

TRPSYN.PWY

FDR: $4.211\text{e-}04$

Coefficient: $-6.98\text{e-}02$

p-value: GenotypeTCR_KO.SiteJejunum

0

-1

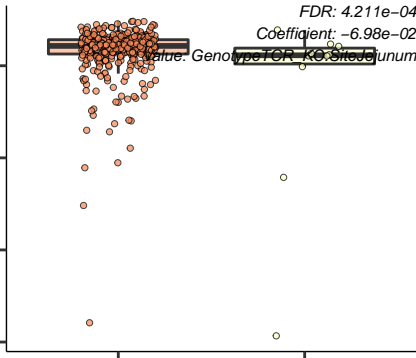
-2

-3

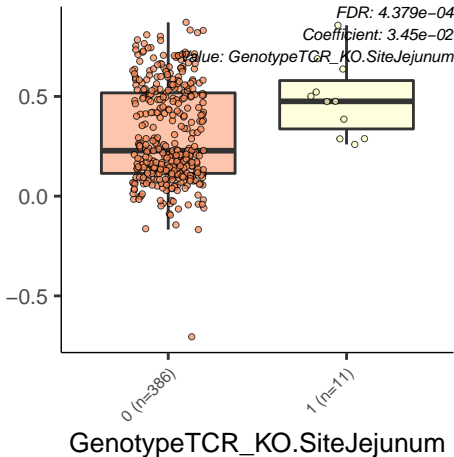
0 (n=386)

1 (n=11)

GenotypeTCR_KO.SiteJejunum



PWY.5659



PHOSLIPSYN.PWY

0.75
0.50
0.25

0 (n=386)

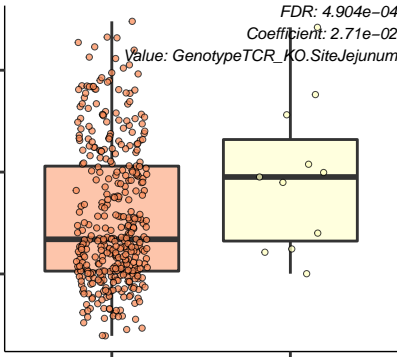
1 (n=11)

GenotypeTCR_KO.SiteJejunum

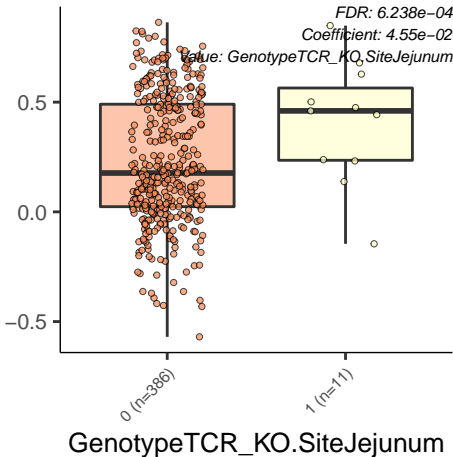
Value: GenotypeTCR_KO.SiteJejunum

Coefficient: 2.71e-02

FDR: 4.904e-04



PWY0.1298



PWY.5973

0.75

0.50

0.25

0 (n=386)

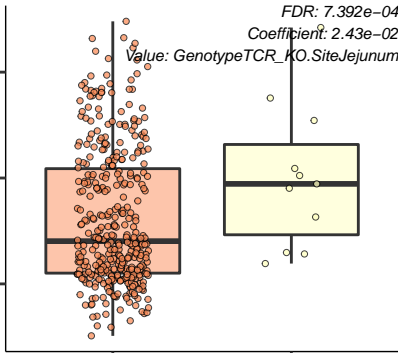
1 (n=11)

GenotypeTCR_KO.SiteJejunum

FDR: 7.392e-04

Coefficient: 2.43e-02

Value: GenotypeTCR_KO.SiteJejunum



PWY.7663

0.75
0.50
0.25

0 (n=386)

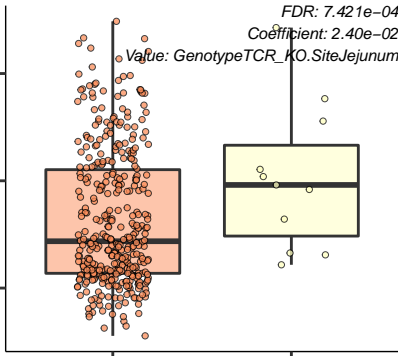
1 (n=11)

GenotypeTCR_KO.SiteJejunum

Value: GenotypeTCR_KO.SiteJejunum

Coefficient: 2.40e-02

FDR: 7.421e-04



PWY.5667

0.75
0.50
0.25

0 (n=386)

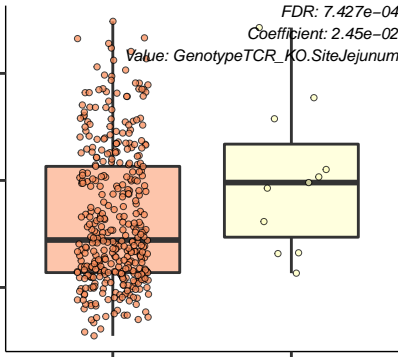
1 (n=11)

GenotypeTCR_KO.SiteJejunum

Value: GenotypeTCR_KO.SiteJejunum

Coefficient: 2.45×10^{-2}

FDR: 7.427×10^{-4}



PWY0.1319

0.75
0.50
0.25

0 (n=386)

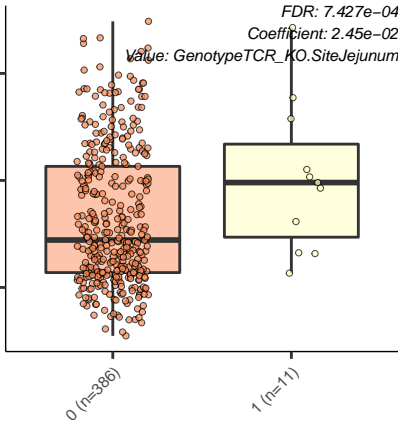
1 (n=11)

GenotypeTCR_KO.SiteJejunum

Value: GenotypeTCR_KO.SiteJejunum

Coefficient: 2.45×10^{-2}

FDR: 7.427×10^{-4}



TRNA.CHARGING.PWY

0.75

0.50

0.25

0 (n=386)

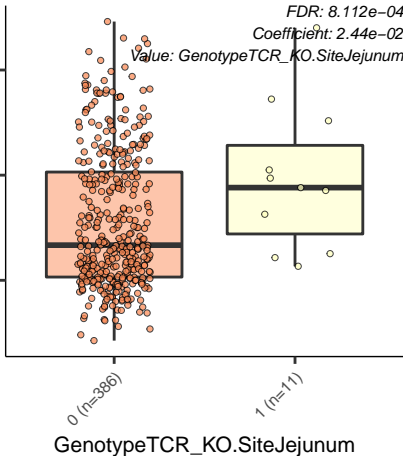
1 (n=11)

GenotypeTCR_KO.SiteJejunum

FDR: 8.112×10^{-4}

Coefficient: 2.44×10^{-2}

Value: GenotypeTCR_KO.SiteJejunum

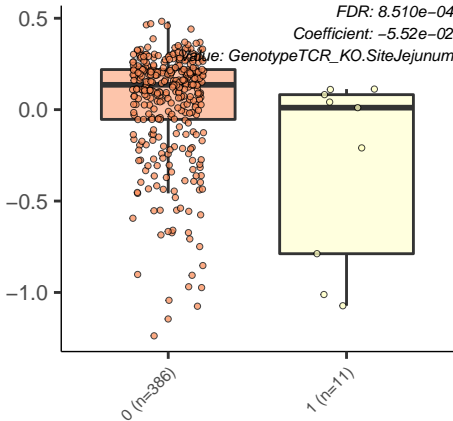


ARGSYN.PWY

FDR: 8.510e-04

Coefficient: -5.52e-02

Value: GenotypeTCR_KO.SiteJejunum



GenotypeTCR_KO.SiteJejunum

PWY.5097

0.75

0.50

0.25

0 (n=386)

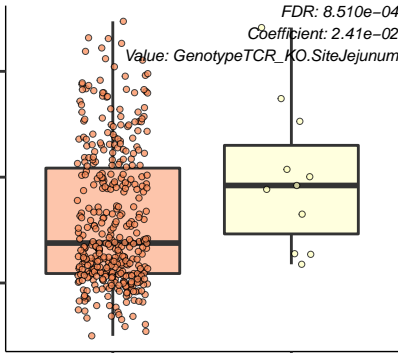
1 (n=11)

