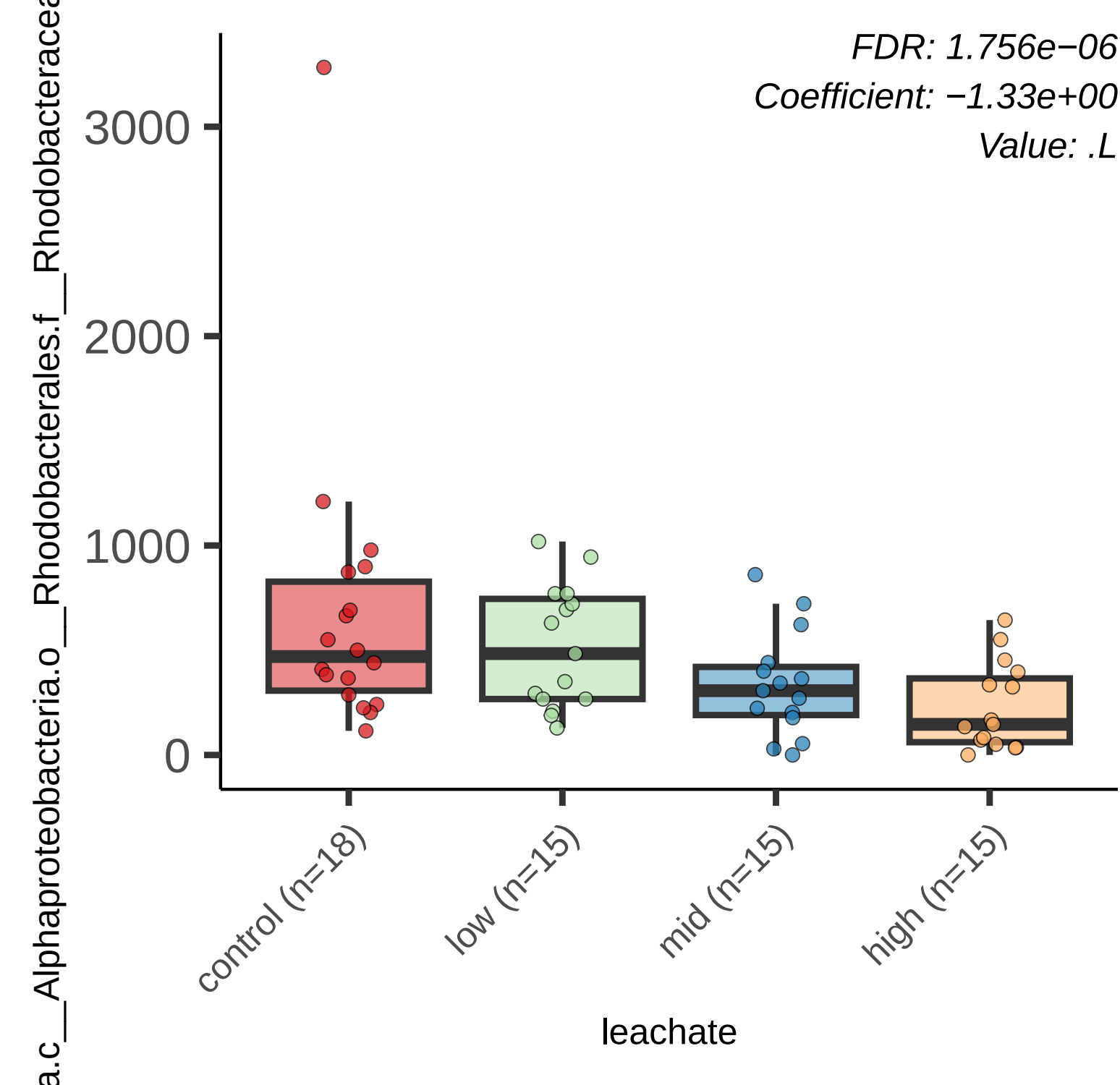
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leachate
