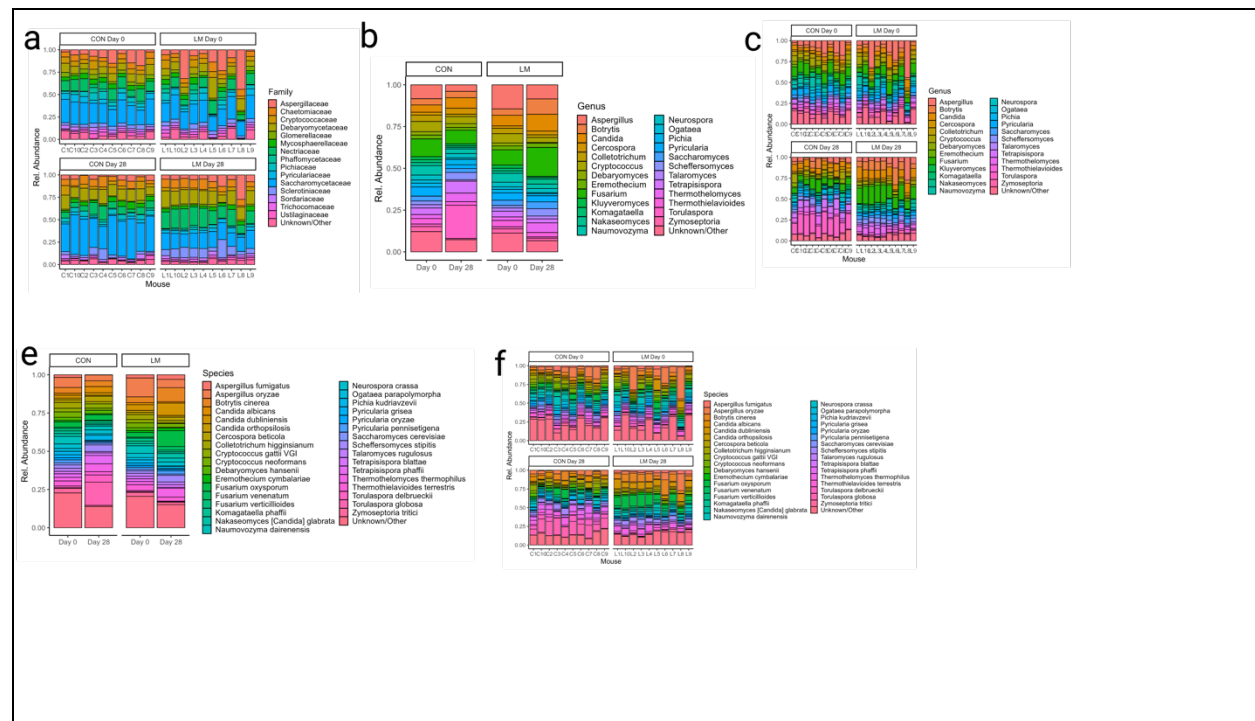
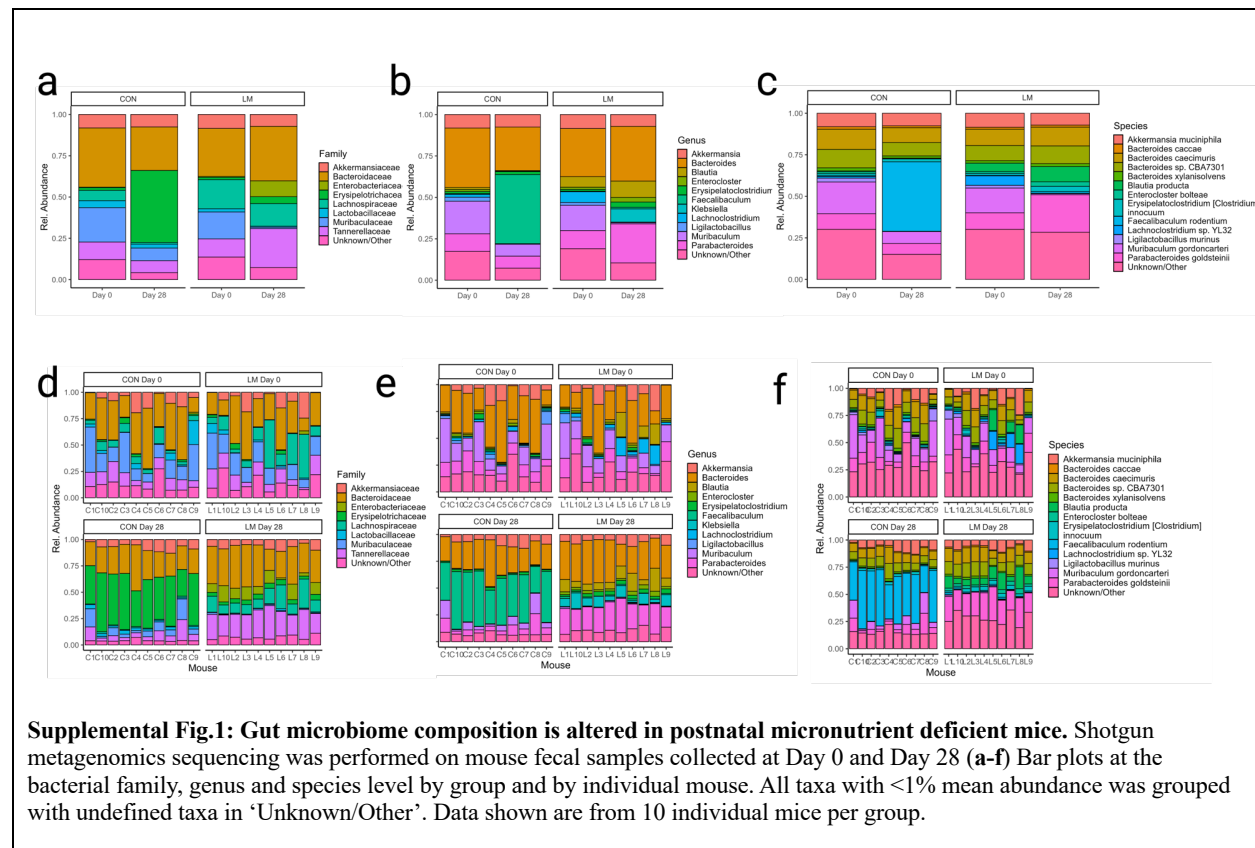
