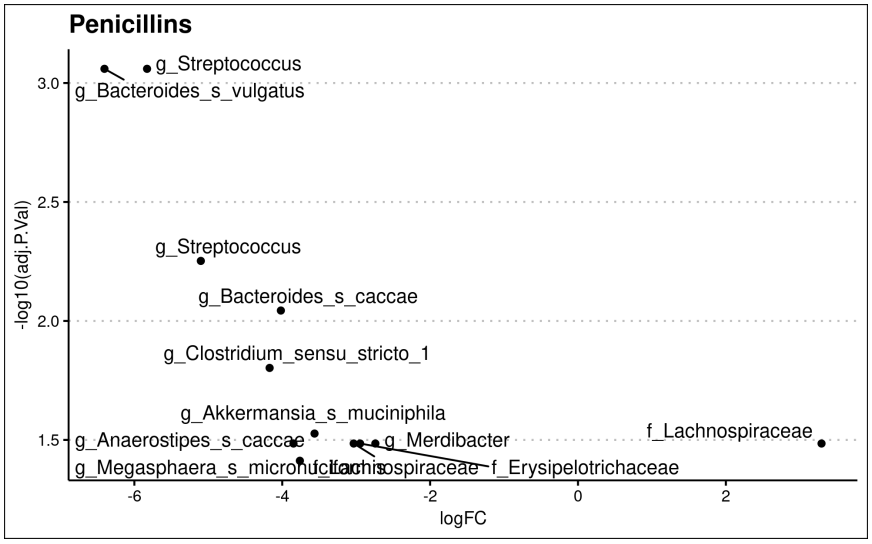
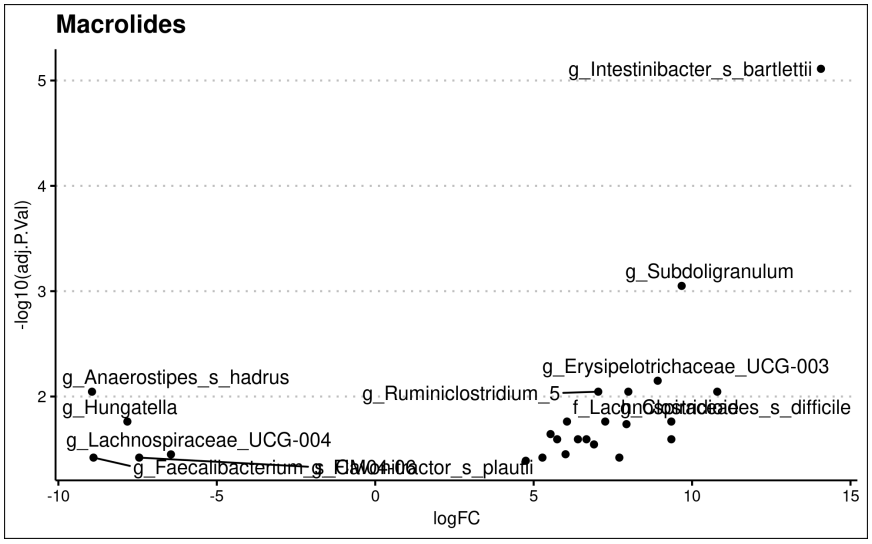
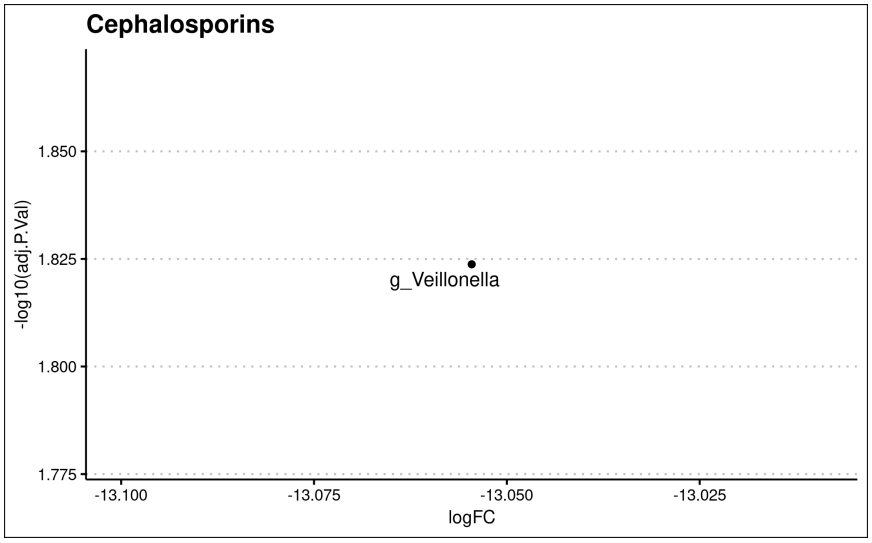
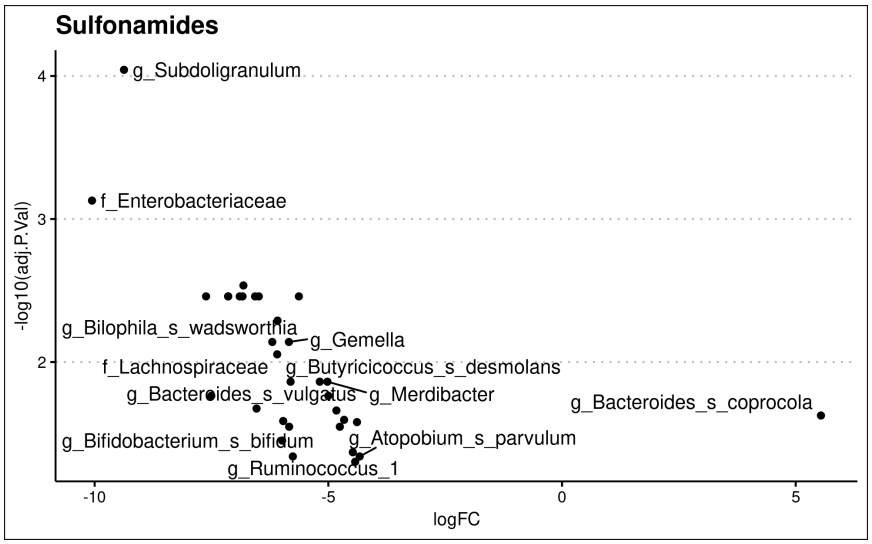
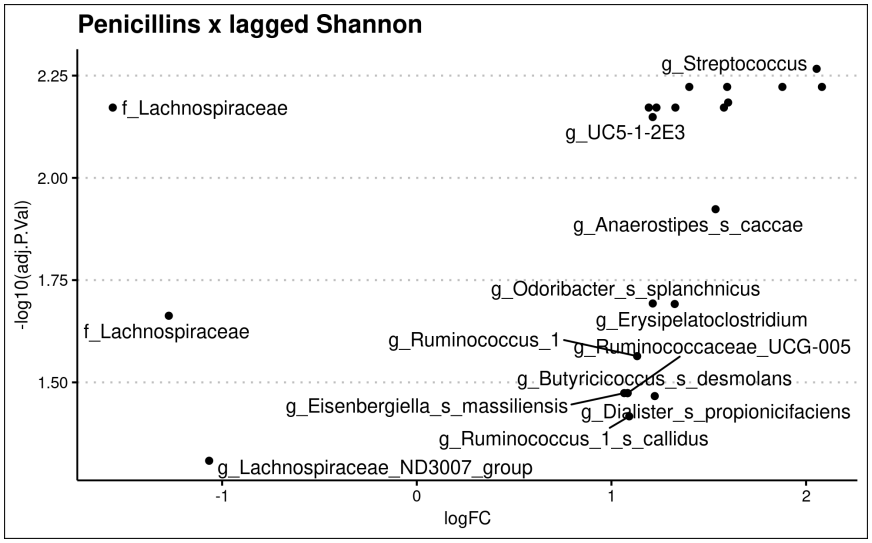
Supplemental Figure 3. Mixed Effects Model of the interaction between lagged Shannon and various classes of antibiotics presented as volcano plots where the y-axis represents decreasing p-value as it increase and the x-axis is log2 fold change. Values in the top right or top left quadrant are significant and have a large effect size.