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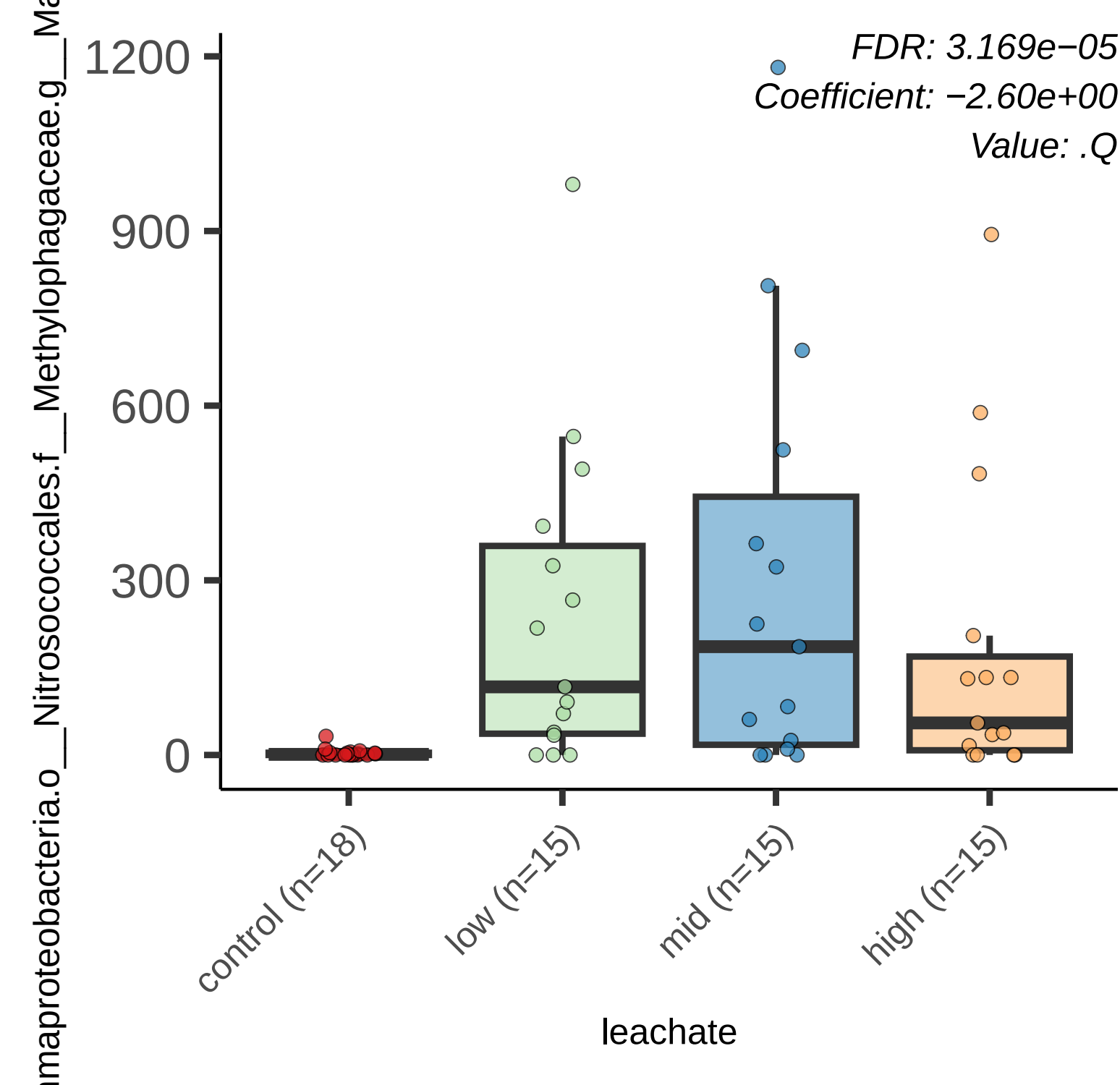
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high (n=15)
