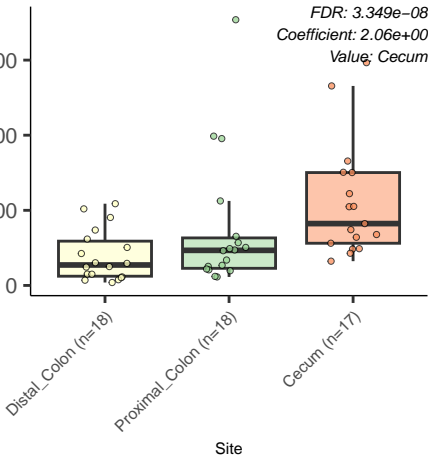
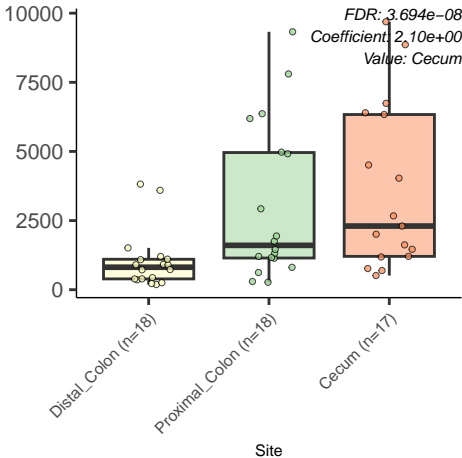


acteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnosp

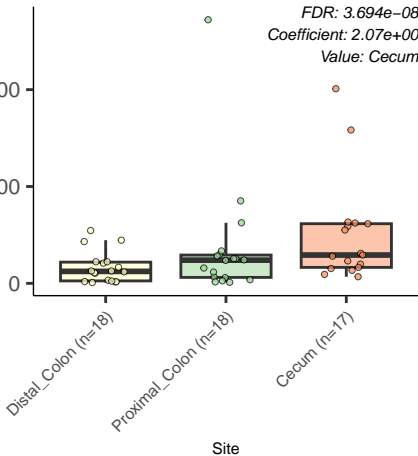


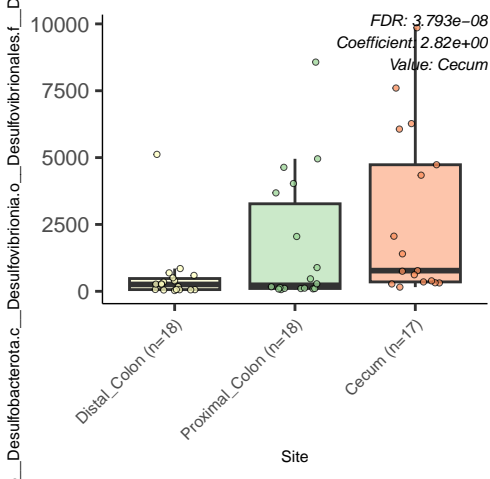
Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__



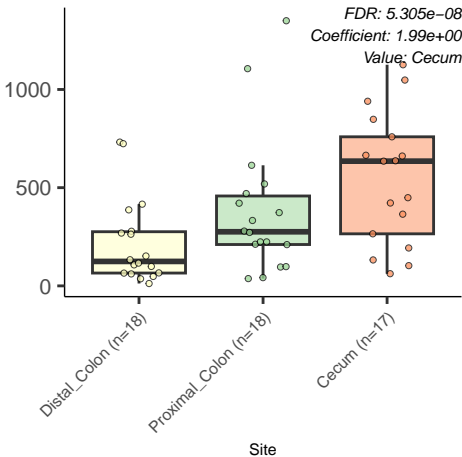
a.p._Firmicutes.c._Clostridia.o._Lachnospirales.f._Lachnospirace

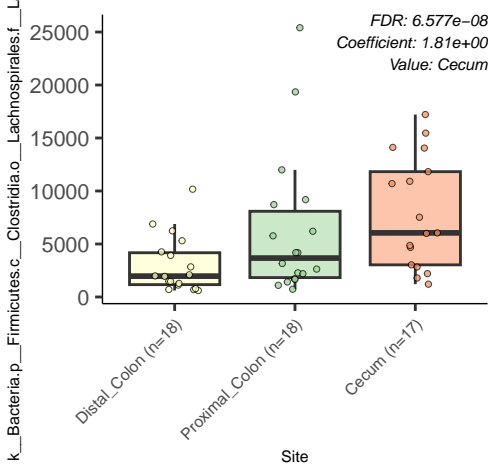
FDR: $3.694e-08$
Coefficient: $2.07e+00$
Value: Cecum



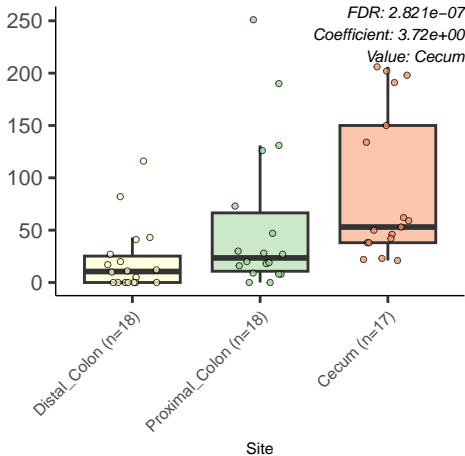


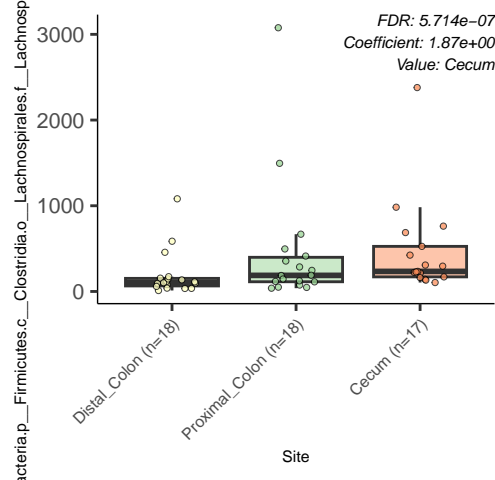
Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachn



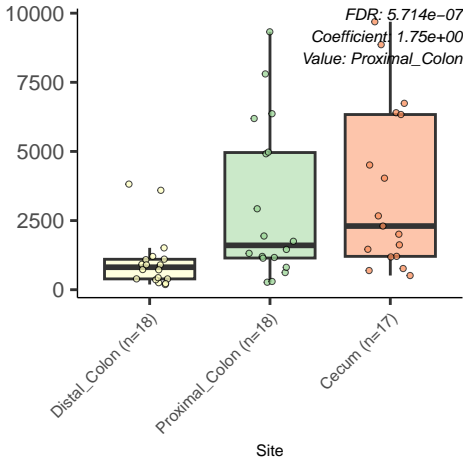


rmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__An

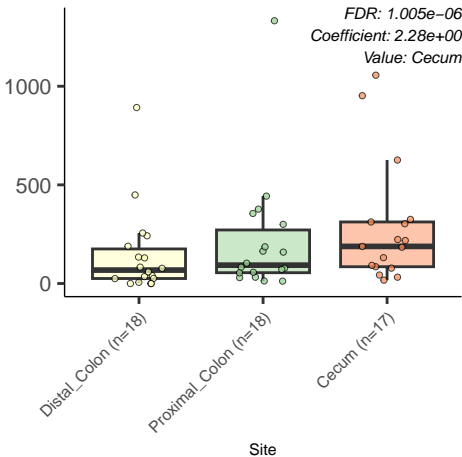




Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g__

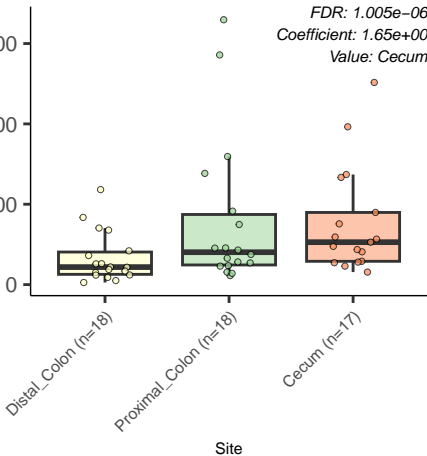


Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae



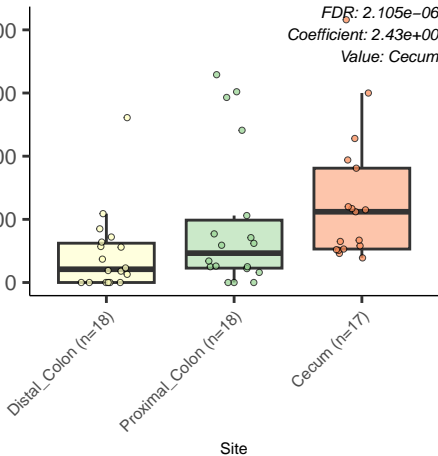
Bacteria.p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Oscillosp

FDR: 1.005e-06
Coefficient: 1.65e+00
Value: Cecum

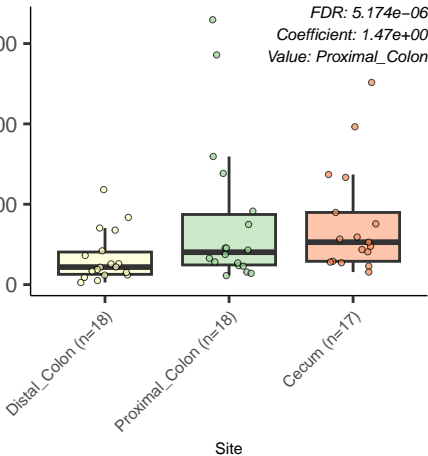


a.p._Firmicutes.c._Clostridia.o._Lachnospirales.f._Lachnospiraceae

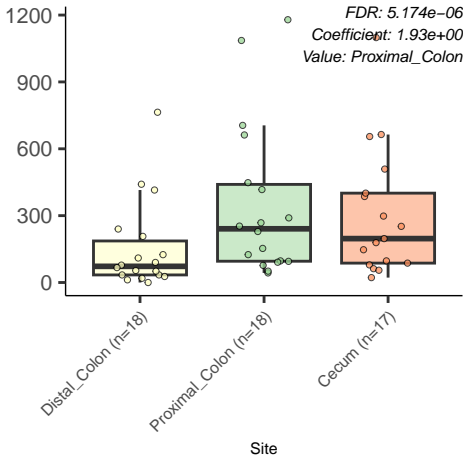
FDR: 2.105e-06
Coefficient: 2.43e+00
Value: Cecum



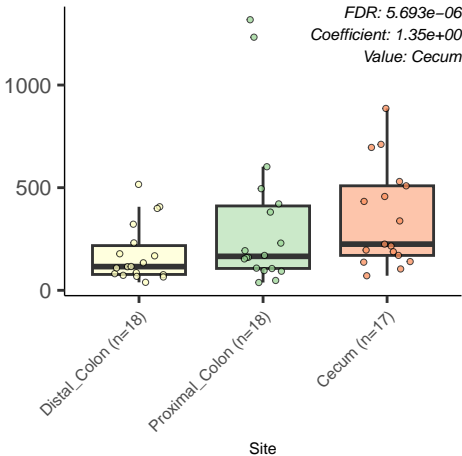
Bacteria.p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Oscillosp



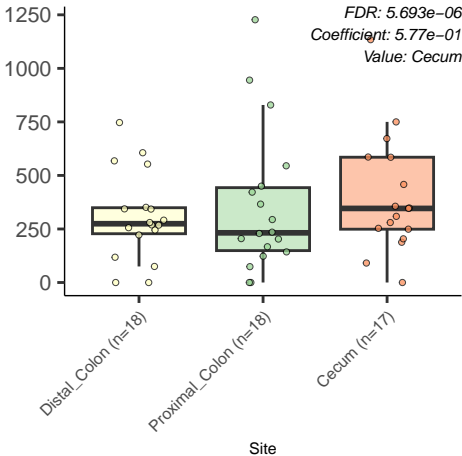
Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillos

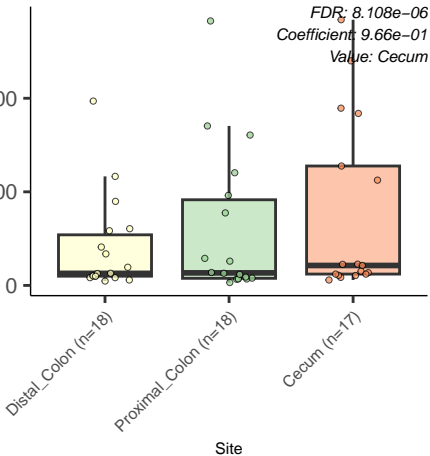


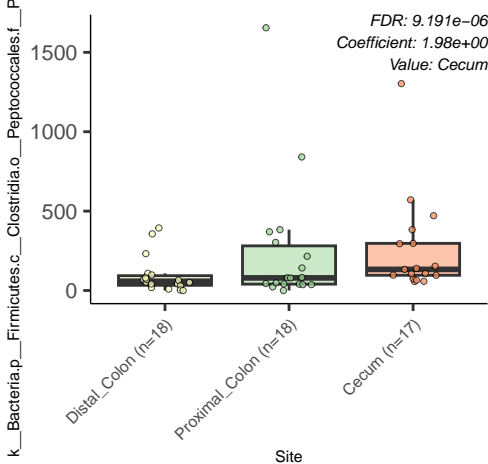
Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Oscillospira