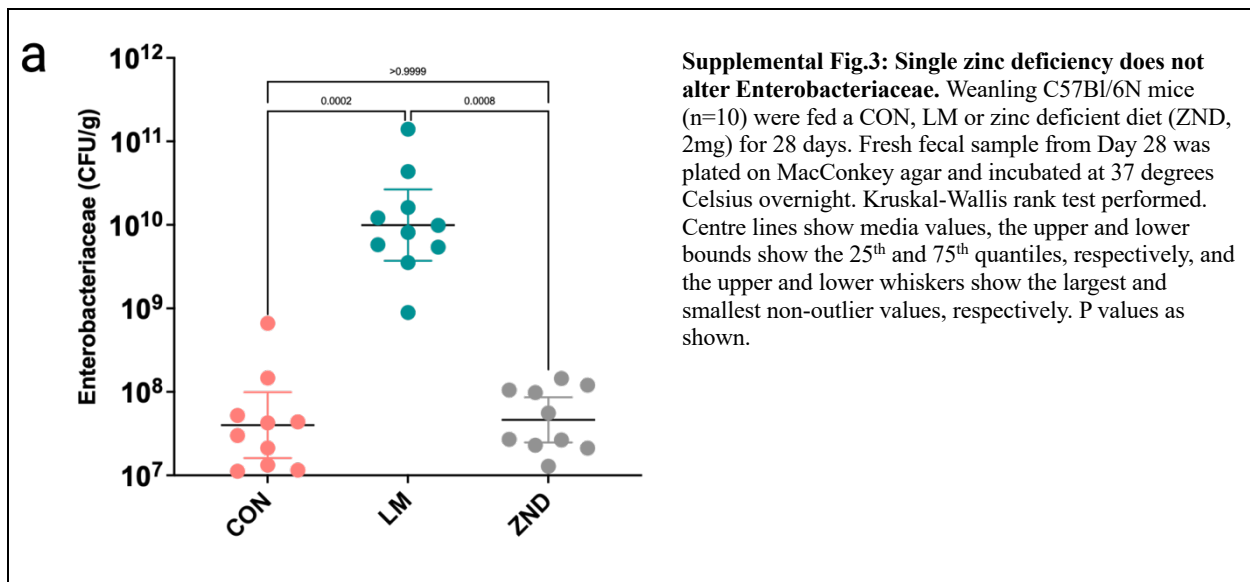
