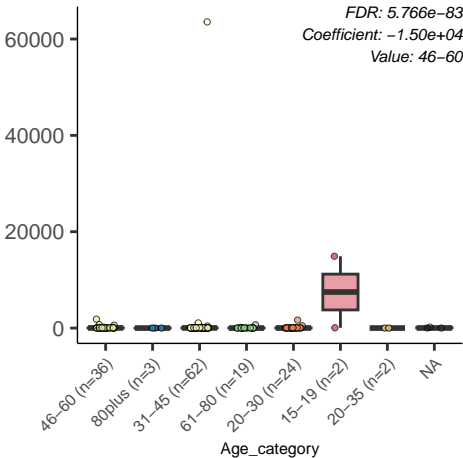
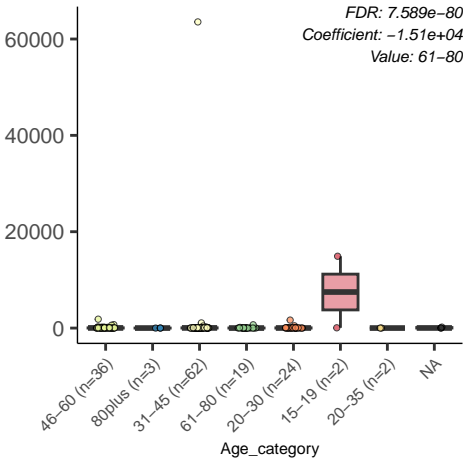
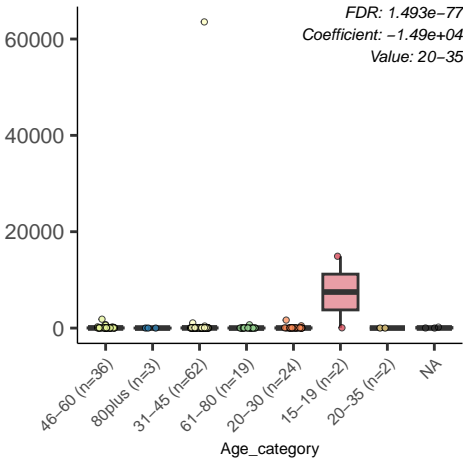


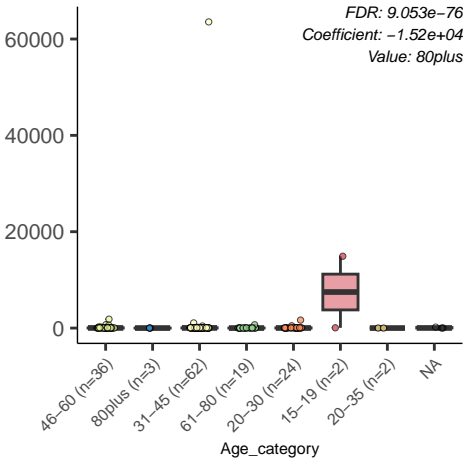
teobacteria.c__Betaproteobacteria.o__Neisseriales.f__Neisseriaceae



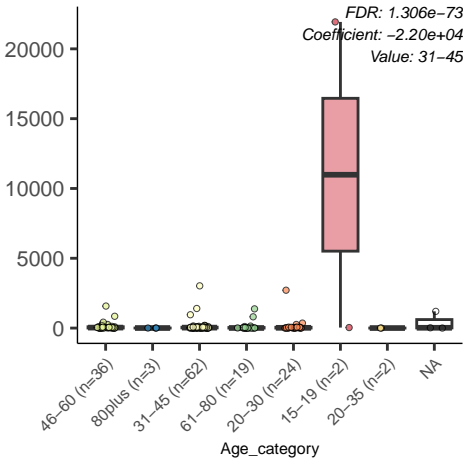


teobacteria.c__Betaproteobacteria.o__Neisseriales.f__Neisseriaceae

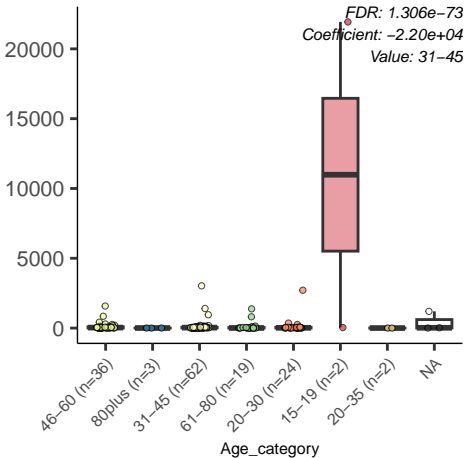


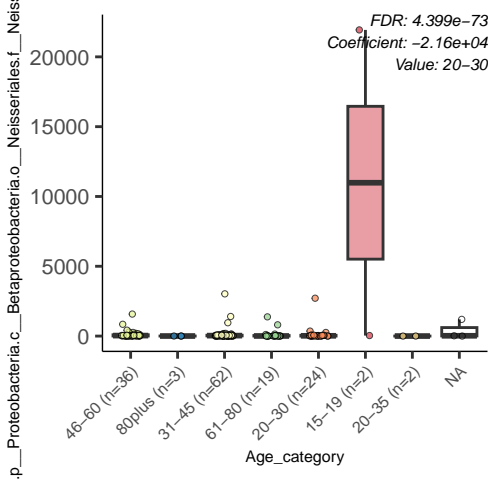


.p__Proteobacteria.c__Betaproteobacteria.o__Neisseriales.f__Neis

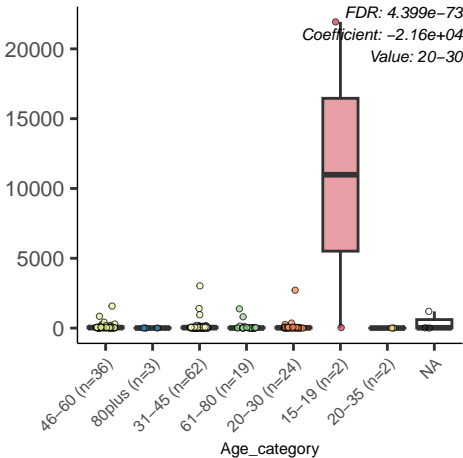


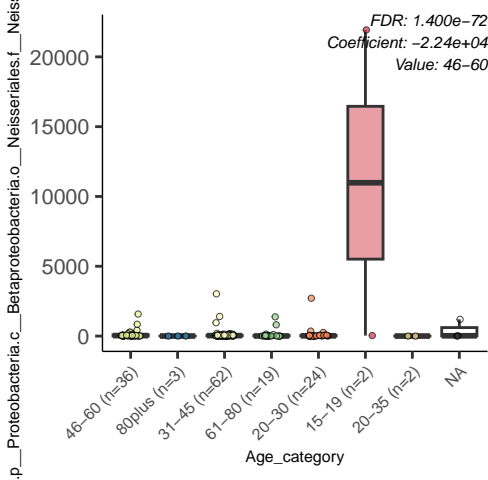
bacteria.c__Betaproteobacteria.o__Neisseriales.f__Neisseriaceae.g

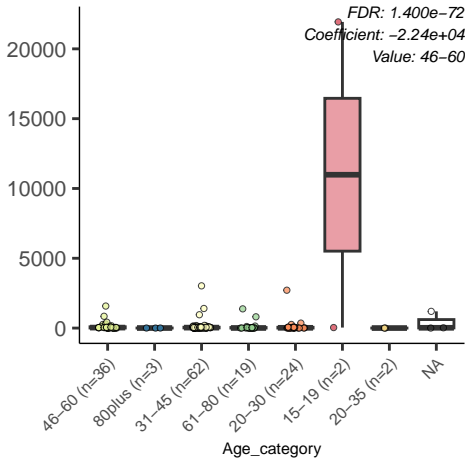




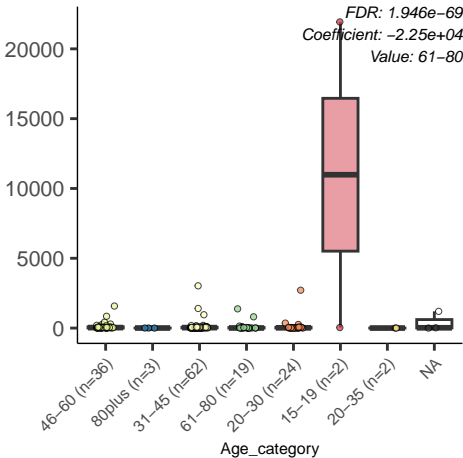
bacteria.c__Betaproteobacteria.o__Neisseriales.f__Neisseriaceae.g



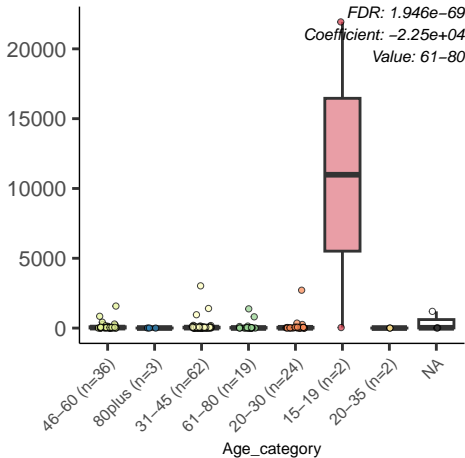


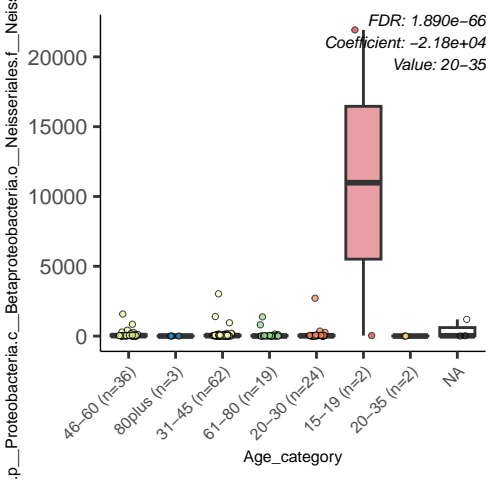


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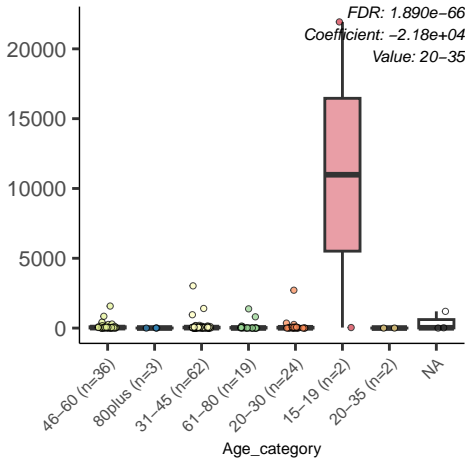


bacteria.c__Betaproteobacteria.o__Neisseriales.f__Neisseriaceae.g

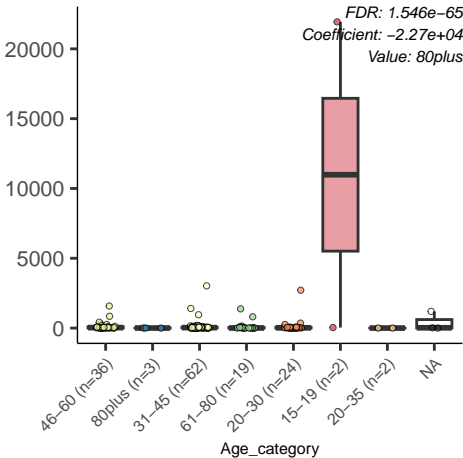




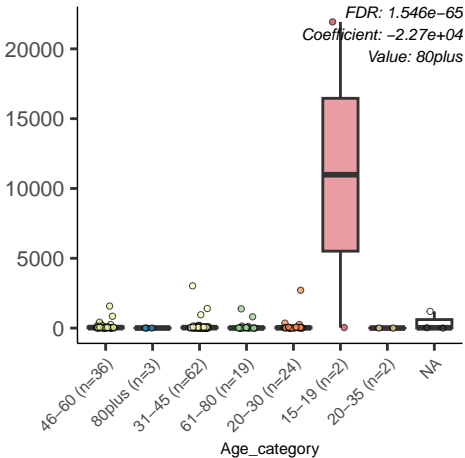
bacteria.c__Betaproteobacteria.o__Neisseriales.f__Neisseriaceae.g

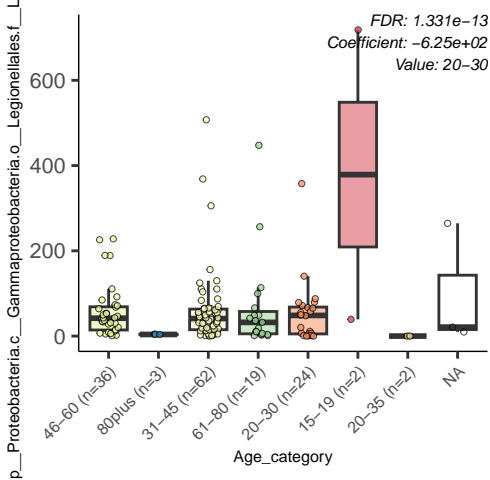


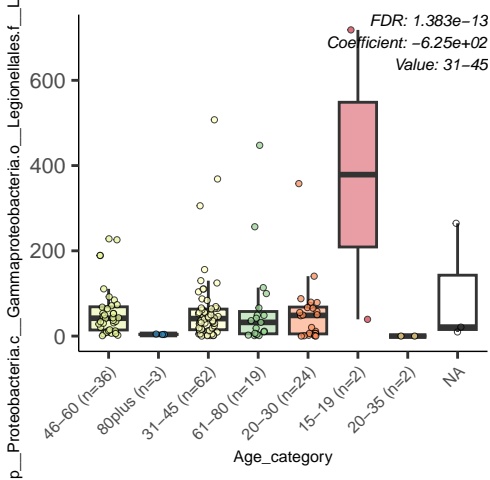
p__Proteobacteria.c__Betaproteobacteria.o__Neisseriales.f__Neis

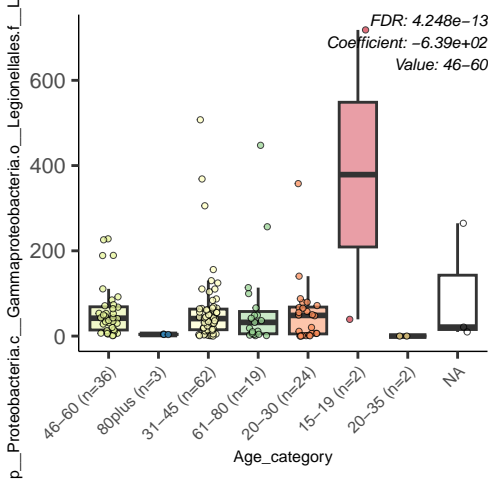


bacteria.c__Betaproteobacteria.o__Neisseriales.f__Neisseriaceae.g

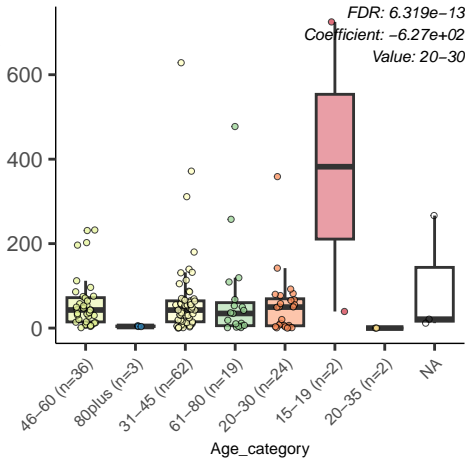




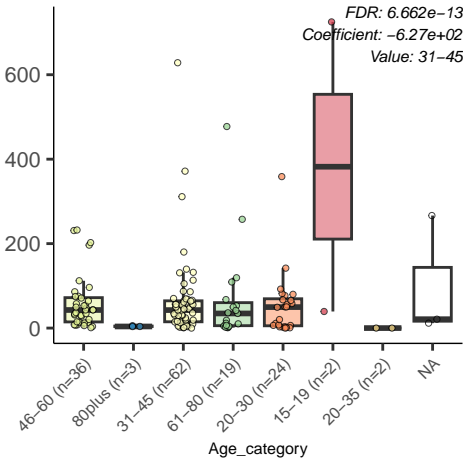


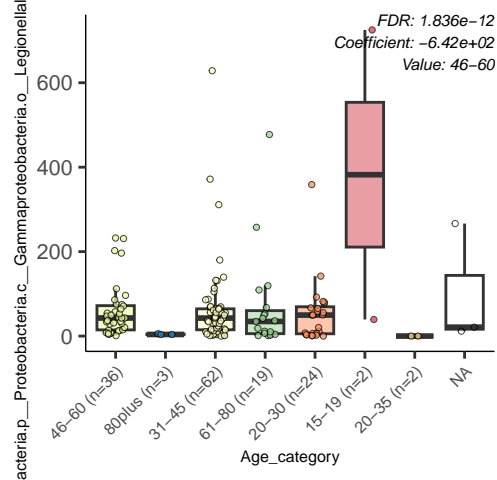


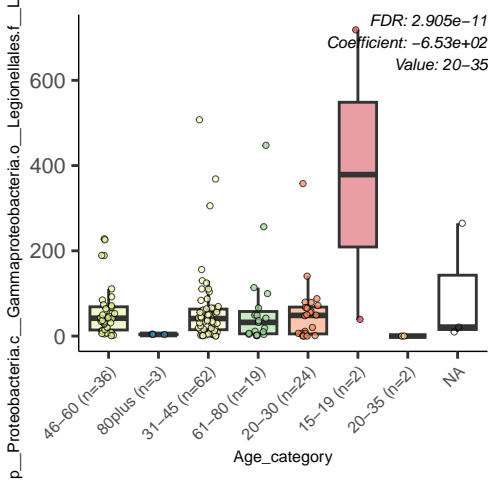
acteria.p__Proteobacteria.c__Gammaproteobacteria.o__Legionella

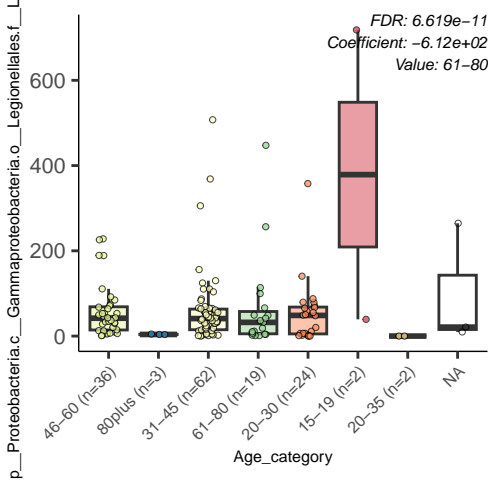


acteria.p__Proteobacteria.c__Gammaproteobacteria.o__Legionella

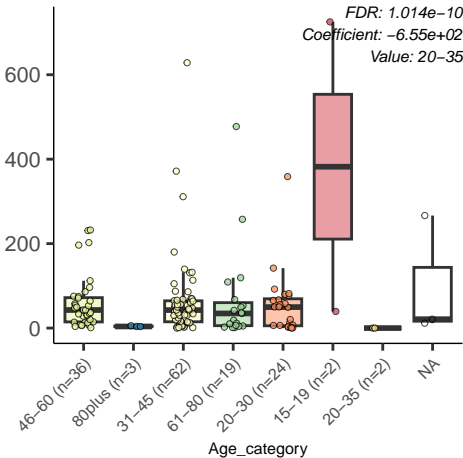


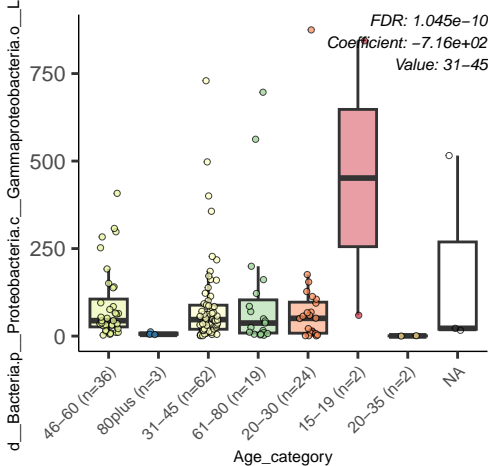


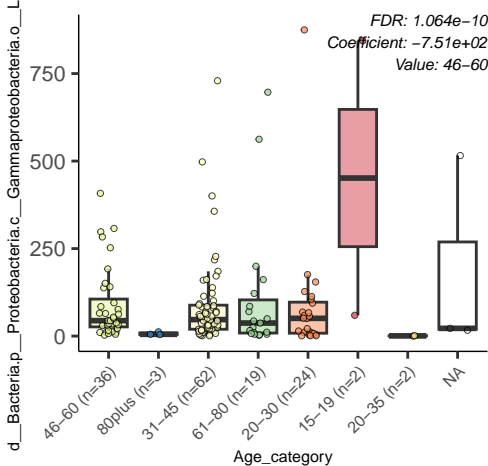


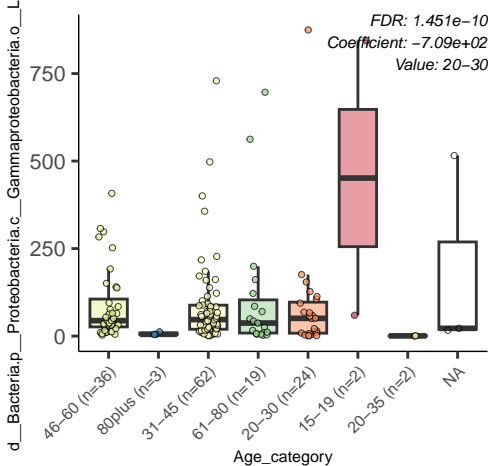


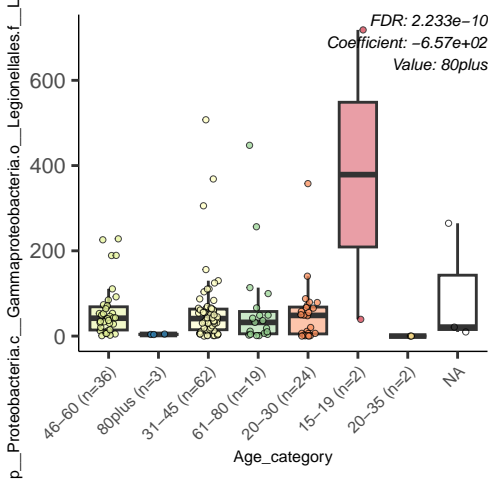
acteria.p__Proteobacteria.c__Gammaproteobacteria.o__Legionella



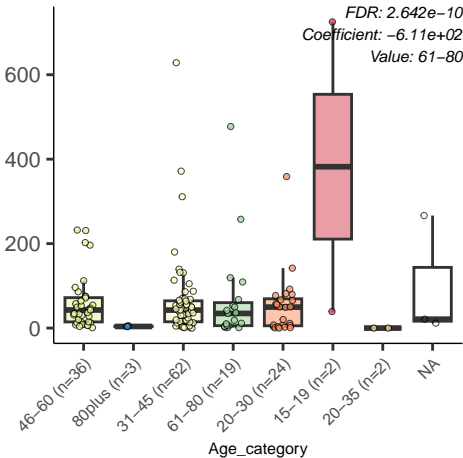




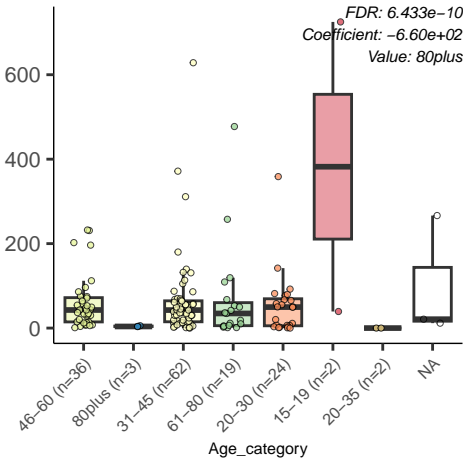


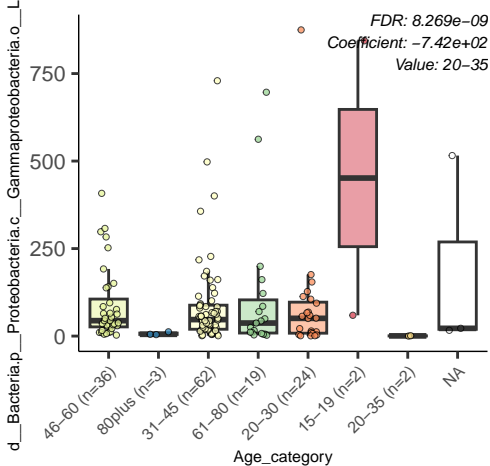


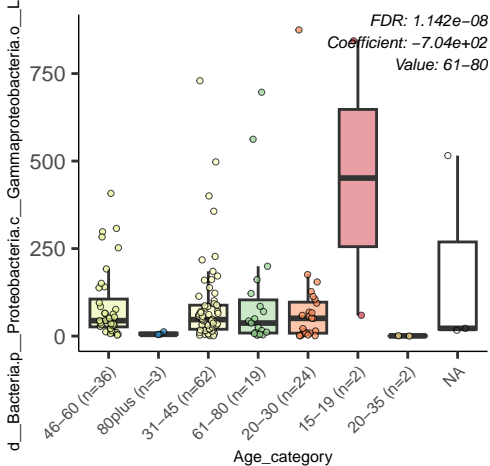
acteria.p__Proteobacteria.c__Gammaproteobacteria.o__Legionella

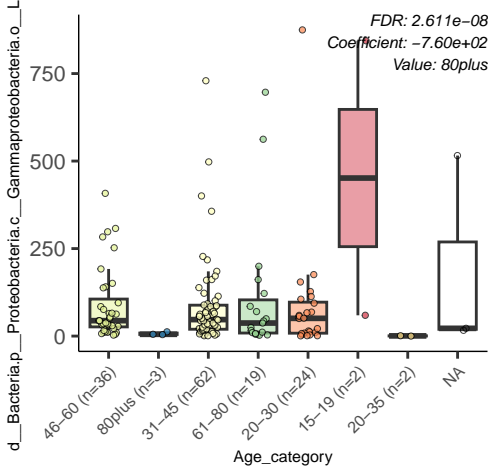


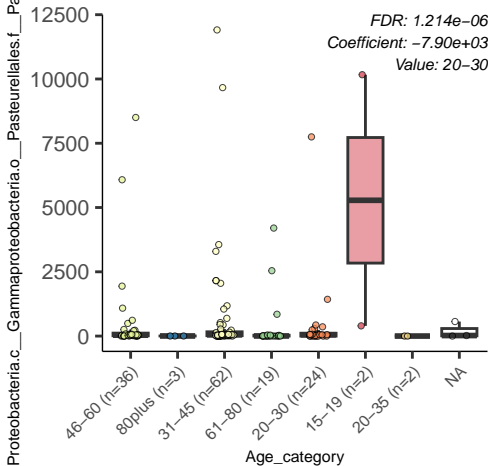
acteria.p__Proteobacteria.c__Gammaproteobacteria.o__Legionella

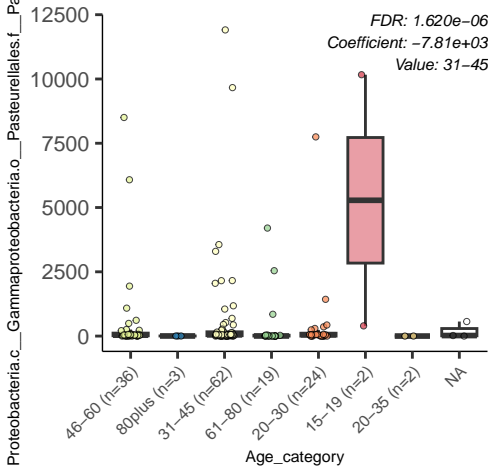


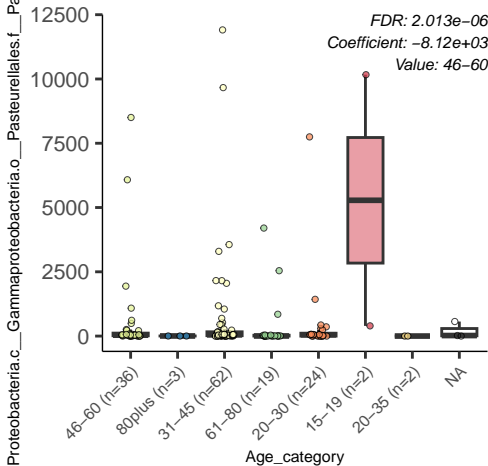






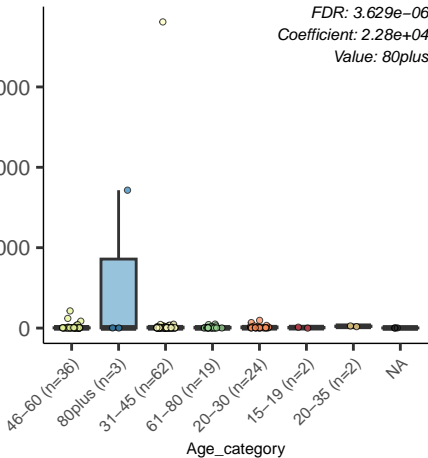


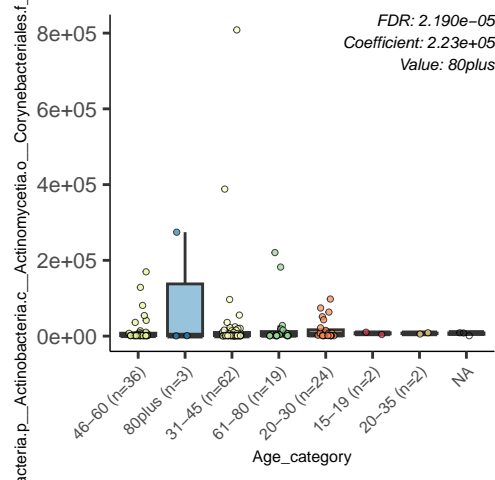




Actinomycetia.o__Corynebacteriales.f__Corynebacteriaceae.g__C

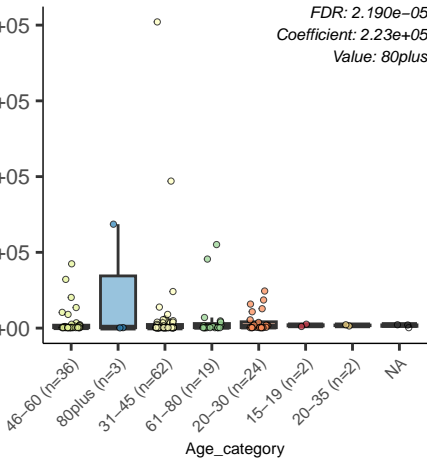
FDR: 3.629e-06
Coefficient: 2.28e+04
Value: 80plus



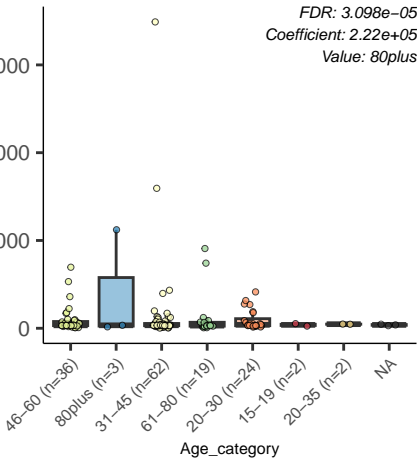


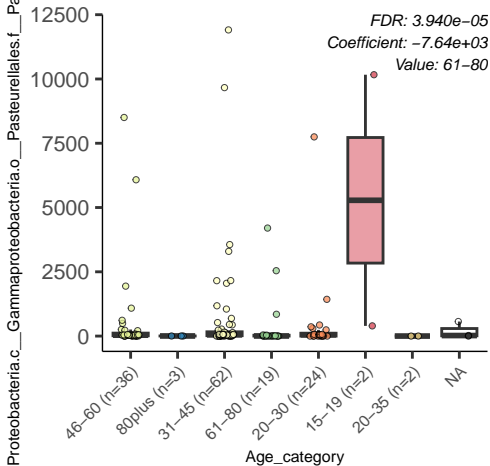
Actinobacteria.c__Actinomycetia.o__Corynebacteriales.f__Coryneb

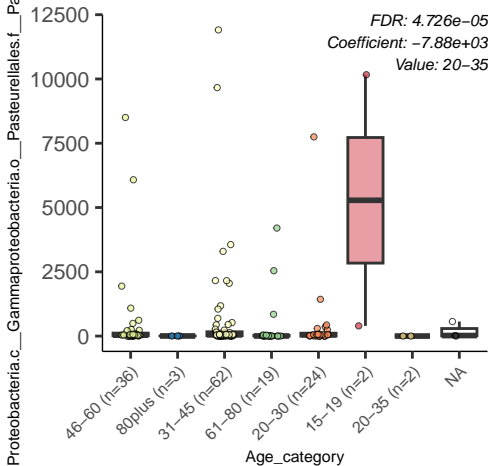
FDR: 2.190e-05
Coefficient: 2.23e+05
Value: 80plus

