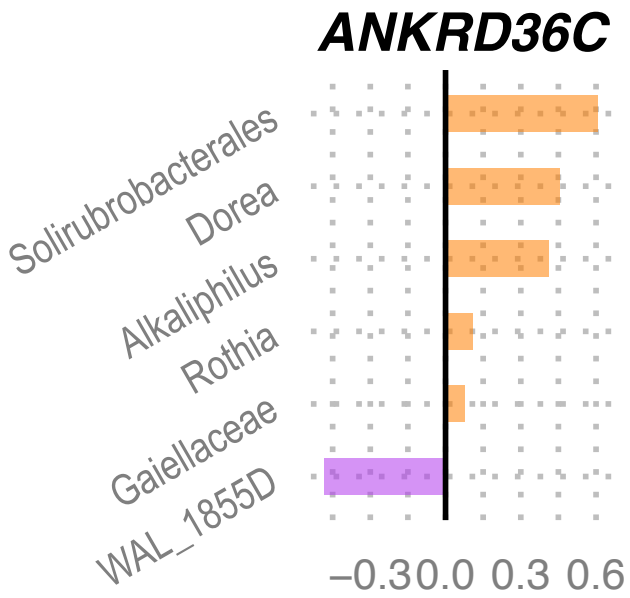
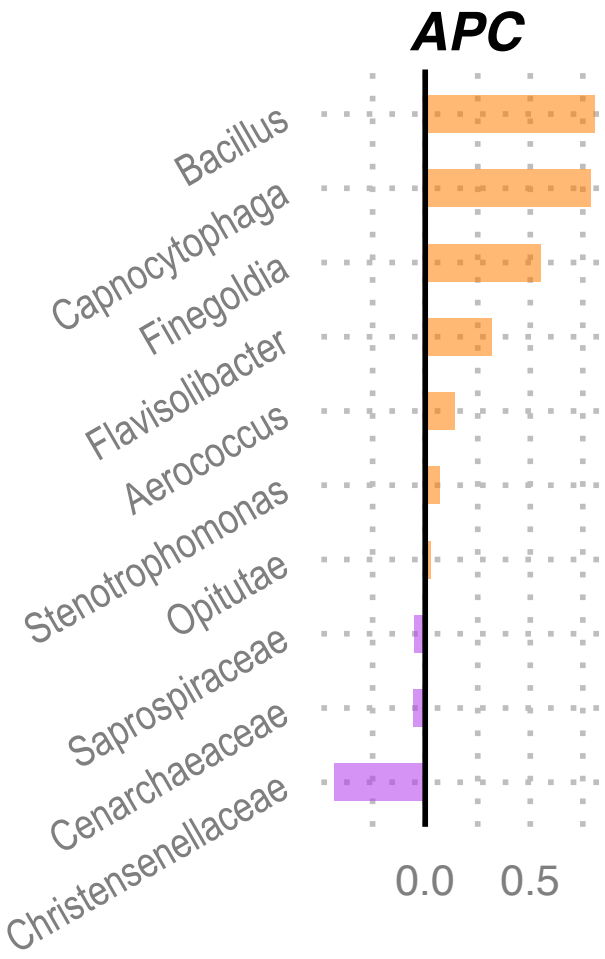
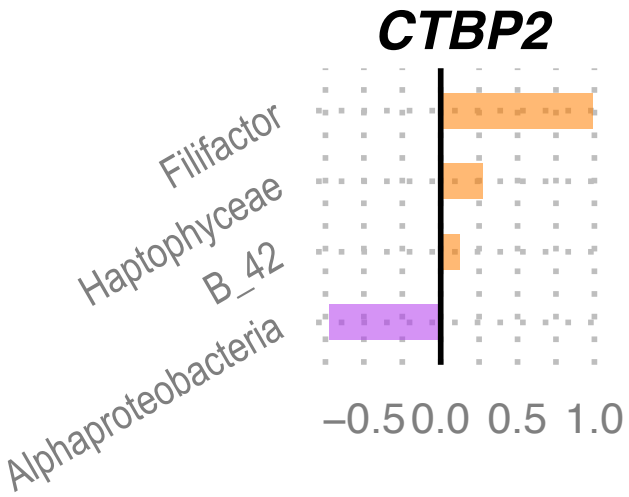
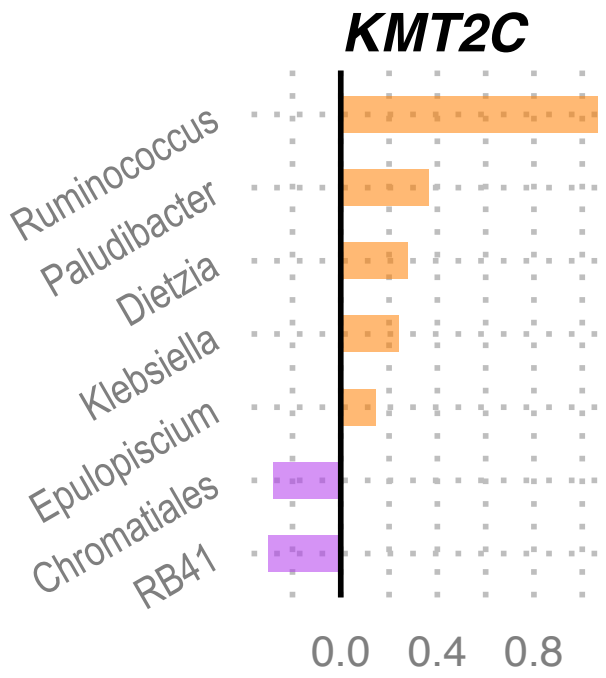
Supplementary Figure 10 | Abundance Barcharts.

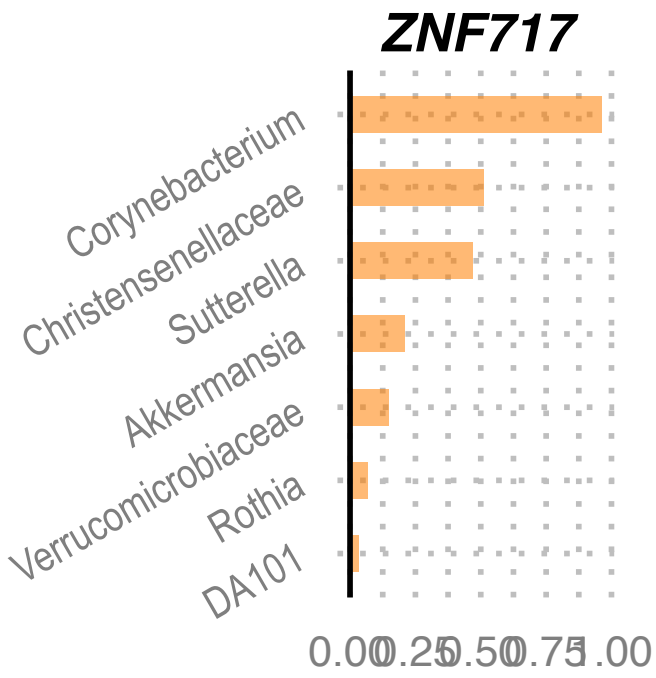
Genes


ANKRD36C
Solirubrobacterales
Dorea
Alkaliphilus
Rothia
Gaiellaceae
WAL_1855D
−0.3
0.0
0.3
0.6


APC
Bacillus
Capnocytophaga
Finegoldia
Flavisolibacter
Aerococcus
Stenotrophomonas
Opitutae
Saprospiraceae
Cenarchaeaceae
Christensenellaceae
0.0
0.5

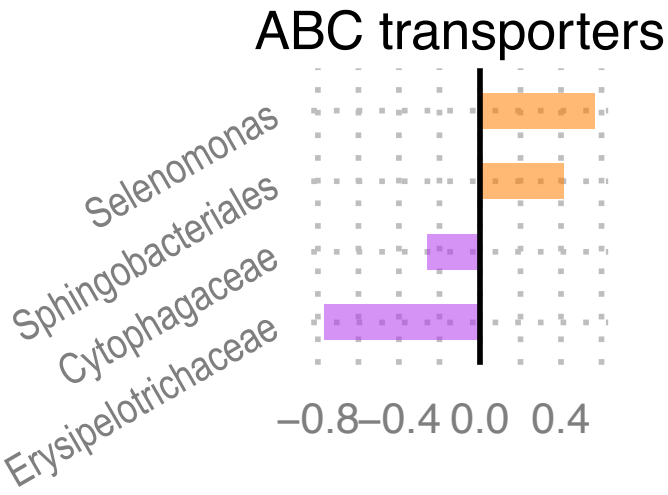

CTBP2
Filifactor
Haptophyceae
B_42
Alphaproteobacteria
−0.5
0.0
0.5
1.0

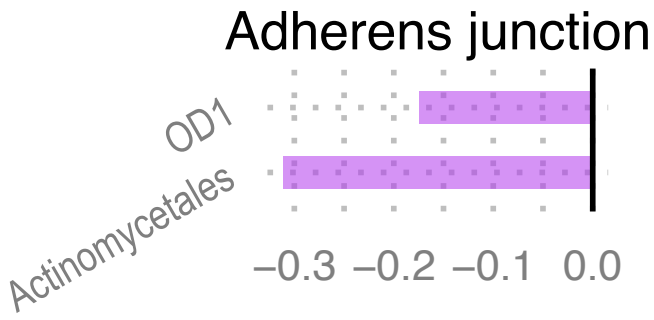

KMT2C
Ruminococcus
Paludibacter
Dietzia
Klebsiella
Epulopiscium
Chromatiales
RB41
0.0
0.4
0.8


ZNF717
Corynebacterium
Christensenellaceae
Sutterella
Akkermansia
Verrucomicrobiaceae
Rothia
DA101
0.00
0.25
0.50
0.75
1.00

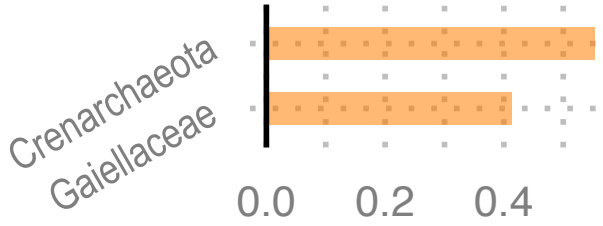
Supplementary Figure 10 | Abundance Barcharts.

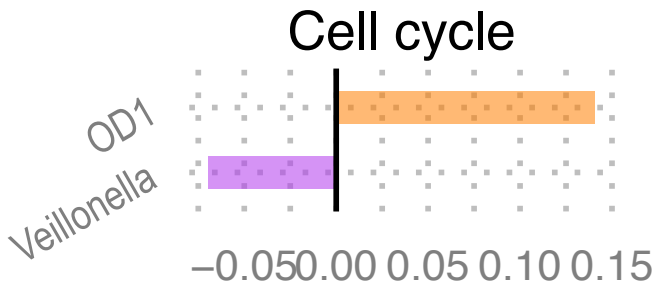
KEGG


ABC transporters
Selenomonas
Sphingobacteriales
Cytophagaceae
Erysipelotrichaceae
–0.8
–0.4
0.0
0.4


Adherens junction
OD1
Actinomycetales
–0.3
–0.2
–0.1
0.0

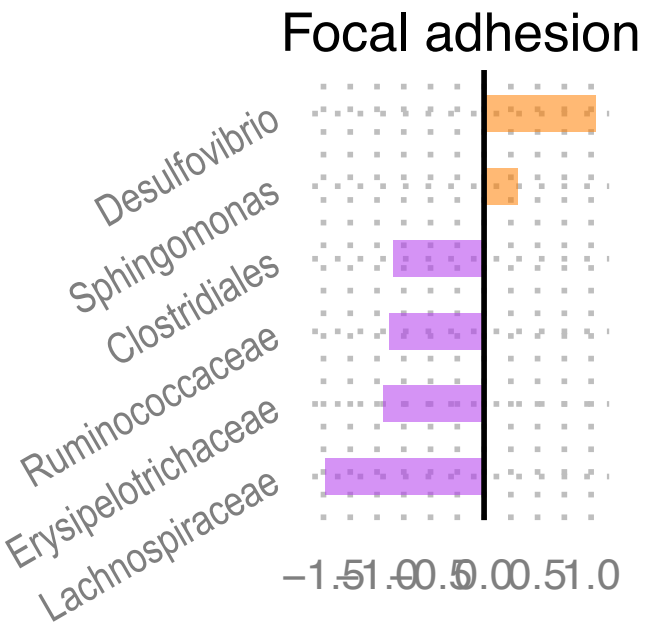
Alanine, aspartate, and glutamate metabolism

