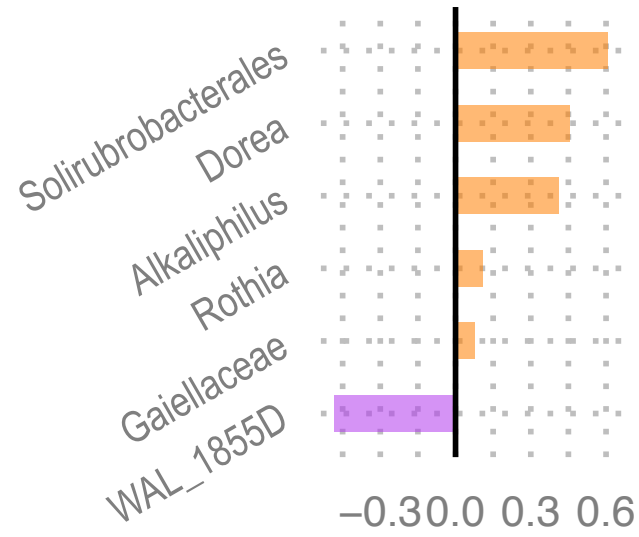


S12 Fig. Large set of abundance plots for the taxa from each of the genes, KEGG pathways, and PID pathways that harbored prevalent LoF mutations and showed significance as a means of predicting the interaction between the mutation and the microbiota. Abundances are plotted as both column dot plots as well as horizontal bar plots of the differences in the mean abundances of a subset of the taxa predicted to interact differentially with tumors with a LoF mutation relative to those without the indicated mutation. These subsets represent those taxa that had a mean difference in abundance of greater than 0.1%, proportionally.

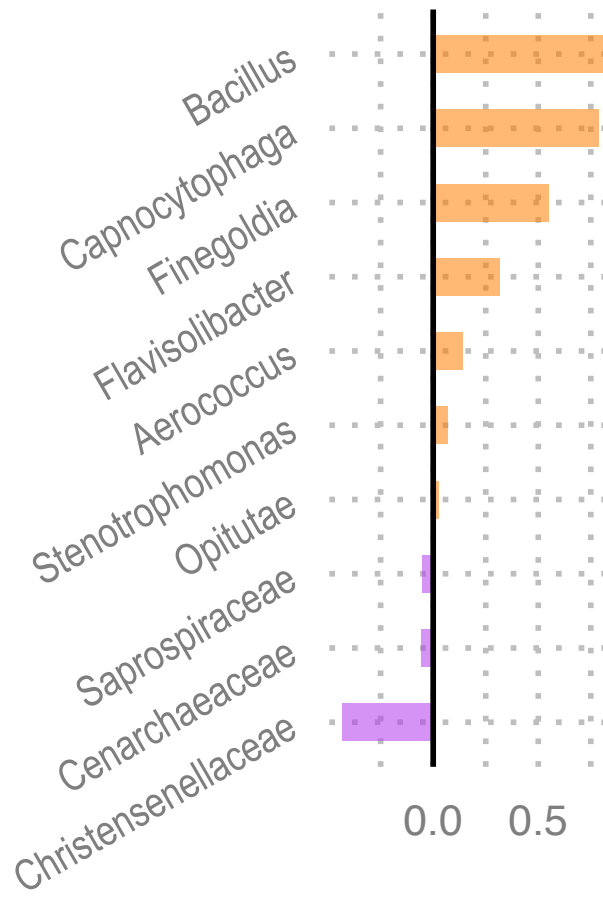
S12 Fig | Abundance Barcharts.

Genes

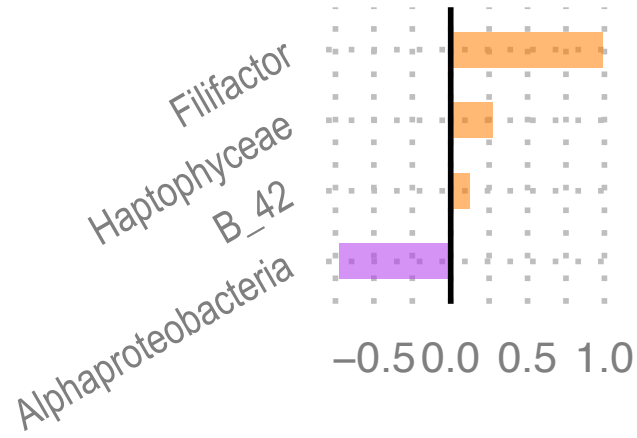
ANKRD36C



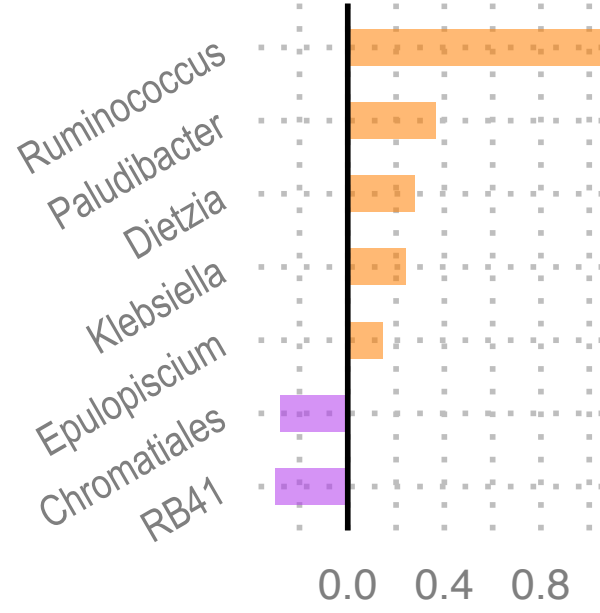
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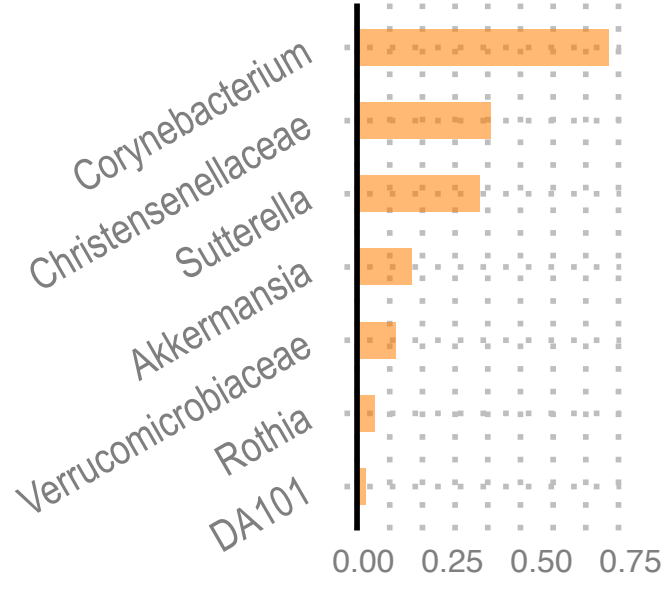
CTBP2



KMT2C



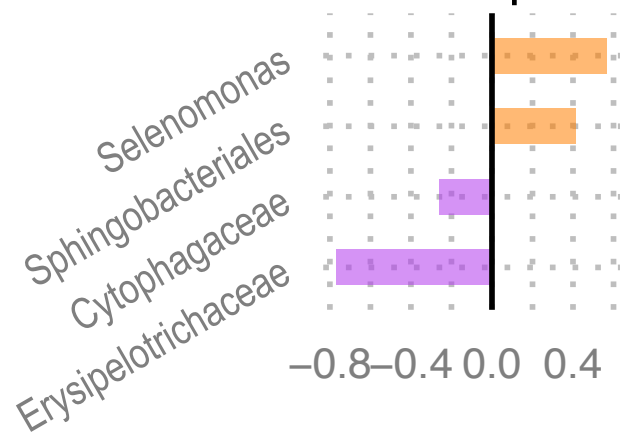
ZNF717



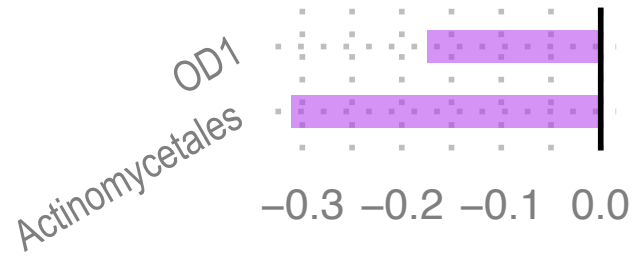
S12 Fig | Abundance Barcharts.