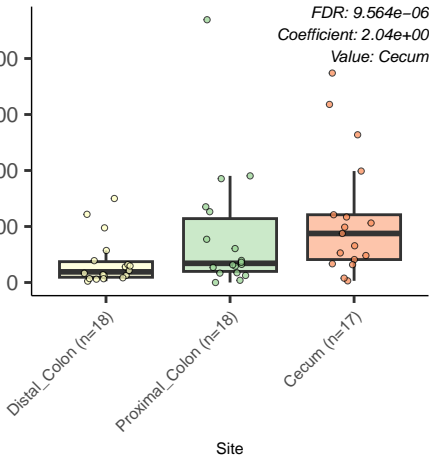
eria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Eubacterium



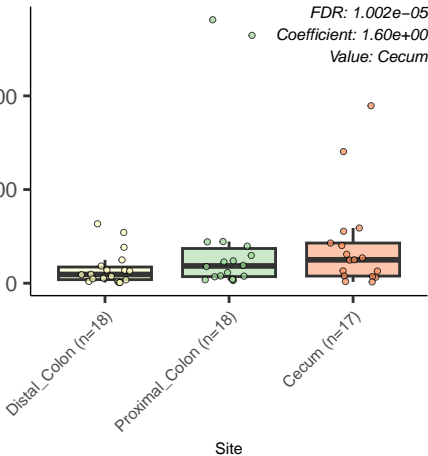




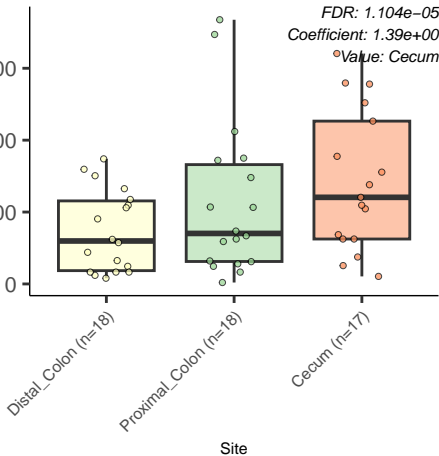
Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g_Lactobacillus.g_Lactobacillus

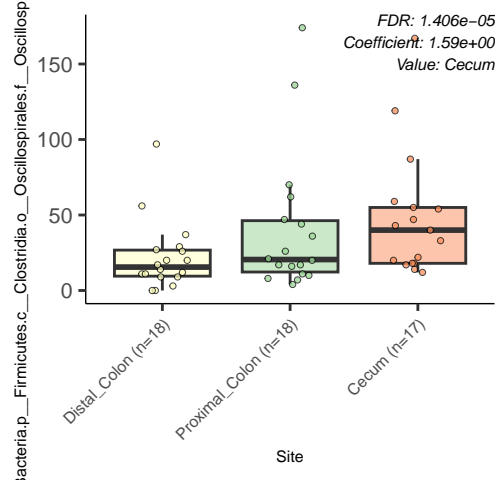


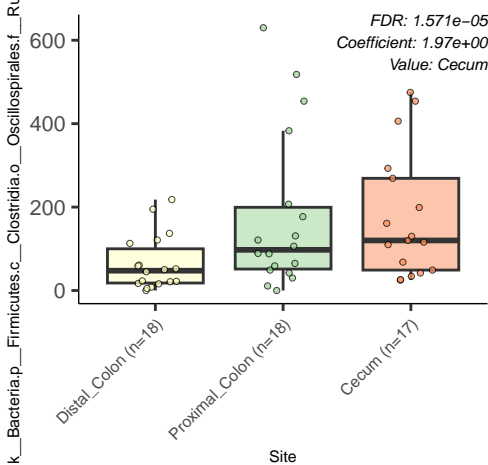
k_Bacteria.p_Firmicutes.c__Clostridia.o__Clostridia.vadinBE



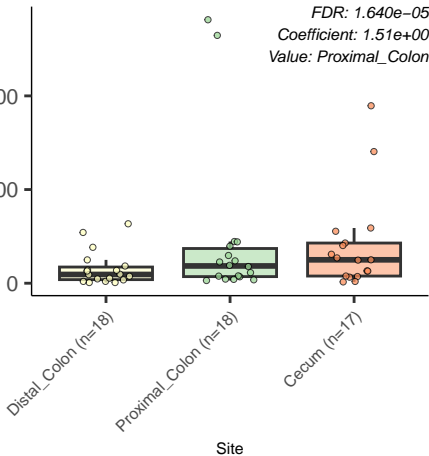
acteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminoc

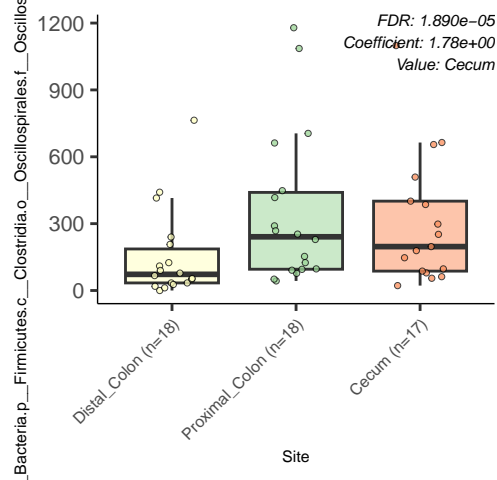


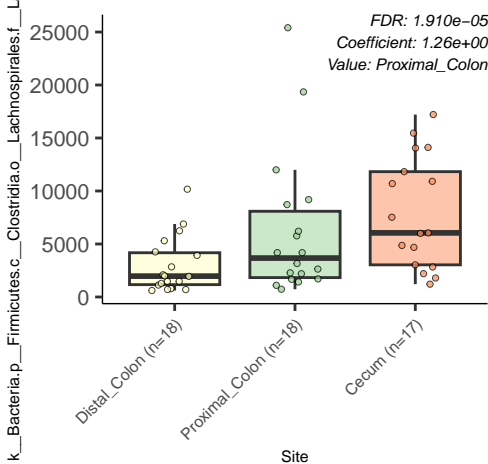




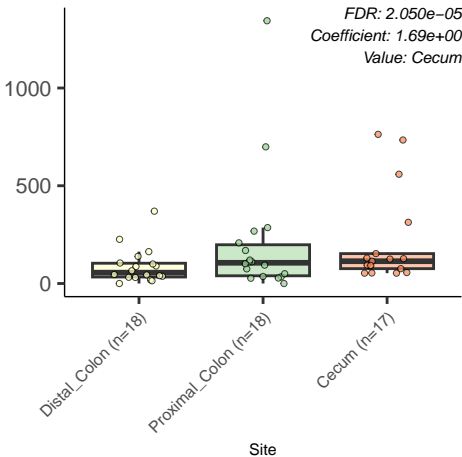
k_Bacteria.p_Firmicutes.c__Clostridia.o__Clostridia.vadinBE

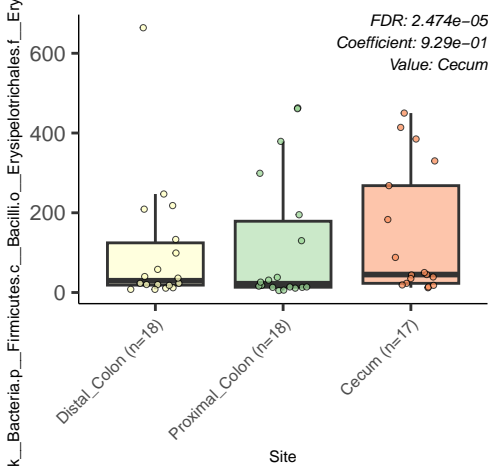


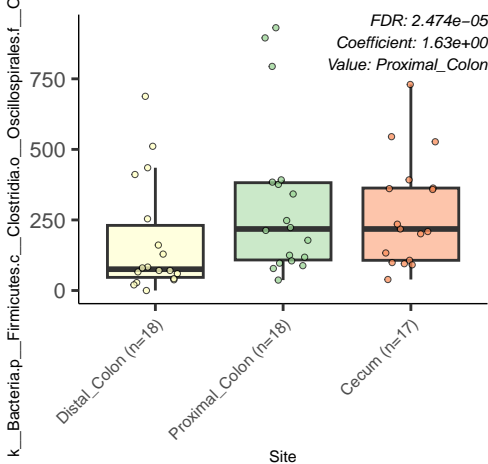




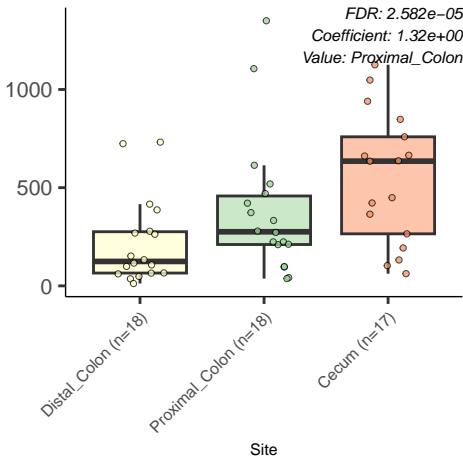
k_Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_La



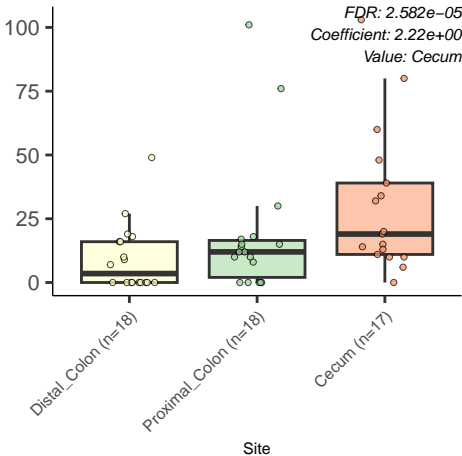


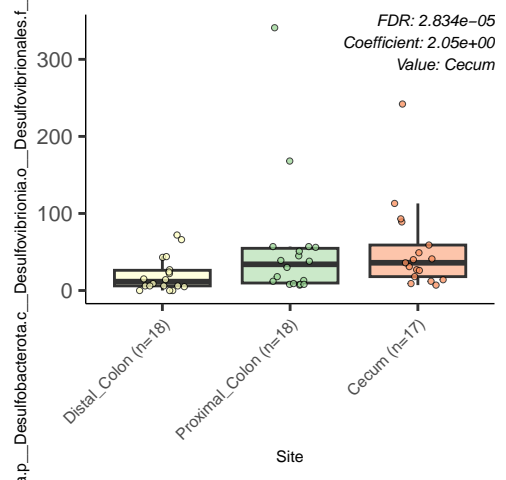


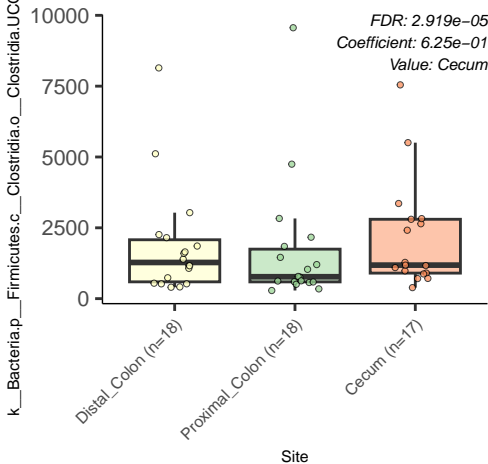
Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachn



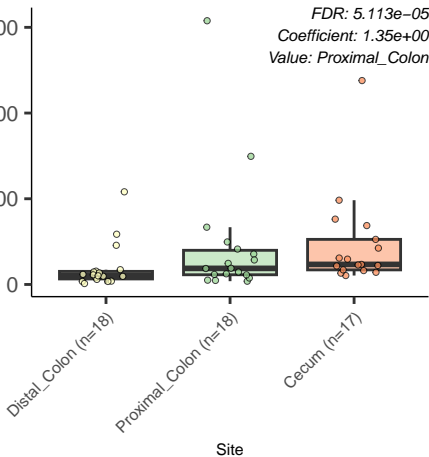
Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachn