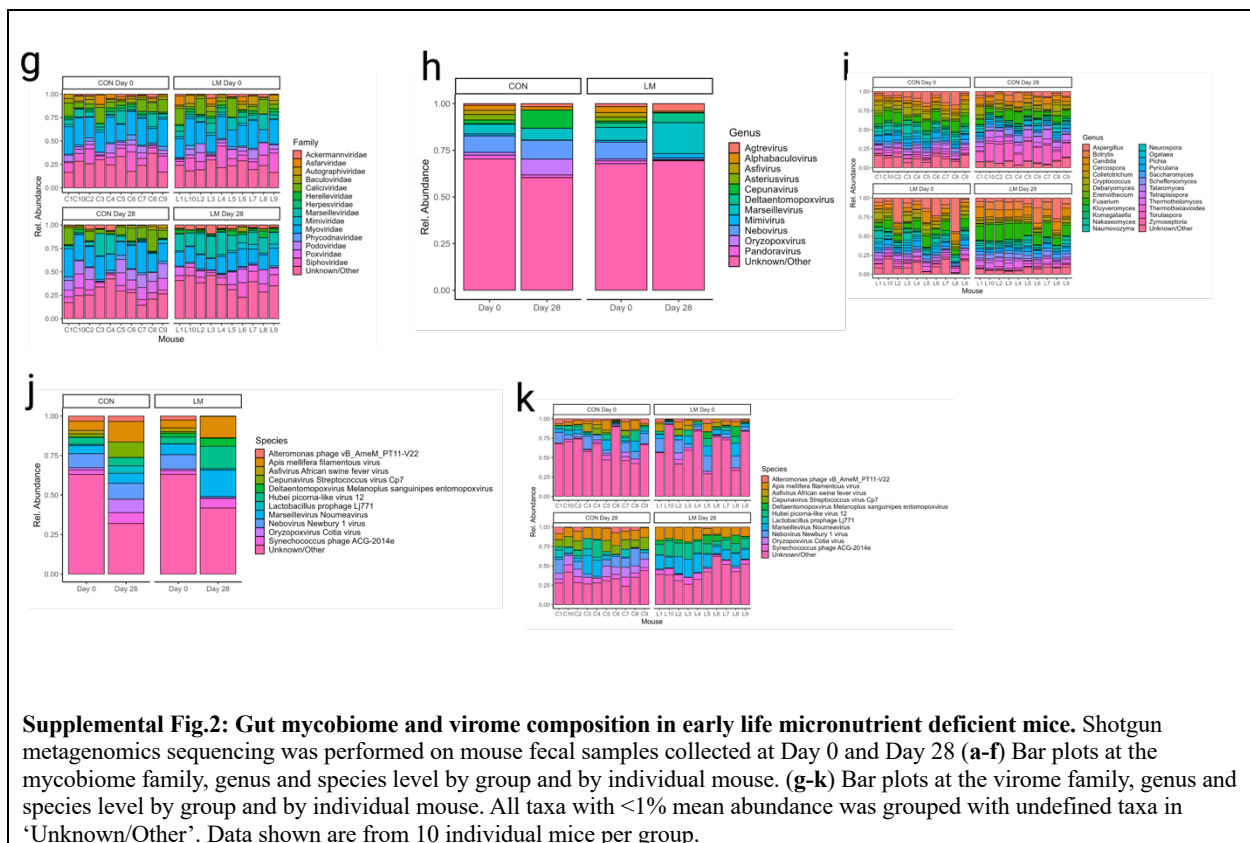
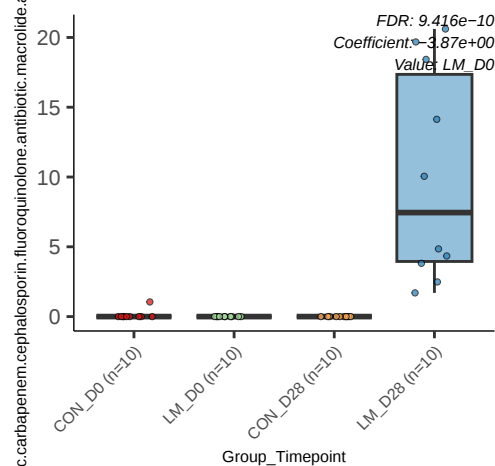