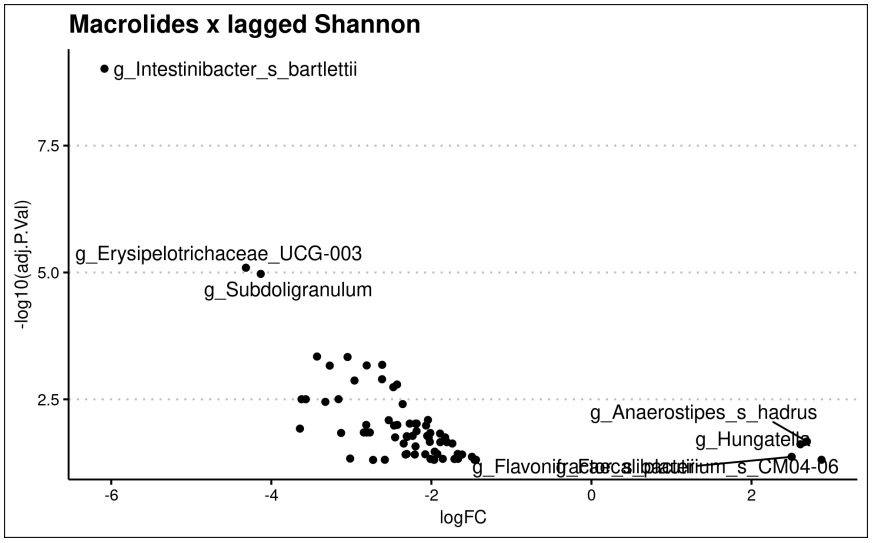


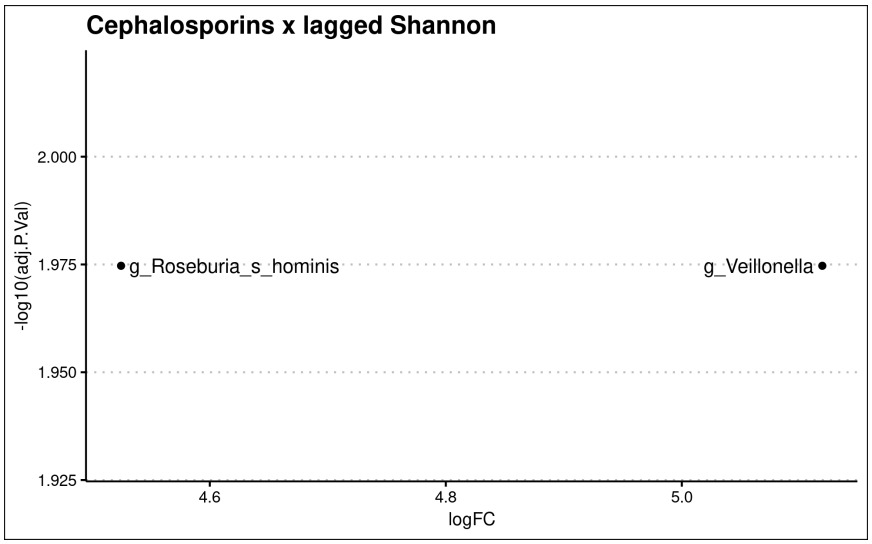


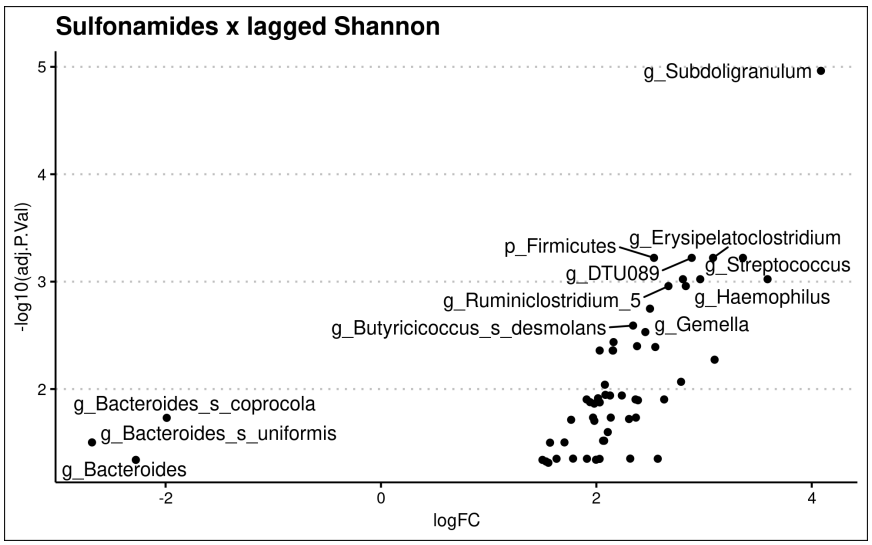

Cephalosporins
1.850
1.825
1.800
1.775
-log10(adj.P.Val)
g_Veillonella
-13.100
-13.075
-13.050
-13.025
logFC


Sulfonamides
4
3
2
-log10(adj.P.Val)
g_Subdoligranulum
f_Enterobacteriaceae
g_Bilophila_s_wadsworthia
g_Gemella
f_Lachnospiraceae
g_Butyricicoccus_s_desmolans
g_Bacteroides_s_vulgatus
g_Merdibacter
g_Bacteroides_s_coprocola
g_Bifidobacterium_s_bifidum
g_Atopobium_s_parvulum
g_Ruminococcus_1
-10
-5
0
5
logFC

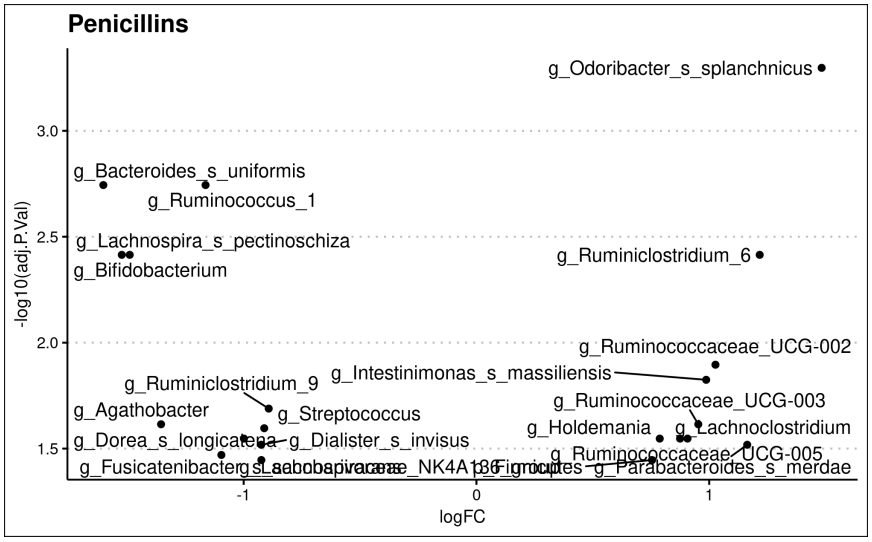

Penicillins x lagged Shannon