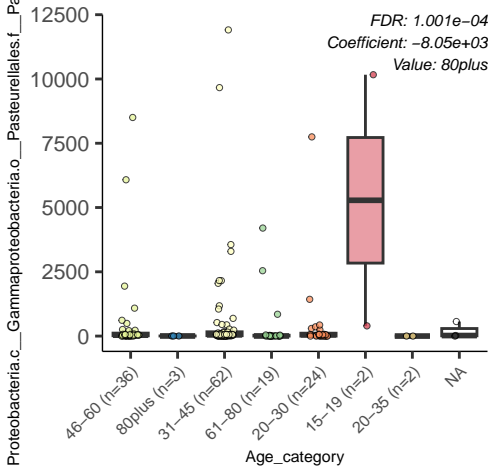


d__Bacteria.p_Actinobacteria.c_Actinomycetia.o_Coryneb

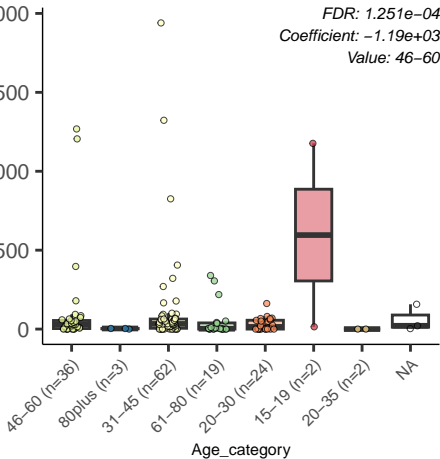




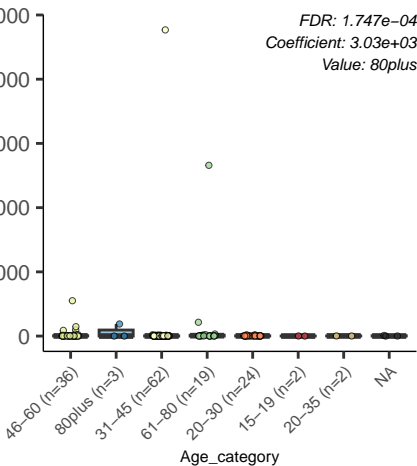




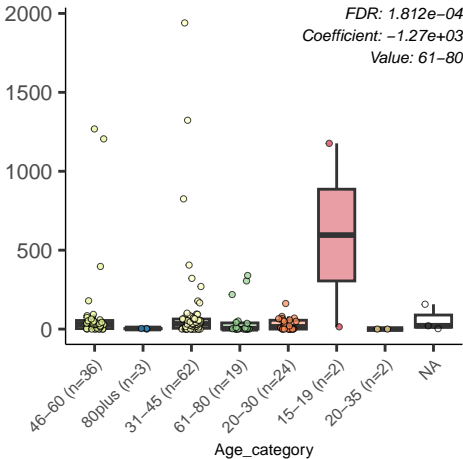
bacteria.c__Betaproteobacteria.o__Neisseriales.f__Neisseriaceae.g



tinomycetia.o__Corynebacteriales.f__Corynebacteriaceae.g__Cory

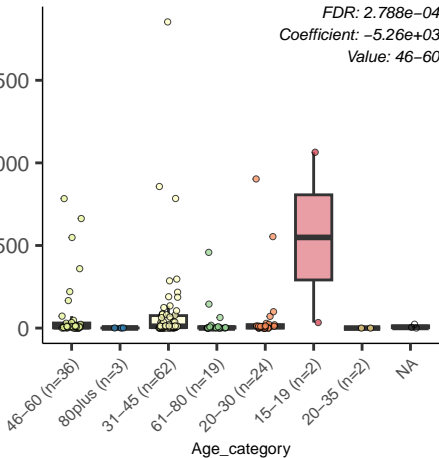


bacteria.c__Betaproteobacteria.o__Neisseriales.f__Neisseriaceae.g



micutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Stre

FDR: $2.788e-04$
Coefficient: $-5.26e+03$
Value: 46-60



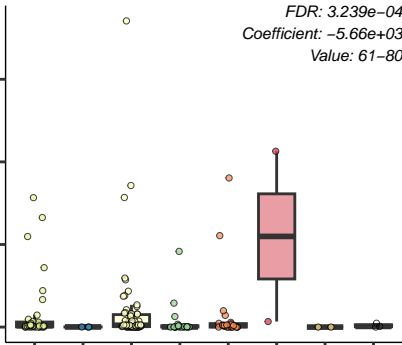
micutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Stre

FDR: 3.239e-04
Coefficient: -5.66e+03
Value: 61-80

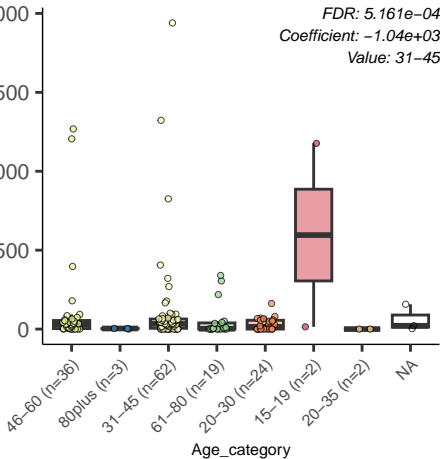
7500
5000
2500
0

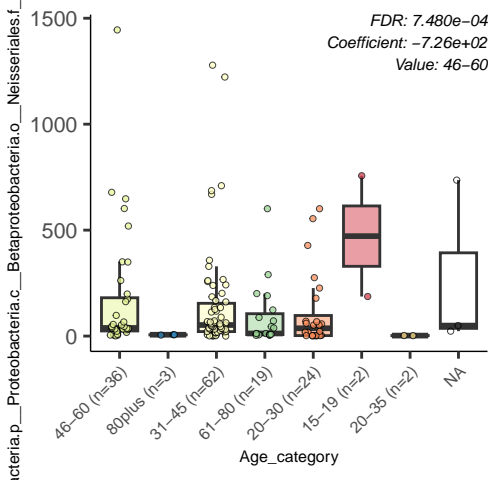
46-60 (n=36)
80plus (n=3)
31-45 (n=62)
61-80 (n=19)
20-30 (n=24)
15-19 (n=2)
20-35 (n=2)
NA

Age_category



bacteria.c__Betaproteobacteria.o__Neisseriales.f__Neisseriaceae.g





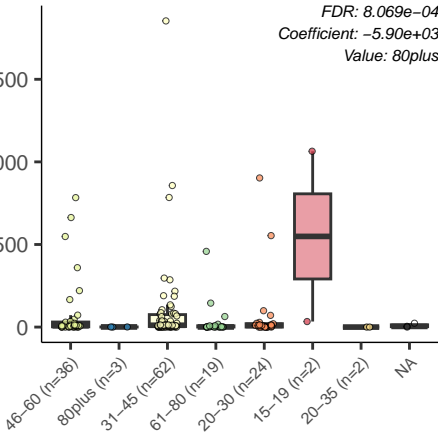
micutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Stre

FDR: 8.069e-04
Coefficient: -5.90e+03
Value: 80plus

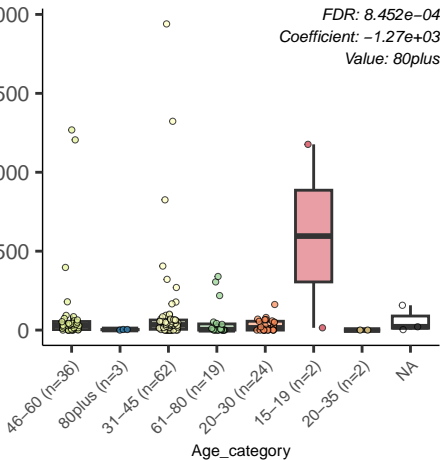
7500
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2500
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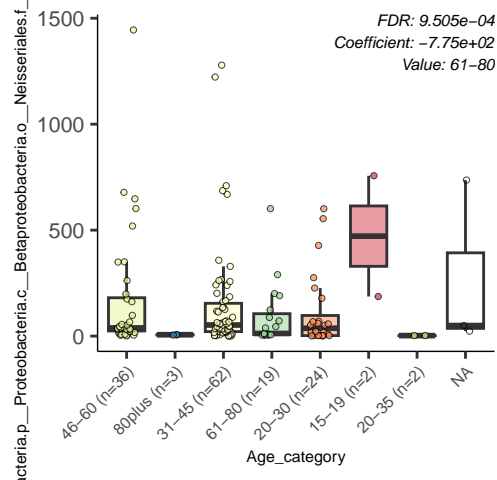
46-60 (n=36)
80plus (n=3)
31-45 (n=62)
61-80 (n=19)
20-30 (n=24)
15-19 (n=2)
20-35 (n=2)
NA

Age_category



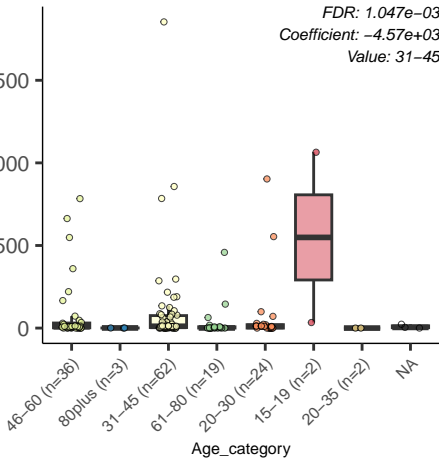
bacteria.c__Betaproteobacteria.o__Neisseriales.f__Neisseriaceae.g



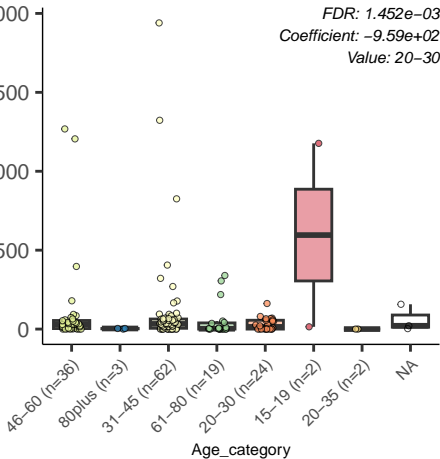


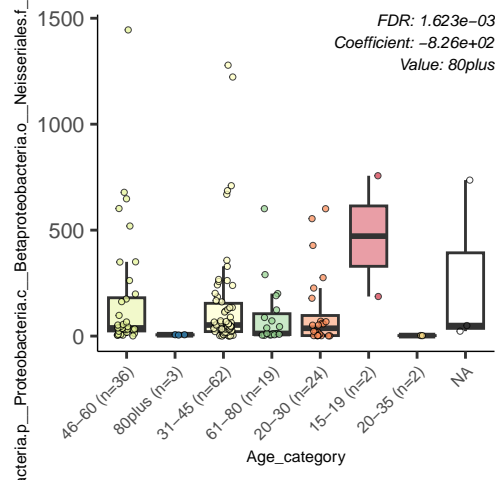
micutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Stre

FDR: $1.047e-03$
Coefficient: $-4.57e+03$
Value: 31-45

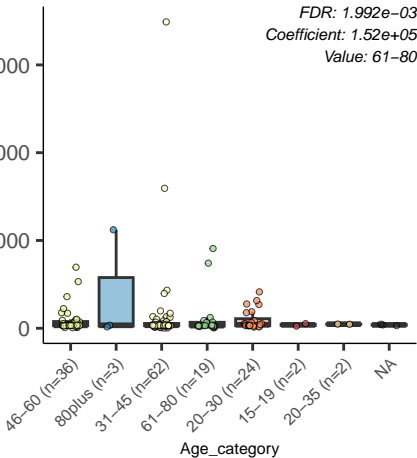


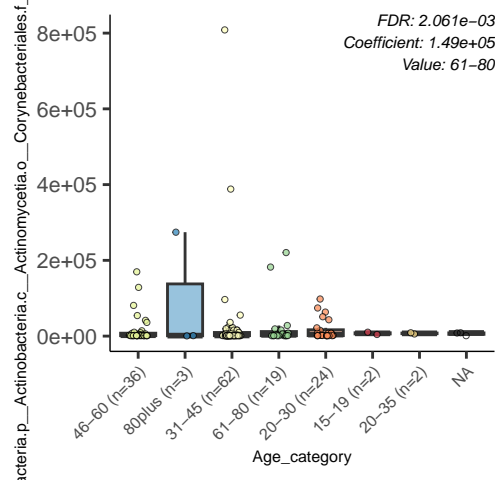
bacteria.c__Betaproteobacteria.o__Neisseriales.f__Neisseriaceae.g

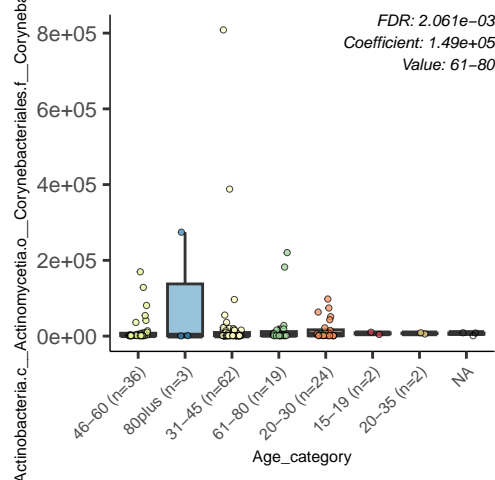


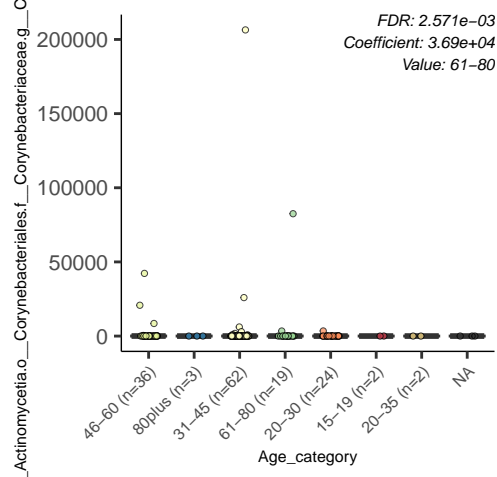


d__Bacteria.p__Actinobacteria.c__Actinomycetia.o__Coryneb



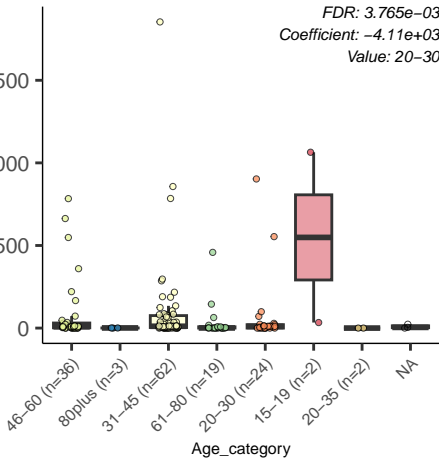




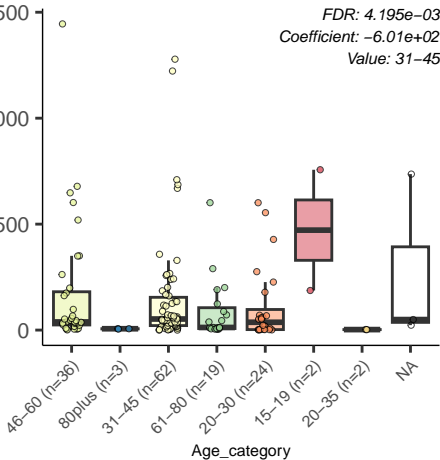


micutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Stre

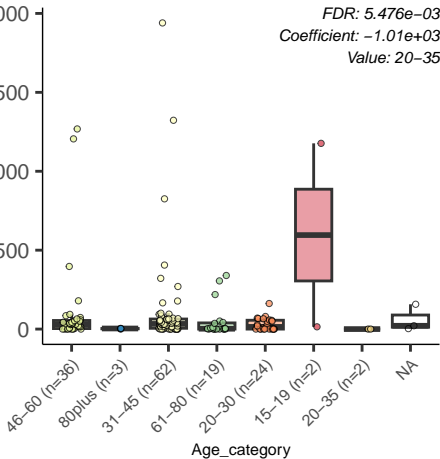
FDR: 3.765e-03
Coefficient: -4.11e+03
Value: 20-30



bacteria.p__Proteobacteria.c__Betaproteobacteria.o__Neisseriales.f

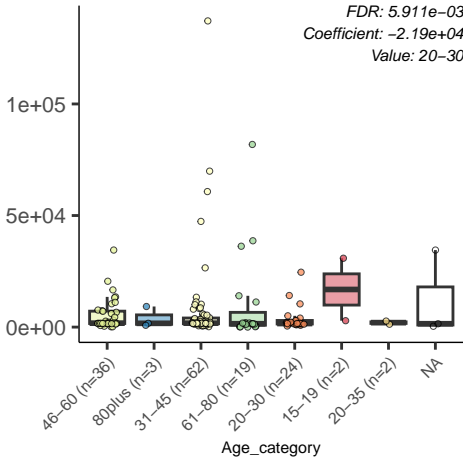


bacteria.c__Betaproteobacteria.o__Neisseriales.f__Neisseriaceae.g



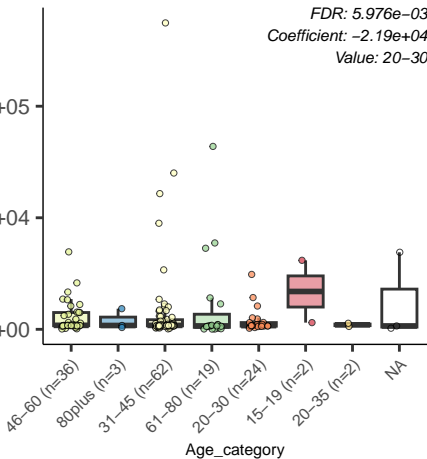
c__Gammaproteobacteria.o__Oceanospirillales.f__Halomonadaceae

FDR: $5.911\text{e-}03$
Coefficient: $-2.19\text{e+}04$
Value: 20-30



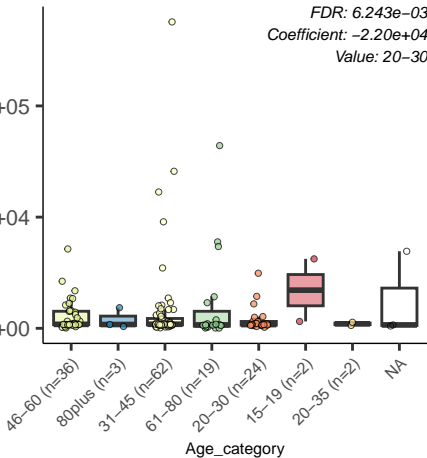
Proteobacteria.c__Gammaproteobacteria.o__Oceanospirillales.f__F

FDR: 5.976e-03
Coefficient: -2.19e+04
Value: 20-30

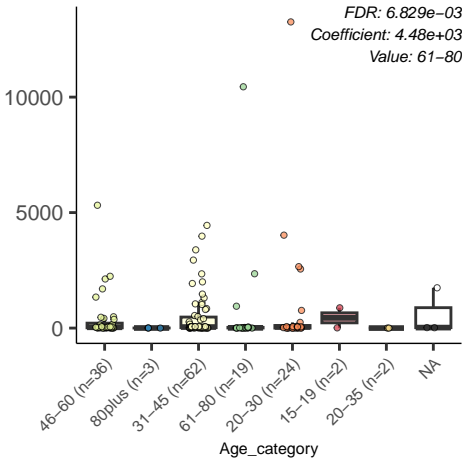


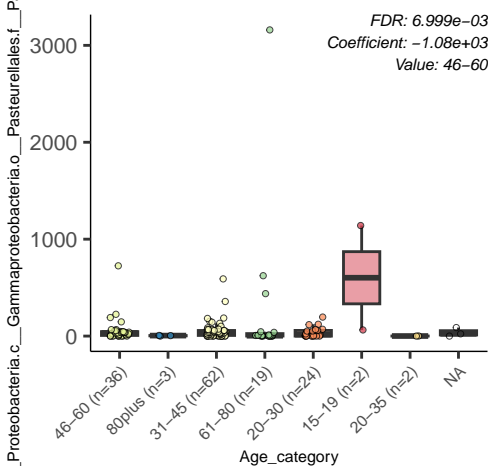
eria.p__Proteobacteria.c__Gammaproteobacteria.o__Oceanospirilla

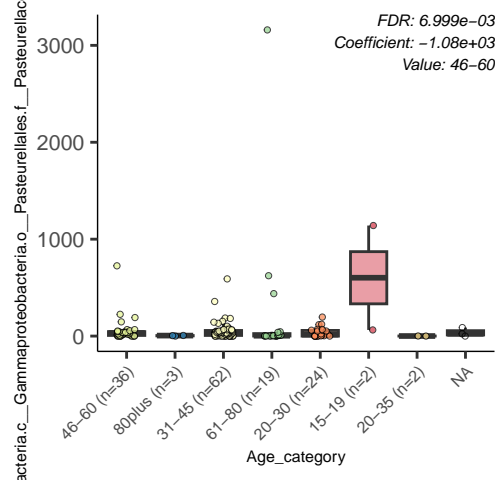
FDR: $6.243e-03$
Coefficient: $-2.20e+04$
Value: 20-30

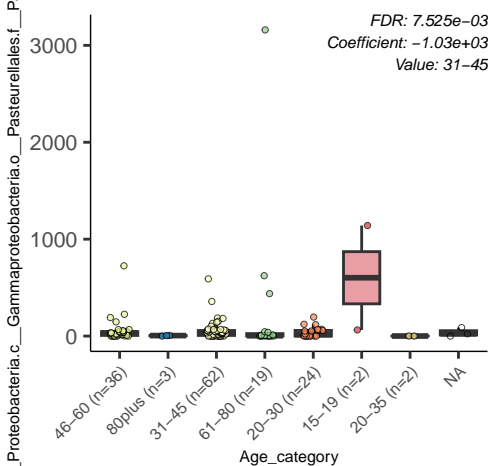


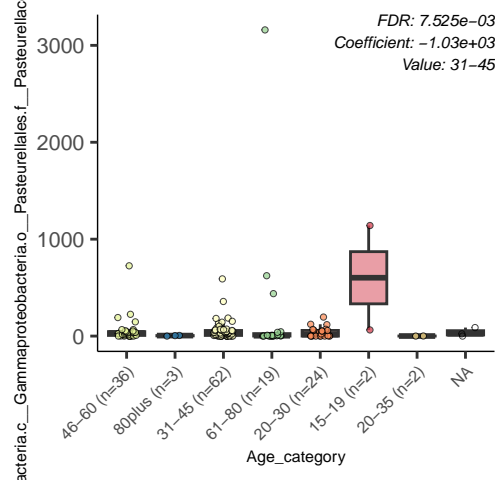
Gamma__Gammaproteobacteria.o__Cardiobacteriales.f__Cardiobacteriaceae





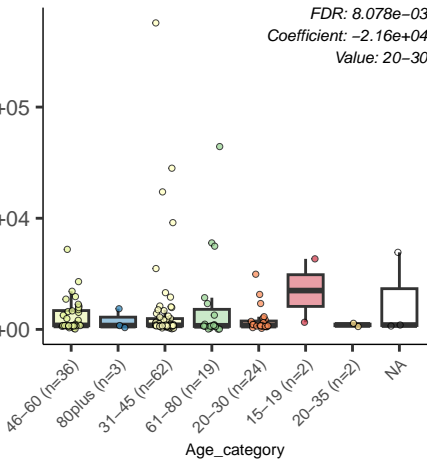


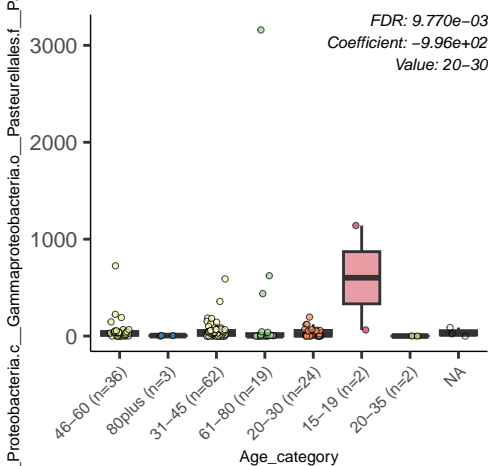


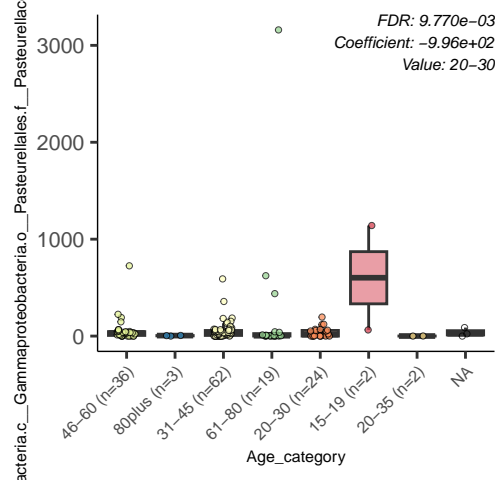


d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Oscillatoriales

FDR: $8.078e-03$
Coefficient: $-2.16e+04$
Value: 20-30

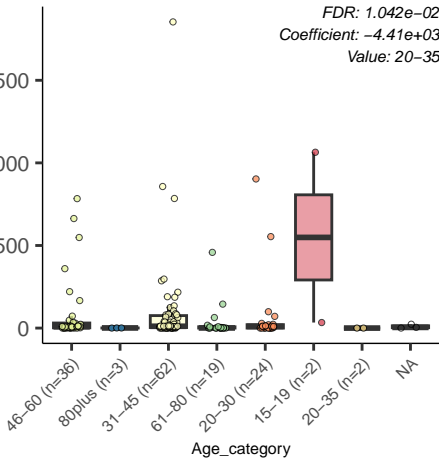




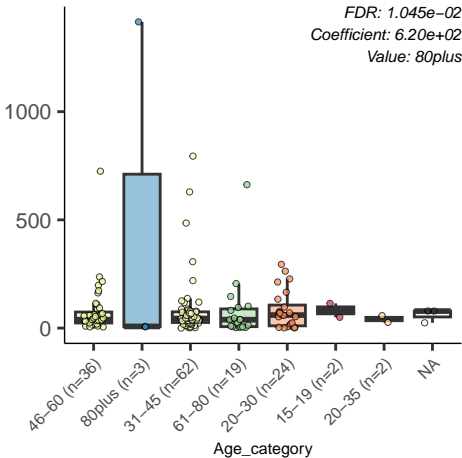


micutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Stre

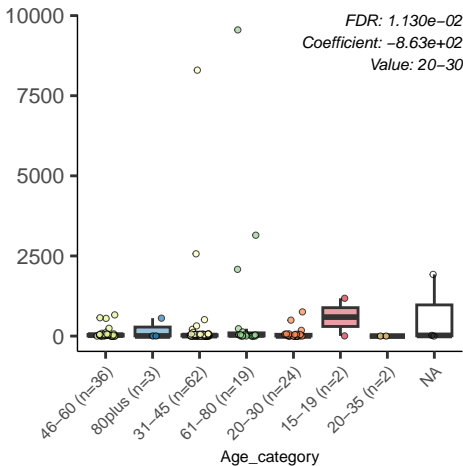
FDR: $1.042e-02$
Coefficient: $-4.41e+03$
Value: 20-35

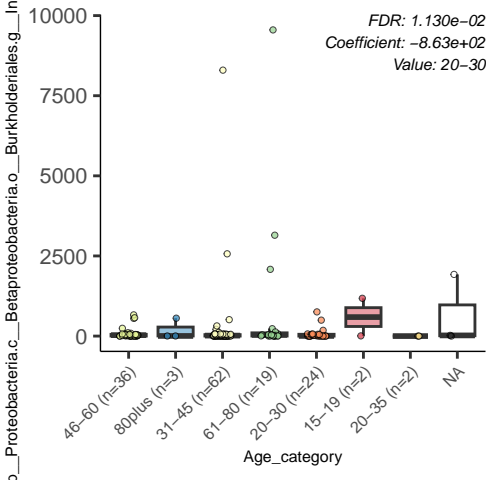


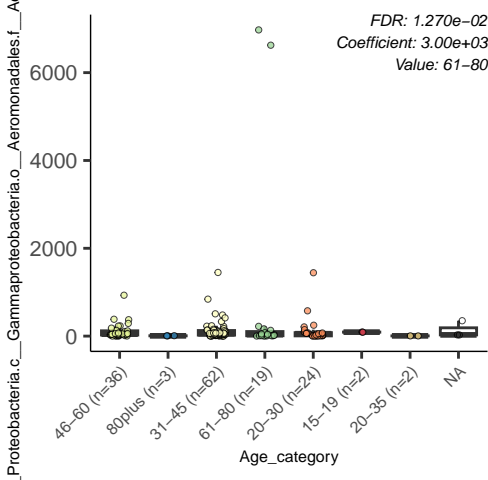
.c__Actinomycetia.o__Candidatus.Nanopelagiales.f__Candidatus.