KEGG

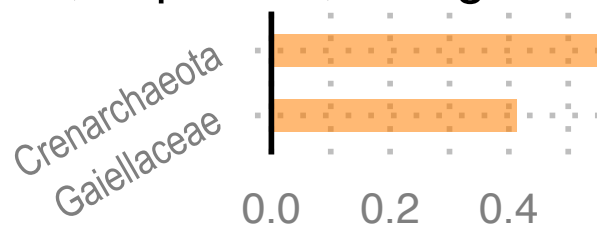
ABC transporters

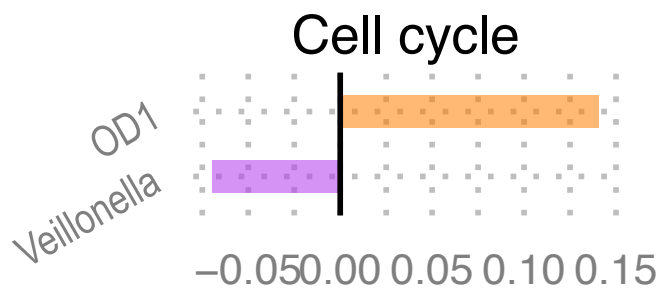


Adherens junction



Alanine, aspartate, and glutamate metabolism

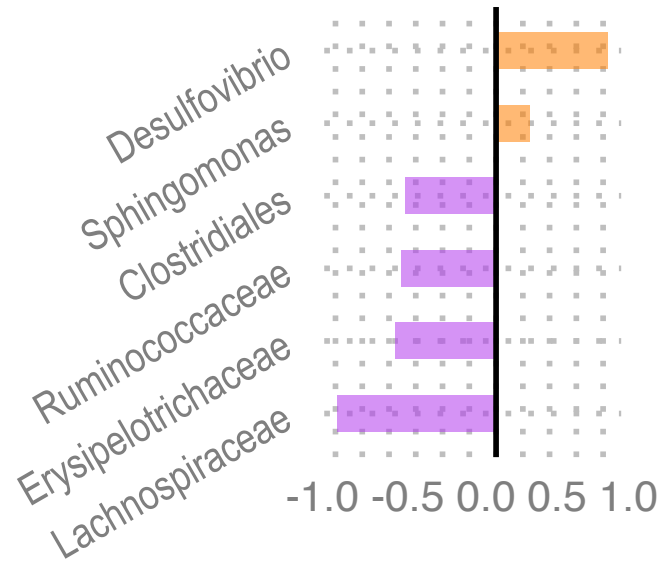




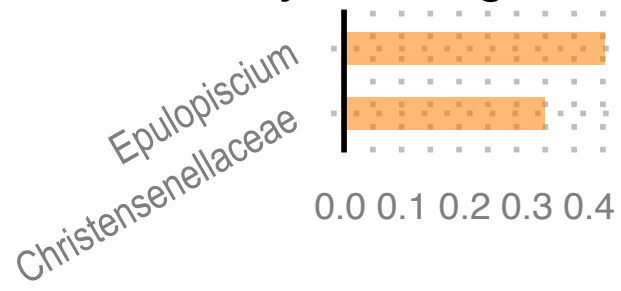
Cysteine and methionine metabolism

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

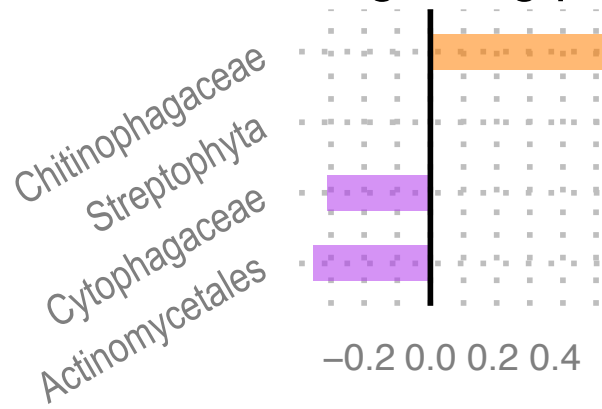
Focal adhesion



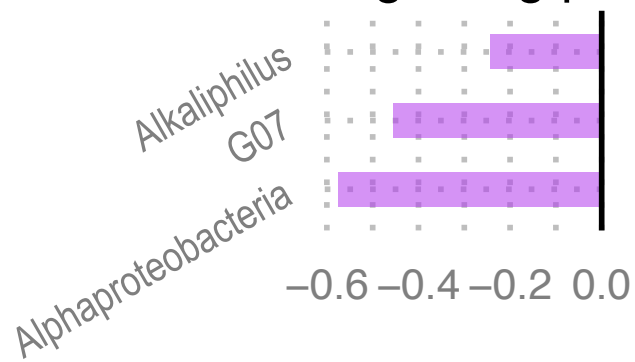
Lysine degradation



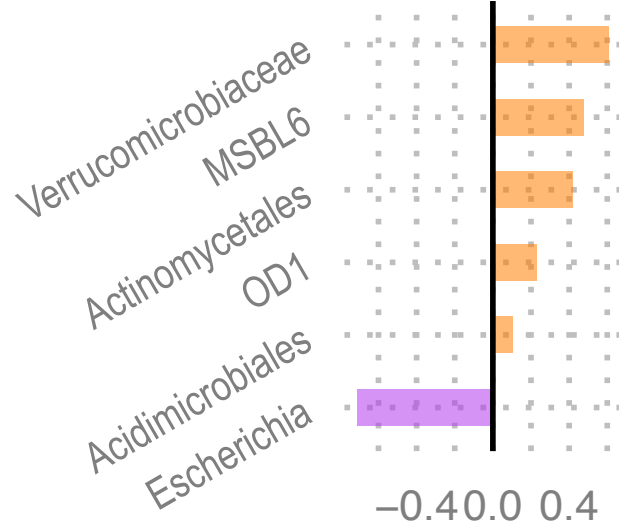
MAPK signaling pathway



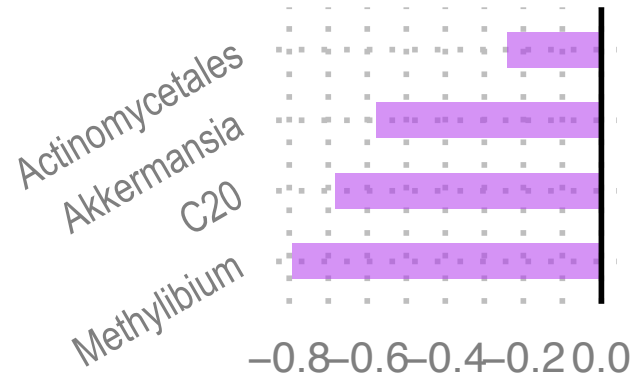
Notch signaling pathway



Oocyte meiosis



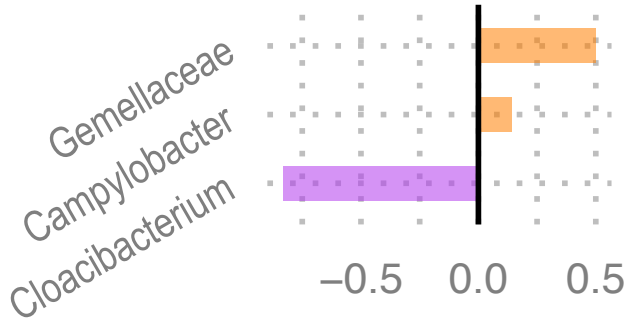
Oxidative phosphorylation



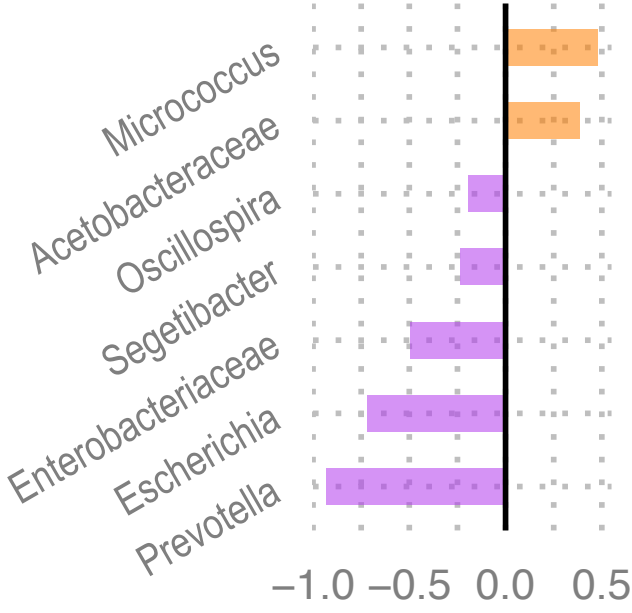
Phosphatidylinositol signaling system

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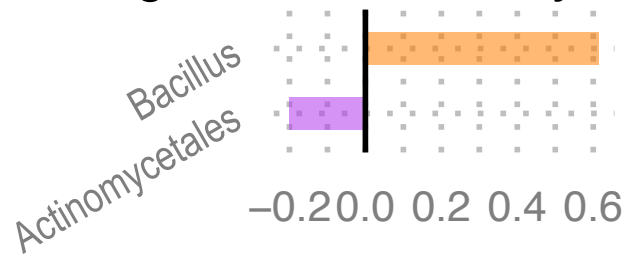
Protein processing in endoplasmic reticulum



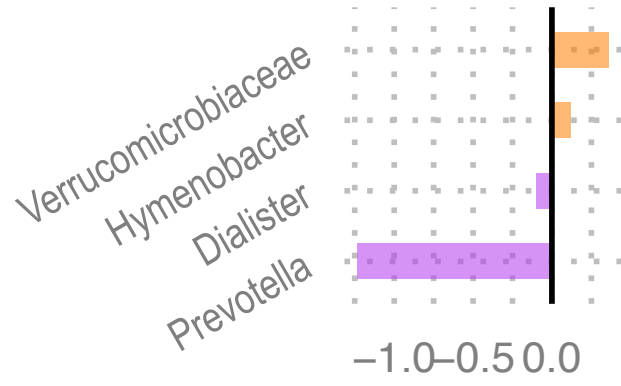
Purine metabolism



Regulation of actin cytoskeleton

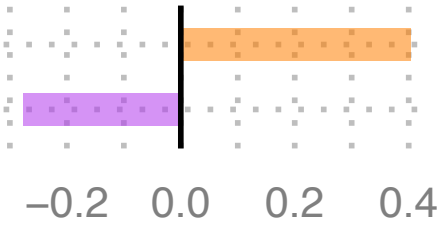


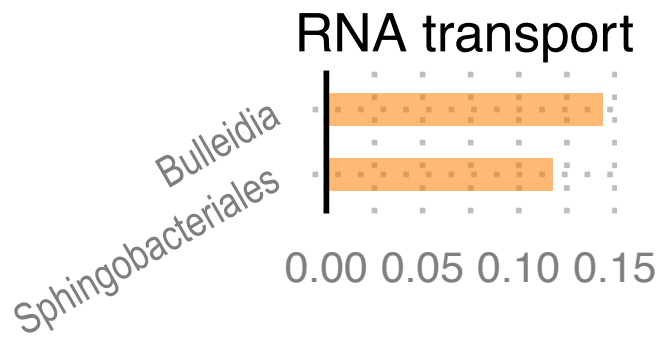
Ribosome



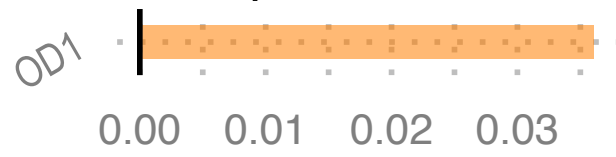
RNA degradation

Prevotella
PeHg47





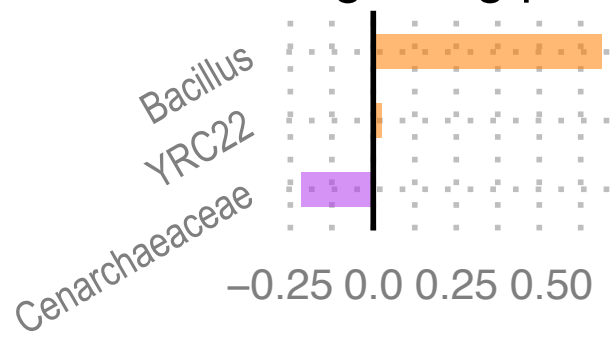
Spliceosome



Ubiquitin mediated proteolysis

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

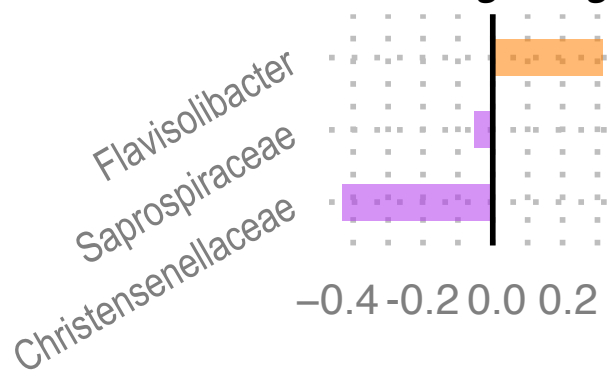
Wnt signaling pathway

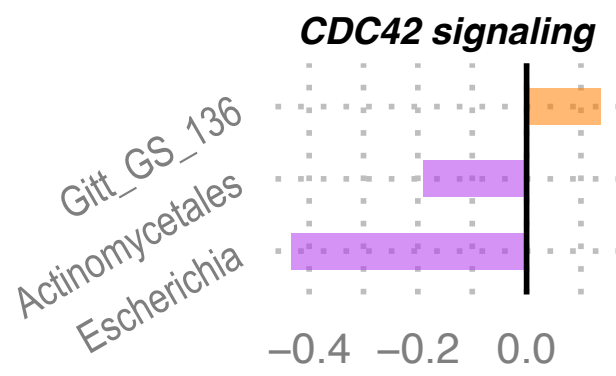


S12 Fig I Abundance Barcharts.