2.25
2.00
1.75
1.50
-log10(adj.P.Val)
g_Streptococcus
f_Lachnospiraceae
g_UC5-1-2E3
g_Anaerostipes_s_caccae
g_Odoribacter_s_splanchnicus
g_Erysipelatoclostridium
f_Lachnospiraceae
g_Ruminococcus_1
g_Ruminococcaceae_UCG-005
g_Butyricicoccus_s_desmolans
g_Eisenbergiella_s_massiliensis
g_Dialister_s_propionicifaciens
g_Ruminococcus_1_s_callidus
g_Lachnospiraceae_ND3007_group
-1
0
1
2
logFC

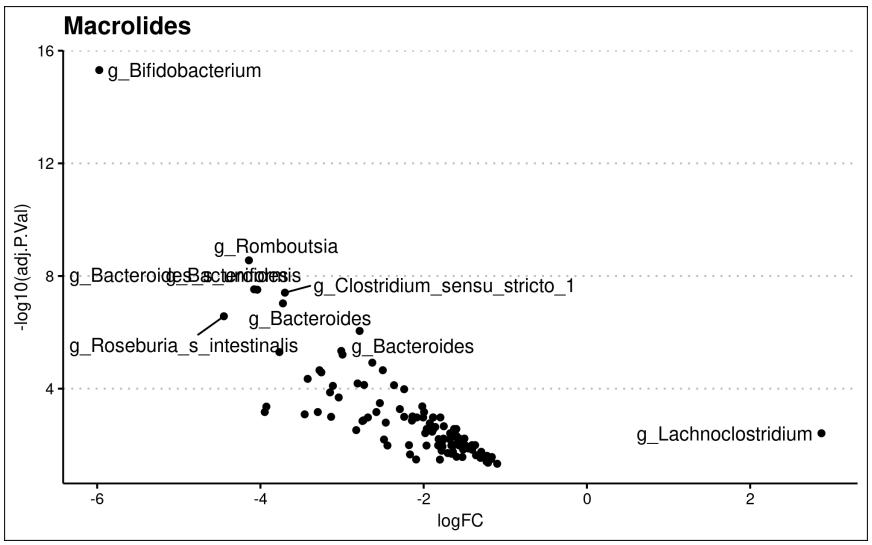

Macrolides x lagged Shannon
g_Intestinibacter_s_bartlettii
g_Erysipelotrichaceae_UCG-003
g_Subdoligranulum
g_Anaerostipes_s_hadrus
g_Hungatella
-log10(adj.P.Val)
logFC