leachate
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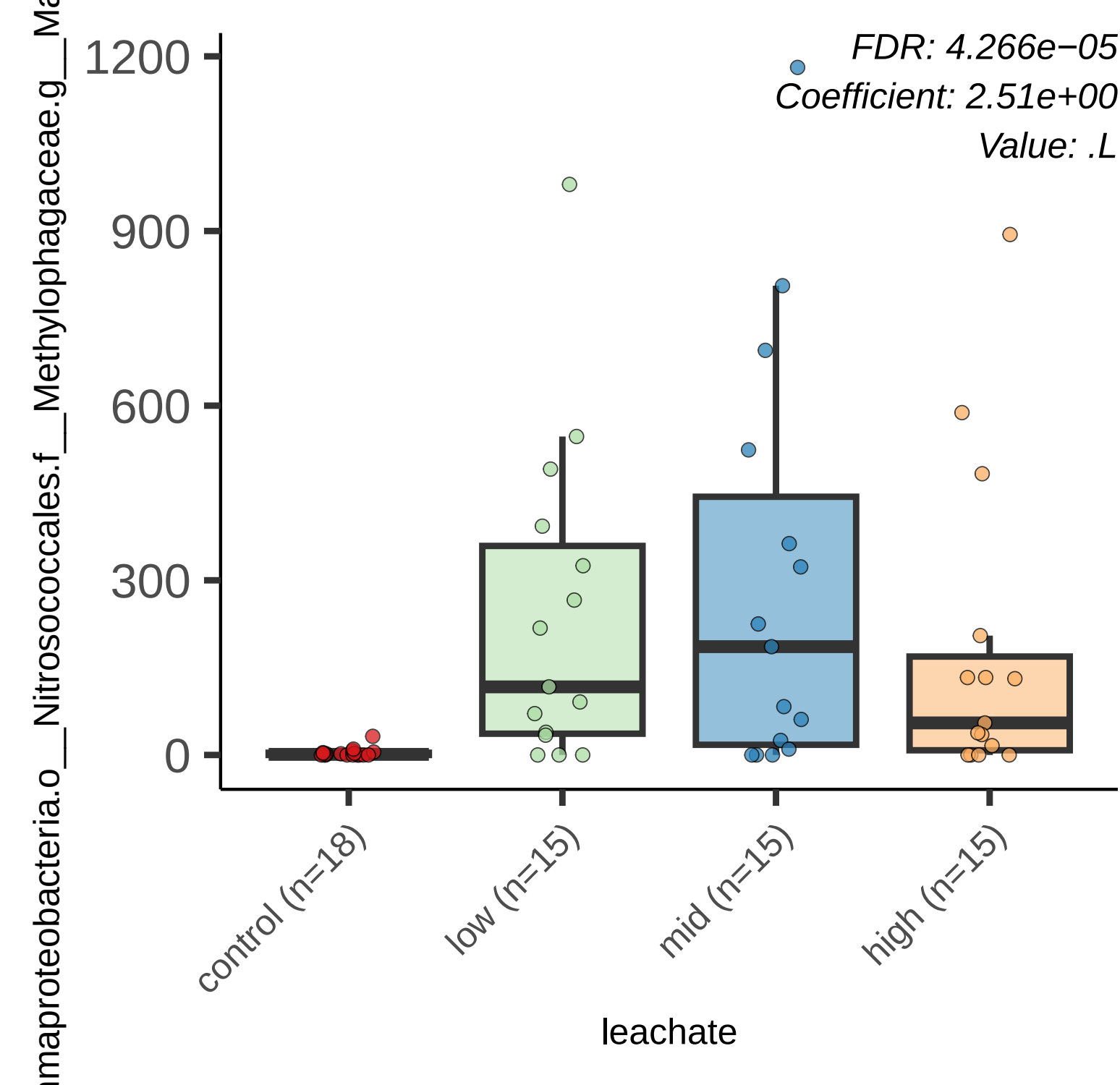