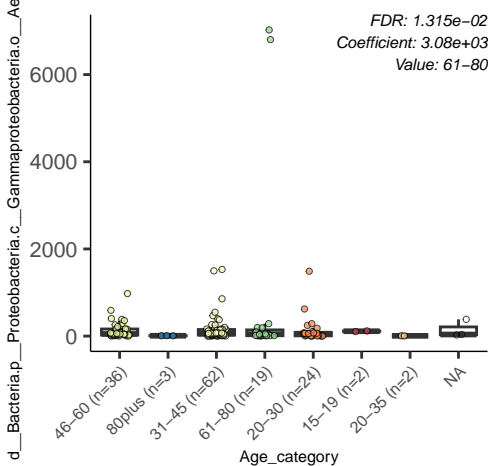


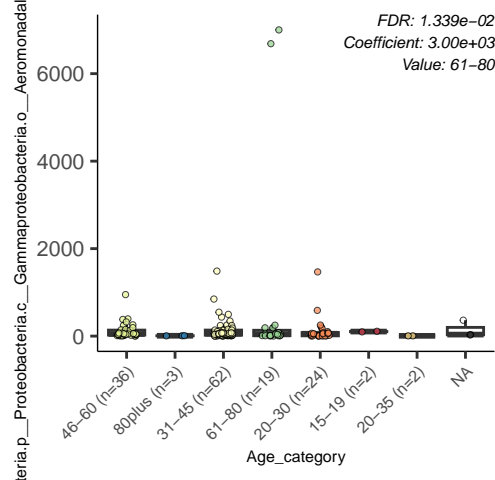
l_Bacteria.p__Proteobacteria.c__Betaproteobacteria.o__Burkholder





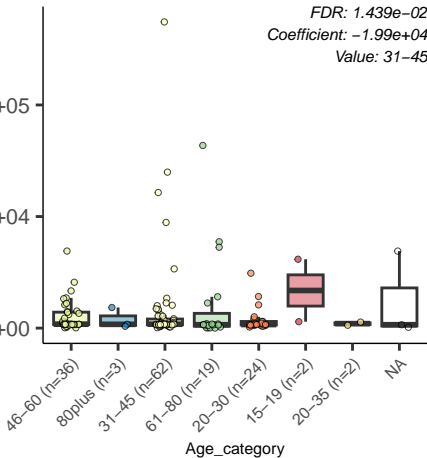




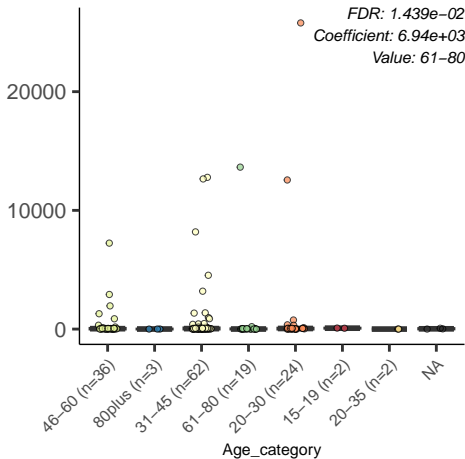


c__Gammaproteobacteria.o__Oceanospirillales.f__Halomonadaceae

FDR: $1.439\text{e-}02$
Coefficient: $-1.99\text{e+}04$
Value: 31-45

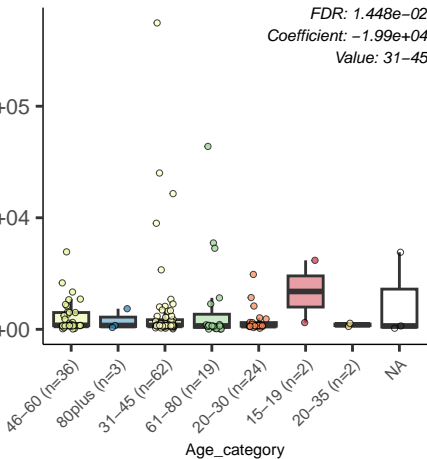


Epsilonproteobacteria.o__Campylobacterales.f__Campylobacteraceae



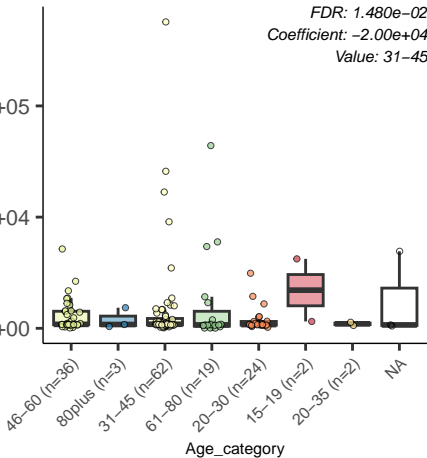
Proteobacteria.c__Gammaproteobacteria.o__Oceanospirillales.f__F

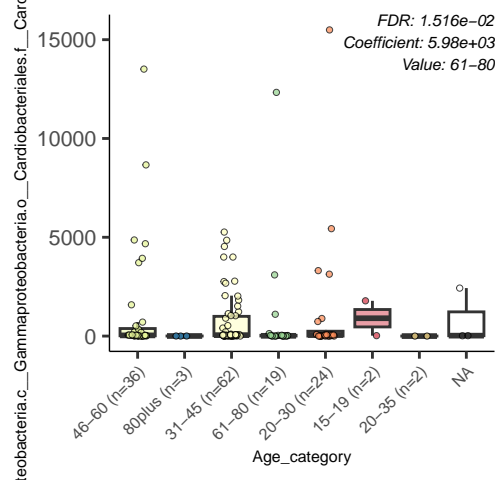
FDR: 1.448×10^{-2}
Coefficient: -1.99×10^4
Value: 31-45

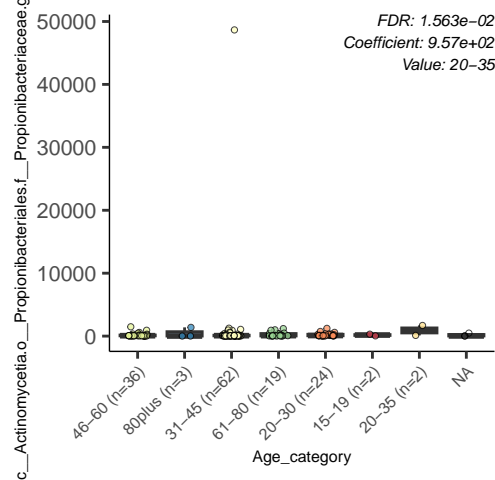


eria.p__Proteobacteria.c__Gammaproteobacteria.o__Oceanospirilla

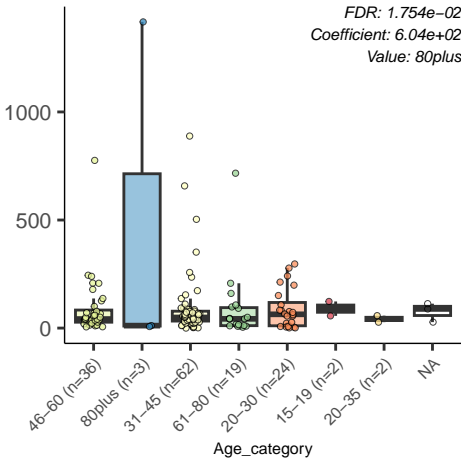
FDR: $1.480e-02$
Coefficient: $-2.00e+04$
Value: 31-45







d_Bacteria.p_Actinobacteria.c_Actinomycetia.o_Candidatus.N



FDR: $1.754e-02$
Coefficient: $6.04e+02$
Value: 80plus

1000

500

0

46-60 (n=36)

80plus (n=3)

31-45 (n=62)

61-80 (n=19)

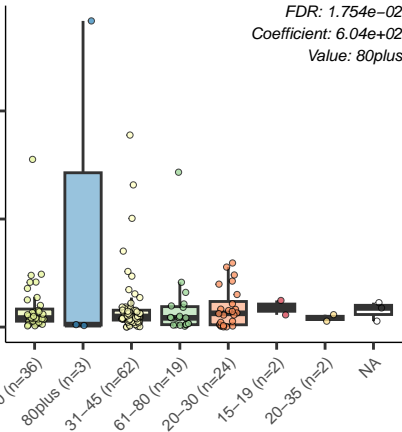
20-30 (n=24)

15-19 (n=2)

20-35 (n=2)

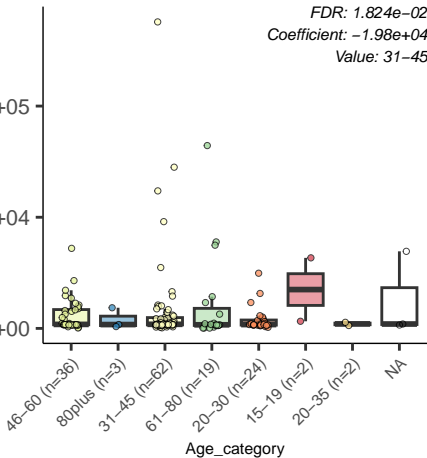
NA

Age_category



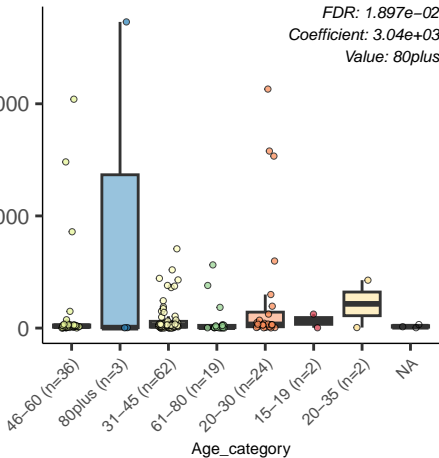
d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Oscillatoriales

FDR: $1.824e-02$
Coefficient: $-1.98e+04$
Value: 31-45



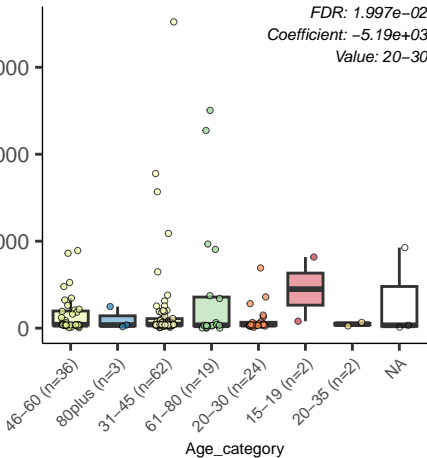
Actinomycetia.o__Corynebacteriales.f__Corynebacteriaceae.g

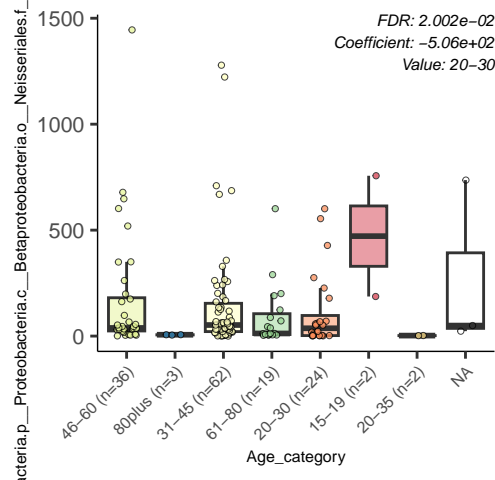
FDR: 1.897e-02
Coefficient: 3.04e+03
Value: 80plus

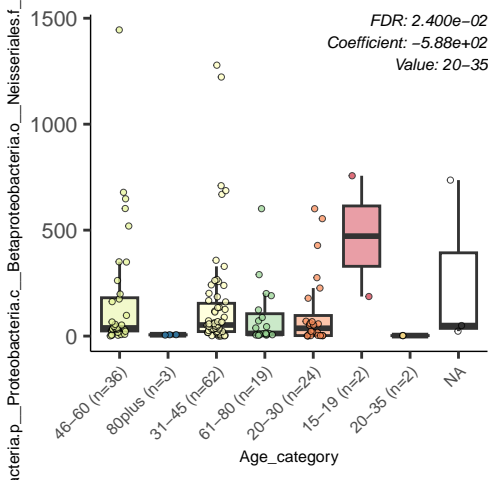


Firmicutes.c__Clostridia.o__Eubacteriales.f__Clostridiaceae.g__C

FDR: 1.997e-02
Coefficient: -5.19e+03
Value: 20-30

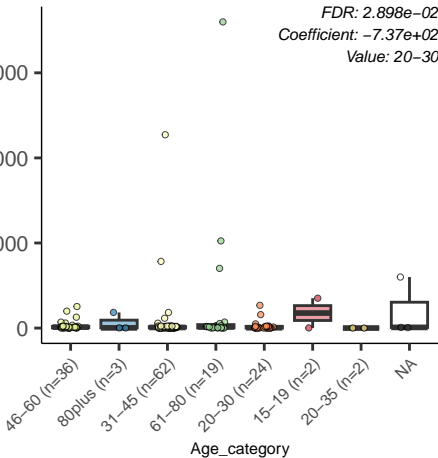


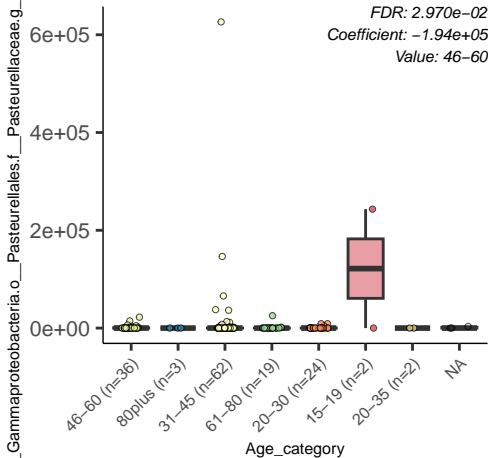


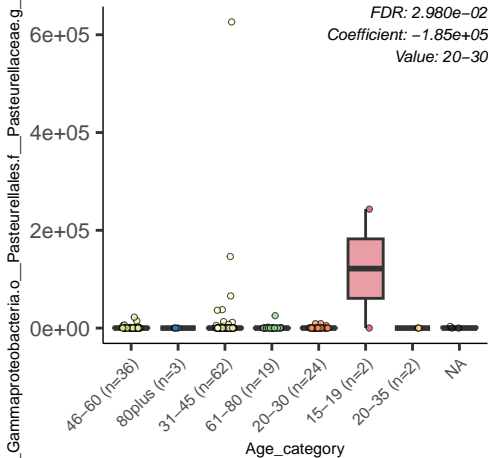


Proteobacteria.c__Betaproteobacteria.o__Burkholderiales.f__Alcal

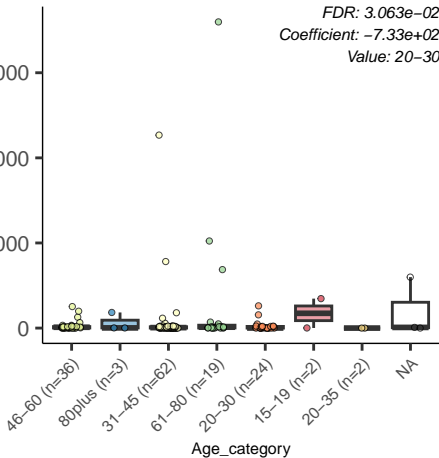
FDR: 2.898e-02
Coefficient: -7.37e+02
Value: 20-30

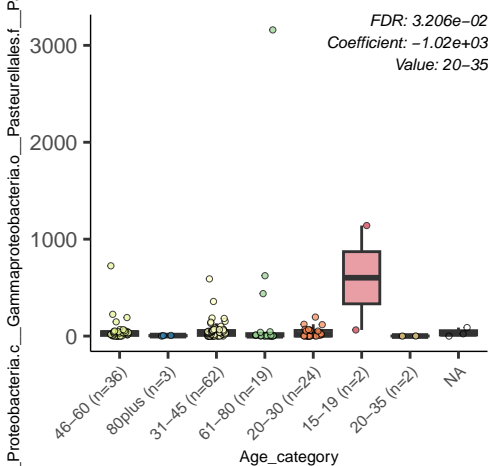


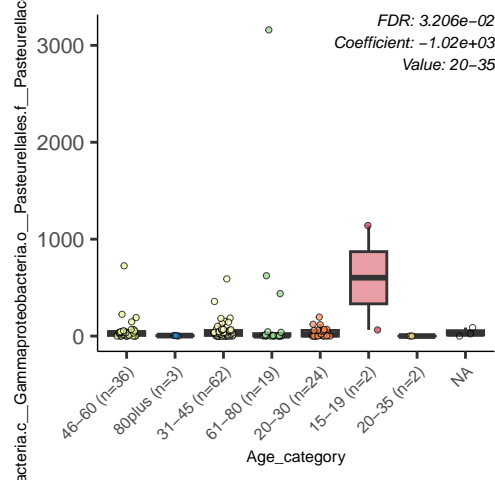




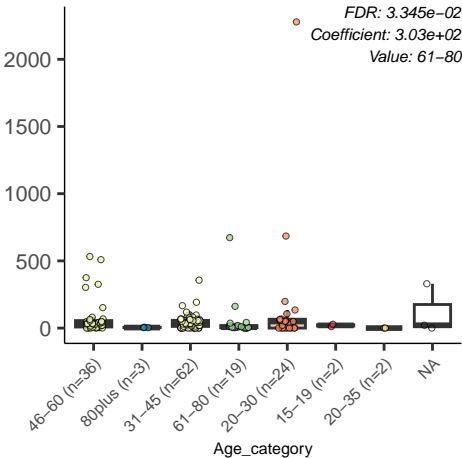
FDR: 3.063e-02
Coefficient: -7.33e+02
Value: 20-30



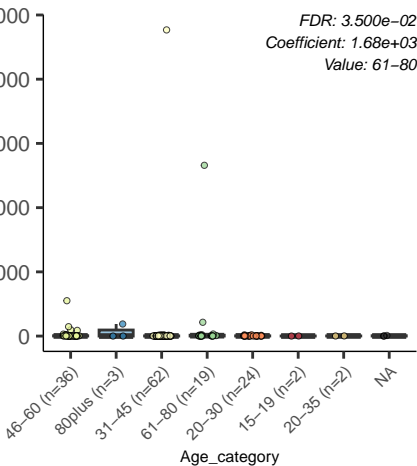




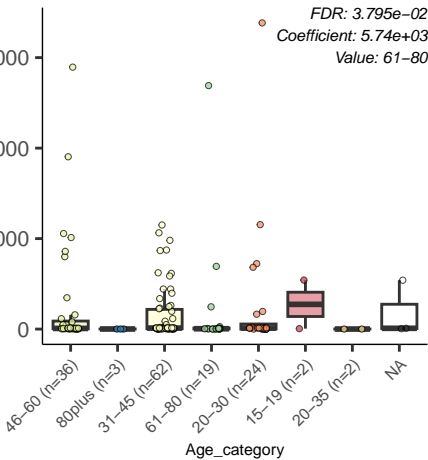
Bacteria.p__Bacteroidetes.c__Flavobacteriia.o__Flavobacteriales.f

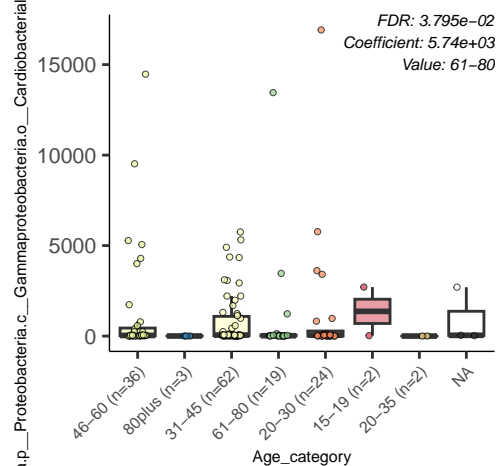


tinomycetia.o__Corynebacteriales.f__Corynebacteriaceae.g__Cory

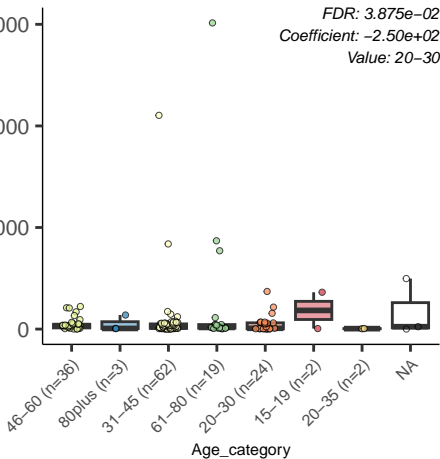


d_Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Car



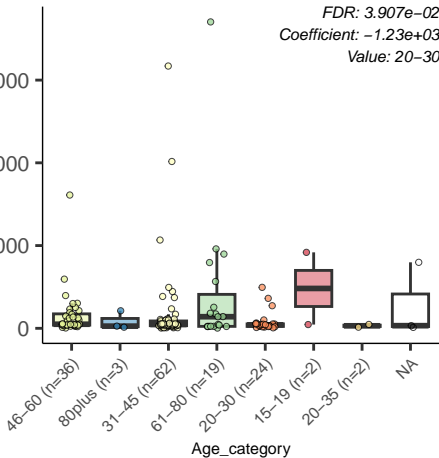


.p__Proteobacteria.c__Alphaproteobacteria.o__Hyphomicrobiales.f

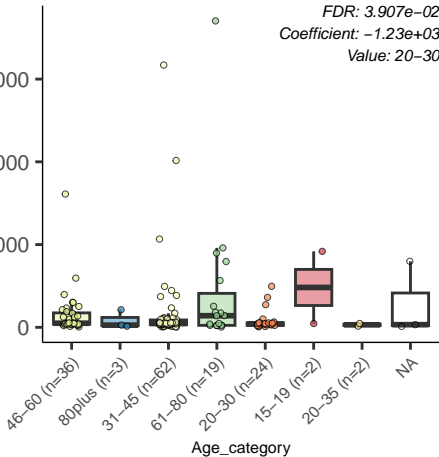


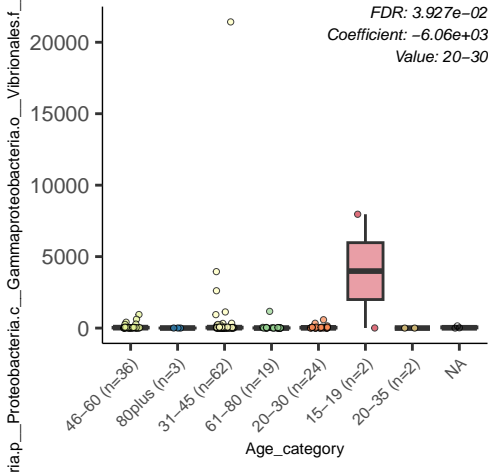
Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Clostridia

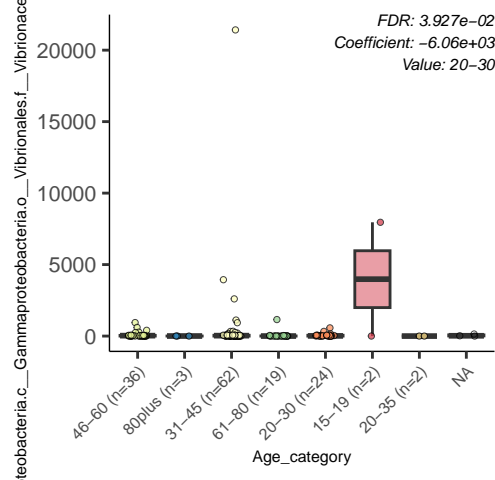
FDR: $3.907e-02$
Coefficient: $-1.23e+03$
Value: 20-30



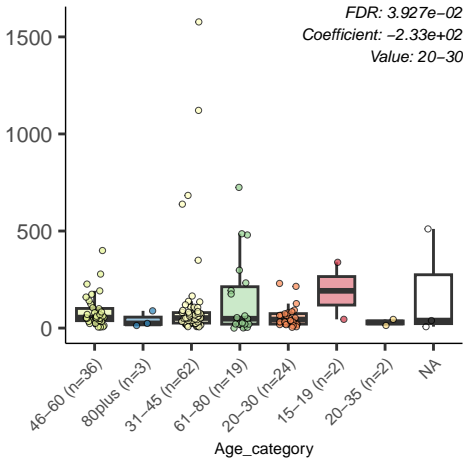
FDR: $3.907e-02$
Coefficient: $-1.23e+03$
Value: 20-30





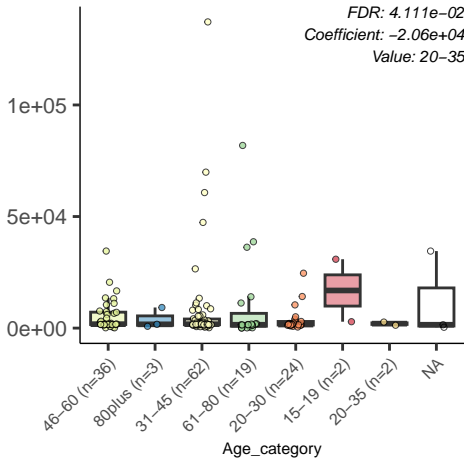


bacteria.o__Synechococcales.f__Synechococcaceae.g__Synechococcus



c__Gammaproteobacteria.o__Oceanospirillales.f__Halomonadacea

FDR: $4.111\text{e-}02$
Coefficient: $-2.06\text{e+}04$
Value: 20-35



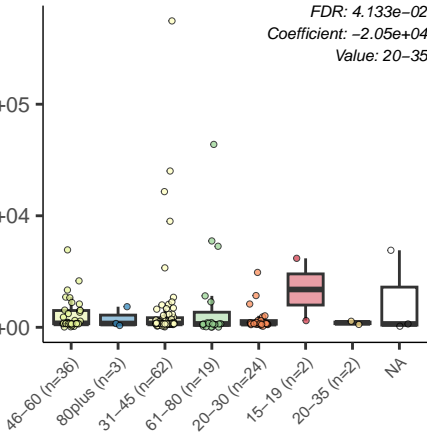
Proteobacteria.c__Gammaproteobacteria.o__Oceanospirillales.f__F

FDR: $4.133e-02$
Coefficient: $-2.05e+04$
Value: 20-35

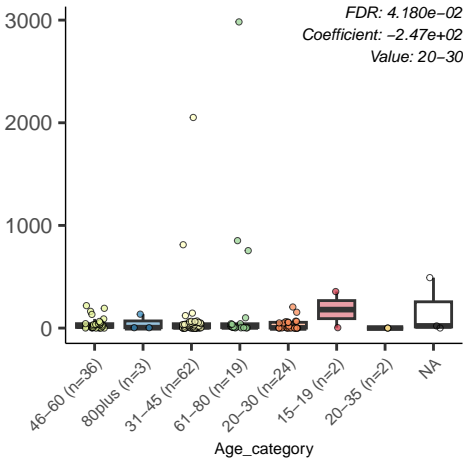
1e+05
5e+04
0e+00

46-60 (n=36)
80plus (n=3)
31-45 (n=62)
61-80 (n=19)
20-30 (n=24)
15-19 (n=2)
20-35 (n=2)
NA

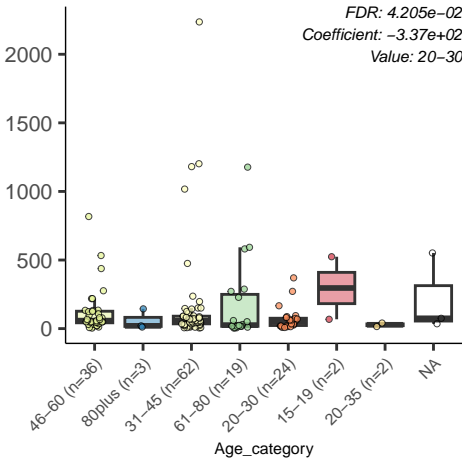
Age_category



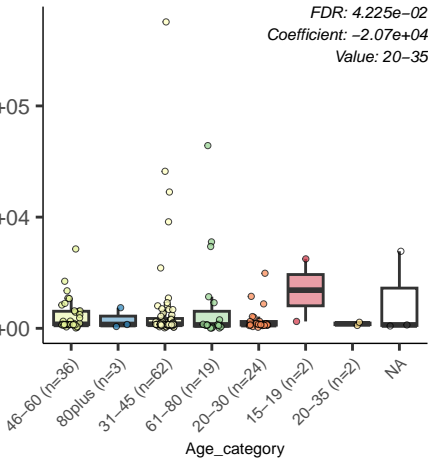
bacteria.c__Alphaproteobacteria.o__Hyphomicrobiales.f__Rhizobiales

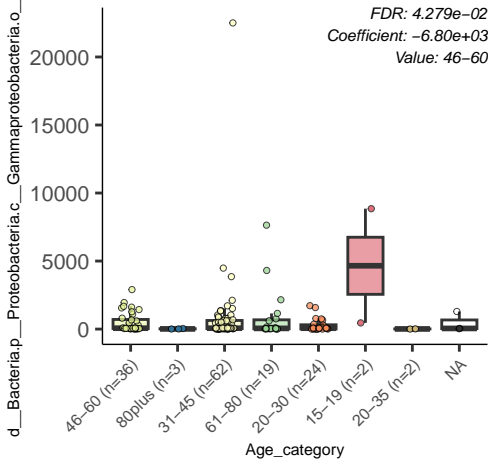


Proteobacteria.c__Alphaproteobacteria.o__Rickettsiales.f__Anap

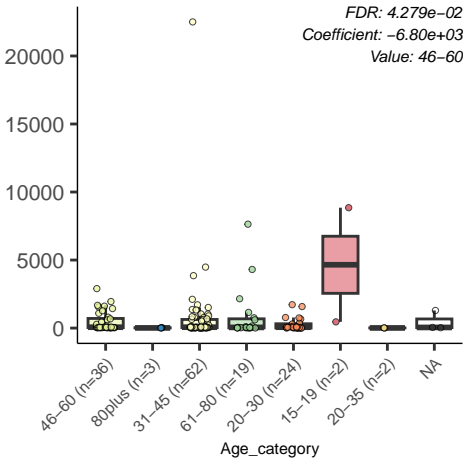


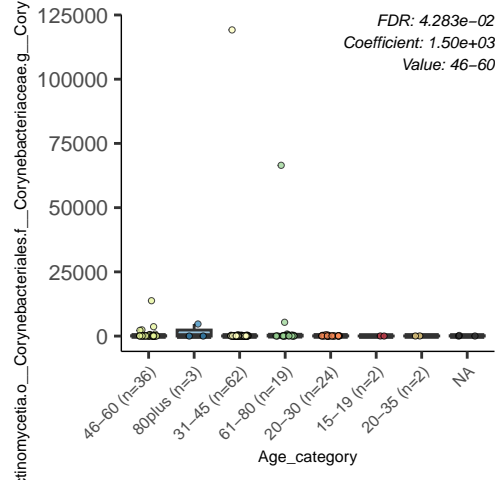
eria.p__Proteobacteria.c__Gammaproteobacteria.o__Oceanospirilla



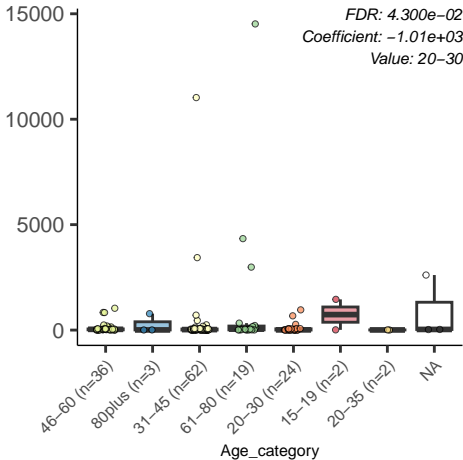


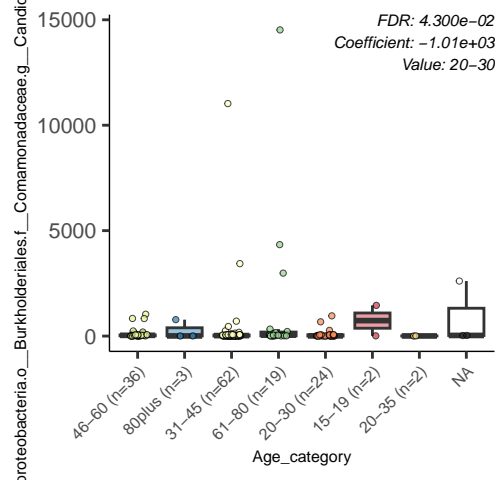
Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Vibrion

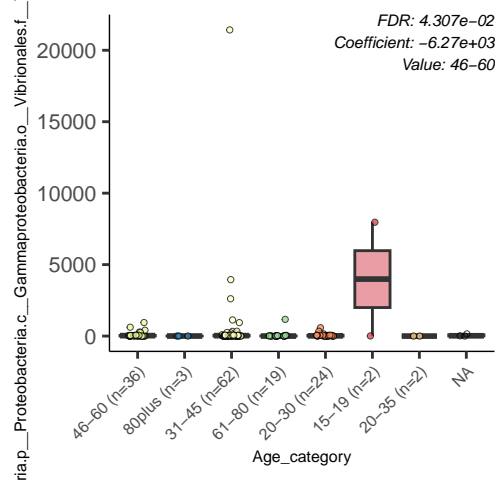


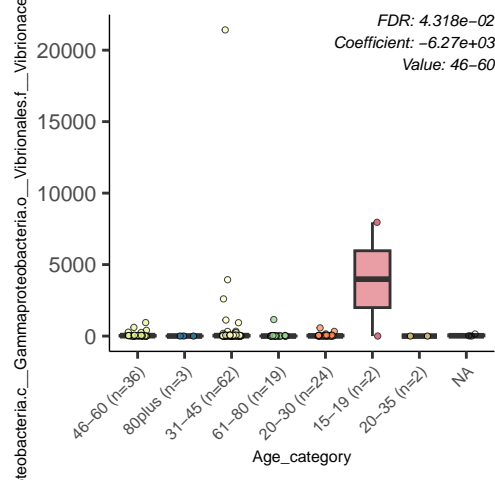


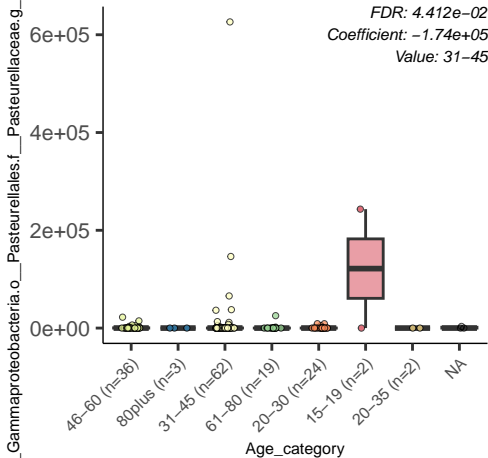
obacteria.c__Betaproteobacteria.o__Burkholderiales.f__Comamonad





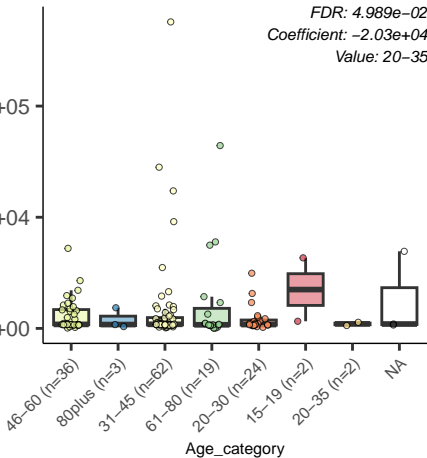


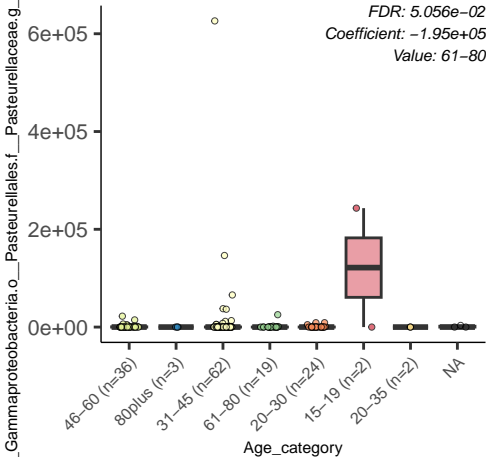




d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Oscillatoriales

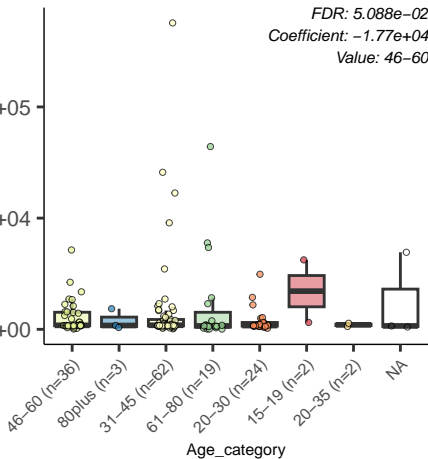
FDR: 4.989×10^{-2}
Coefficient: -2.03×10^4
Value: 20-35





eria.p__Proteobacteria.c__Gammaproteobacteria.o__Oceanospirilla

FDR: $5.088e-02$
Coefficient: $-1.77e+04$
Value: 46-60



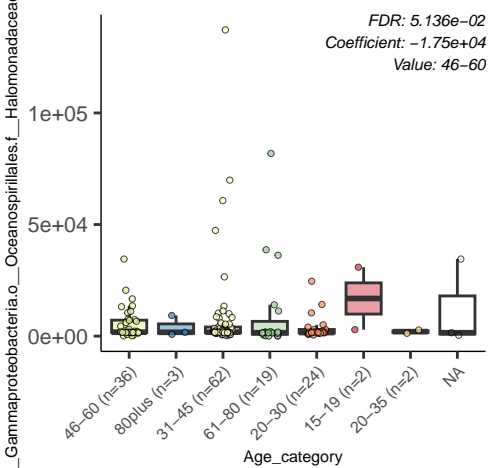
c__Gammaproteobacteria.o__Oceanospirillales.f__Halomonadacea

