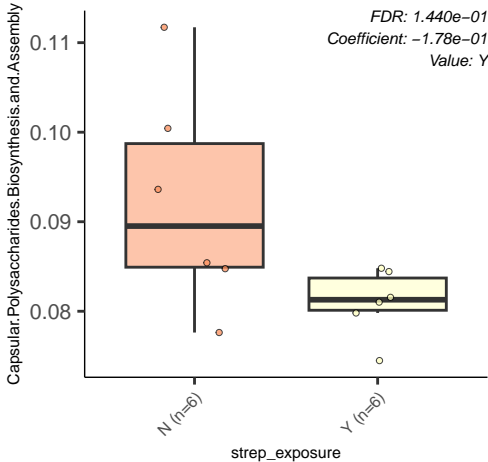
strep_exposure

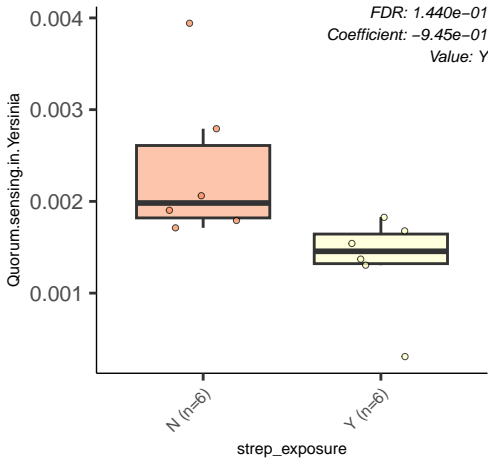




Hyperosmotic.potassium.uptake

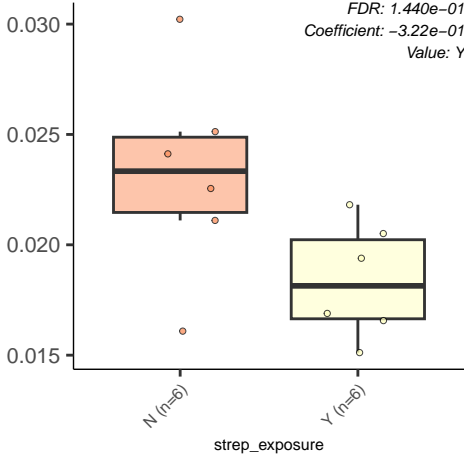


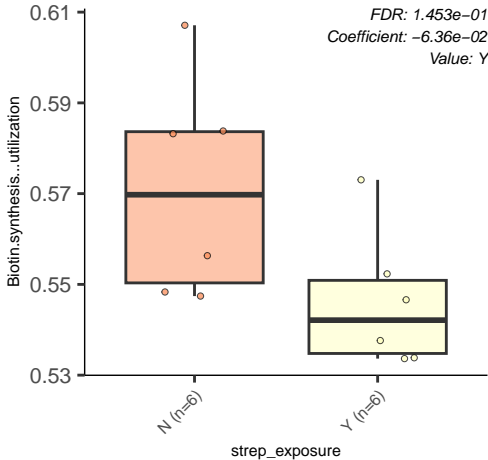




p.Aminobenzoyl.Glutamate.Utilization

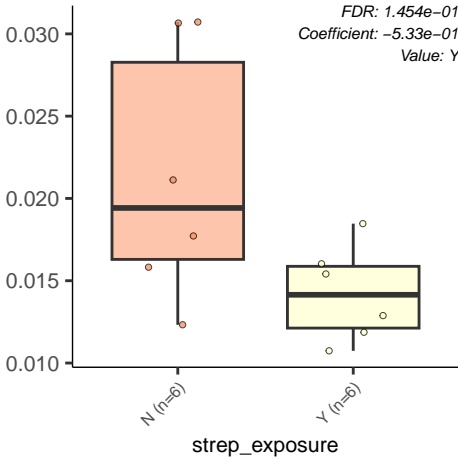
FDR: 1.440e-01
Coefficient: -3.22e-01
Value: Y





The.fimbrial.Stf.cluster

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



Glycogen.metabolism

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

1.00

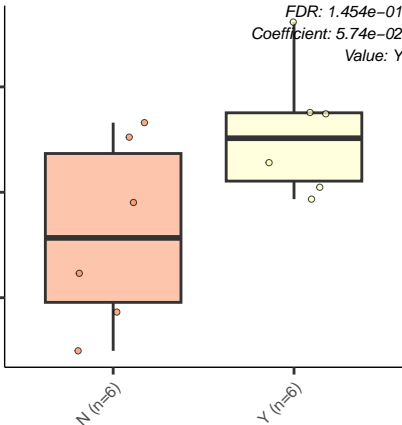
0.96

0.92

N (n=6)

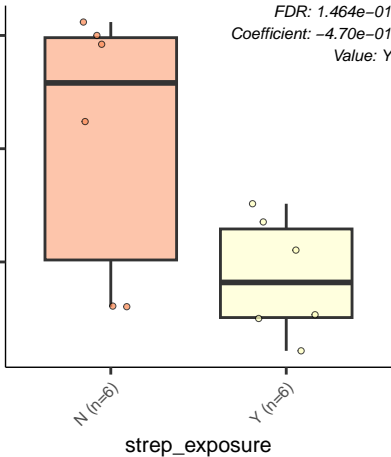
Y (n=6)

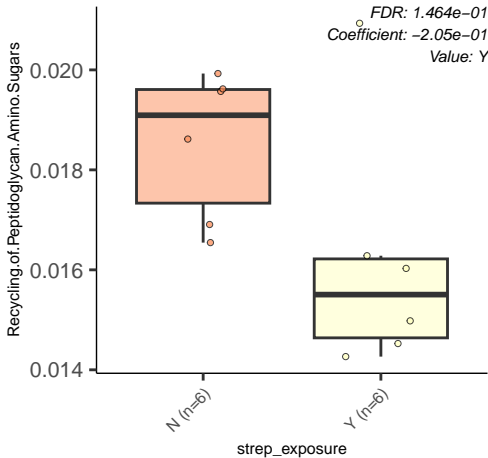
strep_exposure



CBSS.584.1.pcg.841

FDR: 1.464e-01
Coefficient: -4.70e-01
Value: Y





DNA.repair..bacterial.RecBCD.pathway

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

0.40

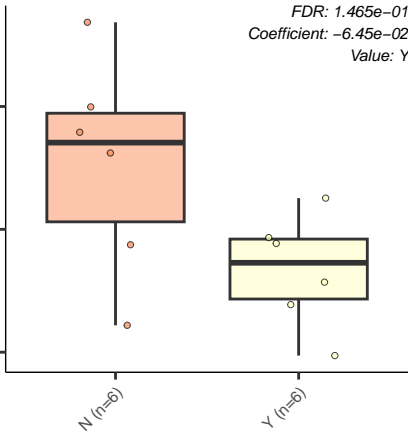
0.38

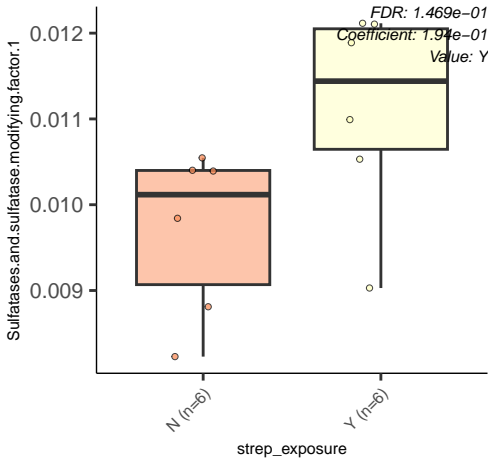
0.36

N (n=6)

Y (n=6)

strep_exposure





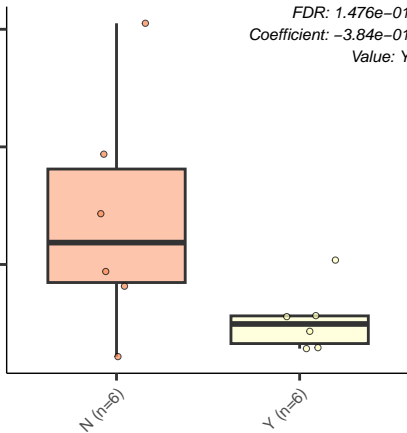
Major.Outer.Membrane.Proteins

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

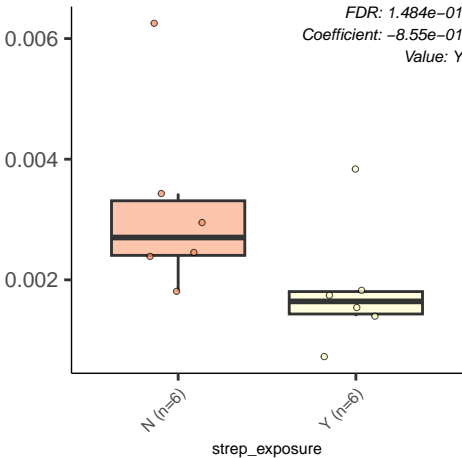
N (n=6)

Y (n=6)

strep_exposure



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



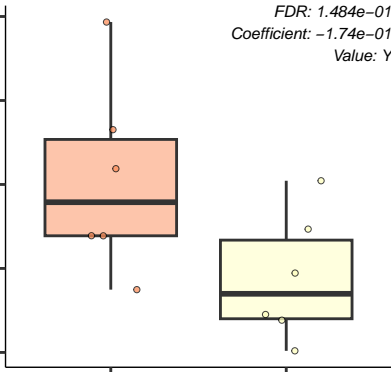
CBSS.246196.1.peg.364

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

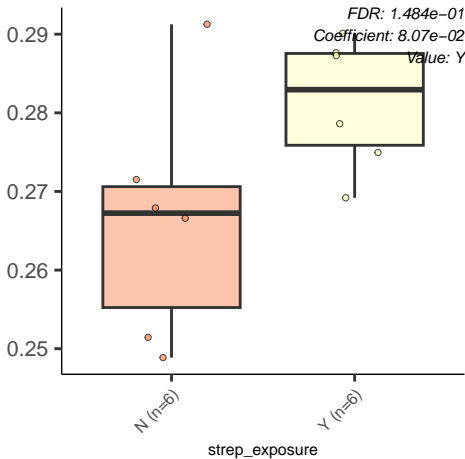
N (n=6)