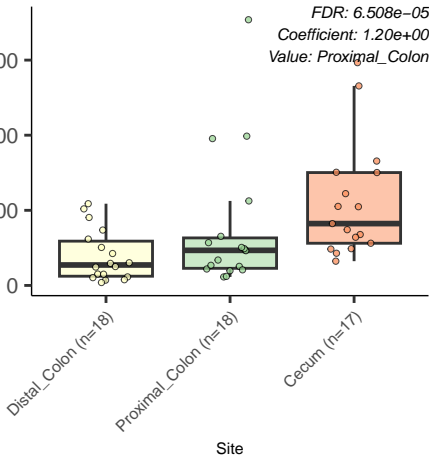


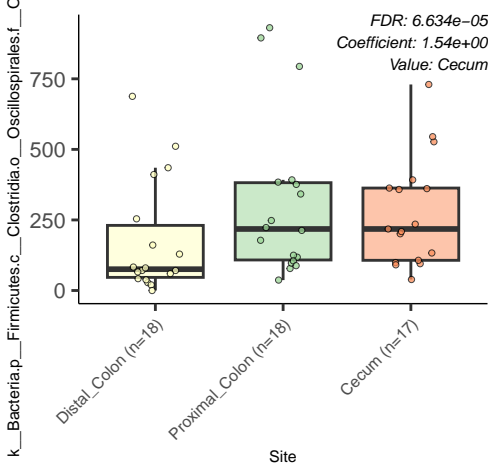


acteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnosp



acteria.p__Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnosp





Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae

1000

500

0

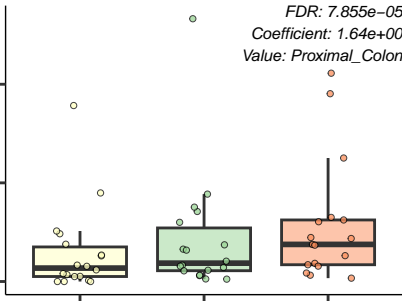
Distal_Colon (n=18)

Proximal_Colon (n=18)

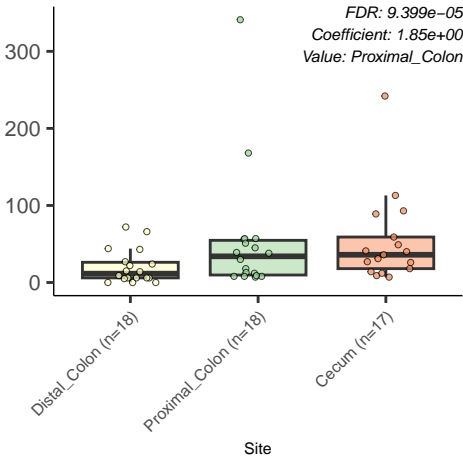
Cecum (n=17)

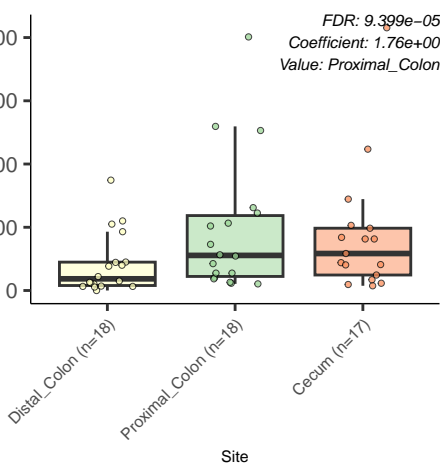
Site

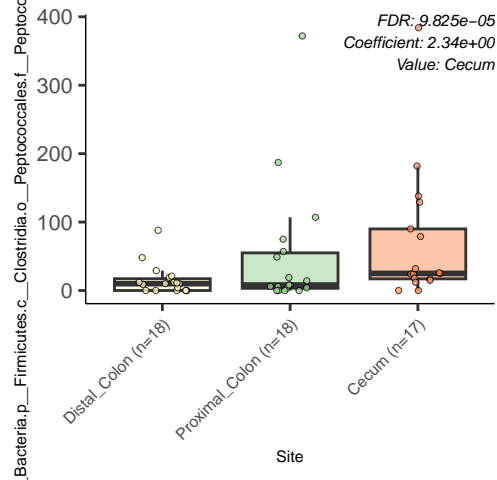
FDR: $7.855e-05$
Coefficient: $1.64e+00$
Value: Proximal_Colon



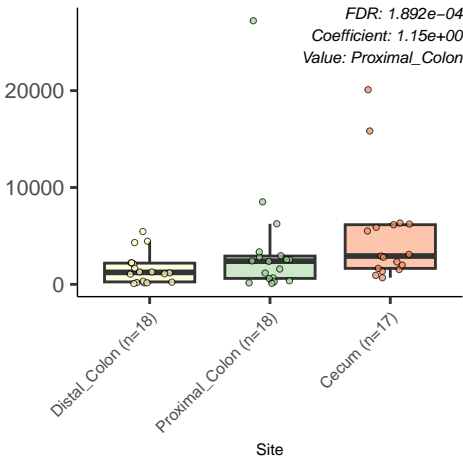
a.p__Desulfobacterota.c__Desulfovibrionia.o__Desulfovibrionales.f.

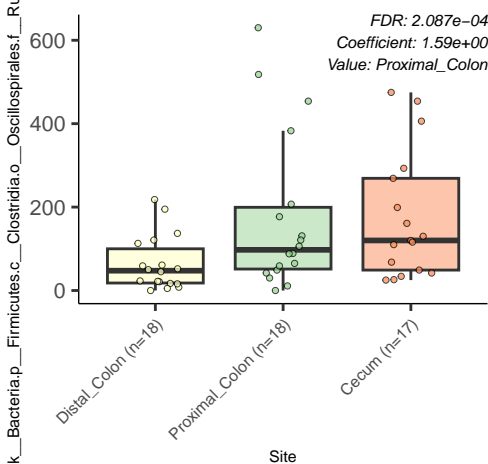






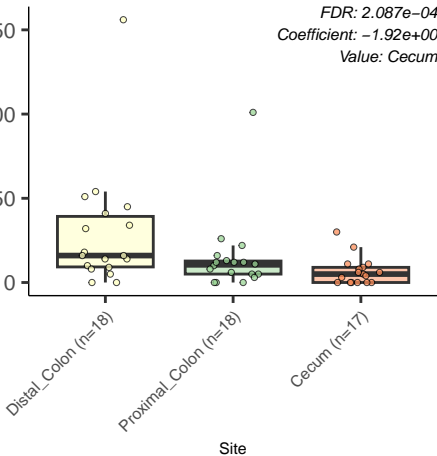
a.p._Firmicutes.c._Clostridia.o._Lachnospirales.f._Lachnospirace

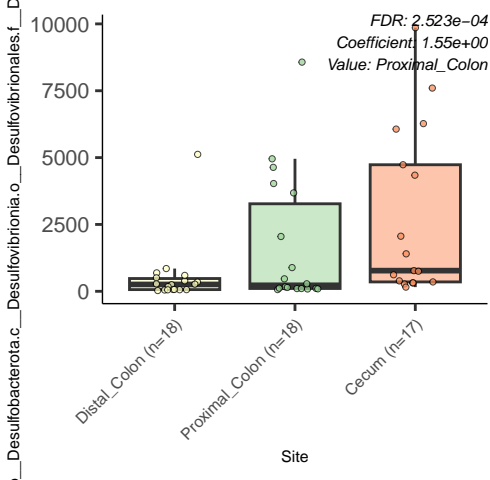




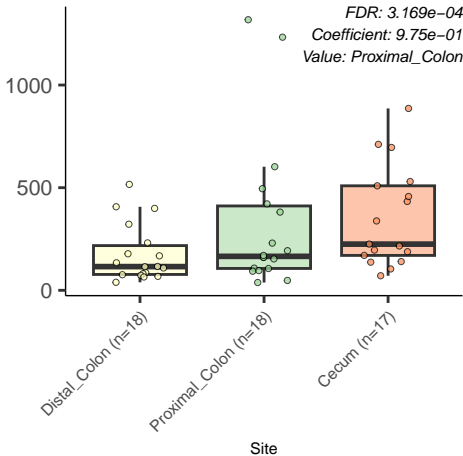
k_Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rho

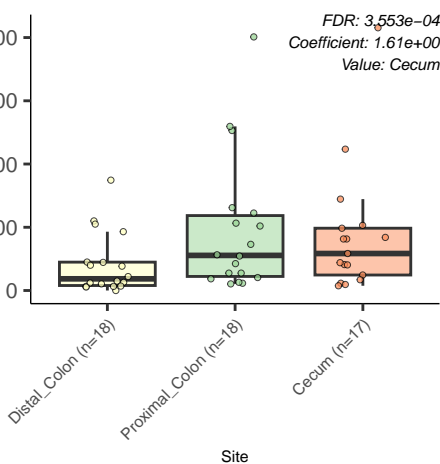
FDR: $2.087e-04$
Coefficient: $-1.92e+00$
Value: Cecum



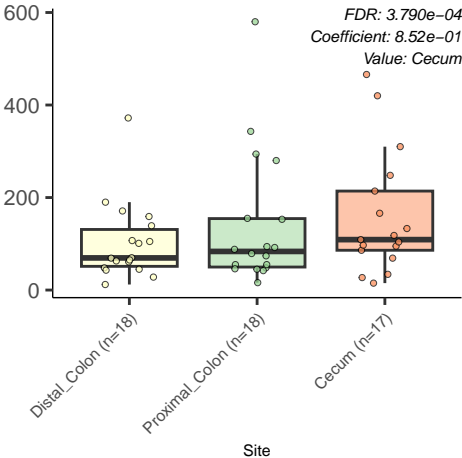


Bacteria.p__Firmicutes.c__Clostridia.o__Oscillospira

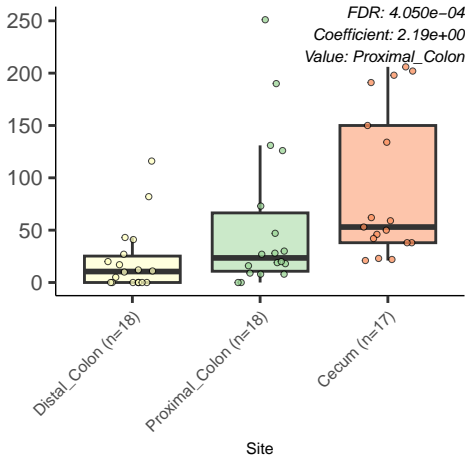


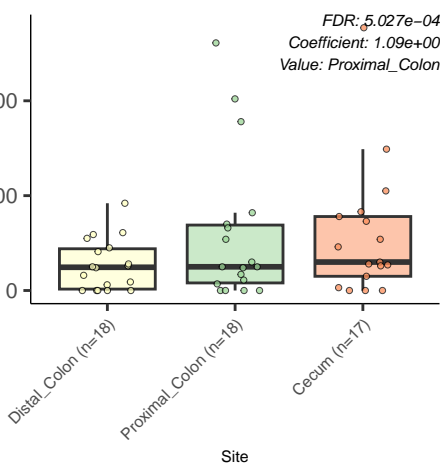


Bacteria.p_Bacteroidota.c_Bacteroidia.o_Bacteroidales.f_Mar



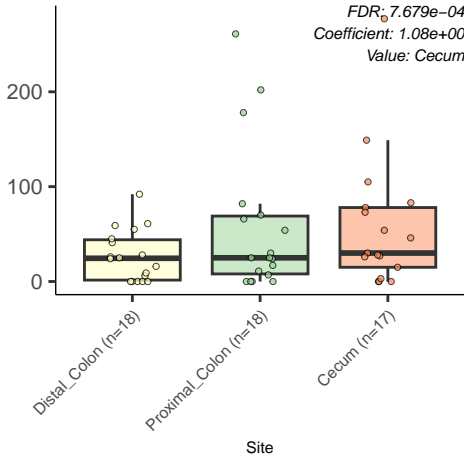
rmicutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__An



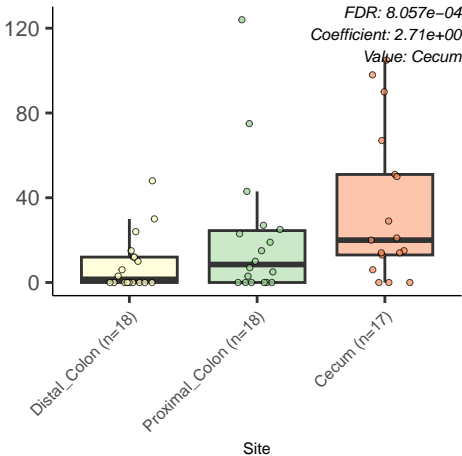


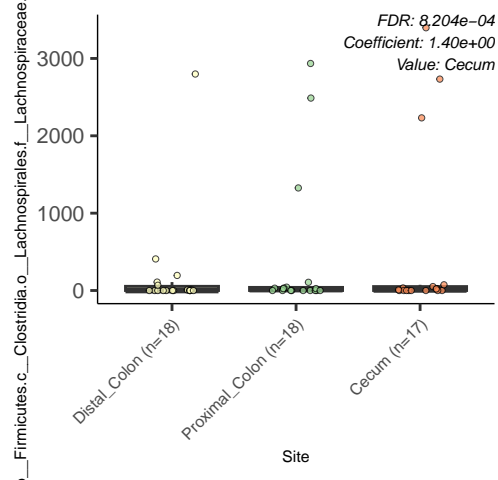
cteria.p__Firmicutes.c__Bacilli.o__Acholeplasmatales.f__Acholeplasma