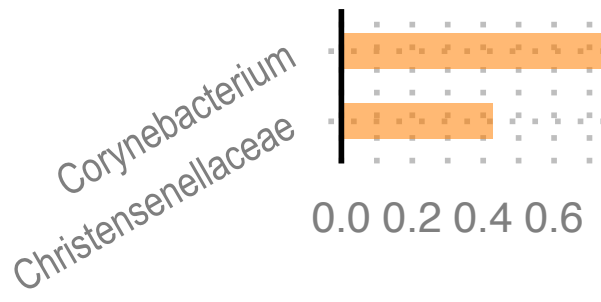
PID

Canonical Wnt signaling pathway

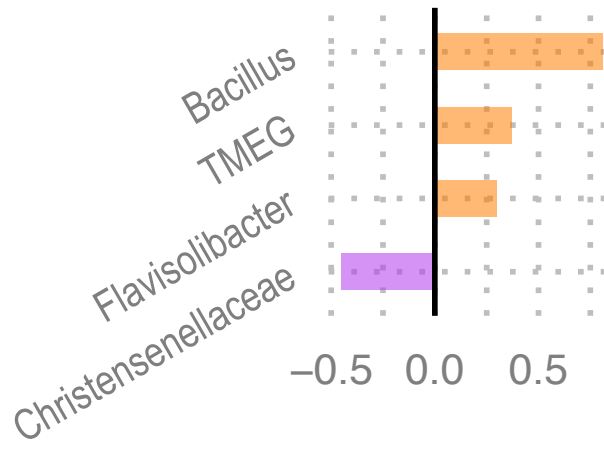




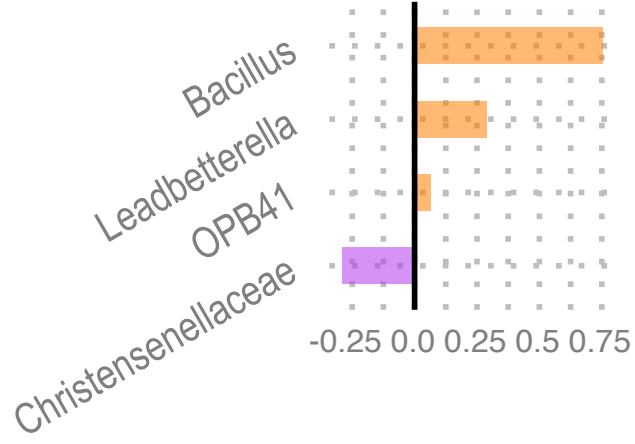
CXCR4-mediated signaling



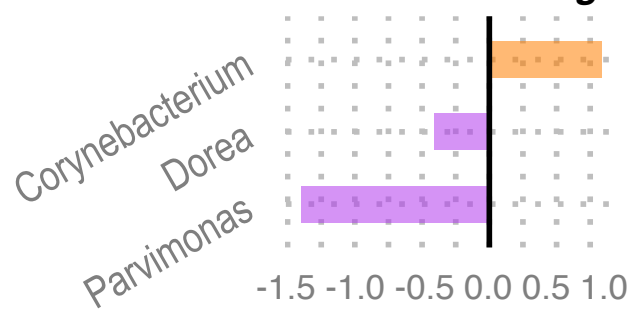
Degradation of beta-catenin



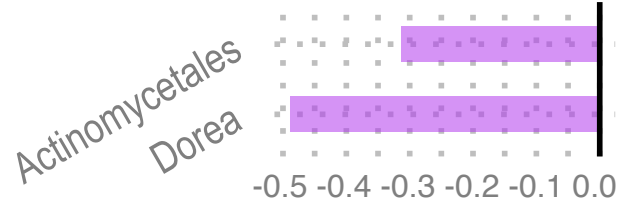
Direct p53 effectors



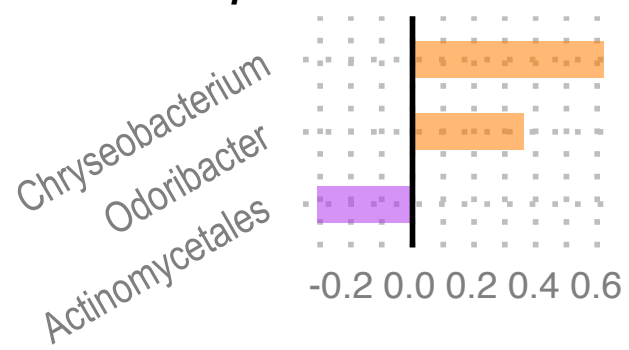
***ErbB1* downstream signaling**



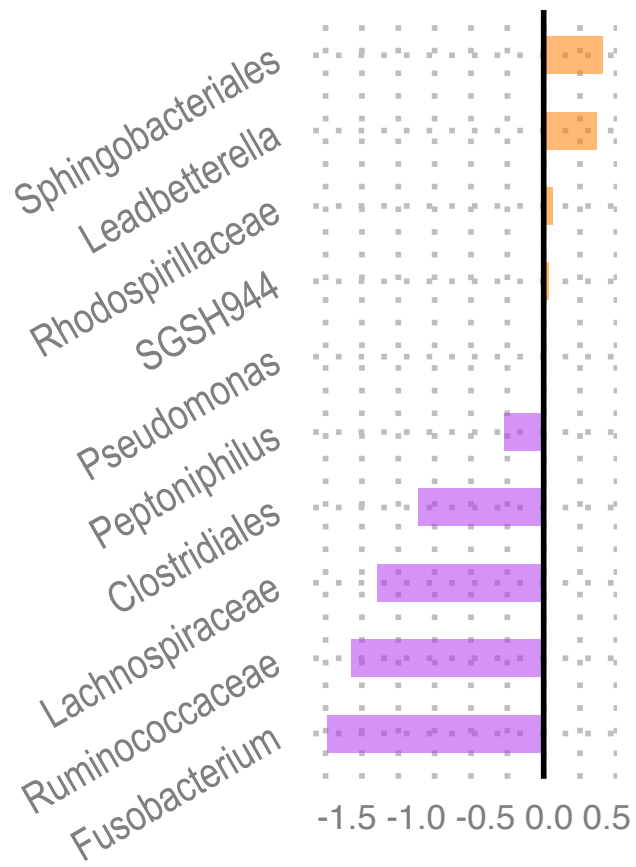
Insulin pathway



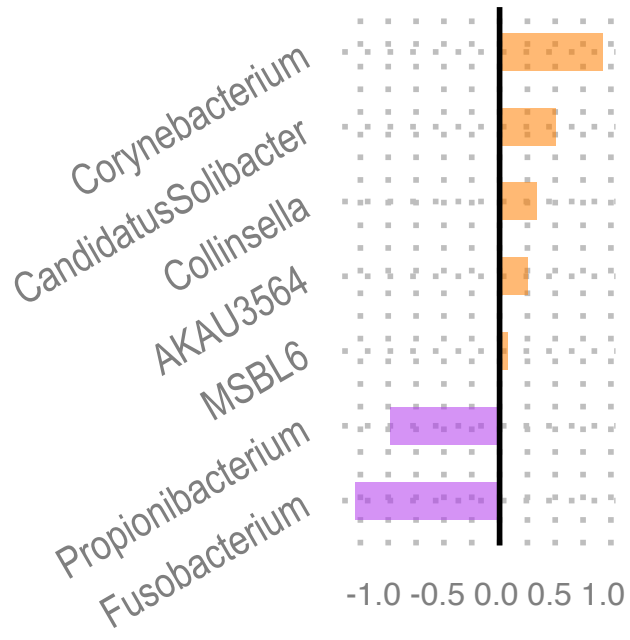
Neurotrophic factor-mediated Trk signaling



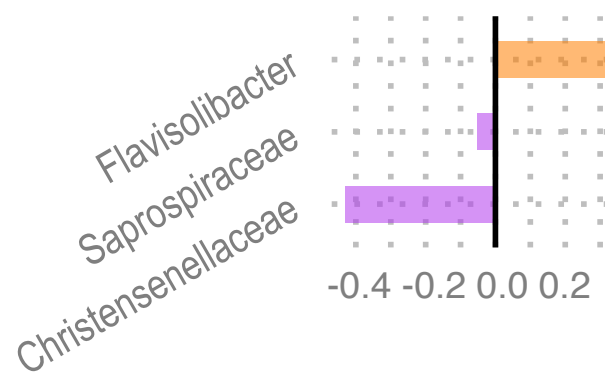
p75 (NTR)-mediated signaling



PDGFR-beta signaling pathway



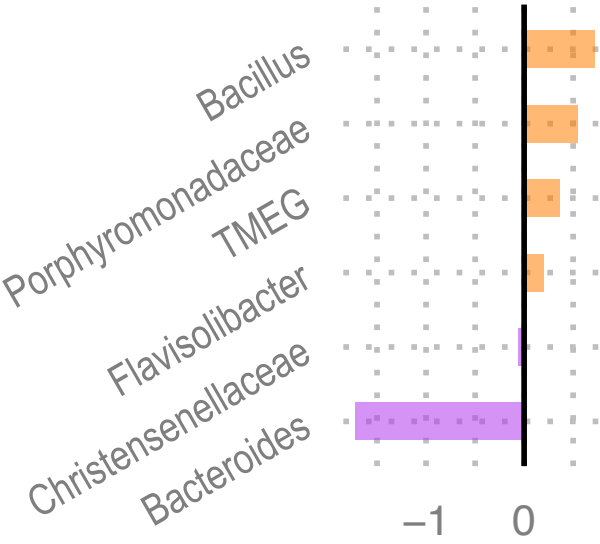
Presenilin action in Notch and Wnt signaling



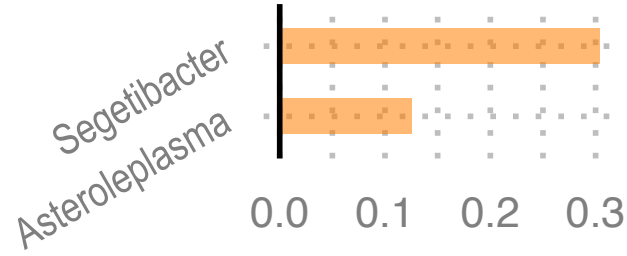
Regulation of CDC42 activity

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

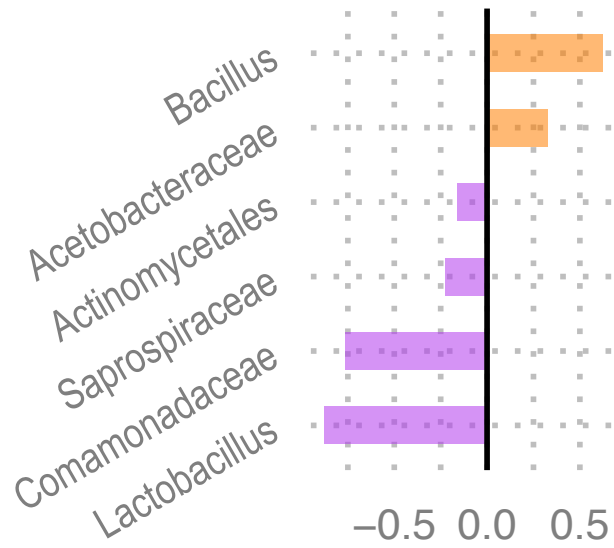
Regulation of nuclear beta-catenin signaling and target gene transcription



Regulation of telomerase



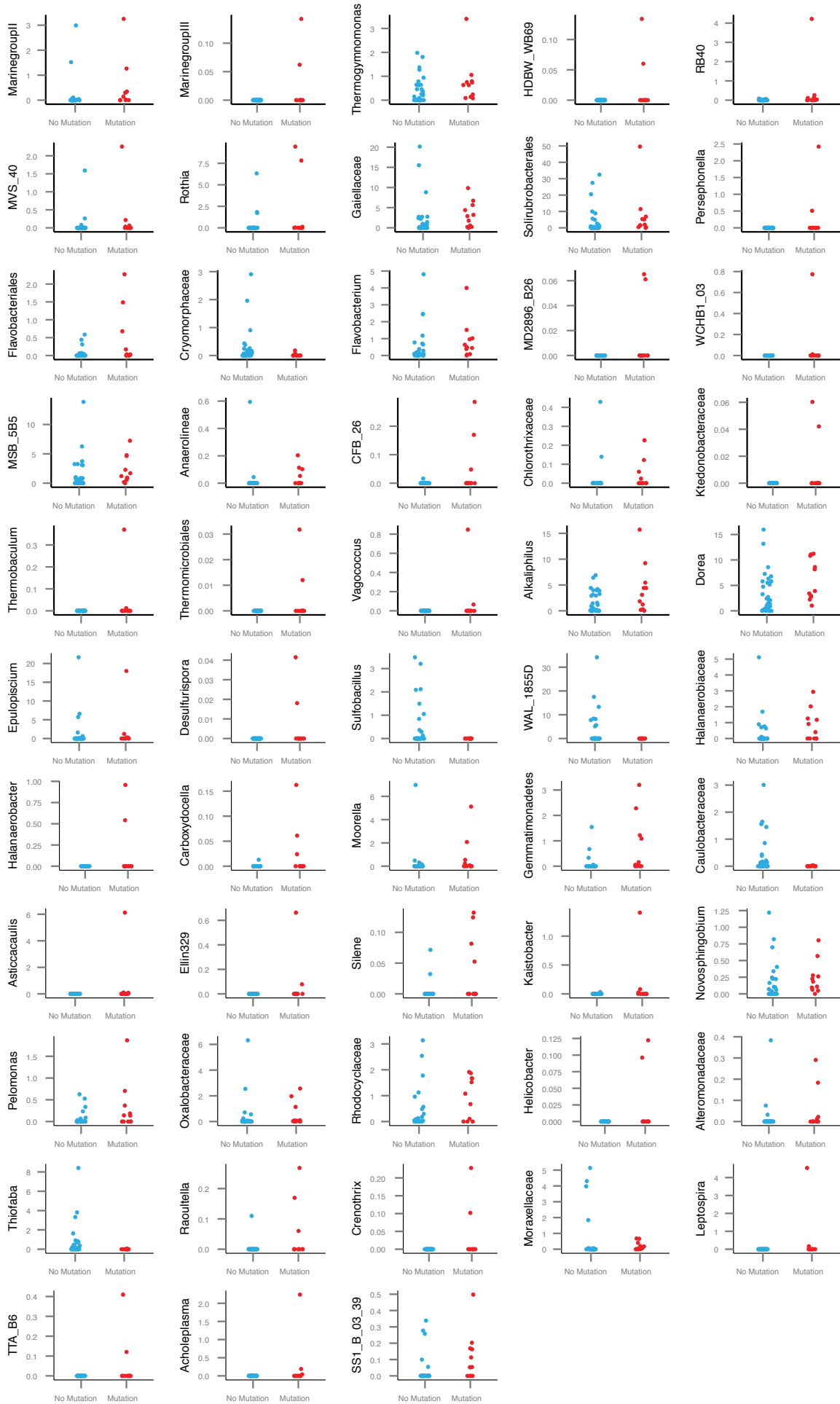
Signaling events mediated by Hepatocyte Growth Factor Receptor (c-Met)