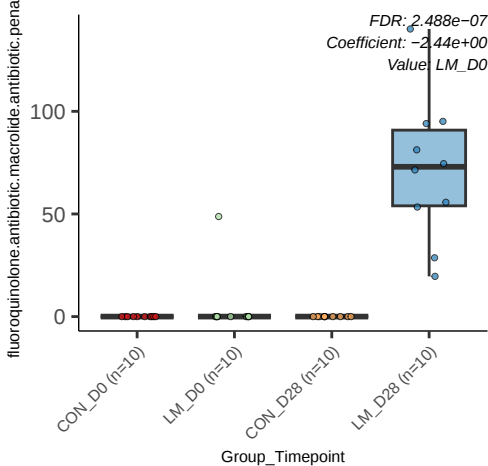
Multiple micronutrient deficiencies in early life cause multi-kingdom alterations in the gut microbiome and intrinsic antibiotic resistance genes in mice

In the format provided by the
authors and unedited

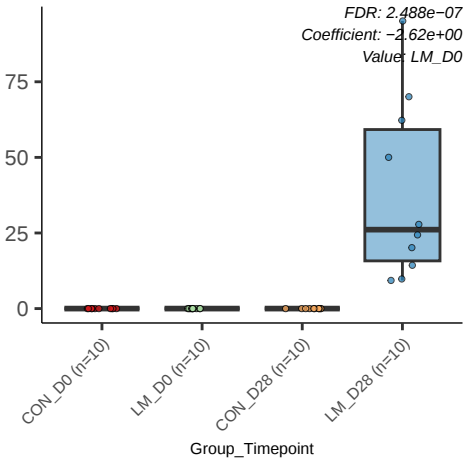




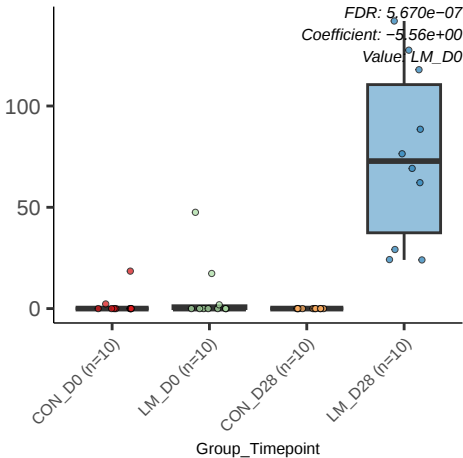


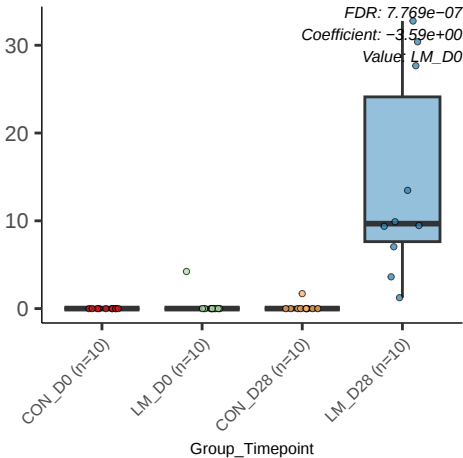


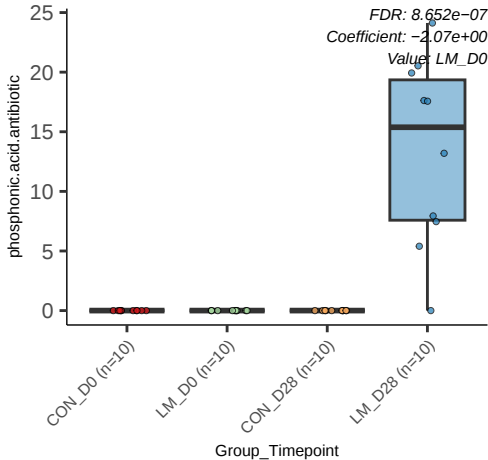
aminocoumarin.antibiotic.carbapenem.peptide.antibiotic.rifamycin