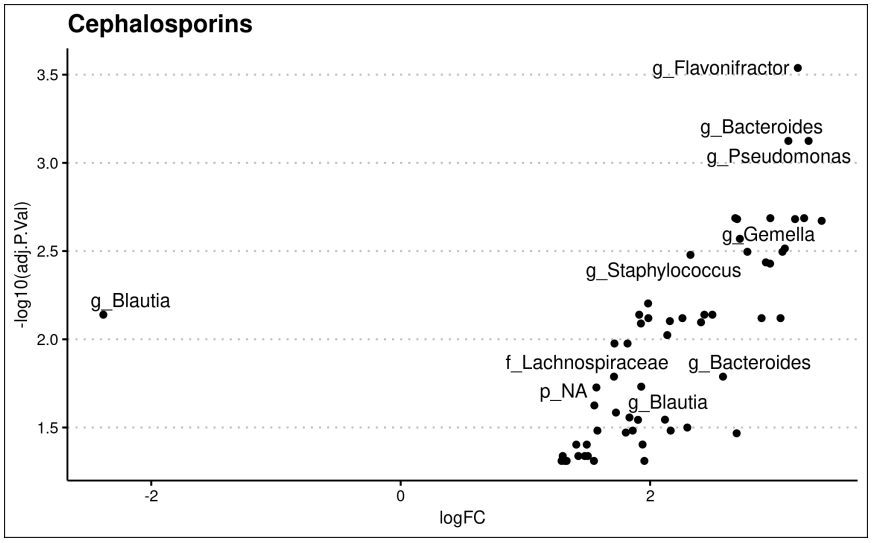

Cephalosporins x lagged Shannon
g_Roseburia_s_hominis
g_Veillonella
-log10(adj.P.Val)
logFC

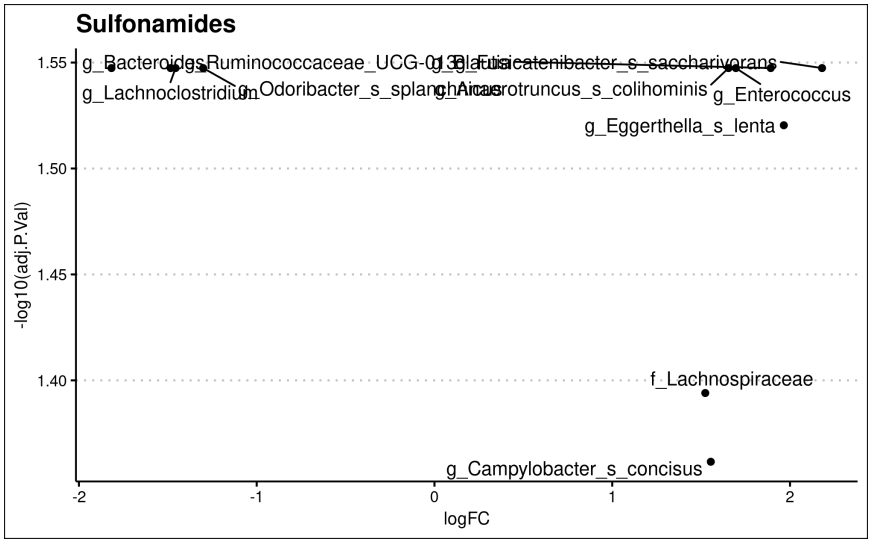

Sulfonamides x lagged Shannon
g_Subdoligranulum
p_Firmicutes
g_Erysipelatoclostridium
g_DTU089
g_Streptococcus
g_Ruminiclostridium_5
g_Haemophilus
g_Butyricicoccus_s_desmolans
g_Gemella
g_Bacteroides_s_coprocola
g_Bacteroides_s_uniformis
g_Bacteroides
-log10(adj.P.Val)
logFC

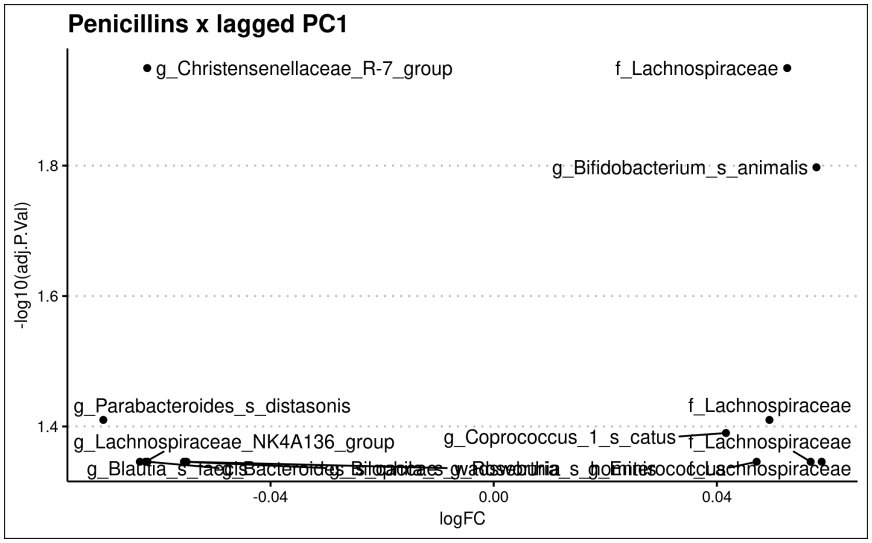
Supplemental Figure 4. Mixed Effects Model of the interaction between lagged PC1 and various classes of antibiotics presented as volcano plots where the y-axis represents decreasing p-value as it increase and the x-axis is log2 fold change. Values in the top right or top left quadrant are significant and have a large effect size.