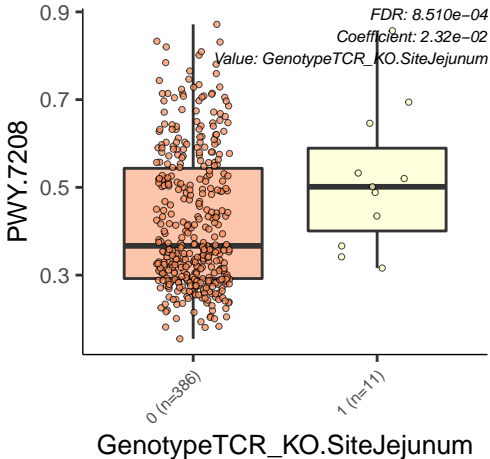
GenotypeTCR_KO.SiteJejunum

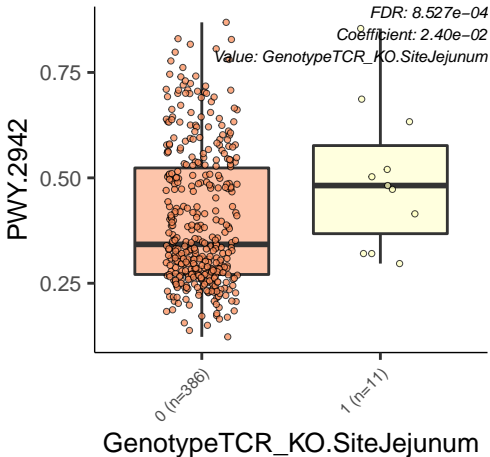
FDR: 8.510e-04

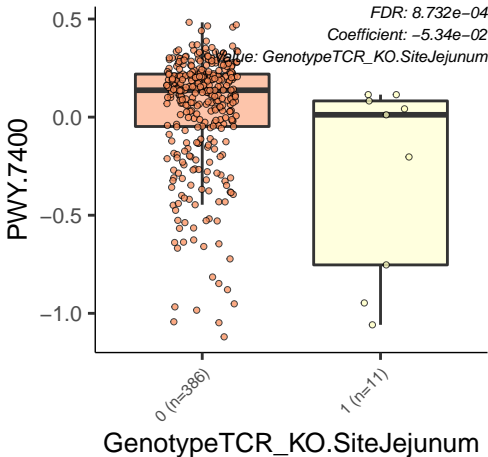
Coefficient: 2.41e-02

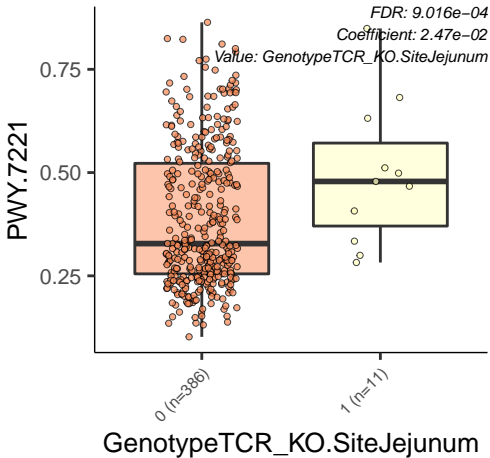
Value: GenotypeTCR_KO.SiteJejunum











PWY.7219

0.75
0.50
0.25

0 (n=386)

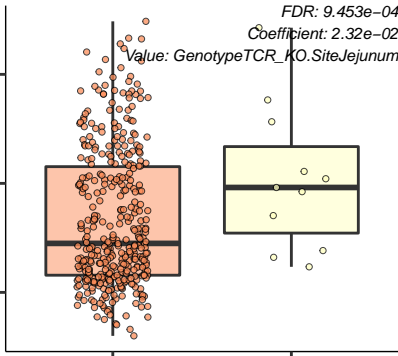
1 (n=11)

GenotypeTCR_KO.SiteJejunum

FDR: 9.453×10^{-4}

Coefficient: 2.32×10^{-2}

Value: GenotypeTCR_KO.SiteJejunum



PEPTIDOGLYCANSYN.PWY

0.75

0.50

0.25

0 (n=386)

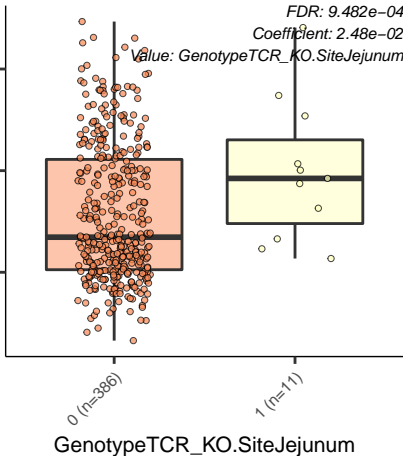
1 (n=11)

GenotypeTCR_KO.SiteJejunum

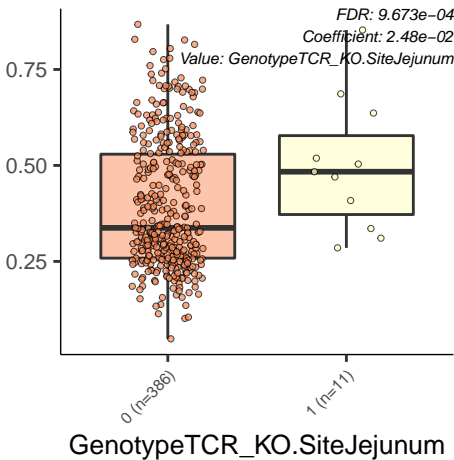
FDR: 9.482×10^{-4}

Coefficient: 2.48×10^{-2}

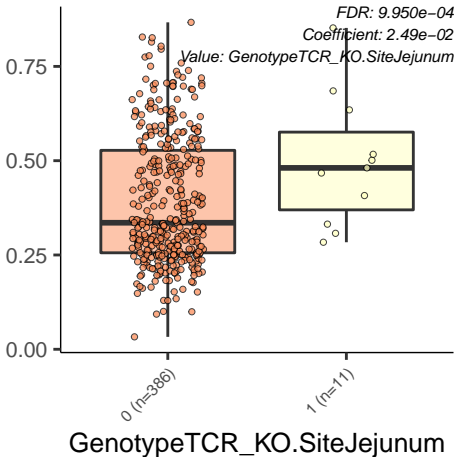
Value: GenotypeTCR_KO.SiteJejunum



PWY.6387



PWY.6385



ANAGLYCOLYSIS.PWY

0.75
0.50
0.25

0 (n=386)

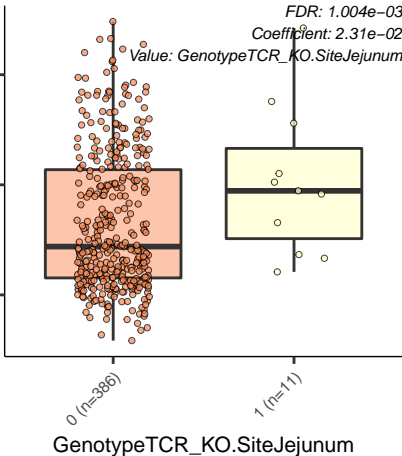
1 (n=11)