FDR: 7.679×10^{-4}
Coefficient: 1.08×10^0
Value: Cecum

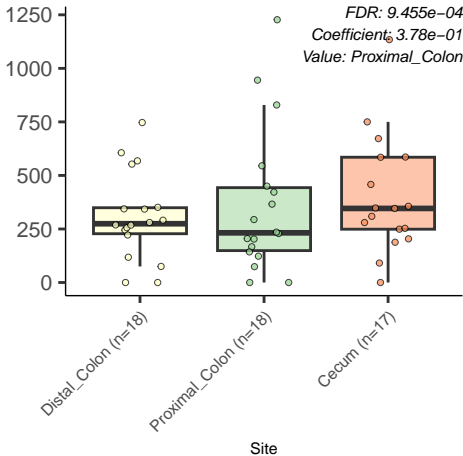


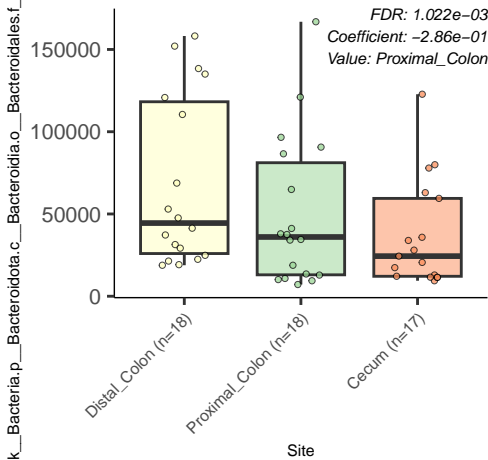
scutes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaer



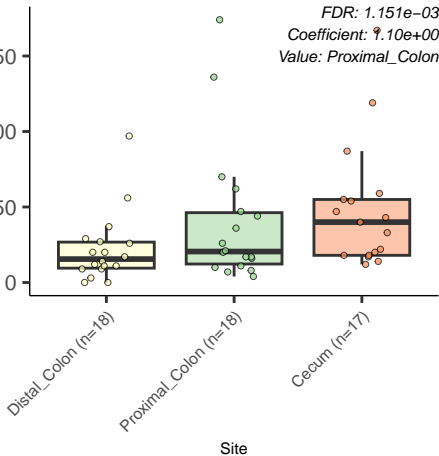


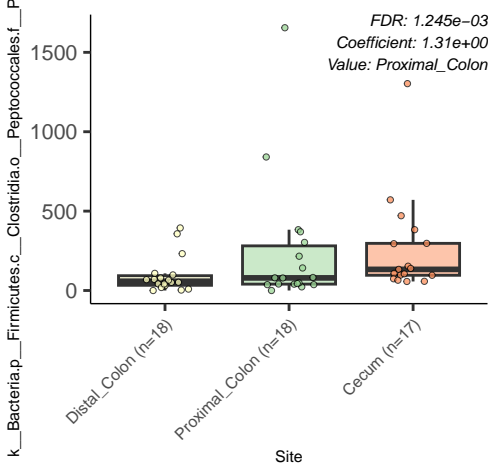
eria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Eubacterium



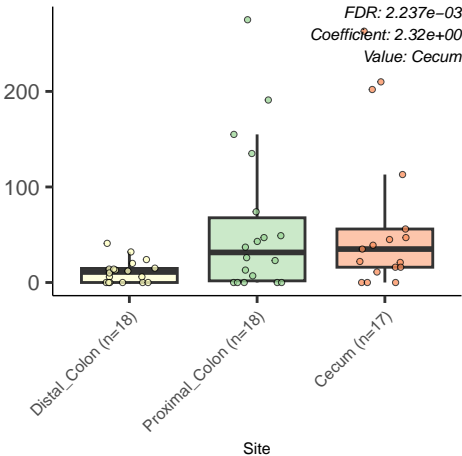


Bacteria.p_Firmicutes.c_Clostridia.o_Oscillospirales.f_Oscillosp





Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachno



k_Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_La

FDR: 2.506e-03
Coefficient: 1.12e+00
Value: Proximal_Colon

1000

500

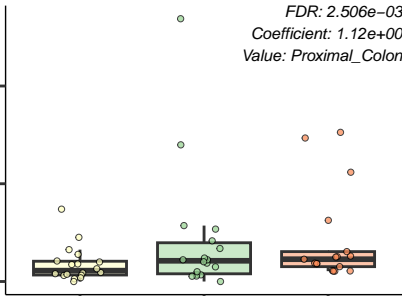
0

Distal_Colon (n=18)

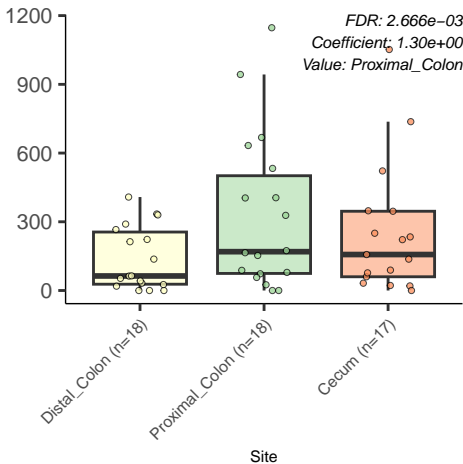
Proximal_Colon (n=18)

Cecum (n=17)

Site

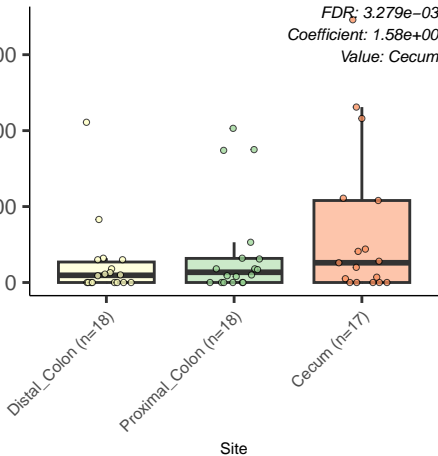


a.p._Firmicutes.c._Clostridia.o._Lachnospirales.f._Lachnospiraceae

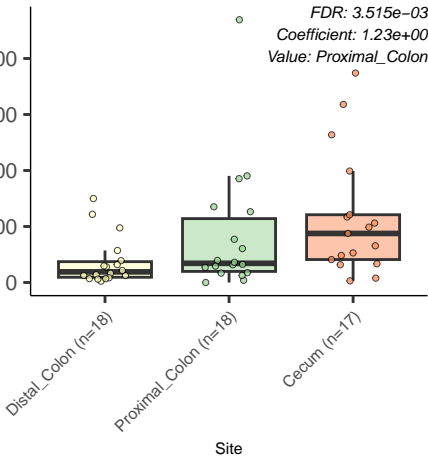


p_Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae

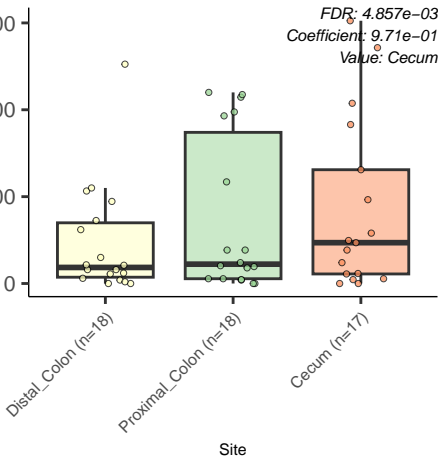
FDR: 3.279e-03
Coefficient: 1.58e+00
Value: Cecum

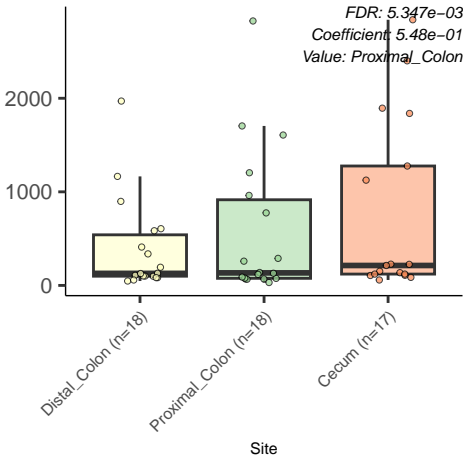


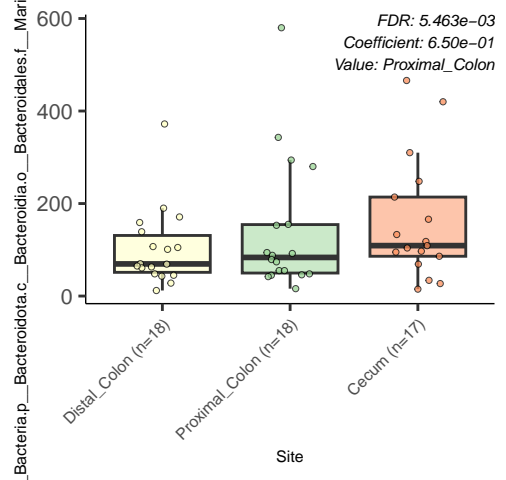
Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnospiraceae.g_Lactobacillus.g_Lactobacillus



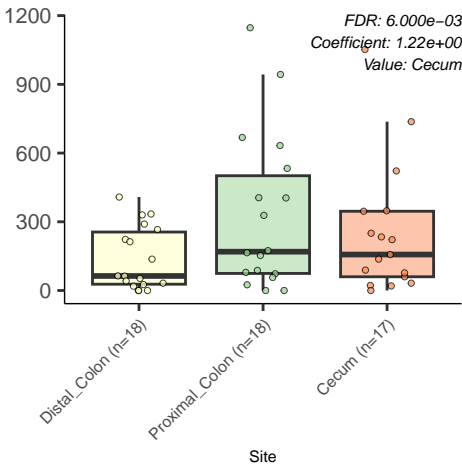
ia.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eg

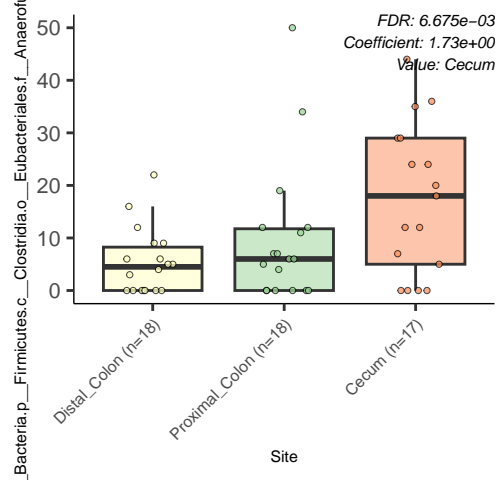




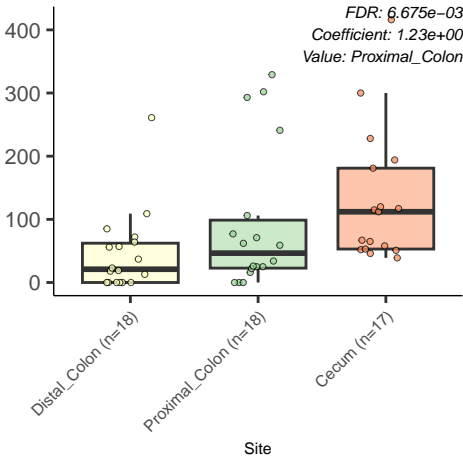


a.p._Firmicutes.c._Clostridia.o._Lachnospirales.f._Lachnospiraceae

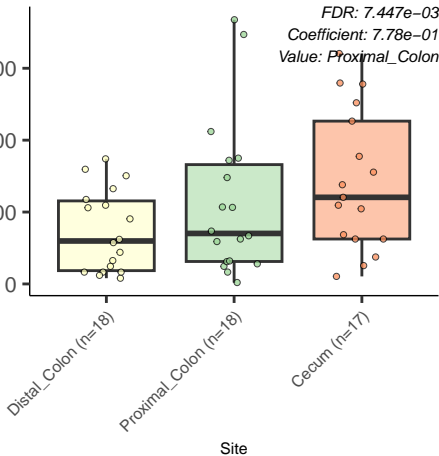


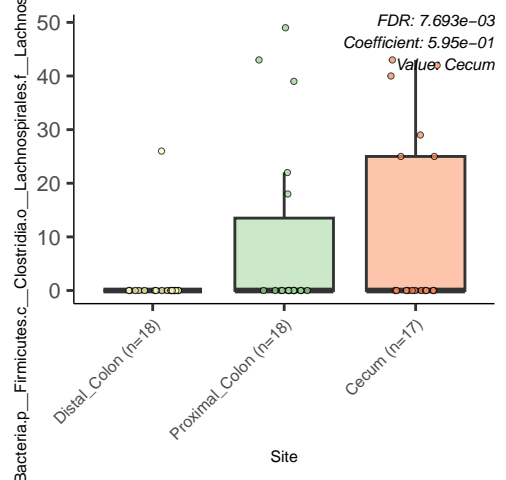


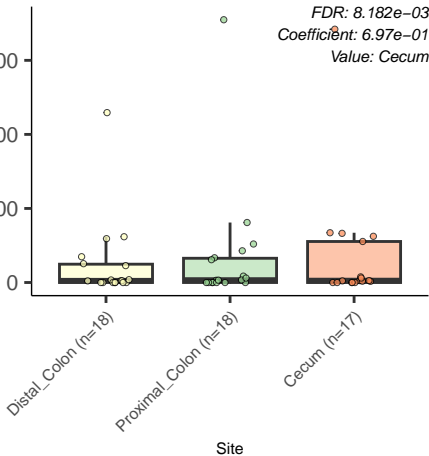
a.p._Firmicutes.c._Clostridia.o._Lachnospirales.f._Lachnospiraceae

