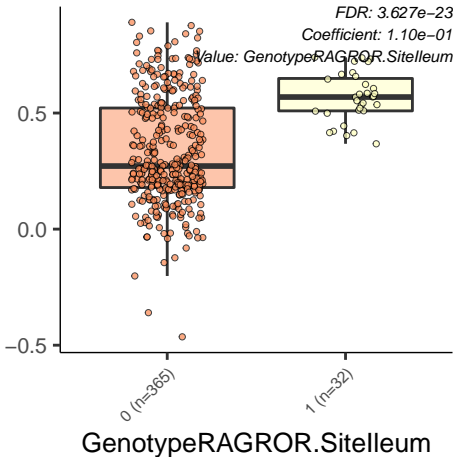
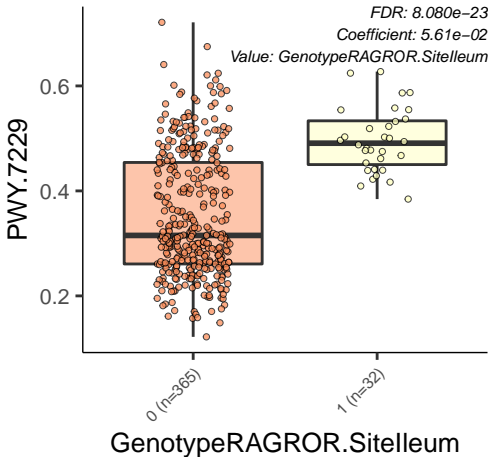


PWY0.1586



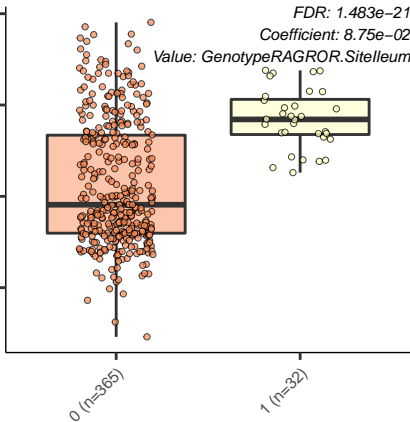


FASYN.ELONG.PWY

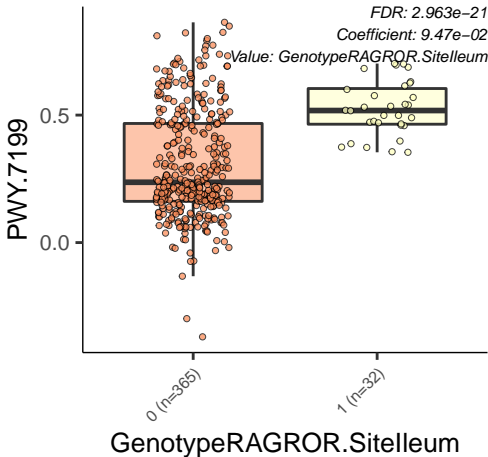
FDR: 1.483e-21

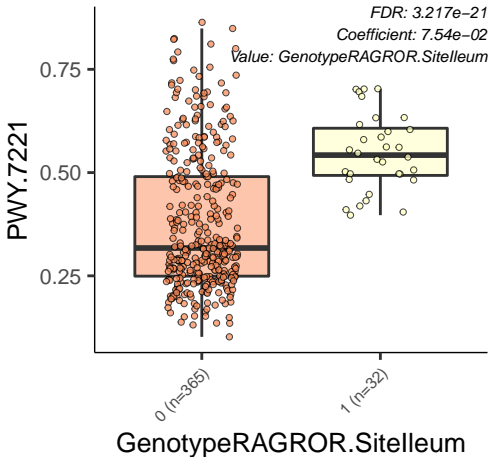
Coefficient: 8.75e-02

Value: GenotypeRAGROR.Sitelleum



GenotypeRAGROR.Sitelleum





PHOSLIPSYN.PWY

FDR: $3.450e-21$

Coefficient: $7.90e-02$

Value: GenotypeRAGROR.Sitelleum

0.75

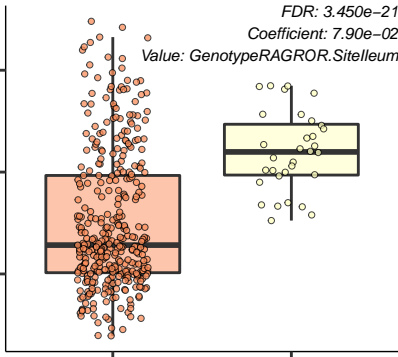
0.50

0.25

0 (n=365)

1 (n=32)

GenotypeRAGROR.Sitelleum



TRNA.CHARGING.PWY

FDR: $3.450e-21$

Coefficient: $7.38e-02$

Value: GenotypeRAGROR.Sitelleum

0.75

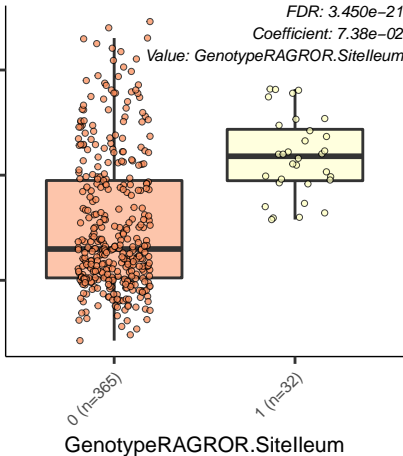
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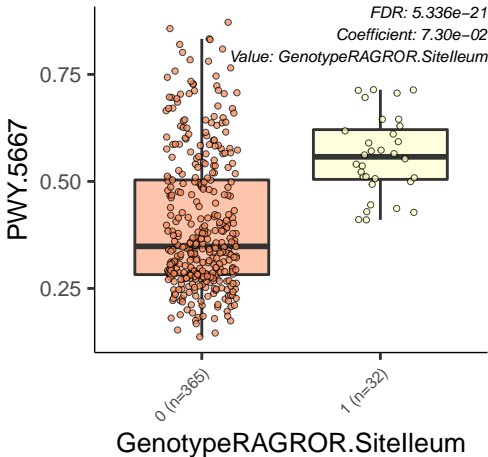
0.25

0 (n=365)

1 (n=32)

GenotypeRAGROR.Sitelleum





PWY0.1319

FDR: 5.336e-21

Coefficient: 7.30e-02

Value: GenotypeRAGROR.Sitelleum

0.75

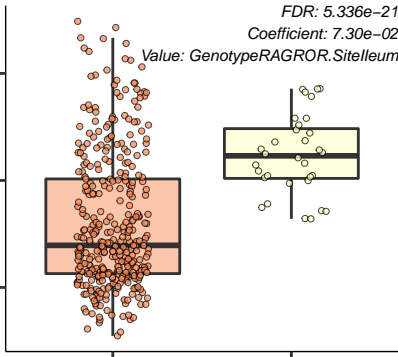
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0.25

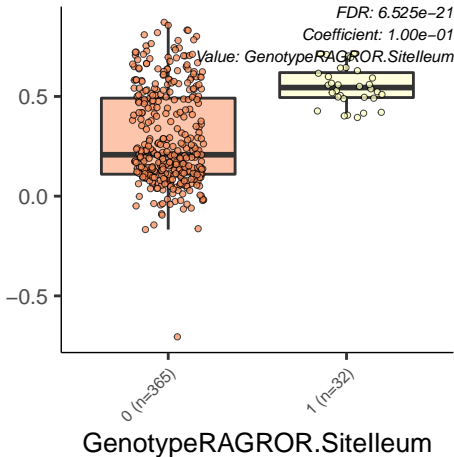
0 (n=365)

1 (n=32)

GenotypeRAGROR.Sitelleum



PWY.5659



PEPTIDOGLYCANSYN.PWY

FDR: 6.556e-21

Coefficient: 7.53e-02

Value: GenotypeRAGROR.Sitelleum

0.75

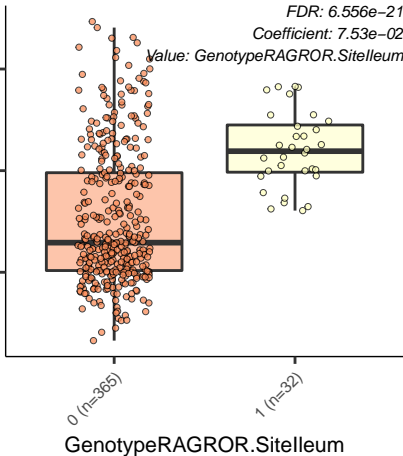
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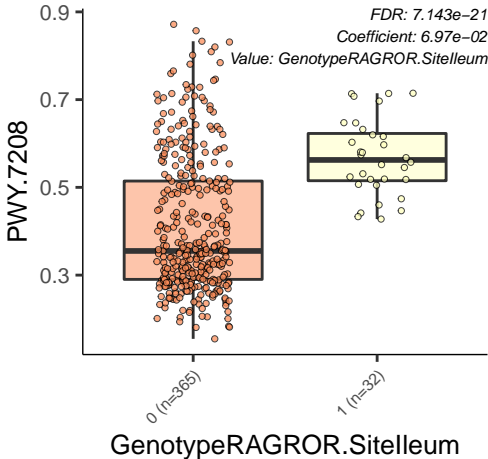
0.25

0 (n=365)

1 (n=32)