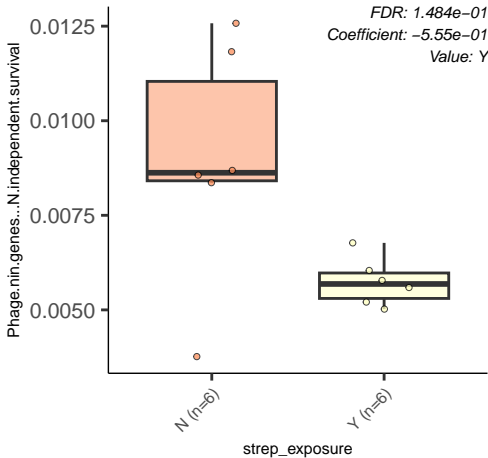
Y (n=6)

strep_exposure



Exopolysaccharide.Biosynthesis





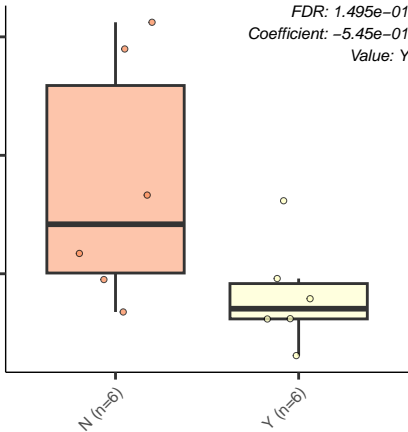
Peptide.ABC.transport.system.Sap

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

N (n=6)

Y (n=6)

strep_exposure



Aromatic.amino.acid.degradation

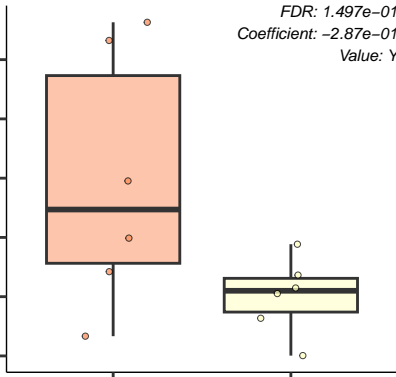
0.060
0.055
0.050
0.045
0.040
0.035

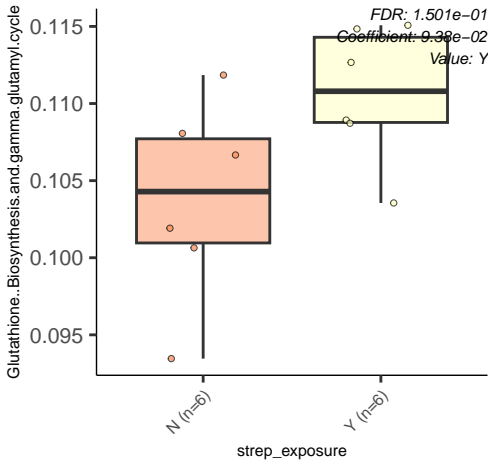
N (n=6)

Y (n=6)

strep_exposure

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





tRNA.aminoacylation..Phe

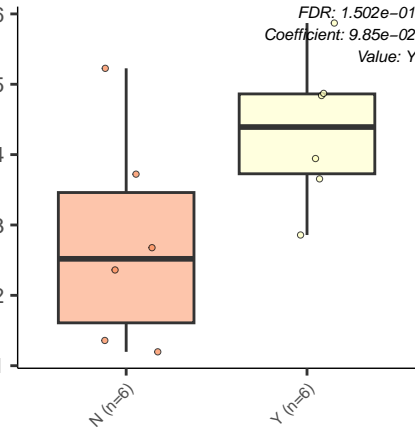
0.26
0.25
0.24
0.23
0.22
0.21

N (n=6)

Y (n=6)

strep_exposure

FDR: 1.502e-01
Coefficient: 9.85e-02
Value: Y



Rubrerythrin

FDR: 1.510e-01

Coefficient: -1.29e-01

Value: Y

0.060

0.056

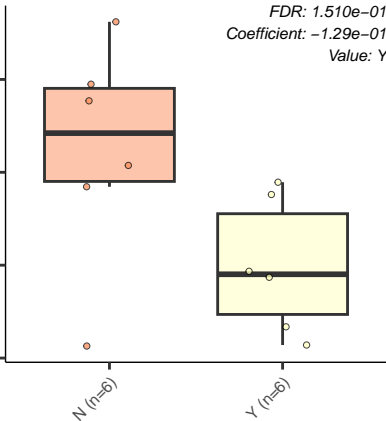
0.052

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

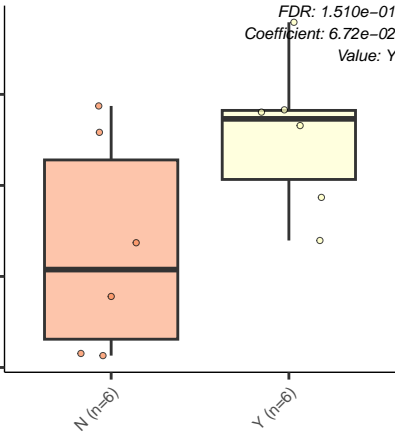
0.130

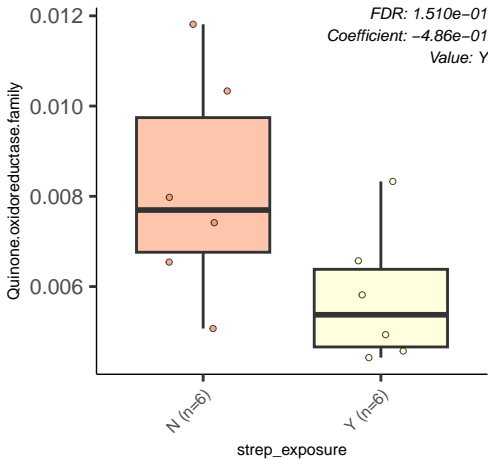
0.125

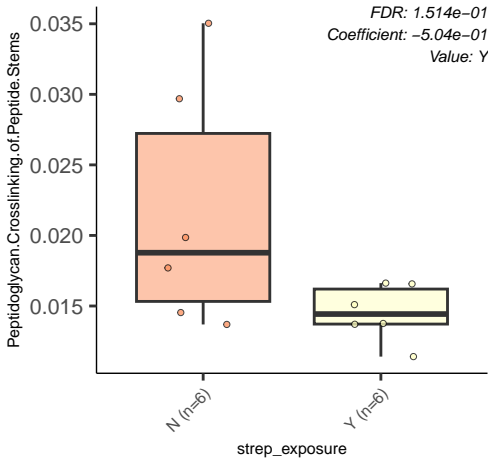
N (n=6)

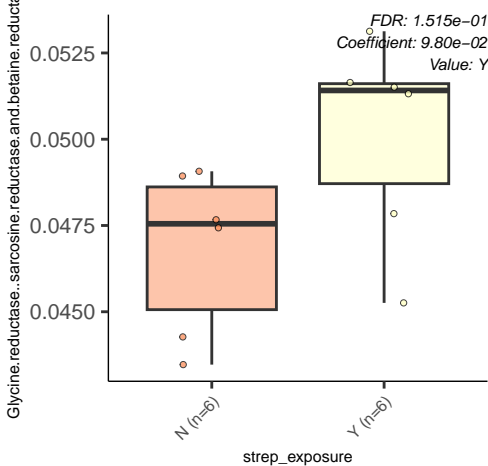
Y (n=6)

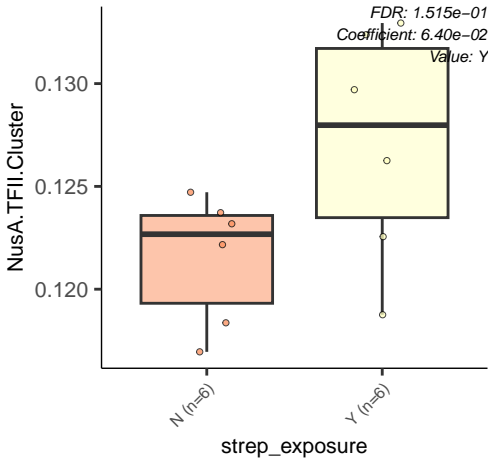
strep_exposure











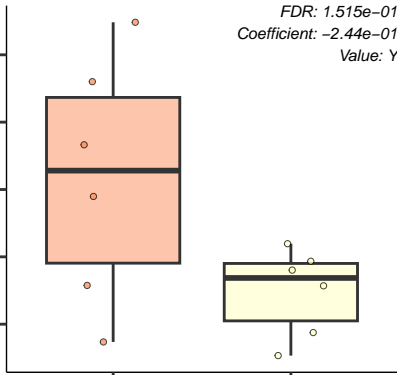
Unknown.sugar.utilization..cluster.yphABCDEFG.