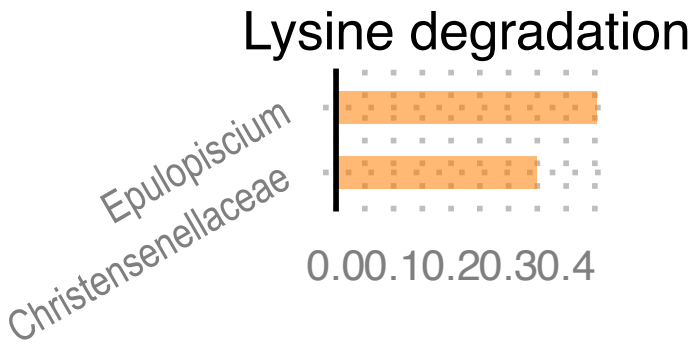


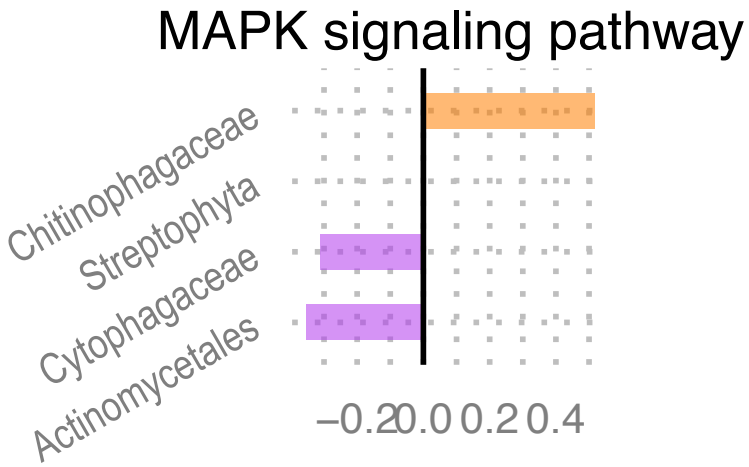

Cell cycle
OD1
Veillonella
−0.05
0.00
0.05
0.10
0.15

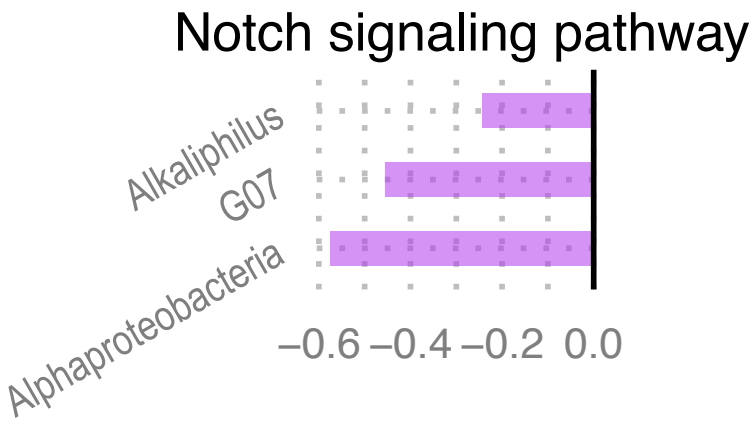
Cysteine and methionine metabolism

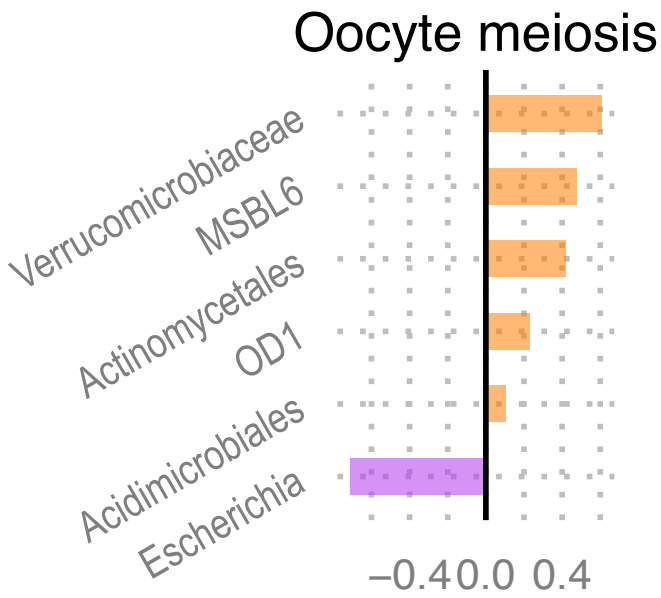
File intentionally blank -no taxa met the abundance-difference threshold for inclusion

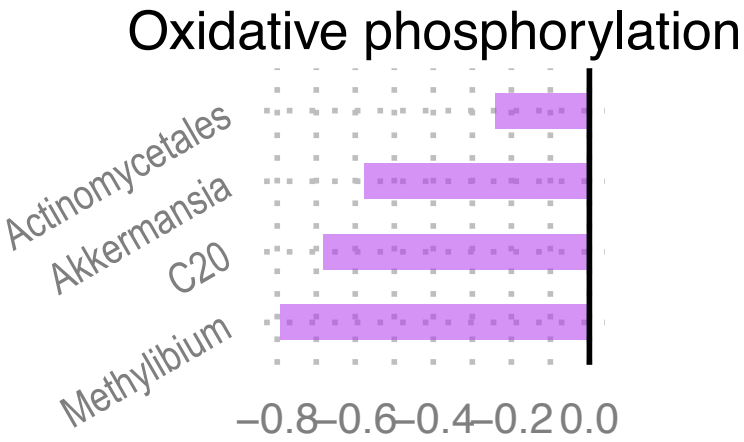

Focal adhesion
Desulfovibrio
Sphingomonas
Clostridiales
Ruminococcaceae
Erysipelotrichaceae
Lachnospiraceae
−1.5
−1.0
−0.5
0.0
0.5
1.0


Lysine degradation
Epulopiscium
Christensenellaceae
0.0
0.1
0.2
0.3
0.4


MAPK signaling pathway
Chitinophagaceae
Streptophyta
Cytophagaceae
Actinomycetales
−0.2
0.0
0.2
0.4


Notch signaling pathway
Alkaliphilus G07
Alphaproteobacteria
–0.6
–0.4
–0.2
0.0

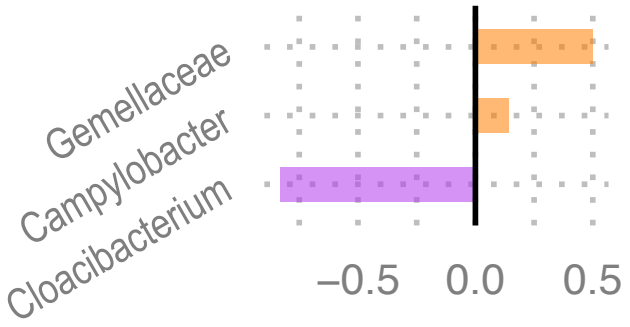

Oocyte meiosis
Verrucomicrobiaceae
MSBL6
Actinomycetales
OD1
Acidimicrobiales
Escherichia
−0.4
0.0
0.4

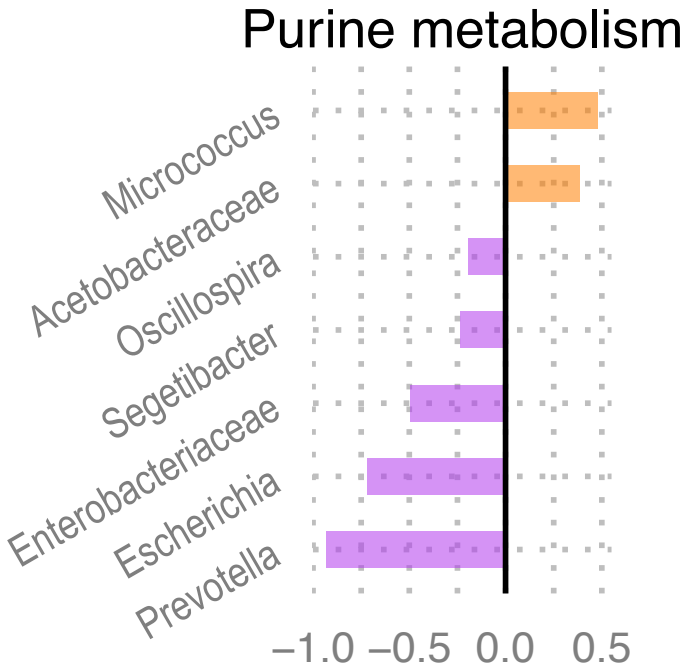

Oxidative phosphorylation
Actinomycetales
Akkermansia
C20
Methylibium
–0.8
–0.6
–0.4
–0.2
0.0

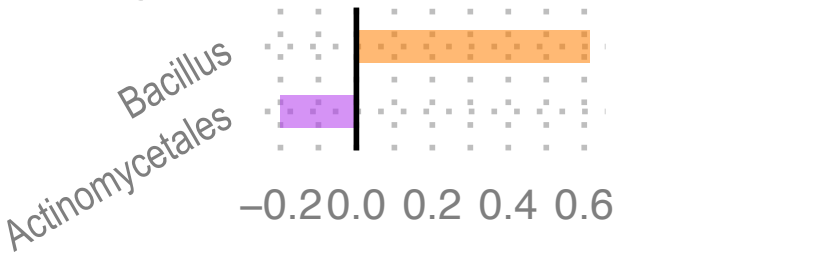
Phosphatidylinositol signaling system

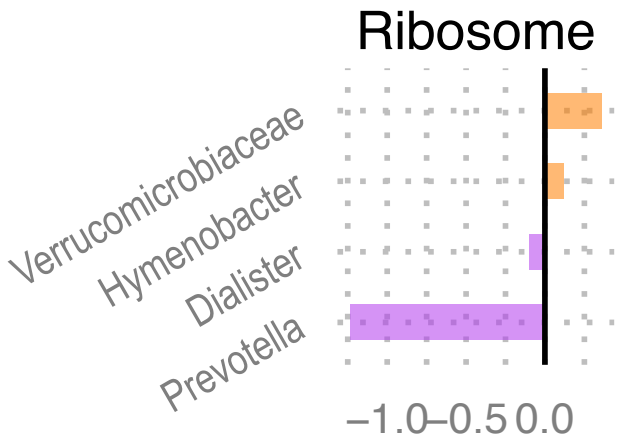
File intentionally blank -no taxa met the abundance-difference threshold for inclusion

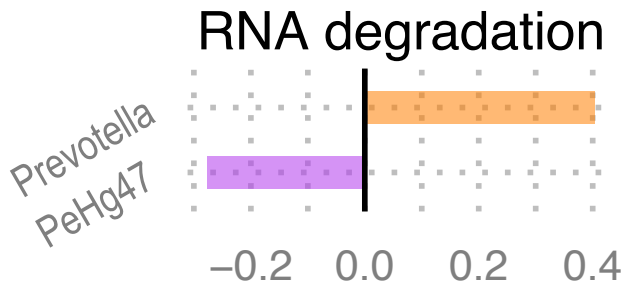
Protein processing in endoplasmic reticulum

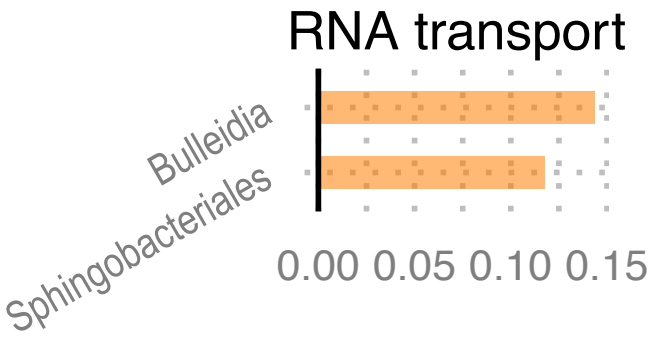


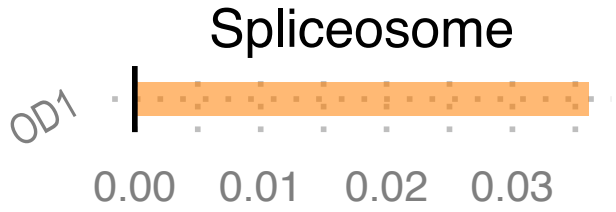

Purine metabolism
Micrococcus
Acetobacteraceae
Oscillospira
Segetibacter
Enterobacteriaceae
Escherichia
Prevotella
−1.0
−0.5
0.0
0.5


Regulation of actin cytoskeleton
Bacillus
Actinomycetales
−0.2
0.0
0.2
0.4
0.6


Ribosome
Verrucomicrobiaceae
Hymenobacter
Dialister
Prevotella
−1.0
−0.5
0.0

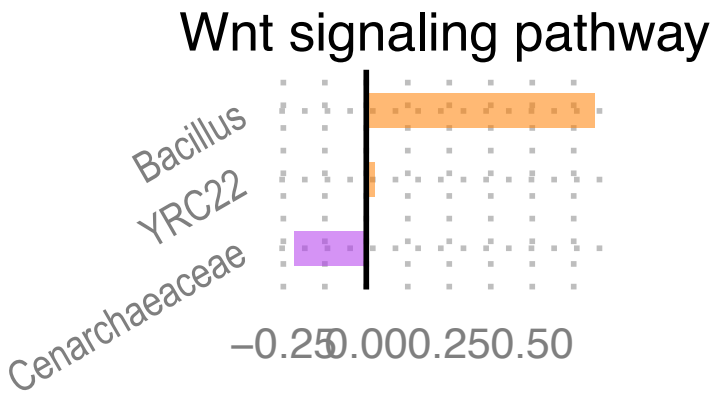

RNA degradation
Prevotella
PeHg47
–0.2
0.0
0.2
0.4


RNA transport
Bulleidia
Sphingobacteriales
0.00
0.05
0.10
0.15


Spliceosome
OD1
0.00
0.01
0.02
0.03

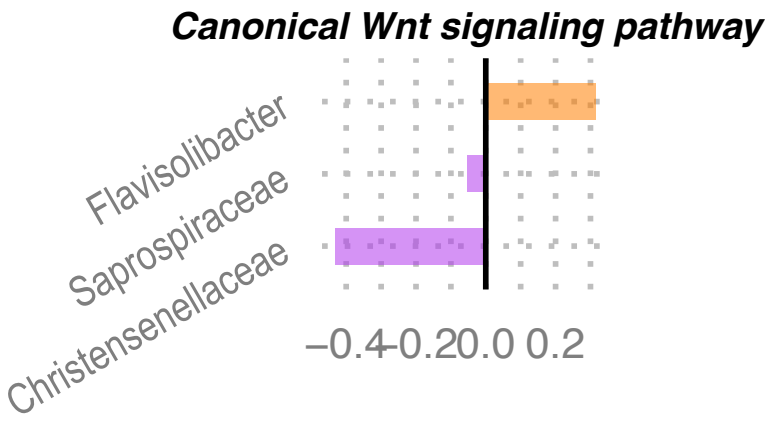
Ubiquitin mediated proteolysis

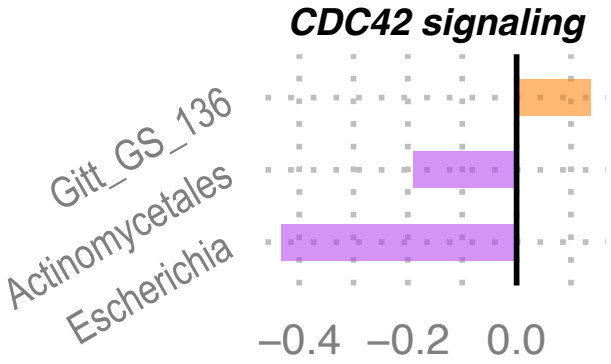
File intentionally blank -no taxa met the abundance-difference threshold for inclusion