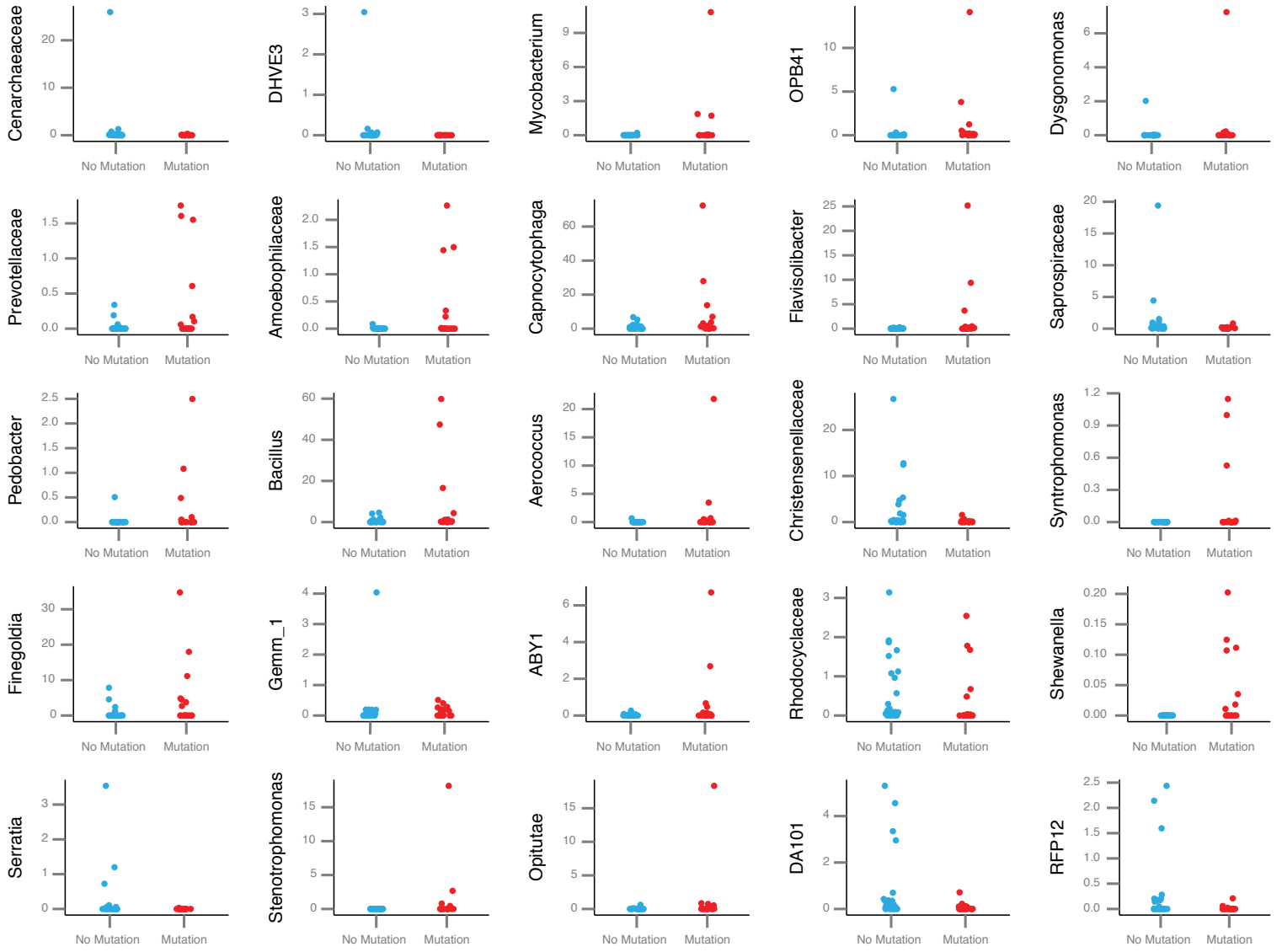
S12 Fig | Abundance Dotplots.