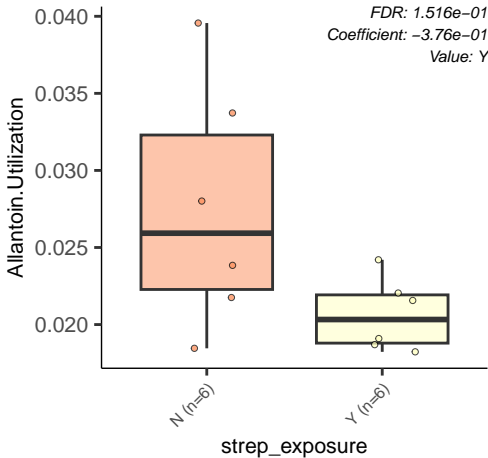
FDR: 1.515e-01
Coefficient: -2.44e-01
Value: Y

N (n=6)

Y (n=6)

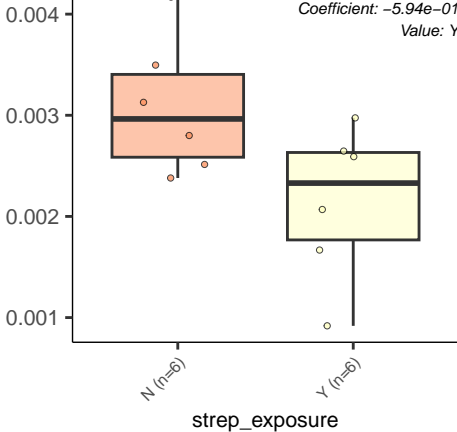
strep_exposure

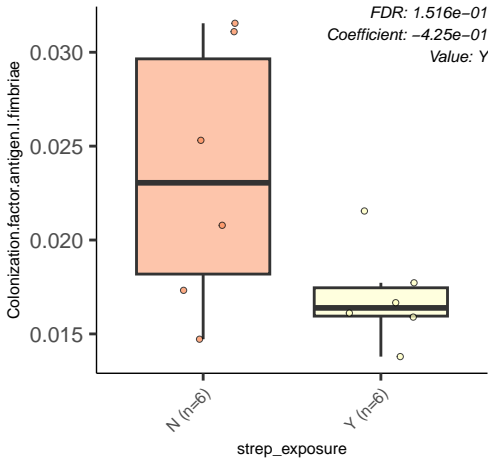




CBSS.318161.14.peg.2599

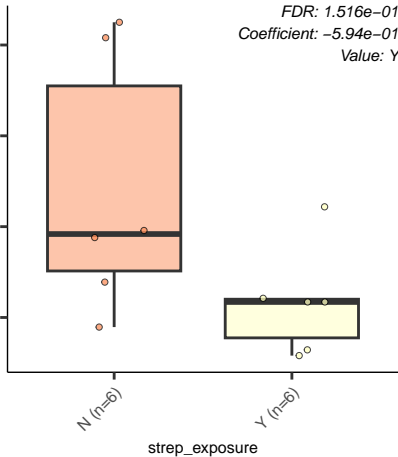
FDR: 1.516e-01
Coefficient: -5.94e-01
Value: Y





Terminal.cytochrome.O.ubiquinol.oxidase

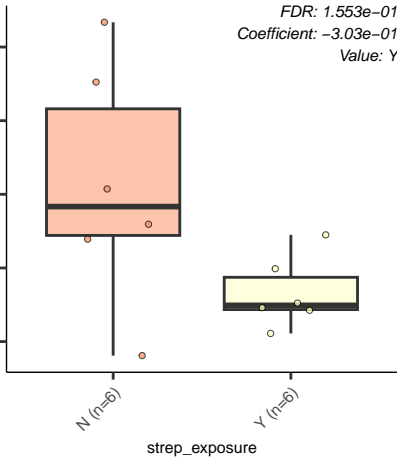
FDR: 1.516e-01
Coefficient: -5.94e-01
Value: Y

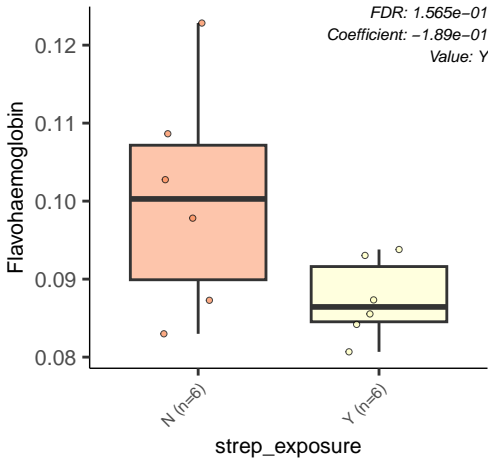


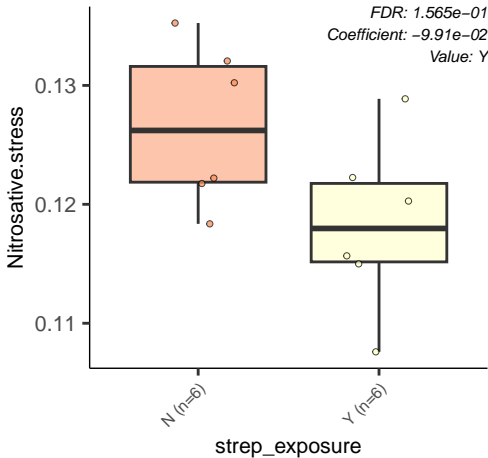
strep_exposure

Unknown.carbohydrate.utilization...cluster.Yeg..

FDR: 1.553e-01
Coefficient: -3.03e-01
Value: Y







Queuosine,Archaeosine.Biosynthesis

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

0.180

0.175

0.170

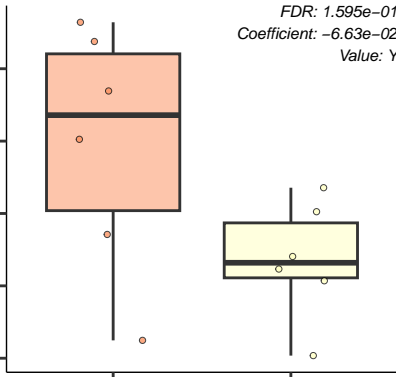
0.165

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

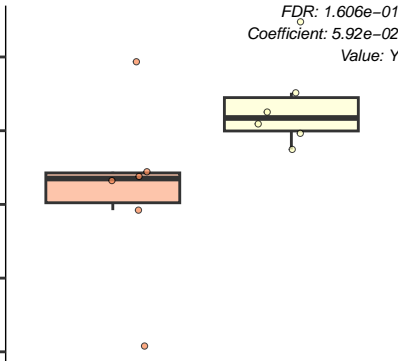
0.27

0.26

N (n=6)

Y (n=6)

strep_exposure



Putative.TldE.TldD.proteolytic.complex

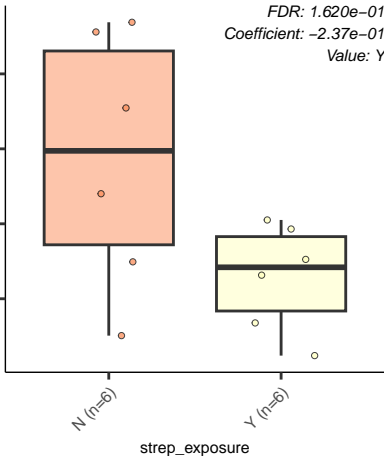
FDR: 1.620e-01
Coefficient: -2.37e-01
Value: Y

N (n=6)

Y (n=6)

strep_exposure

0.0275
0.0250
0.0225
0.0200



CBSS.281090.3.pcg.464

0.13

0.12

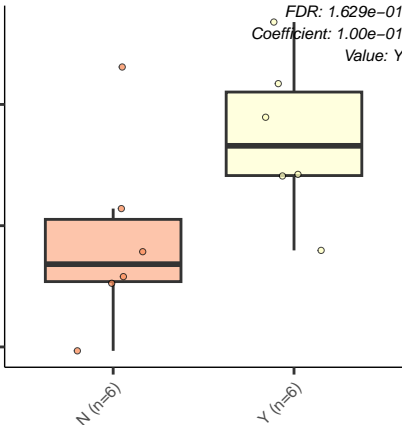
0.11

N (n=6)

Y (n=6)

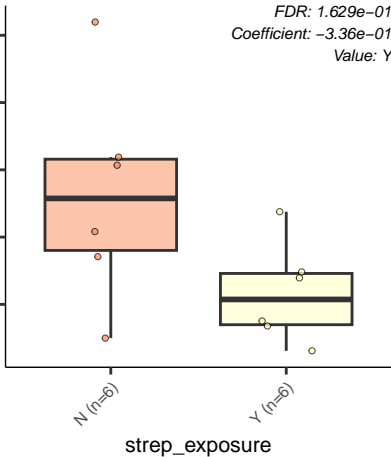
strep_exposure

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



Listeria.Pathogenicity.Island.LIPI.1.extended

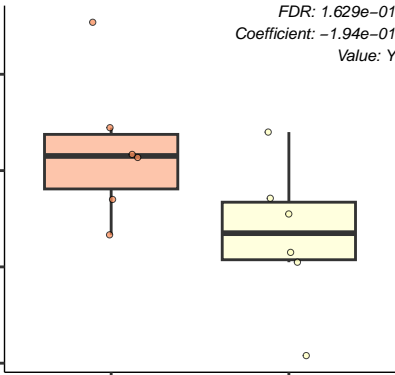
FDR: 1.629e-01
Coefficient: -1.94e-01
Value: Y

0.016
0.014
0.012
0.010

N (n=6)

Y (n=6)

strep_exposure



COG1836

0.0300

0.0275

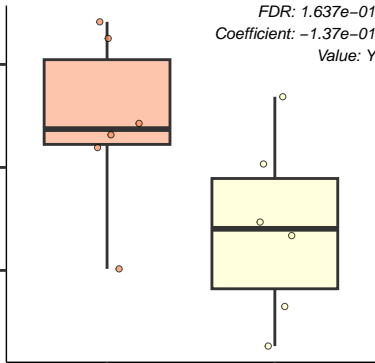
0.0250

N (n=6)

Y (n=6)

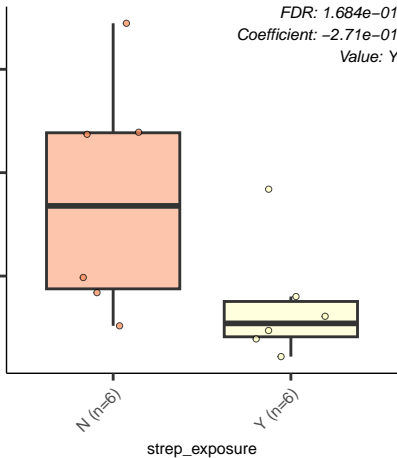
strep_exposure

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

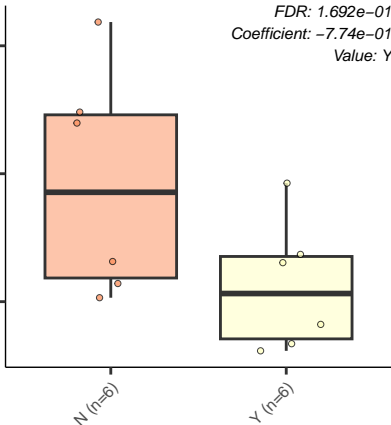
0.002

0.001

N (n=6)

Y (n=6)

strep_exposure



Creatine.and.Creatinine.Degradation

0.035

0.030

0.025

N (n=6)