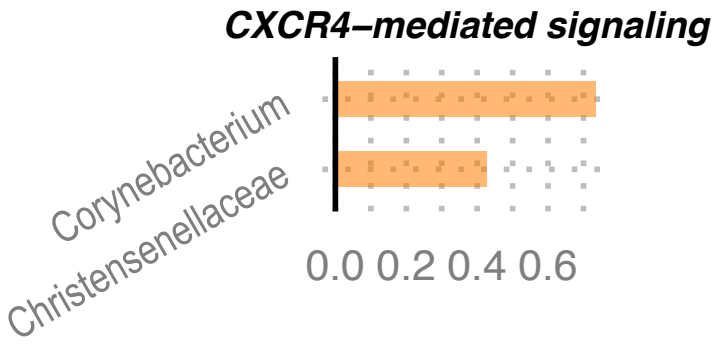

Wnt signaling pathway
Bacillus
YRC22
Cenarchaeaceae
−0.25
0.00
0.25
0.50

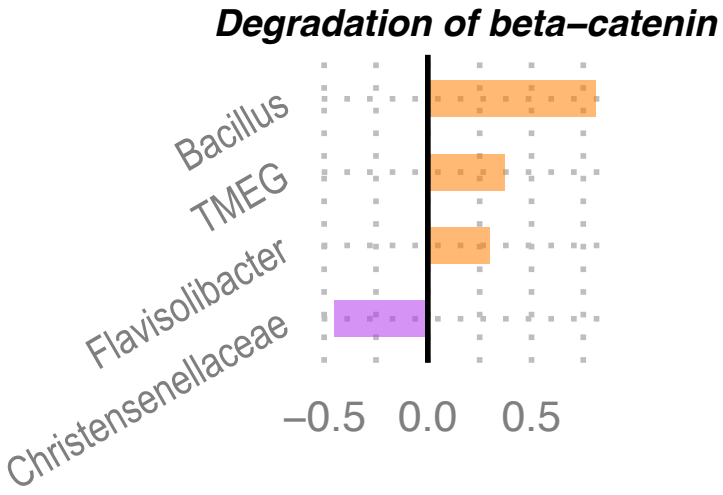
Supplementary Figure 10 | Abundance Barcharts.

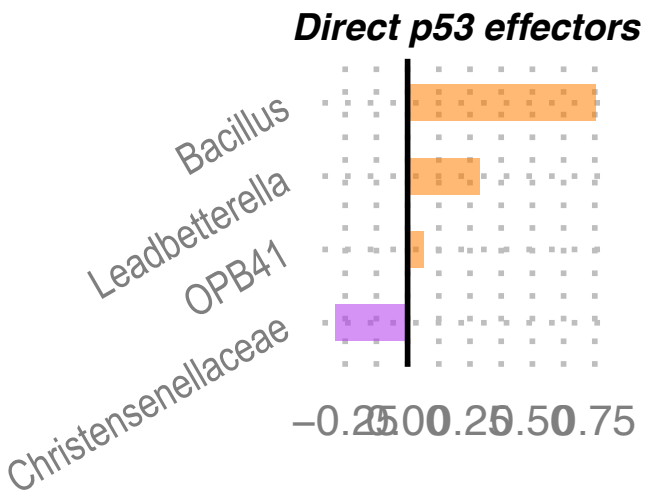
PID

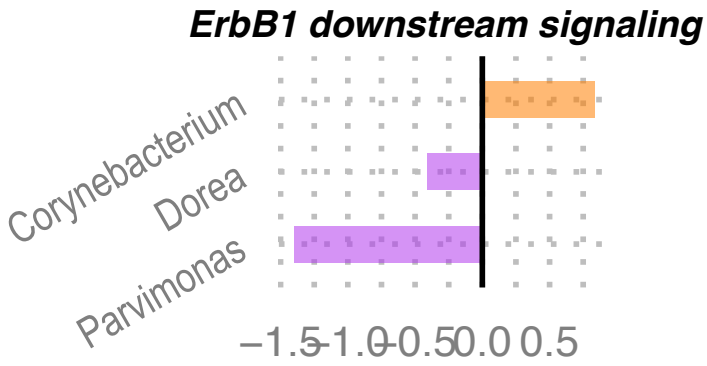

Canonical Wnt signaling pathway
Flavisolibacter
Saprospiraceae
Christensenellaceae
−0.4
−0.2
0.0
0.2

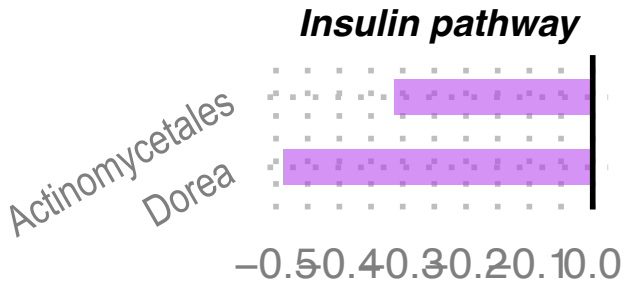

CDC42 signaling
Gitt_GS_136
Actinomycetales
Escherichia
–0.4
–0.2
0.0

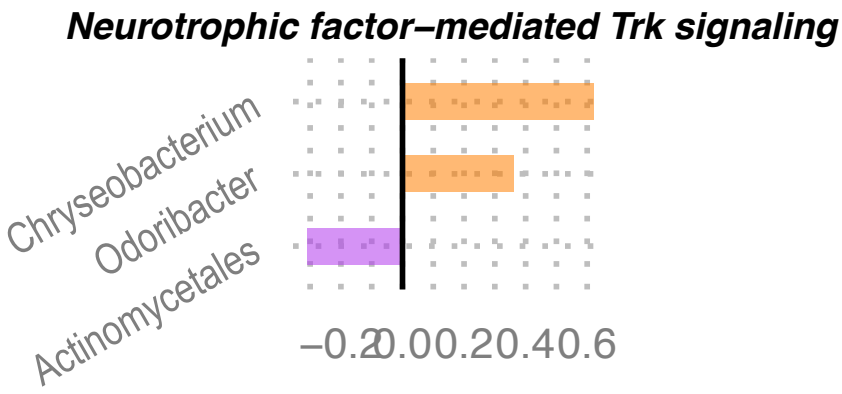

CXCR4–mediated signaling
Corynebacterium
Christensenellaceae
0.0 0.2 0.4 0.6

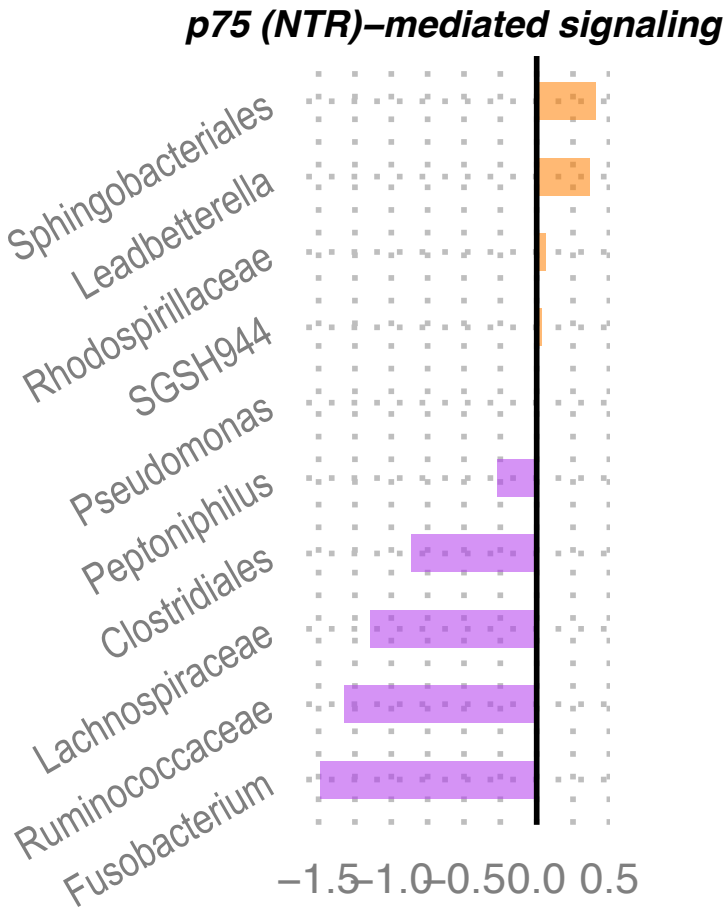

Degradation of beta–catenin
Bacillus
TMEG
Flavisolibacter
Christensenellaceae
–0.5
0.0
0.5

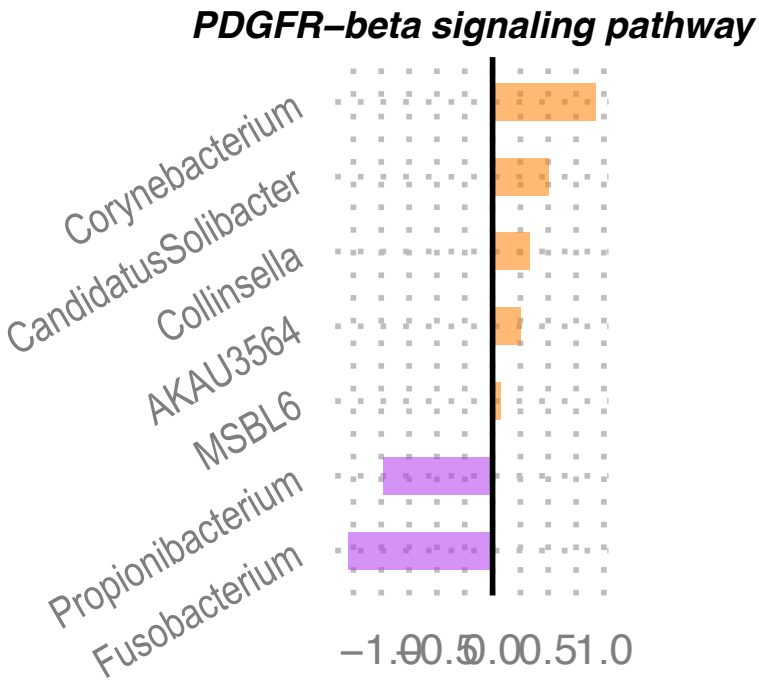

Direct p53 effectors
Bacillus
Leadbetterella
OPB41
Christensenellaceae
−0.25
0.00
0.25
0.50
0.75


ErbB1 downstream signaling
Corynebacterium
Dorea
Parvimonas
−1.5
−1.0
−0.5
0.0
0.5

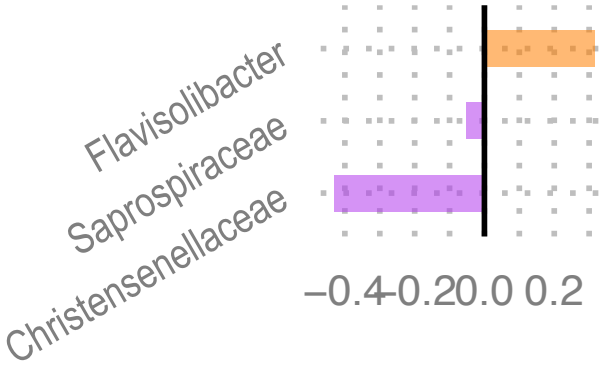

Insulin pathway
Actinomycetales
Dorea
−0.5
−0.4
−0.3
−0.2
−0.1
0.0


Neurotrophic factor–mediated Trk signaling
Chryseobacterium
Odoribacter
Actinomycetales
−0.2
0.0
0.2
0.4
0.6


p75 (NTR)–mediated signaling
Sphingobacteriales
Leadbetterella
Rhodospirillaceae
SGSH944
Pseudomonas
Peptoniphilus
Clostridiales
Lachnospiraceae
Ruminococcaceae
Fusobacterium
−1.5
−1.0
−0.5
0.0
0.5


PDGFR−beta signaling pathway
Corynebacterium
CandidatusSolibacter
Collinsella
AKAU3564
MSBL6
Propionibacterium
Fusobacterium
−1.0
−0.5
0.0
0.5
1.0

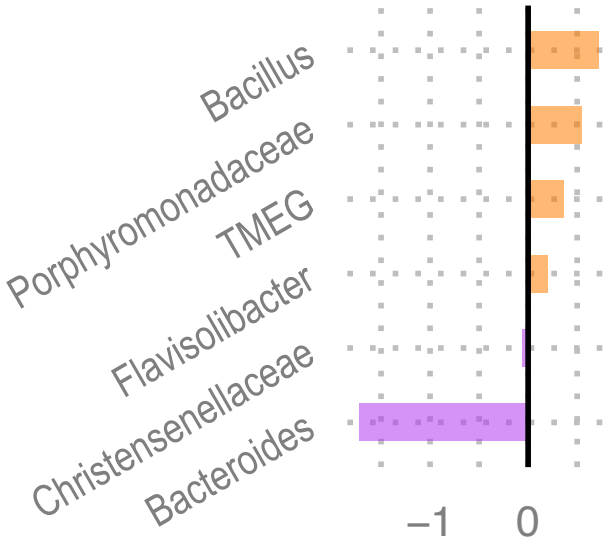
Presenilin action in Notch and Wnt signaling