GenotypeRAGROR.Sitelleum





PWY.6387

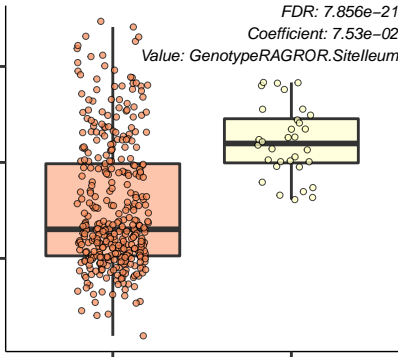
0.75
0.50
0.25

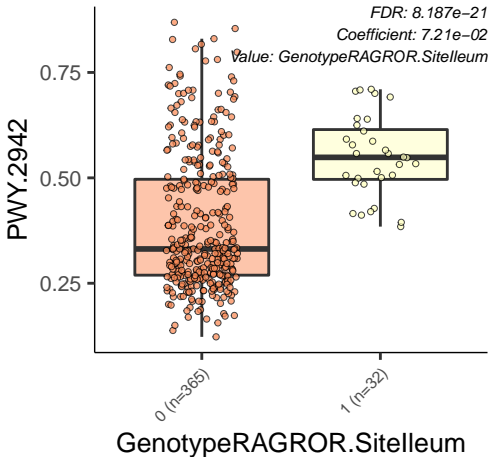
0 (n=365)

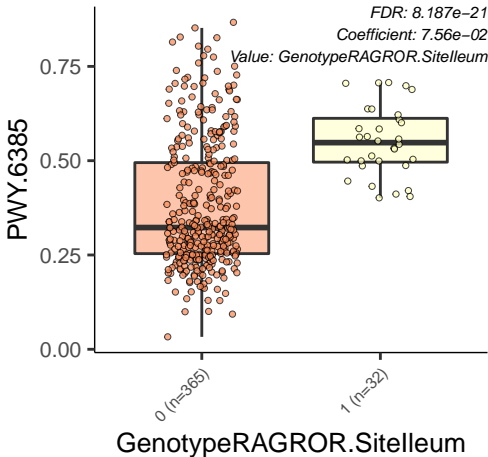
1 (n=32)

GenotypeRAGROR.Sitelleum

FDR: 7.856e-21
Coefficient: 7.53e-02
Value: GenotypeRAGROR.Sitelleum







PWY.7219

FDR: 8.187e-21

Coefficient: 7.01e-02

Value: GenotypeRAGROR.Sitelleum

0.75

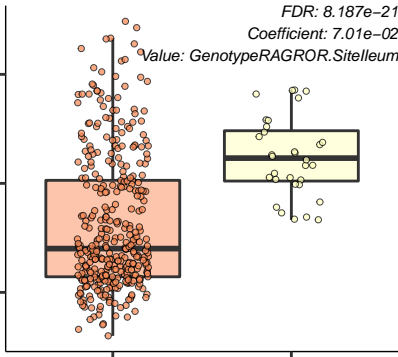
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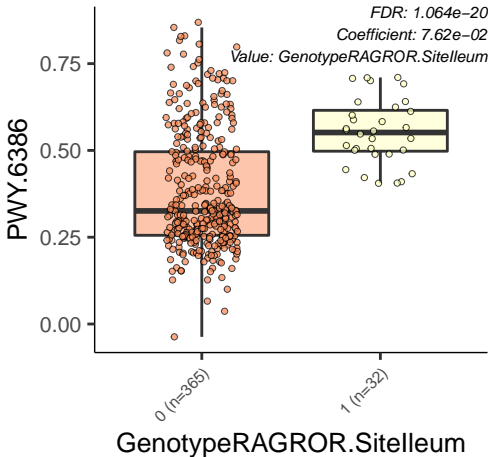
0.25

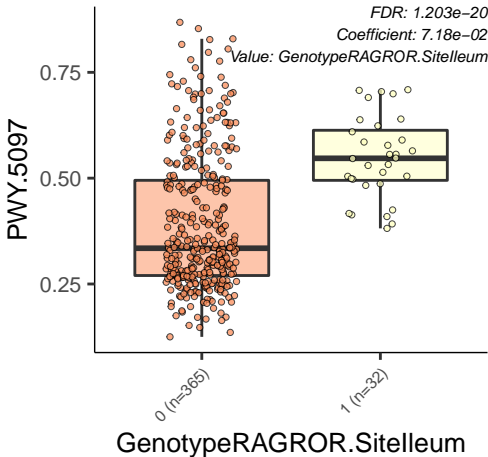
0 (n=365)

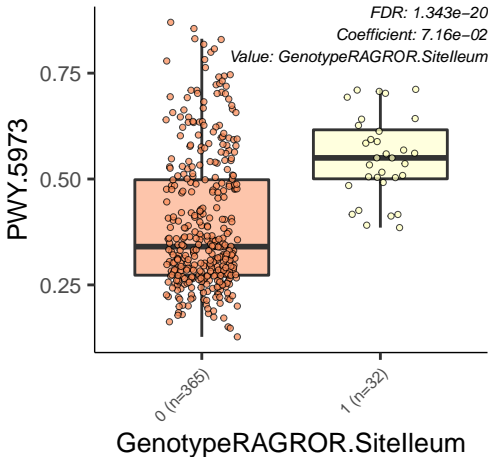
1 (n=32)

GenotypeRAGROR.Sitelleum









ANAGLYCOLYSIS.PWY

FDR: 1.809e-20

Coefficient: 6.95e-02

Value: GenotypeRAGROR.Sitelleum

0.75

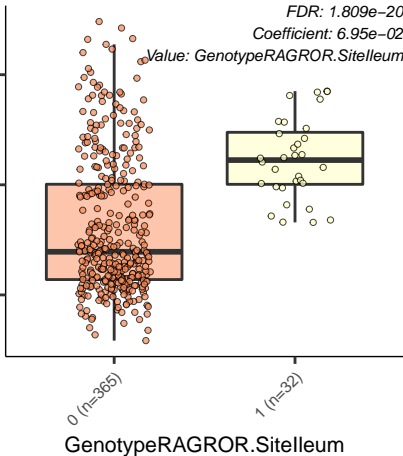
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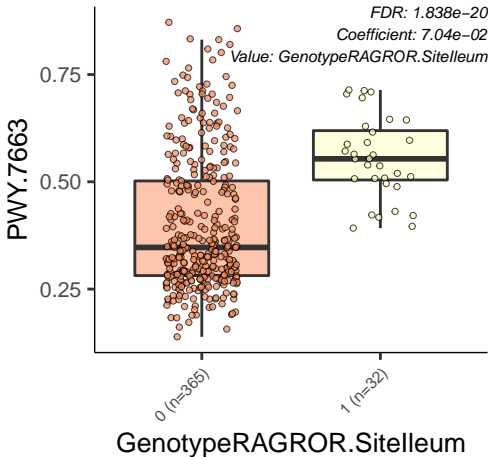
0.25

0 (n=365)

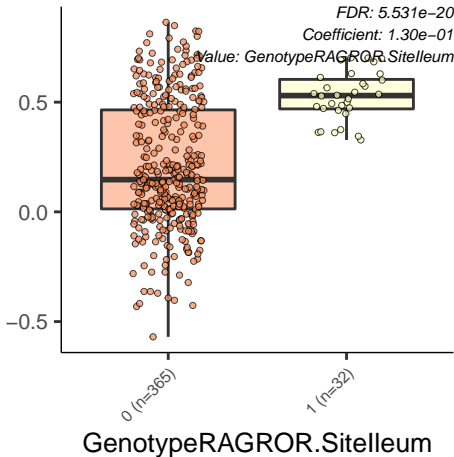
1 (n=32)

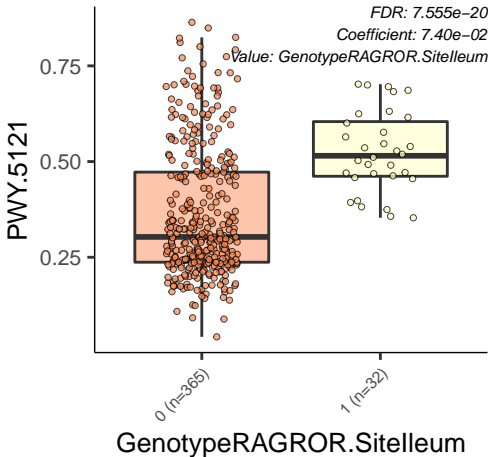
GenotypeRAGROR.Sitelleum





PWY0.1298





PWY4FS.7

FDR: 9.777e-20

Coefficient: 8.73e-02

Value: GenotypeRAGROR.Sitelleum

0.75

0.50

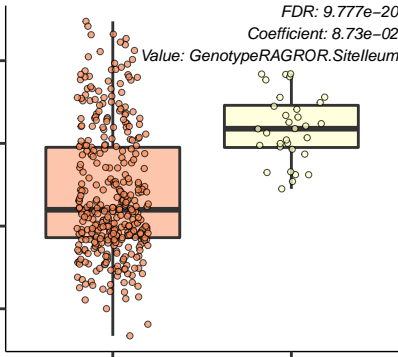
0.25

0.00

0 (n=365)

1 (n=32)

GenotypeRAGROR.Sitelleum



PWY4FS.8

FDR: 9.777e-20

Coefficient: 8.73e-02

Value: GenotypeRAGROR.Sitelleum

0.75

0.50

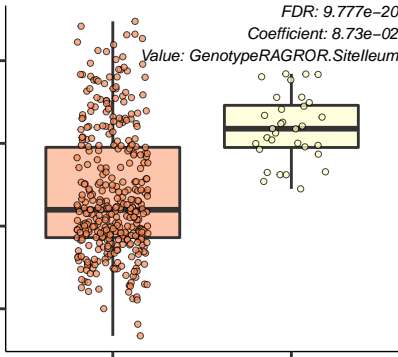
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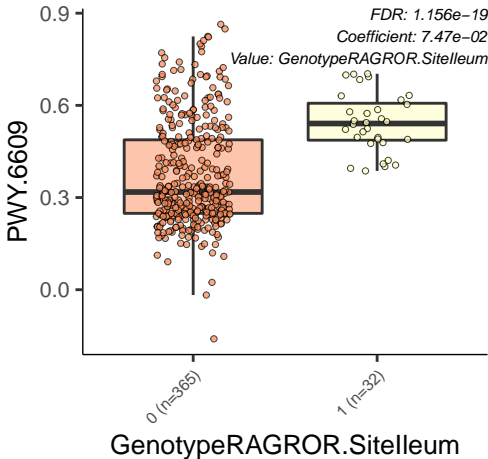
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0 (n=365)