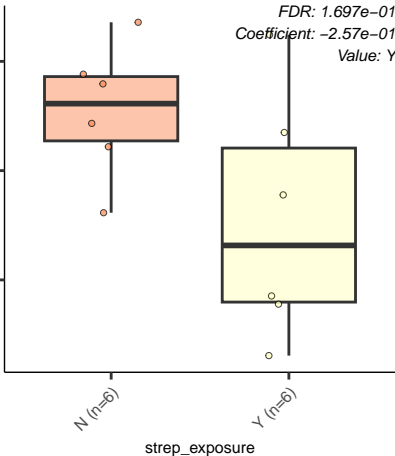
Y (n=6)

strep_exposure

FDR: 1.697e-01

Coefficient: -2.57e-01

Value: Y



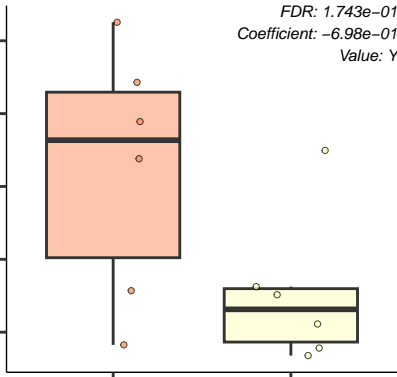
Biogenesis.of.cytochrome.c.oxidases

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

N (n=6)

Y (n=6)

strep_exposure



Flagellum.in.Campylobacter

FDR: 1.750e-01
Coefficient: 1.45e-01
Value: Y

0.060

0.055

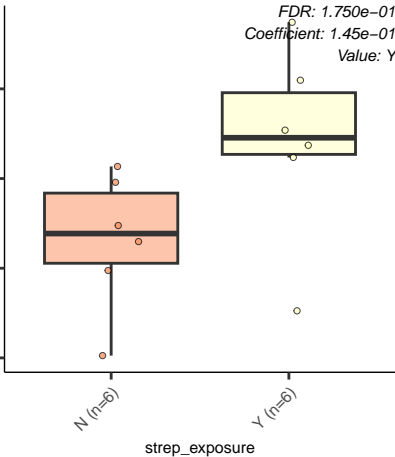
0.050

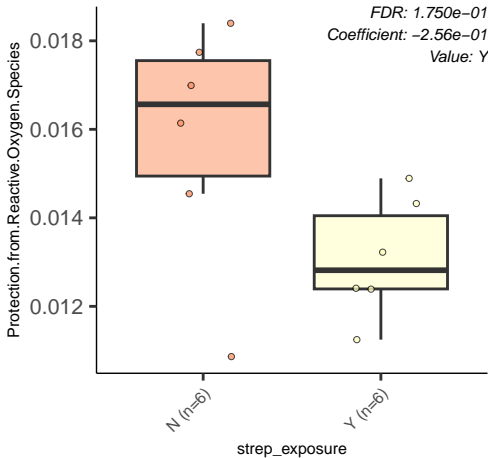
0.045

N (n=6)

Y (n=6)

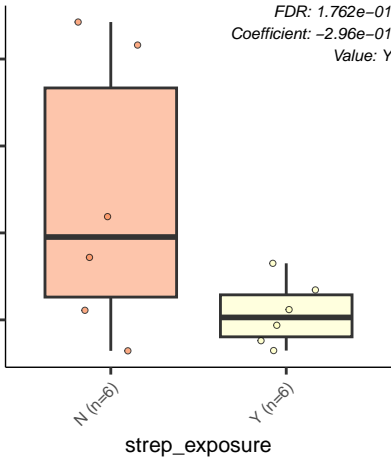
strep_exposure





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

N (n=6)

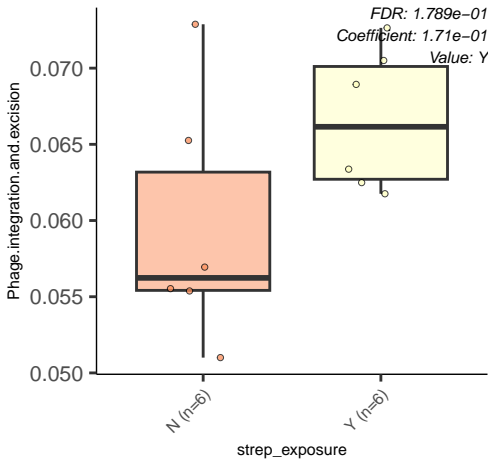
Y (n=6)

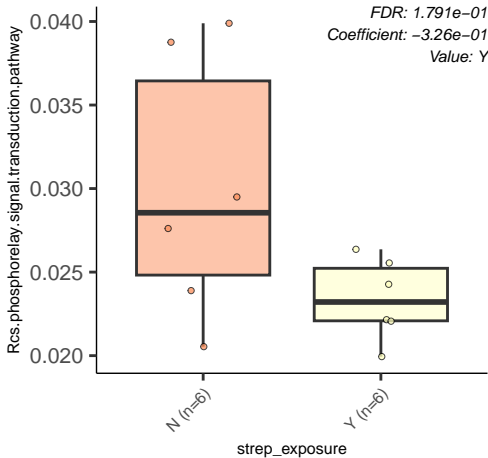
strep_exposure

0.150

0.145

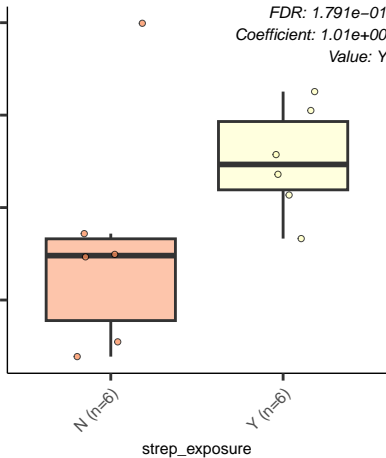
0.140

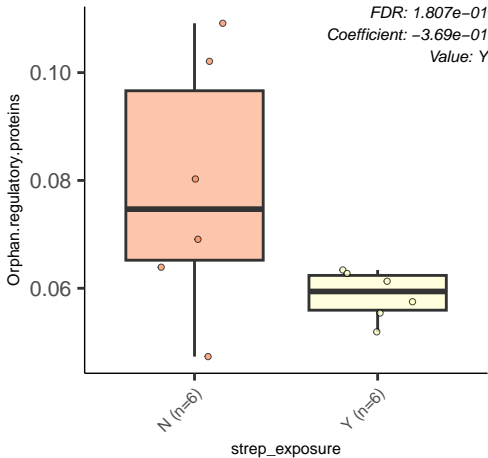




Terminal.cytochrome.C.oxidases

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





Omega.amidase.KE2

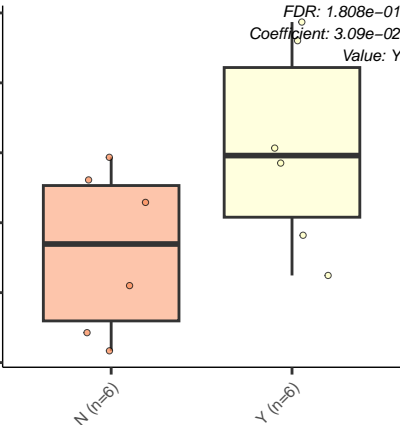
0.72
0.71
0.70
0.69
0.68
0.67

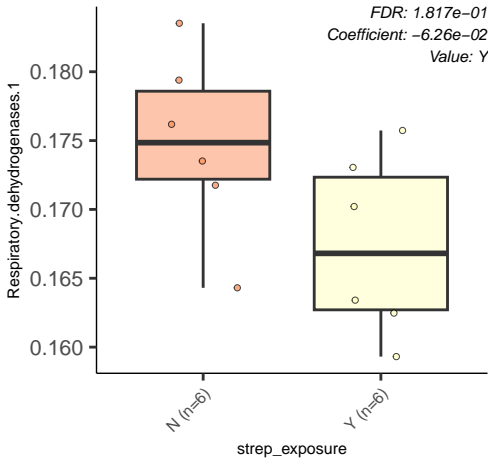
N (n=6)

Y (n=6)

strep_exposure

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





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

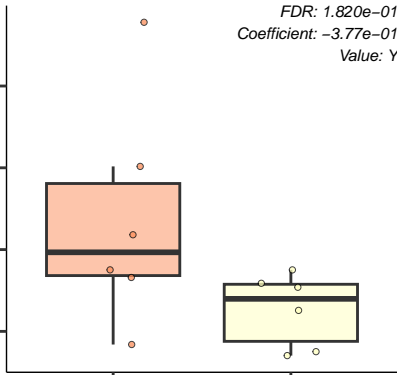
FDR: 1.820e-01
Coefficient: -3.77e-01
Value: Y

0.030
0.025
0.020
0.015

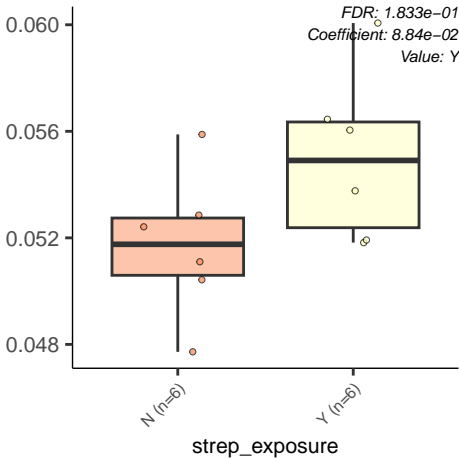
N (n=6)

Y (n=6)

strep_exposure



t6A.synthesis.in.bacteria



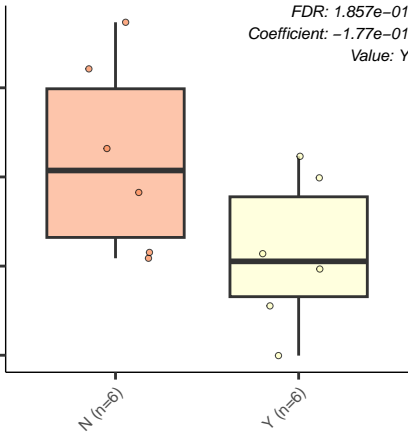
FDR: $1.857e-01$
Coefficient: $-1.77e-01$
Value: Y

0.10
0.09
0.08
0.07

N (n=6)