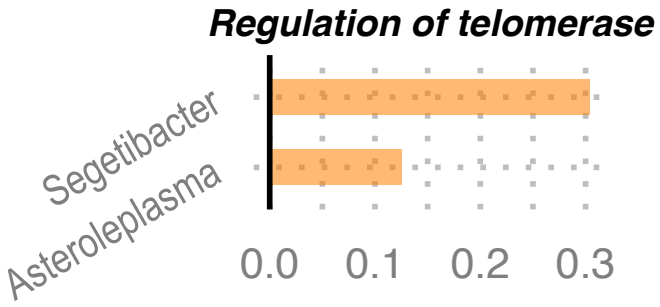


Regulation of CDC42 activity

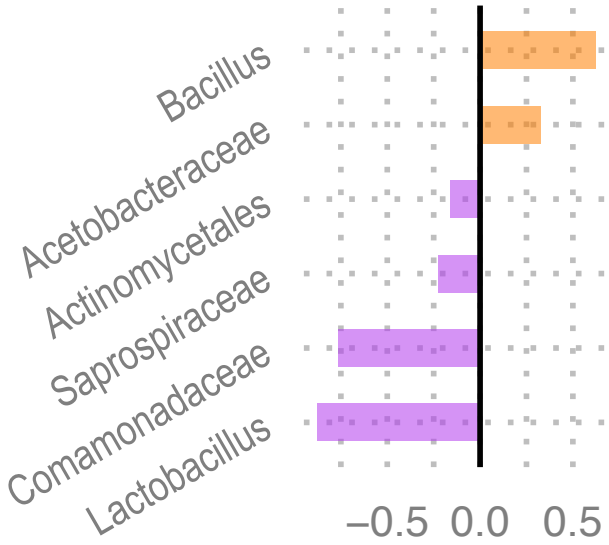
File intentionally blank -no taxa met the abundance-difference threshold for inclusion

Regulation of nuclear beta−catenin signaling and target gene transcription




Regulation of telomerase
Segetibacter
Asteroleplasma
0.0
0.1
0.2
0.3

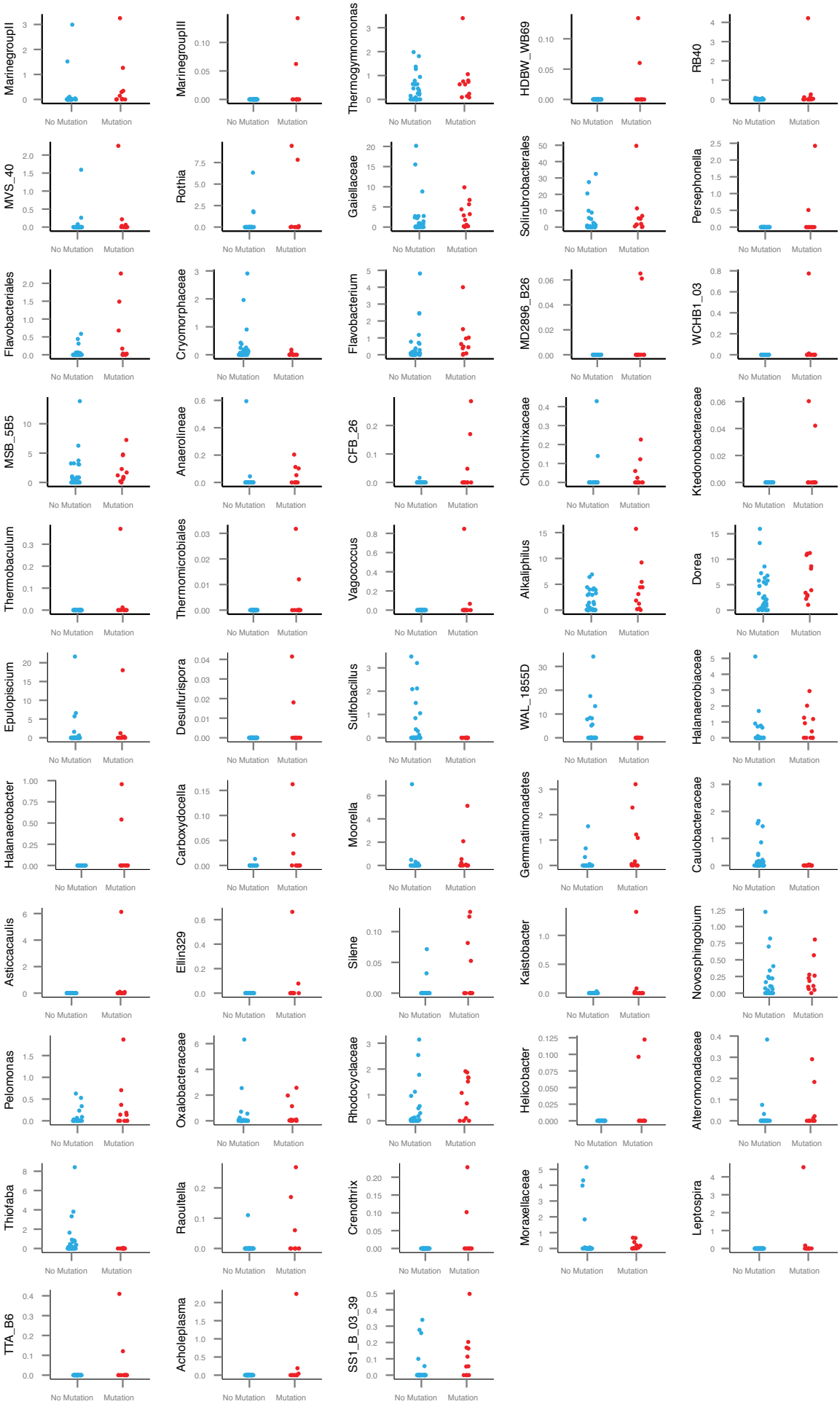
Signaling events mediated by Hepatocyte Growth Factor Receptor (c–Met)



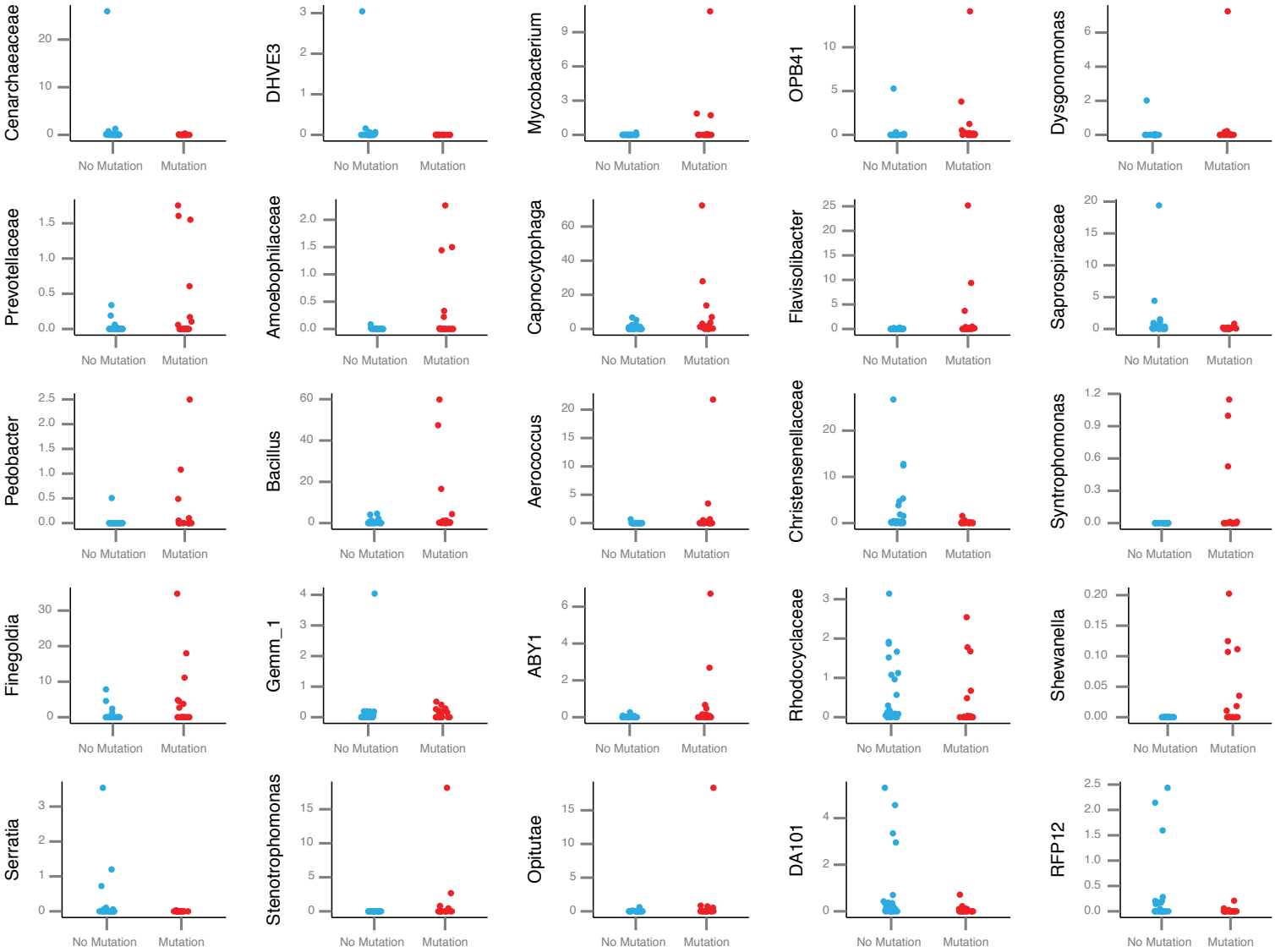
Supplementary Figure 10 | Abundance Dotplots.

Genes

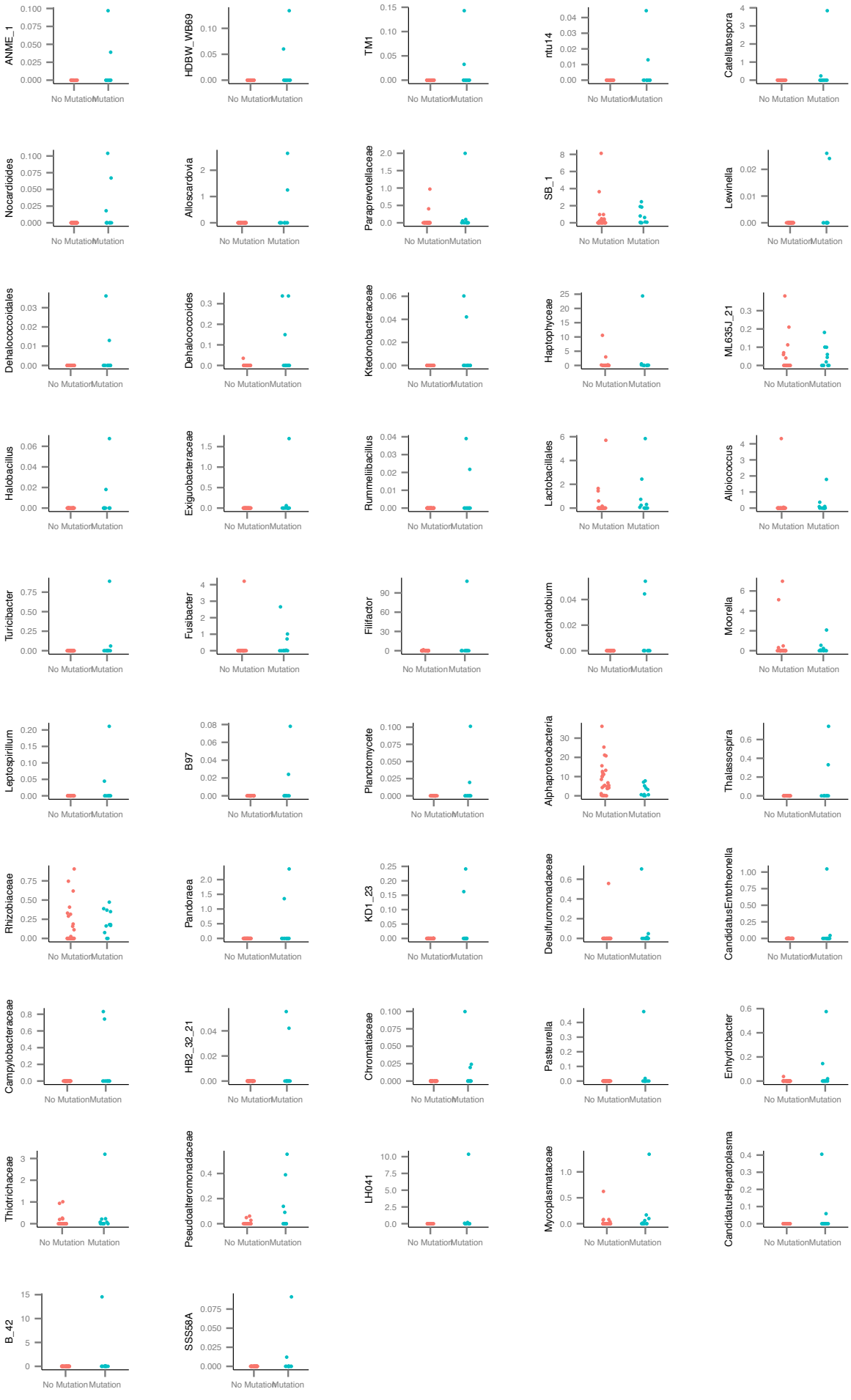
ANKRD36C


MarinegroupII
MarinegroupIII
Thermogymnomonas
HDBW_WB69
RB40
MVS_40
Rothia
Gaiellaceae
Solirubrobacterales
Persephonella
Flavobacteriales
Cryomorphaceae
Flavobacterium
MD2896_B26
WCHB1_03
MSB_5B5
Anaerolineae
CFB_26
Chlorothrixaceae
Ktedonobacteraceae
Thermobaculum
Thermomicrobiales
Vagococcus
Alkaliphilus
Dorea
Epulopiscium
Desulfurispora
Sulfobacillus
WAL_1855D
Halanaerobiaceae
Halanaerobacter
Carboxydocella
Moorella
Gemmatimonadetes
Caulobacteraceae
Asticcacaulis
Ellin329
Silene
Kaistobacter
Novosphingobium
Pelomonas
Oxalobacteraceae
Rhodocyclaceae
Helicobacter
Alteromonadaceae
Thiofaba
Raoultella
Crenothrix
Moraxellaceae
Leptospira
TTA_B6
Acholeplasma
SS1_B_03_39
No Mutation
Mutation