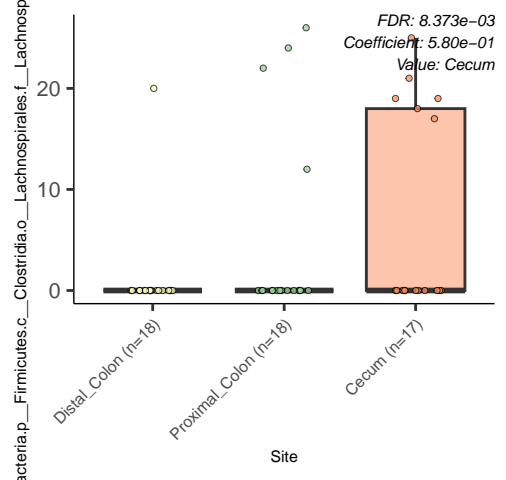


acteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminoc

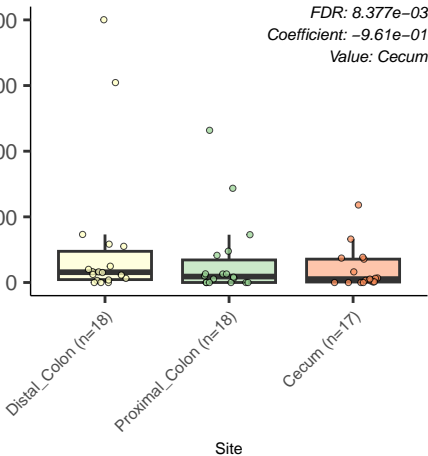


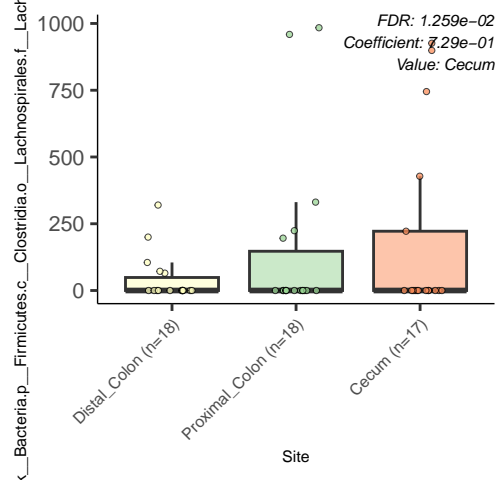


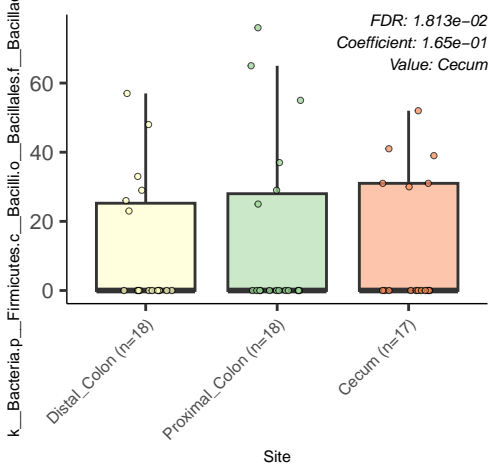


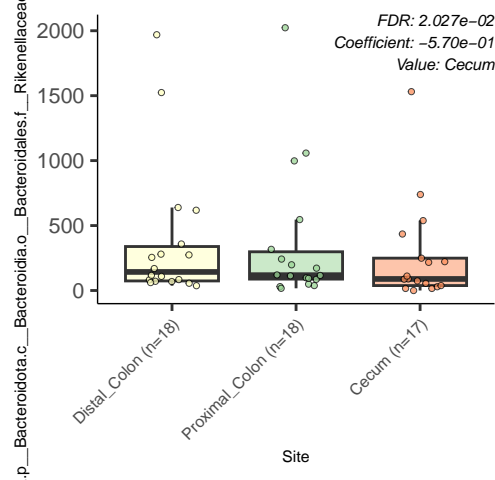


.p__Actinobacteriota.c__Actinobacteria.o__Bifidobacteriales.f__Bifidobacteri



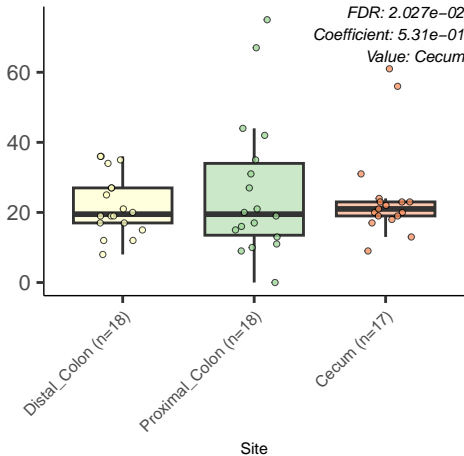




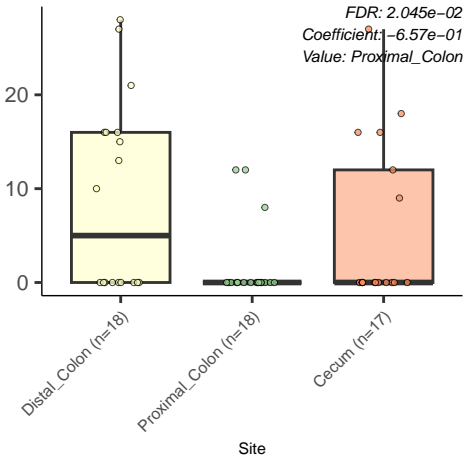


acteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Clostridiaceae

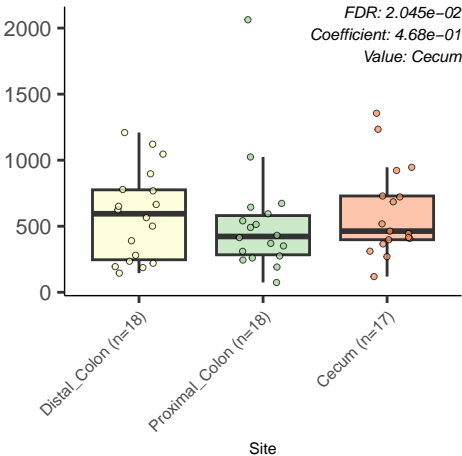
FDR: 2.027e-02
Coefficient: 5.31e-01
Value: Cecum



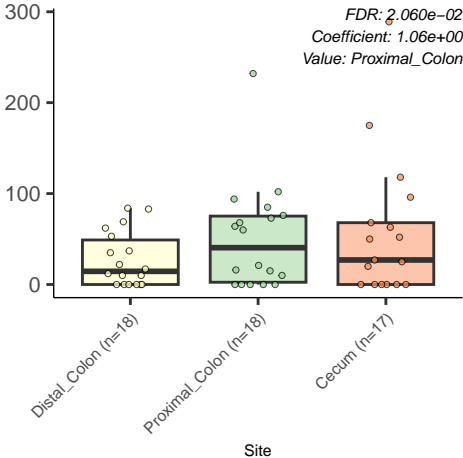
Bacteria.p__Firmicutes.c__Bacilli.o__Erysipelotrichales.f__Erysipel

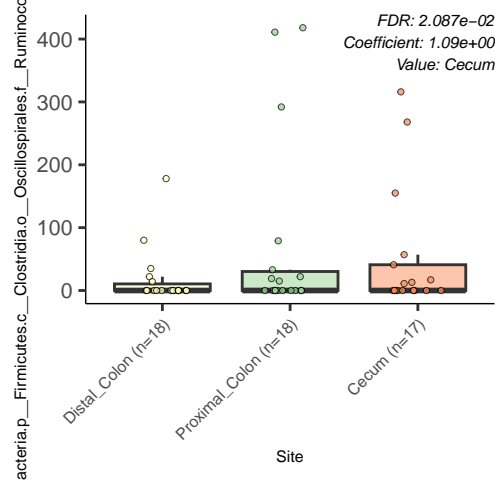


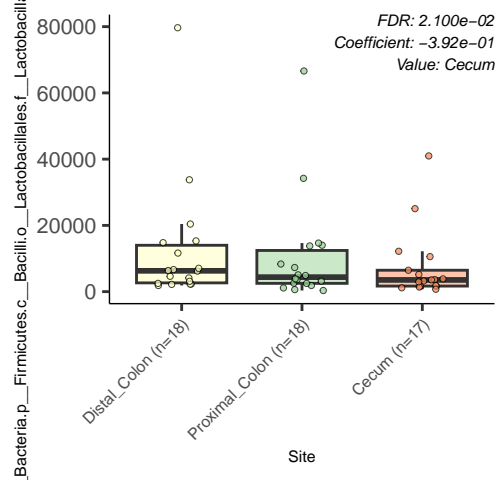
Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachnos

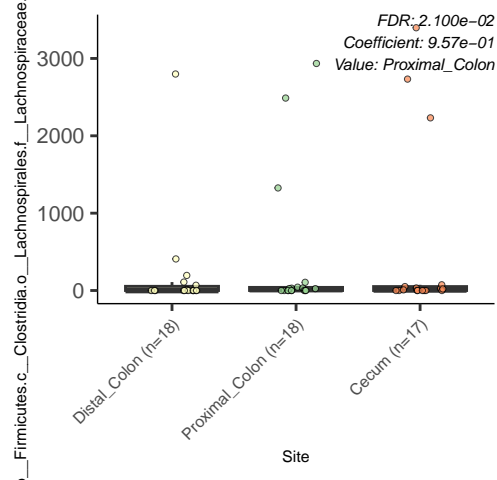


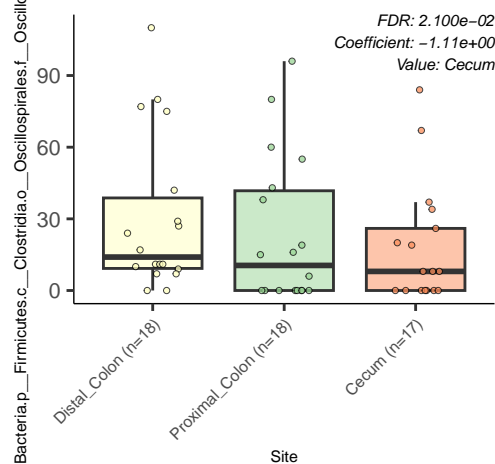
Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g

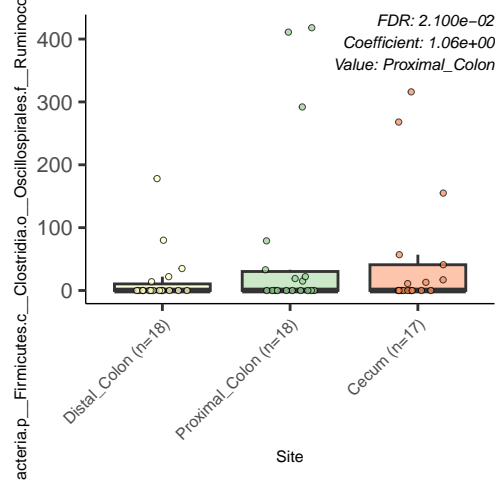












Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Atopob

2000

1000

0

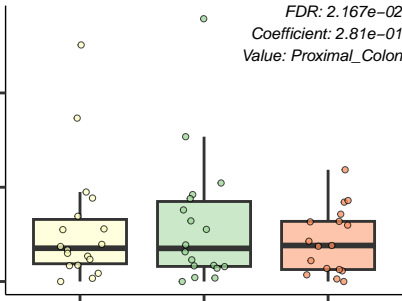
Distal_Colon (n=18)

Proximal_Colon (n=18)

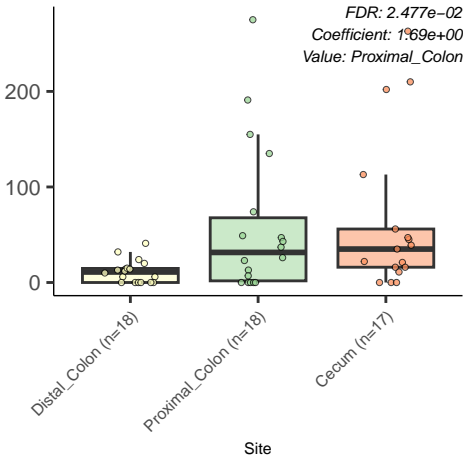
Cecum (n=17)