Y (n=6)

strep_exposure



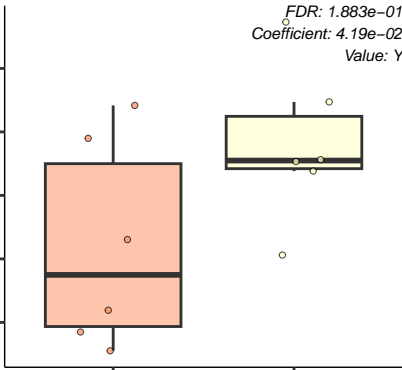
RNA.polymerase.bacterial

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

N (n=6)

Y (n=6)

strep_exposure



Alkanesulfonates.Utilization

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

0.009

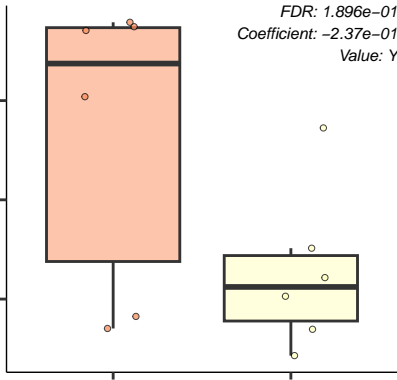
0.008

0.007

N (n=6)

Y (n=6)

strep_exposure



Campylobacter.Iron.Metabolism

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

0.148

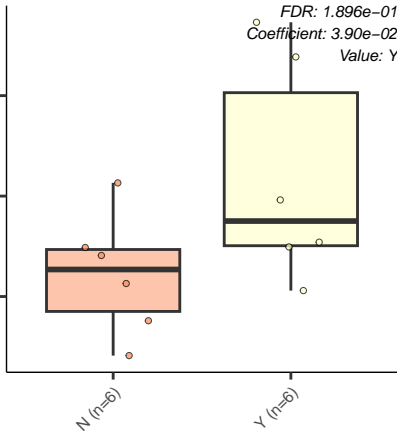
0.144

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

0.075

0.070

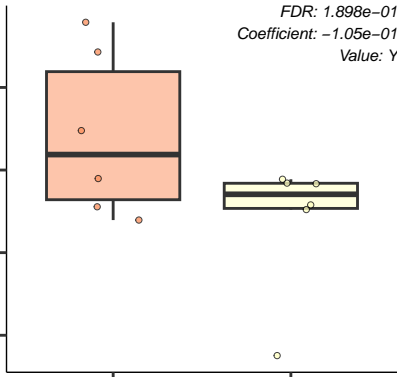
0.065

0.060

N (n=6)

Y (n=6)

strep_exposure



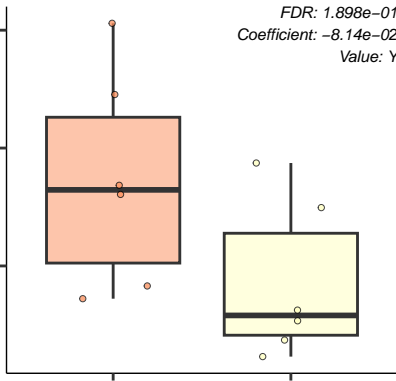
Terminal.cytochrome.oxidases

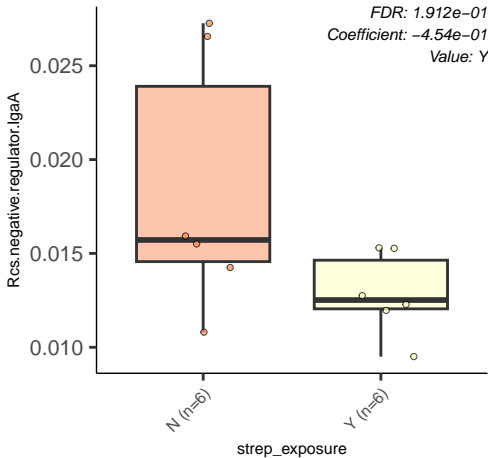
FDR: 1.898e-01
Coefficient: -8.14e-02
Value: Y

N (n=6)

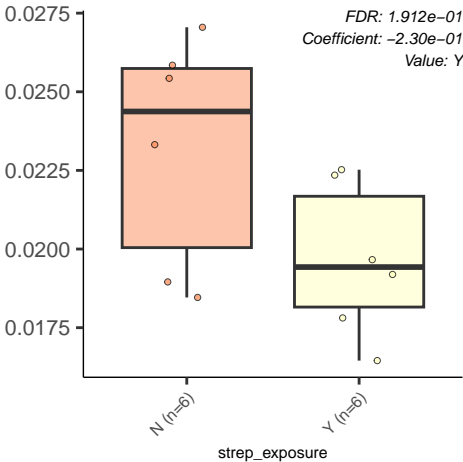
Y (n=6)

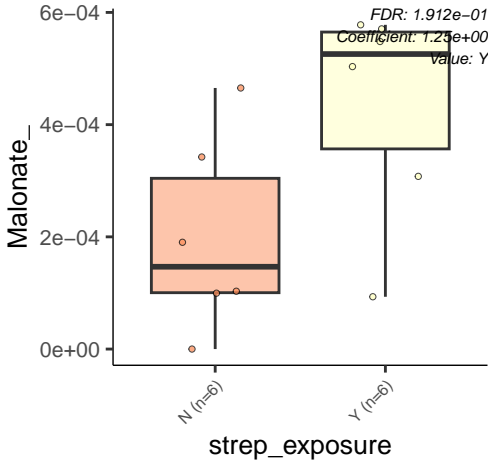
strep_exposure





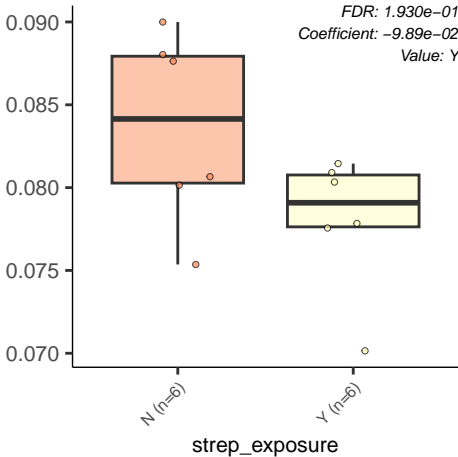
Khodge314.Isoleucine.Biosynthesis





CBSS.498211.3.pcg.1514

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

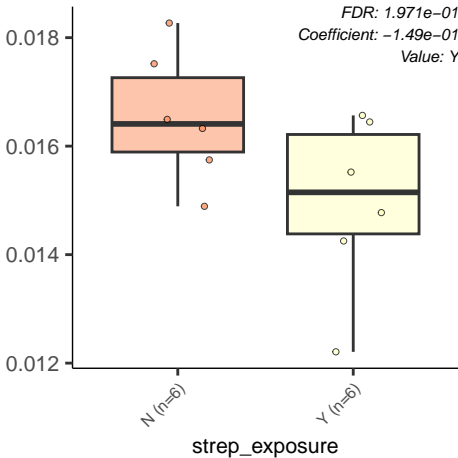


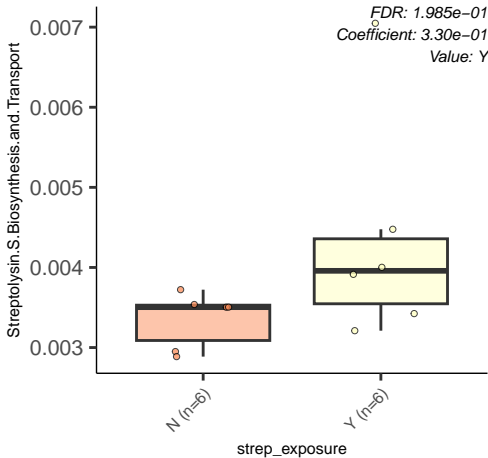
CBSS.316057.3.peg.659

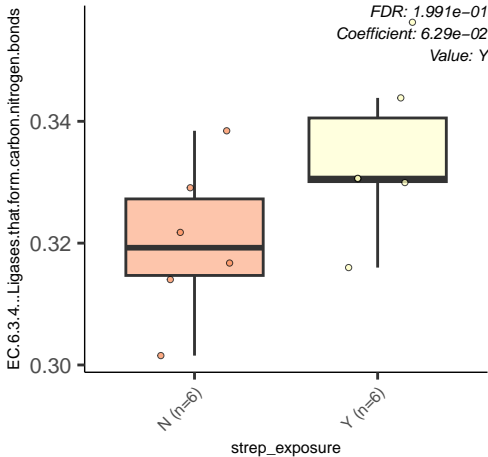
FDR: 1.971e-01

Coefficient: -1.49e-01

Value: Y







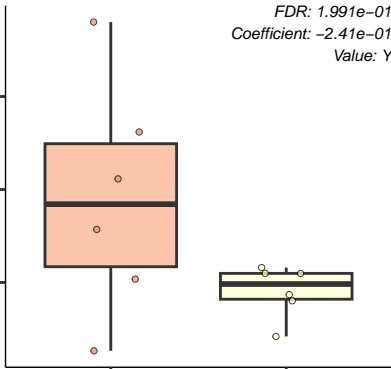
RpoS.Regulators.SG1

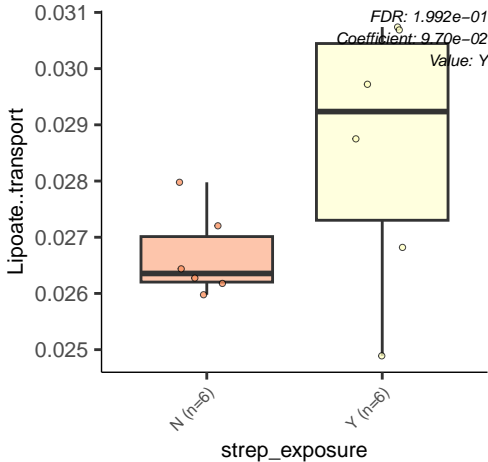
FDR: 1.991e-01
Coefficient: -2.41e-01
Value: Y

N (n=6)