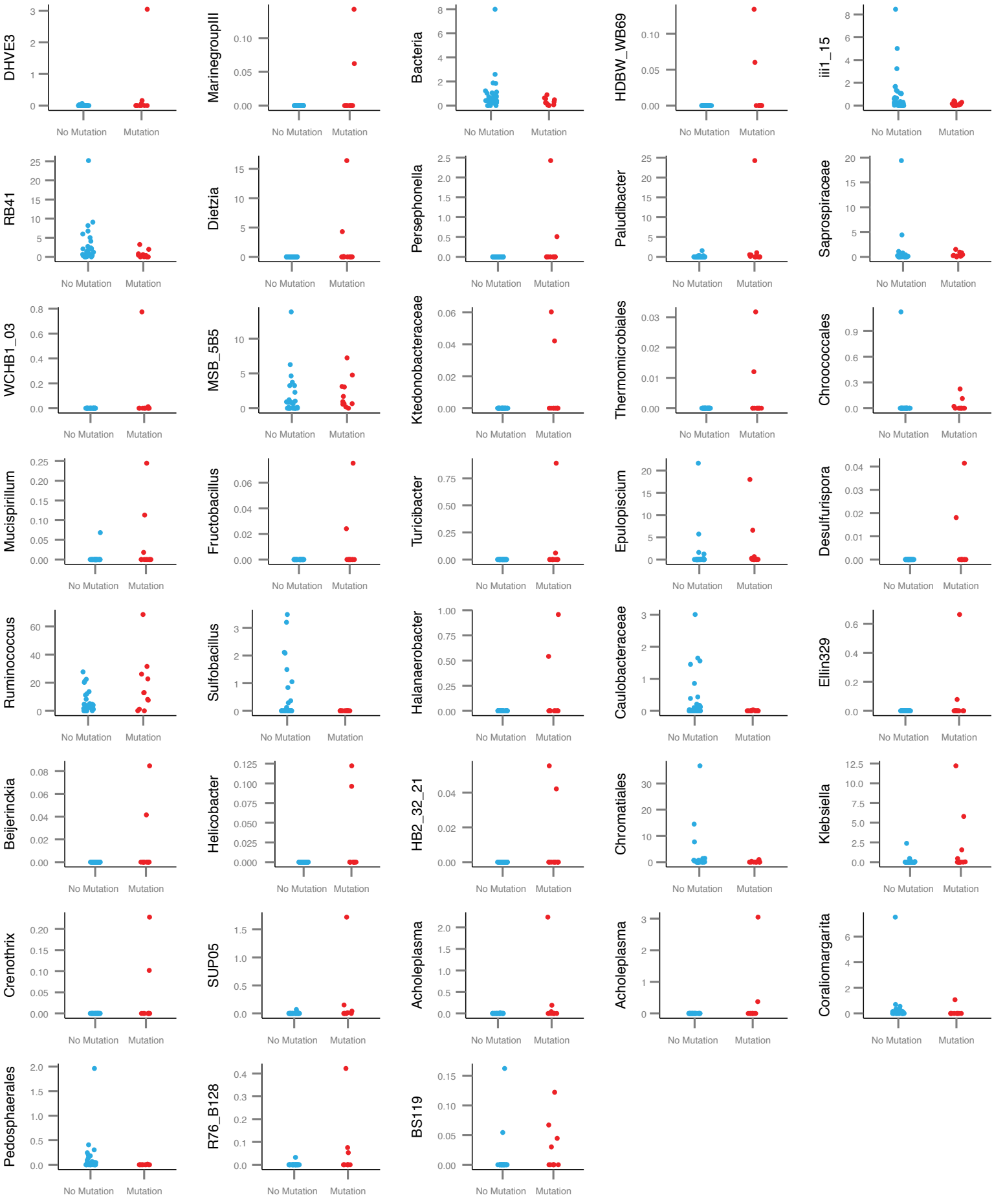
APC


Cenarchaeaceae
DHVE3
Mycobacterium
OPB41
Dysgonomonas
Prevotellaceae
Amoebophilaceae
Capnocytophaga
Flavisolibacter
Saprospiraceae
Pedobacter
Bacillus
Aerococcus
Christensenellaceae
Syntrophomonas
Finegoldia
Gemm_1
ABY1
Rhodocyclaceae
Shewanella
Serratia
Stenotrophomonas
Opitutae
DA101
RFP12
No Mutation
Mutation

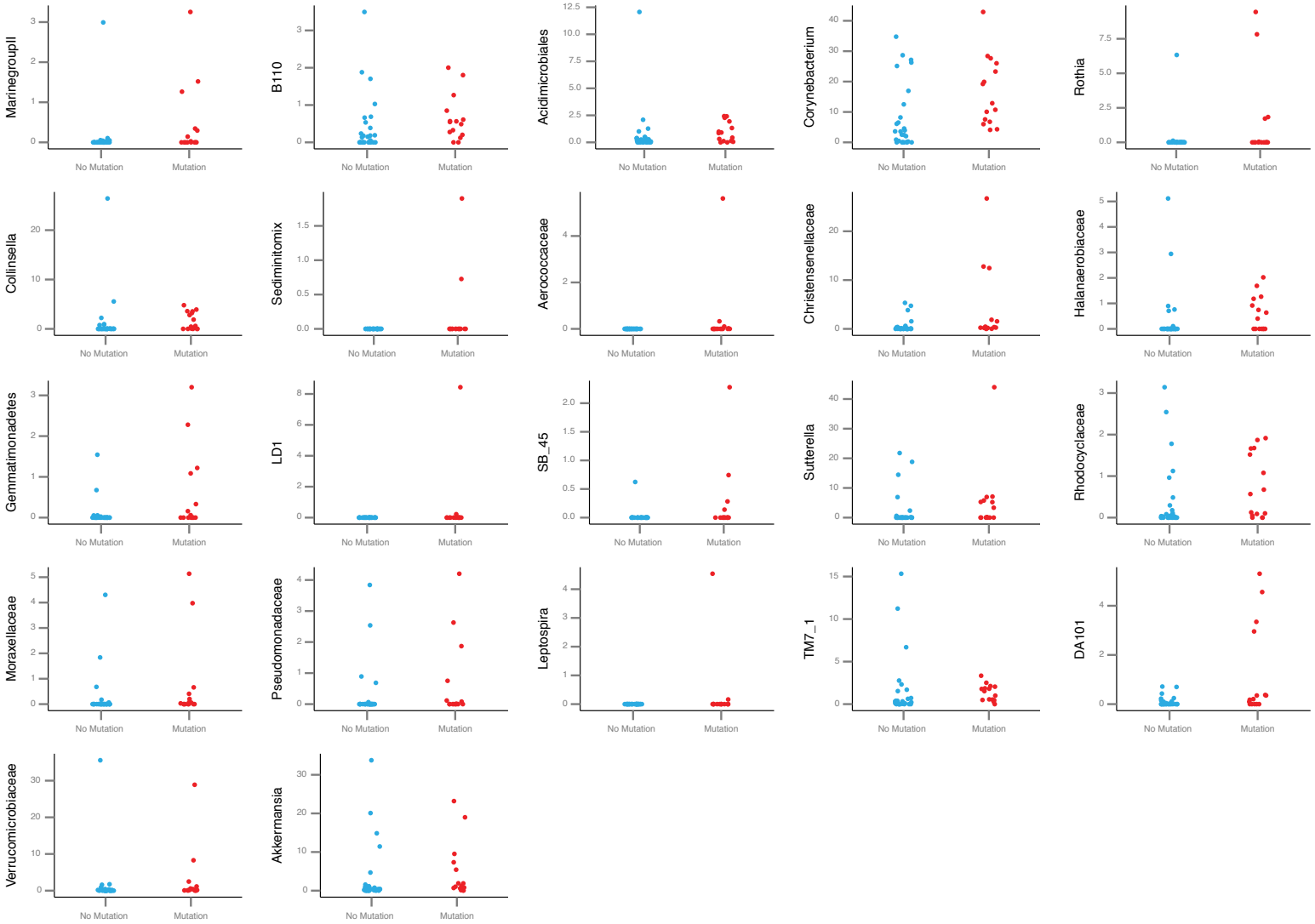
CTBP2


ANME_1
HDBW_WB69
TM1
ntu14
Catellatospora
Nocardioides
Alloscardovia
Paraprevotellaceae
SB_1
Lewinella
Dehalococcoidales
Dehalococcoides
Ktedonobacteraceae
Haptophyceae
ML635J_21
Halobacillus
Exiguobacteraceae
Rummeliibacillus
Lactobacillales
Alloiococcus
Turicibacter
Fusibacter
Filifactor
Acetohalobium
Moorella
Leptospirillum
B97
Planctomycete
Alphaproteobacteria
Thalassospira
Rhizobiaceae
Pandoraea
KD1_23
Desulfuromonadaceae
CandidatusEntotheonella
Campylobacteraceae
HB2_32_21
Chromatiaceae
Pasteurella
Enhydrobacter
Thiotrichaceae
Pseudoalteromonadaceae
LH041
Mycoplasmataceae
CandidatusHepatoplasma
B_42
SSS58A
No Mutation
Mutation

KMT2C


DHVE3
MarinegroupIII
Bacteria
HDBW_WB69
iii1_15
RB41
Dietzia
Persephonella
Paludibacter
Saprospiraceae
WCHB1_03
MSB_5B5
Ktedonobacteraceae
Thermomicrobiales
Chroococcales
Mucispirillum
Fructobacillus
Turicibacter
Epulopiscium
Desulfurispora
Ruminococcus
Sulfobacillus
Halanaerobacter
Caulobacteraceae
Ellin329
Beijerinckia
Helicobacter
HB2_32_21
Chromatiales
Klebsiella
Crenothrix
SUP05
Acholeplasma
Acholeplasma
Coraliomargarita
Pedosphaerales
R76_B128
BS119
No Mutation
Mutation

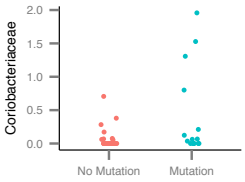
ZNF717

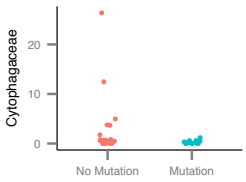

MarinegroupII
B110
Acidimicrobiales
Corynebacterium
Rothia
Collinsella
Sediminitomix
Aerococcaceae
Christensenellaceae
Halanaerobiaceae
Gemmatimonadetes
LD1
SB_45
Sutterella
Rhodocyclaceae
Moraxellaceae
Pseudomonadaceae
Leptospira
TM7_1
DA101
Verrucomicrobiaceae
Akkermansia
No Mutation
Mutation

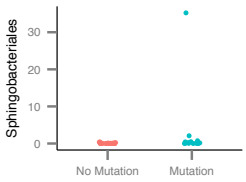
Supplementary Figure 10 | Abundance Dotplots.