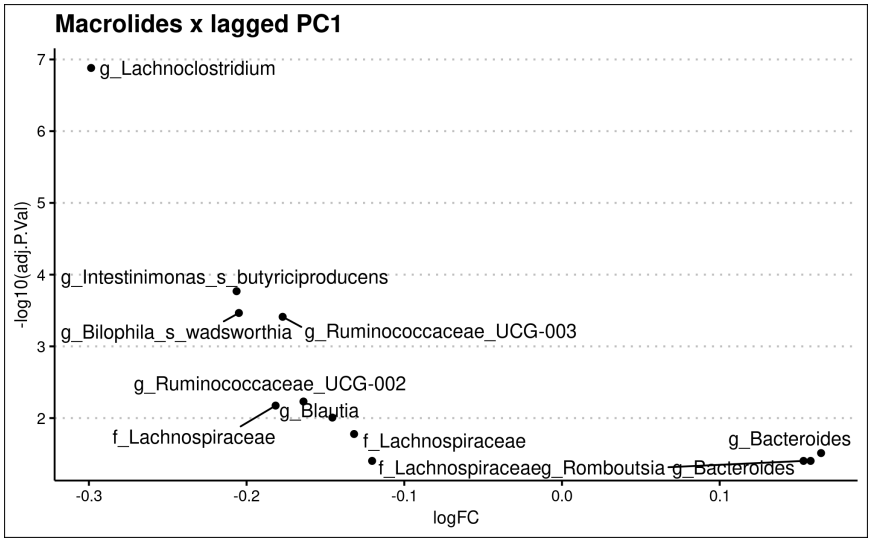


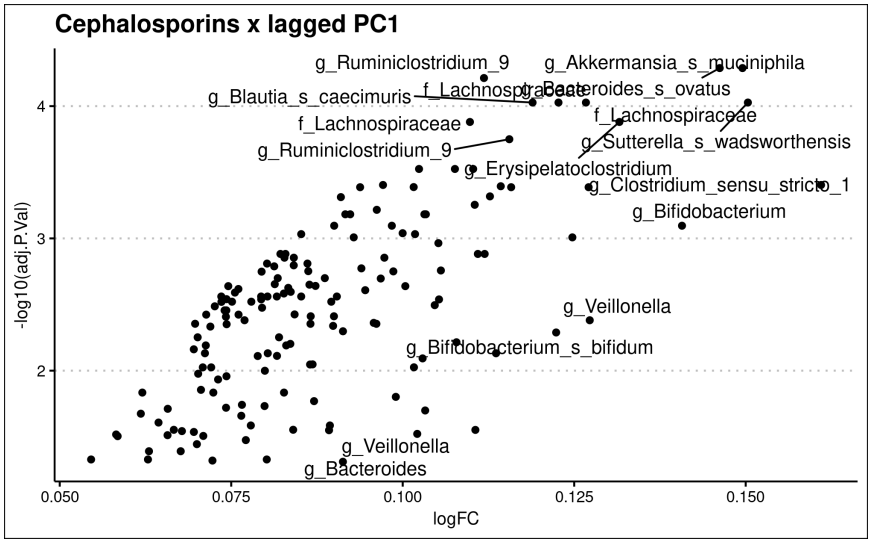


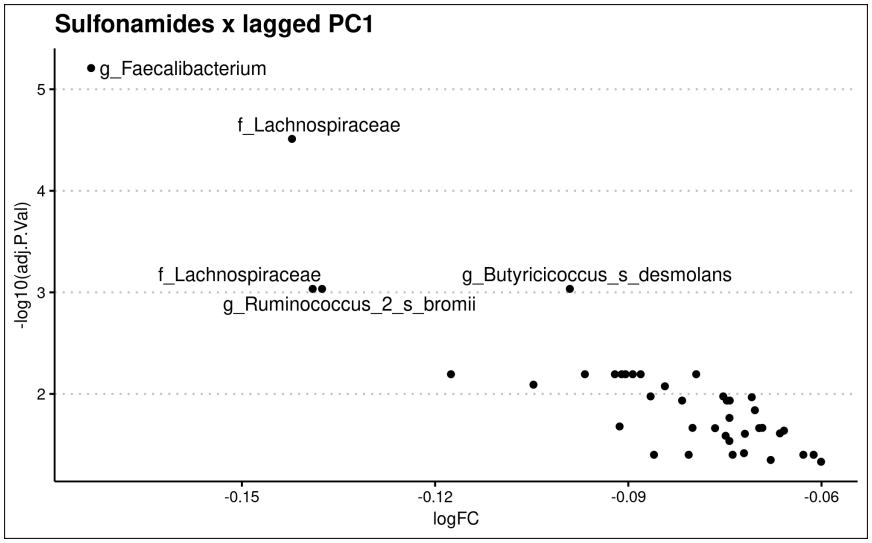

Cephalosporins
g_Flavonifractor
g_Bacteroides
g_Pseudomonas
g_Gemella
g_Staphylococcus
g_Blautia
f_Lachnospiraceae
g_Bacteroides
p_NA
g_Blautia
-log10(adj.P.Val)
logFC