FDR: $5.136e-02$
Coefficient: $-1.75e+04$
Value: 46-60

1e+05
5e+04
0e+00

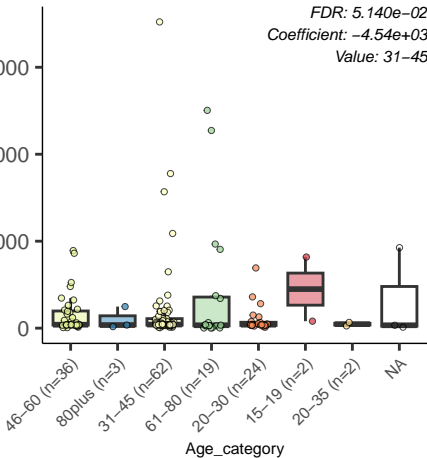
46-60 (n=36)
80plus (n=3)
31-45 (n=62)
61-80 (n=19)
20-30 (n=24)
15-19 (n=2)
20-35 (n=2)
NA

Age_category



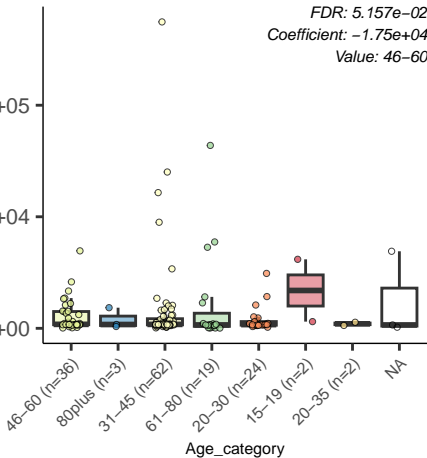
Firmicutes.c_Clostridia.o_Eubacteriales.f_Clostridiaceae.g_C

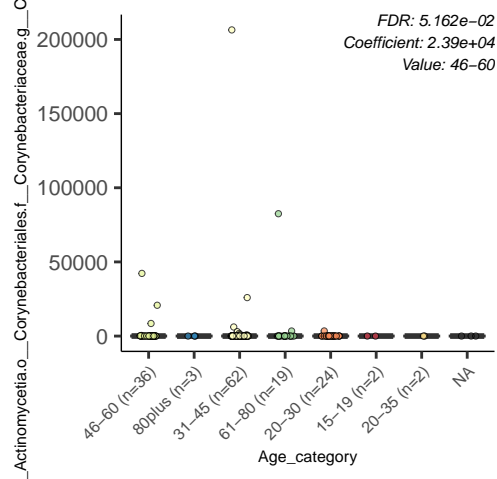
FDR: 5.140×10^{-2}
Coefficient: -4.54×10^3
Value: 31-45

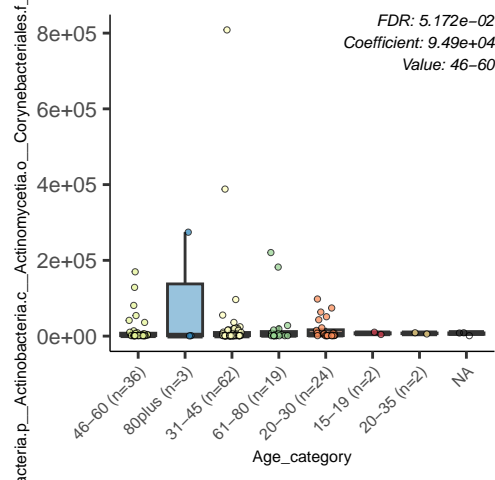


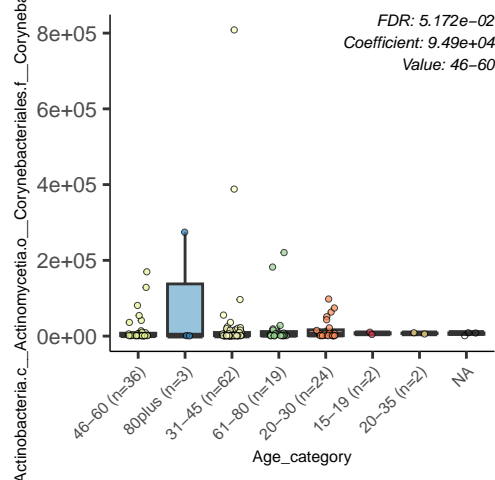
Proteobacteria.c__Gammaproteobacteria.o__Oceanospirillales.f__H

FDR: $5.157e-02$
Coefficient: $-1.75e+04$
Value: 46-60

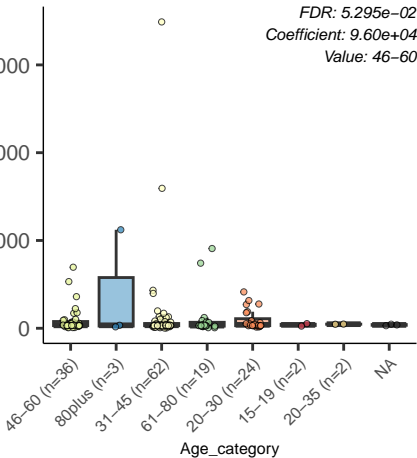


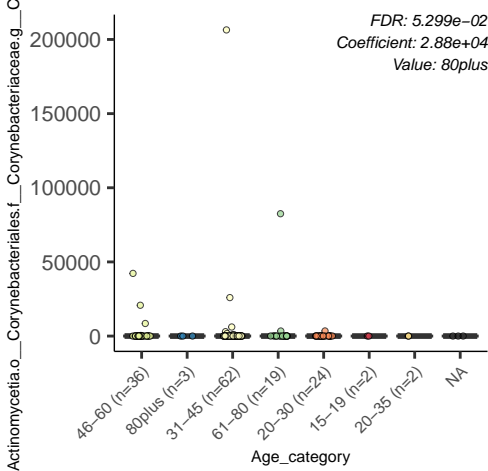


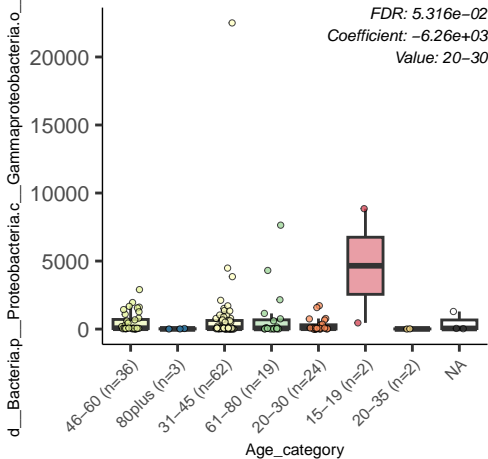




d__Bacteria.p__Actinobacteria.c__Actinomycetia.o__Coryneb

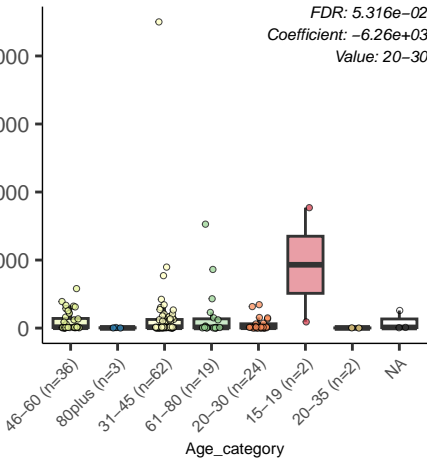


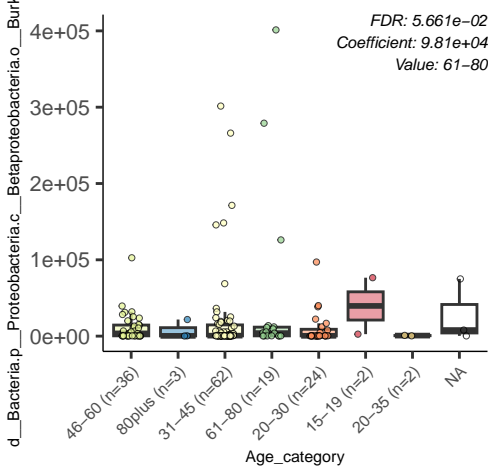




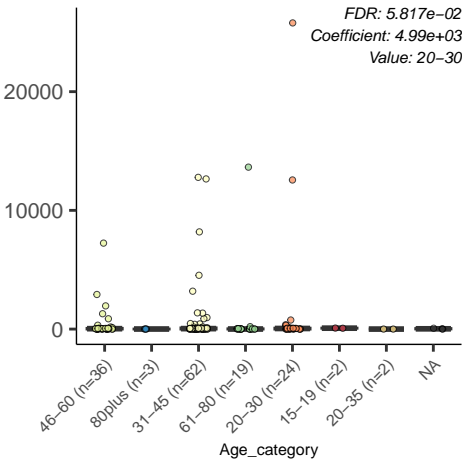
Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Vibrion

FDR: $5.316e-02$
Coefficient: $-6.26e+03$
Value: 20-30



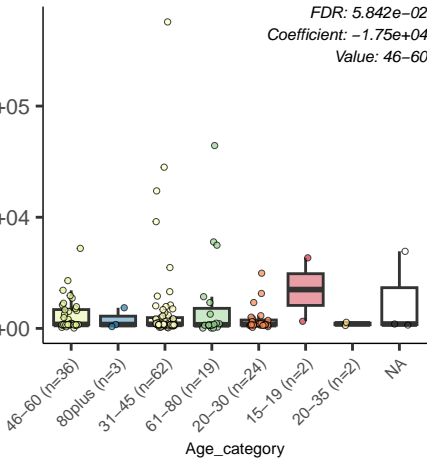


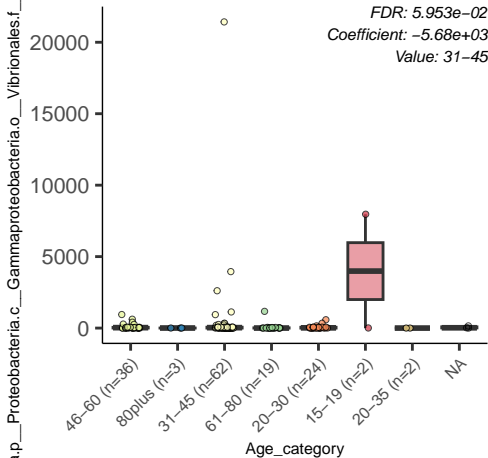
__Epsilonproteobacteria.o__Campylobacteriales.f__Campylobacter



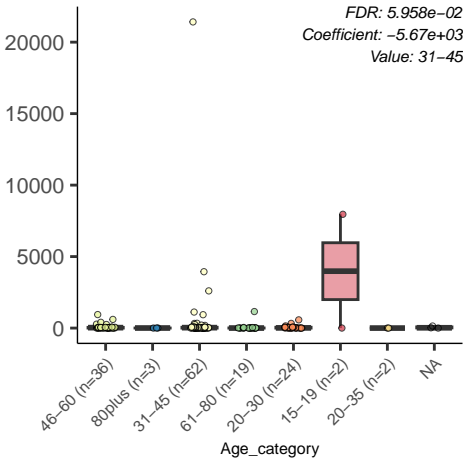
d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Oscillatoriales

FDR: $5.842e-02$
Coefficient: $-1.75e+04$
Value: 46-60

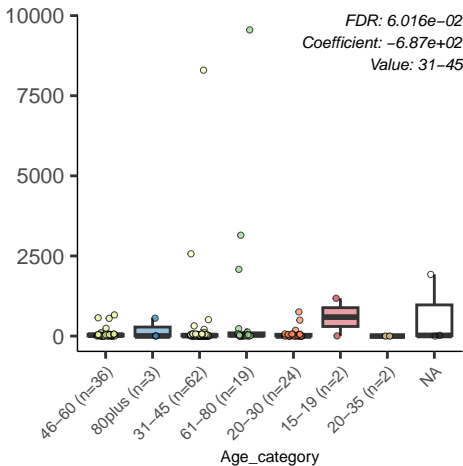


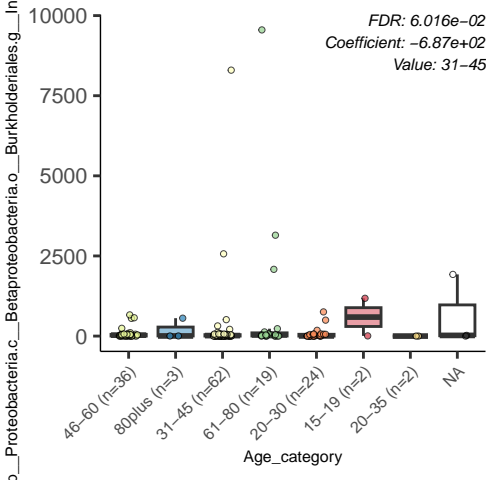


teobacteria.c__Gammaproteobacteria.o__Vibrionales.f__Vibrionaceae



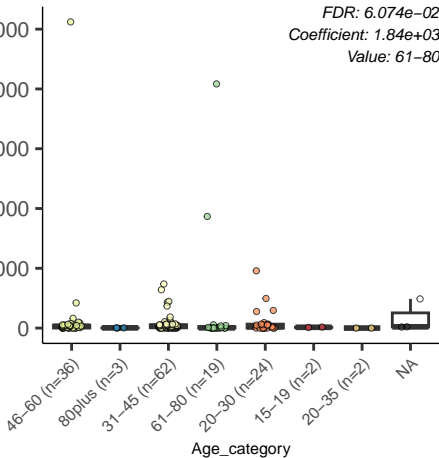
l_Bacteria.p__Proteobacteria.c__Betaproteobacteria.o__Burkholder

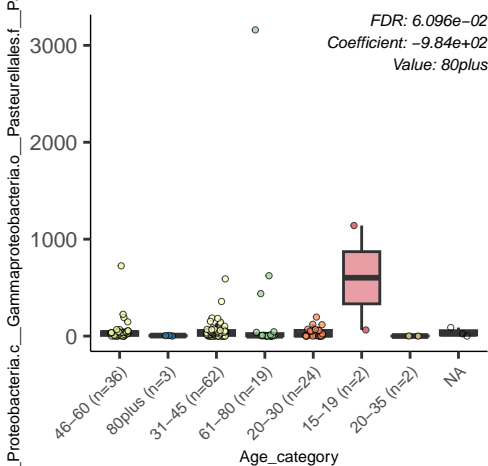


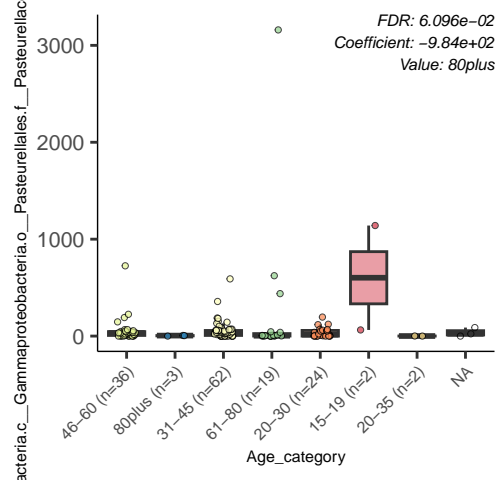


Gammaproteobacteria.o__Pasteurellales.f__Pasteurellaceae.g__Ag

FDR: 6.074e-02
Coefficient: 1.84e+03
Value: 61-80

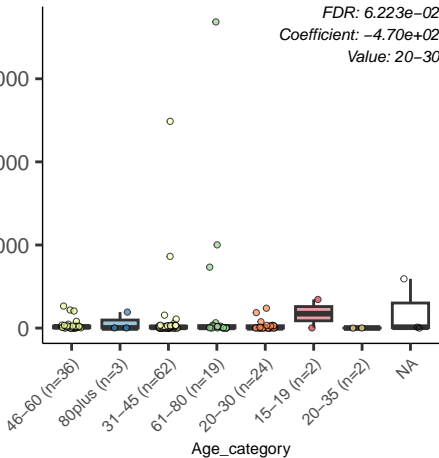






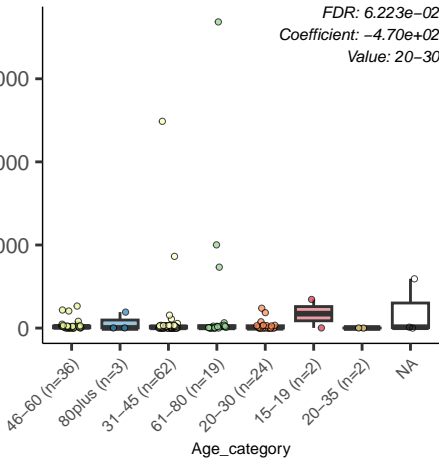
Bacteria.p__Proteobacteria.c__Betaproteobacteria.o__Burkholder

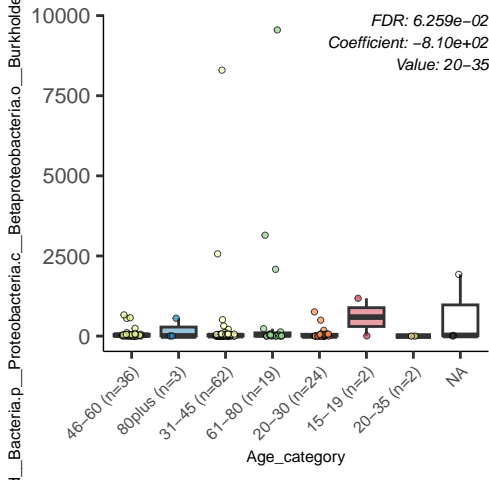
FDR: 6.223e-02
Coefficient: -4.70e+02
Value: 20-30

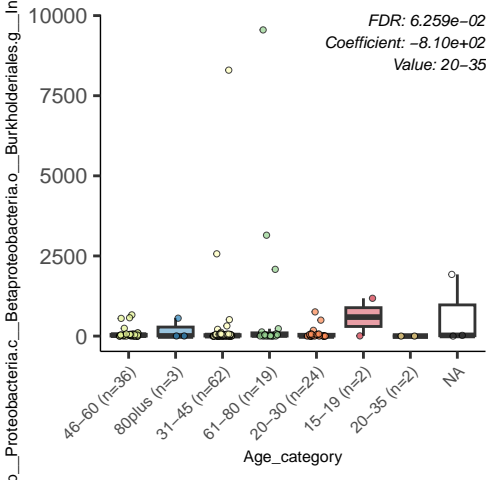


Proteobacteria.c__Betaproteobacteria.o__Burkholderiales.g__Lep

FDR: 6.223e-02
Coefficient: -4.70e+02
Value: 20-30

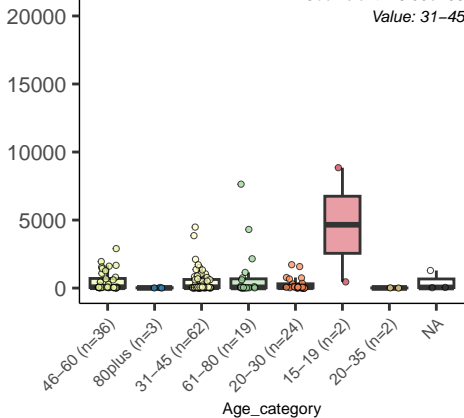




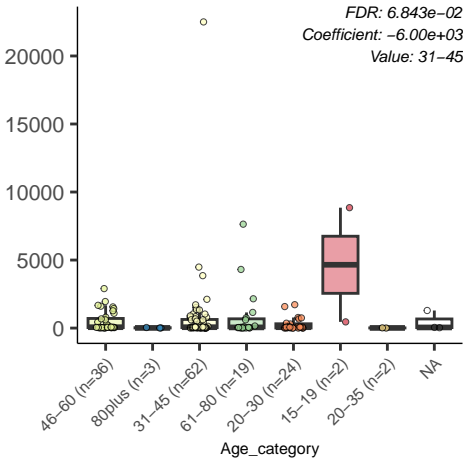


d_Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__

FDR: $6.843e-02$
Coefficient: $-6.00e+03$
Value: 31-45

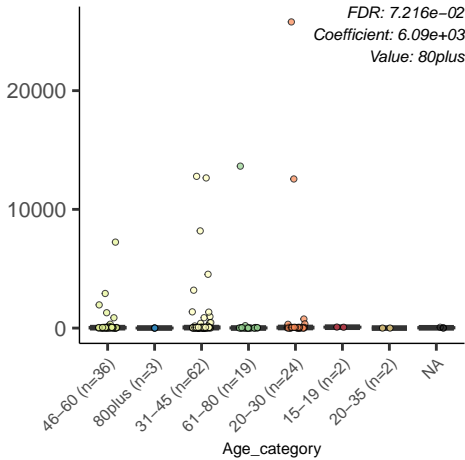


Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Vibrion



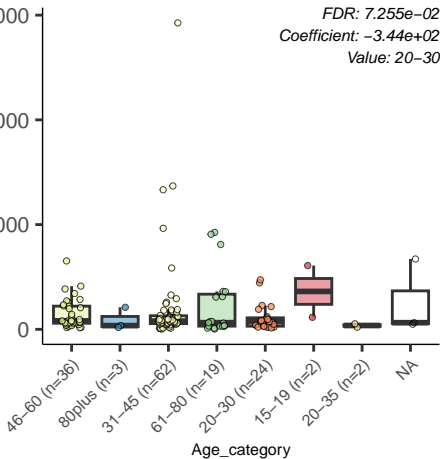
46-60 (n=36)
80plus (n=3)
31-45 (n=62)
61-80 (n=19)
20-30 (n=24)
15-19 (n=2)
20-35 (n=2) NA

Age_category

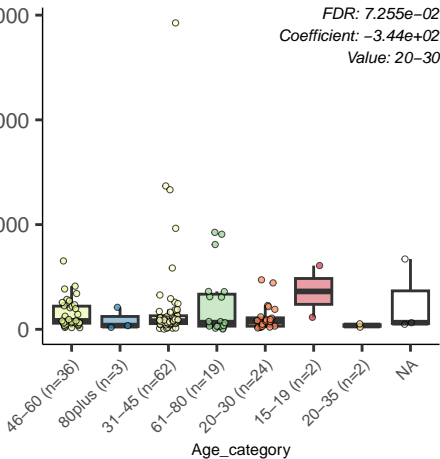


Age_category

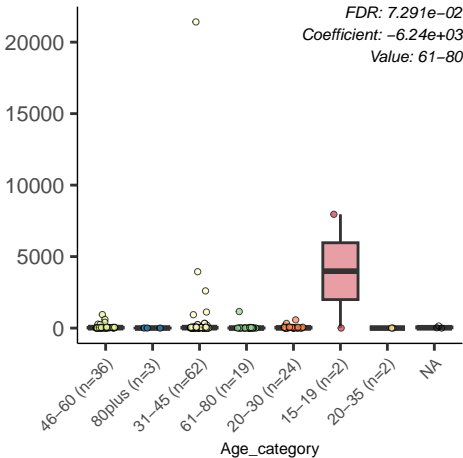
ia.p__Proteobacteria.c__Alphaproteobacteria.o__Hyphomicrobiales

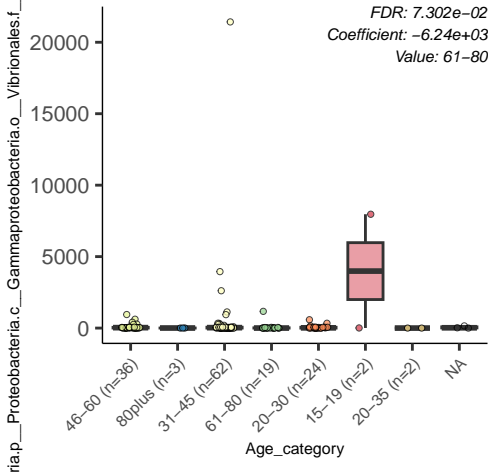


ria.c__Alphaproteobacteria.o__Hyphomicrobiales.g__Candidatus.H

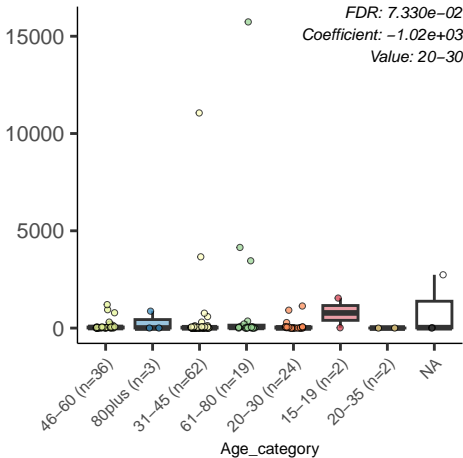


teobacteria.c__Gammaproteobacteria.o__Vibrionales.f__Vibrionaceae



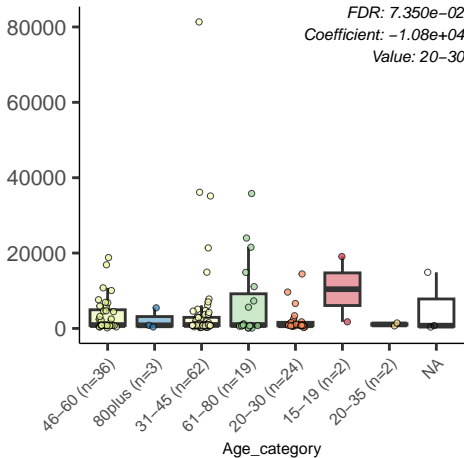


obacteria.c__Betaproteobacteria.o__Burkholderiales.f__Comamonad

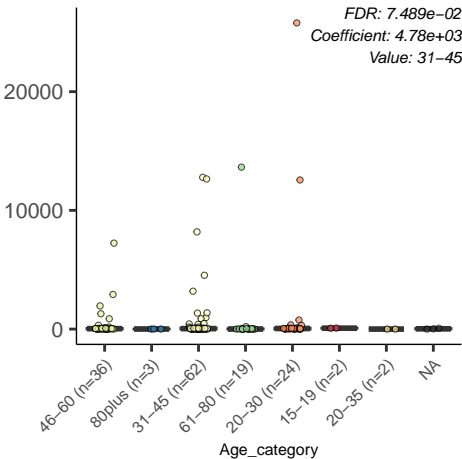


tertia.c__Gammaproteobacteria.o__Pasteurellales.f__Pasteurellaceae

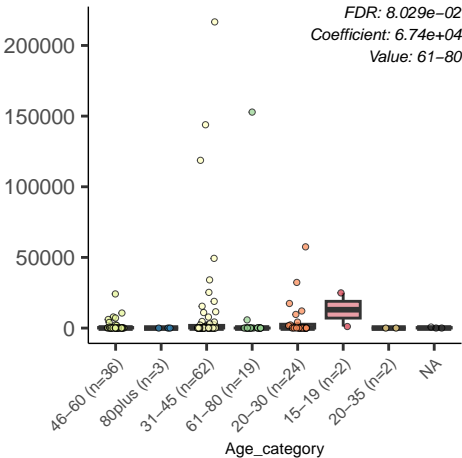
FDR: $7.350e-02$
Coefficient: $-1.08e+04$
Value: 20-30



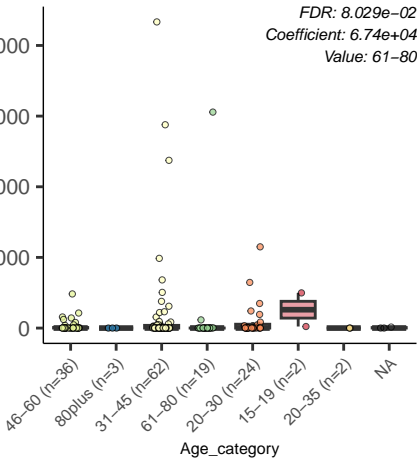
__Epsilonproteobacteria.o__Campylobacteriales.f__Campylobacter

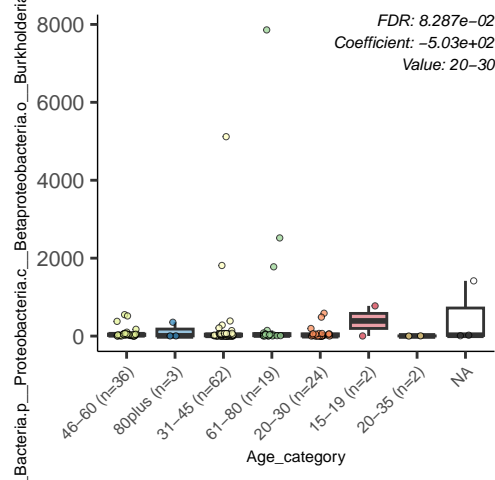


p__Proteobacteria.c__Betaproteobacteria.o__Burkholderiales.f__Bu



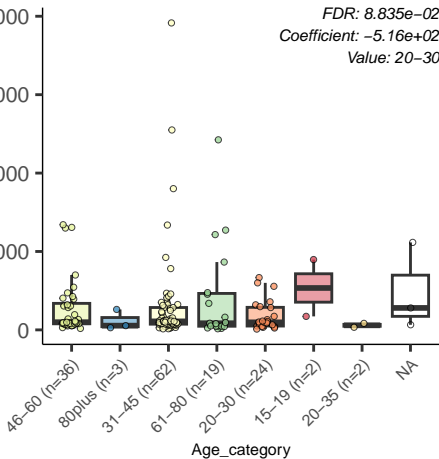
acteria.c__Betaproteobacteria.o__Burkholderiales.f__Burkholderia





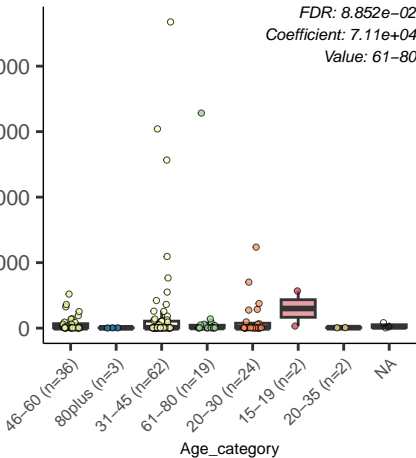
d__Bacteria.p__Cyanobacteria.o__Synechococcales.f__Synech

FDR: $8.835e-02$
Coefficient: $-5.16e+02$
Value: 20-30

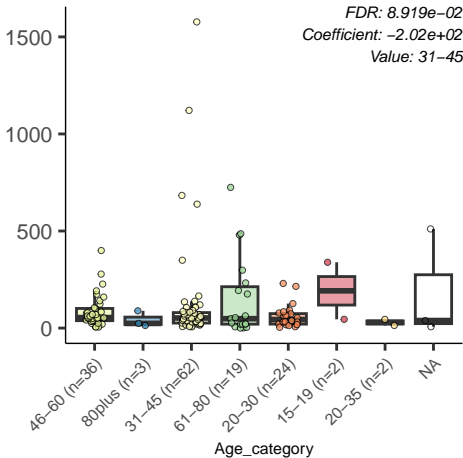


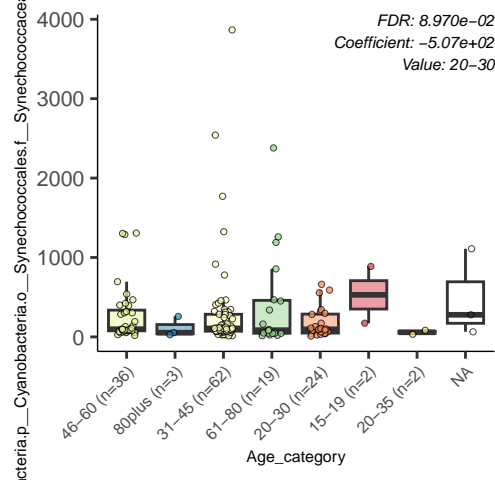
acteria.p__Proteobacteria.c__Betaproteobacteria.o__Burkholderiales

FDR: $8.852e-02$
Coefficient: $7.11e+04$
Value: 61-80



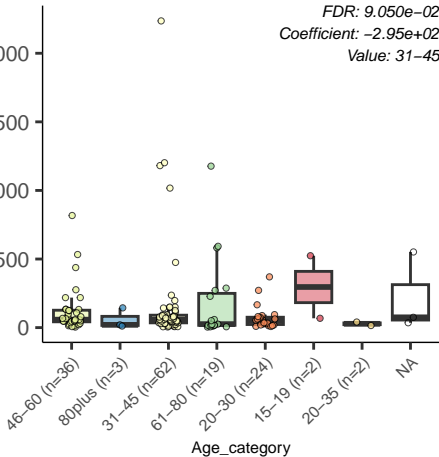
bacteria.o__Synechococcales.f__Synechococcaceae.g__Synechococcus

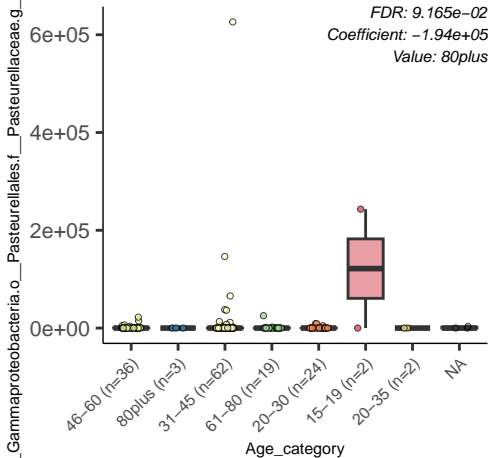




Proteobacteria.c__Alphaproteobacteria.o__Rickettsiales.f__Anap

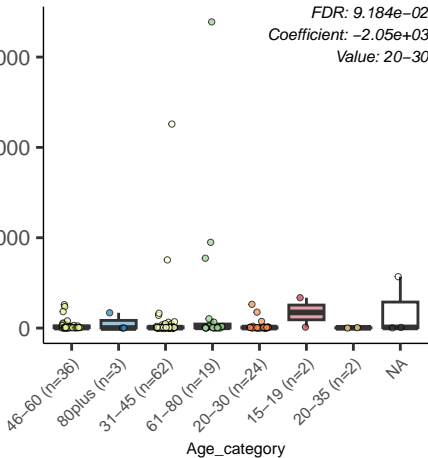
FDR: $9.050e-02$
Coefficient: $-2.95e+02$
Value: 31-45





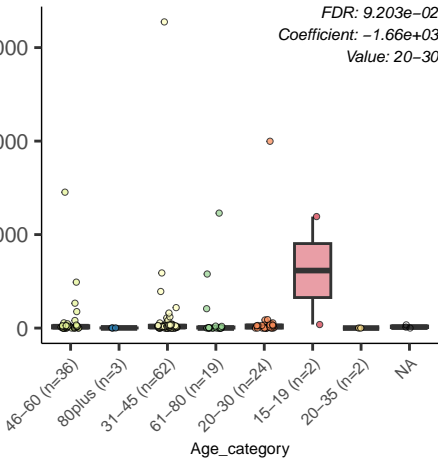
Proteobacteria.c__Betaproteobacteria.o__Burkholderiales.f__Com

FDR: $9.184e-02$
Coefficient: $-2.05e+03$
Value: 20-30

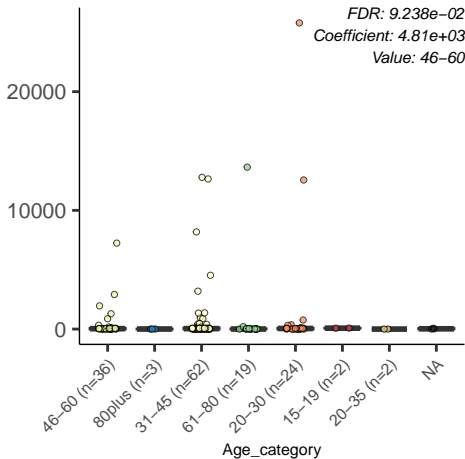


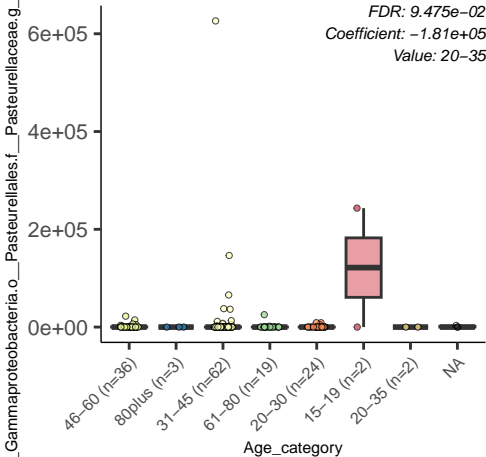
ia.c__Gammaproteobacteria.o__Pasteurellales.f__Pasteurellaceae.