Y (n=6)

strep_exposure





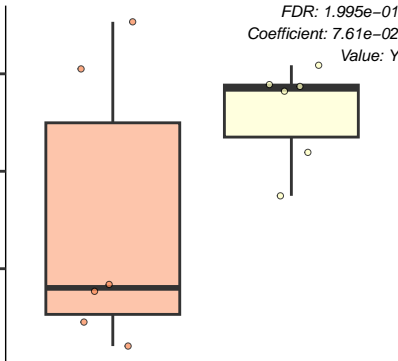
At5g63290

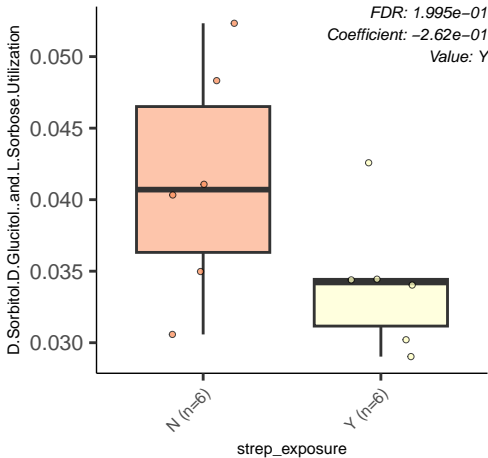
FDR: 1.995e-01
Coefficient: 7.61e-02
Value: Y

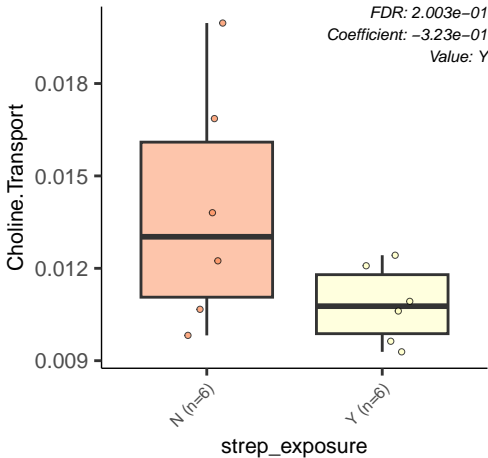
N (n=6)

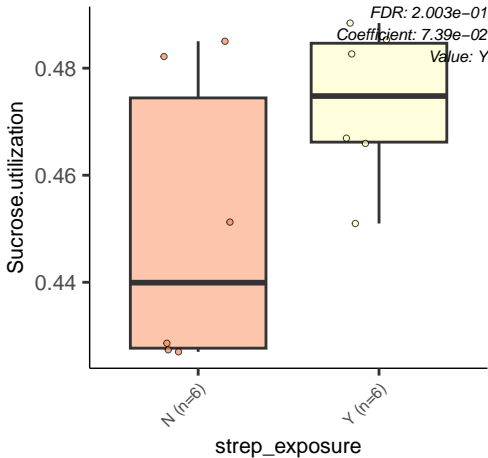
Y (n=6)

strep_exposure

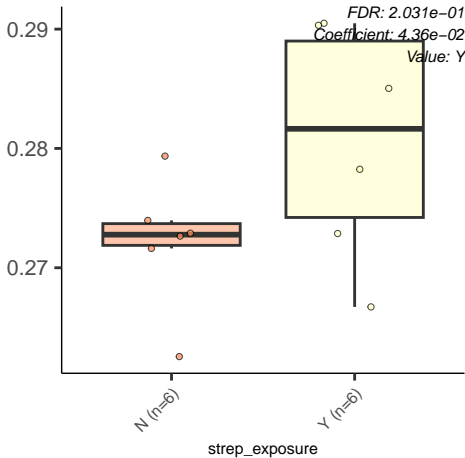






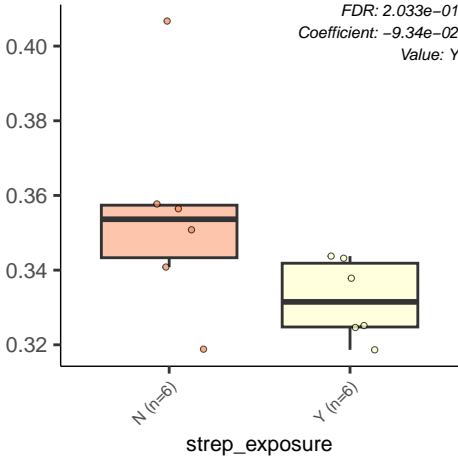


EC.3.4.11...Aminopeptidases



CBSS.258594.1.peg.3339

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



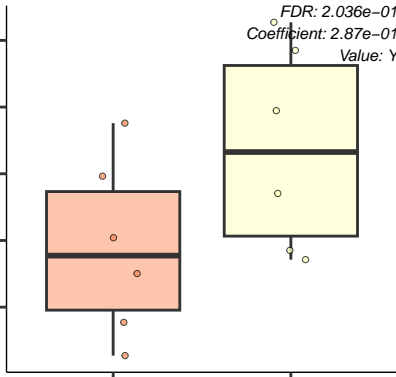
ESAT.6.proteins.secretion.system.in.Firmicutes

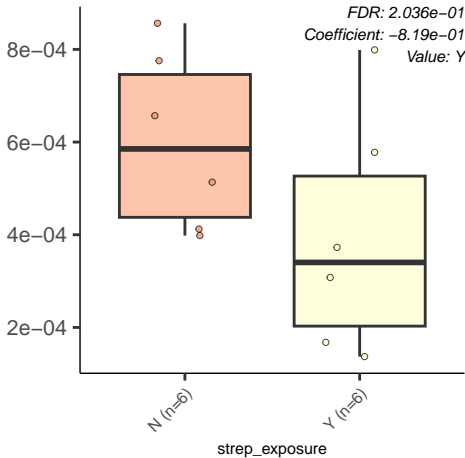
FDR: 2.036e-01
Coefficient: 2.87e-01
Value: Y

N (n=6)

Y (n=6)

strep_exposure





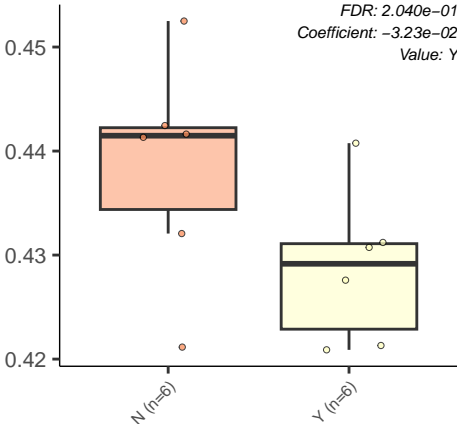
Polyamine.Metabolism

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

N (n=6)

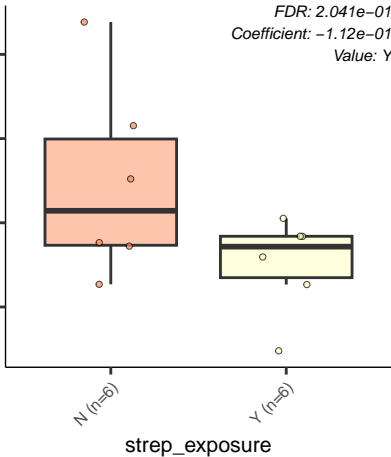
Y (n=6)

strep_exposure



EC.3.4.13...Dipeptidases

FDR: 2.041e-01
Coefficient: -1.12e-01
Value: Y



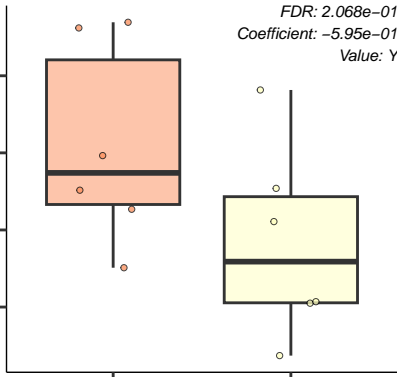
Commensurate.regulon.activation

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

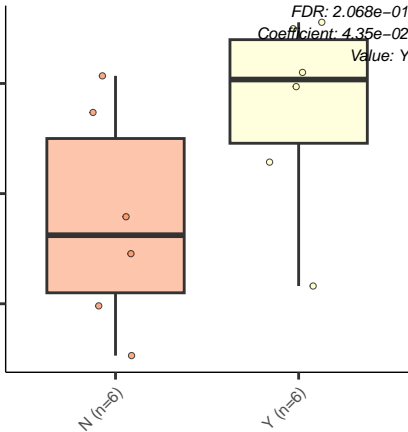
0.32

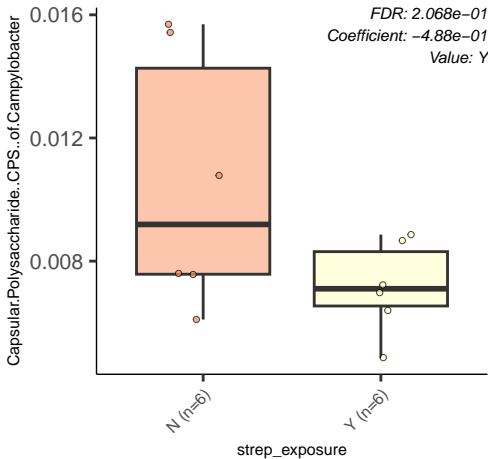
N (n=6)

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

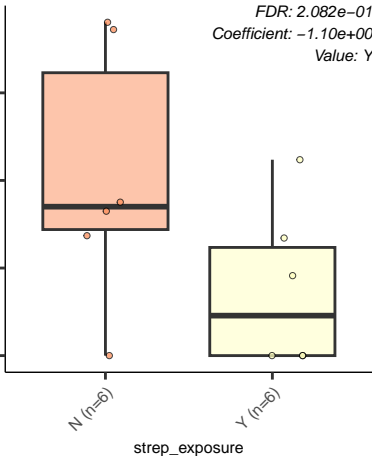
0.00025

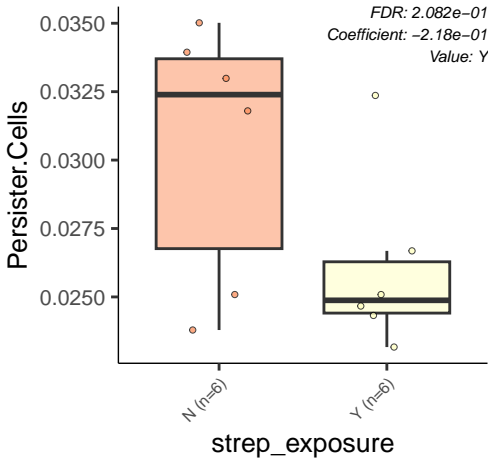
0.00000

N (n=6)