Genes

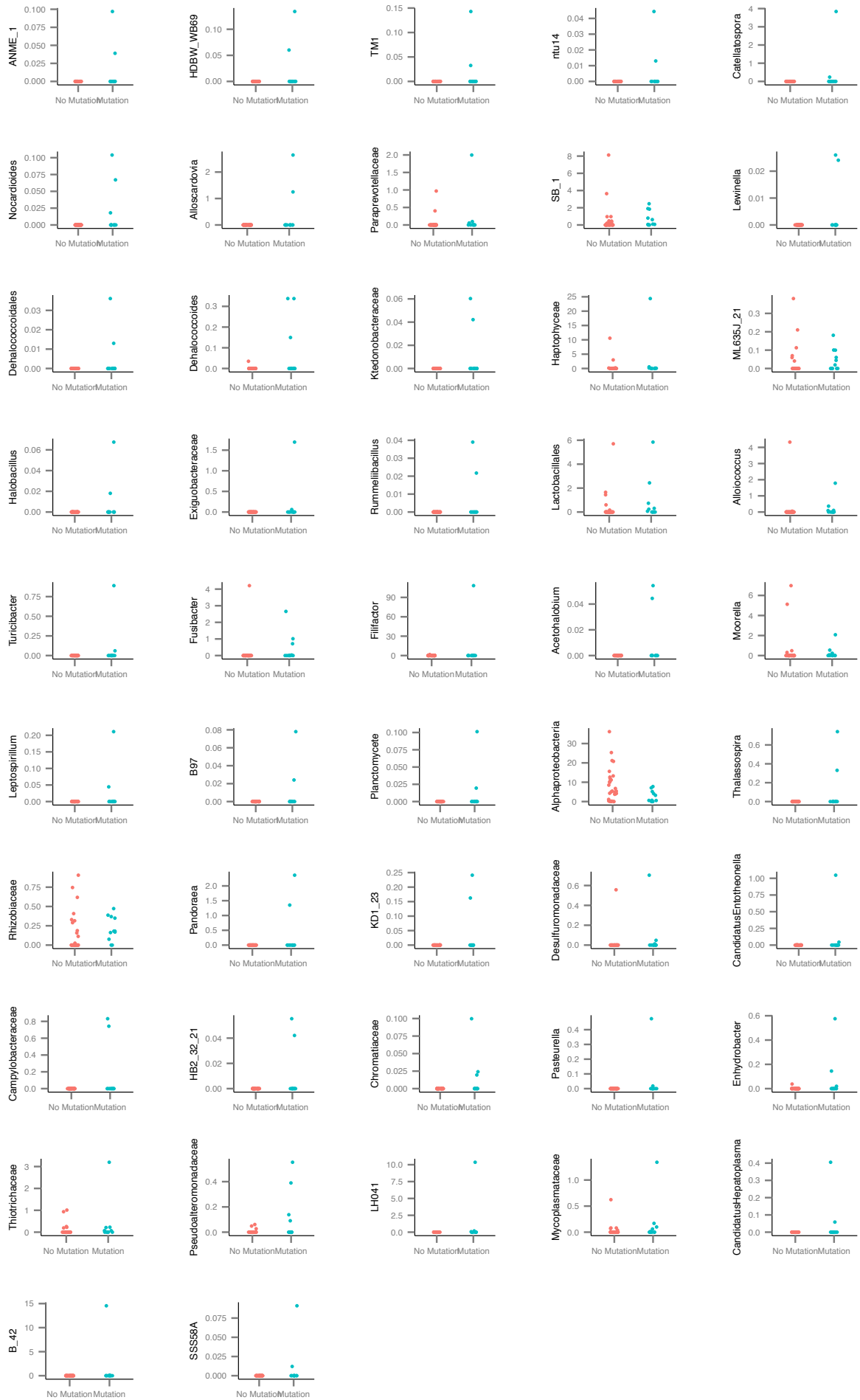
ANKRD36C



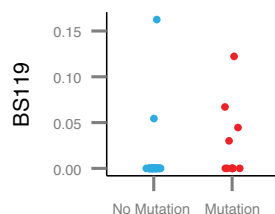
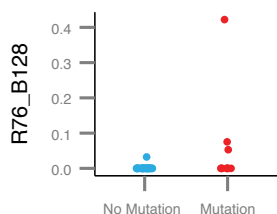
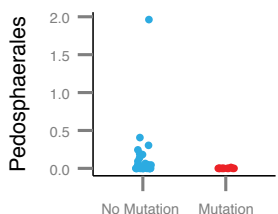
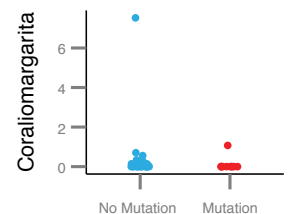
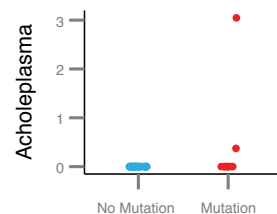
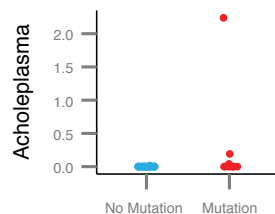
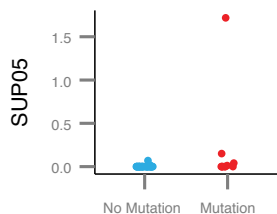
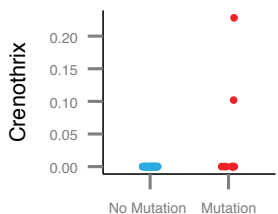
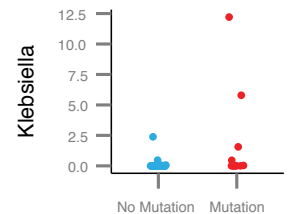
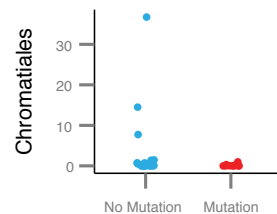
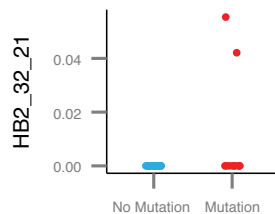
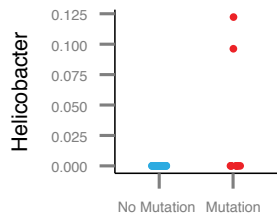
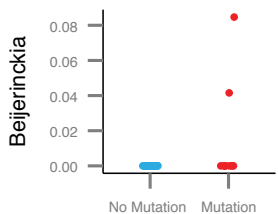
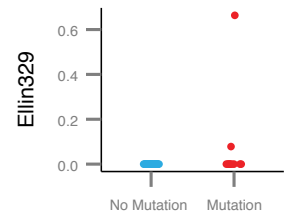
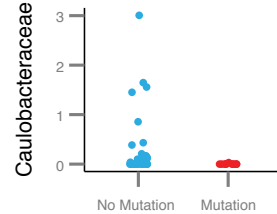
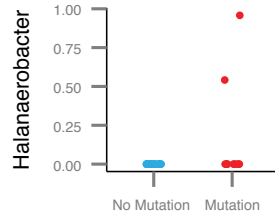
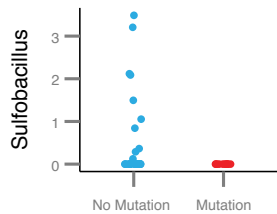
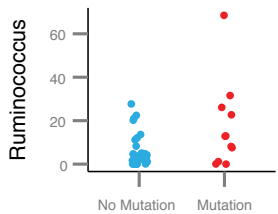
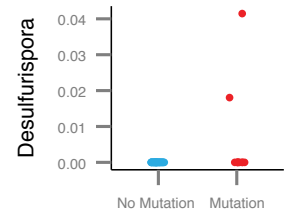
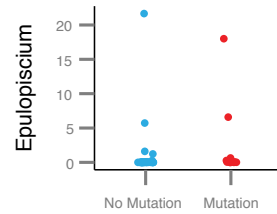
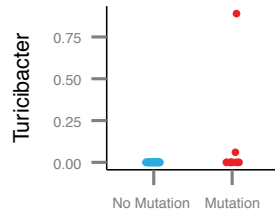
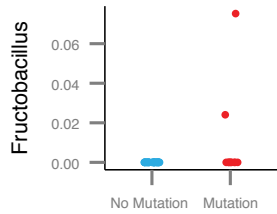
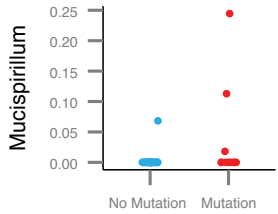
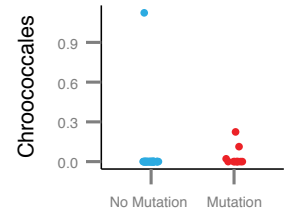
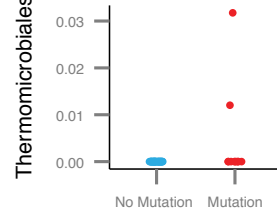
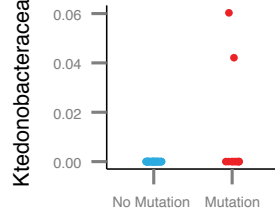
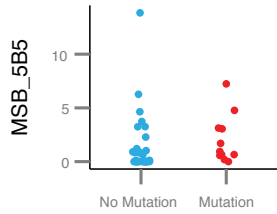
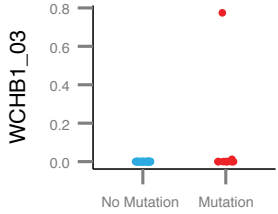
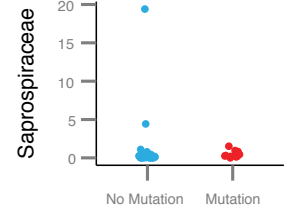
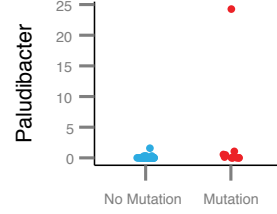
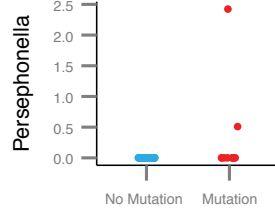
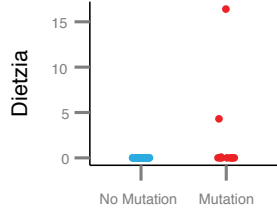
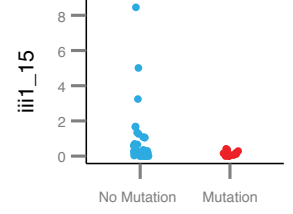
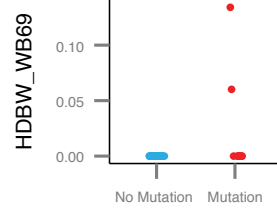
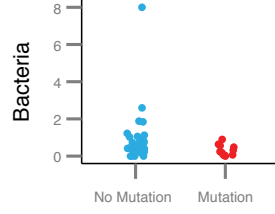
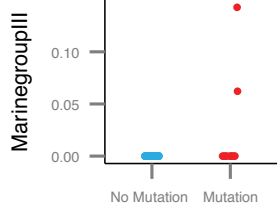
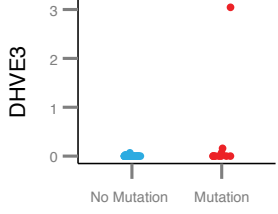
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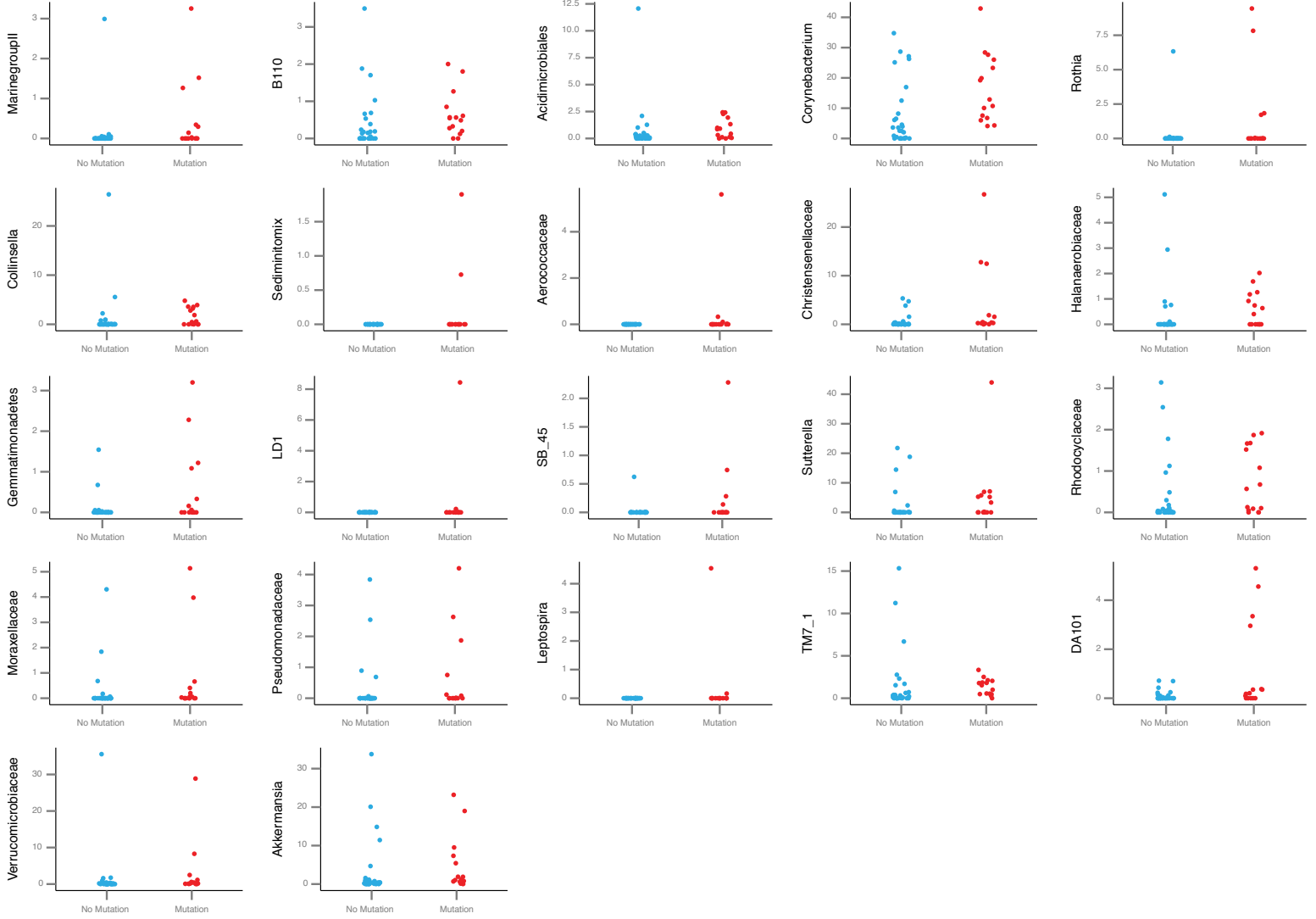
CTBP2



KMT2C



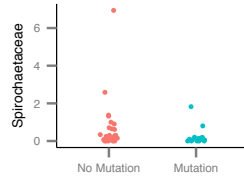
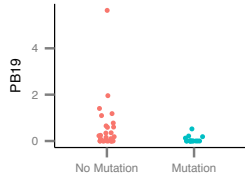
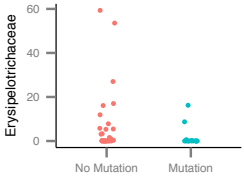
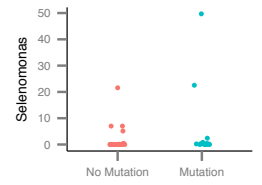
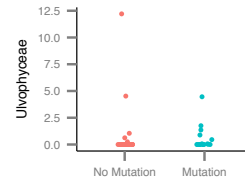
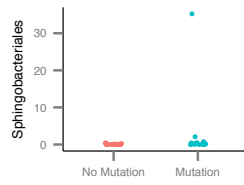
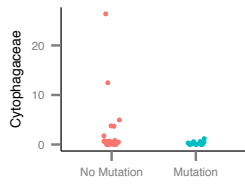
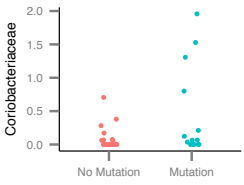
ZNF717



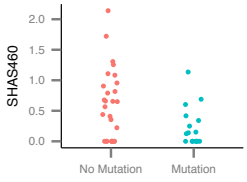
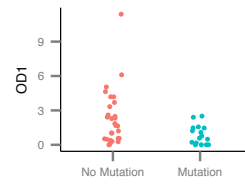
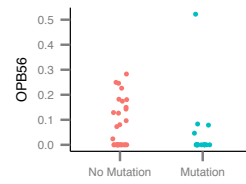
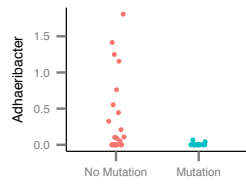
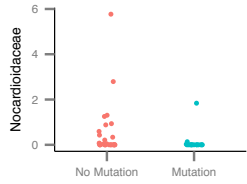
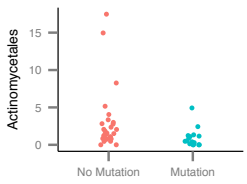
S12 Fig | Abundance Dotplots.

KEGG

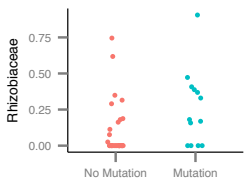
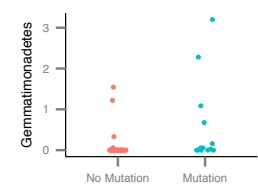
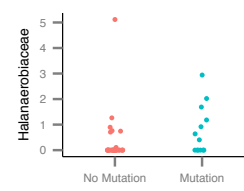
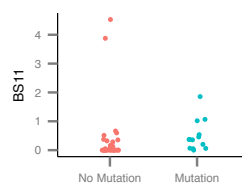
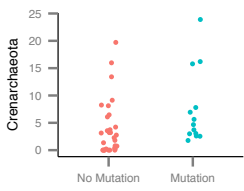
ABC Transporters



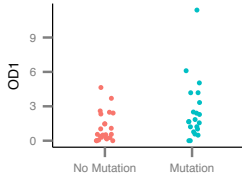
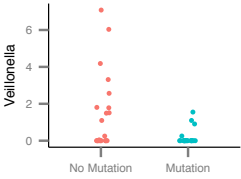
Adherens junctions



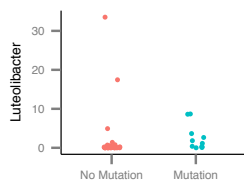
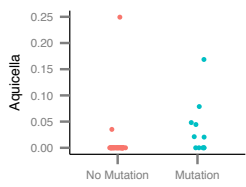
Alanine, aspartate, and glutamate metabolism