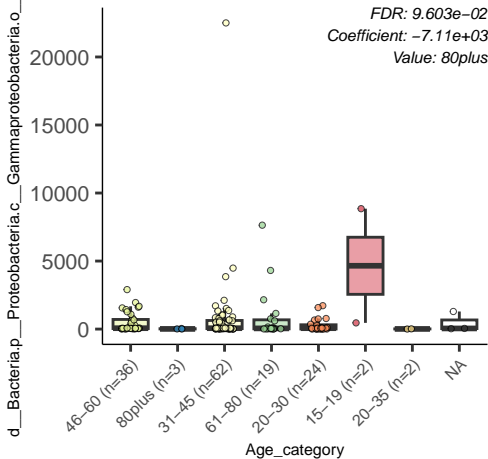
FDR: $9.203e-02$
Coefficient: $-1.66e+03$
Value: 20-30



Epsilonproteobacteria.o__Campylobacterales.f__Campylobacteraceae

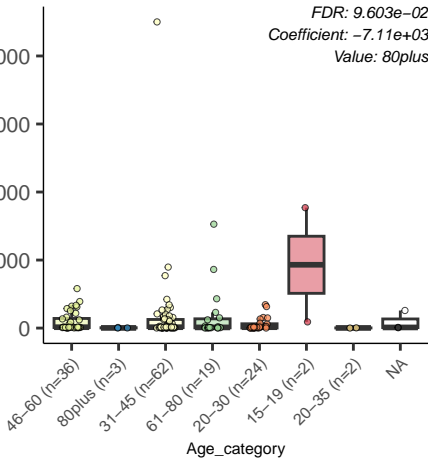






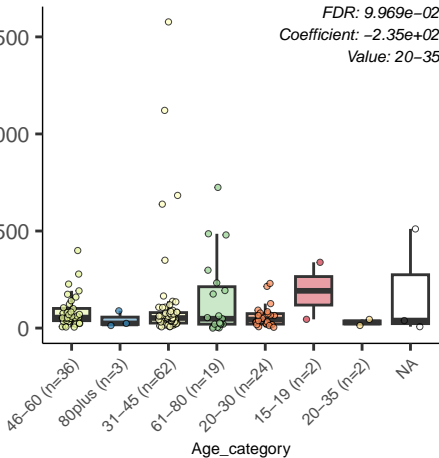
Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Vibrion

FDR: $9.603e-02$
Coefficient: $-7.11e+03$
Value: 80plus



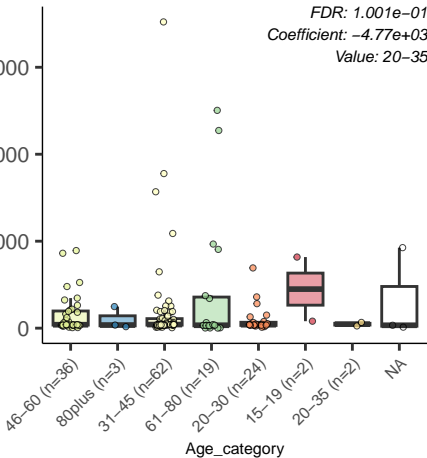
bacteria.o__Synechococcales.f__Synechococcaceae.g__Synechococcus

FDR: 9.969e-02
Coefficient: -2.35e+02
Value: 20-35



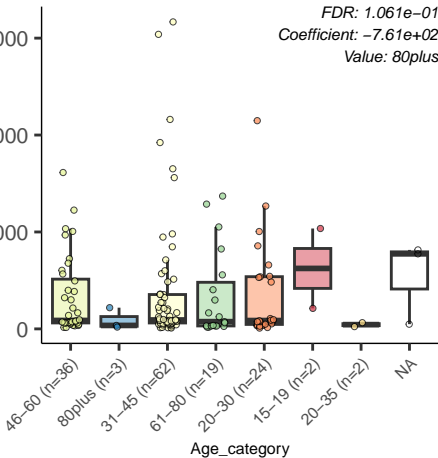
Firmicutes.c__Clostridia.o__Eubacteriales.f__Clostridiaceae.g__C

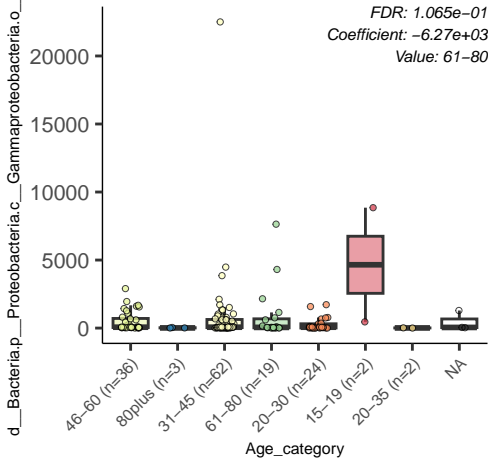
FDR: 1.001e-01
Coefficient: -4.77e+03
Value: 20-35



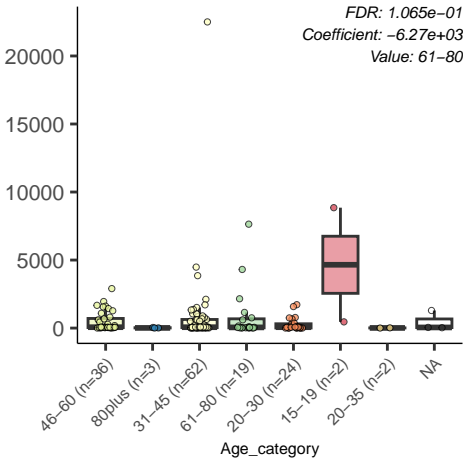
d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o_R

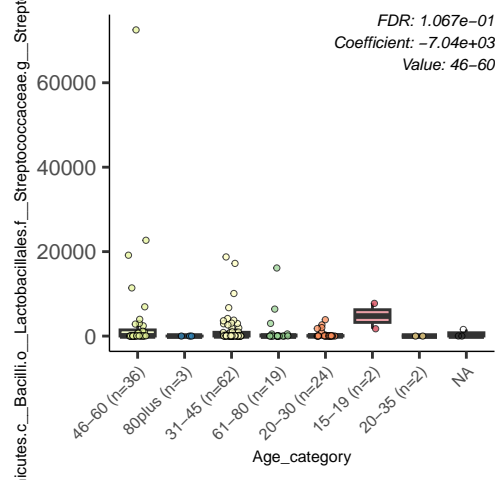
FDR: 1.061e-01
Coefficient: -7.61e+02
Value: 80plus

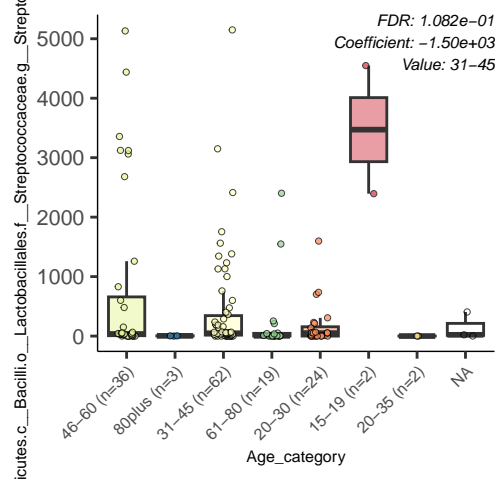


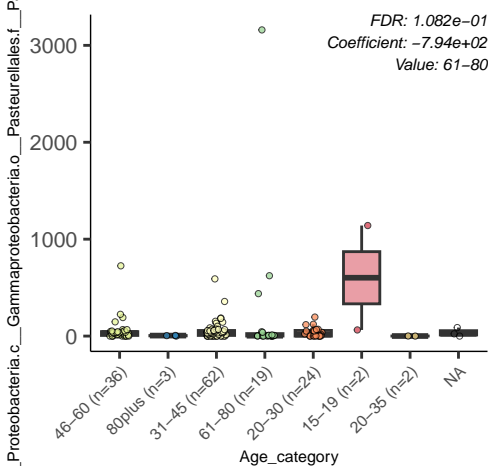


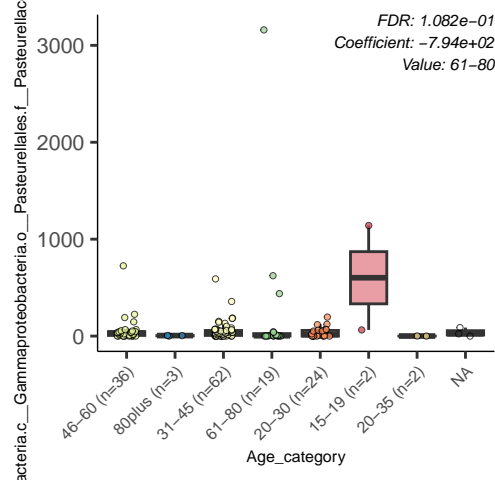
Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Vibrion





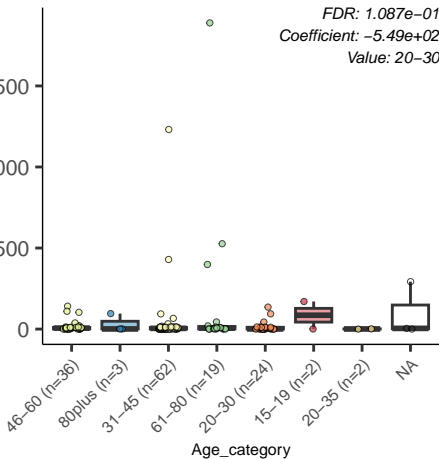






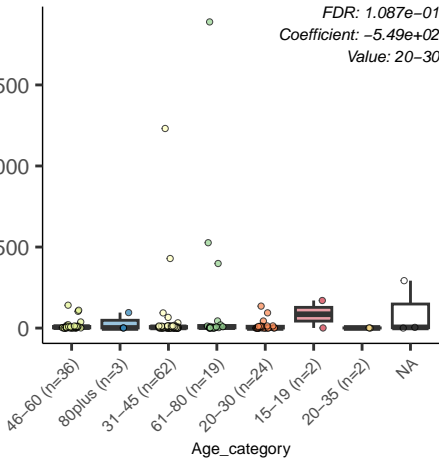
Bacteria.p__Proteobacteria.c__Betaproteobacteria.o__Burkholder

FDR: 1.087e-01
Coefficient: -5.49e+02
Value: 20-30



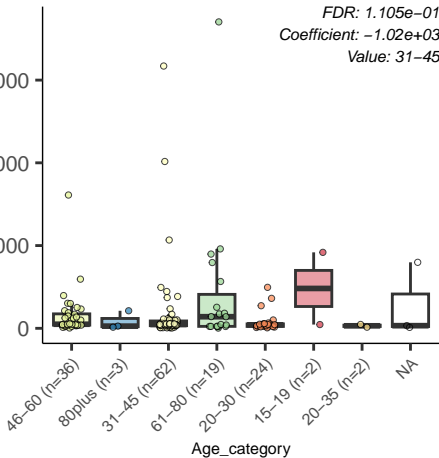
Proteobacteria.c__Betaproteobacteria.o__Burkholderiales.g__Ideo

FDR: 1.087e-01
Coefficient: -5.49e+02
Value: 20-30

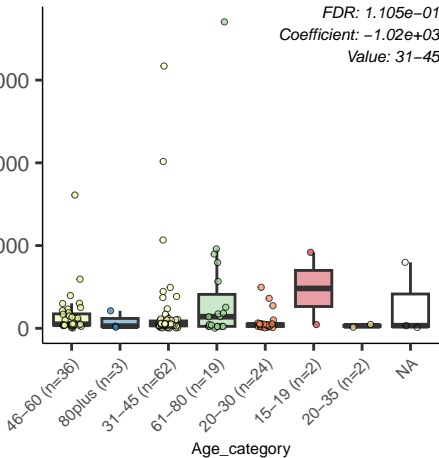


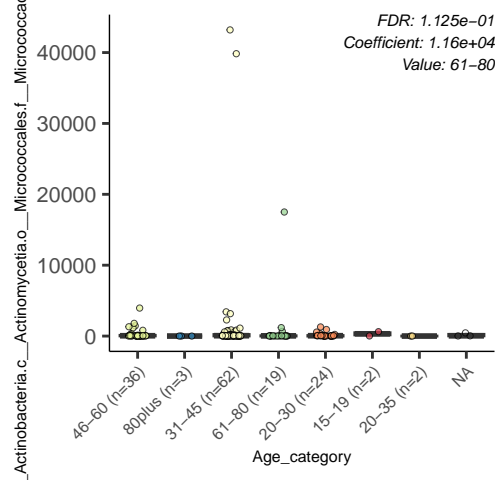
Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Clostridia

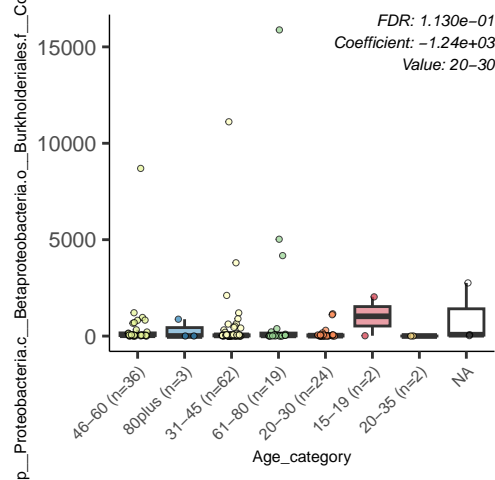
FDR: $1.105e-01$
Coefficient: $-1.02e+03$
Value: 31-45

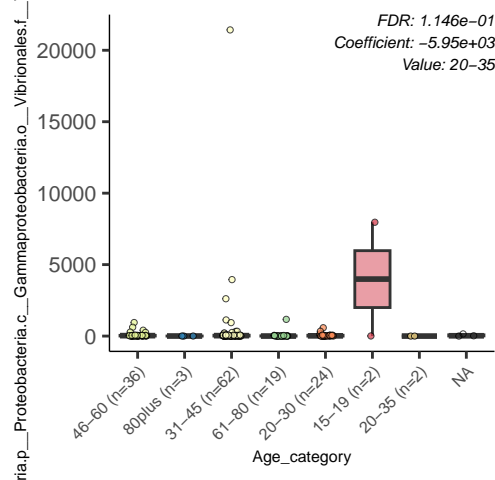


FDR: $1.105e-01$
Coefficient: $-1.02e+03$
Value: 31-45



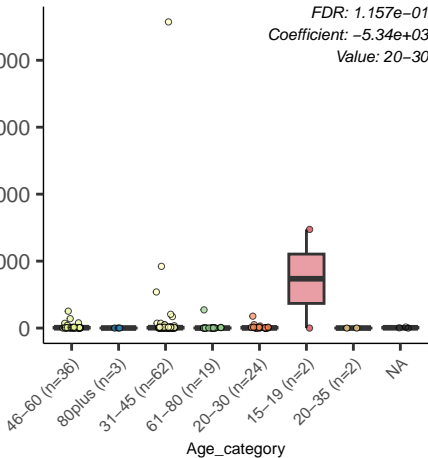


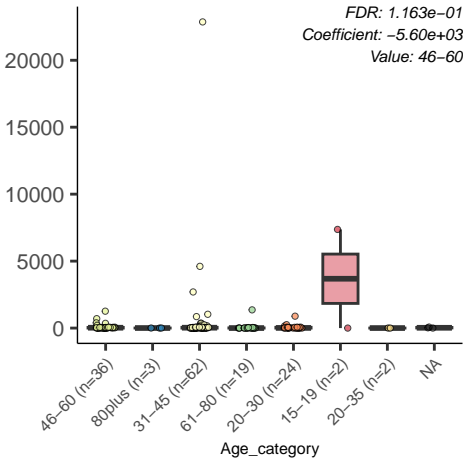




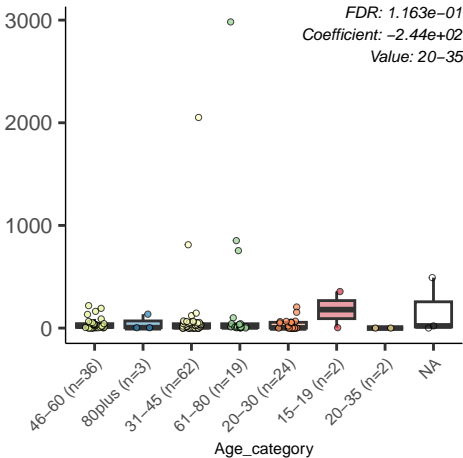
ammaproteobacteria.o__Alteromonadales.f__Pseudoalteromonada

FDR: 1.157e-01
Coefficient: -5.34e+03
Value: 20-30

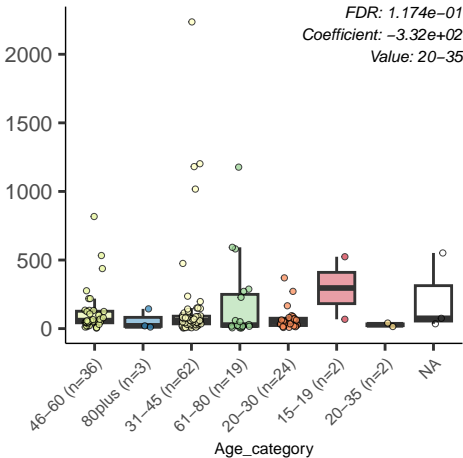


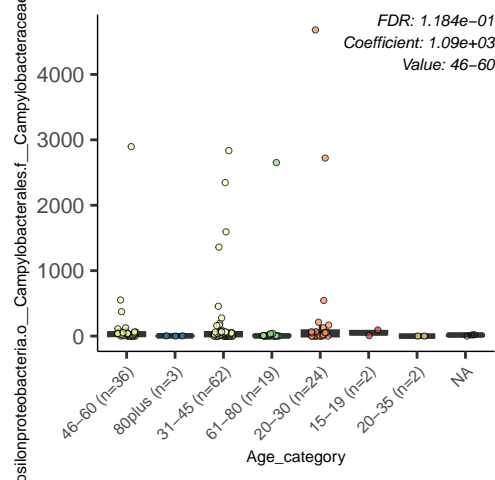


bacteria.c__Alphaproteobacteria.o__Hyphomicrobiales.f__Rhizobiales



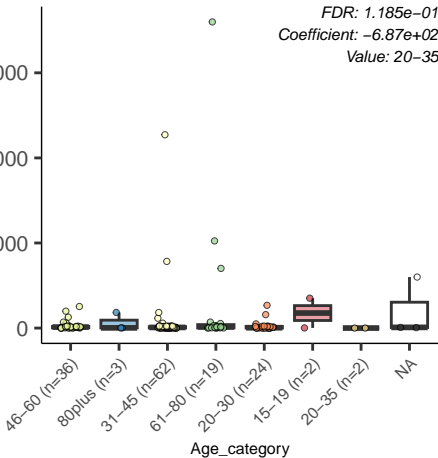
Proteobacteria.c__Alphaproteobacteria.o__Rickettsiales.f__Anap

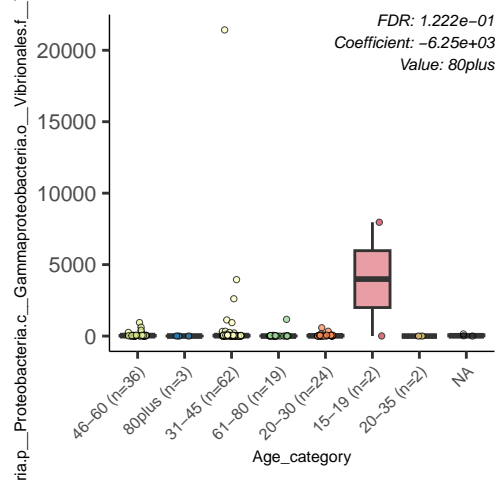




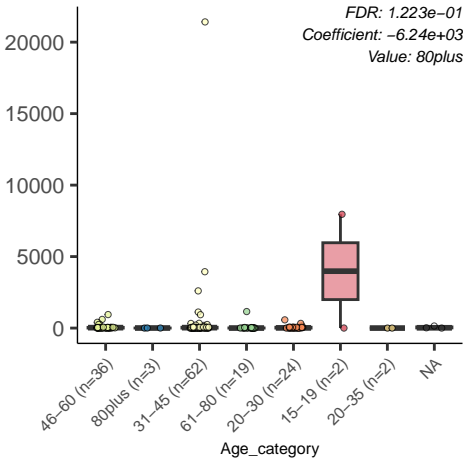
Proteobacteria.c__Betaproteobacteria.o__Burkholderiales.f__Alcal

FDR: 1.185e-01
Coefficient: -6.87e+02
Value: 20-35



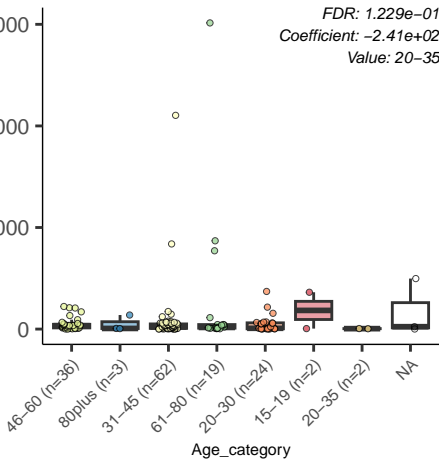


teobacteria.c__Gammaproteobacteria.o__Vibrionales.f__Vibrionaceae

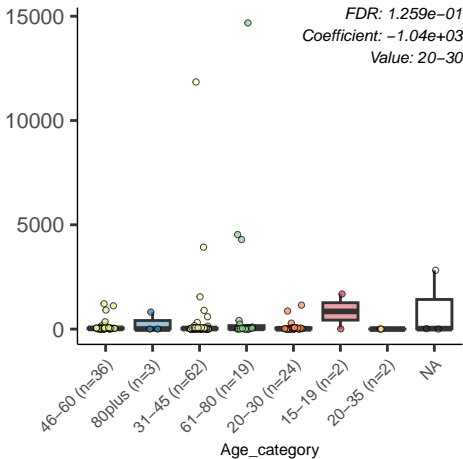


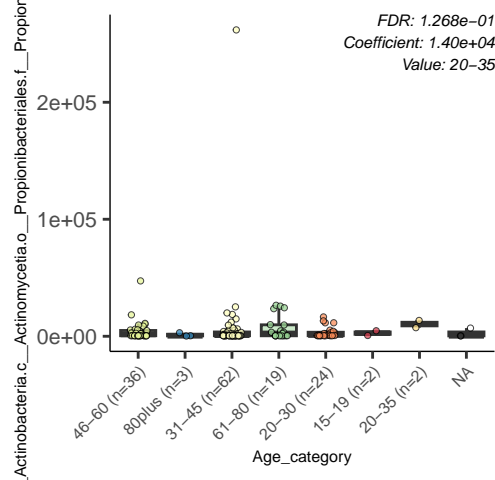
.p__Proteobacteria.c__Alphaproteobacteria.o__Hyphomicrobiales.f

FDR: 1.229e-01
Coefficient: -2.41e+02
Value: 20-35



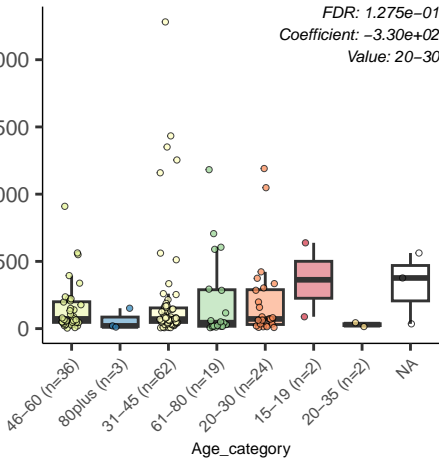
Bacteria.p__Proteobacteria.c__Betaproteobacteria.o__Burkholderia





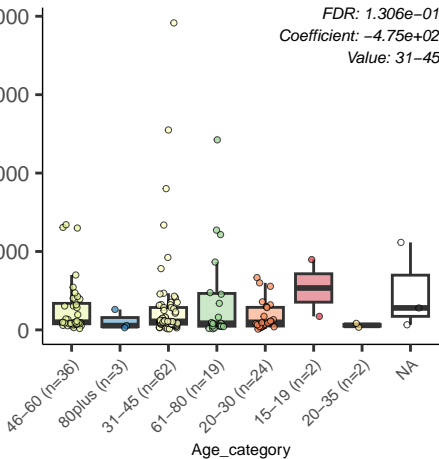
bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rickettsiales

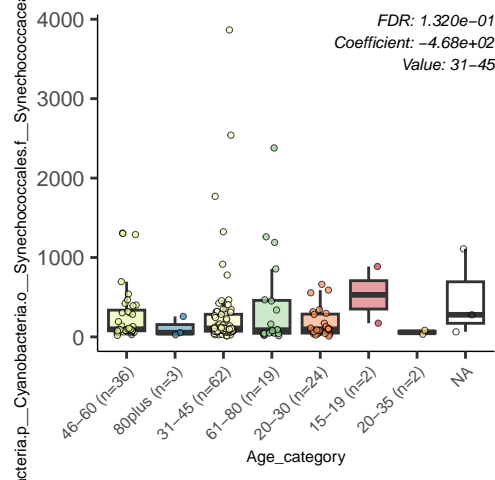
FDR: $1.275e-01$
Coefficient: $-3.30e+02$
Value: 20-30



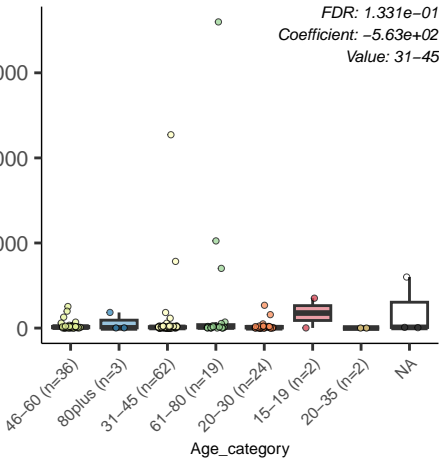
d__Bacteria.p__Cyanobacteria.o__Synechococcales.f__Synech

FDR: 1.306e-01
Coefficient: -4.75e+02
Value: 31-45



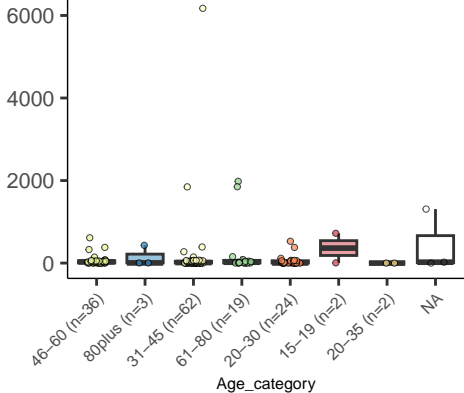


Proteobacteria.c__Betaproteobacteria.o__Burkholderiales.f__Alcal

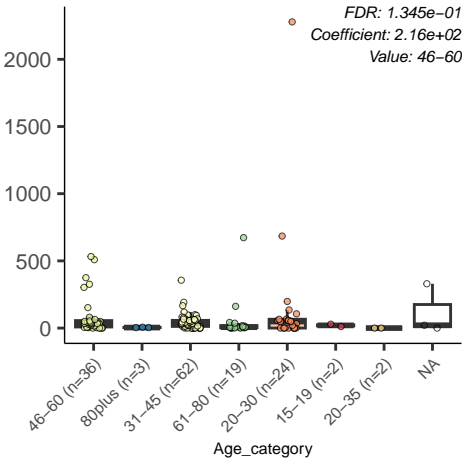


Betaproteobacteria.o__Burkholderiales.f__Comamonadaceae.g

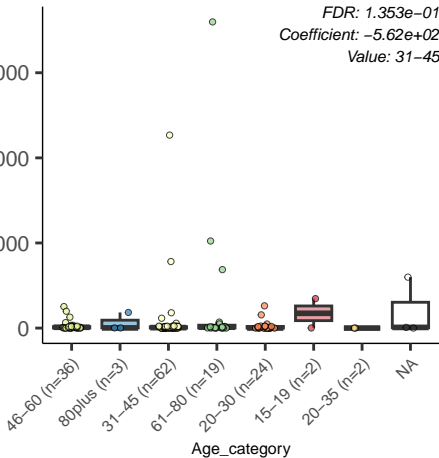
FDR: 1.345e-01
Coefficient: -4.65e+02
Value: 20-30

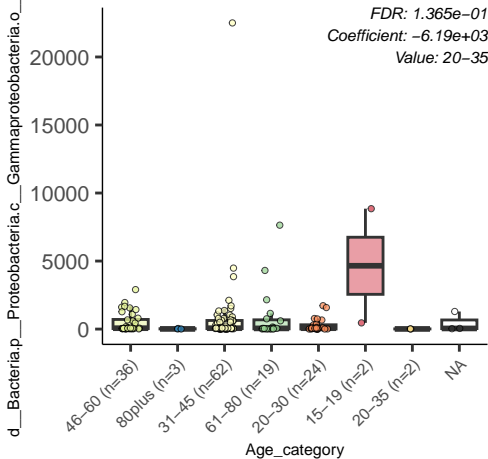


Bacteria.p__Bacteroidetes.c__Flavobacteriia.o__Flavobacteriales.f

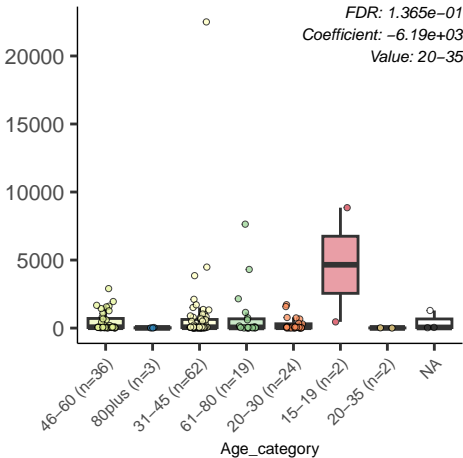


FDR: 1.353e-01
Coefficient: -5.62e+02
Value: 31-45

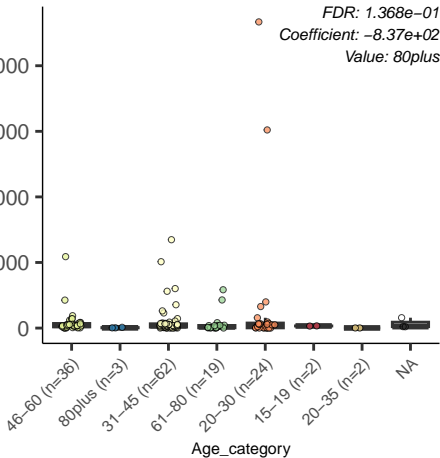




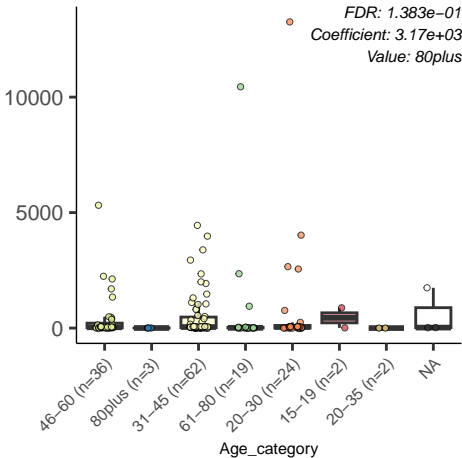
Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Vibrion



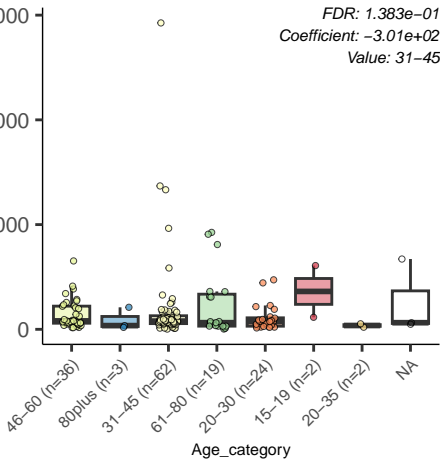
d_Bacteria.p__Proteobacteria.c__Oligoflexia.o__Bacteriov



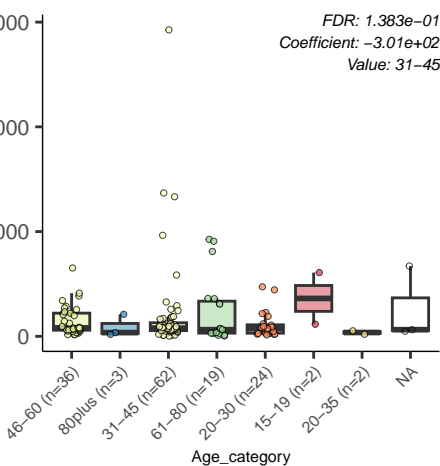
Gamma__Gammaproteobacteria.o__Cardiobacteriales.f__Cardiobacteriaceae



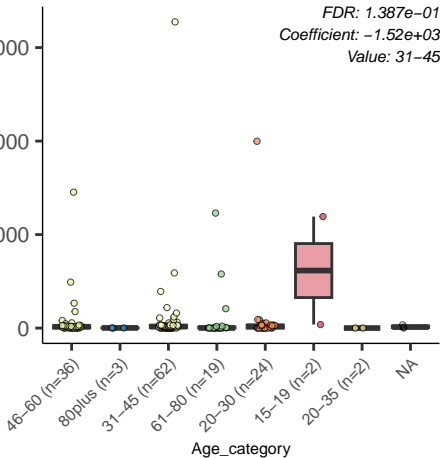
ia.p__Proteobacteria.c__Alphaproteobacteria.o__Hyphomicrobiales

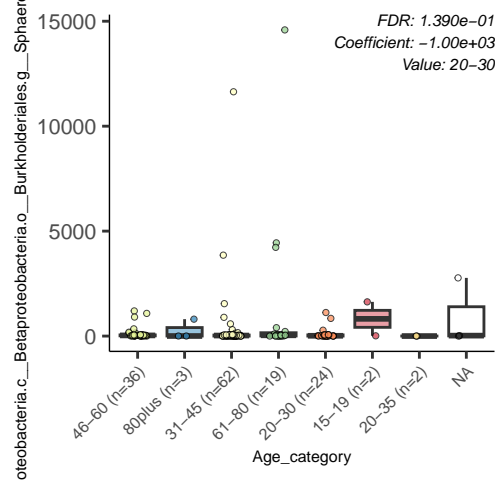


ria.c__Alphaproteobacteria.o__Hyphomicrobiales.g__Candidatus.H

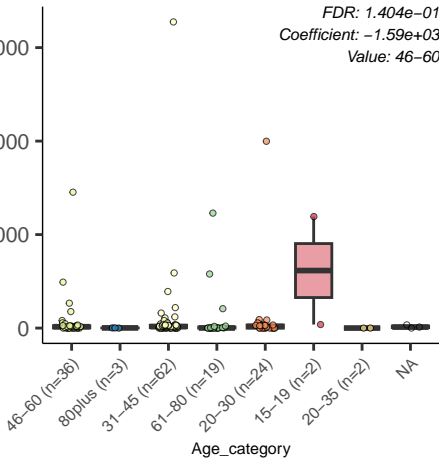


ia.c__Gammaproteobacteria.o__Pasteurellales.f__Pasteurellaceae.