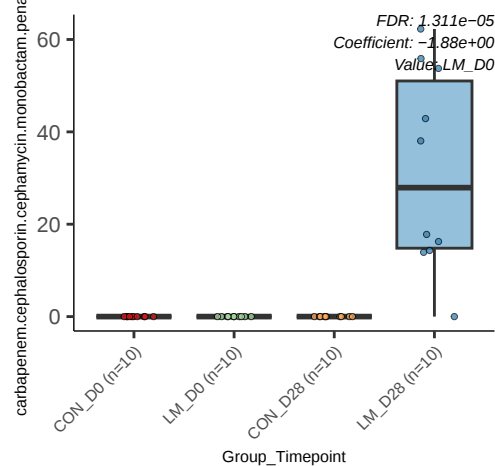


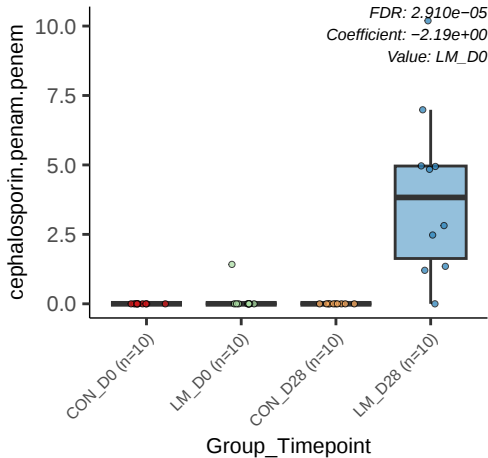
rimidine.antibiotic.fluoroquinolone.antibiotic.glycylcycline.nitrofurantoin



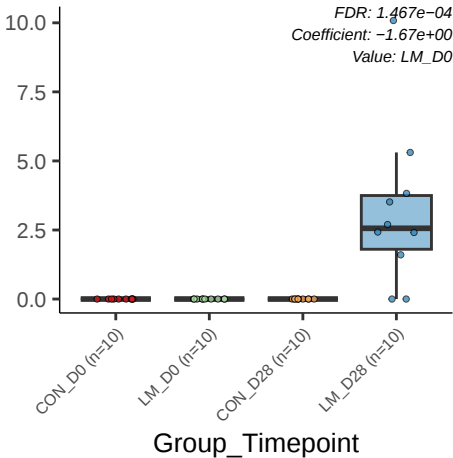








penam.penam



fluoroquinolone.antibiotic

FDR: 2.208×10^{-4}
Coefficient: -1.83×10^0
Value: LM_D0

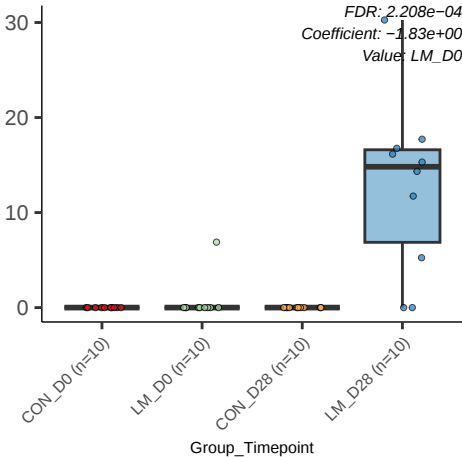
CON_D0 (n=10)

LM_D0 (n=10)

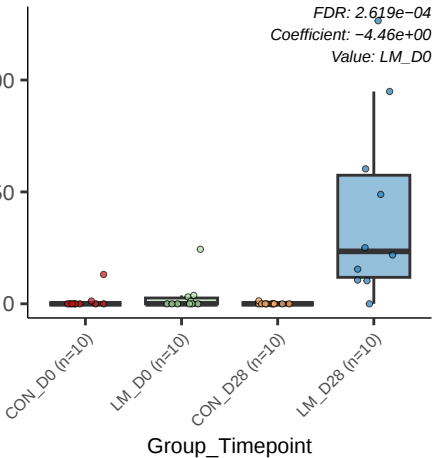
CON_D28 (n=10)

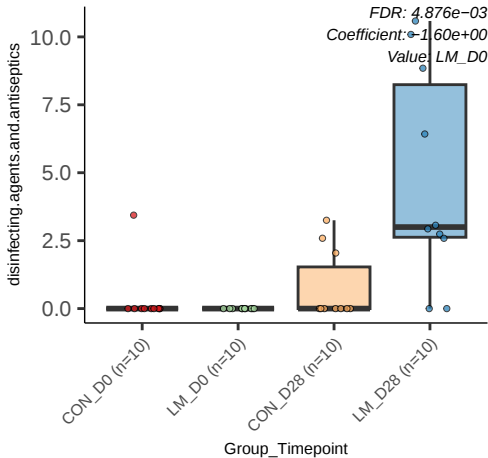
LM_D28 (n=10)