1 (n=32)

GenotypeRAGROR.Sitelleum



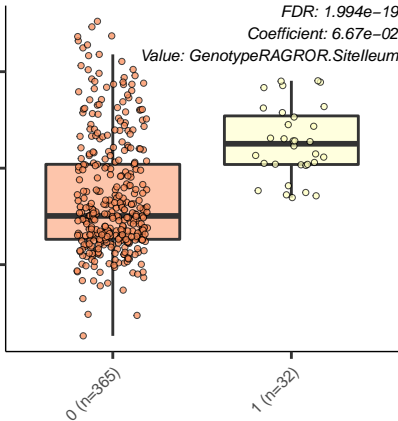


NONOXIPENT.PWY

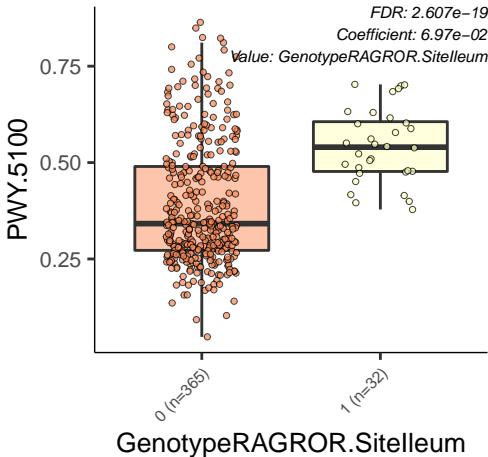
FDR: 1.994e-19

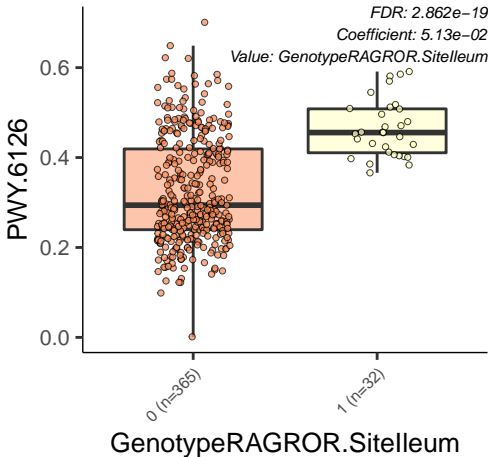
Coefficient: 6.67e-02

Value: GenotypeRAGROR.Sitelleum



GenotypeRAGROR.Sitelleum





COMPLETE.ARO.PWY

0.50
0.25
0.00

0 (n=365)

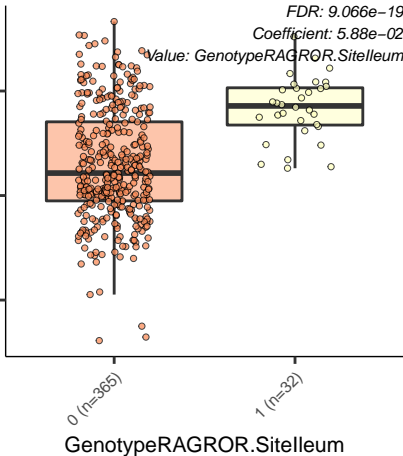
1 (n=32)

GenotypeRAGROR.Sitelleum

Value: GenotypeRAGROR.Sitelleum

FDR: $9.066e-19$

Coefficient: $5.88e-02$



NONMEVIP.PWY

FDR: 9.872e-19

Coefficient: 7.29e-02

Value: GenotypeRAGROR.Sitelleum

0.75

0.50

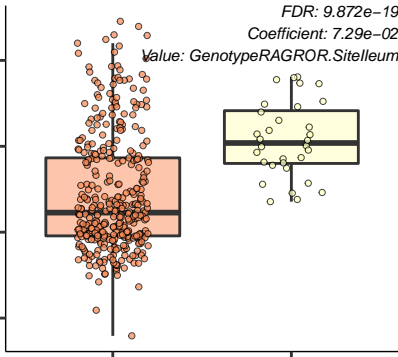
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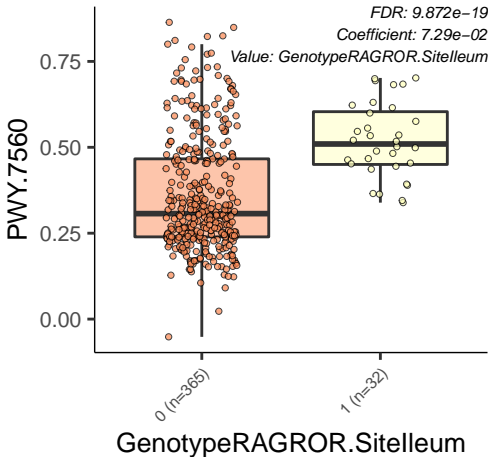
0.00

0 (n=365)

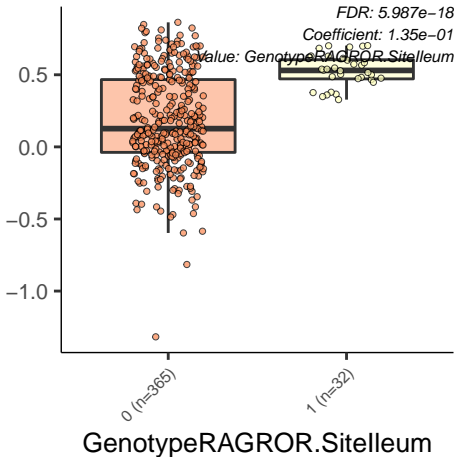
1 (n=32)

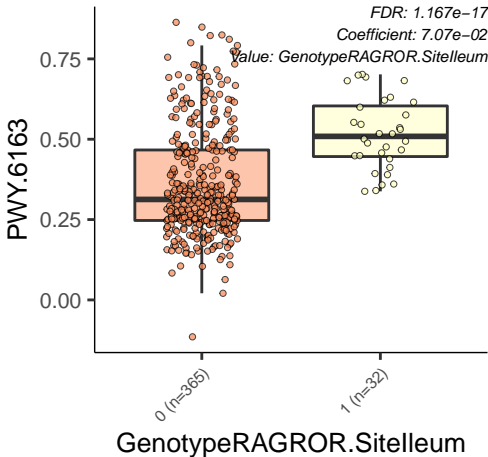
GenotypeRAGROR.Sitelleum

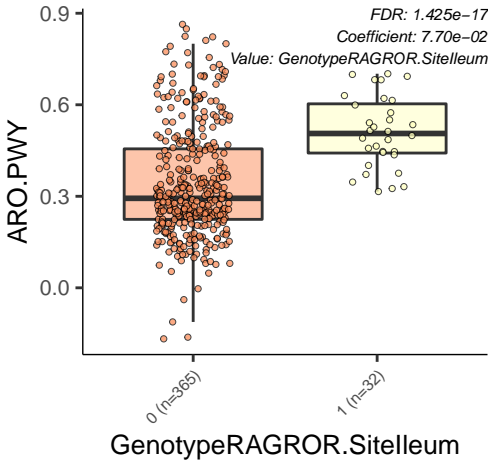




PWY0.1297





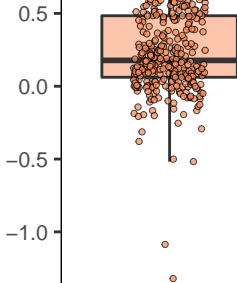


GLCMANNNAUT.PWY

FDR: 9.013e-17

Coefficient: 1.15e-01

Value: GenotypeRAGROR.Sitelleum

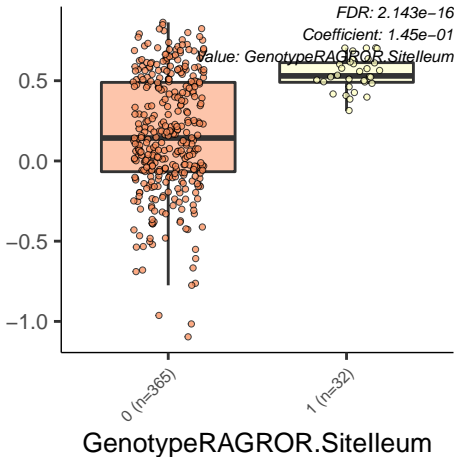


0 (n=365)

1 (n=32)

GenotypeRAGROR.Sitelleum

P161.PWY

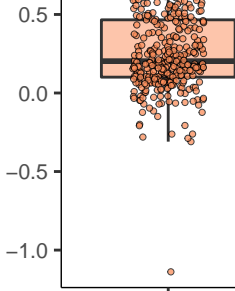


PWY0.1296

FDR: 4.767e-16

Coefficient: 1.02e-01

Value: GenotypeRAGROR.Sitelleum



0 (n=365)

1 (n=32)

GenotypeRAGROR.Sitelleum

POLYISOPRENSYN.PWY

0.4
0.0
-0.4
-0.8

0 (n=365)

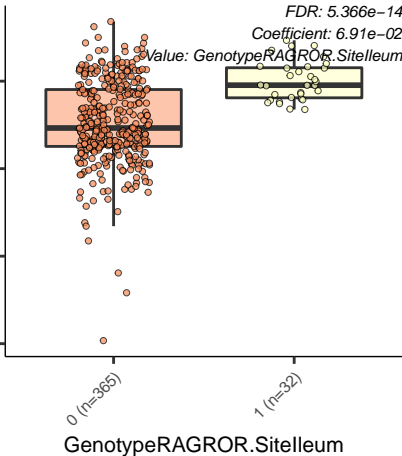
1 (n=32)