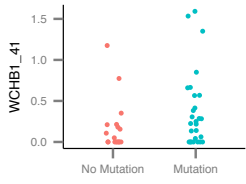
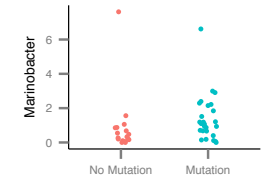
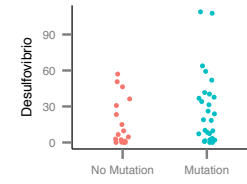
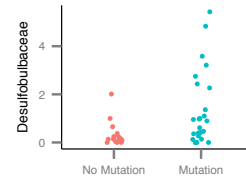
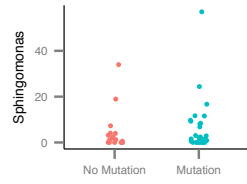
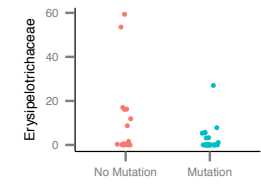
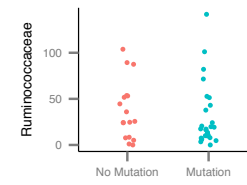
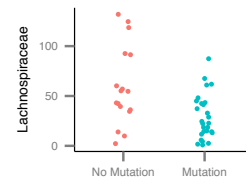
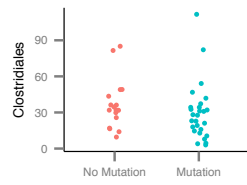
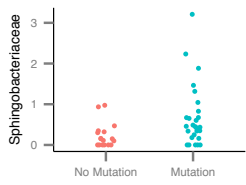
Cell cycle



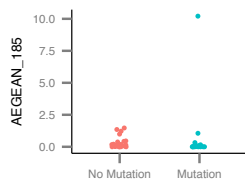
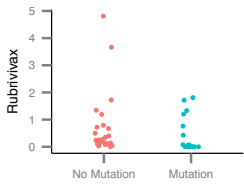
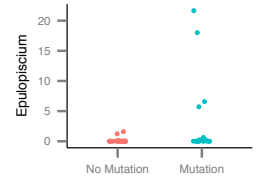
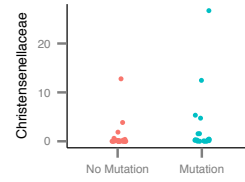
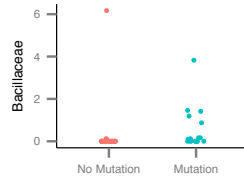
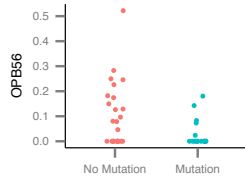
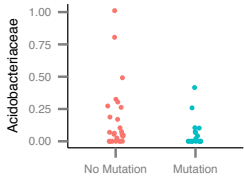
Cysteine and methionine metabolism



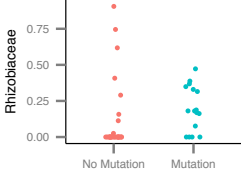
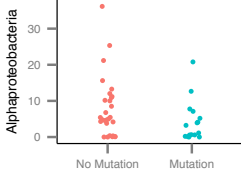
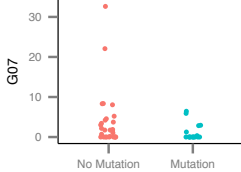
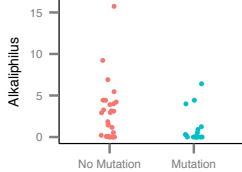
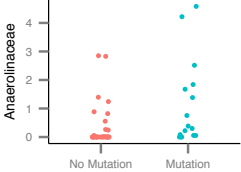
Focal adhesion



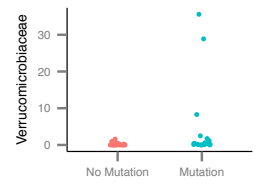
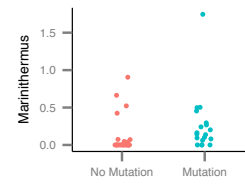
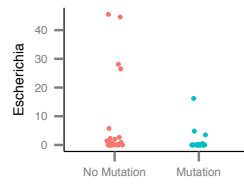
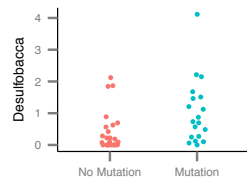
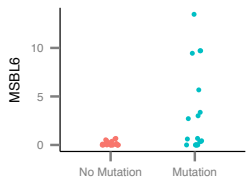
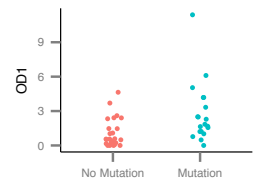
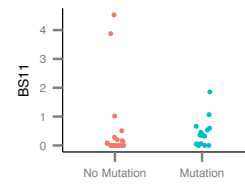
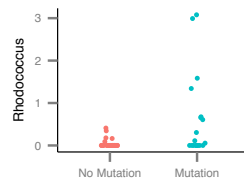
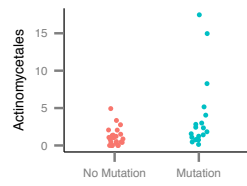
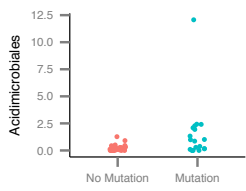
Lysine degradation



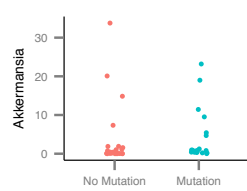
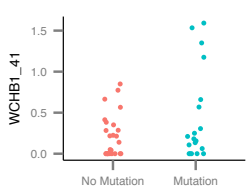
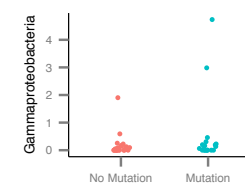
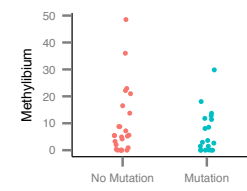
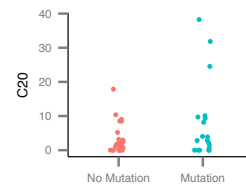
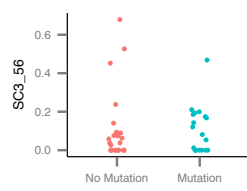
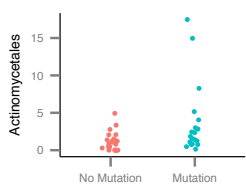
Notch signaling pathway



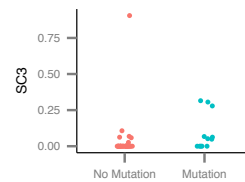
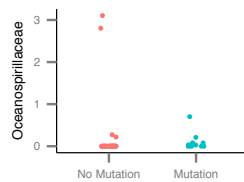
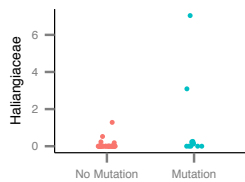
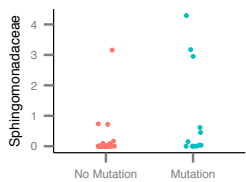
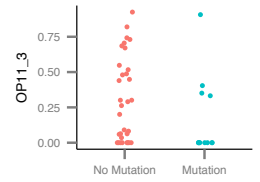
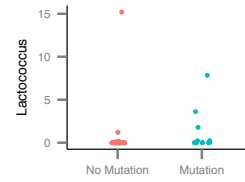
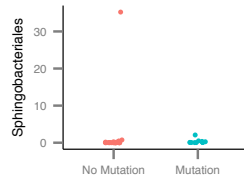
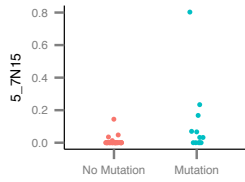
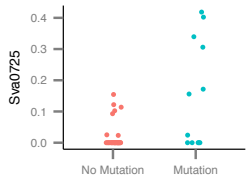
Oocyte meiosis



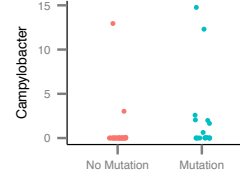
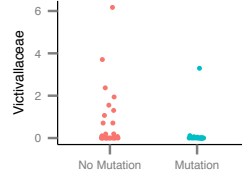
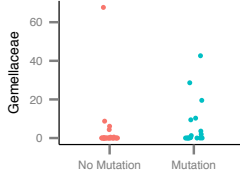
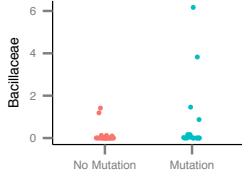
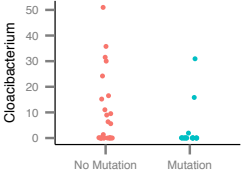
Oxidative phosphorylation



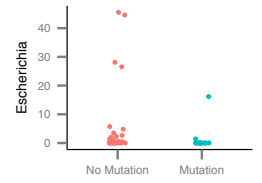
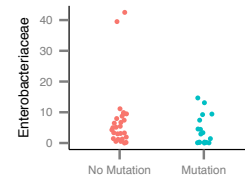
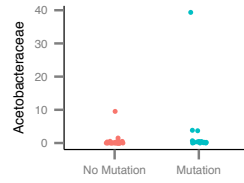
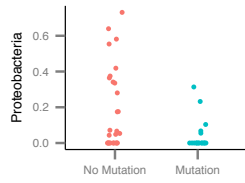
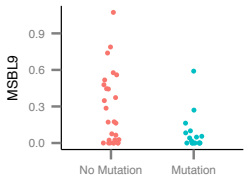
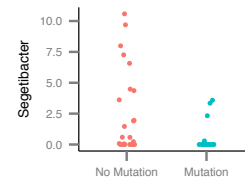
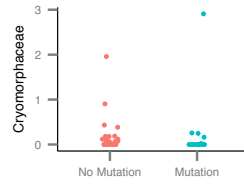
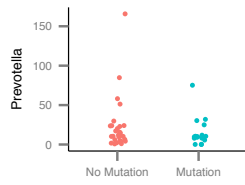
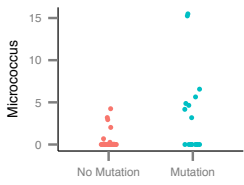
Phosphatidylinositol signaling system



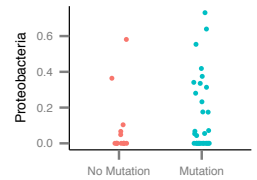
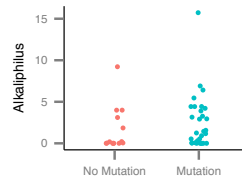
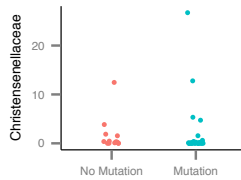
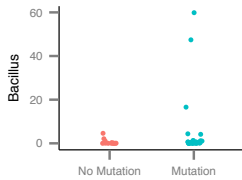
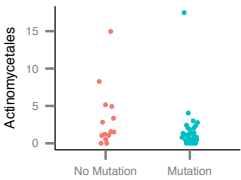
Protein processing in endoplasmic reticulum



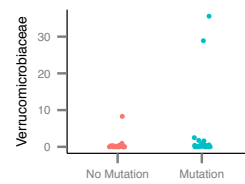
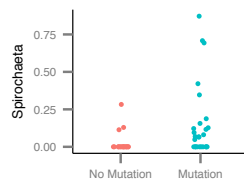
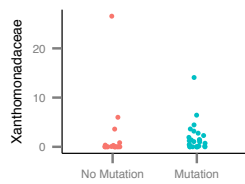
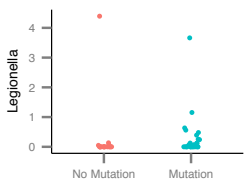
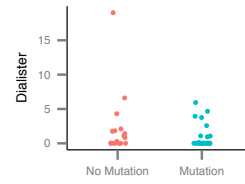
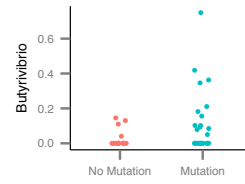
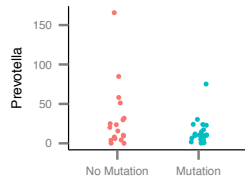
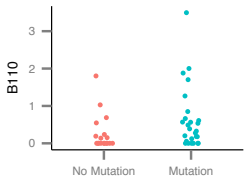
Purine metabolism