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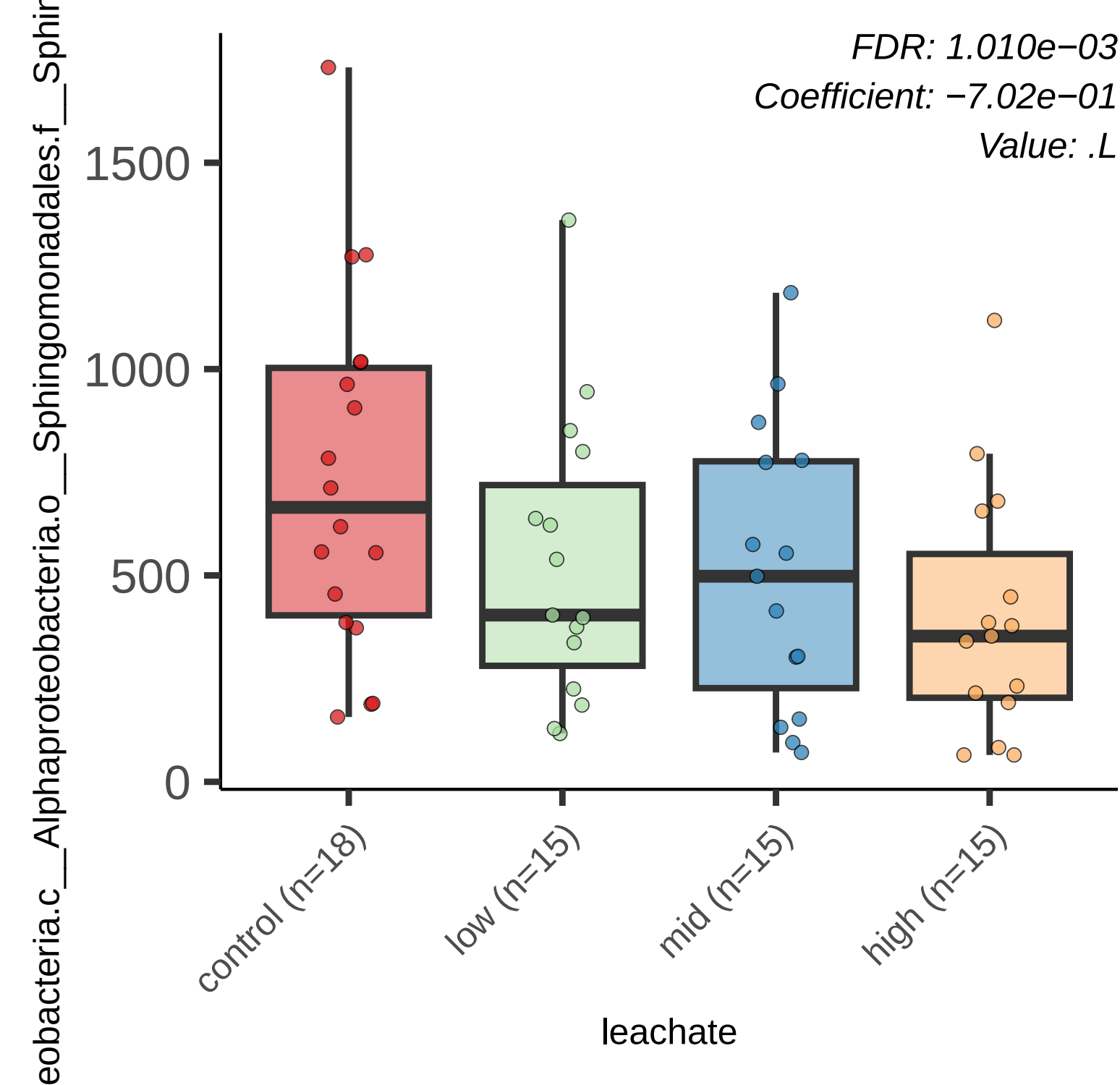
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