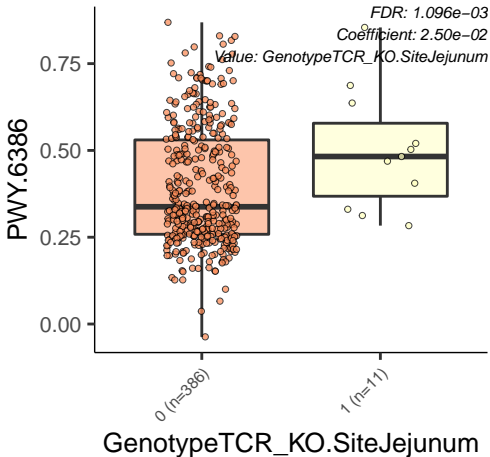
GenotypeTCR_KO.SiteJejunum

Value: GenotypeTCR_KO.SiteJejunum

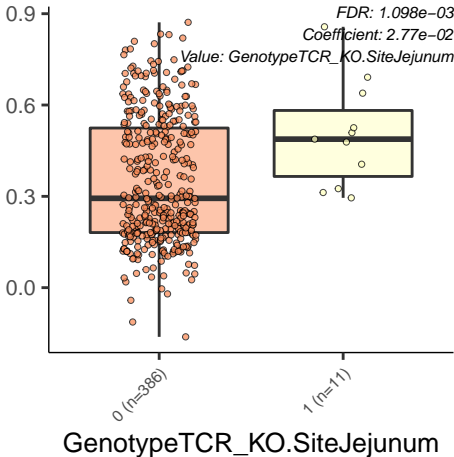
Coefficient: 2.31e-02

FDR: 1.004e-03

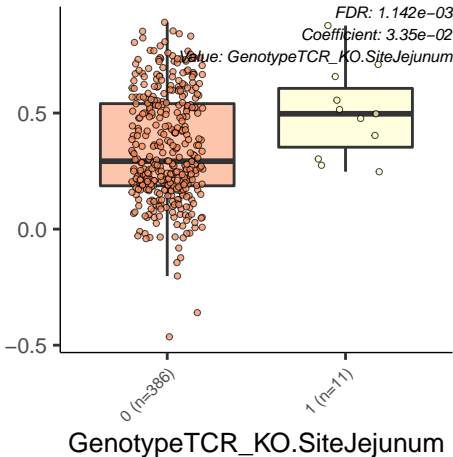


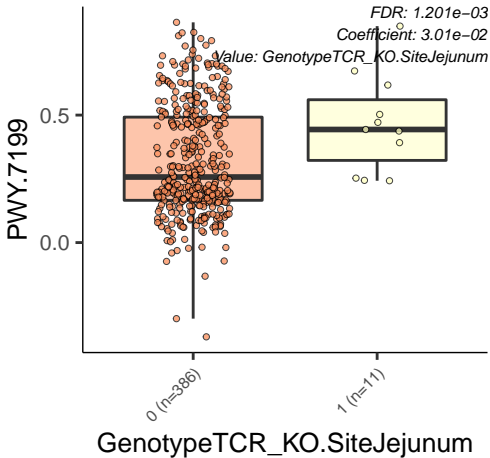


FASYN.ELONG.PWY

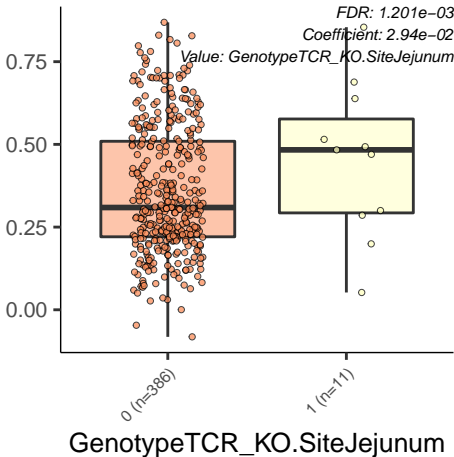


PWY0.1586





PWY4FS.7



PWY4FS.8

0.75
0.50
0.25
0.00

0 (n=386)

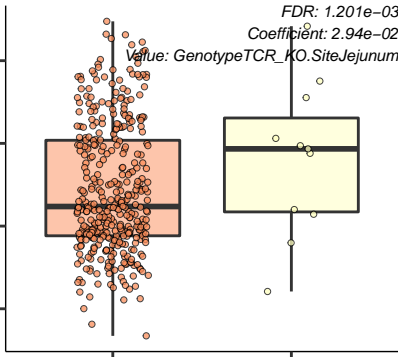
1 (n=11)

GenotypeTCR_KO.SiteJejunum

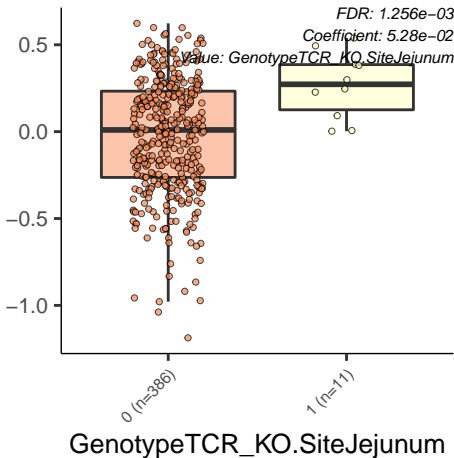
Value: GenotypeTCR_KO.SiteJejunum

Coefficient: 2.94×10^{-2}

FDR: 1.201×10^{-3}



PWY.7187



PWY0.1296

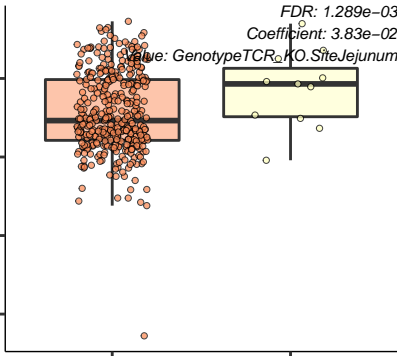
0.5
0.0
-0.5
-1.0

0 (n=386)

1 (n=11)

GenotypeTCR_KO.SiteJejunum

FDR: 1.289e-03
Coefficient: 3.83e-02
Value: GenotypeTCR_KO.SiteJejunum



PWY0.1297

0.5
0.0
-0.5
-1.0

0 (n=386)

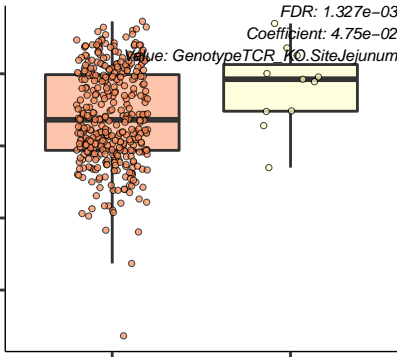
1 (n=11)

GenotypeTCR_KO.SiteJejunum

Value: GenotypeTCR_KO.SiteJejunum

FDR: 1.327×10^{-3}

Coefficient: 4.75×10^{-2}



PWY.5121

0.75
0.50
0.25

0 (n=386)

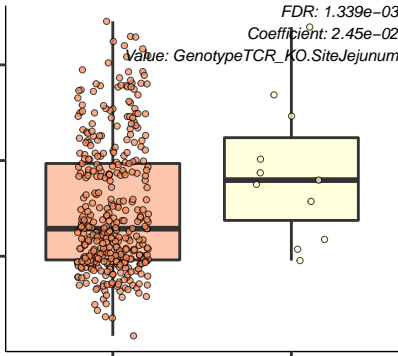
1 (n=11)

GenotypeTCR_KO.SiteJejunum

Value: GenotypeTCR_KO.SiteJejunum

Coefficient: 2.45e-02

FDR: 1.339e-03



HISTSYN.PWY

FDR: 1.411e-03

Coefficient: -5.59e-02

p-value: GenotypeTCR_KO.SiteJejunum

0

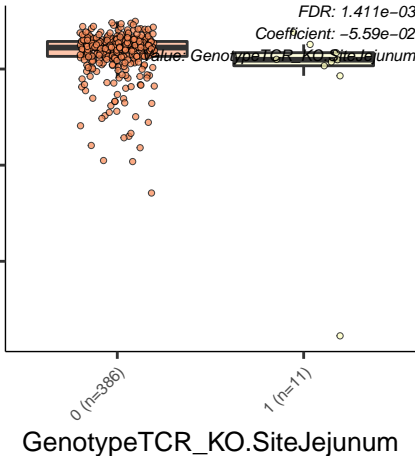
-1

-2

0 (n=386)

1 (n=11)

GenotypeTCR_KO.SiteJejunum



GLCMANNNAUT.PWY

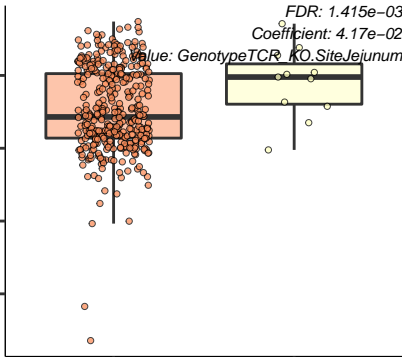
0.5
0.0
-0.5
-1.0

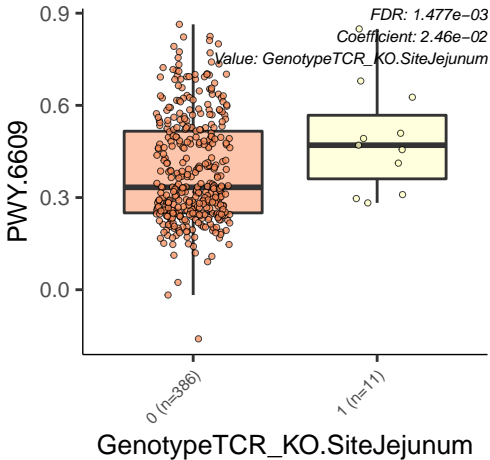
0 (n=386)