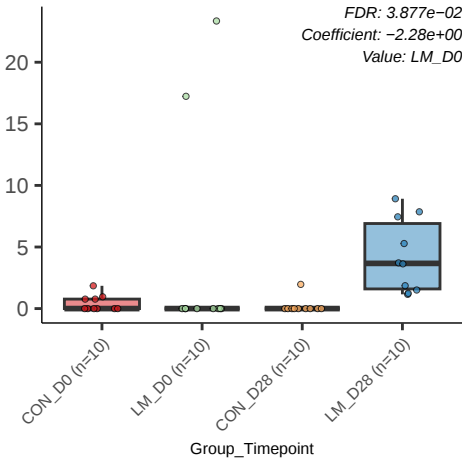
Group_Timepoint



peptide.antibiotic







aminoglycoside.antibiotic

FDR: 5.018e-02
Coefficient: -1.21e+00
Value: LM_D0

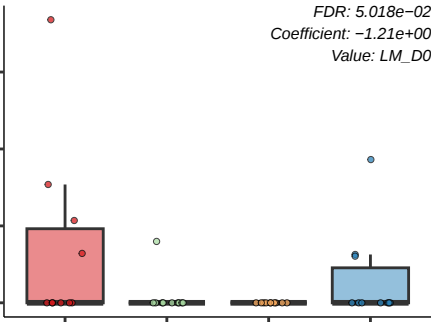
CON_D0 (n=10)

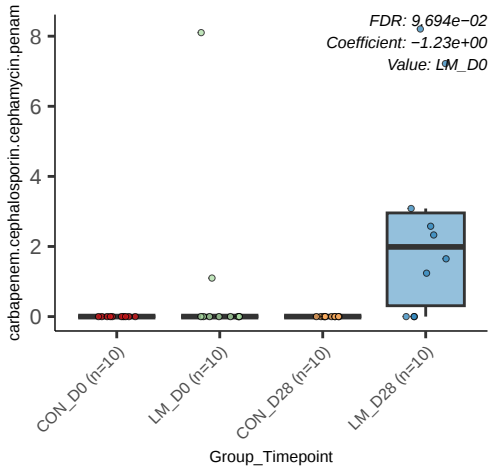
LM_D0 (n=10)

CON_D28 (n=10)

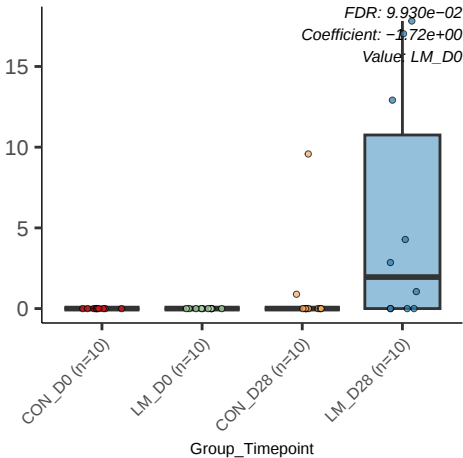
LM_D28 (n=10)