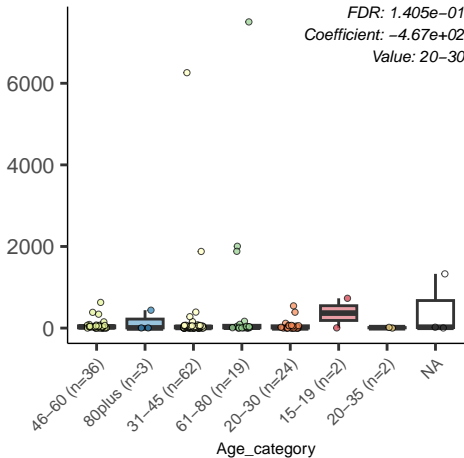


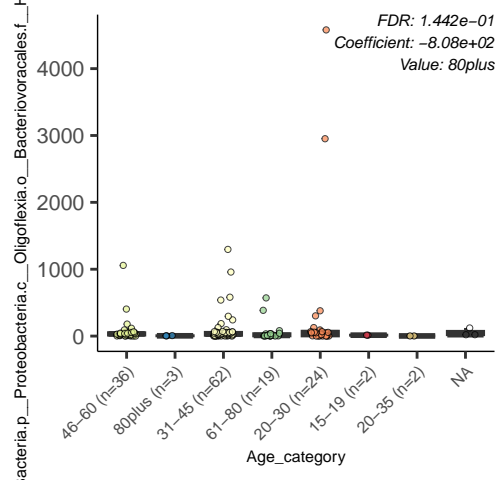
ia.c__Gammaproteobacteria.o__Pasteurellales.f__Pasteurellaceae.

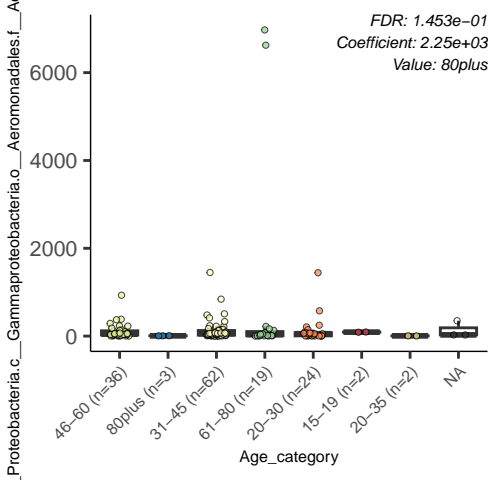


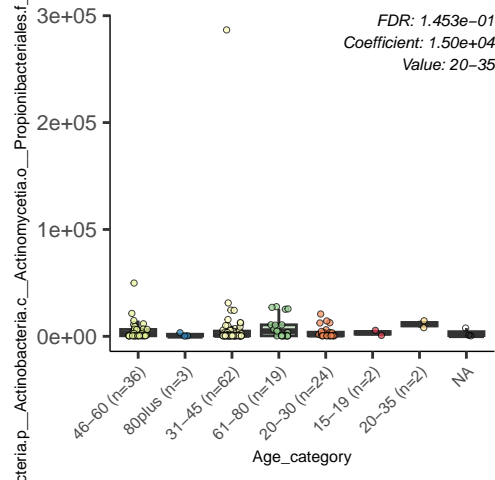
Proteobacteria.c__Betaproteobacteria.o__Burkholderiales.f__Com

FDR: $1.405e-01$
Coefficient: $-4.67e+02$
Value: 20-30

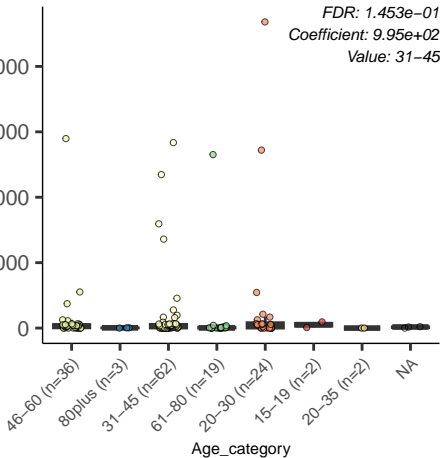






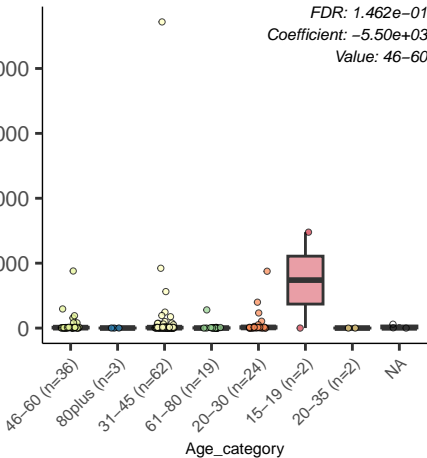


osilonproteobacteria.o__Campylobacterales.f__Campylobacteraceae



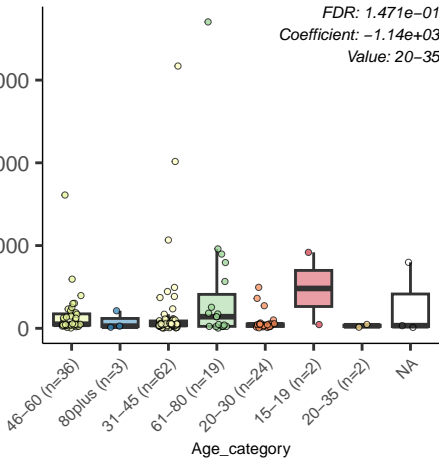
bacteria.c__Gammaproteobacteria.o__Alteromonadales.f__Pseudo

FDR: 1.462e-01
Coefficient: -5.50e+03
Value: 46-60

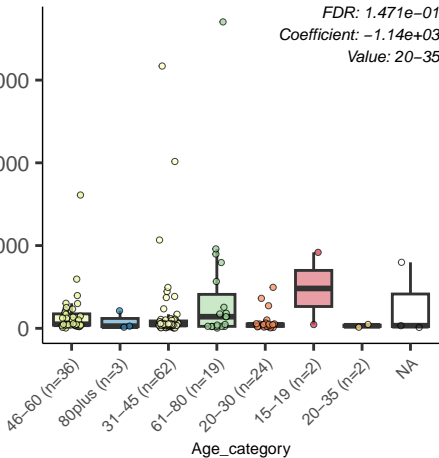


Bacteria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Clostridia

FDR: $1.471\text{e-}01$
Coefficient: $-1.14\text{e}+03$
Value: 20-35

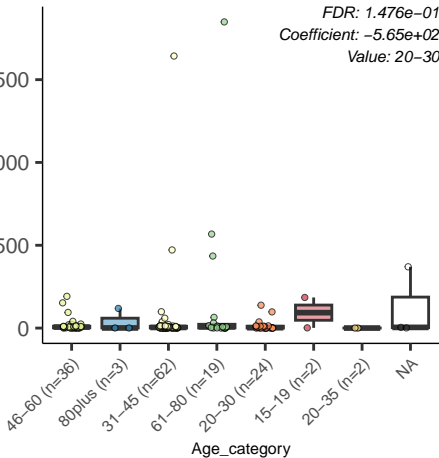


FDR: $1.471\text{e-}01$
Coefficient: $-1.14\text{e}+03$
Value: 20-35



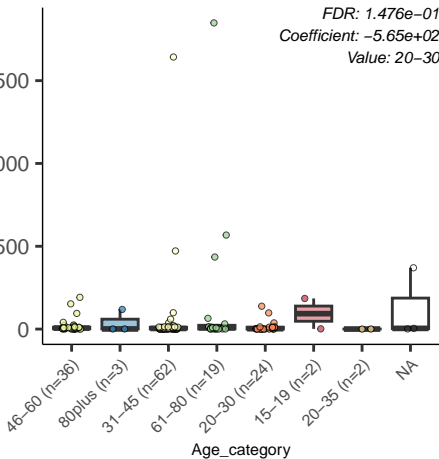
Bacteria.p__Proteobacteria.c__Betaproteobacteria.o__Burkholder

FDR: $1.476e-01$
Coefficient: $-5.65e+02$
Value: 20-30



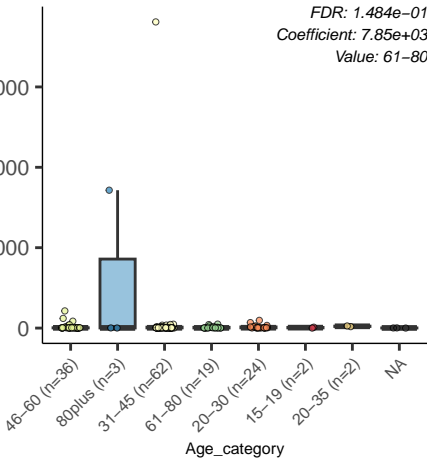
Proteobacteria.c__Betaproteobacteria.o__Burkholderiales.g__Aquini

FDR: 1.476e-01
Coefficient: -5.65e+02
Value: 20-30



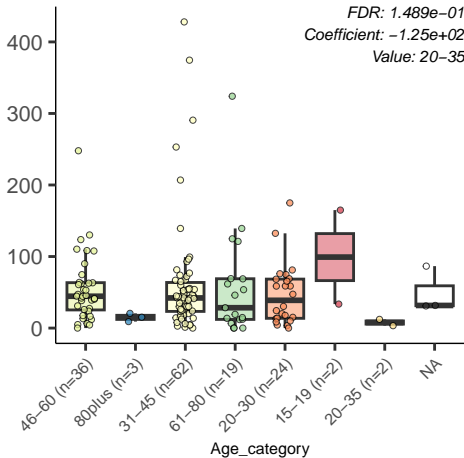
Actinomycetia.o__Corynebacteriales.f__Corynebacteriaceae.g__C

FDR: 1.484e-01
Coefficient: 7.85e+03
Value: 61-80



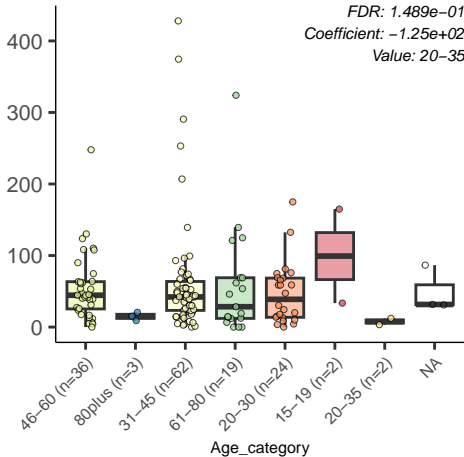
oebacteria.c__Gammaproteobacteria.o__Oceanospirillales.f__Halor

FDR: $1.489\text{e-}01$
Coefficient: $-1.25\text{e}+02$
Value: 20-35



maproteobacteria.o__Oceanospirillales.f__Halomonadaceae.g__Ca

FDR: 1.489e-01
Coefficient: -1.25e+02
Value: 20-35



icutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Strept

FDR: 1.496e-01
Coefficient: -6.21e+03
Value: 31-45

60000

40000

20000

0

Age_category

46-60 (n=36)

80plus (n=3)

31-45 (n=62)

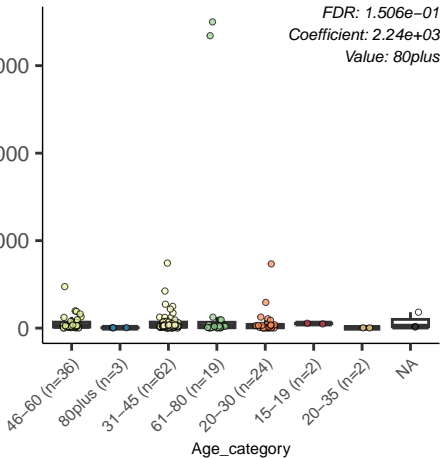
61-80 (n=19)

20-30 (n=24)

15-19 (n=2)

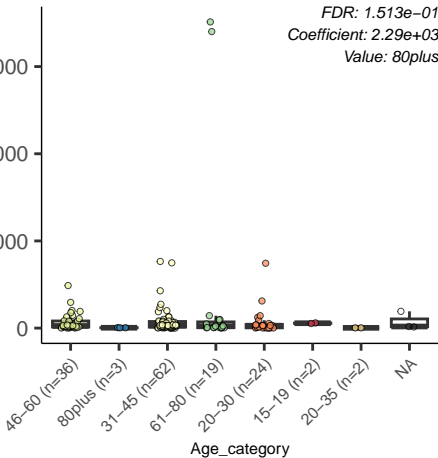
20-35 (n=2)

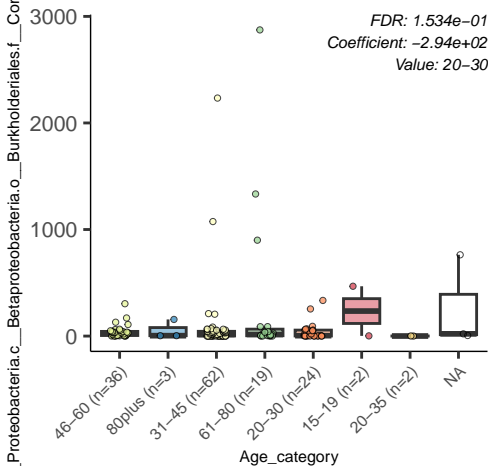
NA



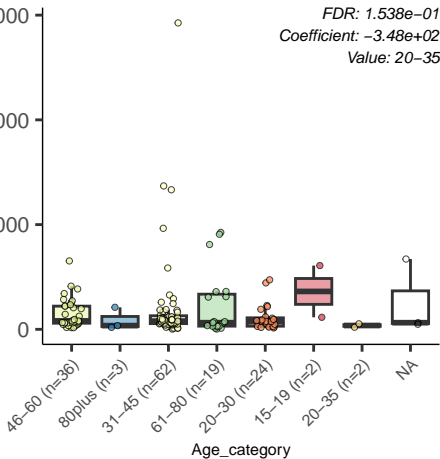
d__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Ae

FDR: 1.513e-01
Coefficient: 2.29e+03
Value: 80plus

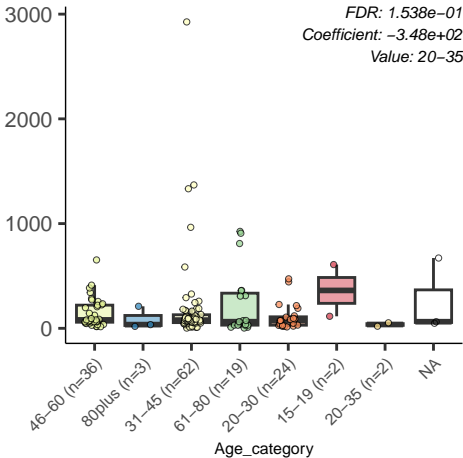




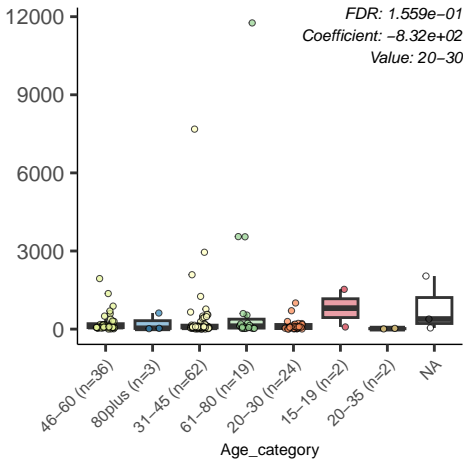
ia.p__Proteobacteria.c__Alphaproteobacteria.o__Hyphomicrobiales



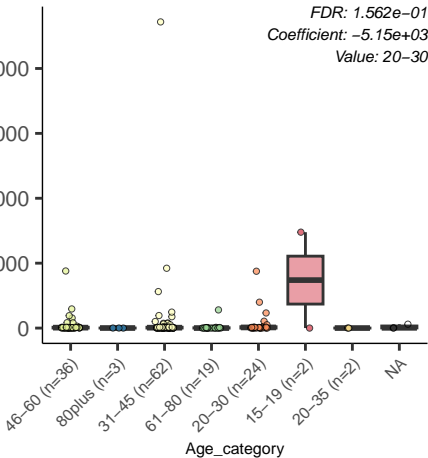
ria.c__Alphaproteobacteria.o__Hyphomicrobiales.g__Candidatus.H

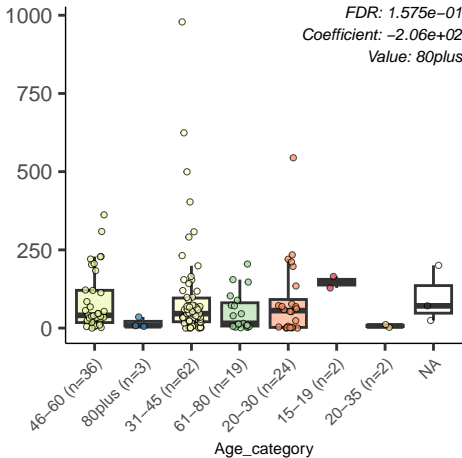


bacteria.p__Proteobacteria.c__Betaproteobacteria.o__Burkholderia

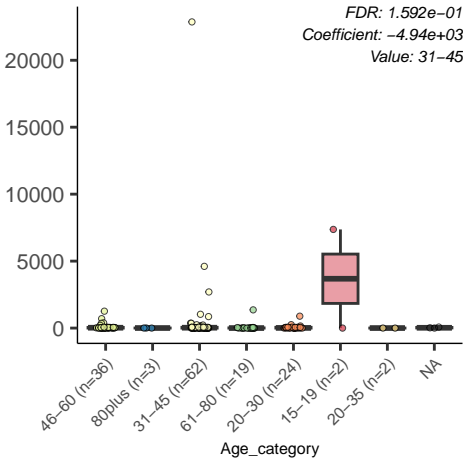


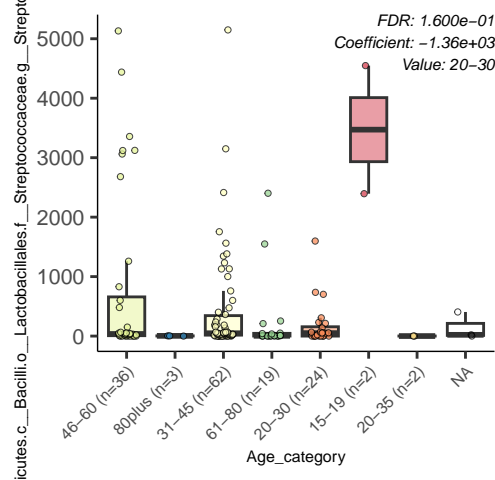
bacteria.c__Gammaproteobacteria.o__Alteromonadales.f__Pseudo



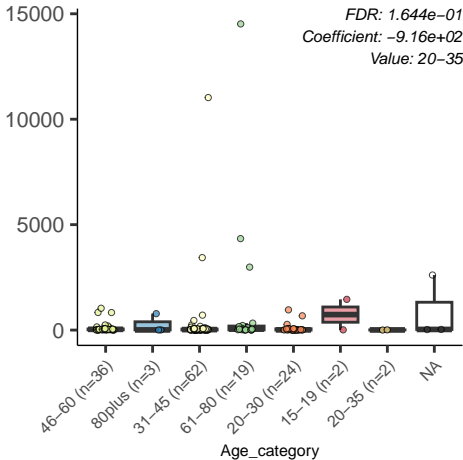


ammaproteobacteria.o__Alteromonadales.f__Pseudoalteromonada

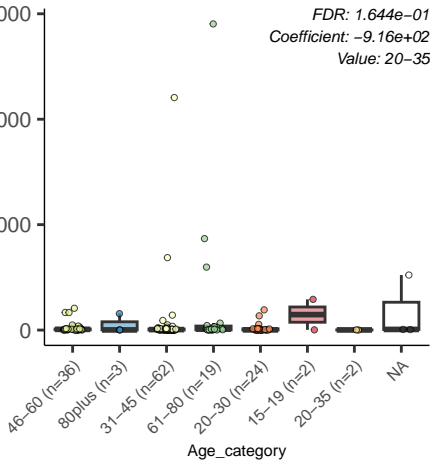


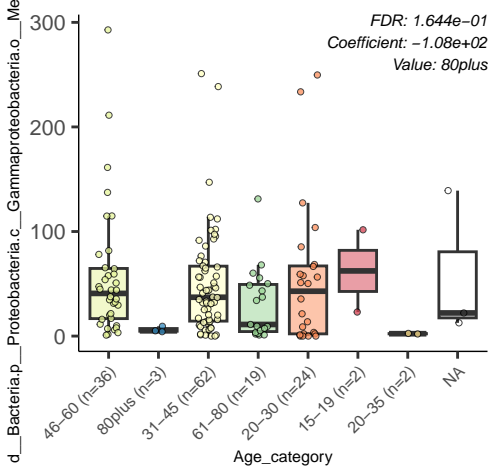


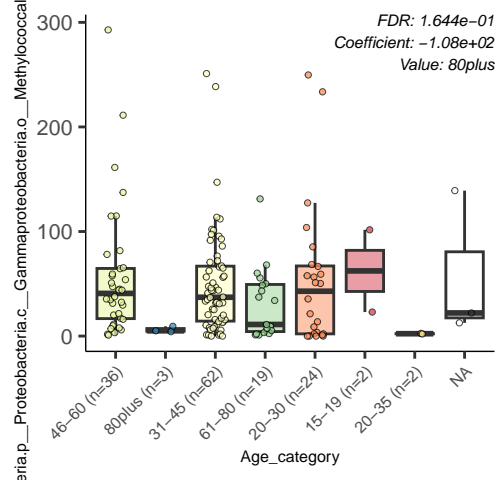
obacteria.c__Betaproteobacteria.o__Burkholderiales.f__Comamonad



proteobacteria.o__Burkholderiales.f__Comamonadaceae.g__Candido

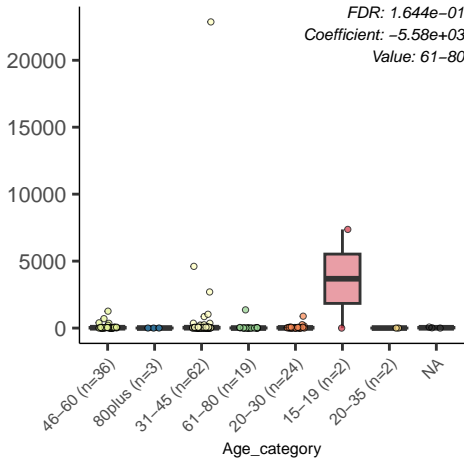






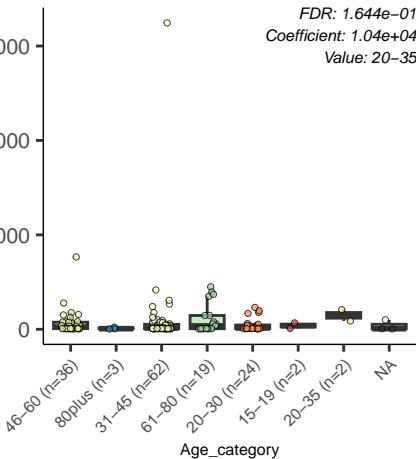
ammaproteobacteria.o__Alteromonadales.f__Pseudoalteromonada

FDR: $1.644e-01$
Coefficient: $-5.58e+03$
Value: 61-80



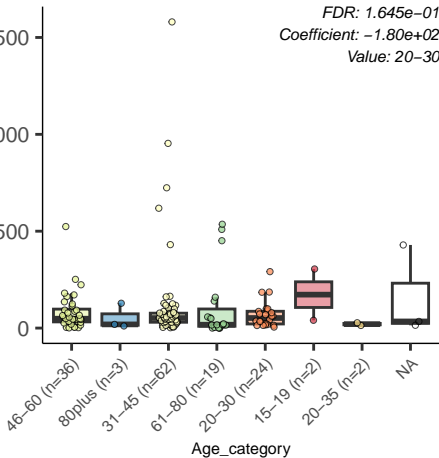
ria.c__Actinomycetia.o__Propionibacteriales.f__Propionibacteriaceae

FDR: 1.644e-01
Coefficient: 1.04e+04
Value: 20-35

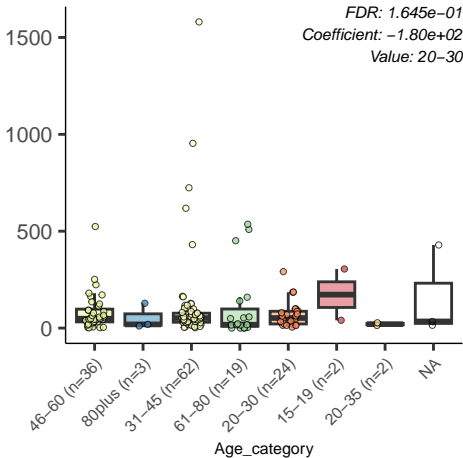


ia.p__Bacteroidetes.c__Flavobacteriia.o__Flavobacteriales.f__Flavo

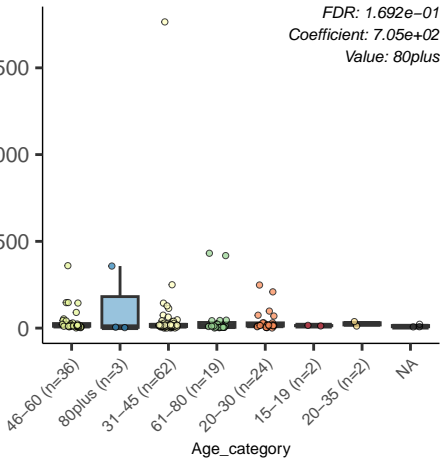
FDR: 1.645e-01
Coefficient: -1.80e+02
Value: 20-30



cteroidetes.c__Flavobacteriia.o__Flavobacteriales.f__Flavobacteriia

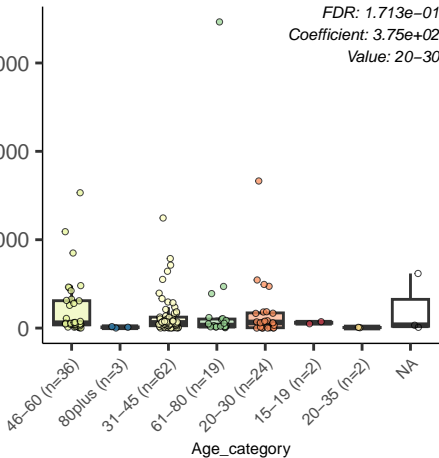


icutes.c__Tissierellia.o__Tissierellales.f__Peptoniphilaceae.g__Ana



Bacteroidetes.c__Spingobacteriia.o__Spingobacteriales.f__Sph

FDR: 1.713e-01
Coefficient: 3.75e+02
Value: 20-30



icutes.c__Bacilli.o__Lactobacillales.f__Streptococcaceae.g__Strept

FDR: 1.714e-01
Coefficient: -6.83e+03
Value: 61-80

60000

40000

20000

0

46-60 (n=36)

80plus (n=3)

31-45 (n=62)

61-80 (n=19)

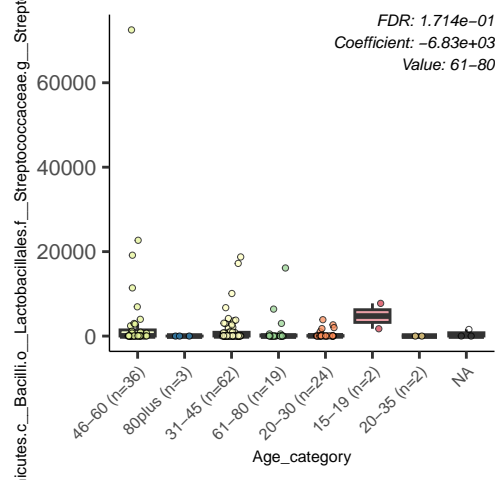
20-30 (n=24)

15-19 (n=2)

20-35 (n=2)