1 (n=11)

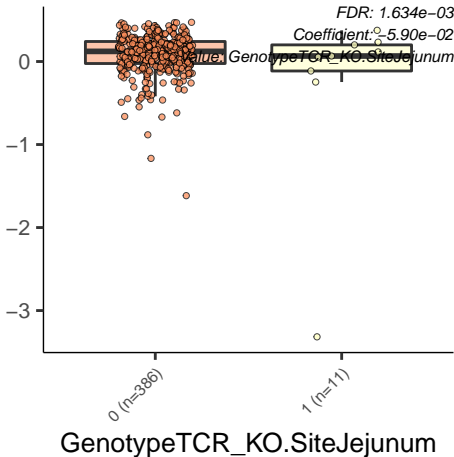
GenotypeTCR_KO.SiteJejunum

FDR: 1.415e-03
Coefficient: 4.17e-02
Value: GenotypeTCR_KO.SiteJejunum





PANTO.PWY



NONOXIPENT.PWY

0.75
0.50
0.25

0 (n=386)

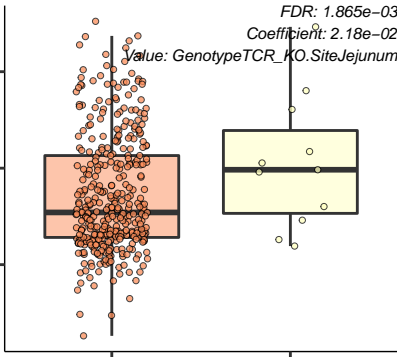
1 (n=11)

GenotypeTCR_KO.SiteJejunum

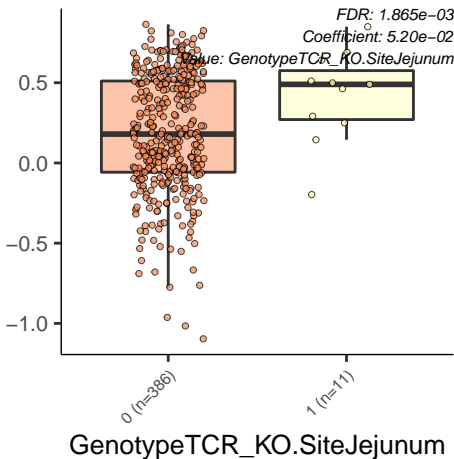
Value: GenotypeTCR_KO.SiteJejunum

Coefficient: 2.18e-02

FDR: 1.865e-03



P161.PWY



NONMEVIP.PWY

0.75
0.50
0.25
0.00

0 (n=386)

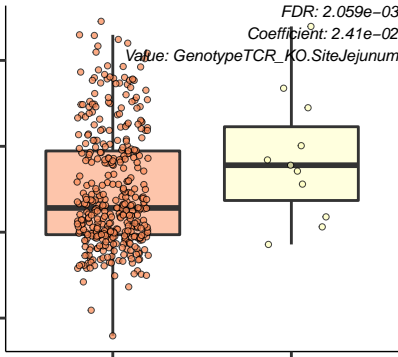
1 (n=11)

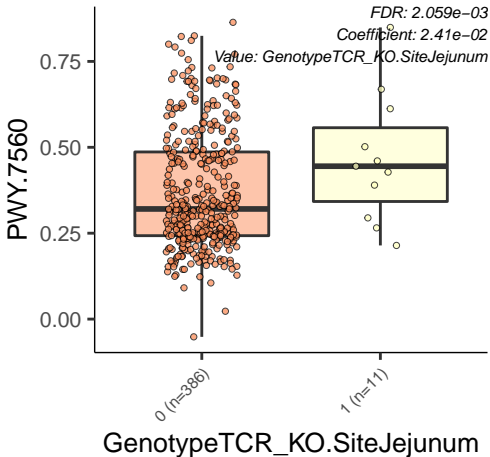
GenotypeTCR_KO.SiteJejunum

Value: GenotypeTCR_KO.SiteJejunum

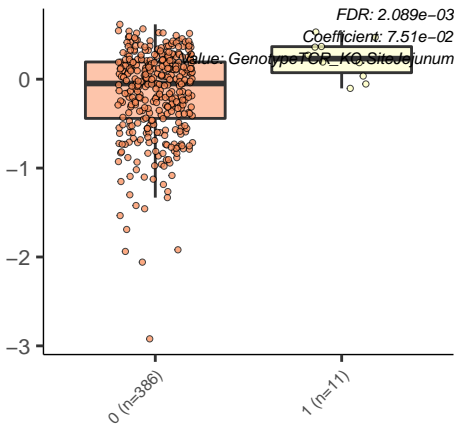
Coefficient: 2.41e-02

FDR: 2.059e-03

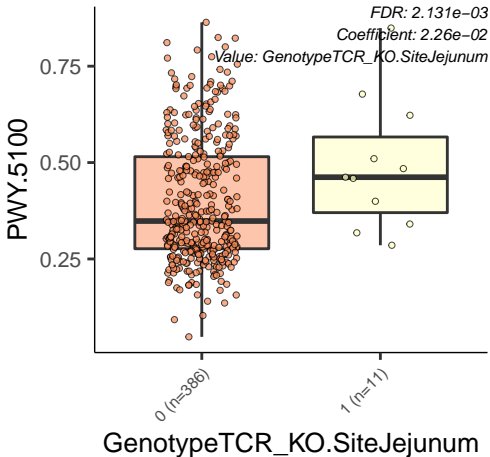




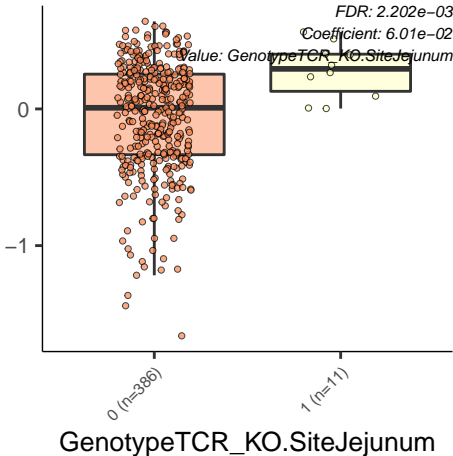
PWY.7200



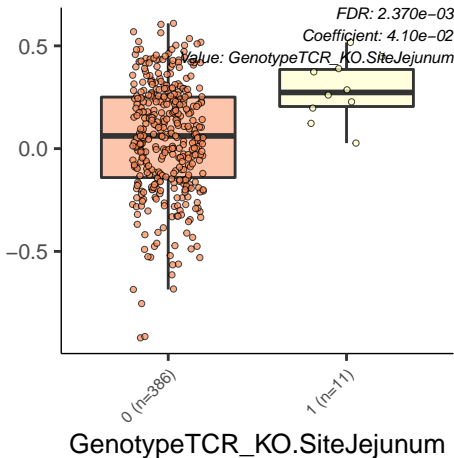
GenotypeTCR_KO.SiteJejunum



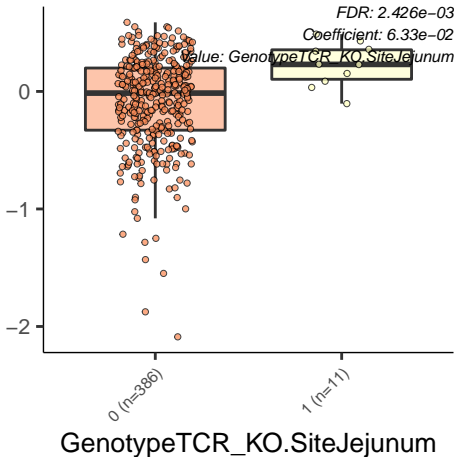
PWY0.166



PWY.841



PWY.7196



PWY.6163

0.75
0.50
0.25
0.00

0 (n=386)

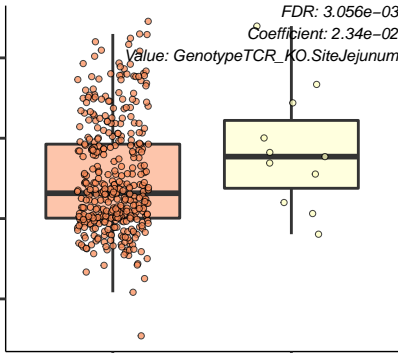
1 (n=11)