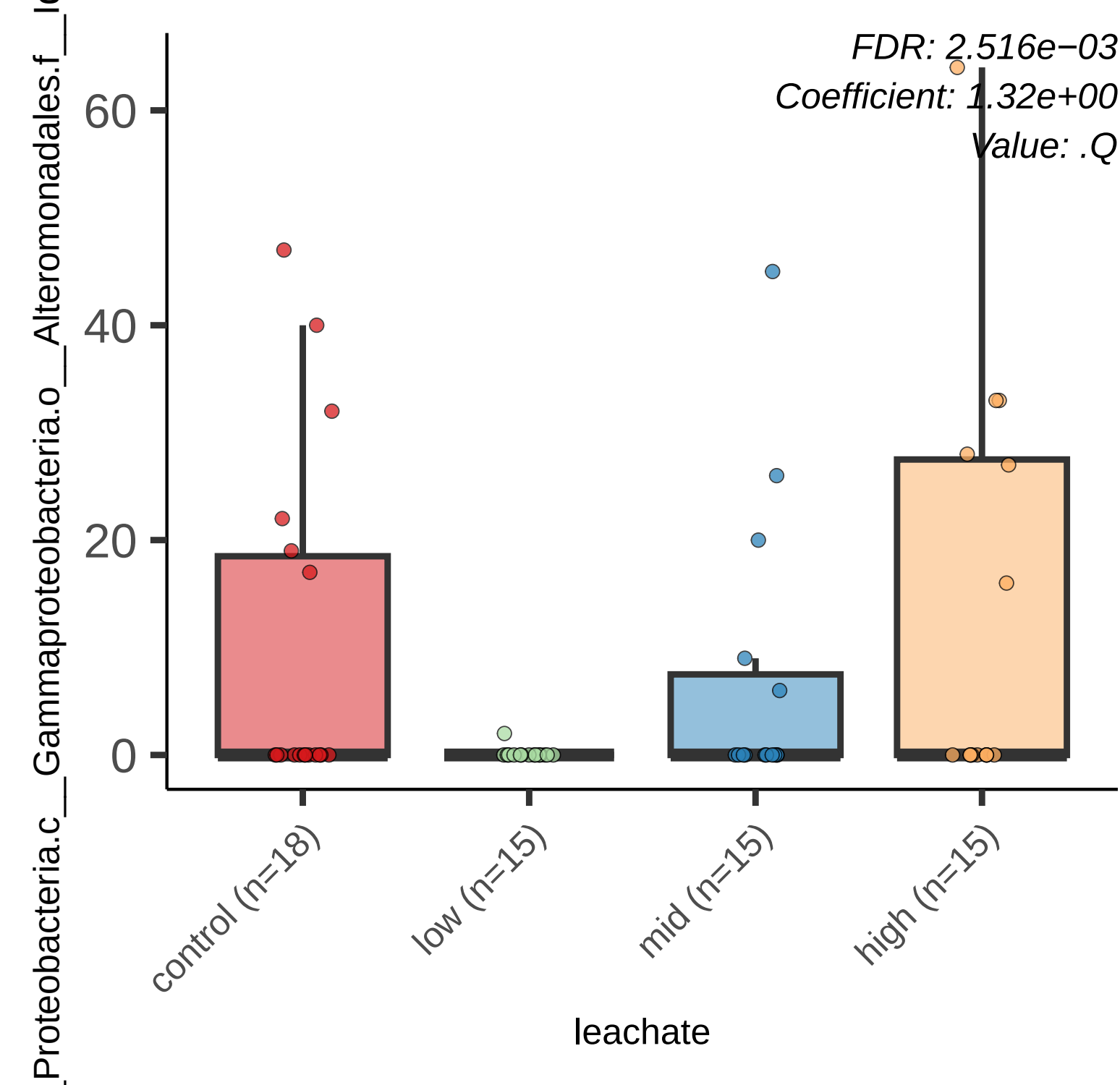
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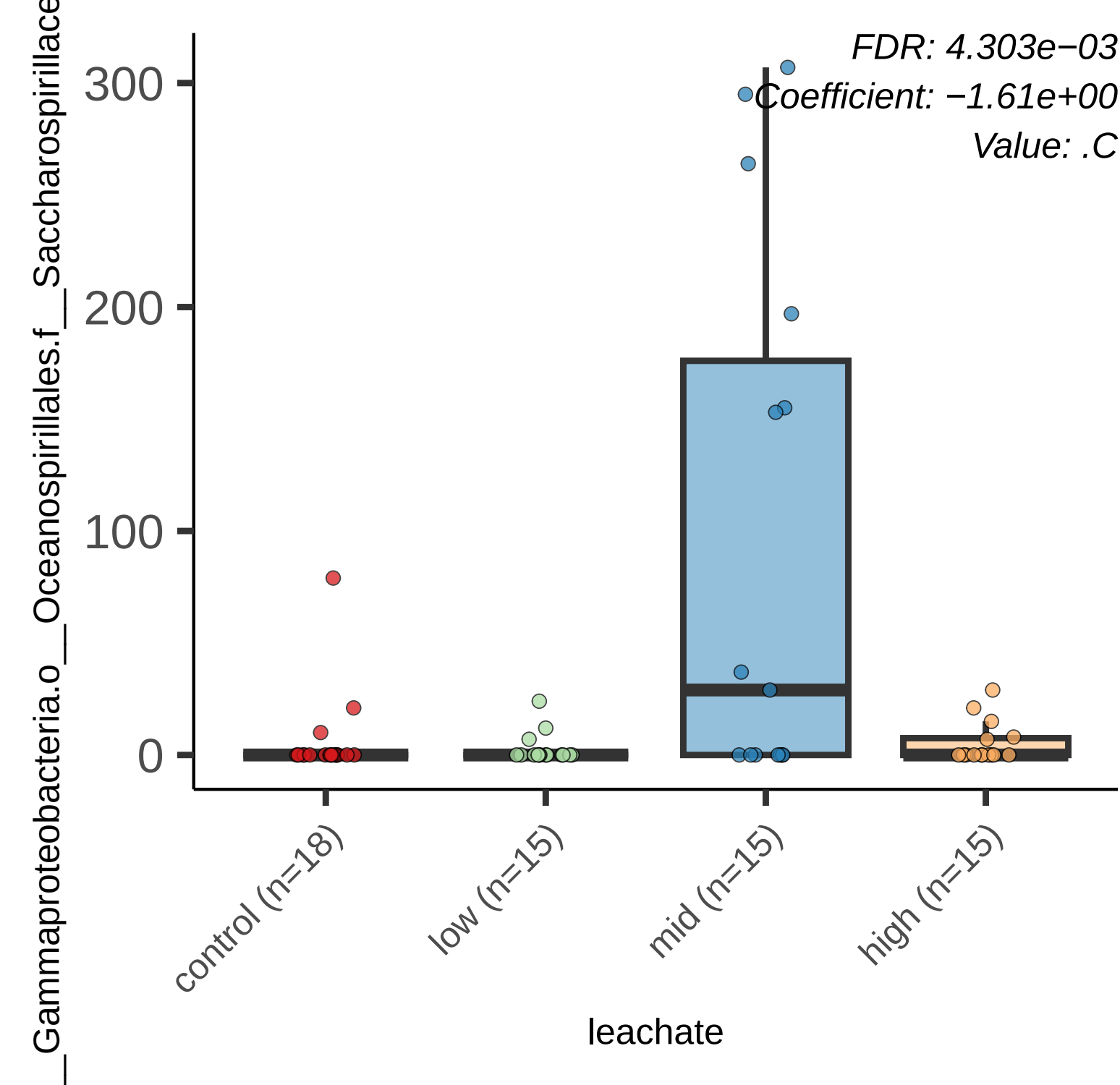