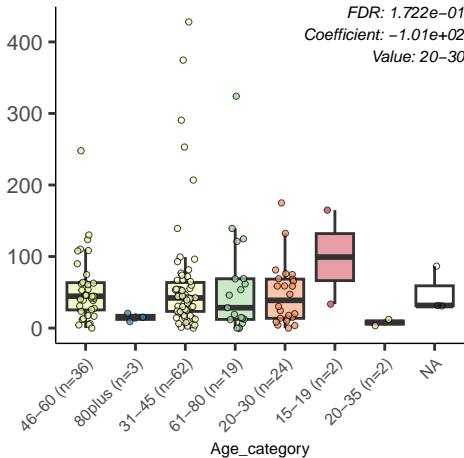
NA

Age_category



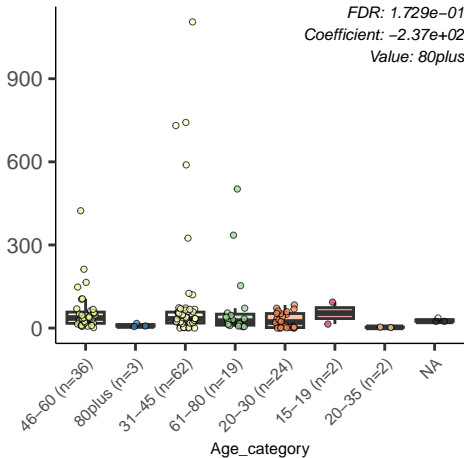
maproteobacteria.o__Oceanospirillales.f__Halomonadaceae.g__Ca

FDR: $1.722e-01$
Coefficient: $-1.01e+02$
Value: 20-30

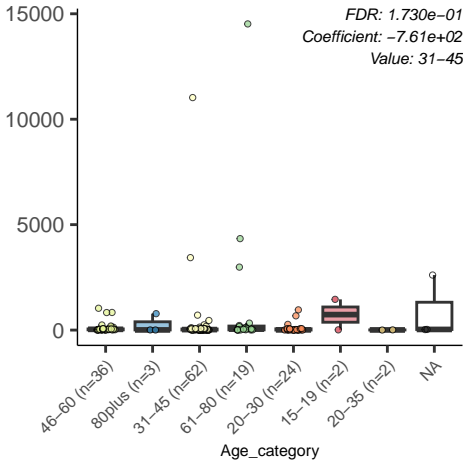


Bacteria.p_Actinobacteria.c_Actinomycetia.o_Micrococcales.f_C

FDR: 1.729e-01
Coefficient: -2.37e+02
Value: 80plus

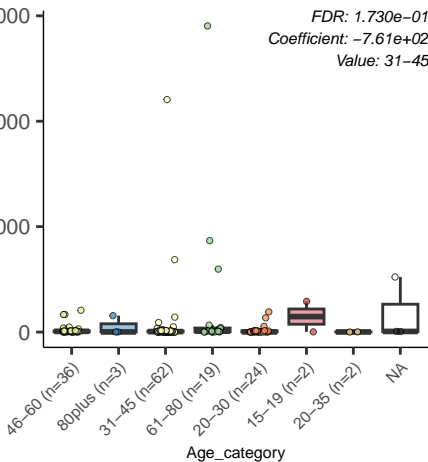


obacteria.c__Betaproteobacteria.o__Burkholderiales.f__Comamonad



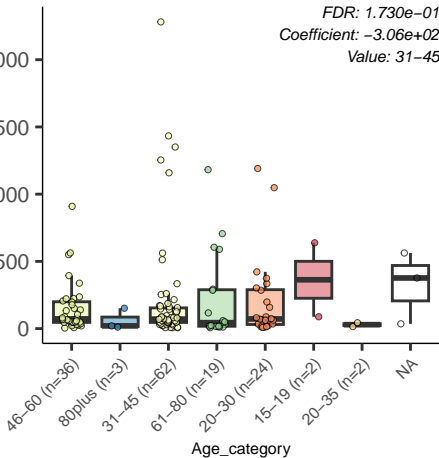
proteobacteria.o__Burkholderiales.f__Comamonadaceae.g__Candido

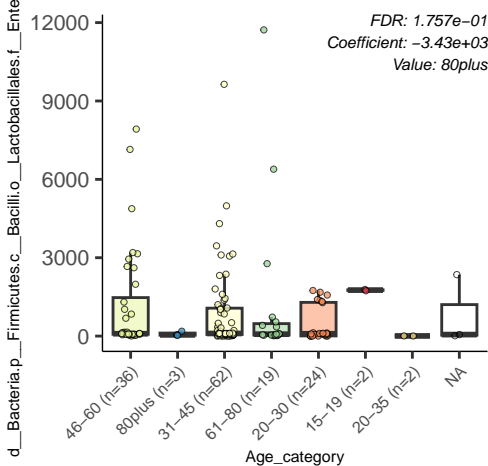
FDR: 1.730e-01
Coefficient: -7.61e+02
Value: 31-45

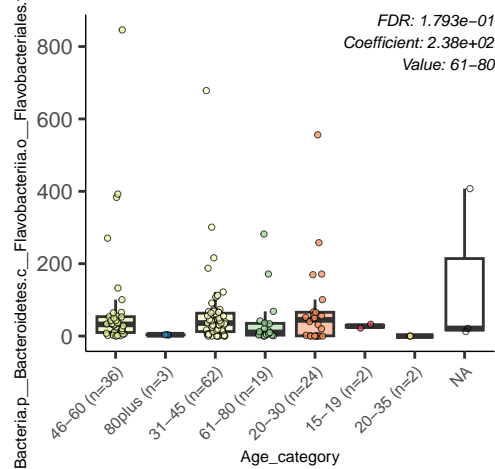


bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rickettsiales

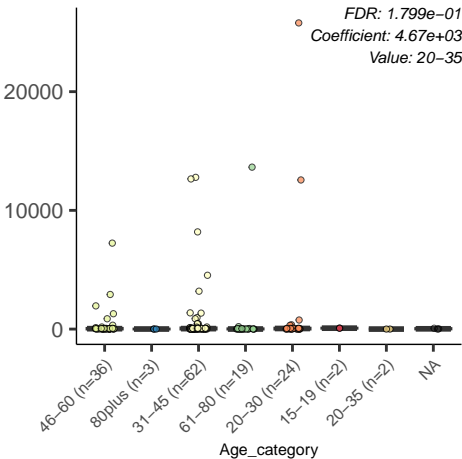
FDR: $1.730e-01$
Coefficient: $-3.06e+02$
Value: 31-45



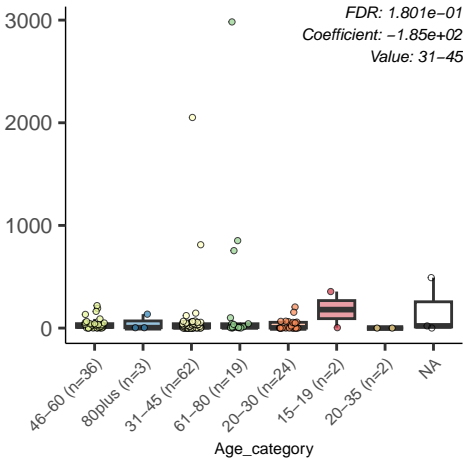


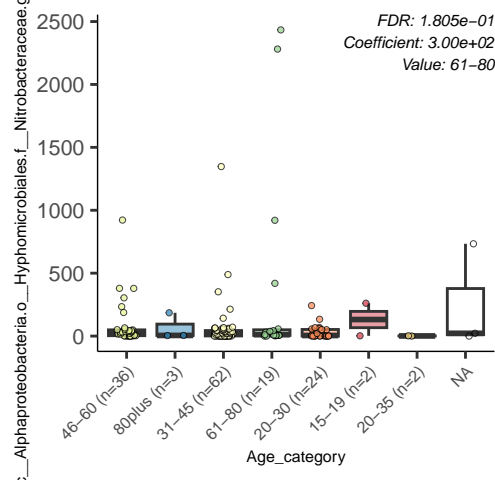


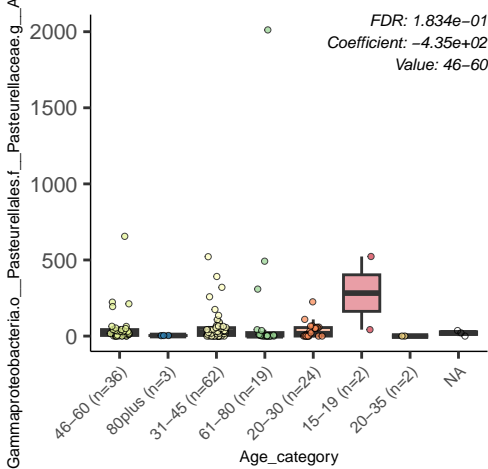
__Epsilonproteobacteria.o__Campylobacterales.f__Campylobacter



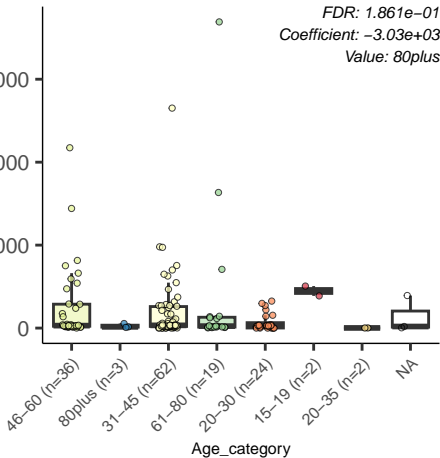
bacteria.c__Alphaproteobacteria.o__Hyphomicrobiales.f__Rhizobia





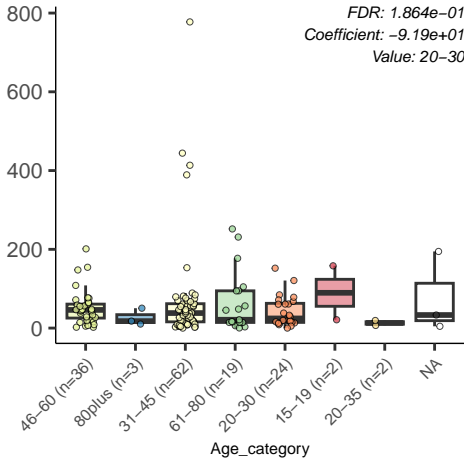


acteria.p_Firmicutes.c_Bacilli.o_Lactobacillales.f_Enterococcae



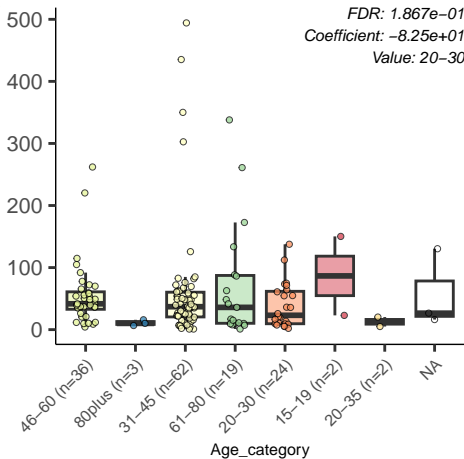
phaproteobacteria.o__Rickettsiales.f__Rickettsiaceae.g__Rickettsia

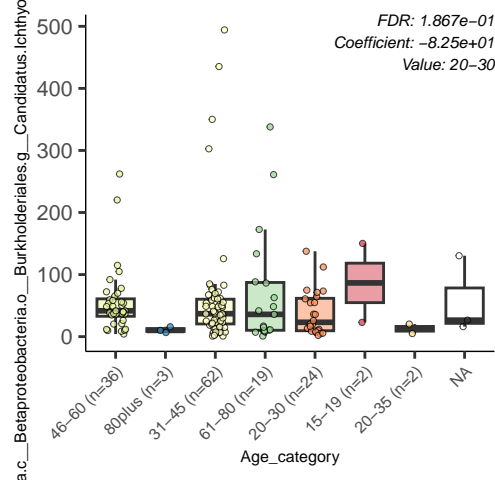
FDR: $1.864e-01$
Coefficient: $-9.19e+01$
Value: 20-30



ia.p__Proteobacteria.c__Betaproteobacteria.o__Burkholderiales.g

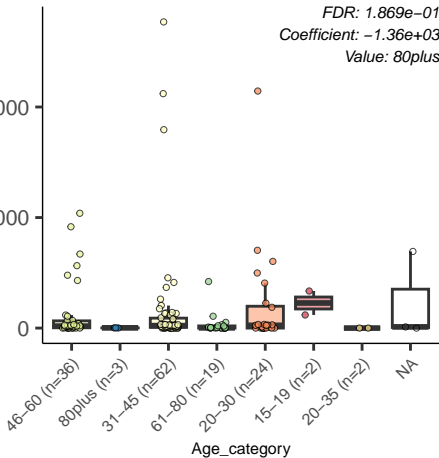
FDR: 1.867e-01
Coefficient: -8.25e+01
Value: 20-30

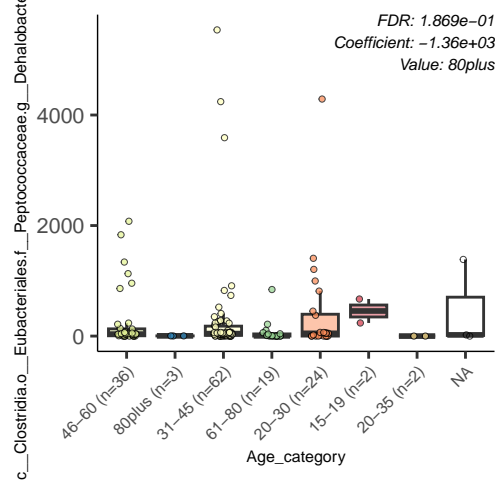


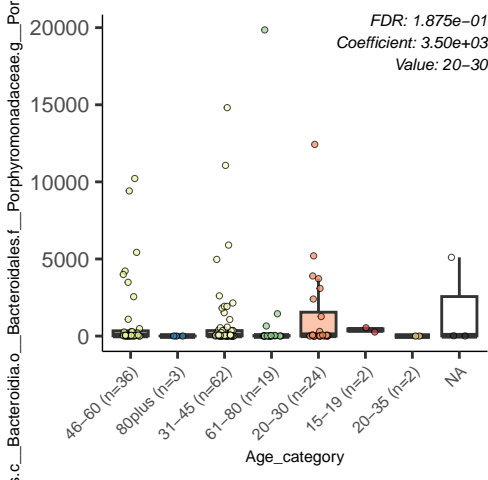


eria.p__Firmicutes.c__Clostridia.o__Eubacteriales.f__Peptococcaceae

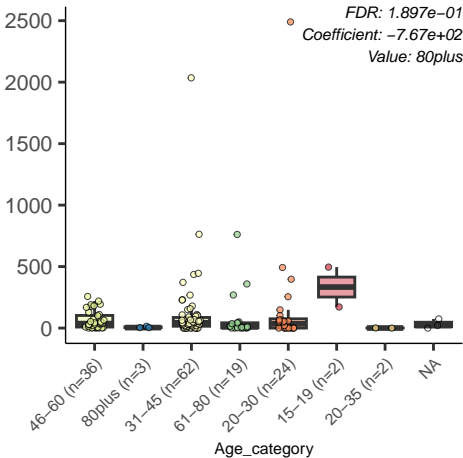
FDR: 1.869e-01
Coefficient: -1.36e+03
Value: 80plus





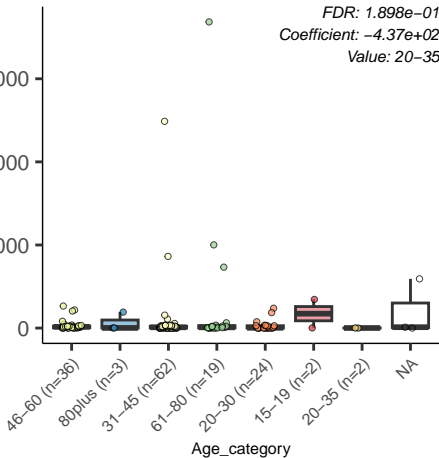


eria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae



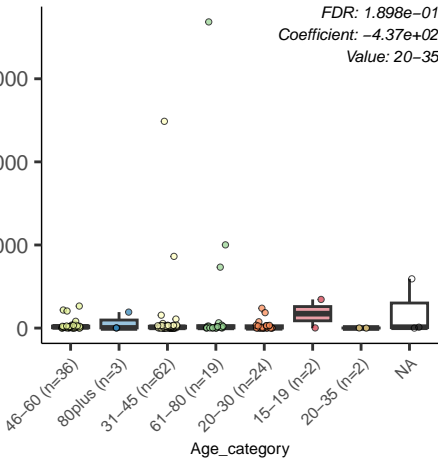
Bacteria.p__Proteobacteria.c__Betaproteobacteria.o__Burkholder

FDR: 1.898e-01
Coefficient: -4.37e+02
Value: 20-35



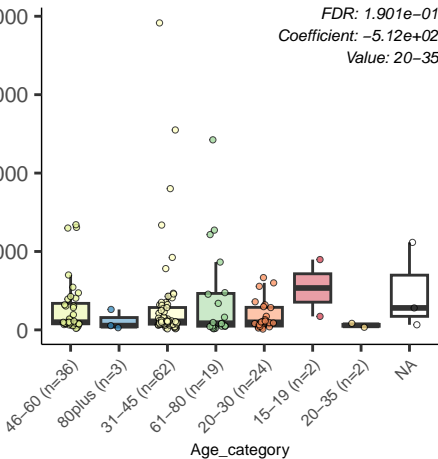
Proteobacteria.c__Betaproteobacteria.o__Burkholderiales.g__Lept

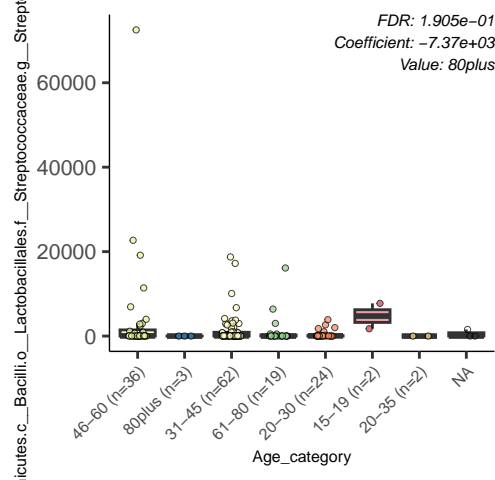
FDR: 1.898e-01
Coefficient: -4.37e+02
Value: 20-35

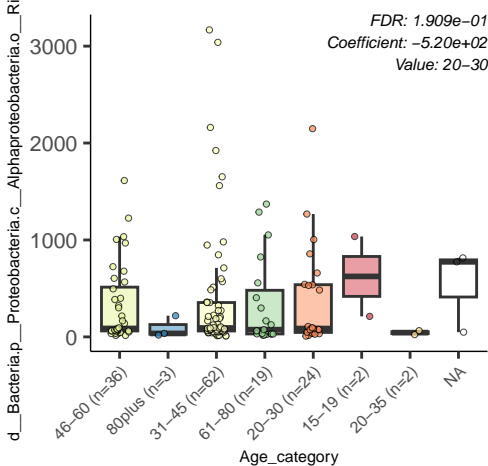


d__Bacteria.p__Cyanobacteria.o__Synechococcales.f__Synech

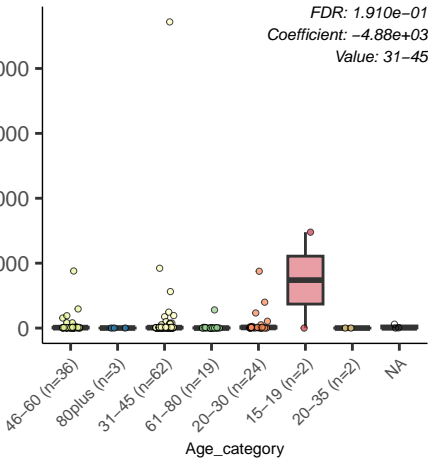
FDR: $1.901e-01$
Coefficient: $-5.12e+02$
Value: 20-35

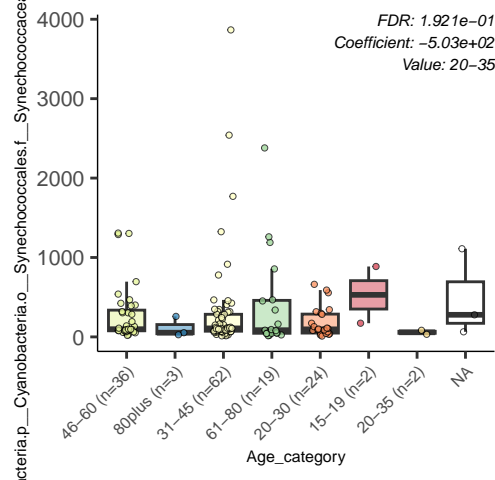






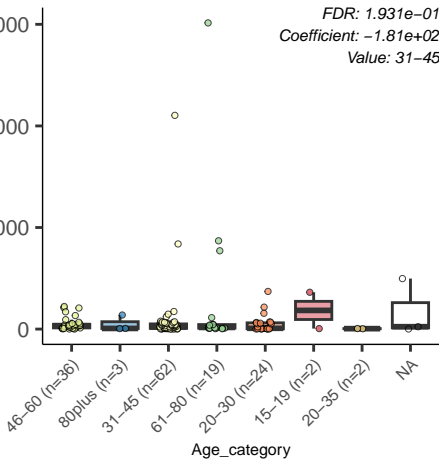
bacteria.c__Gammaproteobacteria.o__Alteromonadales.f__Pseudo

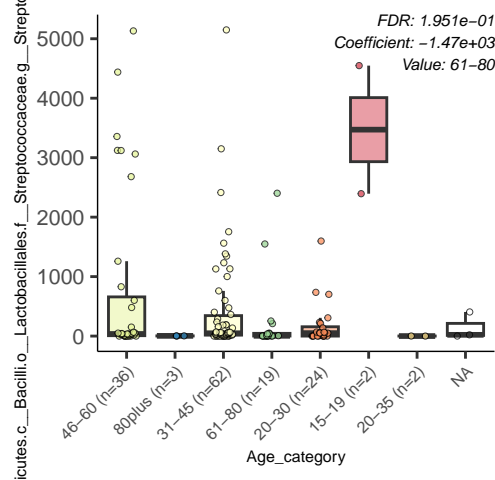




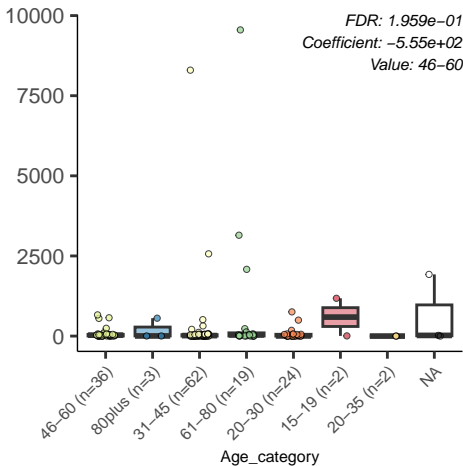
.p__Proteobacteria.c__Alphaproteobacteria.o__Hyphomicrobiales.f

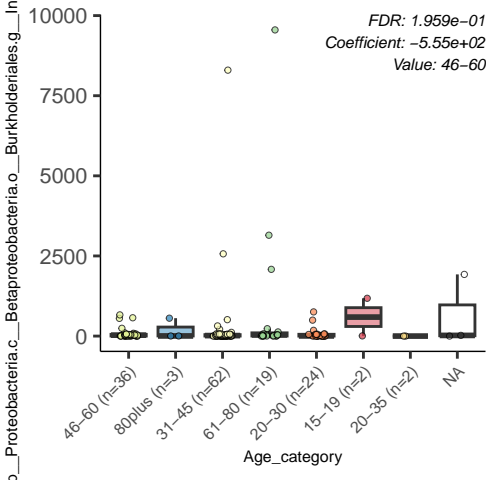
FDR: 1.931e-01
Coefficient: -1.81e+02
Value: 31-45



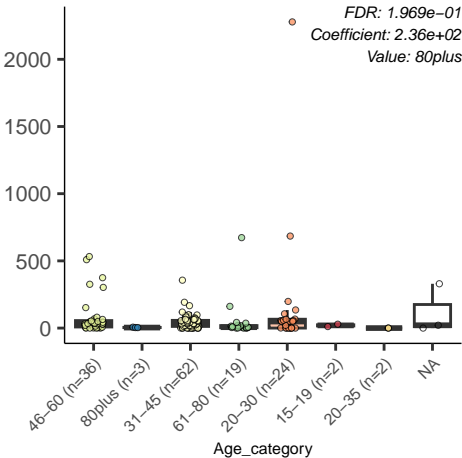


l_Bacteria.p__Proteobacteria.c__Betaproteobacteria.o__Burkholder

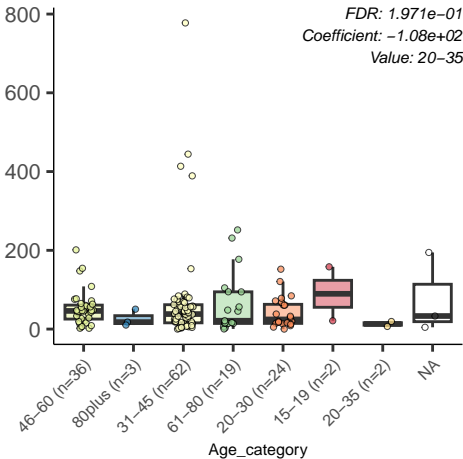




Bacteria.p__Bacteroidetes.c__Flavobacteriia.o__Flavobacteriales.f

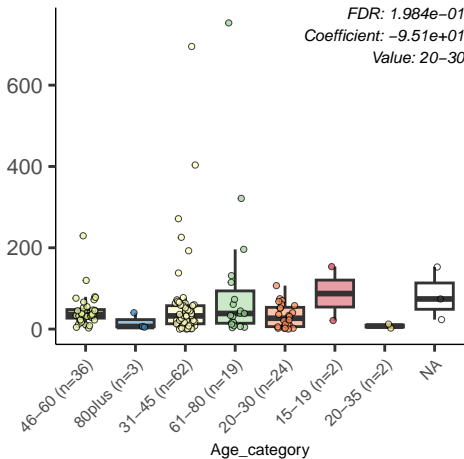


phaproteobacteria.o__Rickettsiales.f__Rickettsiaceae.g__Rickettsia



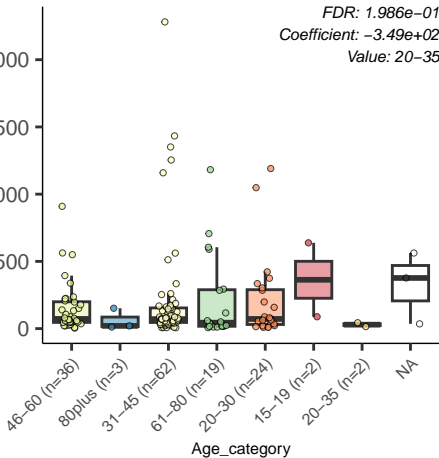
Proteobacteria.c__Betaproteobacteria.o__Burkholderiales.f__Con

FDR: $1.984e-01$
Coefficient: $-9.51e+01$
Value: 20-30

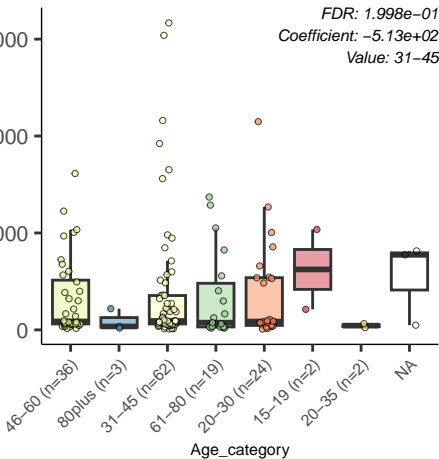


bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rickettsiales

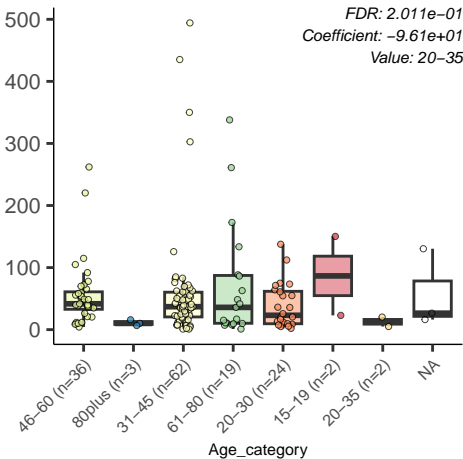
FDR: $1.986e-01$
Coefficient: $-3.49e+02$
Value: 20-35

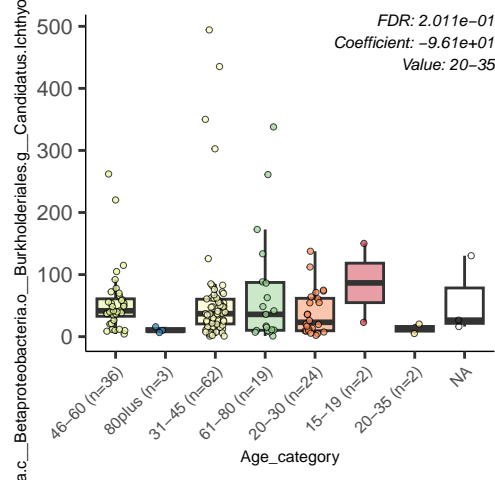


d__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o_R



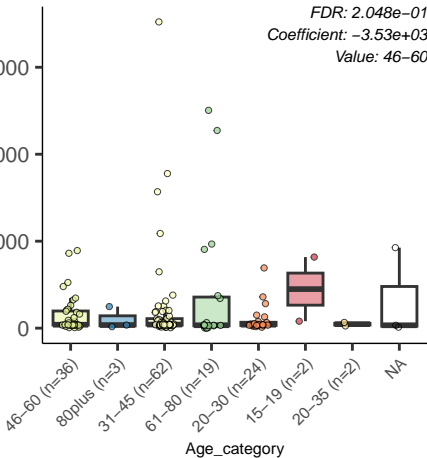
ia.p__Proteobacteria.c__Betaproteobacteria.o__Burkholderiales.g



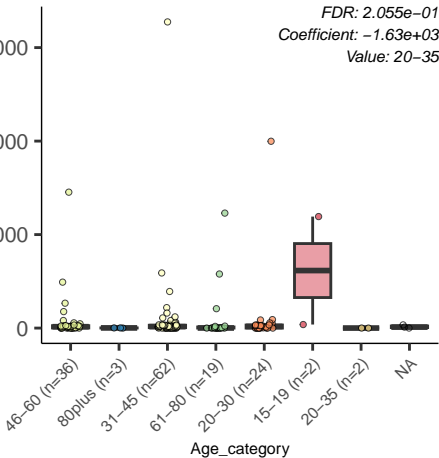


Firmicutes.c__Clostridia.o__Eubacteriales.f__Clostridiaceae.g__C

FDR: 2.048e-01
Coefficient: -3.53e+03
Value: 46-60

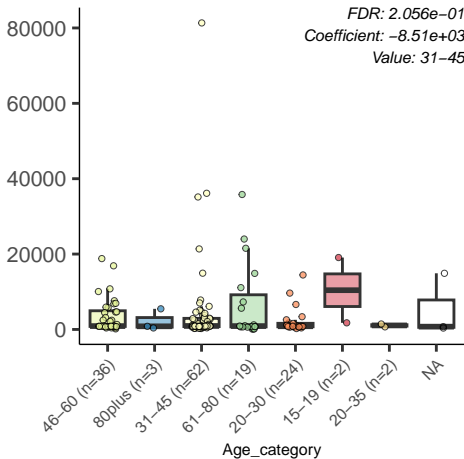


ia.c__Gammaproteobacteria.o__Pasteurellales.f__Pasteurellaceae.