GenotypeRAGROR.Sitelleum

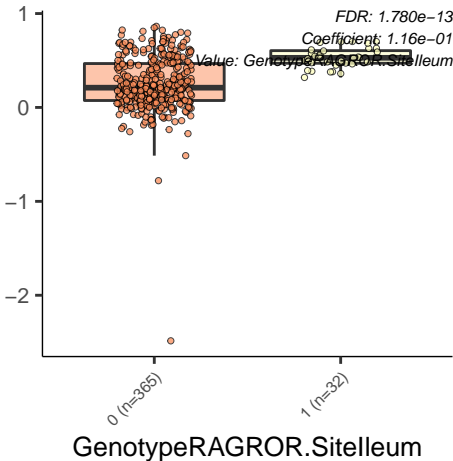
Value: GenotypeRAGROR.Sitelleum

Coefficient: 6.91×10^{-2}

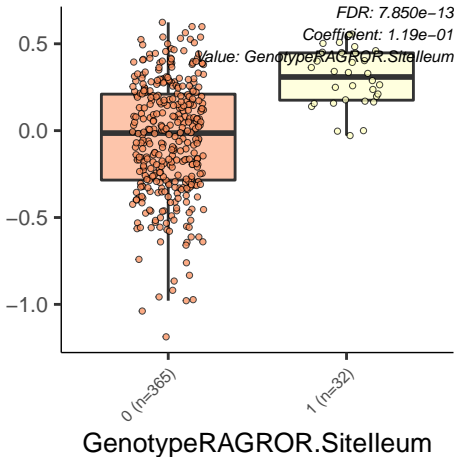
FDR: 5.366×10^{-14}



UDPNAGSYN.PWY



PWY.7187



PWY0.166

0
-1

0 (n=365)

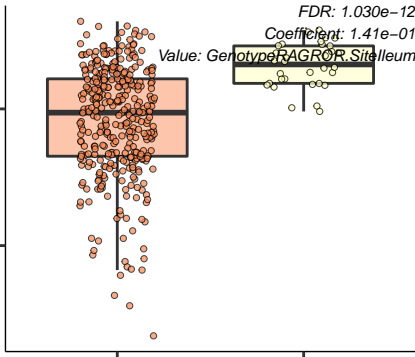
1 (n=32)

GenotypeRAGROR.Sitelleum

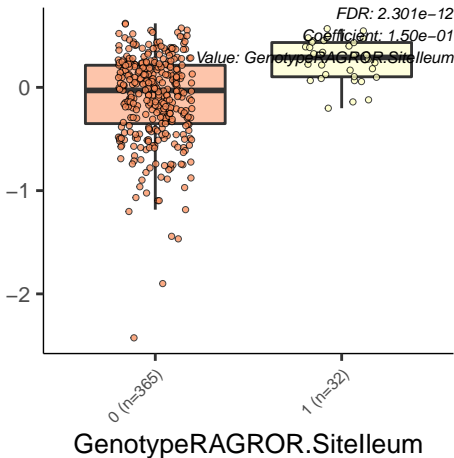
Value: GenotypeRAGROR.Sitelleum

Coefficient: 1.41e-01

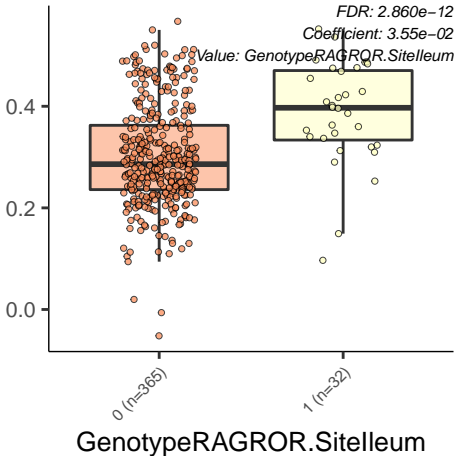
FDR: 1.030e-12

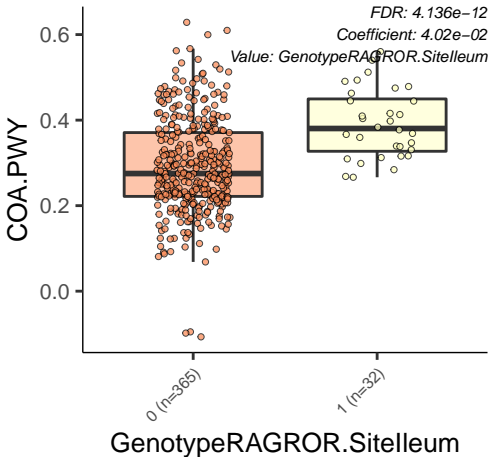


PWY.6125

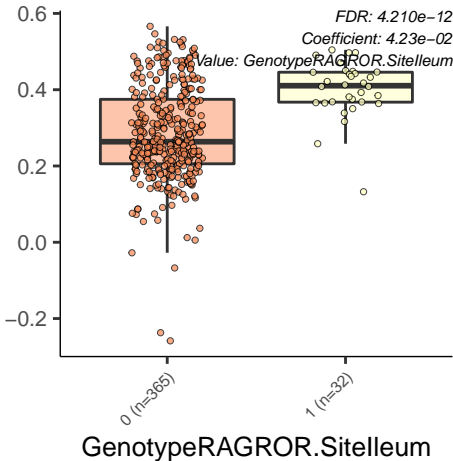


GLUCONEO.PWY

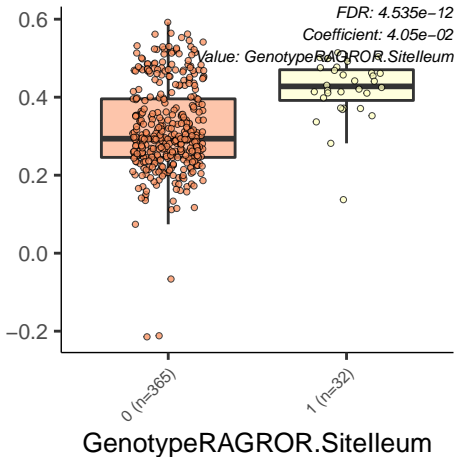




PWY.5484



GLYCOLYSIS



PWY.5505

FDR: 1.698e-11

Coefficient: -2.04e-01

Value: GenotypeRAGROR.Sitelleum

0

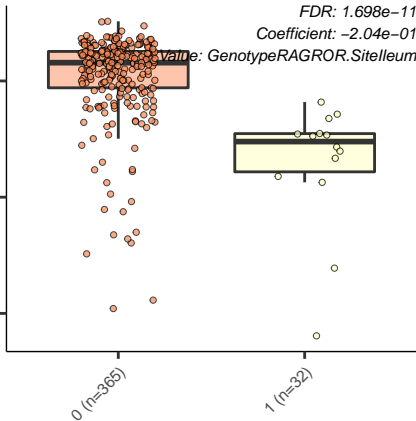
-1

-2

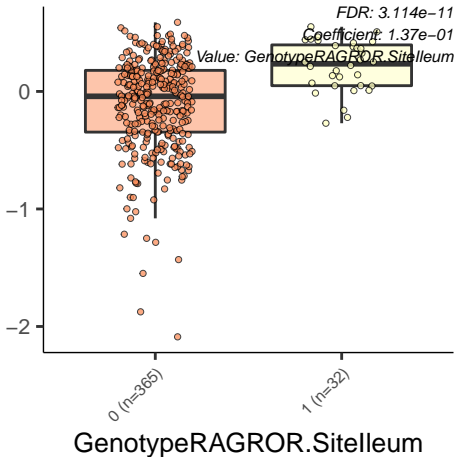
0 (n=365)

1 (n=32)