GenotypeTCR_KO.SiteJejunum

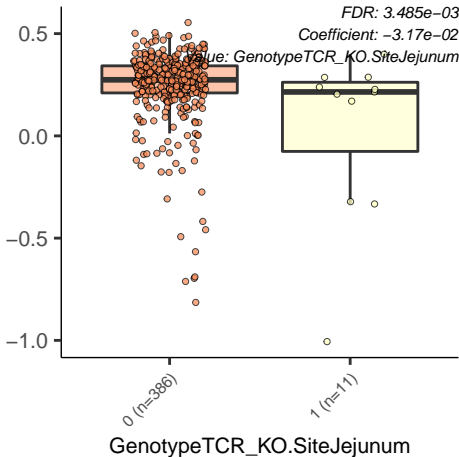
Value: GenotypeTCR_KO.SiteJejunum

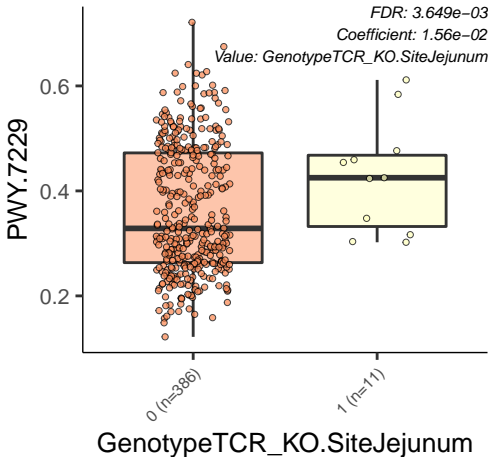
Coefficient: 2.34×10^{-2}

FDR: 3.056×10^{-3}

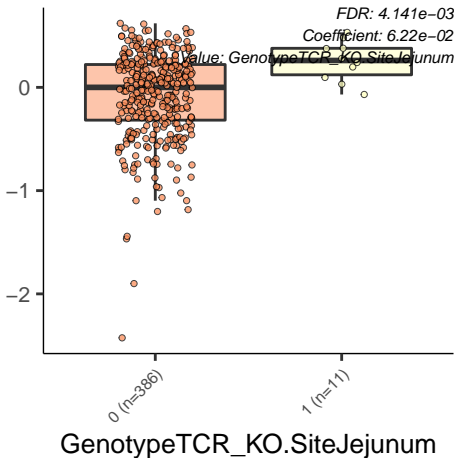


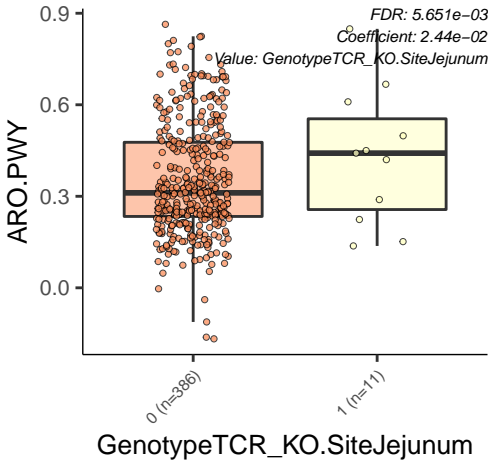
BRANCHED.CHAIN.AA.SYN.PWY



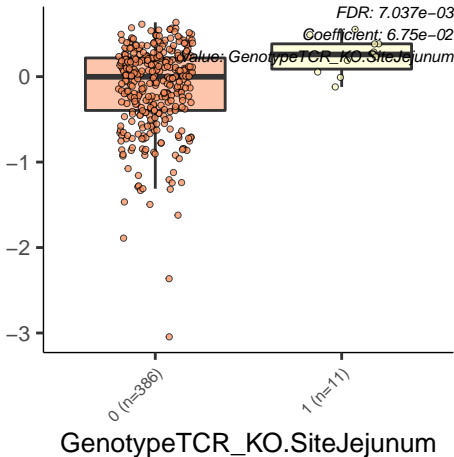


PWY.6125

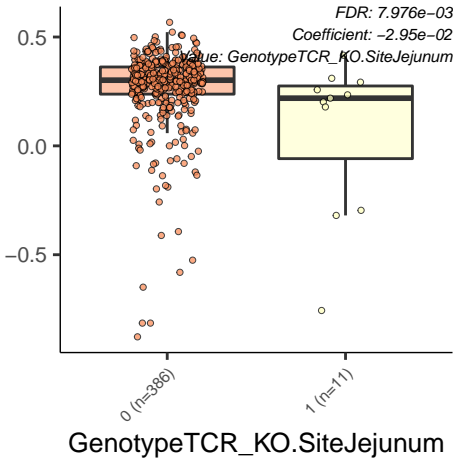




PWY.7228



PWY.5101

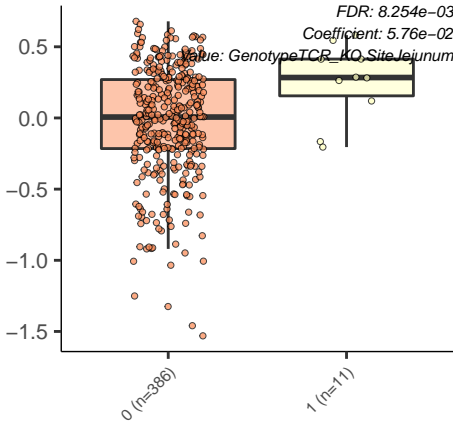


P124.PWY

FDR: $8.254e-03$

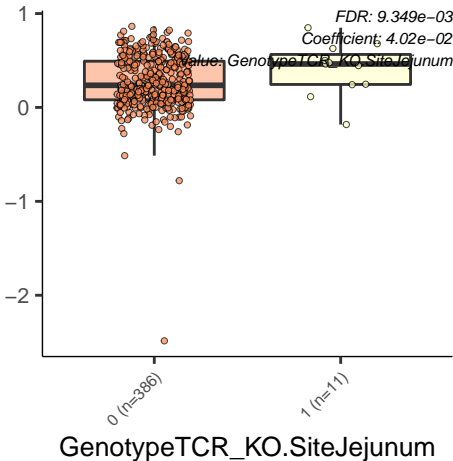
Coefficient: $5.76e-02$

Value: GenotypeTCR_KO.SiteJejunum



GenotypeTCR_KO.SiteJejunum

UDPNAGSYN.PWY



COMPLETE.ARO.PWY

0.50

0.25

0.00

0 (n=386)

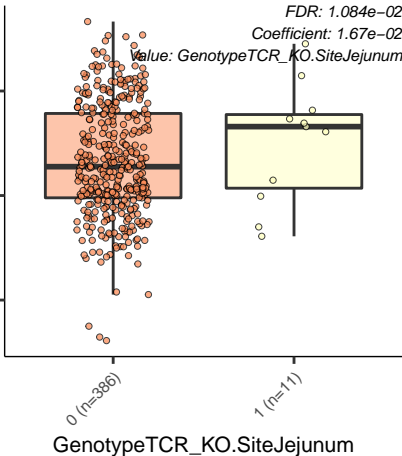
1 (n=11)