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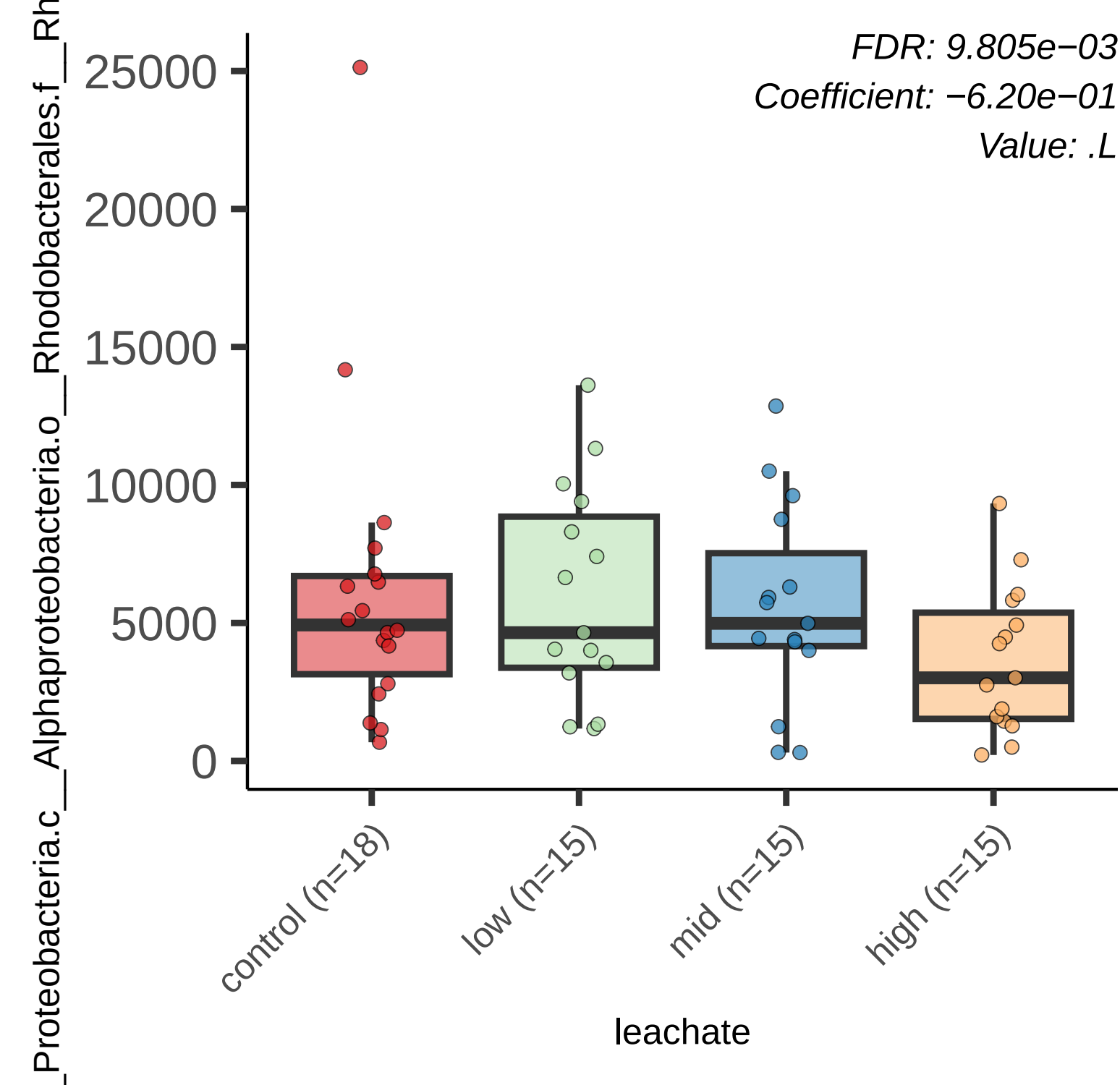