GenotypeRAGROR.Sitelleum



PWY.7196

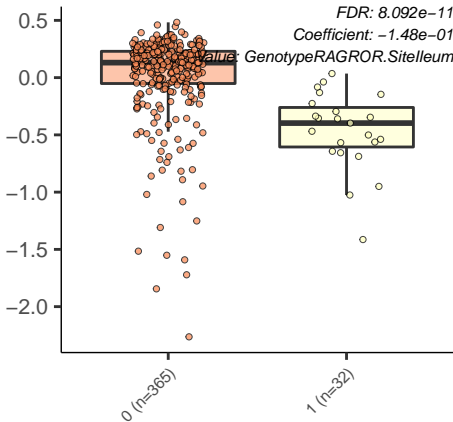


ARGSYNBSUB.PWY

FDR: 8.092e-11

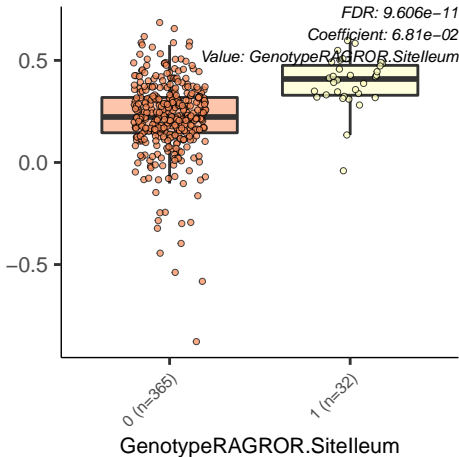
Coefficient: -1.48e-01

Value: GenotypeRAGROR.Sitelleum

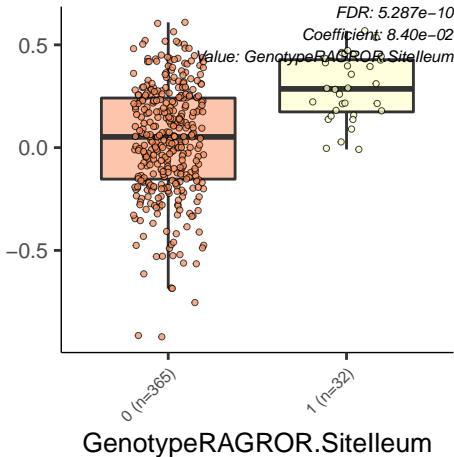


GenotypeRAGROR.Sitelleum

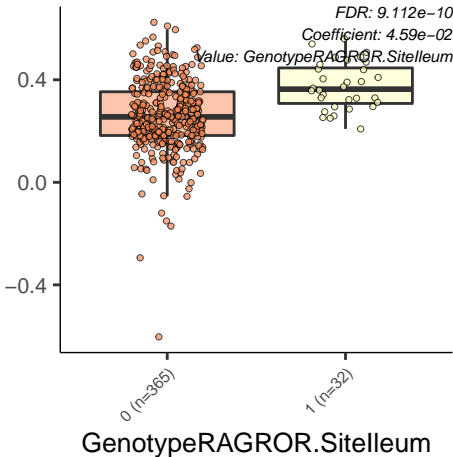
DAPLYSINESYN.PWY



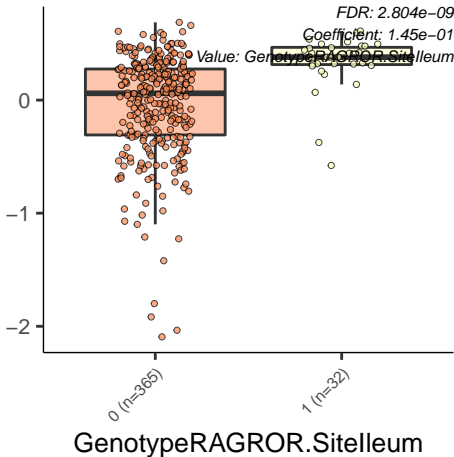
PWY.841



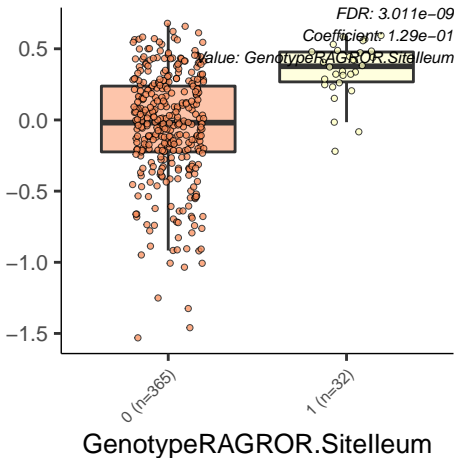
PWY.6151



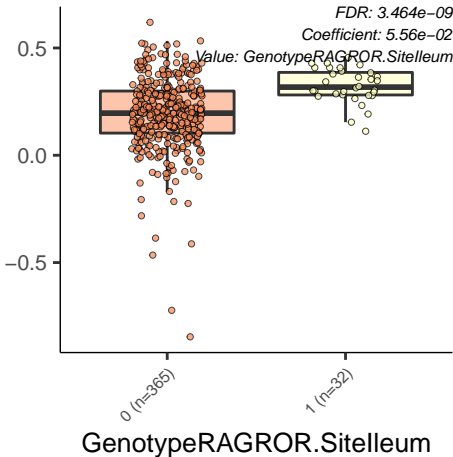
PWY.7392



P124.PWY



OANTIGEN.PWY



PWY.7184

-1

0

GenotypeRAGROR.Sitelleum

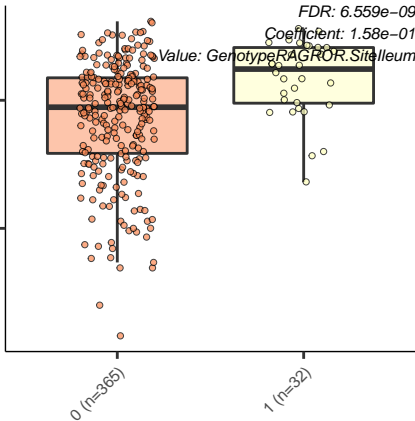
0 (n=365)

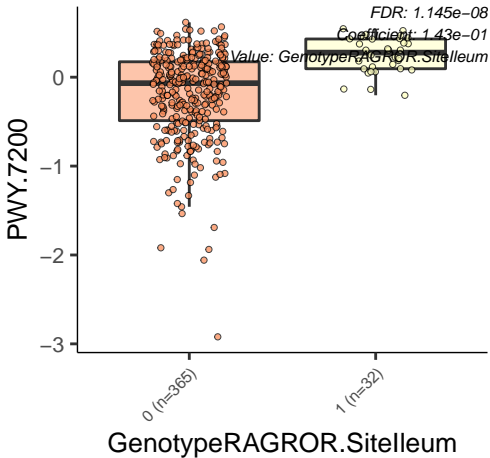
1 (n=32)

Value: GenotypeRAGROR.Sitelleum

Coefficient: 1.58e-01

FDR: 6.559e-09





P122.PWY

FDR: 2.017e-08

Coefficient: 1.60e-01

Value: GenotypeRAGROR.Sitelleum

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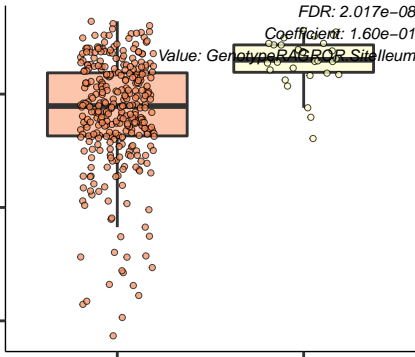
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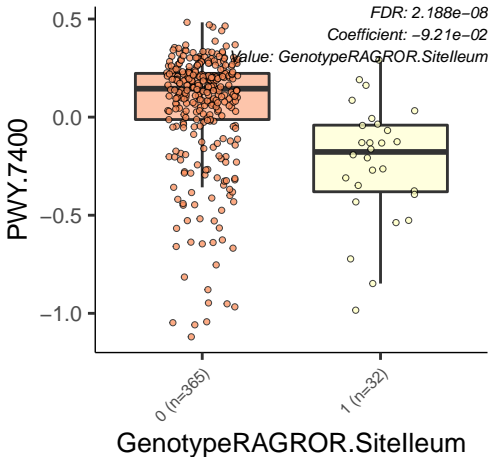
-2

0 (n=365)

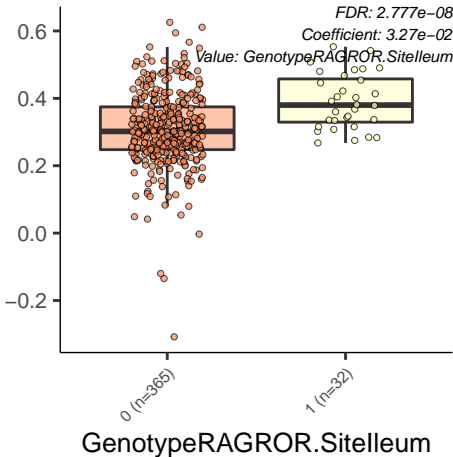
1 (n=32)