Sulfonamides
g_Lachnoclostridium
g_Odoribacter_s_splanchnicus
g_Enterococcus
g_Eggerthella_s_lenta
f_Lachnospiraceae
g_Campylobacter_s_concisus
-log10(adj.P.Val)
logFC

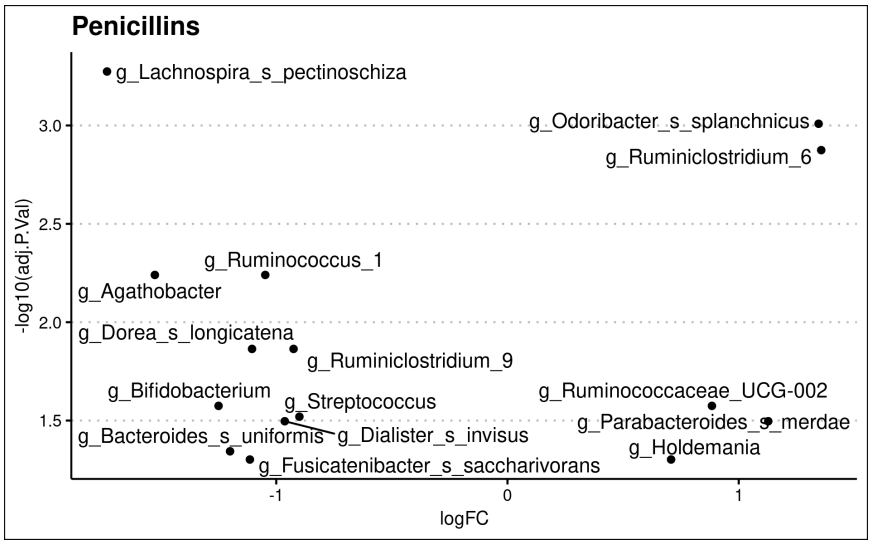

Penicillins x lagged PC1
g_Christensenellaceae_R-7_group
f_Lachnospiraceae
g_Bifidobacterium_s_animalis
g_Parabacteroides_s_distasonis
f_Lachnospiraceae
g_Lachnospiraceae_NK4A136_group
g_Coprococcus_1_s_catus
f_Lachnospiraceae
-log10(adj.P.Val)
logFC

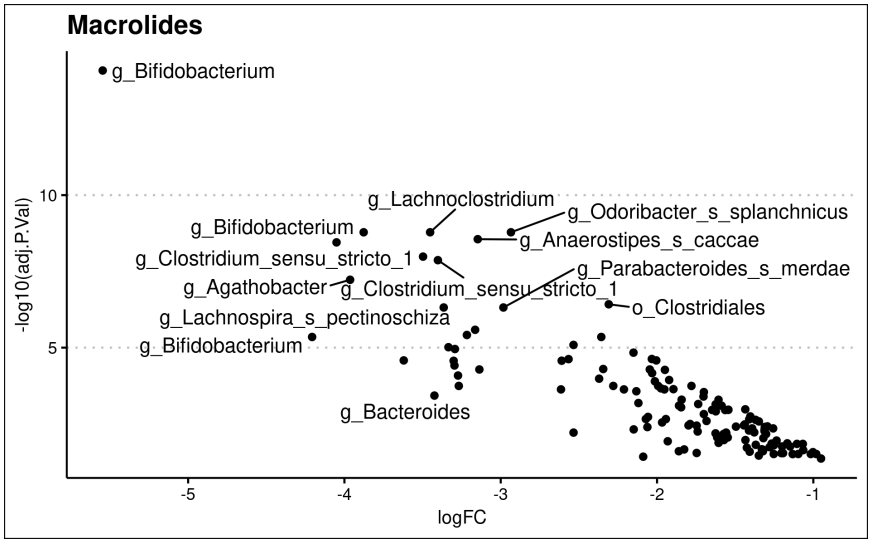

Macrolides x lagged PC1
g_Lachnoclostridium
g_Intestinimonas_s_butyriciproducens
g_Bilophila_s_wadsworthia
g_Ruminococcaceae_UCG-003
g_Ruminococcaceae_UCG-002
g_Blautia
f_Lachnospiraceae
f_Lachnospiraceae
g_Bacteroides
f_Lachnospiraceae
g_Romboutsia
g_Bacteroides
-log10(adj.P.Val)
logFC

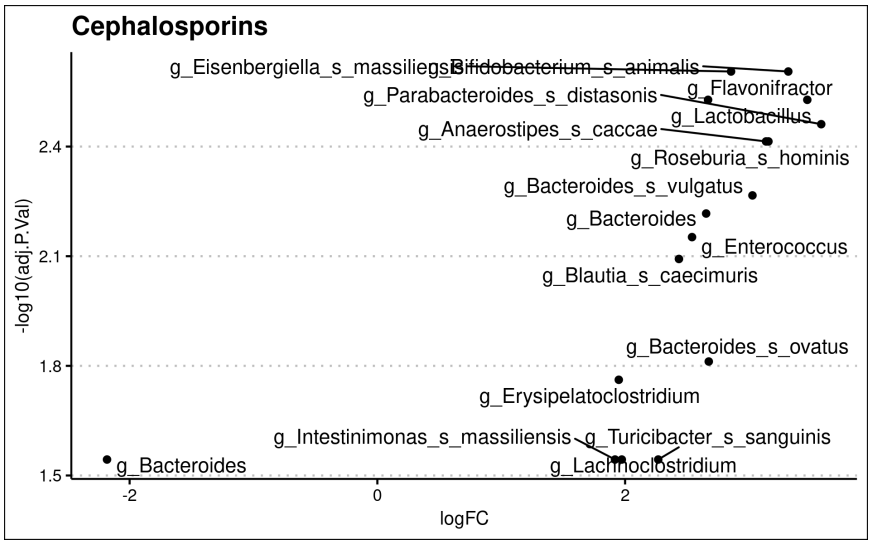

Cephalosporins x lagged PC1
g_Ruminiclostridium_9
g_Akkermansia_s_muciniphila
g_Blautia_s_caecimuris
f_Lachnospiraceae
g_Bacteroides_s_ovatus
f_Lachnospiraceae
g_Ruminiclostridium_9
g_Sutterella_s_wadsworthensis
g_Erysipelatoclostridium
g_Clostridium_sensu_stricto_1
g_Bifidobacterium
g_Veillonella
g_Bifidobacterium_s_bifidum
g_Veillonella
g_Bacteroides
-log10(adj.P.Val)
logFC