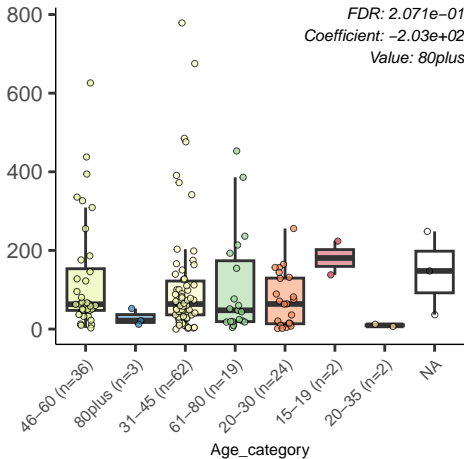
terial.c__Gammaproteobacteria.o__Pasteurellales.f__Pasteurellaceae

FDR: 2.056e-01
Coefficient: -8.51e+03
Value: 31-45

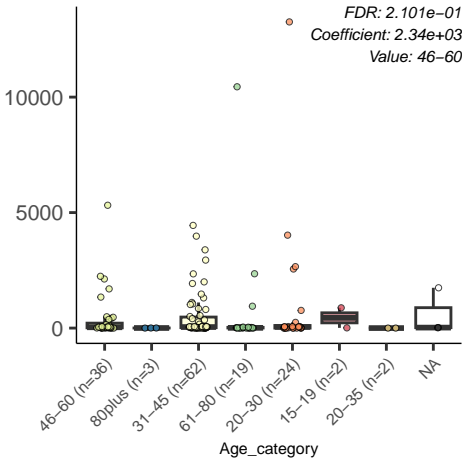


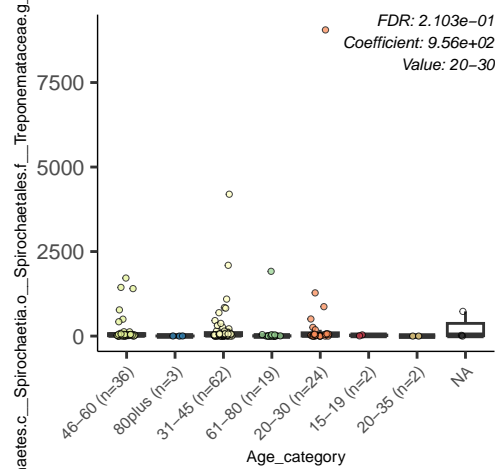
d__Bacteria.p__Cyanobacteria.o__Oscillatoriales.f__Oscillatoria

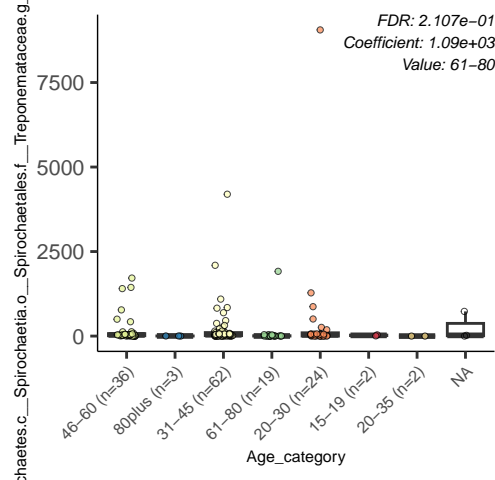
FDR: 2.071e-01
Coefficient: -2.03e+02
Value: 80plus

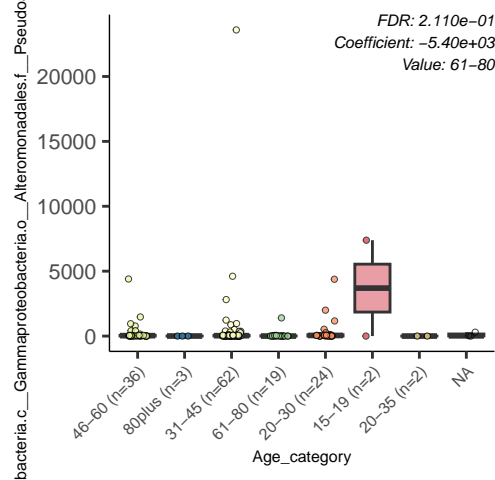


Gamma__Gammaproteobacteria.o__Cardiobacteriales.f__Cardiobacteriaceae



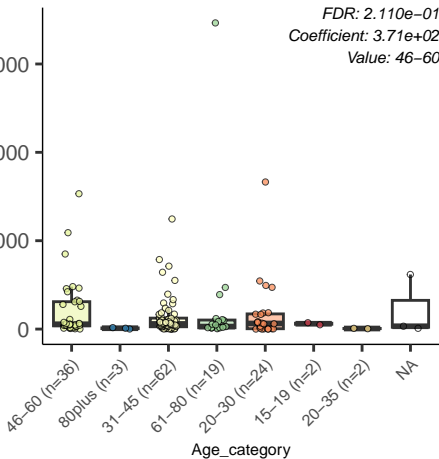


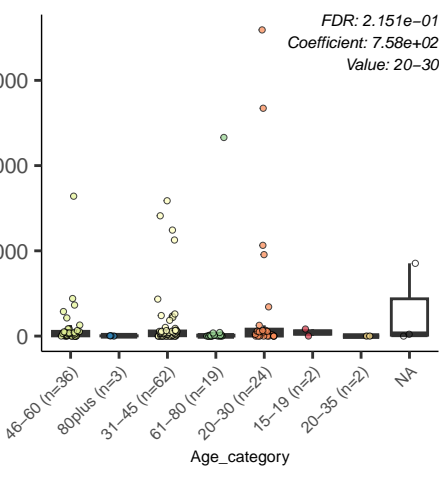


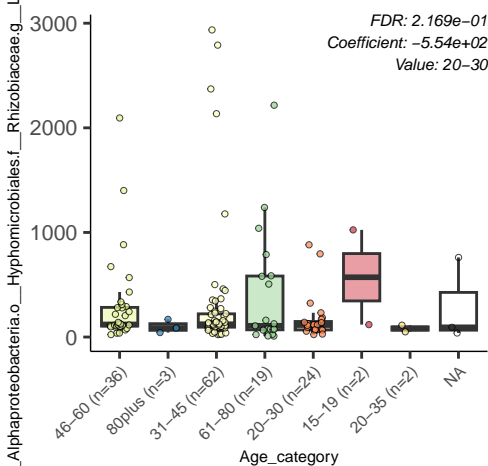


Bacteroidetes.c__Spingobacteriia.o__Spingobacteriales.f__Sphingobacterium

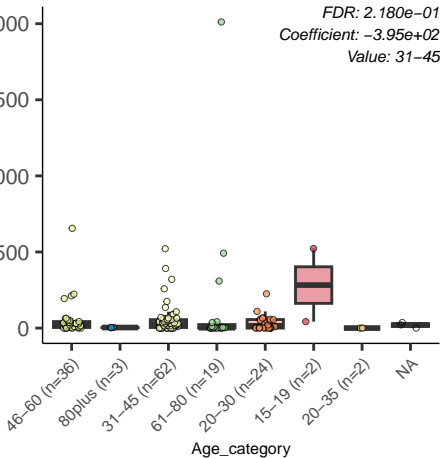
FDR: 2.110e-01
Coefficient: 3.71e+02
Value: 46-60





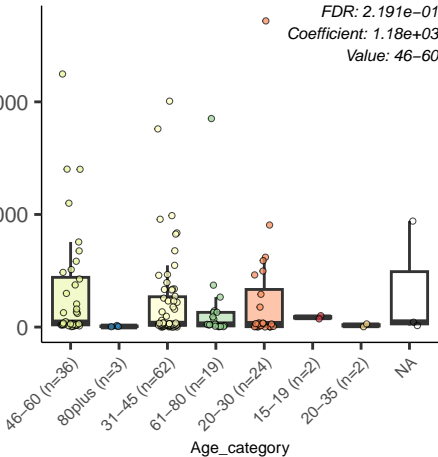


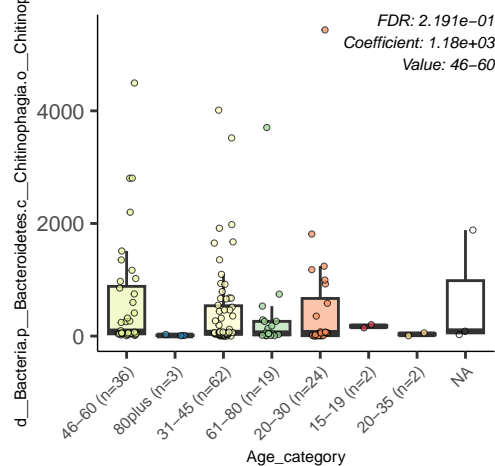
Gamma__Gammaproteobacteria.o__Pasteurellales.f__Pasteurellaceae.g__A



d__Bacteria.p__Bacteroidetes.c__Chitinophagia

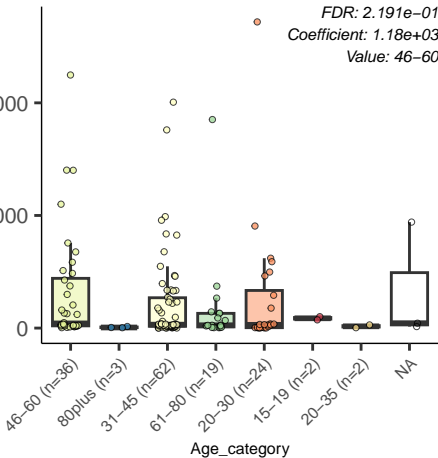
FDR: 2.191e-01
Coefficient: 1.18e+03
Value: 46-60





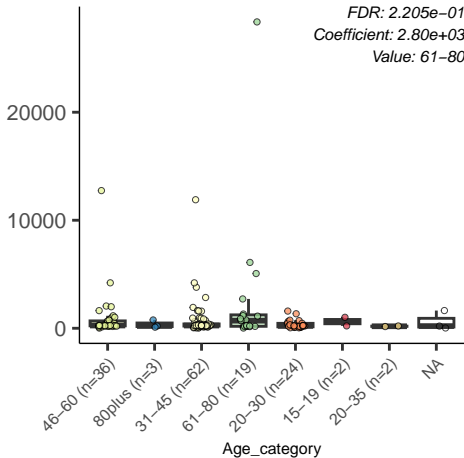
Bacteria.p__Bacteroidetes.c__Chitinophagia.o__Chitinophagales.f

FDR: 2.191e-01
Coefficient: 1.18e+03
Value: 46-60



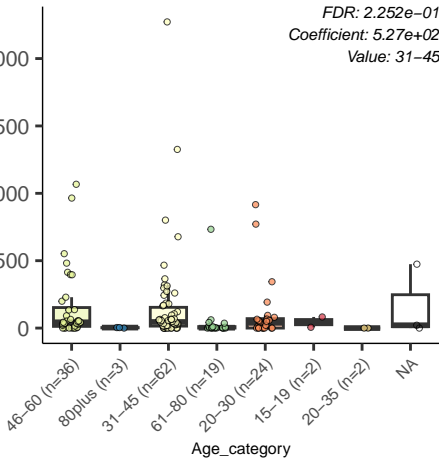
ia.p__Actinobacteria.c__Actinomycetia.o__Micrococcales.f__Micro

FDR: 2.205e-01
Coefficient: 2.80e+03
Value: 61-80



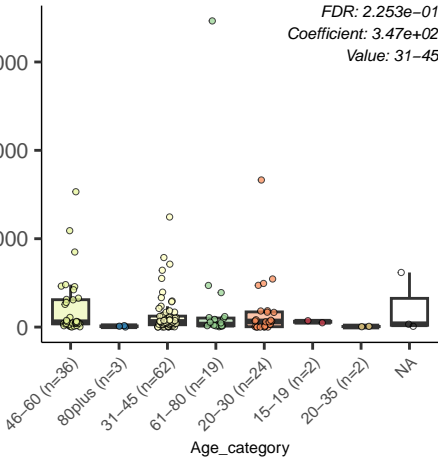
Flavobacteriia.o__Flavobacteriales.f__Flavobacteriaceae.g__Cap

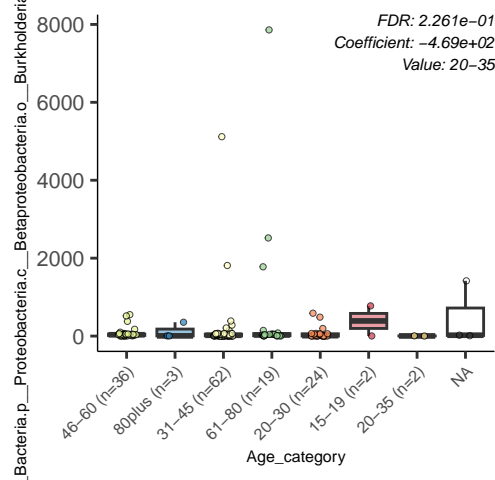
FDR: 2.252e-01
Coefficient: 5.27e+02
Value: 31-45

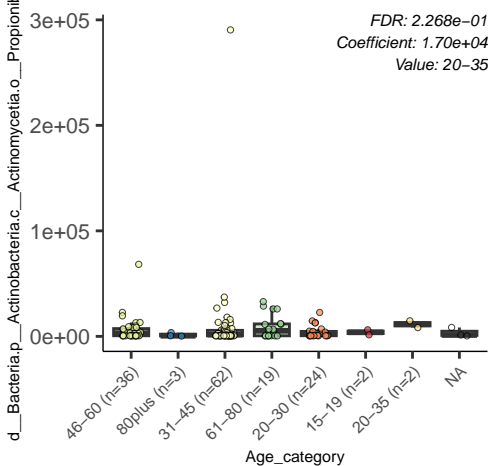


Bacteroidetes.c__Spingobacteriia.o__Spingobacteriales.f__Sphingobacteriales

FDR: 2.253e-01
Coefficient: 3.47e+02
Value: 31-45

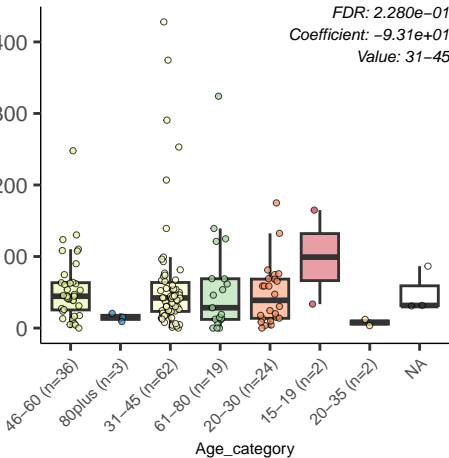






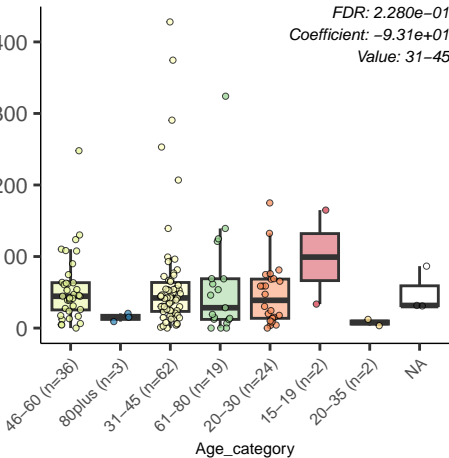
teobacteria.c__Gammaproteobacteria.o__Oceanospirillales.f__Halor

FDR: 2.280e-01
Coefficient: -9.31e+01
Value: 31-45



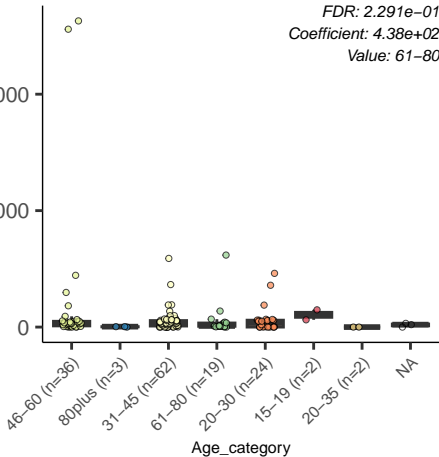
maproteobacteria.o__Oceanospirillales.f__Halomonadaceae.g__Ca

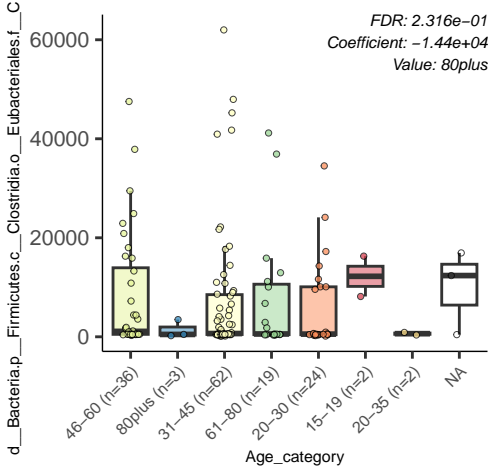
FDR: 2.280e-01
Coefficient: -9.31e+01
Value: 31-45



es.c__Clostridia.o__Eubacteriales.f__Oscillospiraceae.g__Faecalib

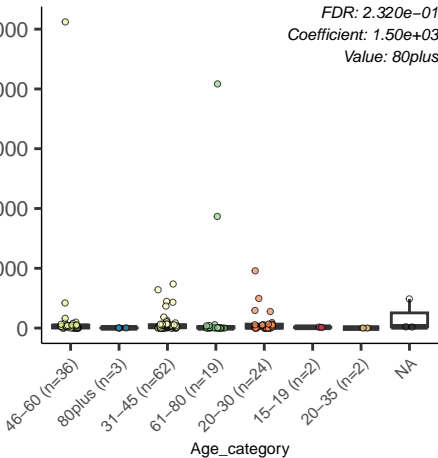
FDR: 2.291e-01
Coefficient: 4.38e+02
Value: 61-80





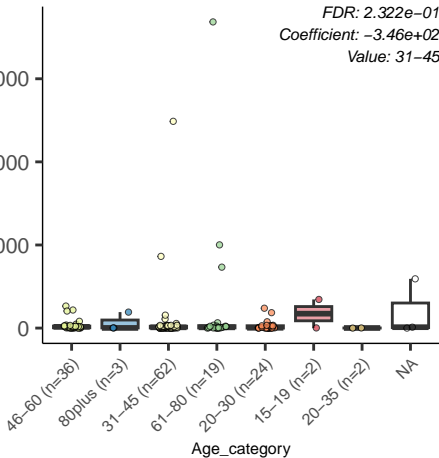
Gammaproteobacteria.o__Pasteurellales.f__Pasteurellaceae.g__Ag

FDR: 2.320e-01
Coefficient: 1.50e+03
Value: 80plus

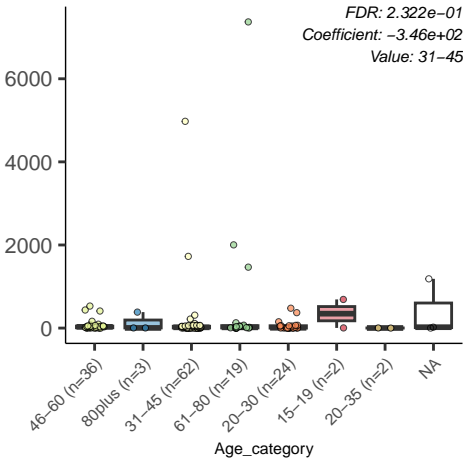


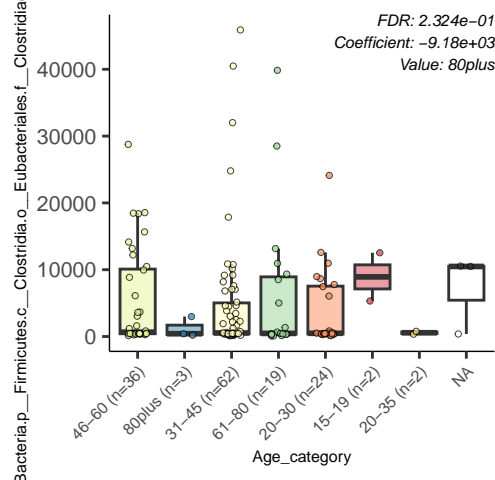
Bacteria.p__Proteobacteria.c__Betaproteobacteria.o__Burkholder

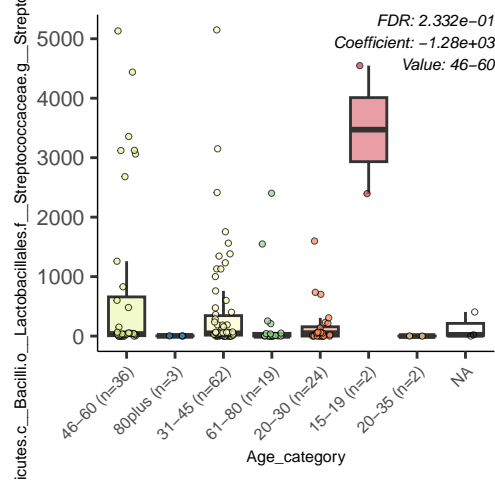
FDR: 2.322e-01
Coefficient: -3.46e+02
Value: 31-45

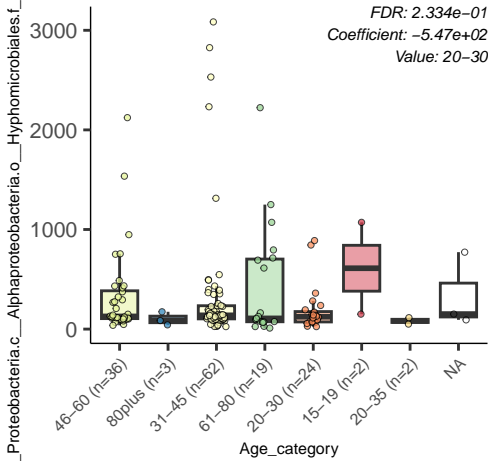


Proteobacteria.c__Betaproteobacteria.o__Burkholderiales.g__Lept



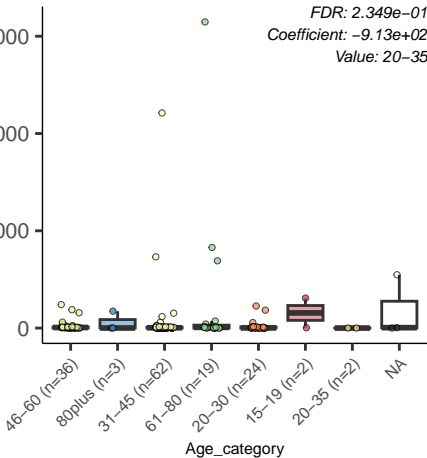




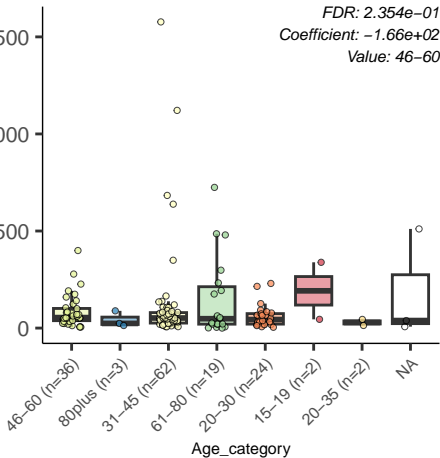


obacteria.c__Betaproteobacteria.o__Burkholderiales.f__Comamonad

FDR: 2.349e-01
Coefficient: -9.13e+02
Value: 20-35

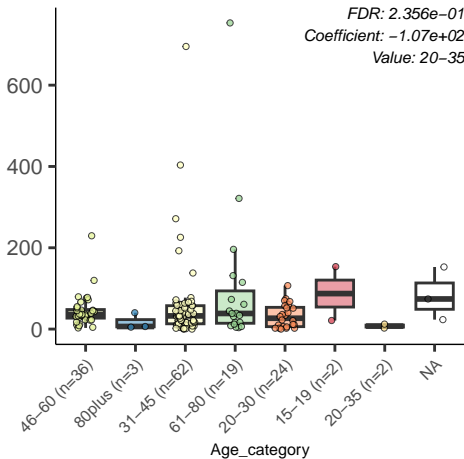


bacteria.o__Synechococcales.f__Synechococcaceae.g__Synechococcus



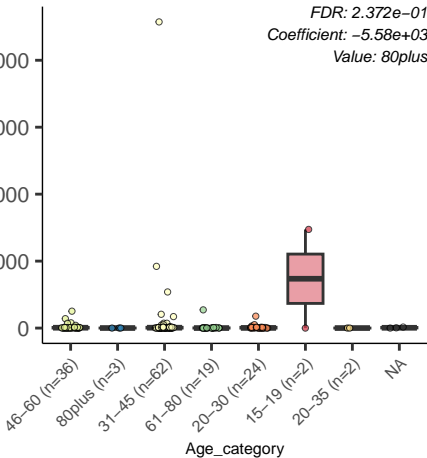
Proteobacteria.c__Betaproteobacteria.o__Burkholderiales.f__Con

FDR: $2.356e-01$
Coefficient: $-1.07e+02$
Value: 20-35

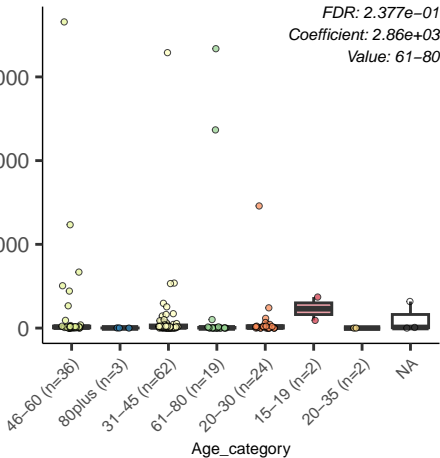


ammaproteobacteria.o__Alteromonadales.f__Pseudoalteromonada

FDR: 2.372e-01
Coefficient: -5.58e+03
Value: 80plus

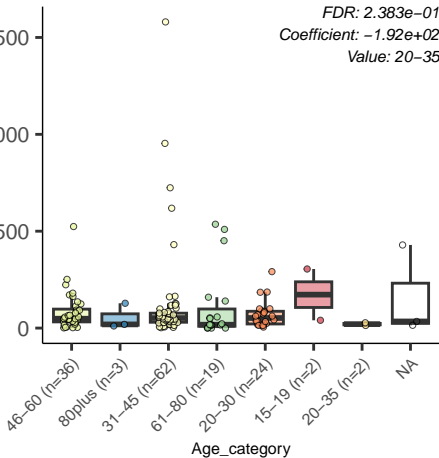


robacteria.c__Betaproteobacteria.o__Neisseriales.f__Neisseriaceae

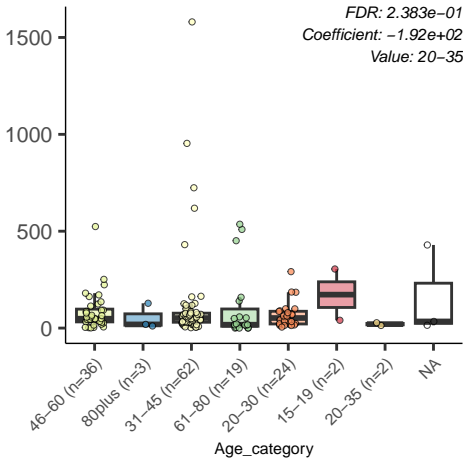


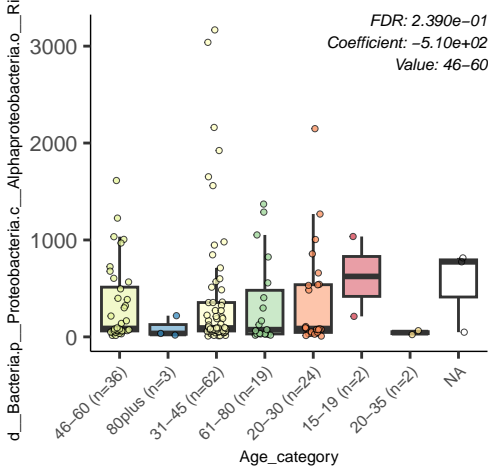
ia.p__Bacteroidetes.c__Flavobacteriia.o__Flavobacteriales.f__Flavo

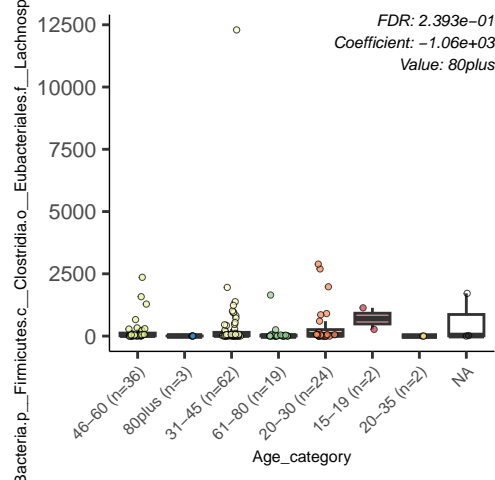
FDR: 2.383e-01
Coefficient: -1.92e+02
Value: 20-35

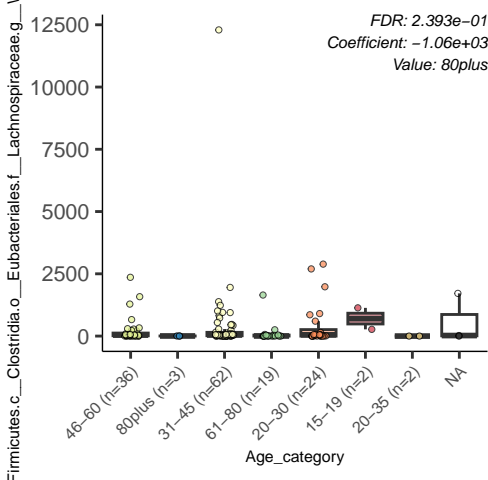


cteroidetes.c__Flavobacteriia.o__Flavobacteriales.f__Flavobacteria

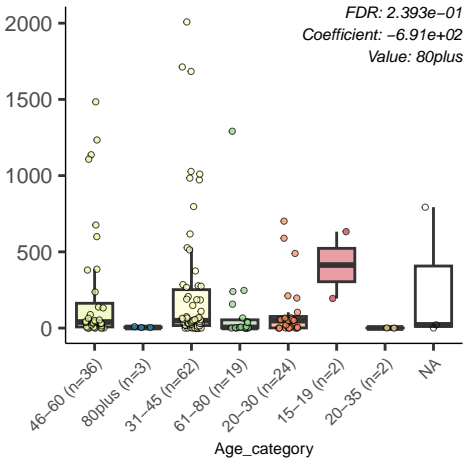


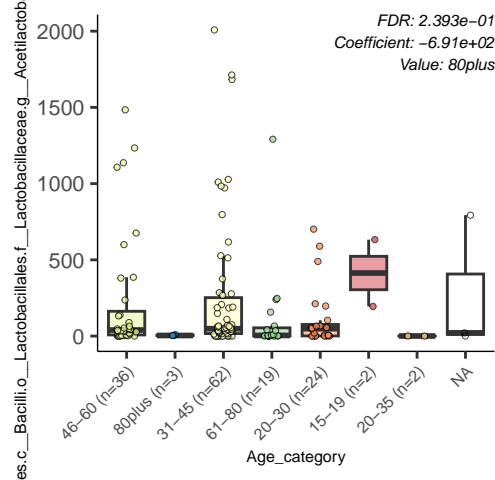




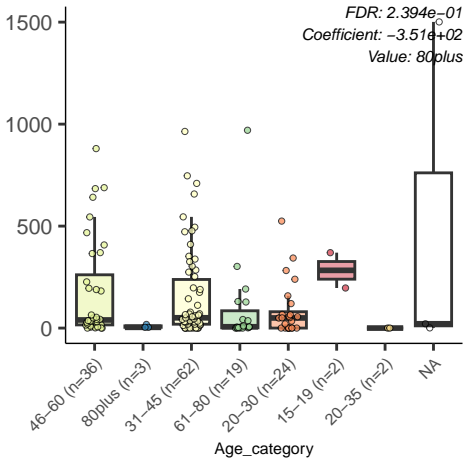


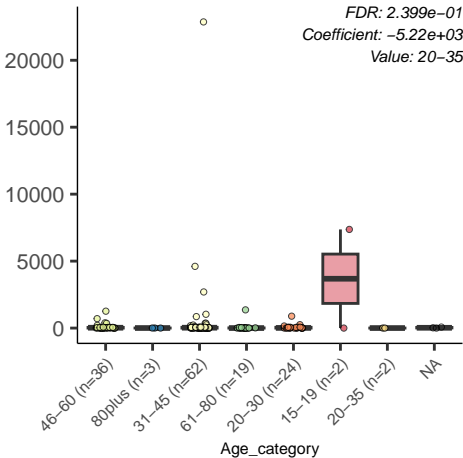
acteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillaceae

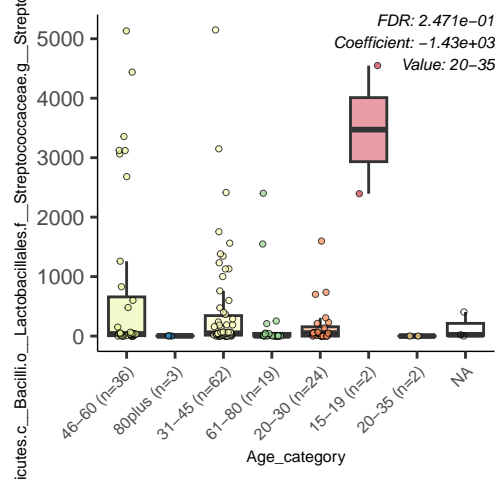


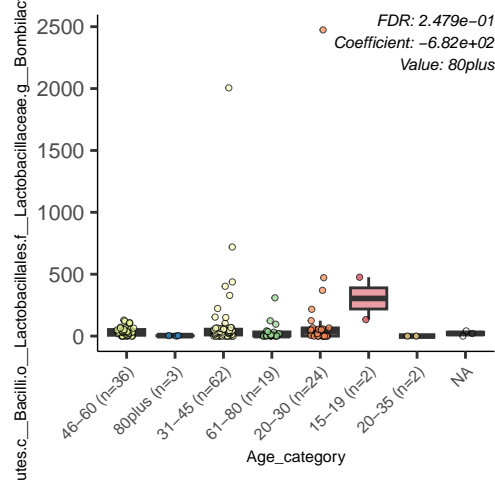


eria.p__Firmicutes.c__Bacilli.o__Bacillales.f__Bacillaceae.g__Bacil



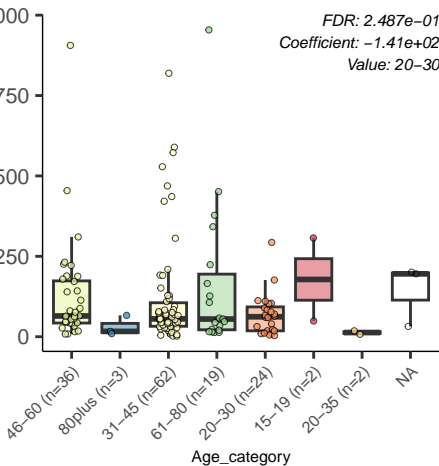






d__Bacteria.p__Proteobacteria.c__Betaproteobacteria.o__Nitros

FDR: 2.487e-01
Coefficient: -1.41e+02
Value: 20-30



Gamma__proteobacteria.o__Pasteurellales.f__Pasteurellaceae.g__A