GenotypeRAGROR.Sitelleum

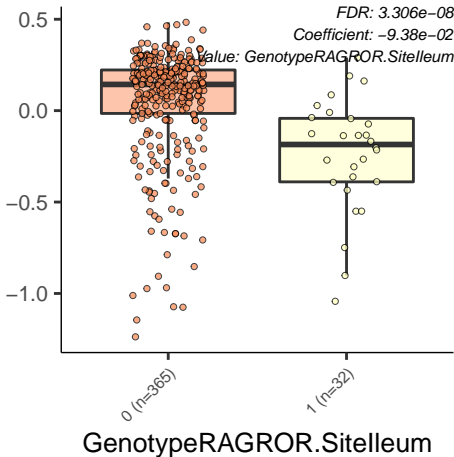




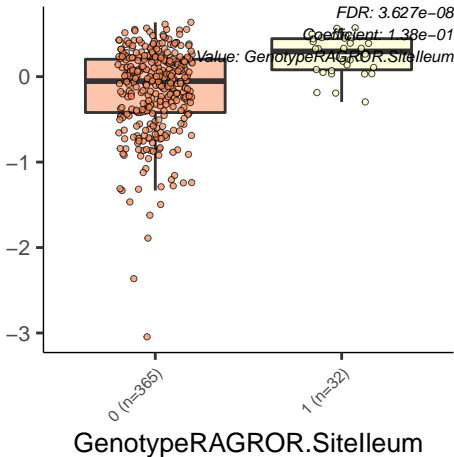
THRESYN.PWY

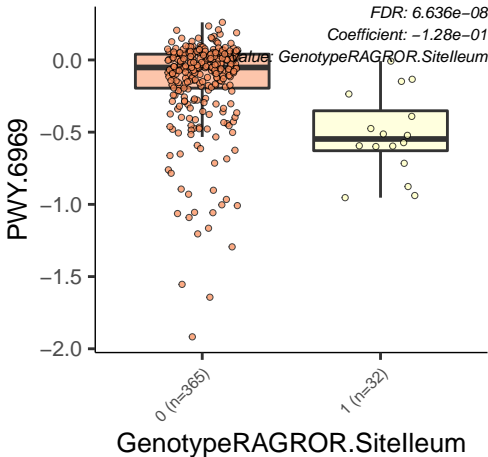


ARGSYN.PWY

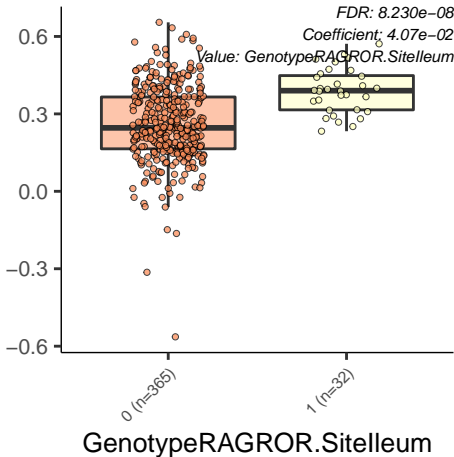


PWY.7228

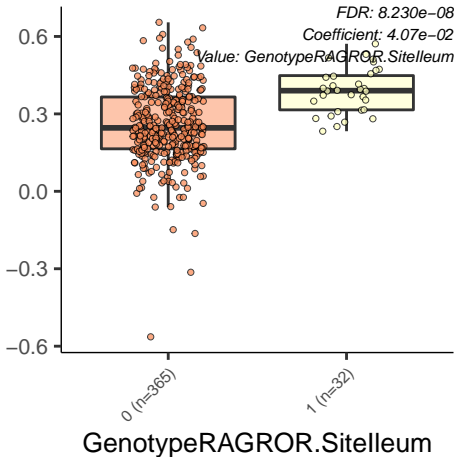




PWY.7220



PWY.7222

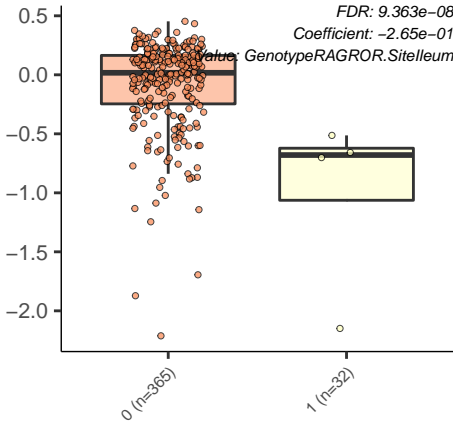


COBALSYN.PWY

FDR: 9.363e-08

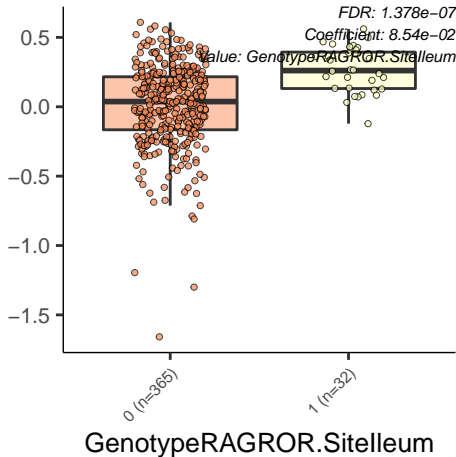
Coefficient: -2.65e-01

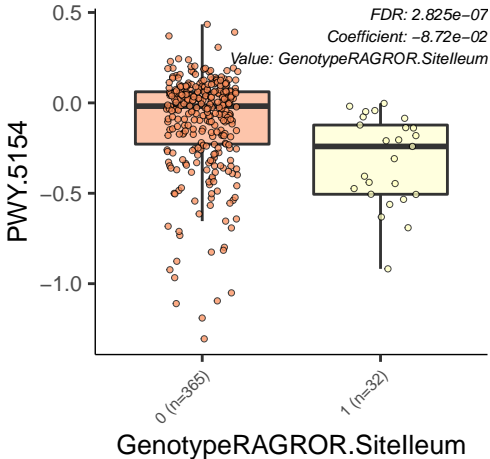
Value: GenotypeRAGROR.Sitelleum



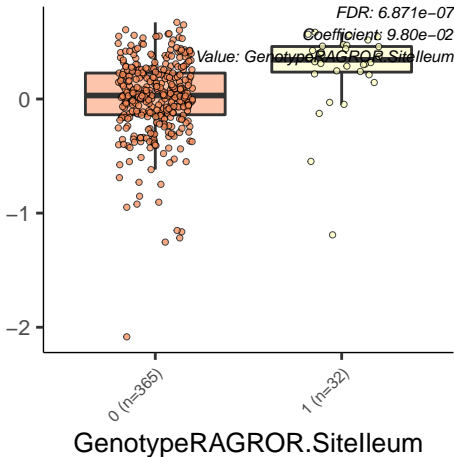
GenotypeRAGROR.Sitelleum

PWY0.162





PWY.6471



DENOVOPURINE2.PWY

0

-1

-2

-3

0 (n=365)

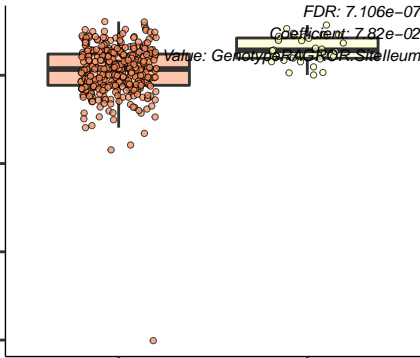
1 (n=32)

GenotypeRAGROR.Sitelleum

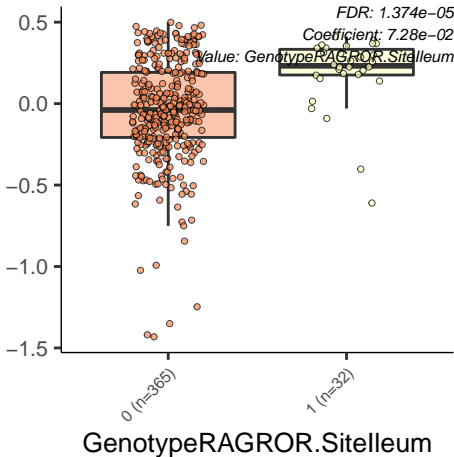
FDR: 7.106e-07

Coefficient: 7.82e-02

Value: GenotypeRAGROR.Sitelleum



COLANSYN.PWY



PYRIDNUCSAL.PWY

FDR: 2.355e-05

Coefficient: -1.13e-01

Value: GenotypeRAGROR.Sitelleum

0

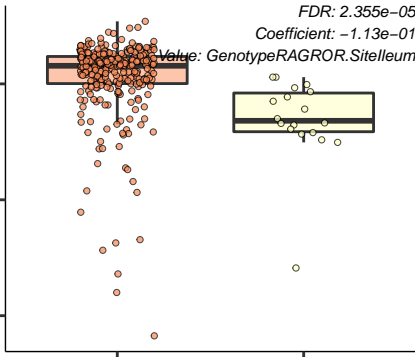
-1

-2

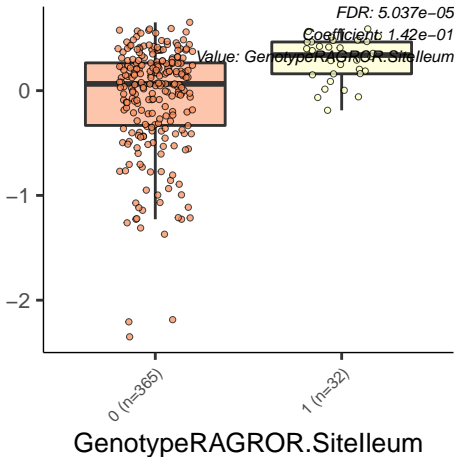
0 (n=365)

1 (n=32)

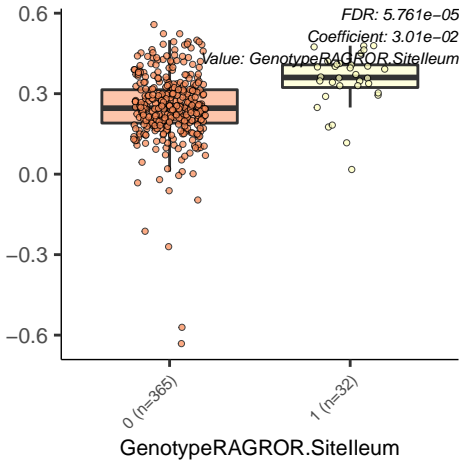
GenotypeRAGROR.Sitelleum



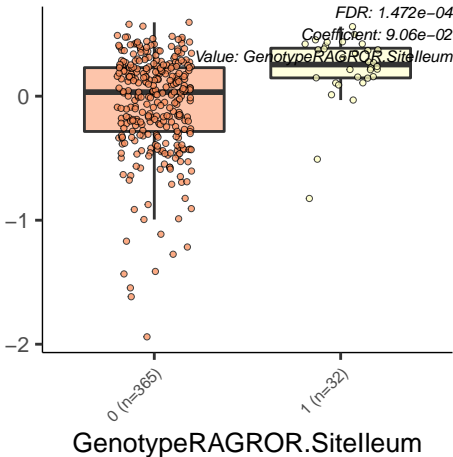
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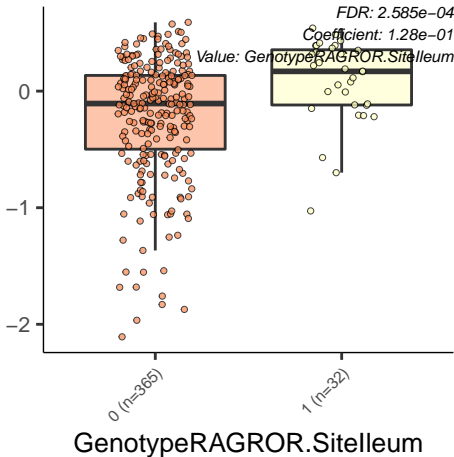
ANAEROFRUCAT.PWY



PWY.7234



PWY.7197



HISTSYN.PWY

FDR: 2.439e-03

Coefficient: -5.64e-02

Value: GenotypeRAGROR.Sitelleum

0

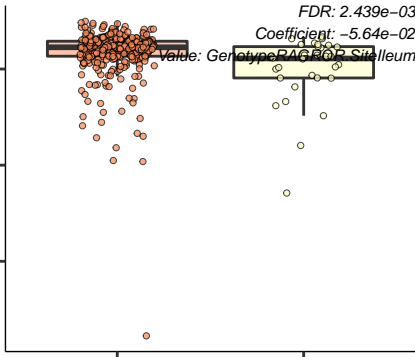
-1

-2

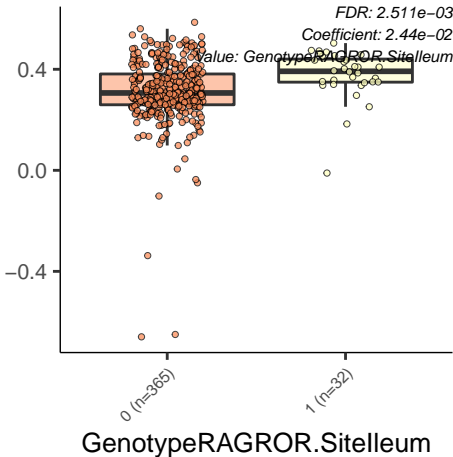
0 (n=365)