Site

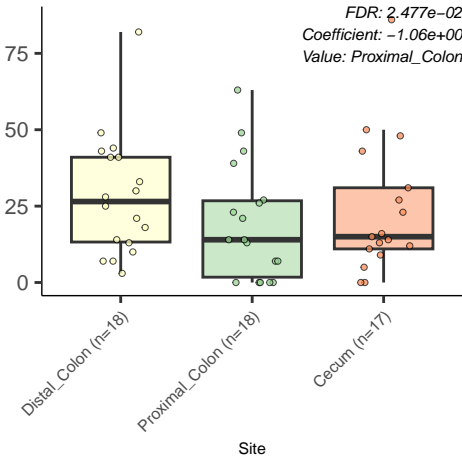
FDR: 2.167e-02
Coefficient: 2.81e-01
Value: Proximal_Colon

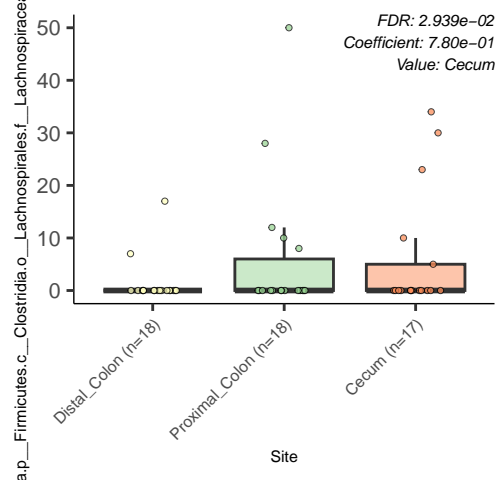


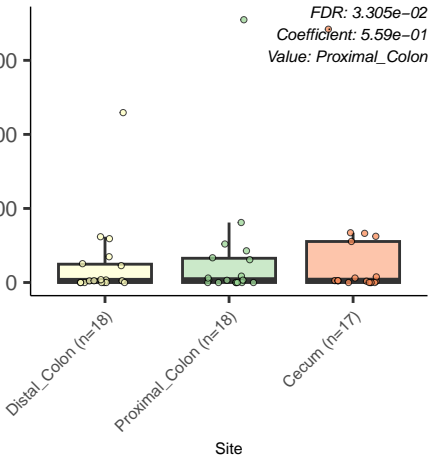
Bacteria.p_Firmicutes.c_Clostridia.o_Lachnospirales.f_Lachno

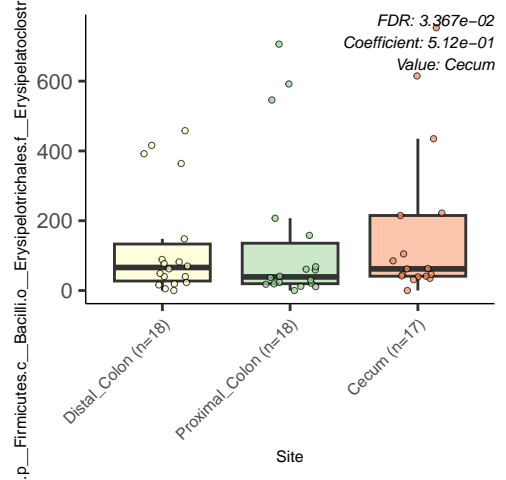


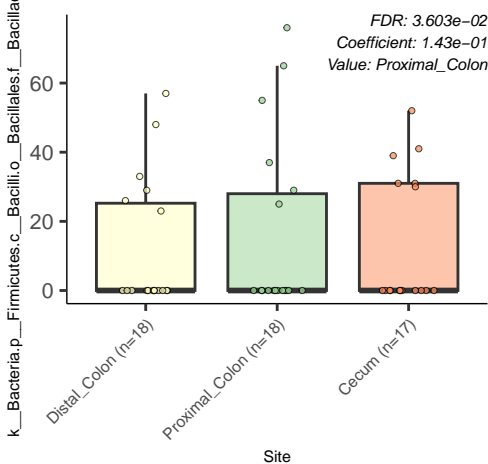
k_Bacteria.p_Firmicutes.c_Clostridia.o_Oscillospirales.f



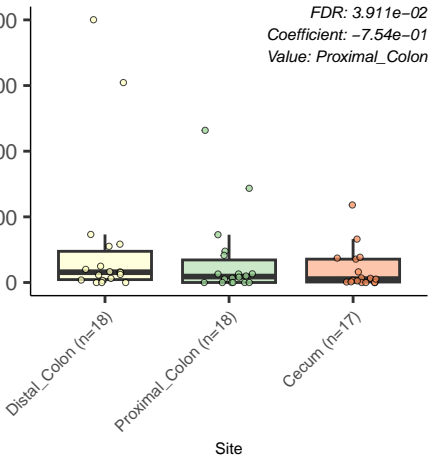


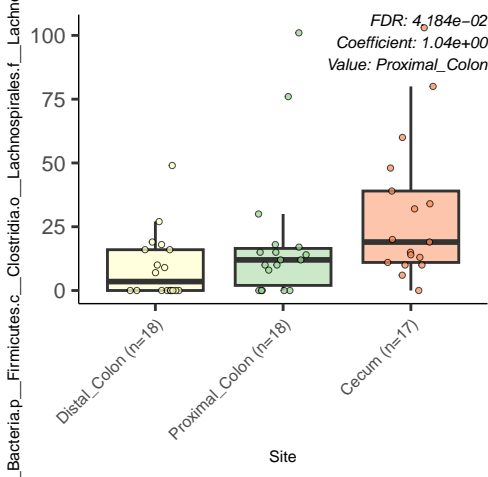






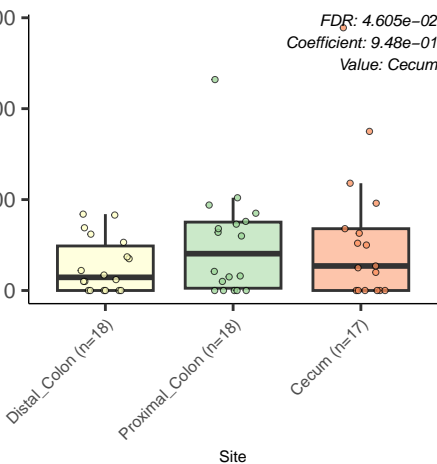
p_Actinobacteriota.c_Actinobacteria.o_Bifidobacteriales.f_Bifidobacteri



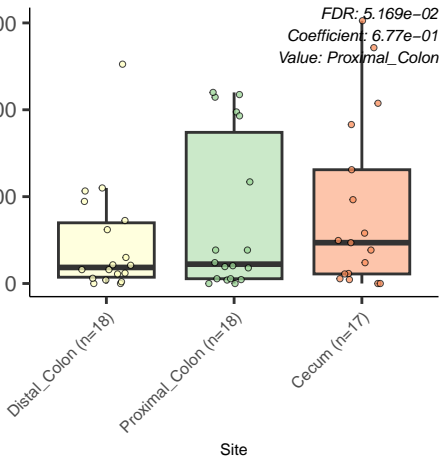


Firmicutes.c__Clostridia.o__Lachnospirales.f__Lachnospiraceae.g

FDR: $4.605e-02$
Coefficient: $9.48e-01$
Value: Cecum



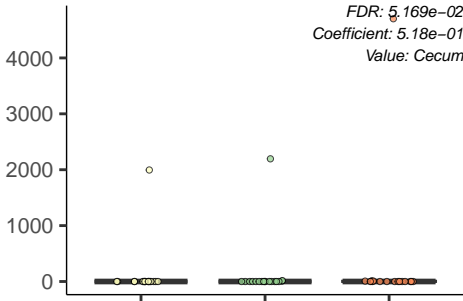
ia.p__Actinobacteriota.c__Coriobacteriia.o__Coriobacteriales.f__Eg

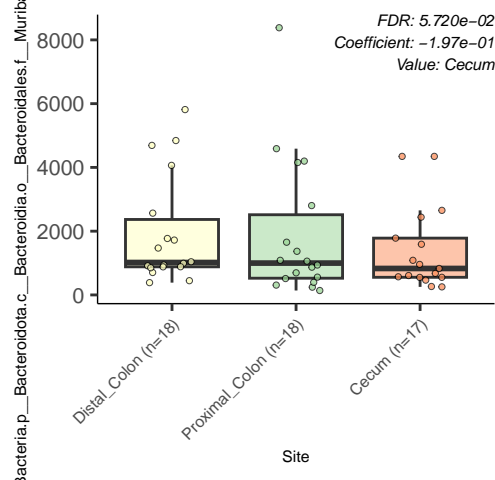


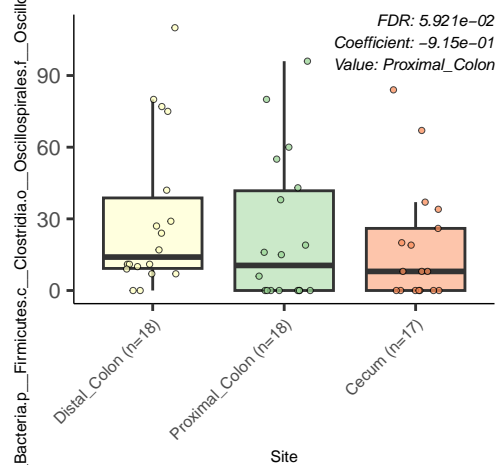
Cecum (n=17)

Site

FDR: 5.169e-02
Coefficient: 5.18e-01
Value: Cecum

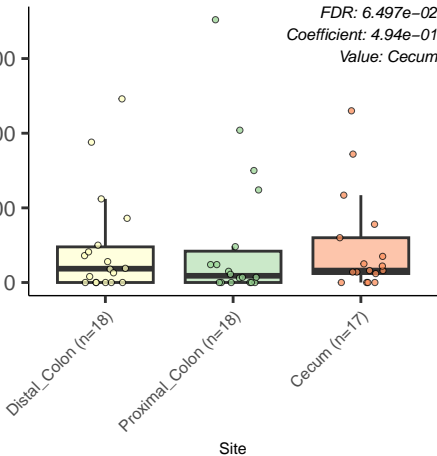


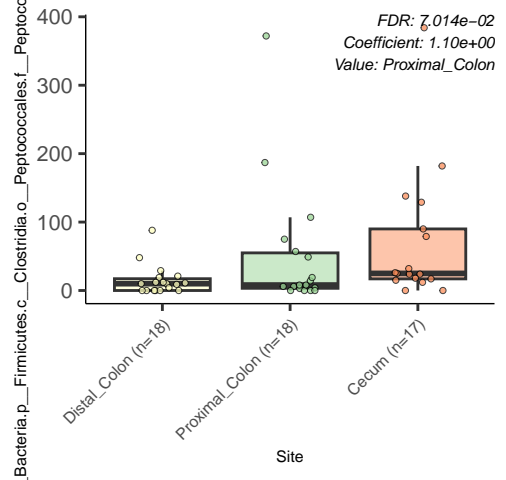




Bacteria.p_Firmicutes.c_Clostridia.o_Monoglobales.f_Monog

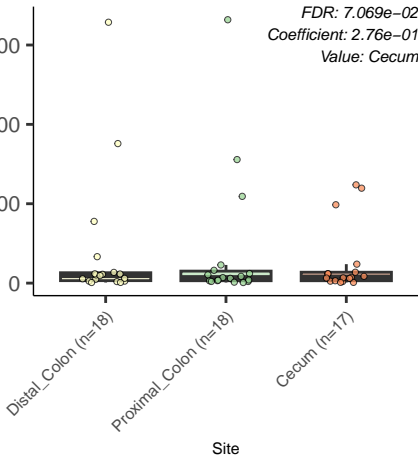
FDR: $6.497e-02$
Coefficient: $4.94e-01$
Value: Cecum

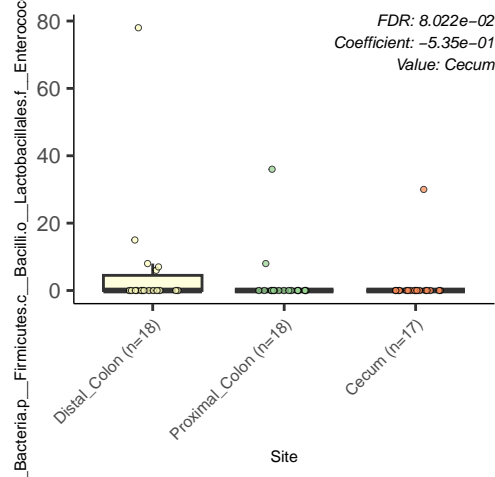




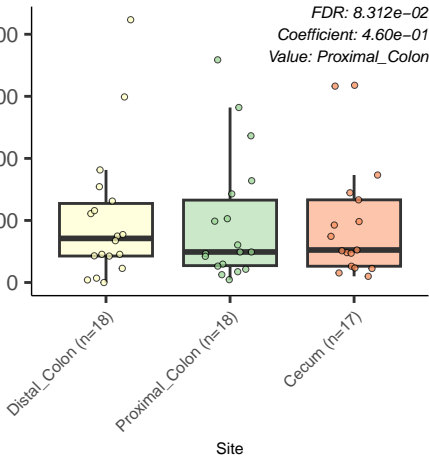
Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobac