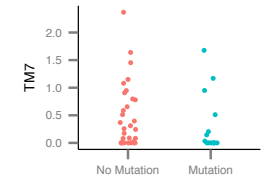
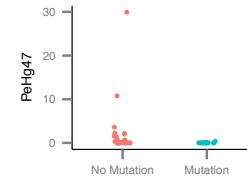
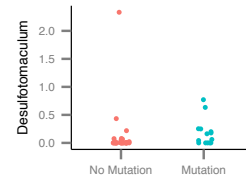
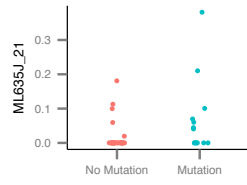
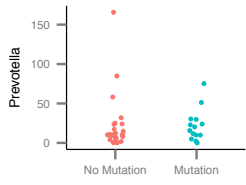
Regulation of actin cytoskeleton



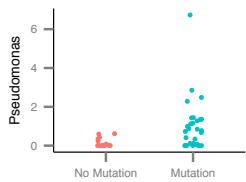
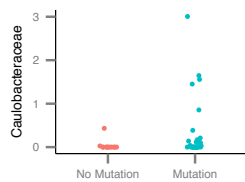
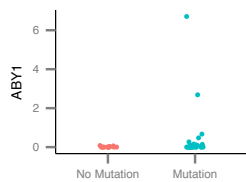
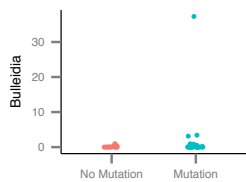
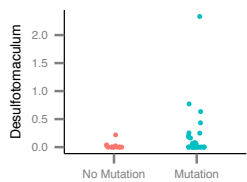
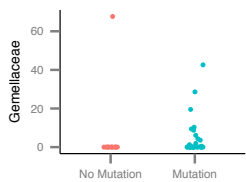
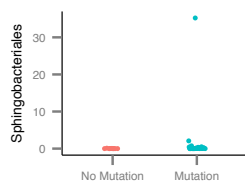
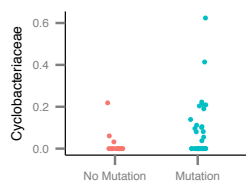
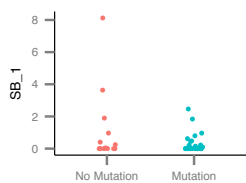
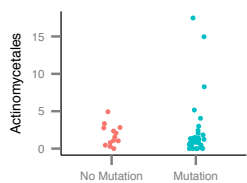
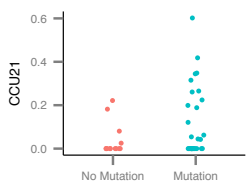
Ribosome



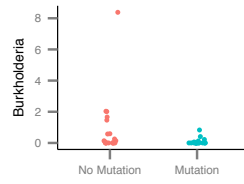
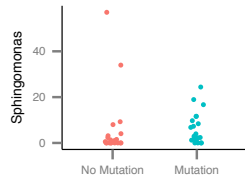
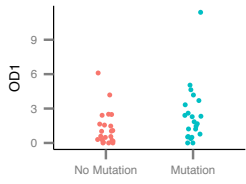
RNA degradation



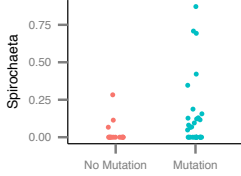
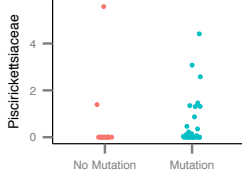
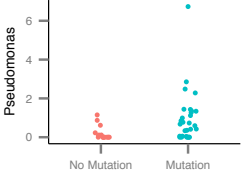
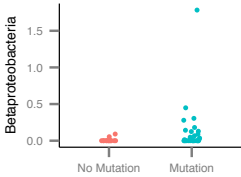
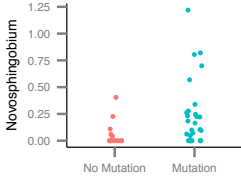
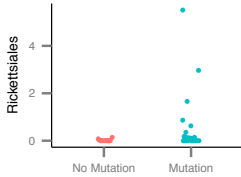
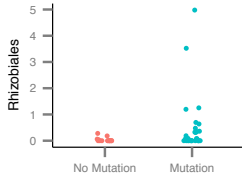
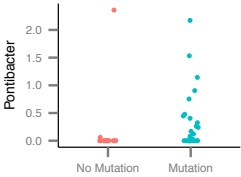
RNA transport



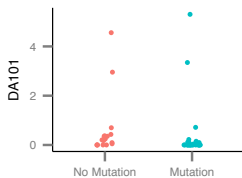
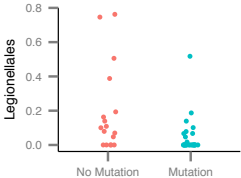
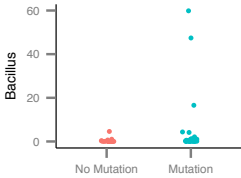
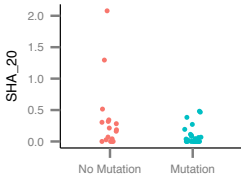
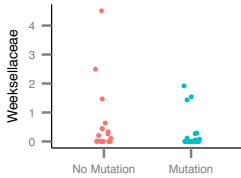
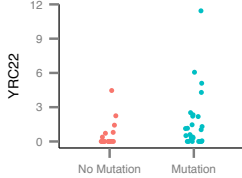
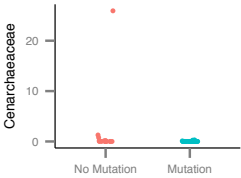
Spliceosome



Ubiquitin mediated proteolysis



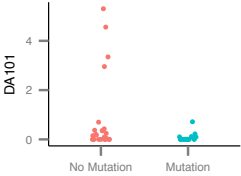
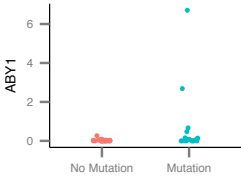
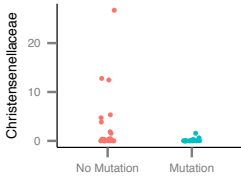
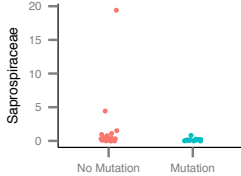
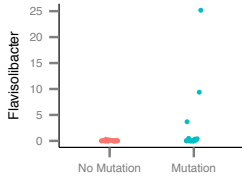
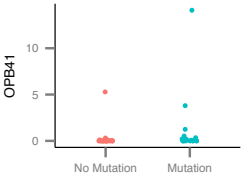
Wnt signaling pathway



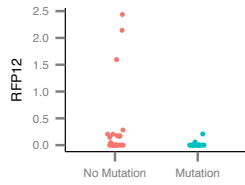
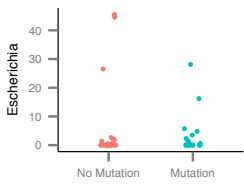
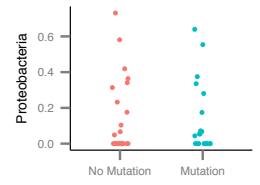
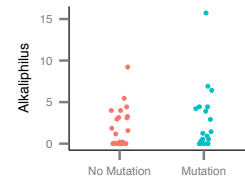
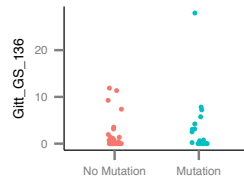
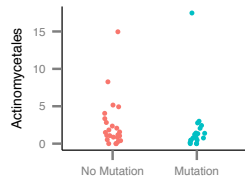
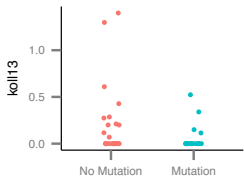
S12 Fig I Abundance Dotplots.

PID

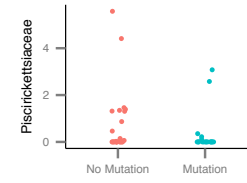
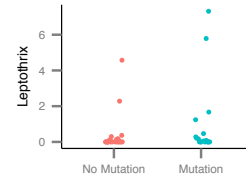
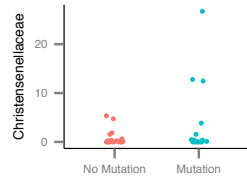
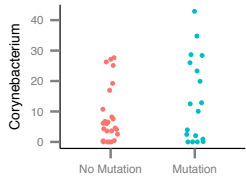
Canonical Wnt signaling pathway



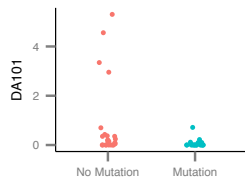
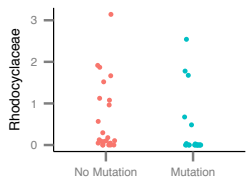
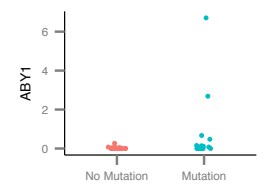
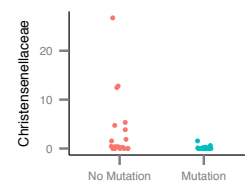
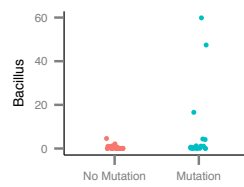
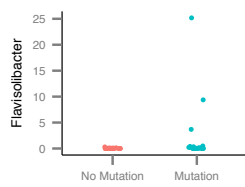
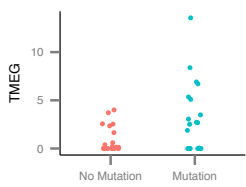
CDC42 signaling



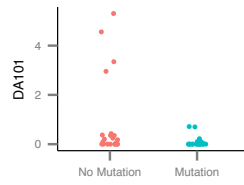
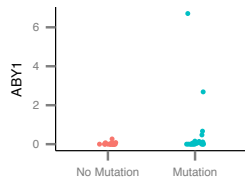
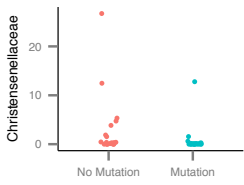
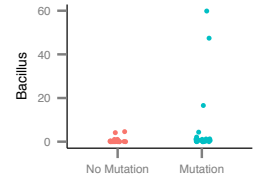
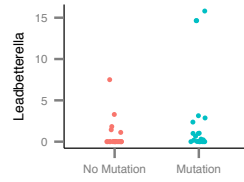
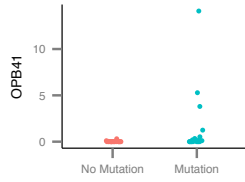
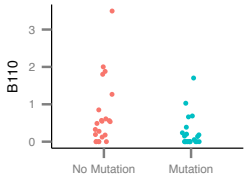
CXCR4-mediated signaling



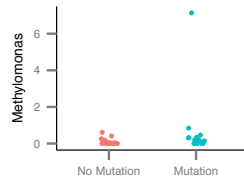
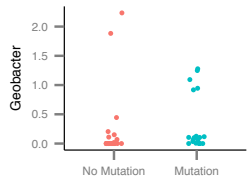
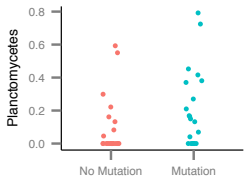
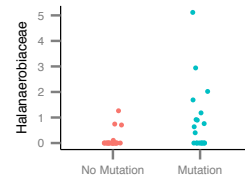
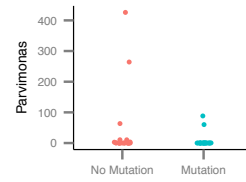
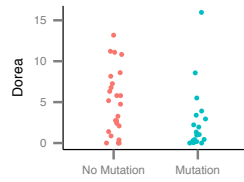
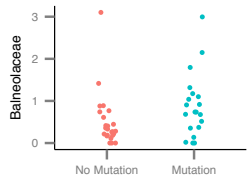
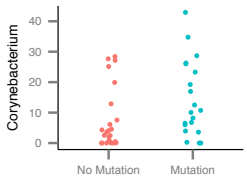
Degradation of beta-catenin



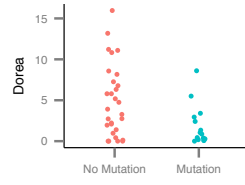
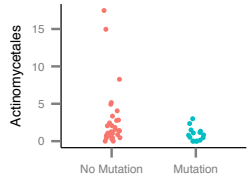
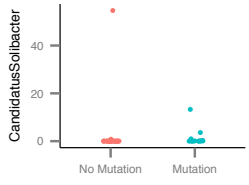
Direct p53 effectors