Group_Timepoint

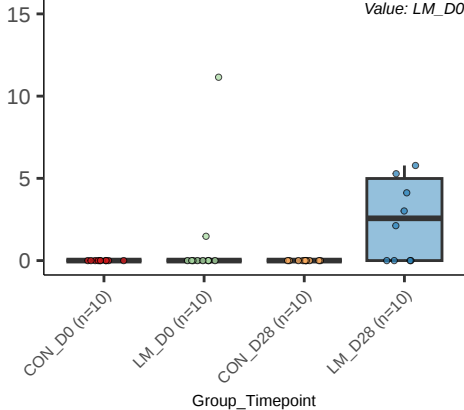




biotic.pleuromutilin.anticbiotic.streptogramin.A.anticbiotic.streptogramin

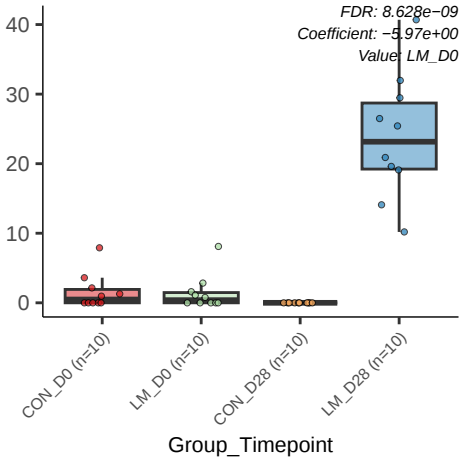


FDR: $1.493\text{e-}01$
Coefficient: $-1.15\text{e}+00$
Value: LM_D0

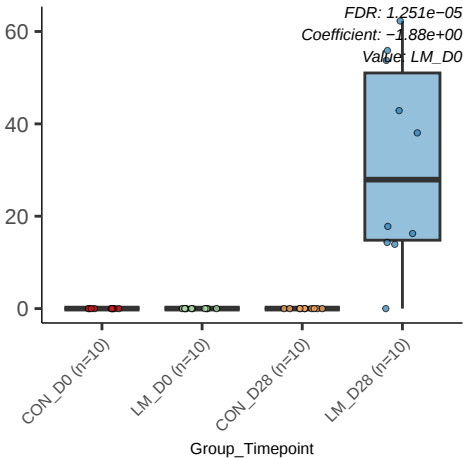


Supplementary Materials 1: We used MaAsLin2 (v1.10.0) to look for associations between counts of antibiotic resistance drug classes within the treatment groups. Data represents drug class per group (RPKM) (two-sided MaAsLin2, P values FDR corrected, Value is comparison to LM_D0).

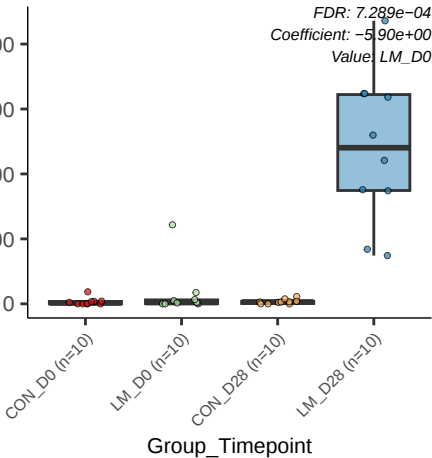
antibiotic.inactivation



reduced.permeability.to.antibiotic

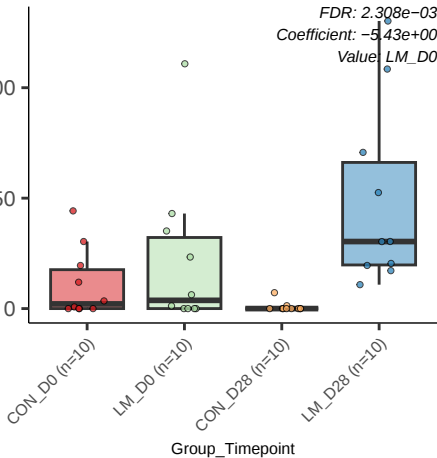


antibiotic.efflux



antibiotic.target.alteration

FDR: 2.308×10^{-3}
Coefficient: -5.43×10^0
Value: LM_D0



antibiotic.target.replacement

FDR: 7.090×10^{-2}
Coefficient: -1.57×10^0
Value: LM_D0

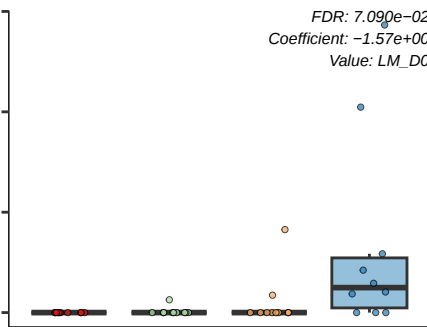
CON_D0 (n=10)

LM_D0 (n=10)

CON_D28 (n=10)

LM_D28 (n=10)

Group_Timepoint



antibiotic.efflux.reduced.permeability.to.antibiotic

FDR: 1.242e-01
Coefficient: -1.15e+00
Value: LM_D0

15
10
5
0

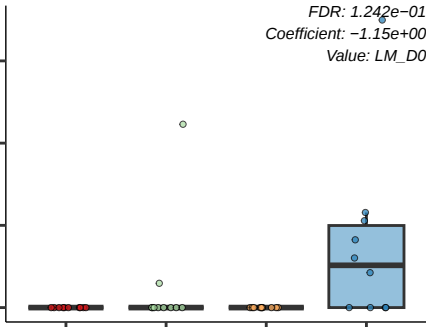
CON_D0 (n=10)

LM_D0 (n=10)