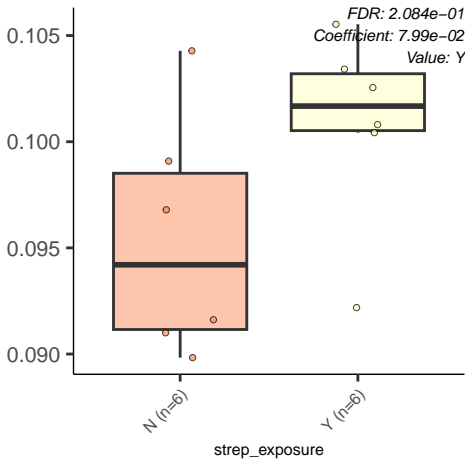
Y (n=6)

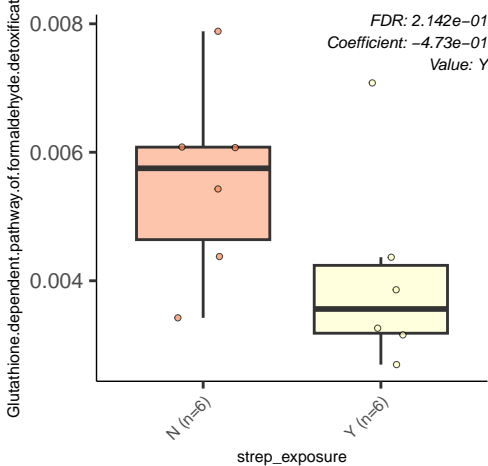
strep_exposure





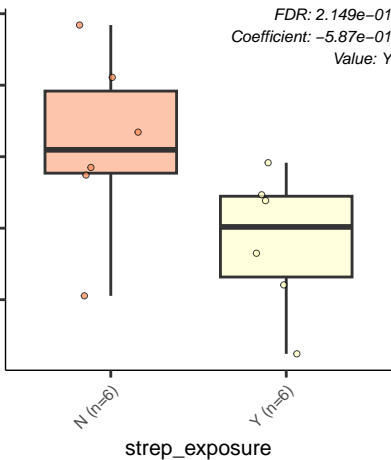
Thioredoxin.disulfide.reductase





CBSS.316275.9.peg.382

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



The.fimbrial.Sfm.cluster

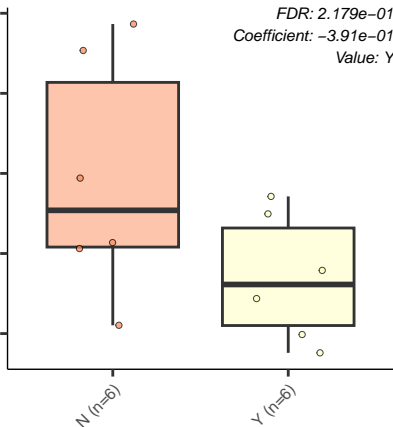
0.035
0.030
0.025
0.020
0.015

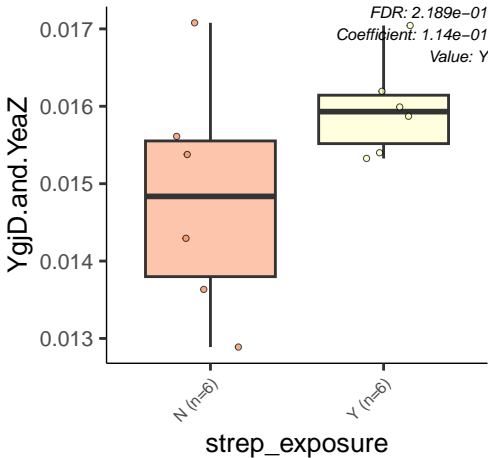
FDR: 2.179e-01
Coefficient: -3.91e-01
Value: Y

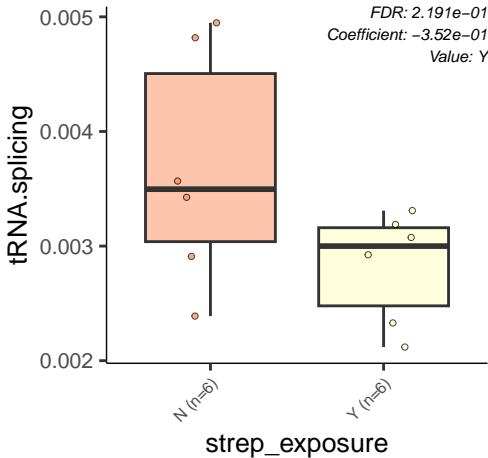
N (n=6)

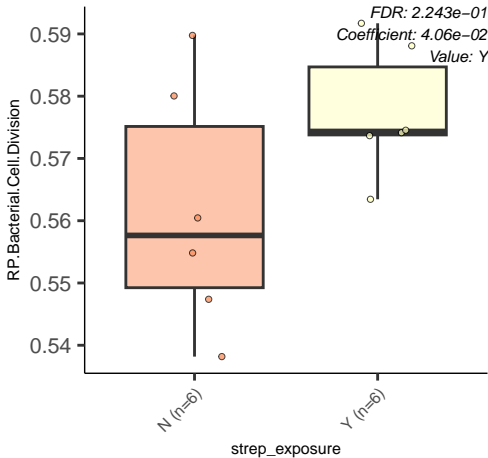
Y (n=6)

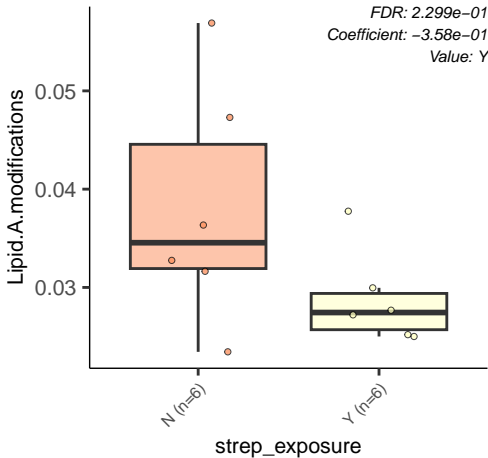
strep_exposure

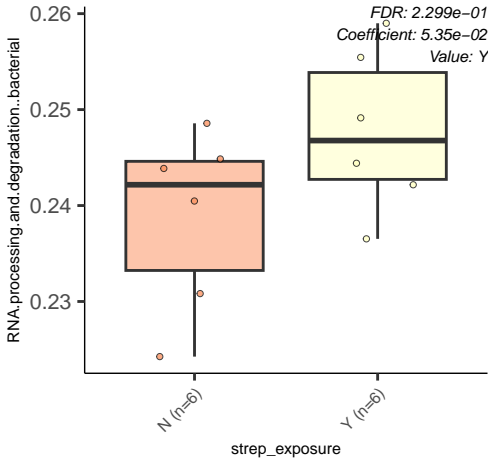












A.DNA.integrity.scanning.protein.that.co.occurs.with.Rad

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

N (n=6)

Y (n=6)

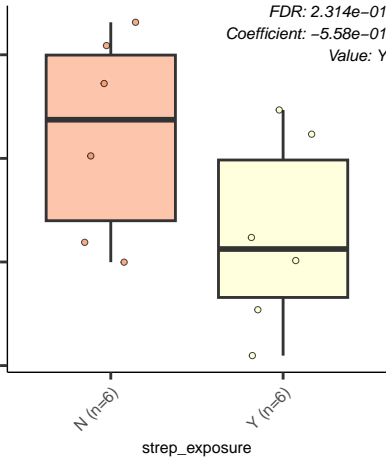
strep_exposure

0.0020

0.0015

0.0010

0.0005



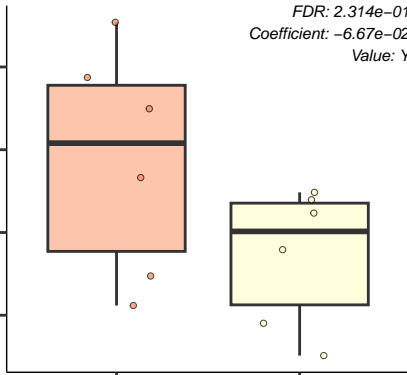
LOS.core.oligosaccharide.biosynthesis

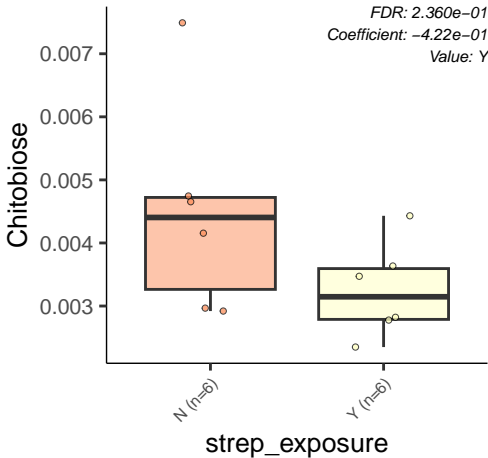
FDR: 2.314e-01
Coefficient: -6.67e-02
Value: Y

N (n=6)

Y (n=6)

strep_exposure





Entner.Doudoroff.Pathway

FDR: 2.360e-01

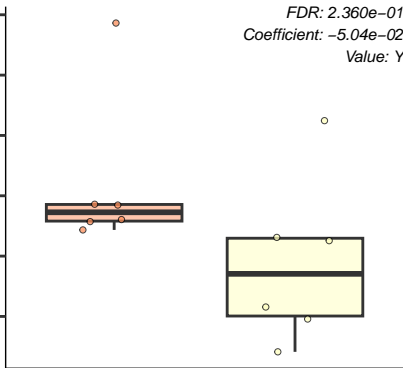
Coefficient: -5.04e-02

Value: Y

N (n=6)

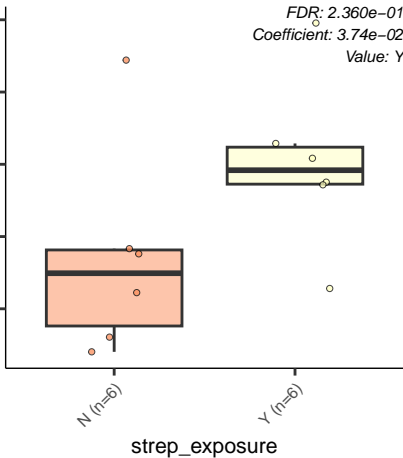
Y (n=6)