GenotypeTCR_KO.SiteJejunum

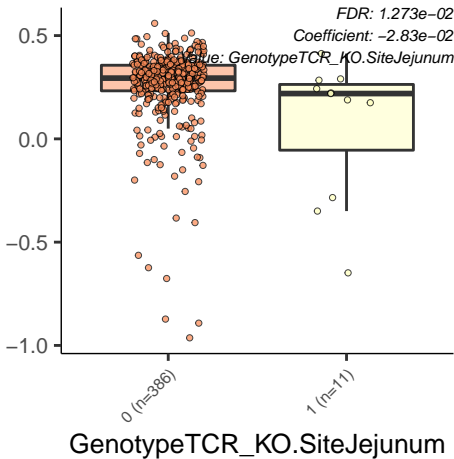
FDR: 1.084e-02

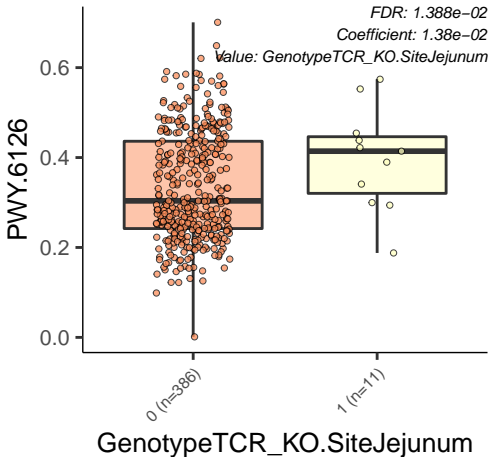
Coefficient: 1.67e-02

Value: GenotypeTCR_KO.SiteJejunum

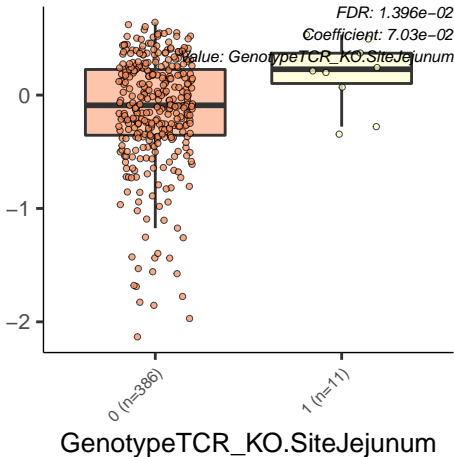


PWY.7111

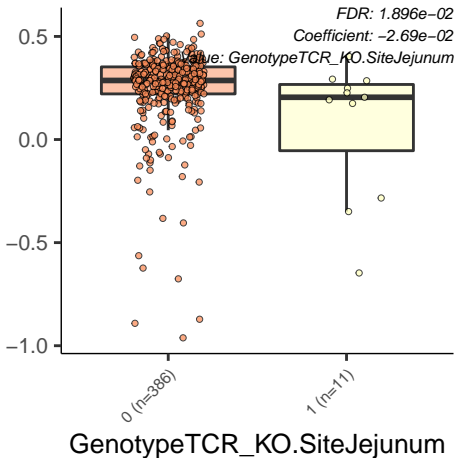




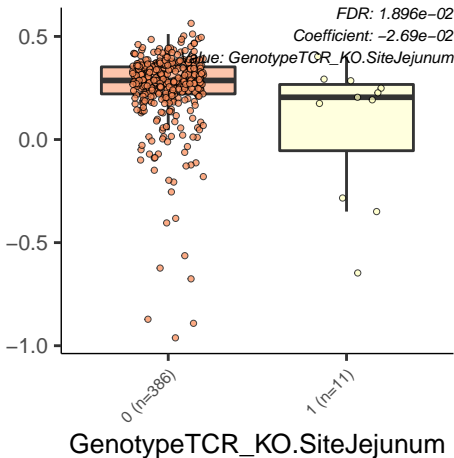
P122.PWY



ILEUSYN.PWY



VALSYN.PWY



DENOVOPURINE2.PWY

0

-1

-2

-3

0 (n=386)

1 (n=11)

GenotypeTCR_KO.SiteJejunum

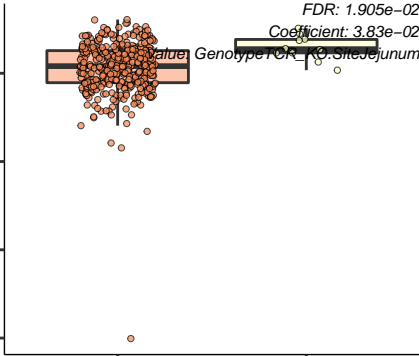
Value

GenotypeTCR_KO.SiteJejunum

Coefficient: $3.83e-02$

FDR: $1.905e-02$

GenotypeTCR_KO.SiteJejunum



PWY.7184

-1

0

0 (n=386)

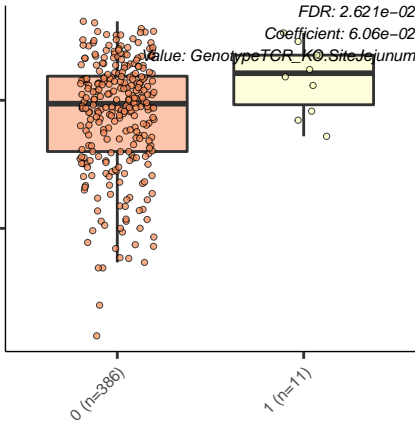
1 (n=11)

GenotypeTCR_KO.SiteJejunum

Value: GenotypeTCR_KO.SiteJejunum

Coefficient: 6.06e-02

FDR: 2.621e-02



PWY0.162

FDR: 2.790e-02

Coefficient: 3.75e-02

Value: GenotypeTCR_KO.SiteJejunum

0.5

0.0

-0.5

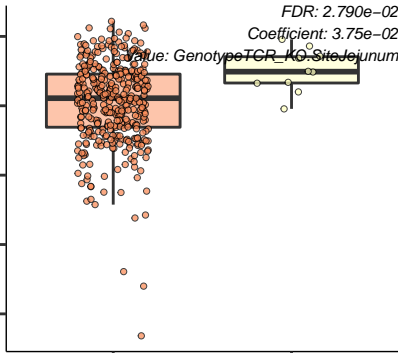
-1.0

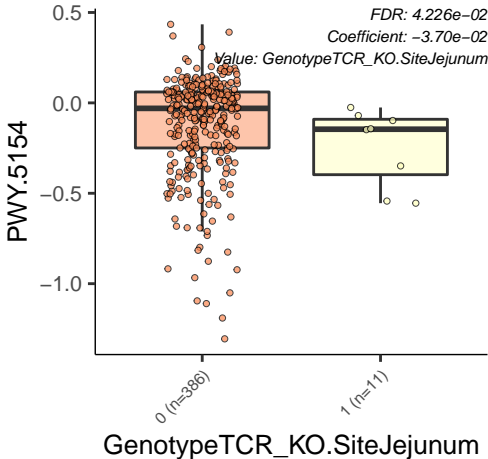
-1.5

0 (n=386)

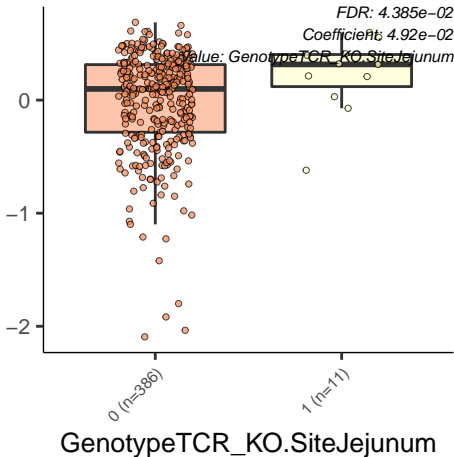
1 (n=11)