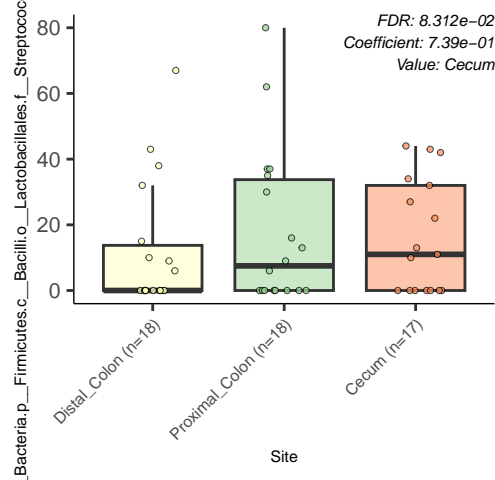
FDR: 7.069×10^{-2}
Coefficient: 2.76×10^{-1}
Value: Cecum

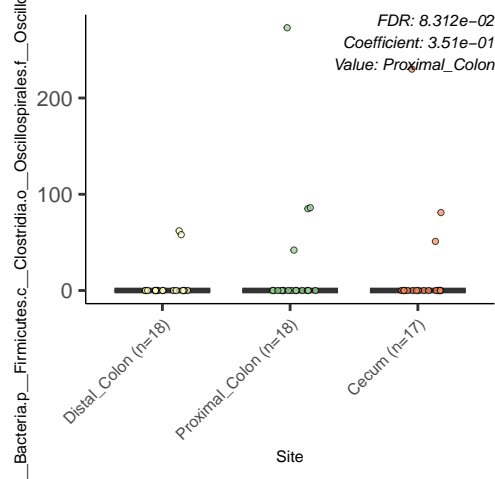


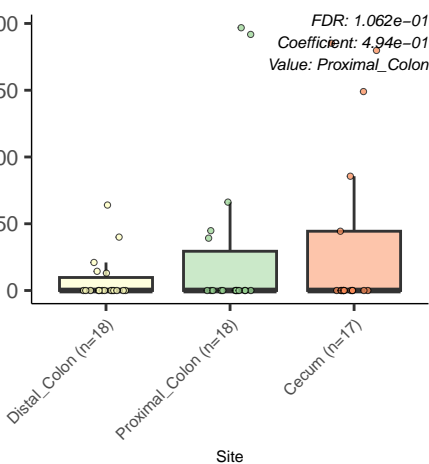


bacteria.p__Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Tanner



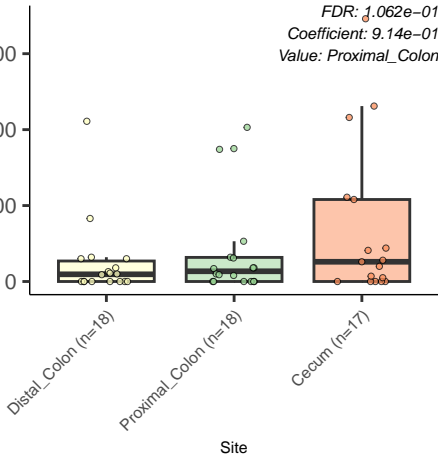


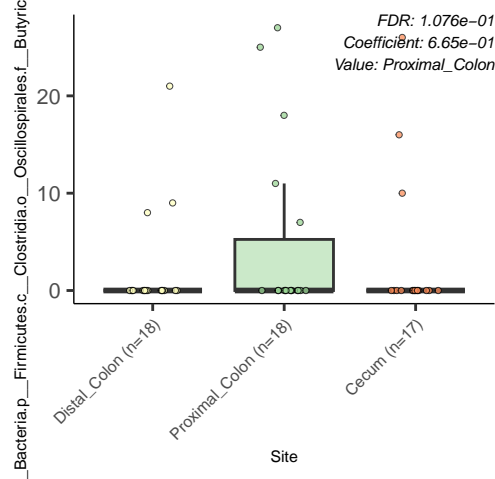




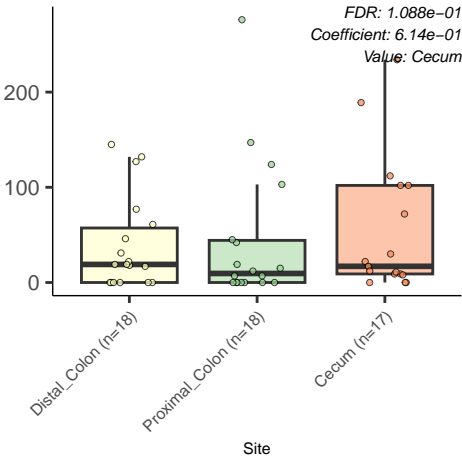
p_Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminococcaceae

FDR: $1.062e-01$
Coefficient: $9.14e-01$
Value: Proximal_Colon



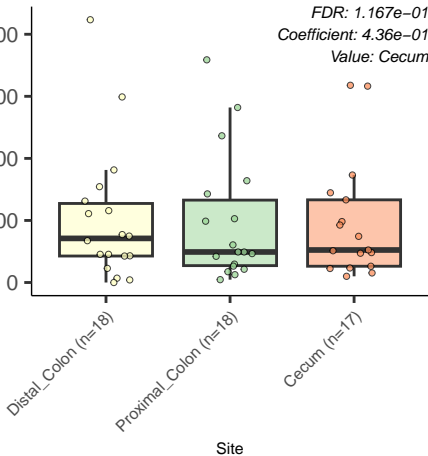


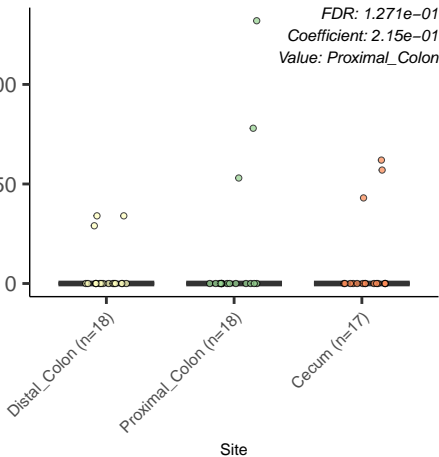
utes.c__Clostridia.o__Peptostreptococcales.Tissierellales.f__Anaerob

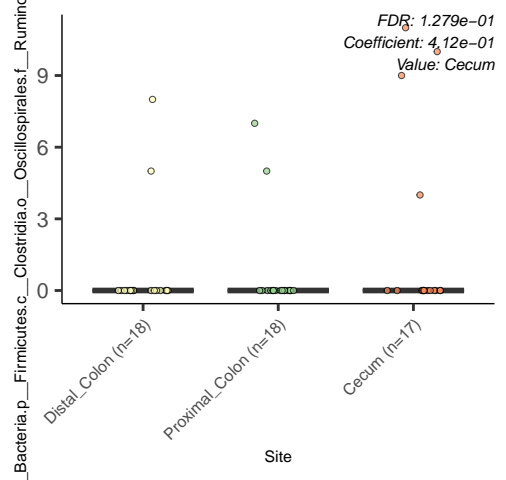


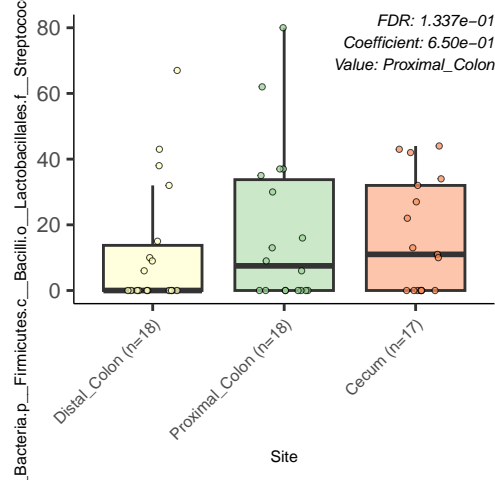
Bacteria.p_Bacteroidota.c_Bacteroidia.o_Bacteroidales.f_Tanner

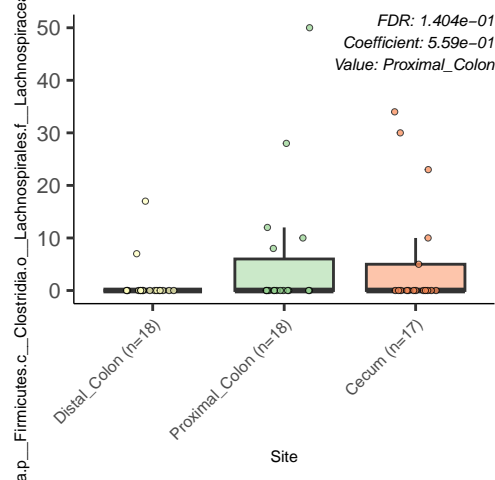
FDR: 1.167e-01
Coefficient: 4.36e-01
Value: Cecum

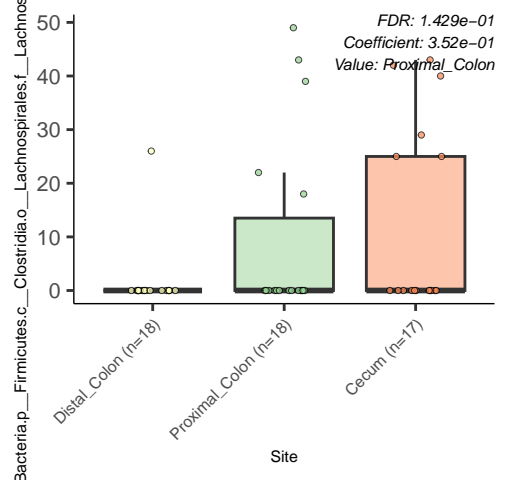


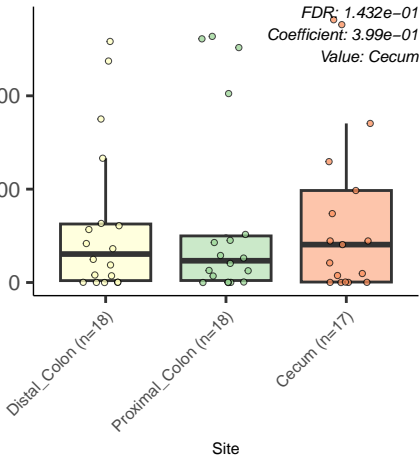




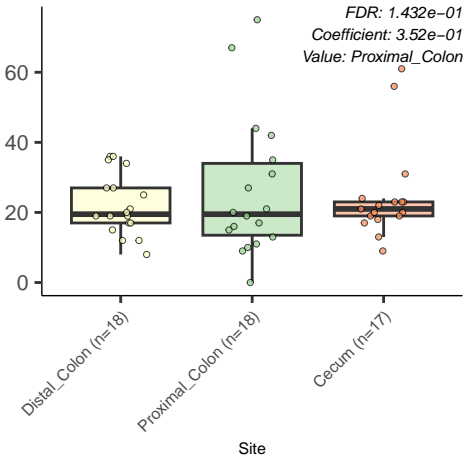


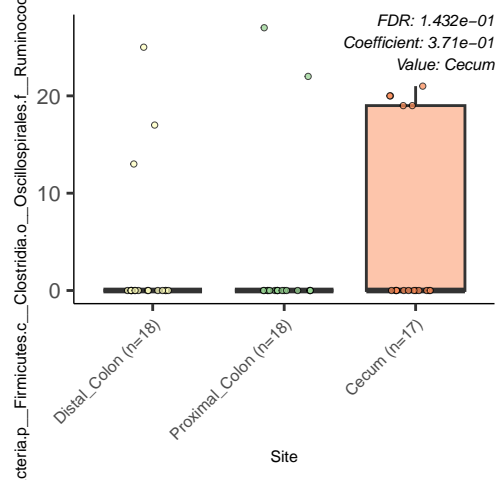


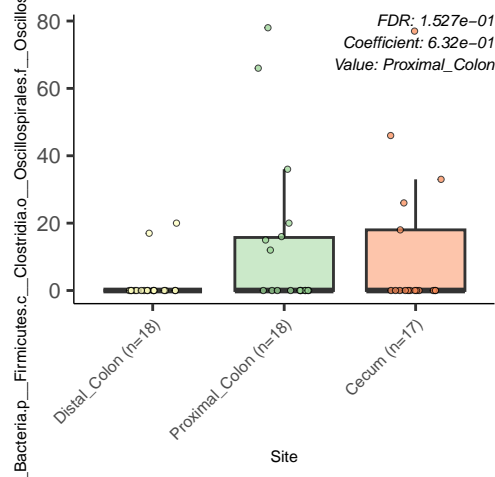


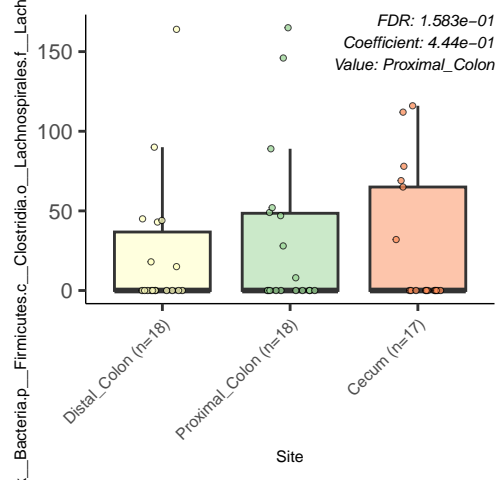


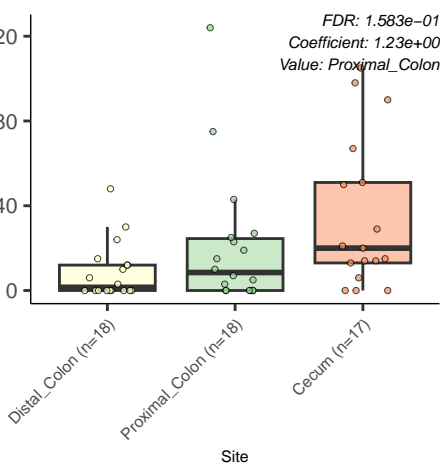
acteria.p__Firmicutes.c__Clostridia.o__Clostridiales.f__Clostridiaceae