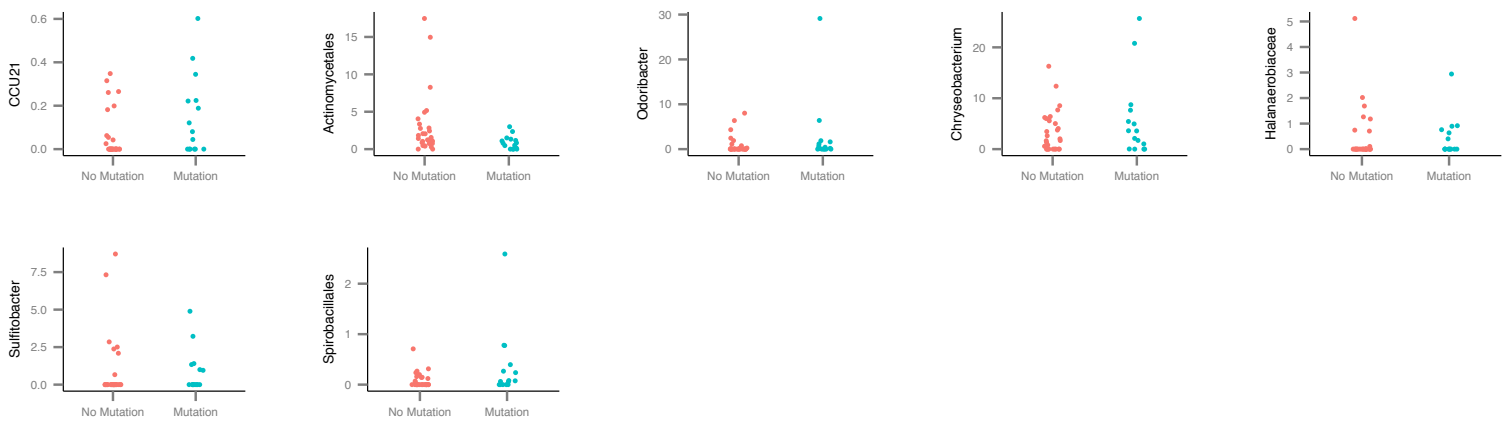
ErbB1 downstream signaling



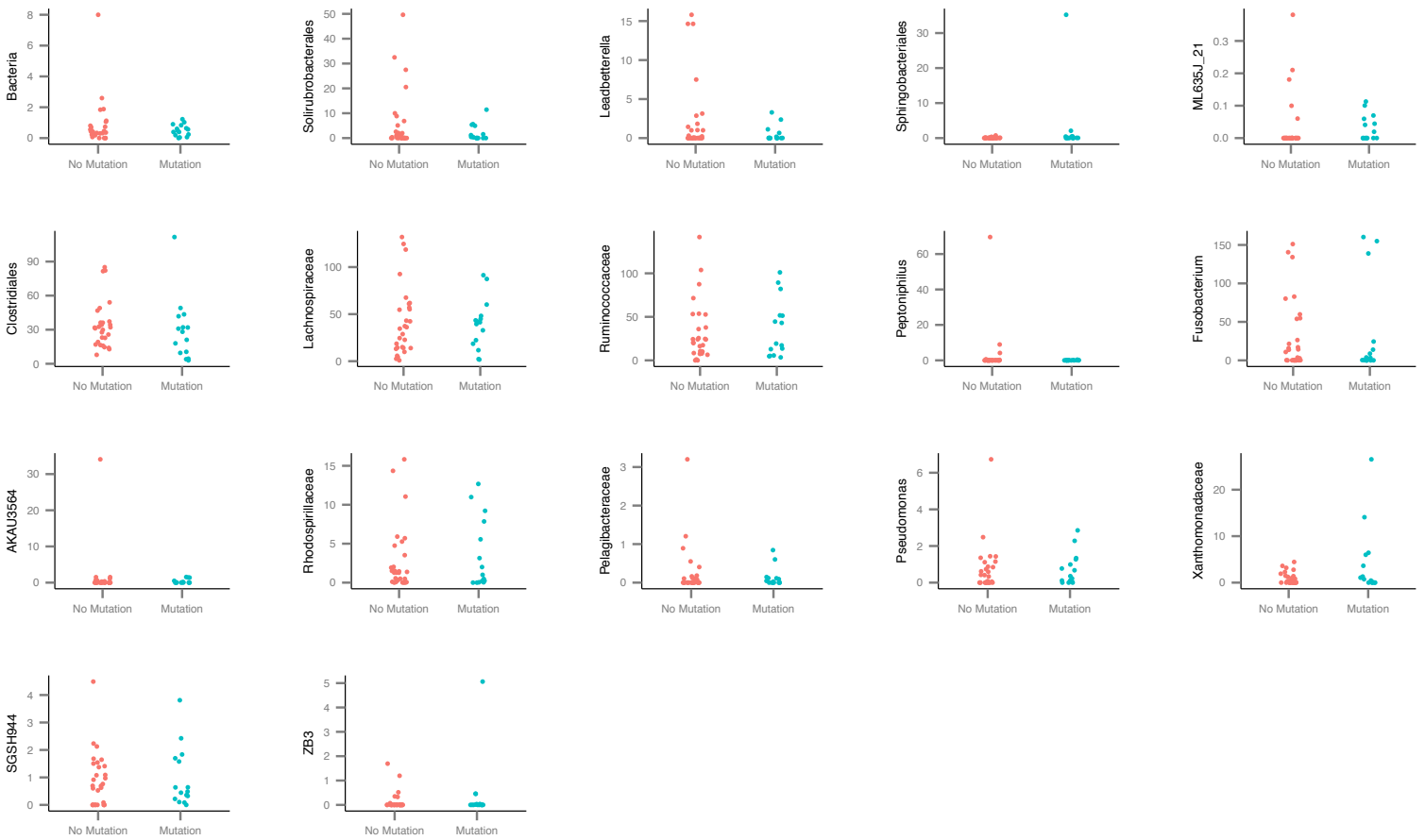
Insulin pathway



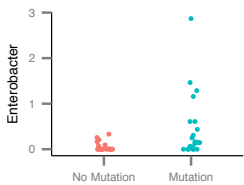
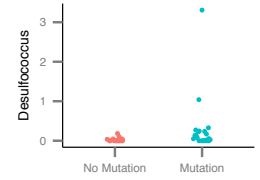
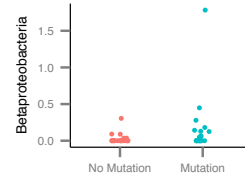
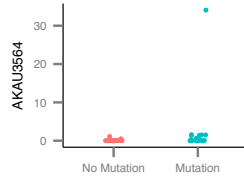
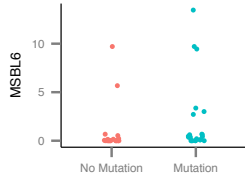
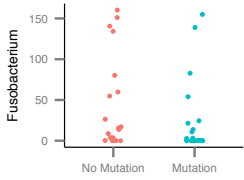
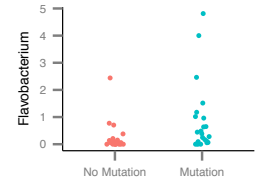
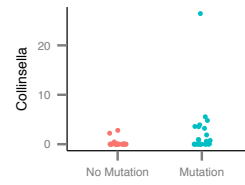
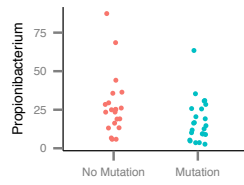
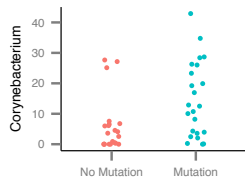
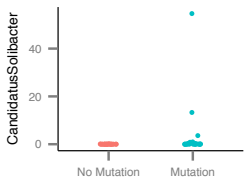
Neurotrophic factor-mediated Trk signaling



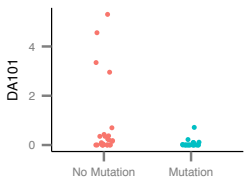
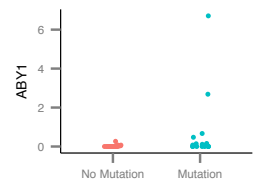
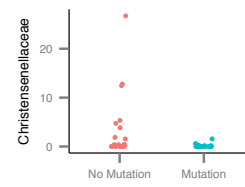
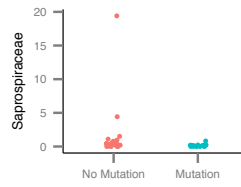
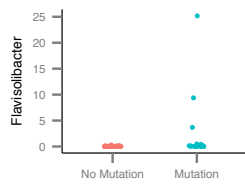
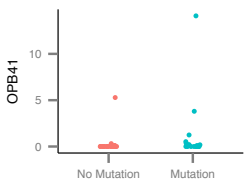
p75 (NTR)-mediated signaling



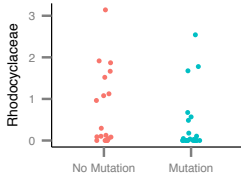
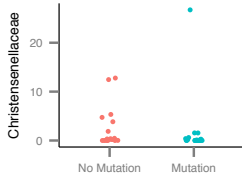
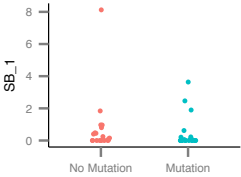
PDGFR-beta signaling pathway



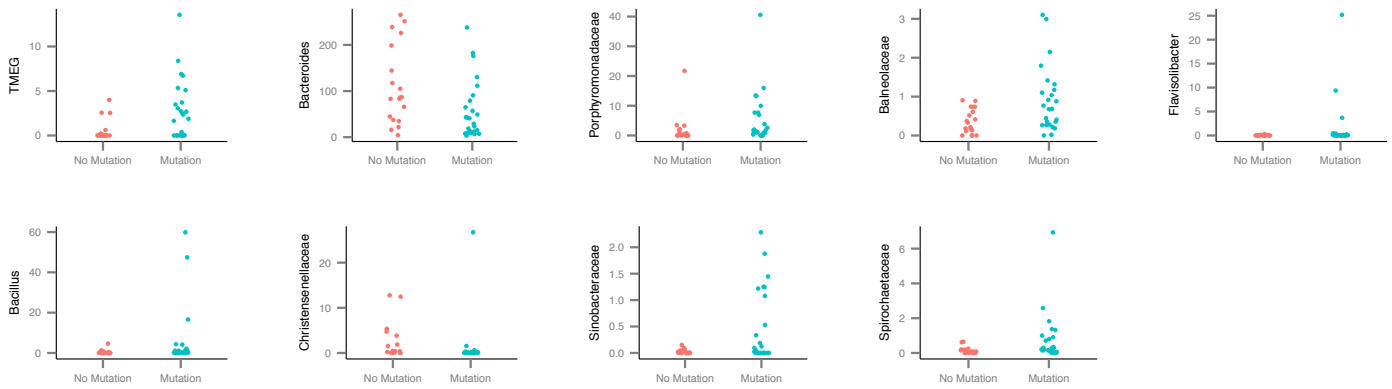
Presenilin action in Notch and Wnt signaling



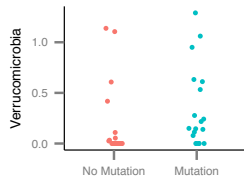
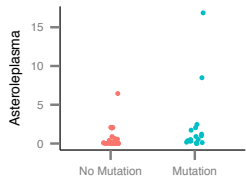
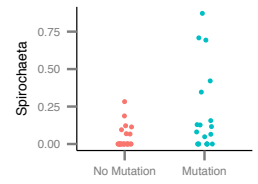
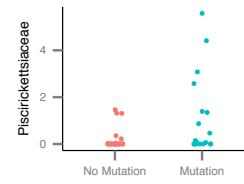
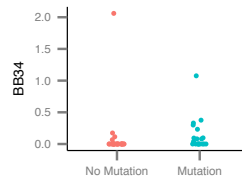
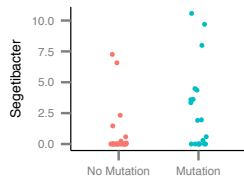
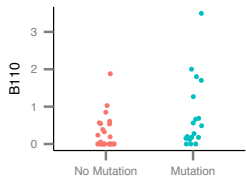
Regulation of CDC42 activity



Regulation of nuclear beta-catenin signaling and target gene transcription



Regulation of telomerase



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