GenotypeTCR_KO.SiteJejunum

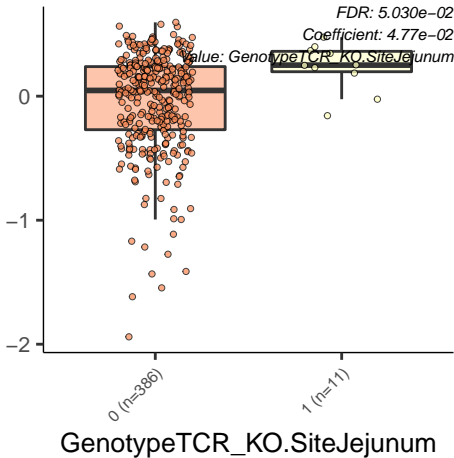




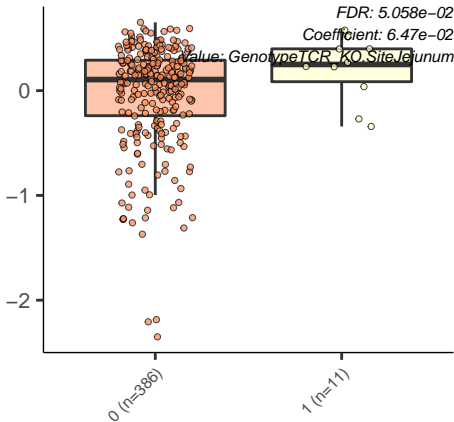
PWY.7392



PWY.7234

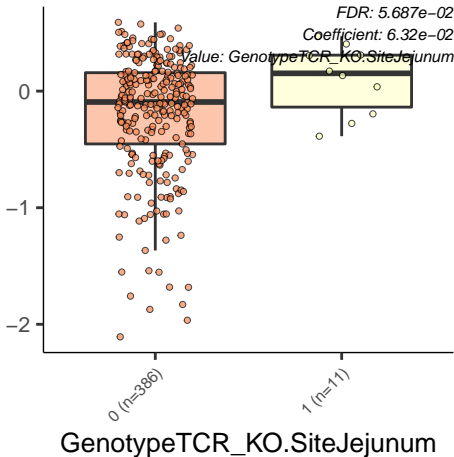


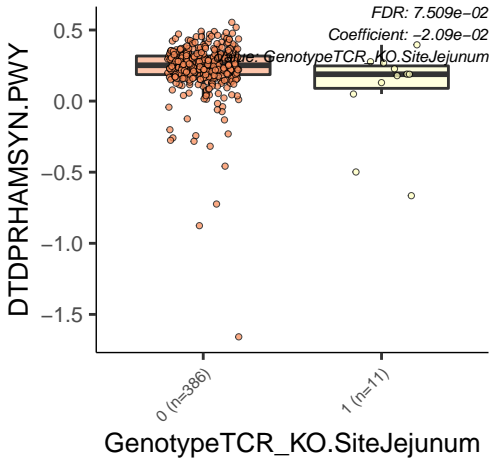
PWY.2941



GenotypeTCR_KO.SiteJejunum

PWY.7197



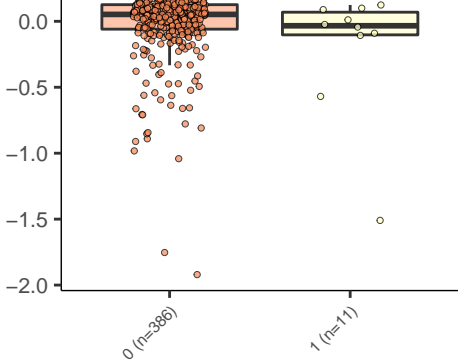


FERMENTATION.PWY

FDR: 8.244e-02

Coefficient: -3.30e-02

Value: GenotypeTCR_KO.SiteJejunum



GenotypeTCR_KO.SiteJejunum

POLYISOPRENSYN.PWY

0.4
0.0
-0.4
-0.8

0 (n=386)

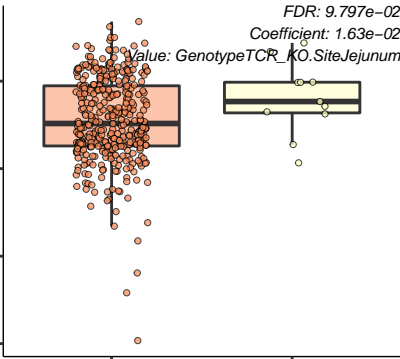
1 (n=11)

GenotypeTCR_KO.SiteJejunum

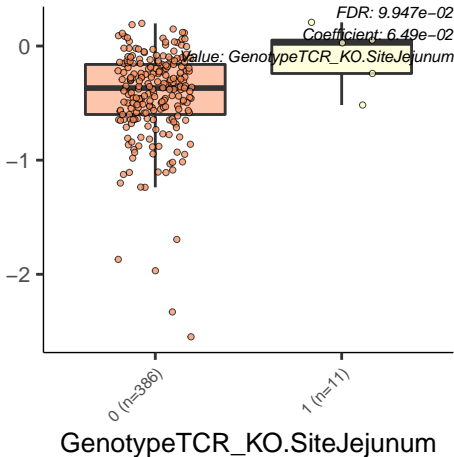
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Coefficient: 1.63e-02

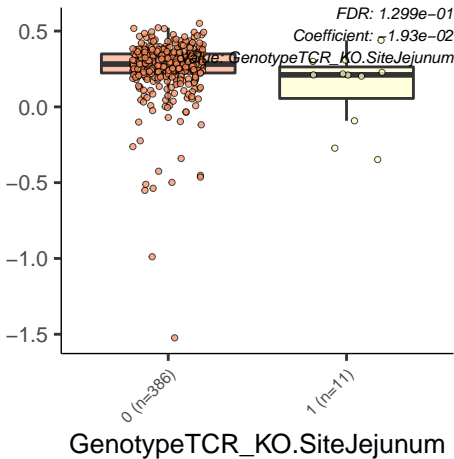
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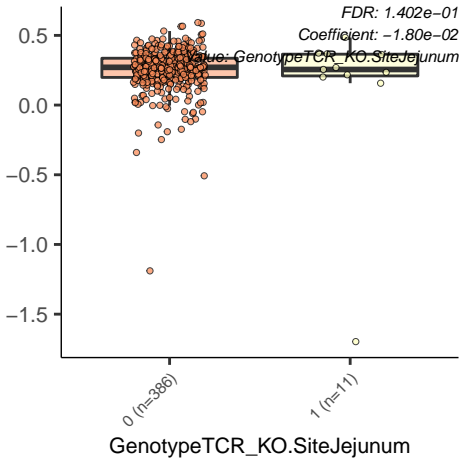
PRPP.PWY



PWY.6737



GLYCOGENSYNTH.PWY



PWY.5103

FDR: 1.431e-01

Coefficient: -2.28e-02

Value: GenotypeTCR_KO.SiteJejunum

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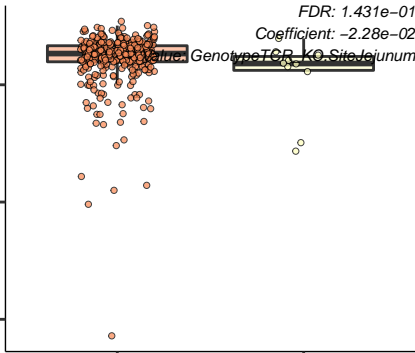
-1

-2

0 (n=386)

1 (n=11)

GenotypeTCR_KO.SiteJejunum



DAPLYSINESYN.PWY

FDR: 1.466e-01

Coefficient: 1.72e-02

Value: GenotypeTCR_KO.SiteJejunum

0.5

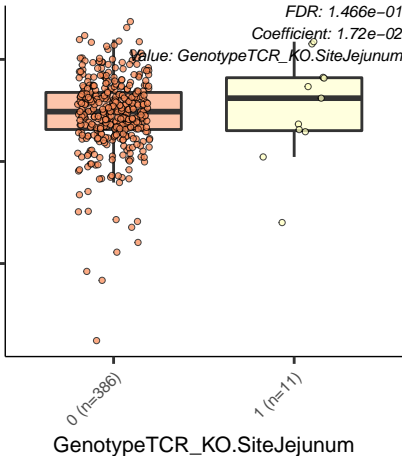
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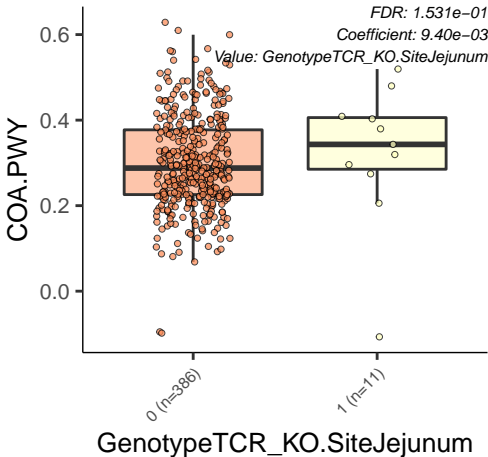
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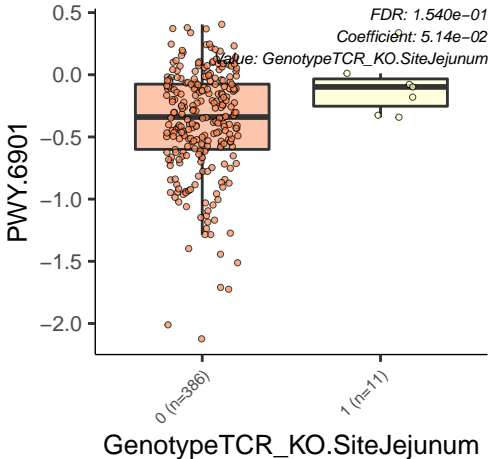
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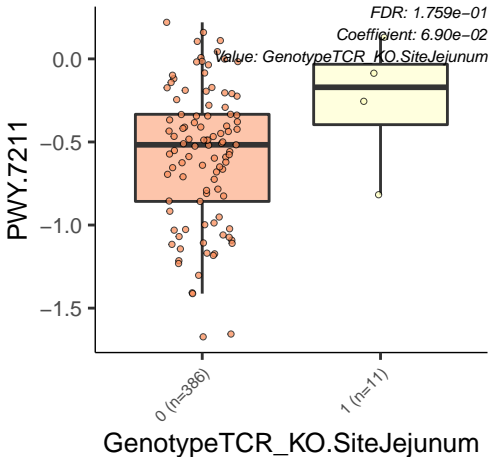
1 (n=11)