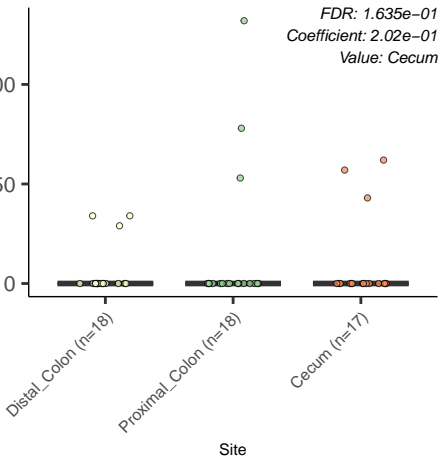


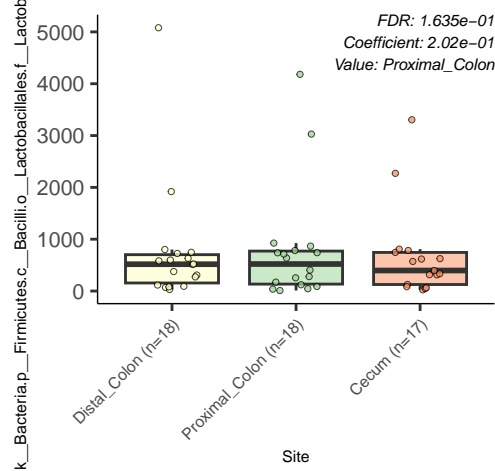


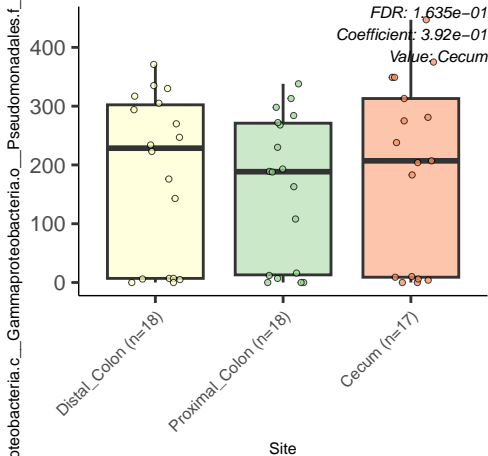


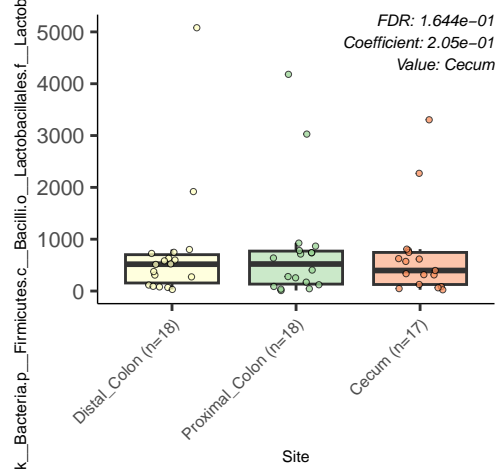


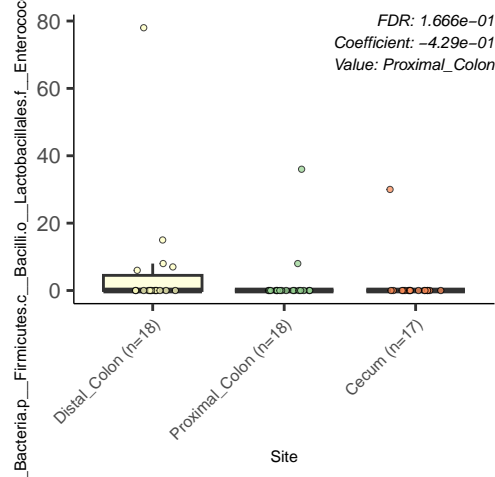






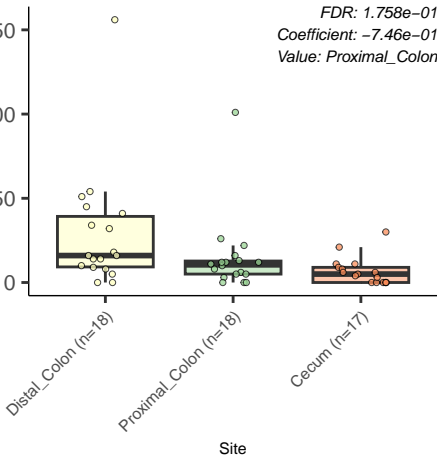


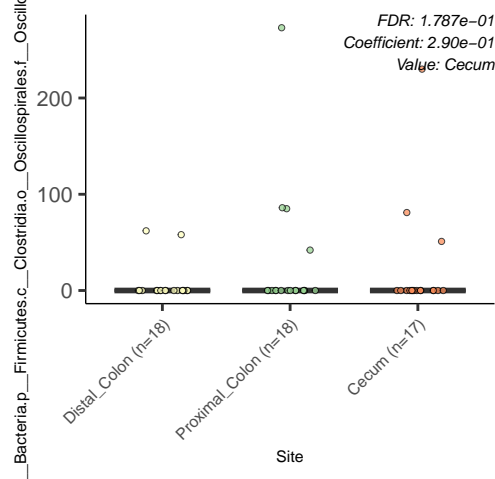


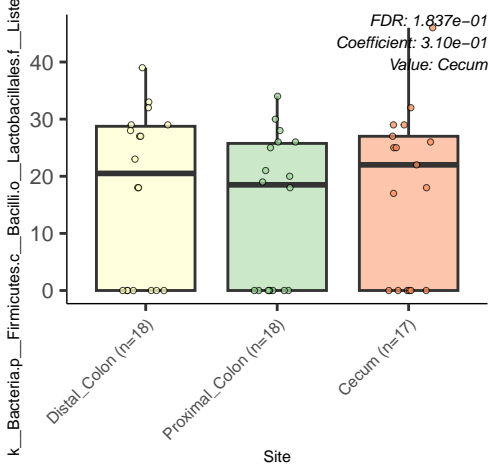


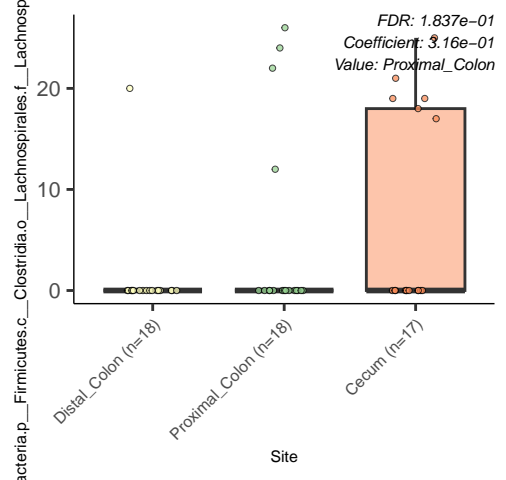
k_Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rho

FDR: 1.758e-01
Coefficient: -7.46e-01
Value: Proximal_Colon



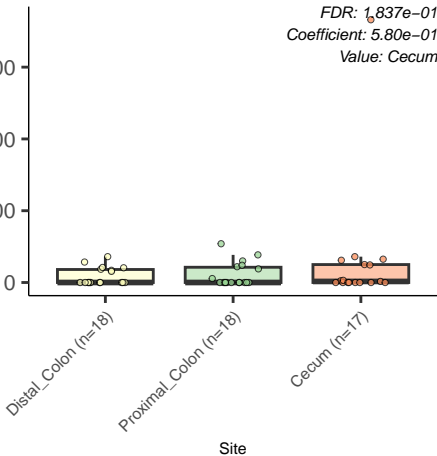






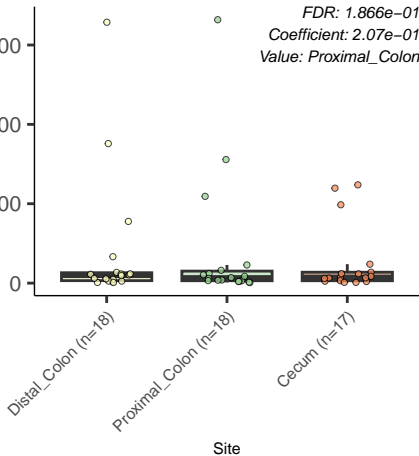
oteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Ent

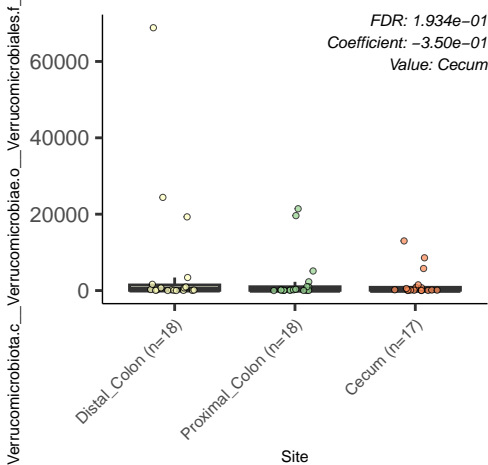
FDR: $1.837e-01$
Coefficient: $5.80e-01$
Value: Cecum



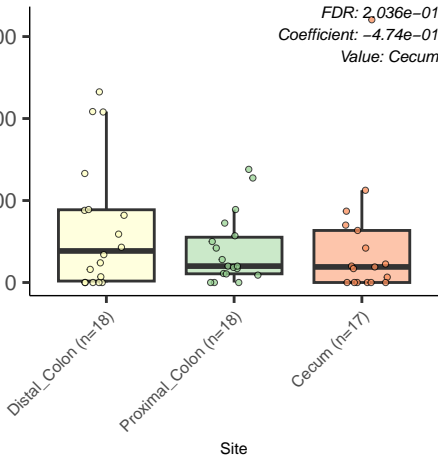
Bacteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobac

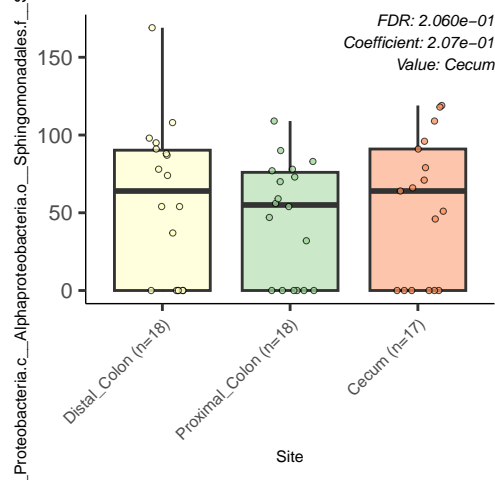
FDR: 1.866e-01
Coefficient: 2.07e-01
Value: Proximal_Colon

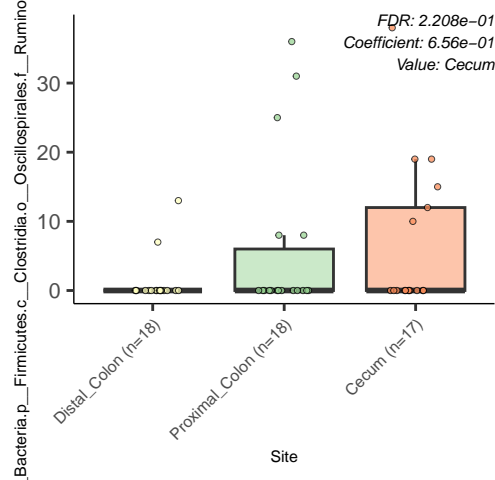




acteria.p__Firmicutes.c__Clostridia.o__Oscillospirales.f__Ruminoc







k_Bacteria.p__Cyanobacteria.c__Vampirivibrionia.o__Gastrana

FDR: 2.396e-01
Coefficient: 6.32e-01
Value: Proximal_Colon