1 (n=32)

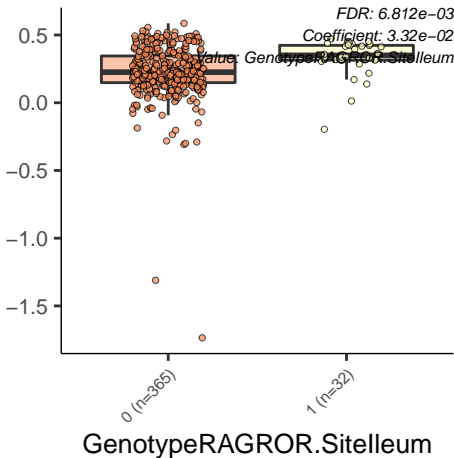
GenotypeRAGROR.Sitelleum

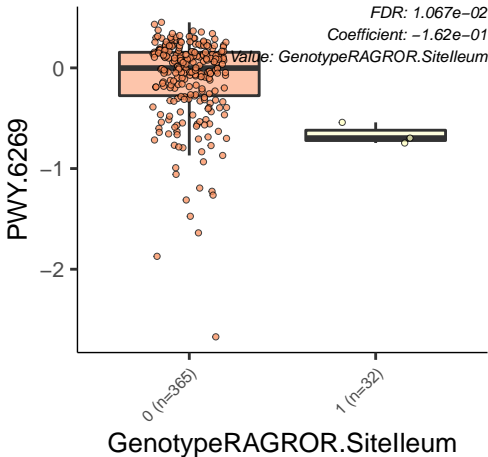


CALVIN.PWY

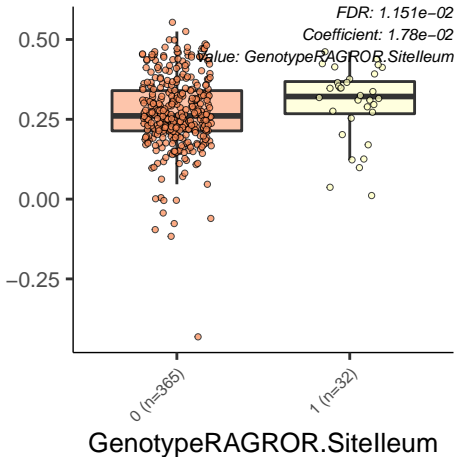


PWY.5695

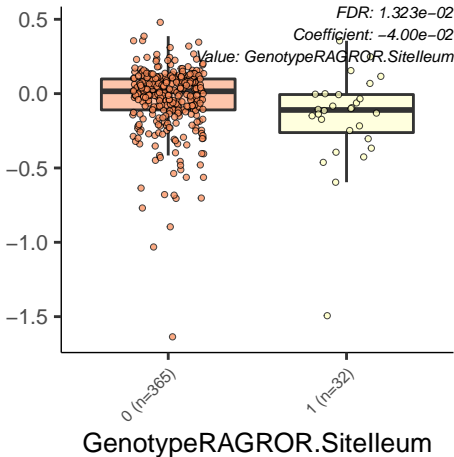




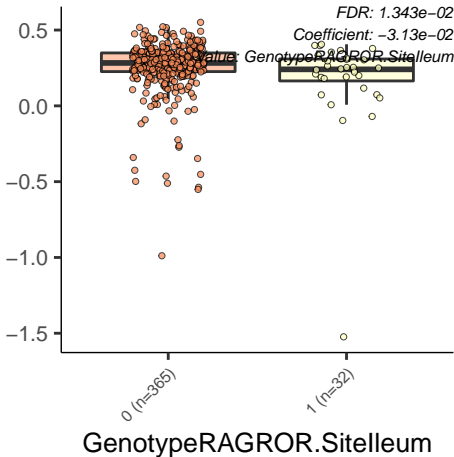
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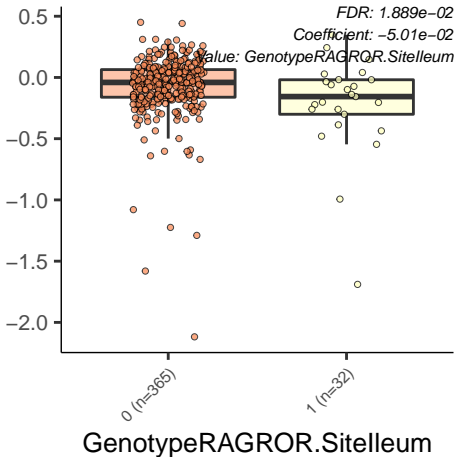
PENTOSE.P.PWY



PWY.6737



PWY.6612



ASPASN.PWY

0
-1
-2

0 (n=365)

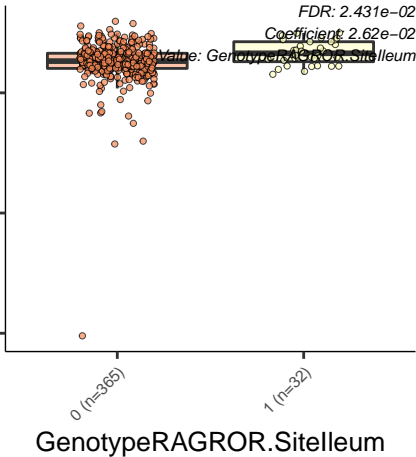
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GenotypeRAGROR.Sitelleum

Value: GenotypeRAGROR.Sitelleum

Coefficient: 2.62e-02

FDR: 2.431e-02

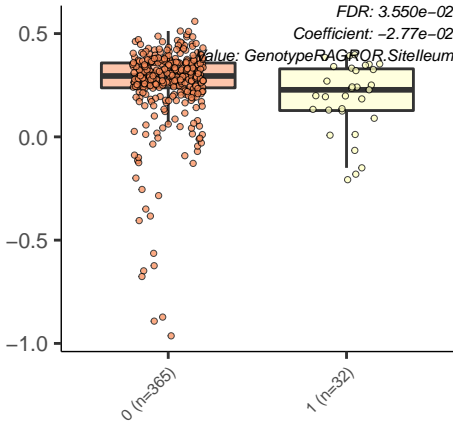


PWY.7111

FDR: 3.550e-02

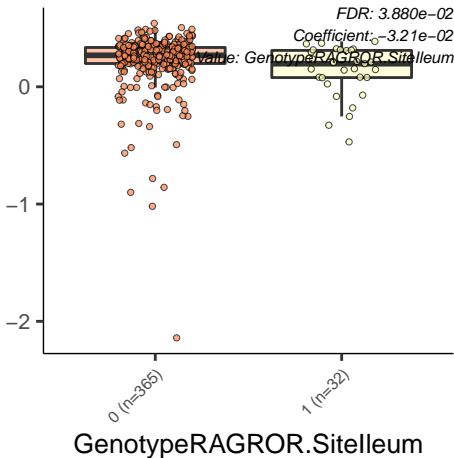
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Value: GenotypeRAGROR.Sitelleum

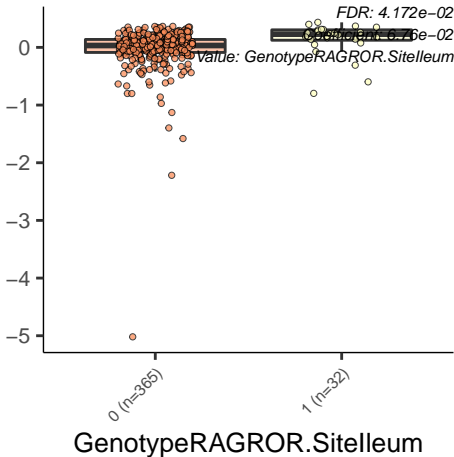


GenotypeRAGROR.Sitelleum

PWY.5103



P441.PWY



GLUTORN.PWY

0

-1

-2

0 (n=365)

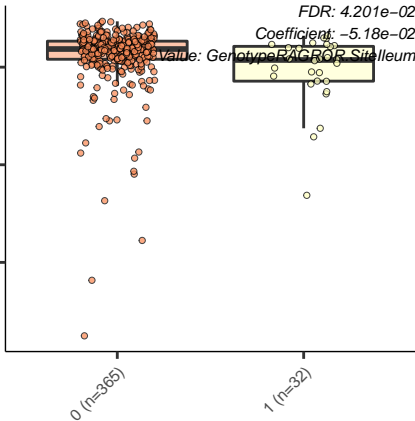
1 (n=32)

GenotypeRAGROR.Sitelleum

FDR: 4.201e-02

Coefficient: -5.18e-02

Value: GenotypeRAGROR.Sitelleum



PWY.5509

FDR: 4.201e-02

Coefficient: -1.56e-01

Value: GenotypeRAGROR.Sitelleum

0

-1

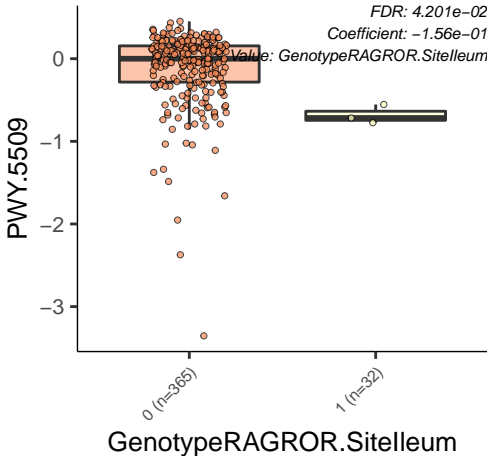
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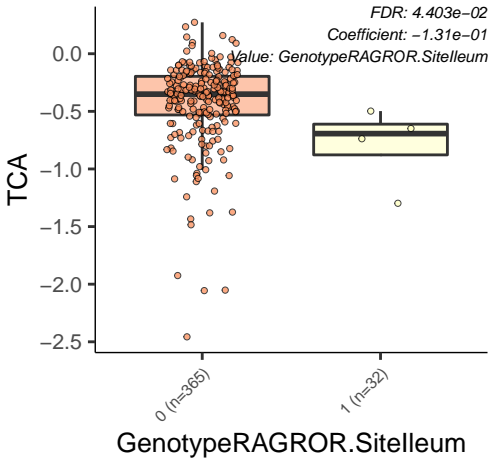
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0 (n=365)