GenotypeTCR_KO.SiteJejunum







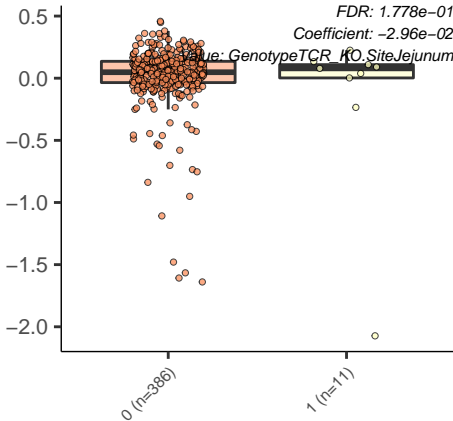


FOLSYN.PWY

FDR: 1.778e-01

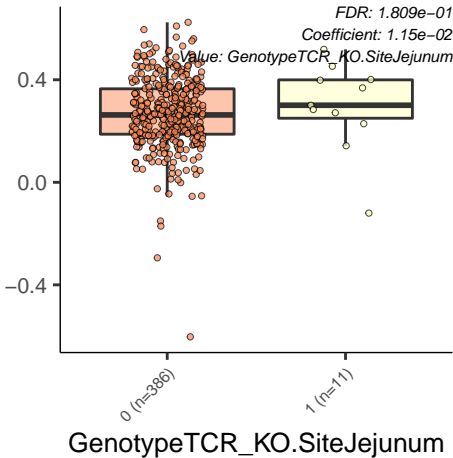
Coefficient: -2.96e-02

t-value: GenotypeTCR_KO.SiteJejunum



GenotypeTCR_KO.SiteJejunum

PWY.6151



PWY.621

0
-1

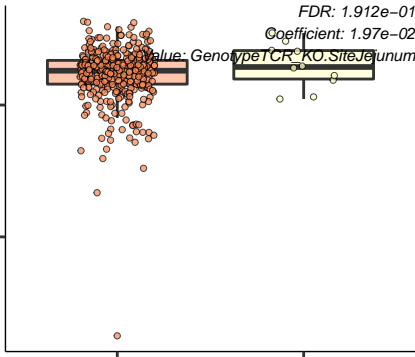
0 (n=386)

1 (n=11)

GenotypeTCR_KO.SiteJejunum

Value: GenotypeTCR_KO.SiteJejunum

FDR: 1.912e-01
Coefficient: 1.97e-02

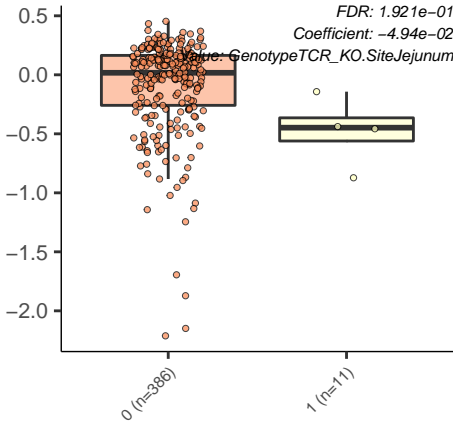


COBALSYN.PWY

FDR: 1.921e-01

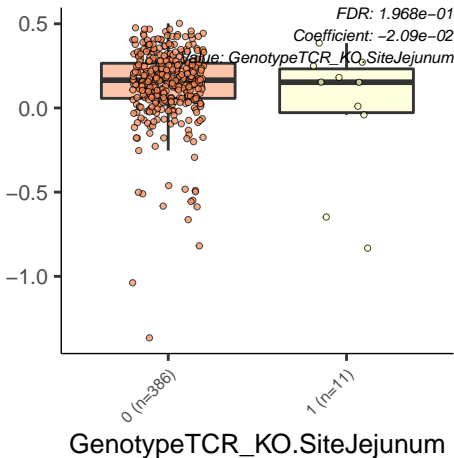
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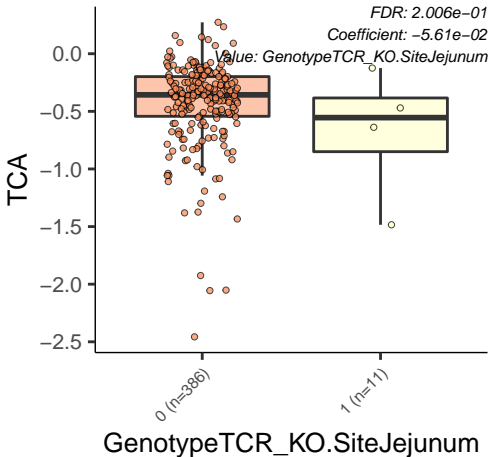
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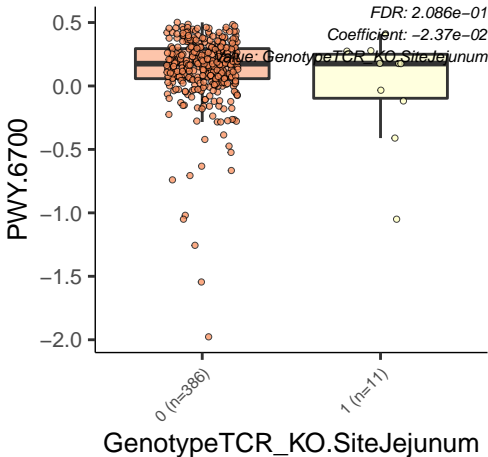


GenotypeTCR_KO.SiteJejunum

PANTOSYN.PWY







PYRIDNUCSAL.PWY

FDR: 2.104e-01

Coefficient: -3.99e-02

Value: GenotypeTCR_KO.SiteJejunum

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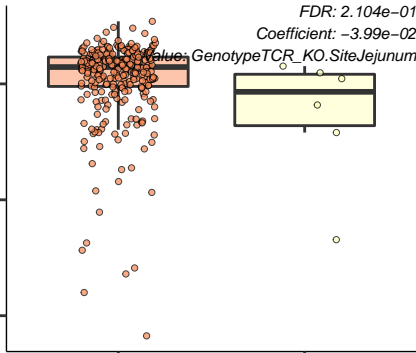
-1

-2

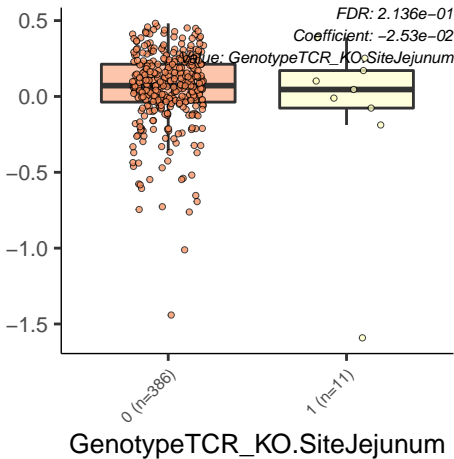
0 (n=386)

1 (n=11)

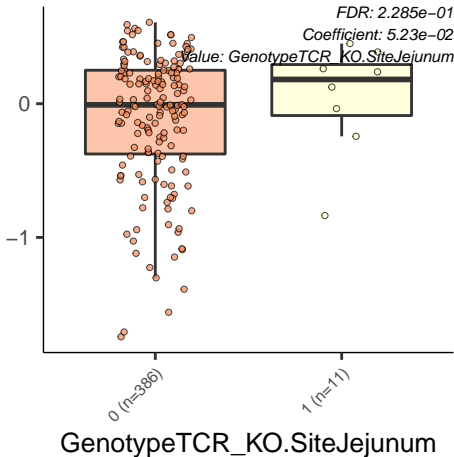
GenotypeTCR_KO.SiteJejunum



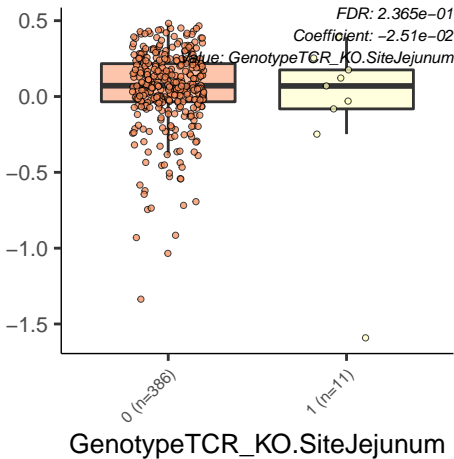
PWY.6147



LACTOSECAT.PWY



PWY.7539



PWY.6471