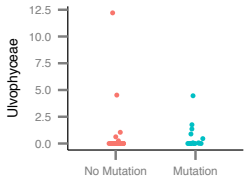
KEGG

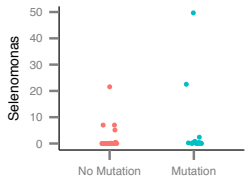
ABC Transporters

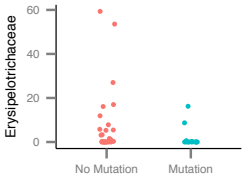


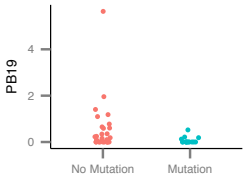


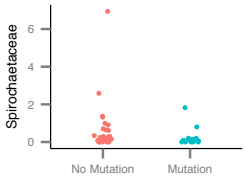




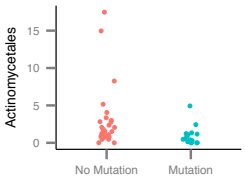


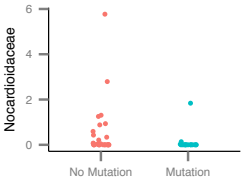


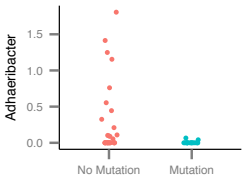


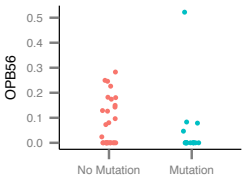


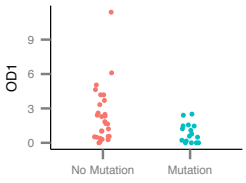
Adherens junctions

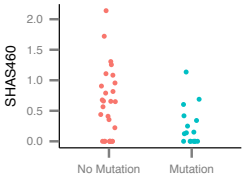




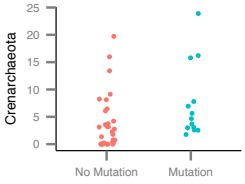


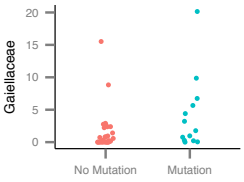


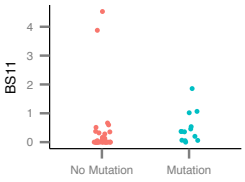


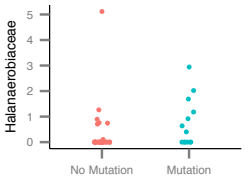


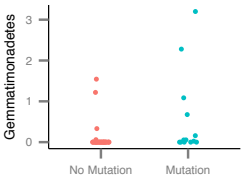
Alanine, aspartate, and glutamate metabolism

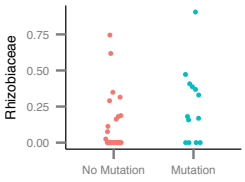




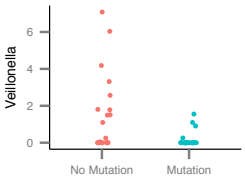


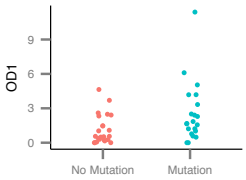




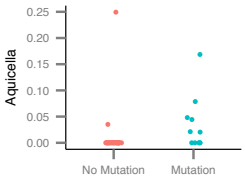


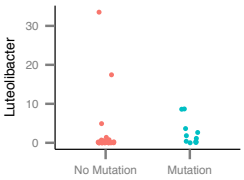
Cell cycle


Veillonella
6
4
2
0
No Mutation
Mutation

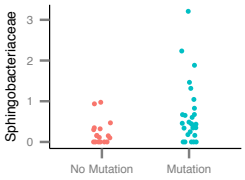

OD1
9
6
3
0
No Mutation
Mutation

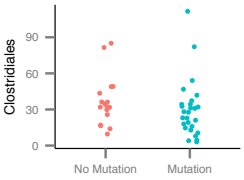
Cysteine and methionine metabolism

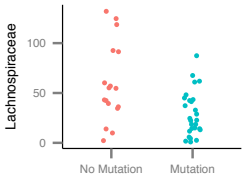


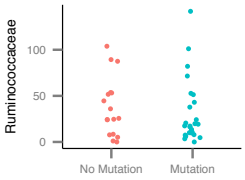


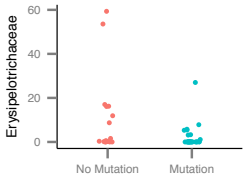
Focal adhesion

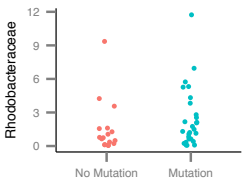


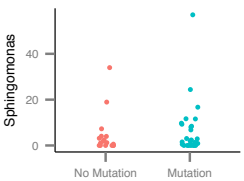


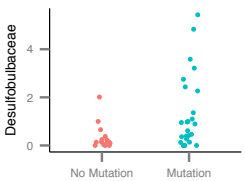


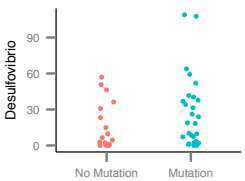


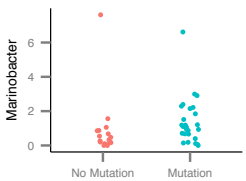




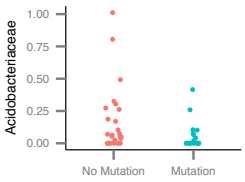


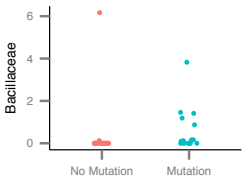


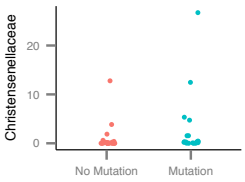


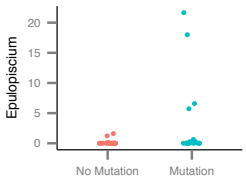


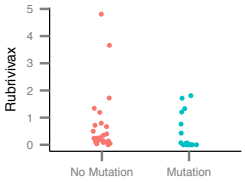
Lysine degradation

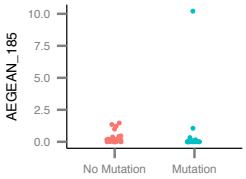




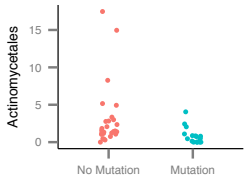


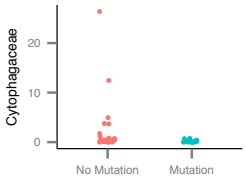


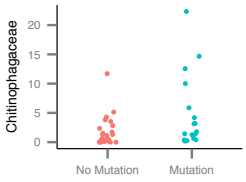


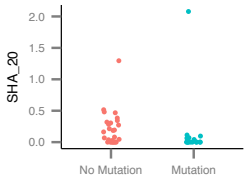


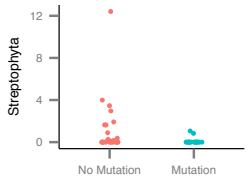
MAPK signaling pathway

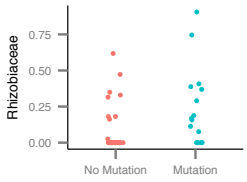




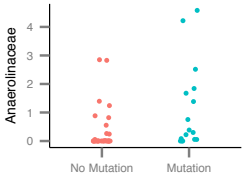


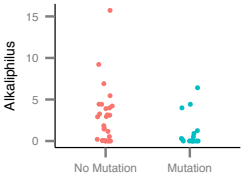


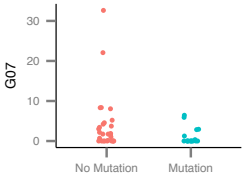


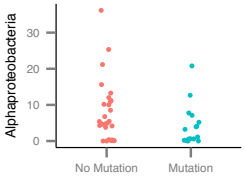


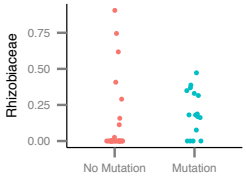
Notch signaling pathway



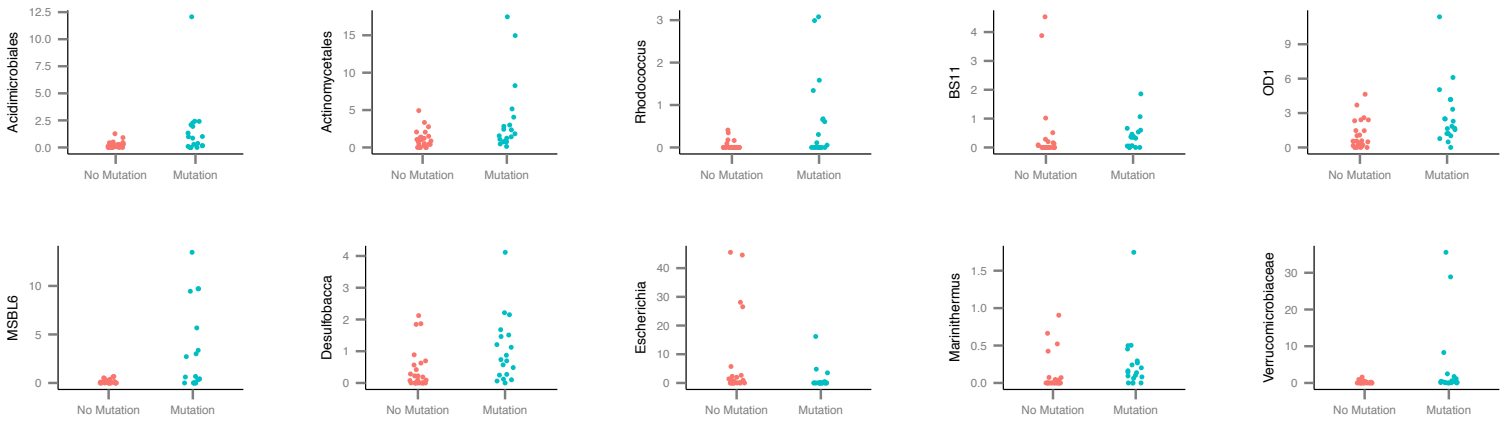




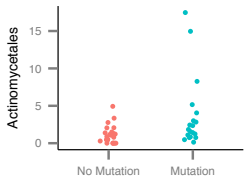


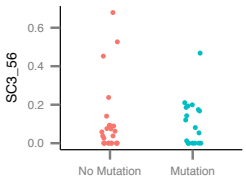


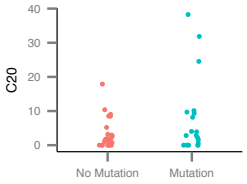
Oocyte meiosis

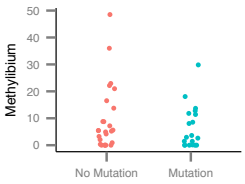


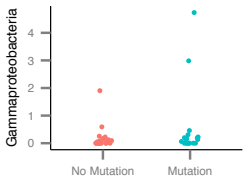
Oxidative phosphorylation

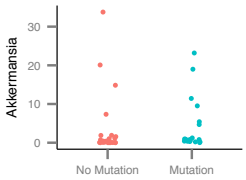




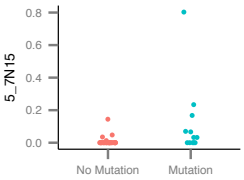


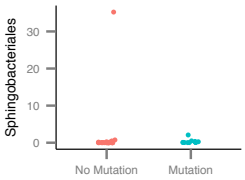


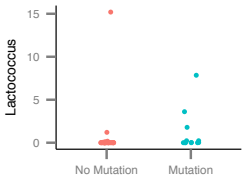


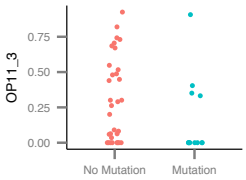


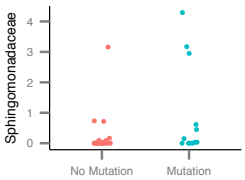
Phosphatidylinositol signaling system

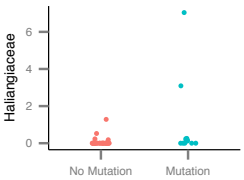


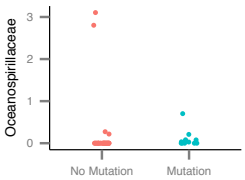


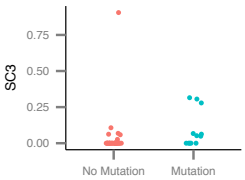




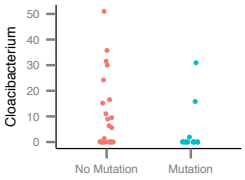


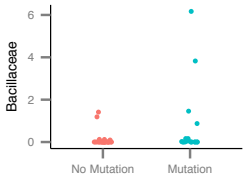


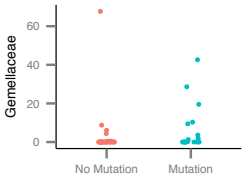


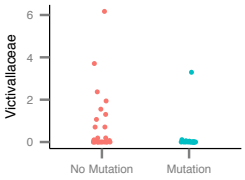


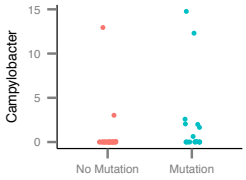
Protein processing in endoplasmic reticulum



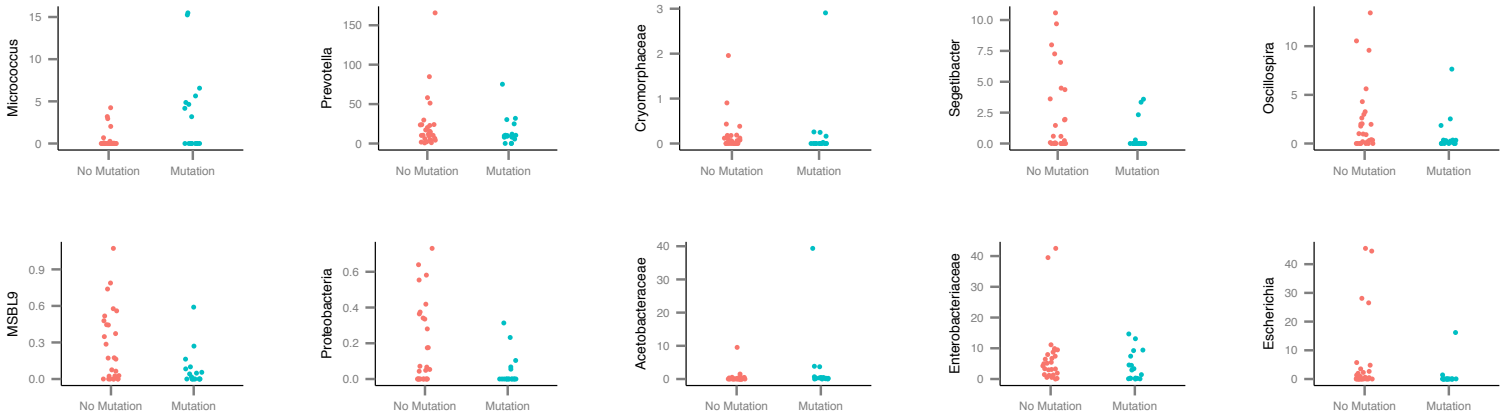




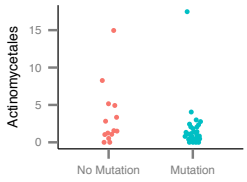


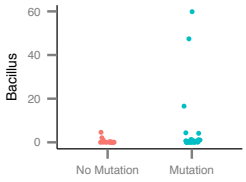


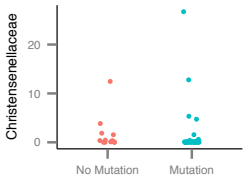
Purine metabolism

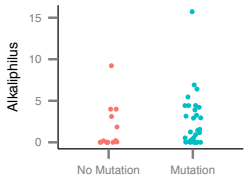


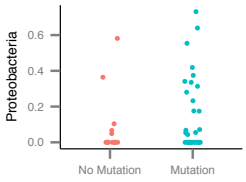
Regulation of actin cytoskeleton



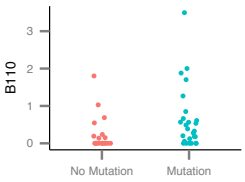








Ribosome


B110
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2
1
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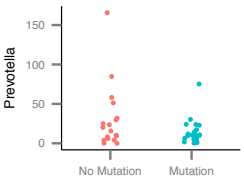
Mutation