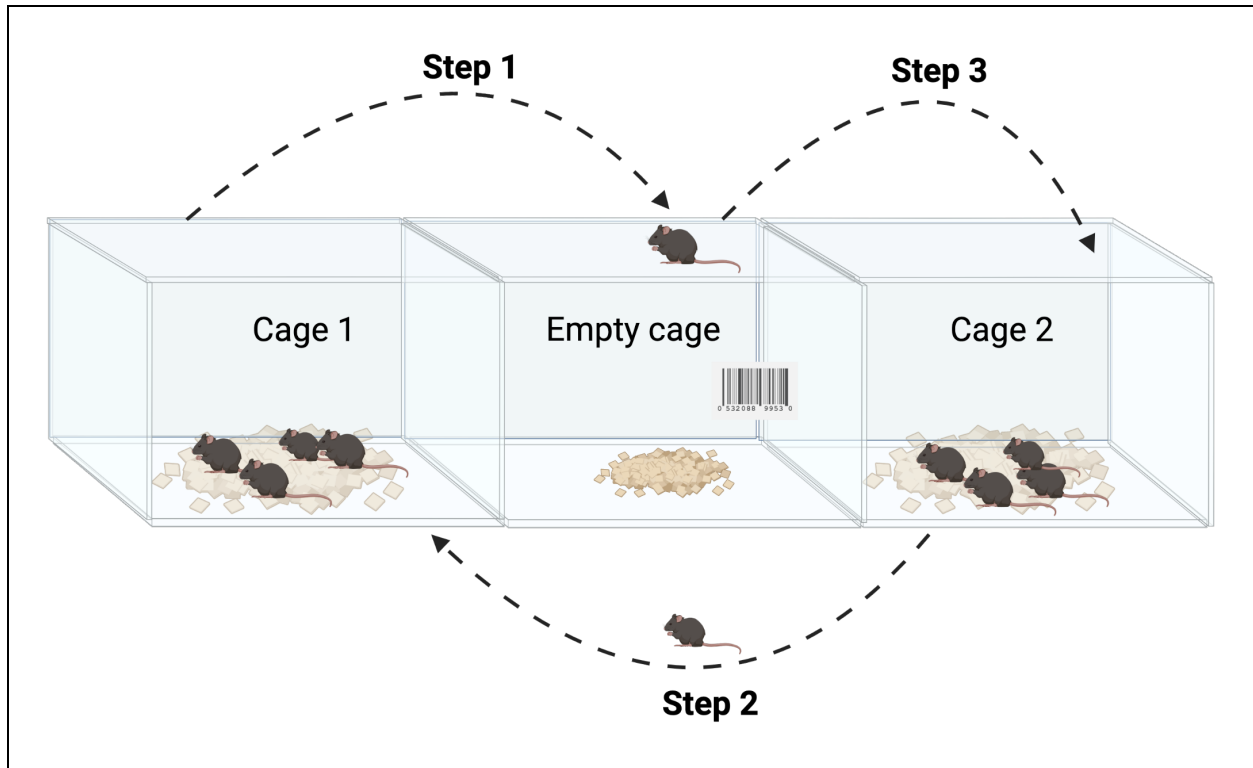
CON_D28 (n=10)

LM_D28 (n=10)

Group_Timepoint



Supplementary Materials 2: We used MaAsLin2 (v1.10.0) to look for associations between counts of antibiotic resistance mechanisms within the treatment groups. Data represents ARG mechanisms per group (RPKM) (two-sided MaAsLin2, P values FDR corrected, Value is comparison to LM_D0).



Materials and Methods:

Cage swapping to prevent gut microbiome cage effect. (use litter mates or mice that were shipped together)

We obtained one clean, autoclaved cage to use for this process. For this experiment 10 mice were housed 5 mice per cage making two cages per group, i.e., control group mice $n=10$ was divided into two cages, CON cage 1 and CON cage 2.

Step 1: Once a week, mice with some of their bedding and cage ID tag from CON cage 1 were placed into a clean new empty cage temporarily.

Step 2: CON mice from cage 2 along with some of their bedding and cage ID tag were then transferred to the now uninhabited cage 1.

Step 3: The cage 1 CON mice in the temporary holding cage were placed into the uninhabited CON cage 2. Mice were observed for 30 minutes for any abnormal change in behavior such fighting. Steps 1-3 was repeated for the LM groups with change of gloves between treatment groups.