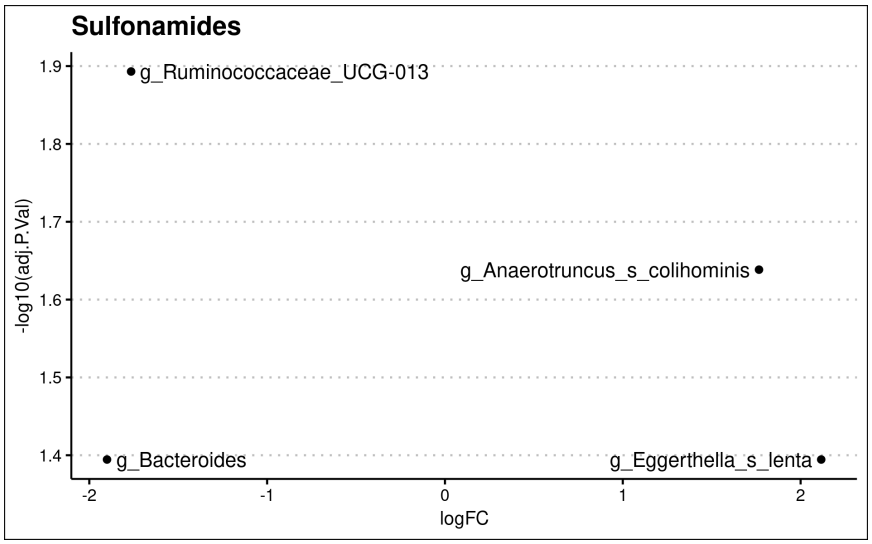

Sulfonamides x lagged PC1
g_Faecalibacterium
f_Lachnospiraceae
f_Lachnospiraceae
g_Butyricicoccus_s_desmolans
g_Ruminococcus_2_s_bromii
-log10(adj.P.Val)
logFC

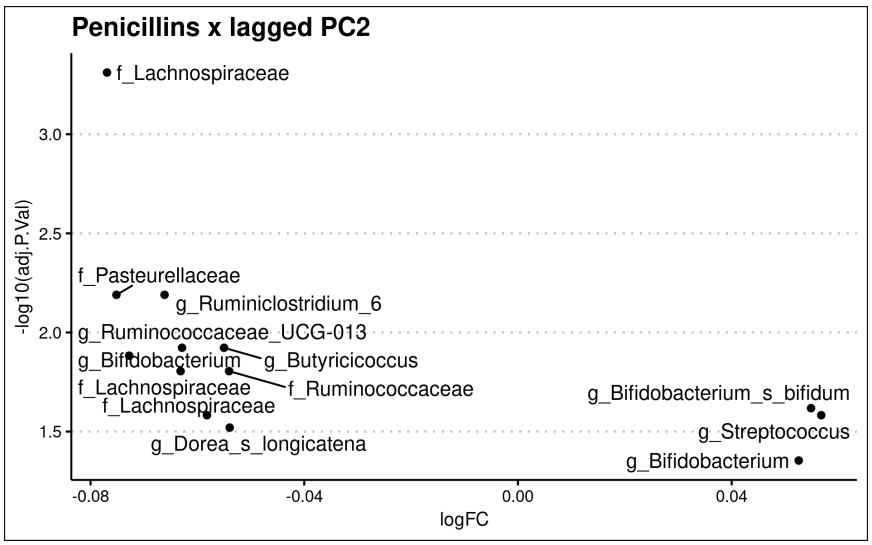
Supplemental Figure 5. Mixed Effects Model of the interaction between lagged PC2 and various classes of antibiotics presented as volcano plots where the y-axis represents decreasing p-value as it increase and the x-axis is log2 fold change. Values in the top right or top left quadrant are significant and have a large effect size.