Prevotella
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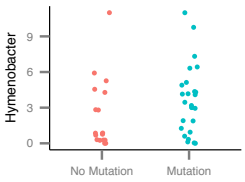
Hymenobacter
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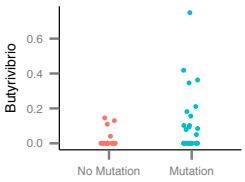
Butyrivibrio
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0.4
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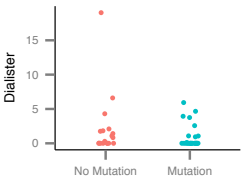
Mutation


Dialister
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5
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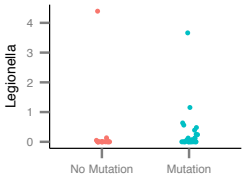
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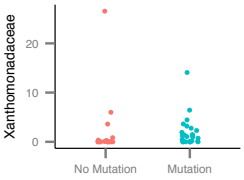
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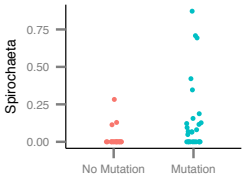
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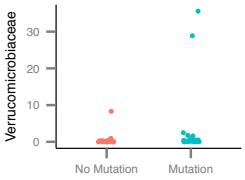
Mutation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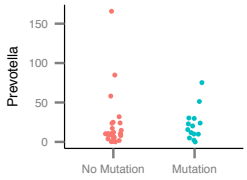
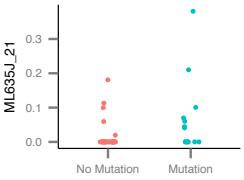
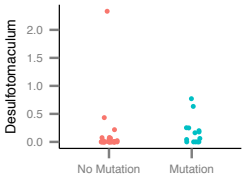
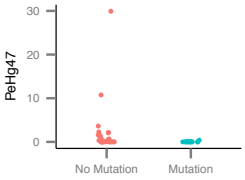
Mutation

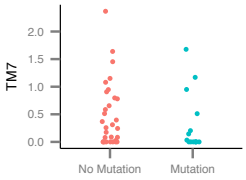
RNA degradation



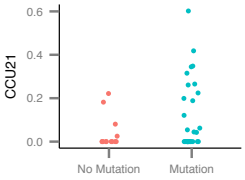


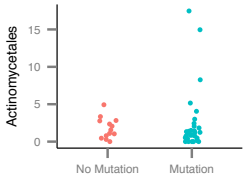


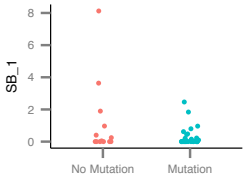


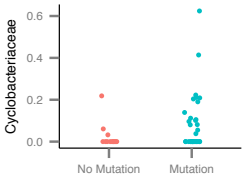


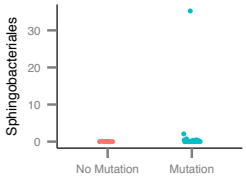
RNA transport

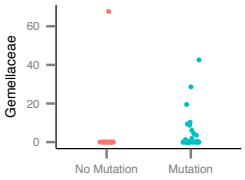


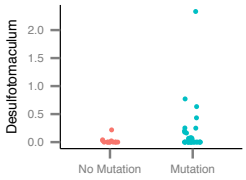


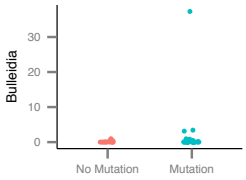


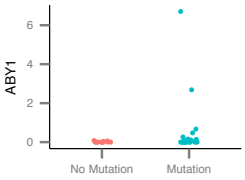


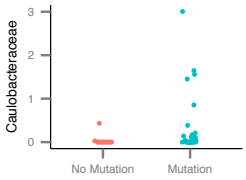


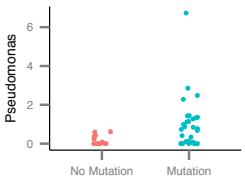




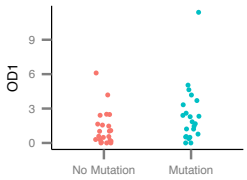


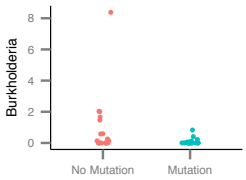




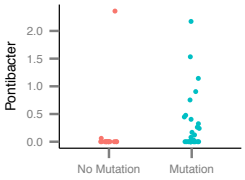


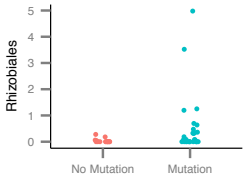
Spliceosome

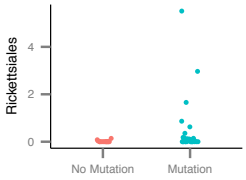


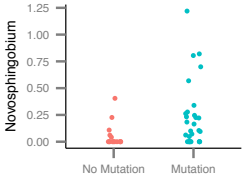


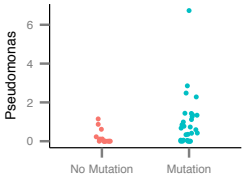
Ubiquitin mediated proteolysis

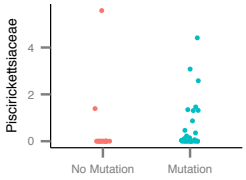


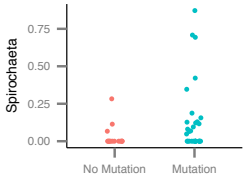




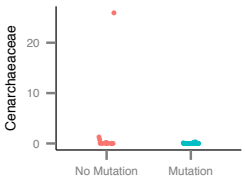


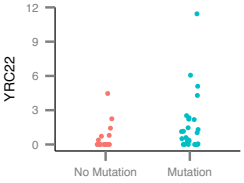


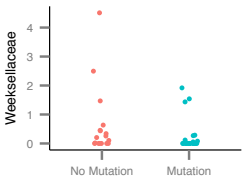


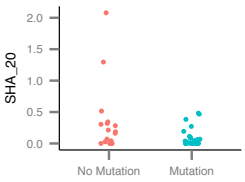


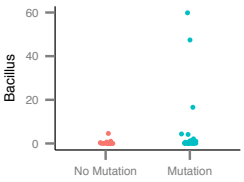
Wnt signaling pathway

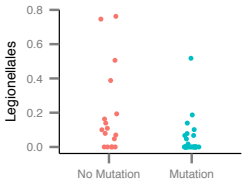


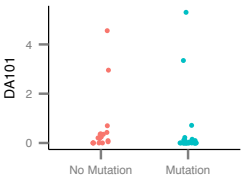








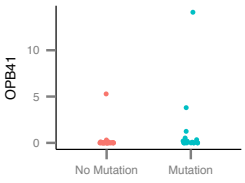


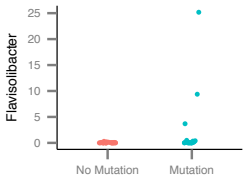


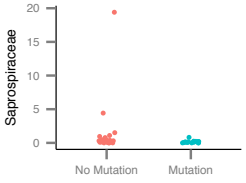
Supplementary Figure 10 | Abundance Dotplots.