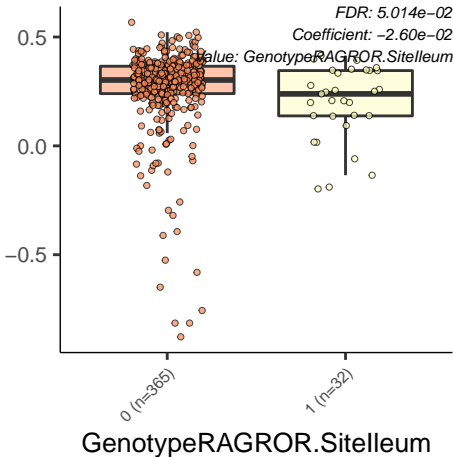
1 (n=32)

GenotypeRAGROR.Sitelleum

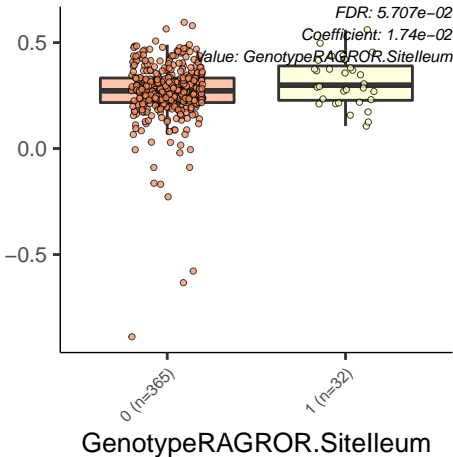




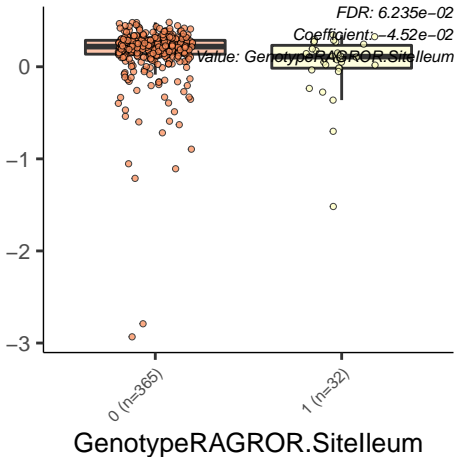
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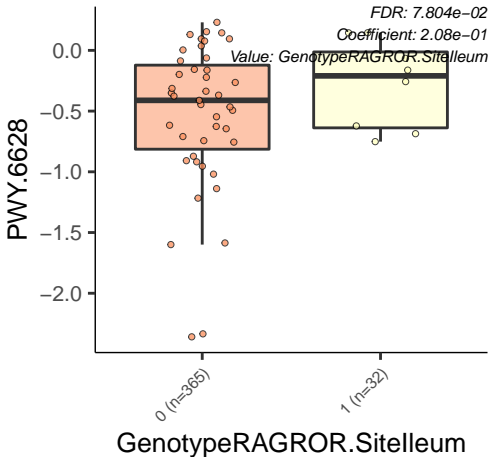


PWY.6123

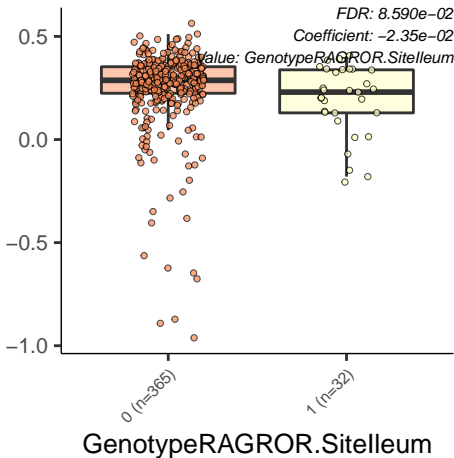


TRPSYN.PWY

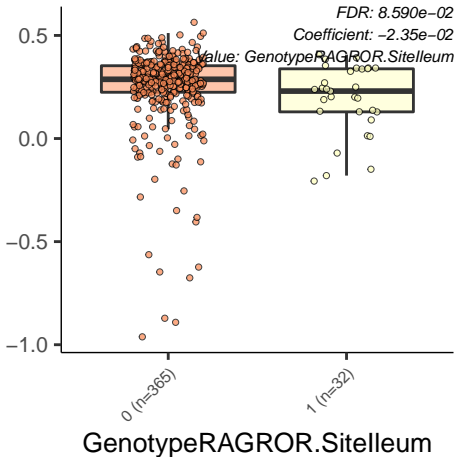




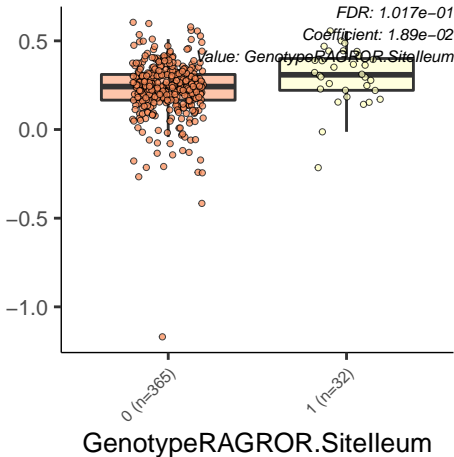
ILEUSYN.PWY



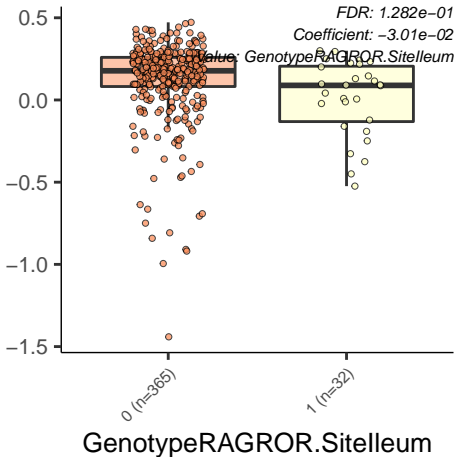
VALSYN.PWY



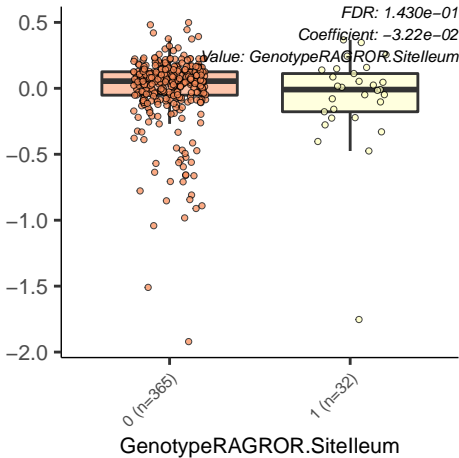
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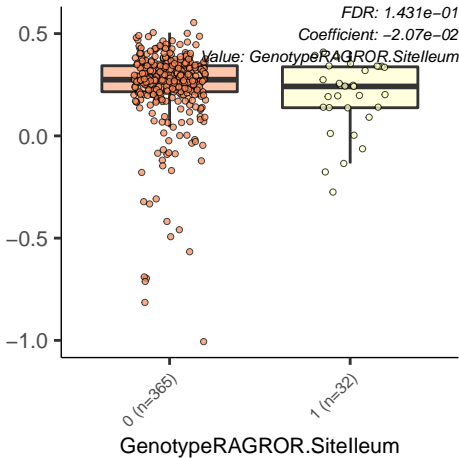
PWY.7242



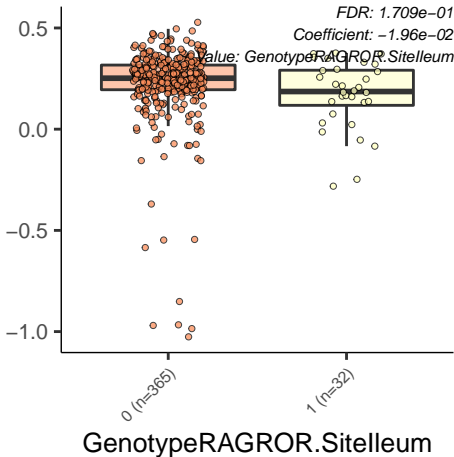
FERMENTATION.PWY



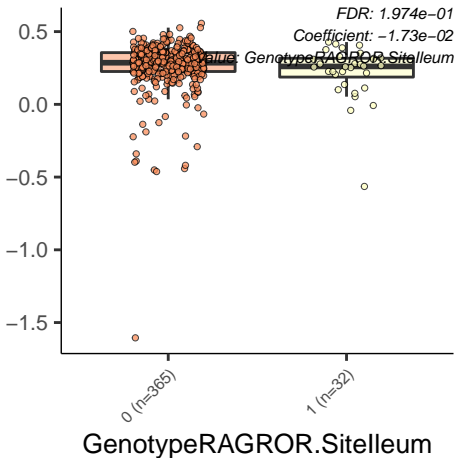
BRANCHED.CHAIN.AA.SYN.PWY



SER.GLYSYN.PWY



GLYCOCAT.PWY



GALACTUROCAT.PWY