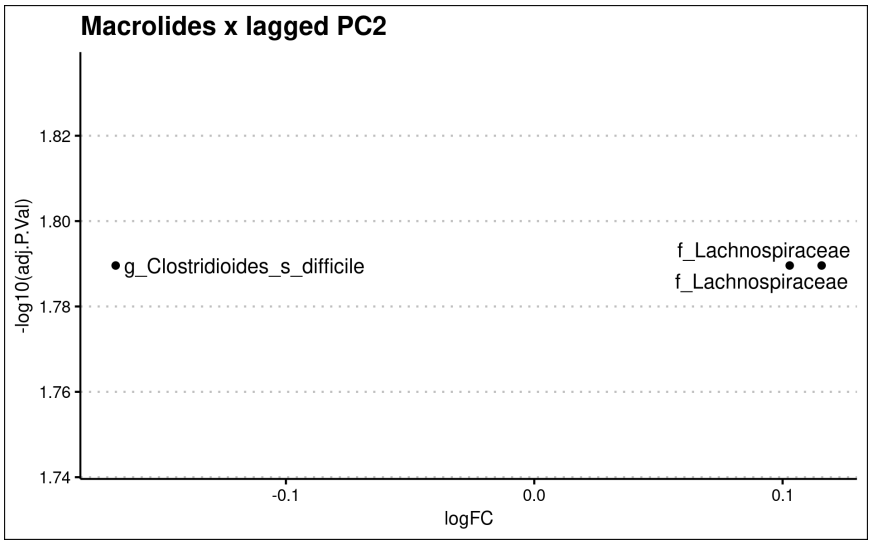


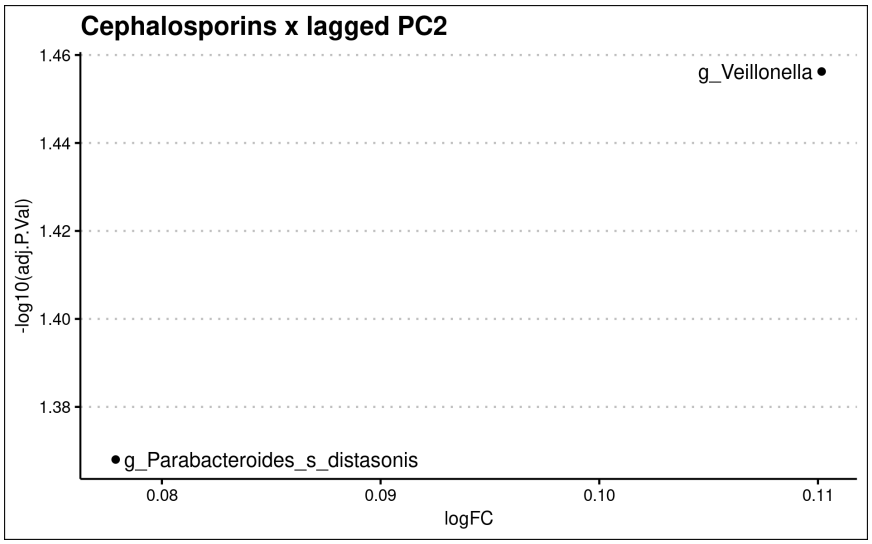


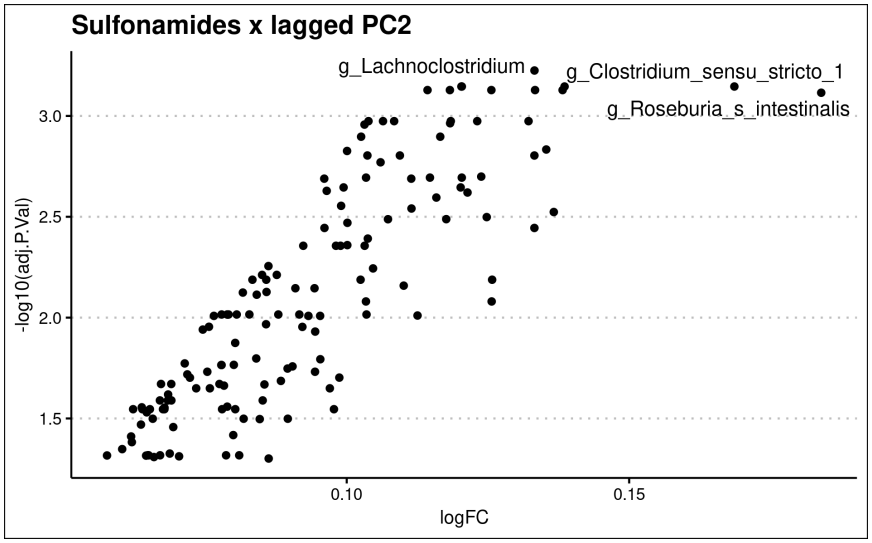

Cephalosporins
g_Eisenbergiella_s_massiliensis
g_Bifidobacterium_s_animalis
g_Flavonifractor
g_Parabacteroides_s_distasonis
g_Lactobacillus
g_Anaerostipes_s_caccae
g_Roseburia_s_hominis
g_Bacteroides_s_vulgatus
g_Bacteroides
g_Enterococcus
g_Blautia_s_caecimuris
g_Bacteroides_s_ovatus
g_Erysipelatoclostridium
g_Intestinimonas_s_massiliensis
g_Turicibacter_s_sanguinis
g_Bacteroides
g_Lachnoclostridium
-log10(adj.P.Val)
2.4
2.1
1.8
1.5
-2
0
2
logFC


Sulfonamides
g_Ruminococcaceae_UCG-013
g_Anaerotruncus_s_colihominis
g_Bacteroides
g_Eggerthella_s_lenta
-log10(adj.P.Val)
1.9
1.8
1.7
1.6
1.5
1.4
-2
-1
0
1
2
logFC


Penicillins x lagged PC2
f_Lachnospiraceae
f_Pasteurellaceae
g_Ruminiclostridium_6
g_Ruminococcaceae_UCG-013
g_Bifidobacterium
g_Butyricicoccus
f_Lachnospiraceae
f_Ruminococcaceae
f_Lachnospiraceae
g_Bifidobacterium_s_bifidum
g_Streptococcus
g_Dorea_s_longicatena
g_Bifidobacterium
-log10(adj.P.Val)
3.0
2.5
2.0
1.5
-0.08
-0.04
0.00
0.04
logFC


Macrolides x lagged PC2
1.82
1.80
1.78
1.76
1.74
-log10(adj.P.Val)
g_Clostridioides_s_difficile
f_Lachnospiraceae
f_Lachnospiraceae
-0.1
0.0
0.1
logFC


Cephalosporins x lagged PC2
1.46
1.44
1.42
1.40
1.38
-log10(adj.P.Val)
g_Veillonella
g_Parabacteroides_s_distasonis
0.08
0.09
0.10
0.11
logFC


Sulfonamides x lagged PC2
3.0
2.5
2.0
1.5
-log10(adj.P.Val)
g_Lachnoclostridium
g_Clostridium_sensu_stricto_1
g_Roseburia_s_intestinalis
0.10
0.15
logFC