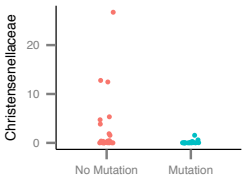
PID

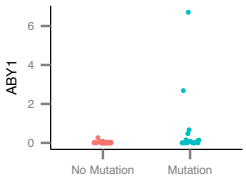
Canonical Wnt signaling pathway

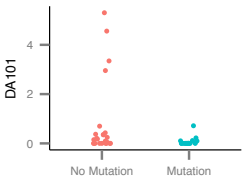




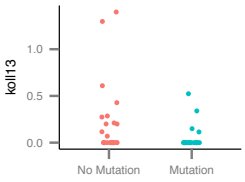


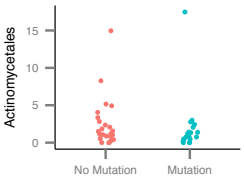


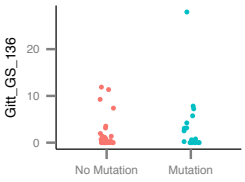


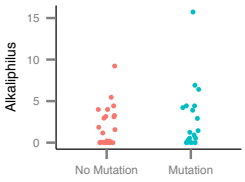


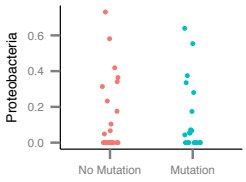
CDC42 signaling

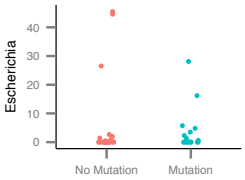


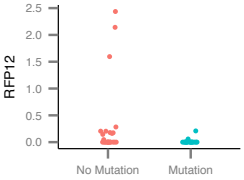




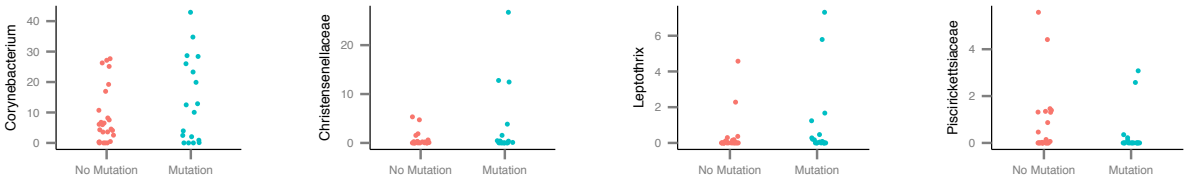




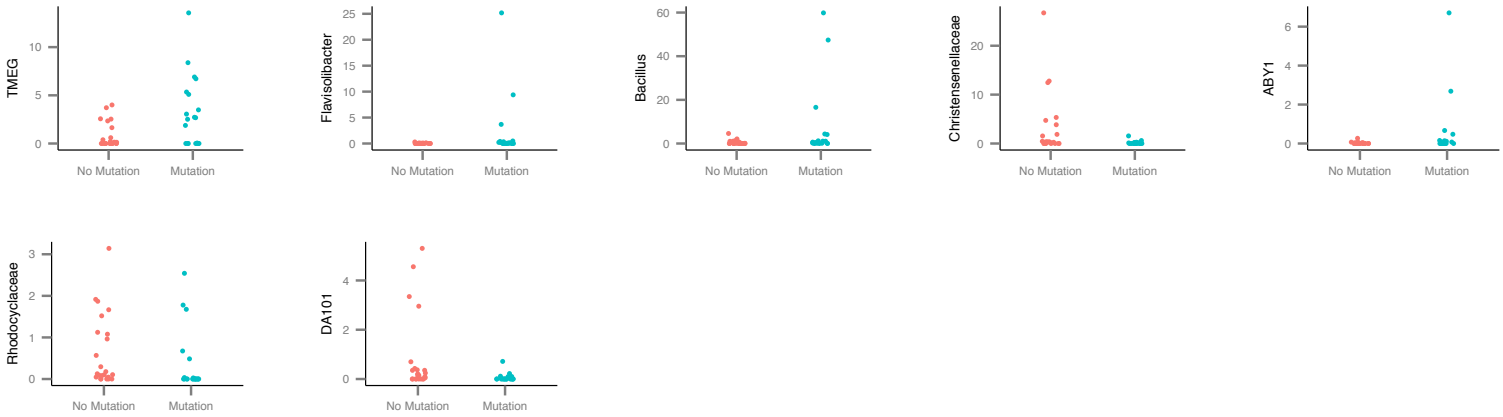




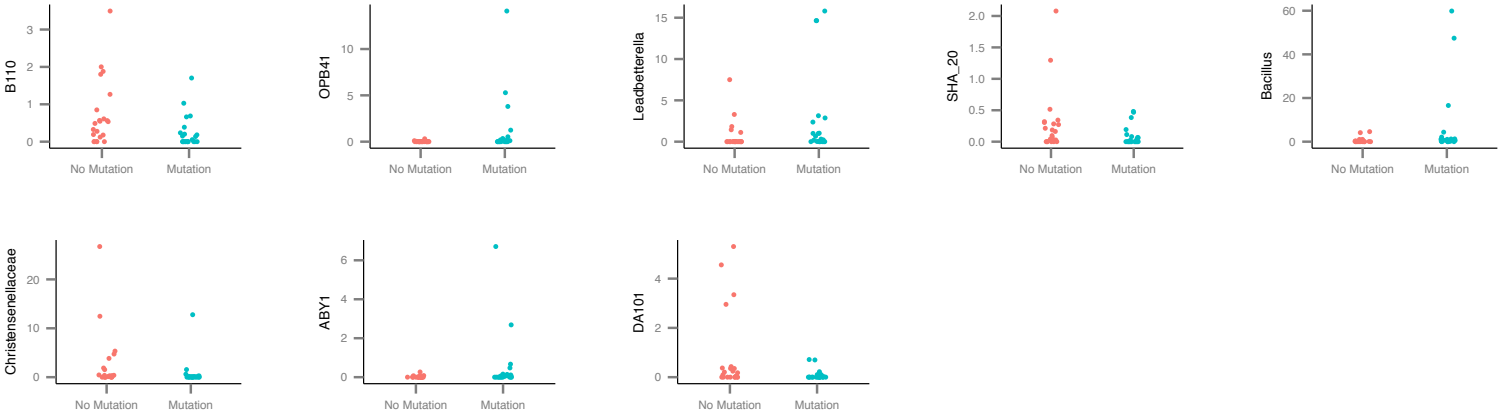
CXCR4-mediated signaling



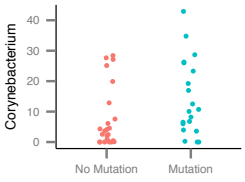
Degradation of beta-catenin

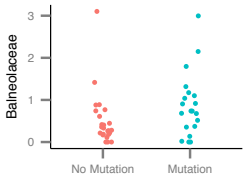


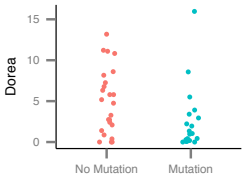
Direct p53 effectors

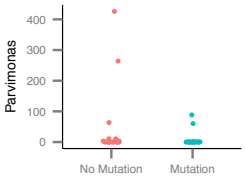


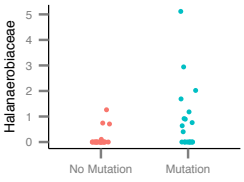
ErbB1 downstream signaling

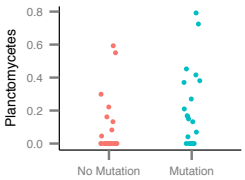


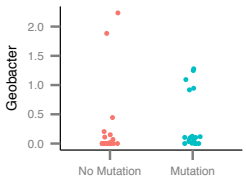


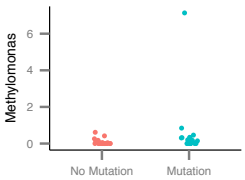




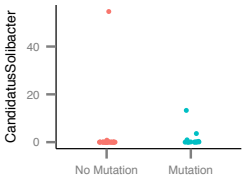


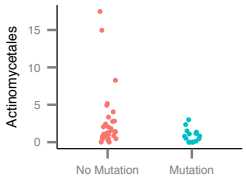


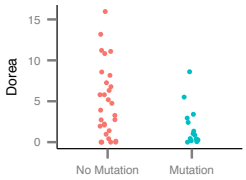




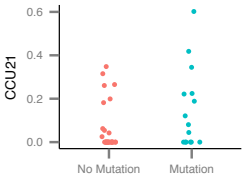
Insulin pathway

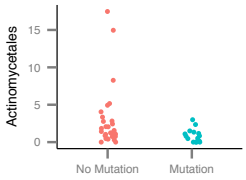


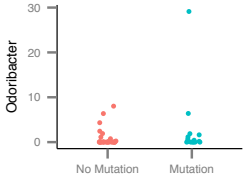


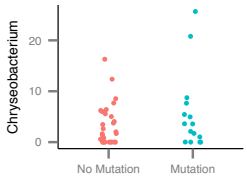


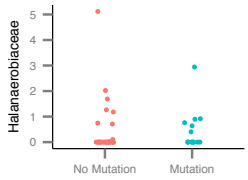
Neurotrophic factor-mediated Trk signaling

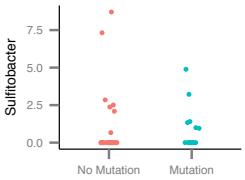


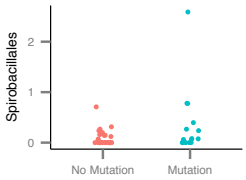




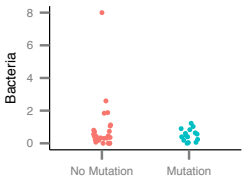


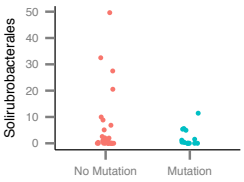


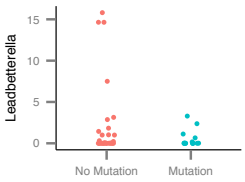


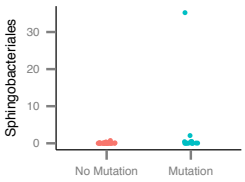


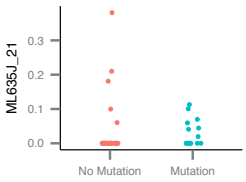
p75 (NTR)-mediated signaling

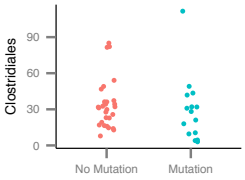


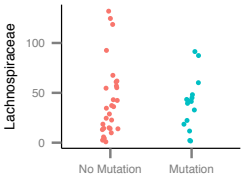


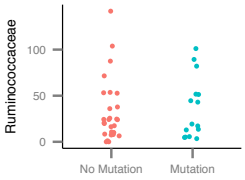


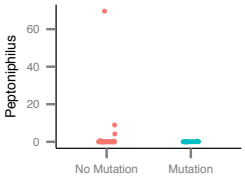


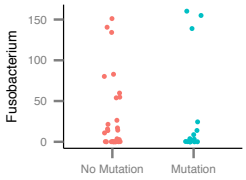


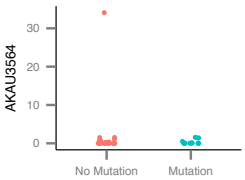


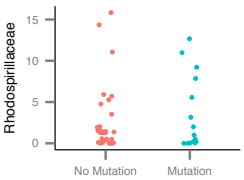


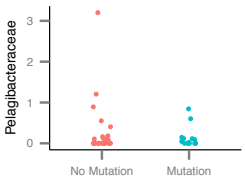


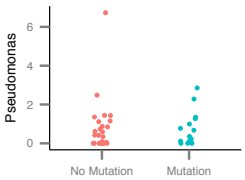


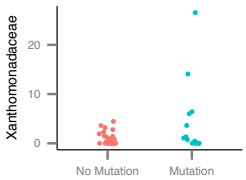


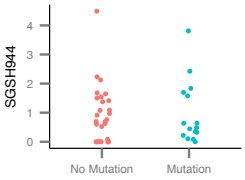


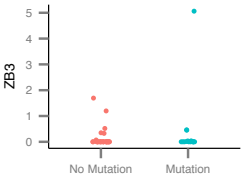




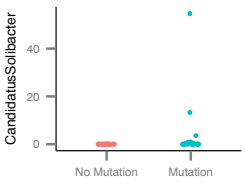


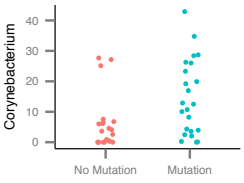


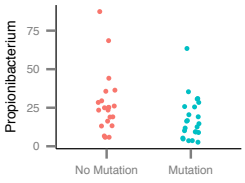


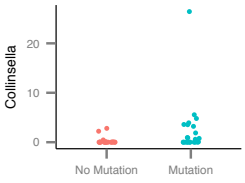


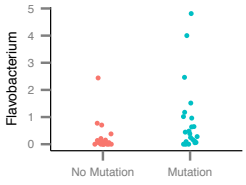
PDGFR-beta signaling pathway

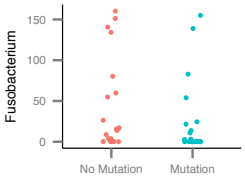


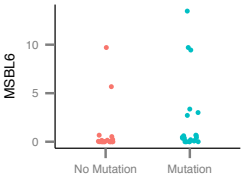


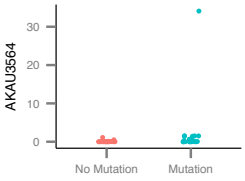


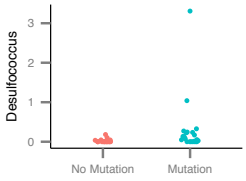


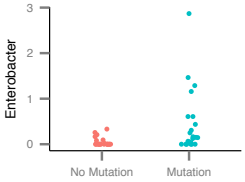




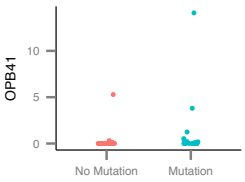


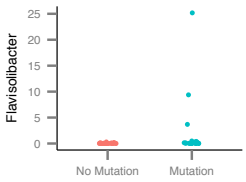


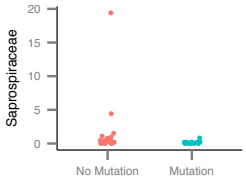


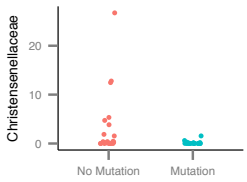


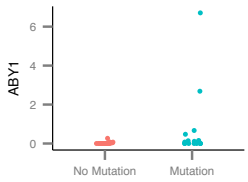
Presenilin action in Notch and Wnt signaling

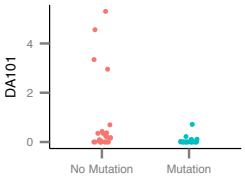




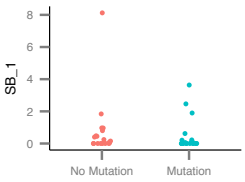


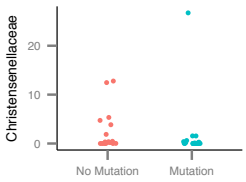


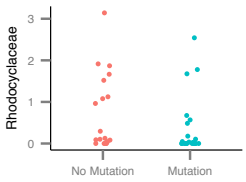




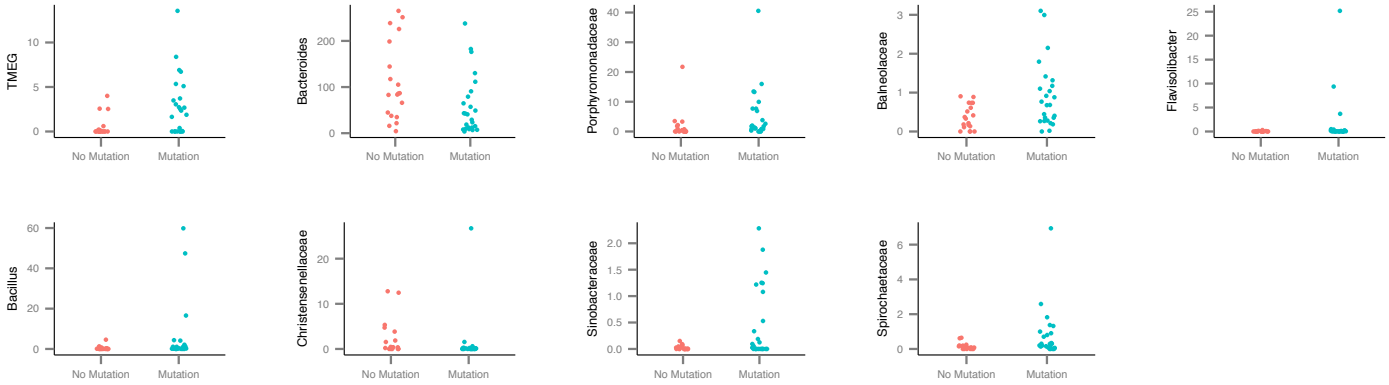
Regulation of CDC42 activity



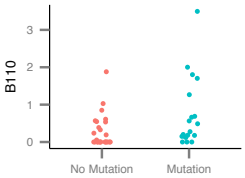


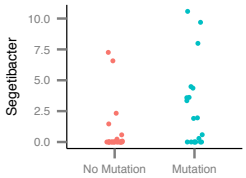


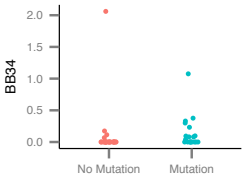
Regulation of nuclear beta-catenin signaling and target gene transcription

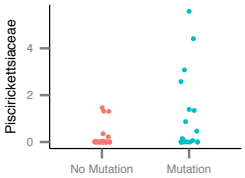


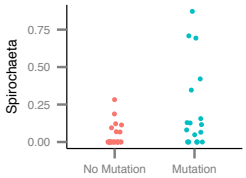
Regulation of telomerase

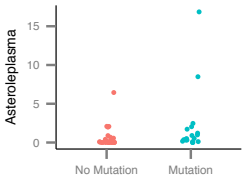
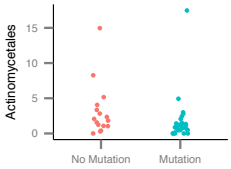
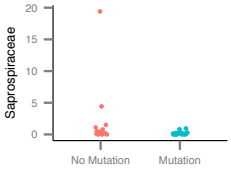
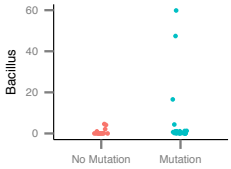
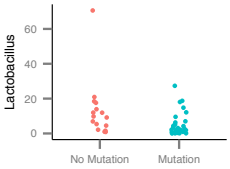
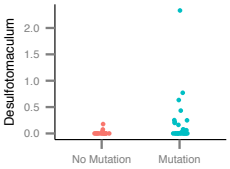
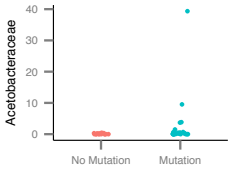
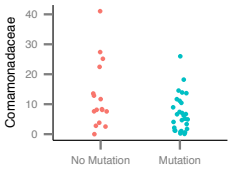












Signaling events mediated by Hepatocyte Growth Factor Receptor (c-Met)