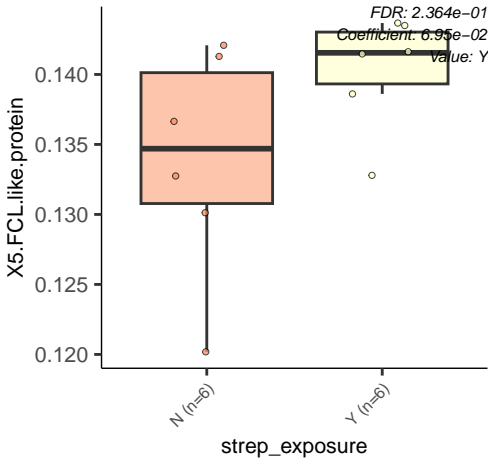
strep_exposure



Fermentations..Mixed.acid

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





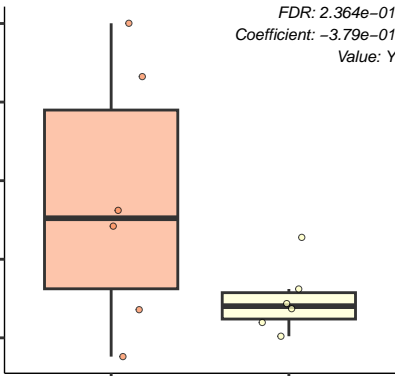
Putrescine.utilization.pathways

FDR: 2.364e-01
Coefficient: -3.79e-01
Value: Y

N (n=6)

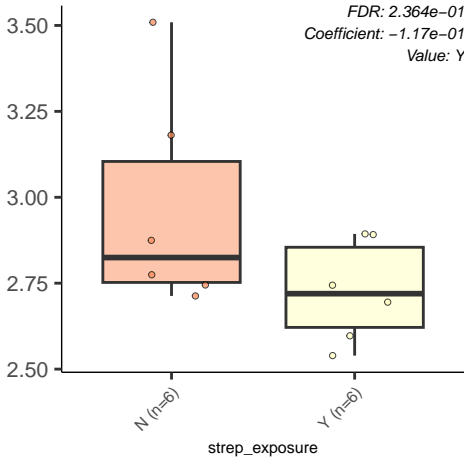
Y (n=6)

strep_exposure



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

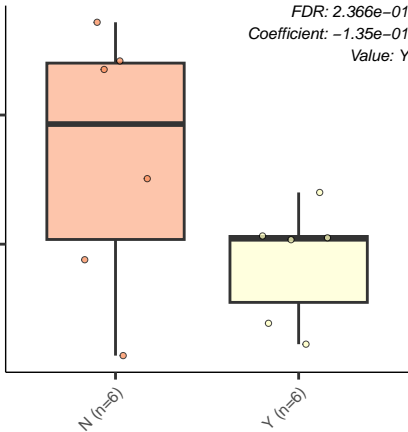
0.09

0.08

N (n=6)

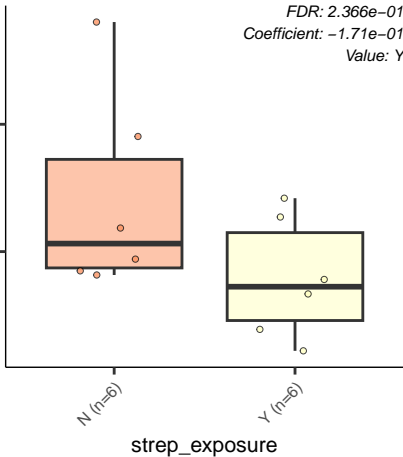
Y (n=6)

strep_exposure



Ubiquinone.Biosynthesis

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



CytR.regulation

FDR: 2.390e-01

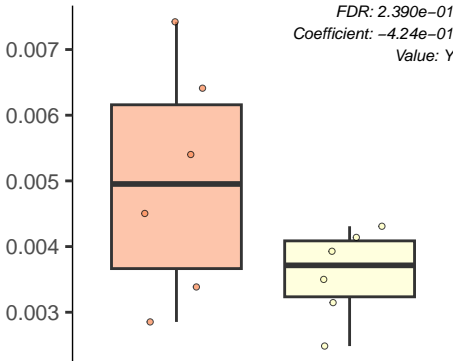
Coefficient: -4.24e-01

Value: Y

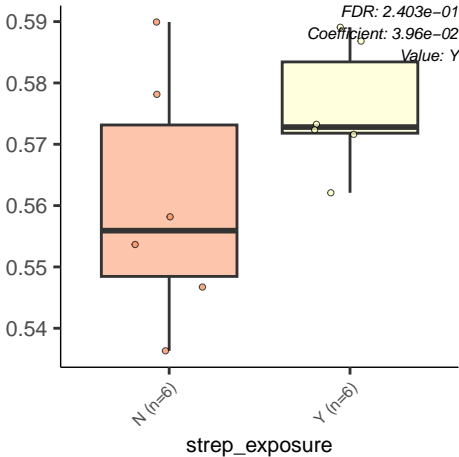
N (n=6)

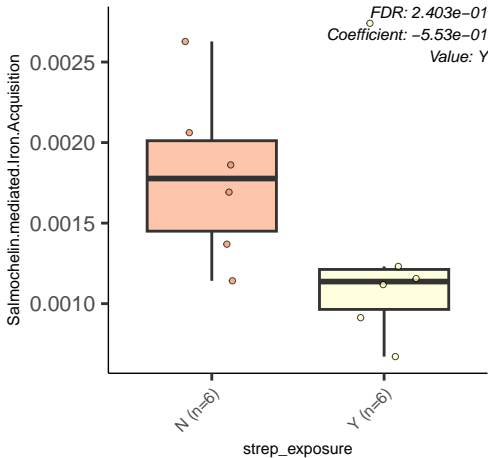
Y (n=6)

strep_exposure



Bacterial.Cell.Division





EC.3.4.21...Serine.endopeptidase

0.015

0.013

0.011

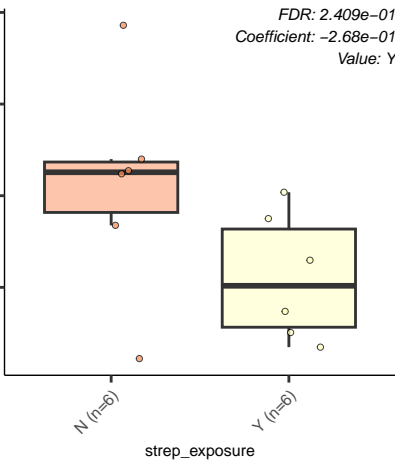
0.009

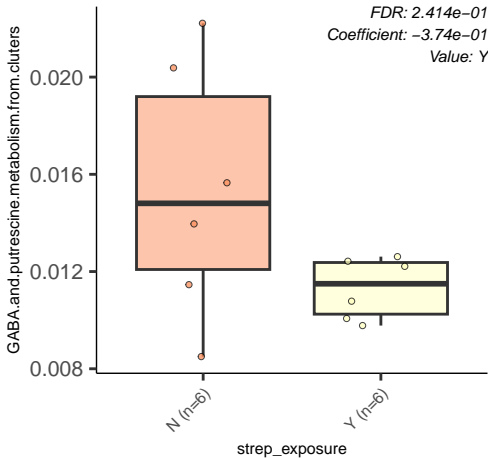
N (n=6)

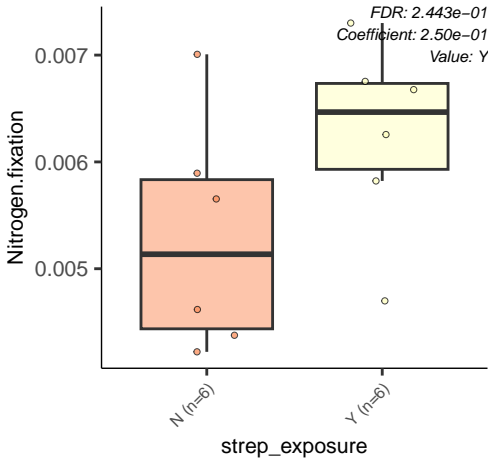
Y (n=6)

strep_exposure

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







Cobalamin

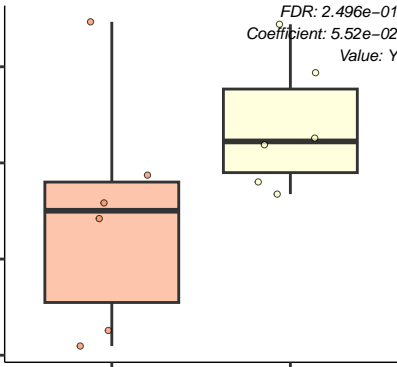
0.26
0.25
0.24
0.23

N (n=6)

Y (n=6)

strep_exposure

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



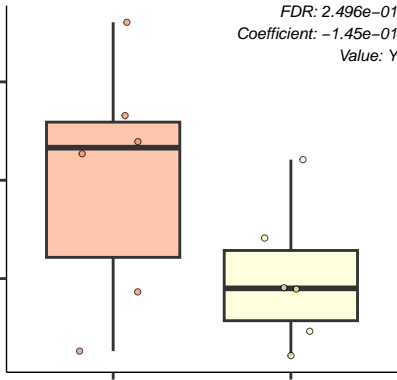
Small.acid.soluble.spore.proteins

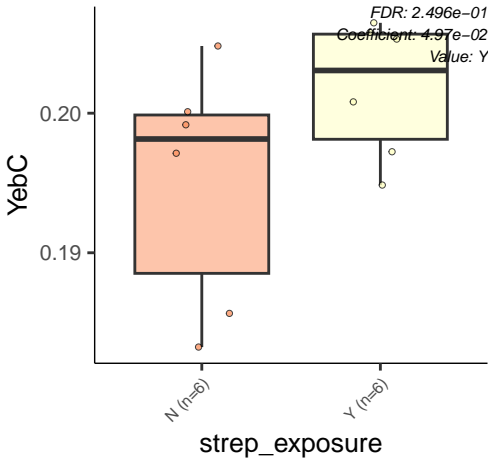
FDR: 2.496e-01
Coefficient: -1.45e-01
Value: Y

N (n=6)

Y (n=6)

strep_exposure





tRNA.aminoacylation..Tyr

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

N (n=6)

Y (n=6)

strep_exposure

0.110
0.105
0.100
0.095
0.090