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leachate
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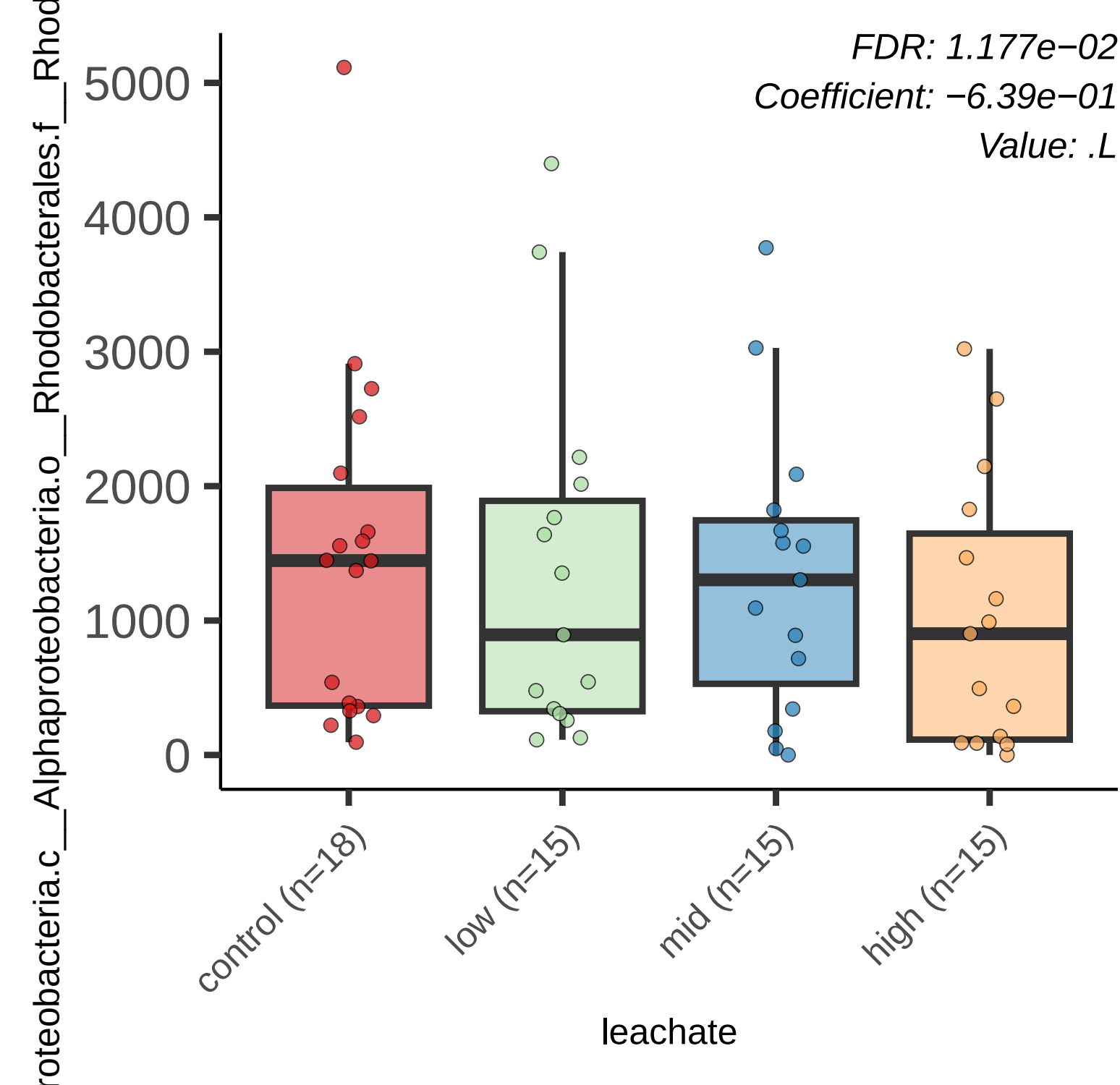
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leachate
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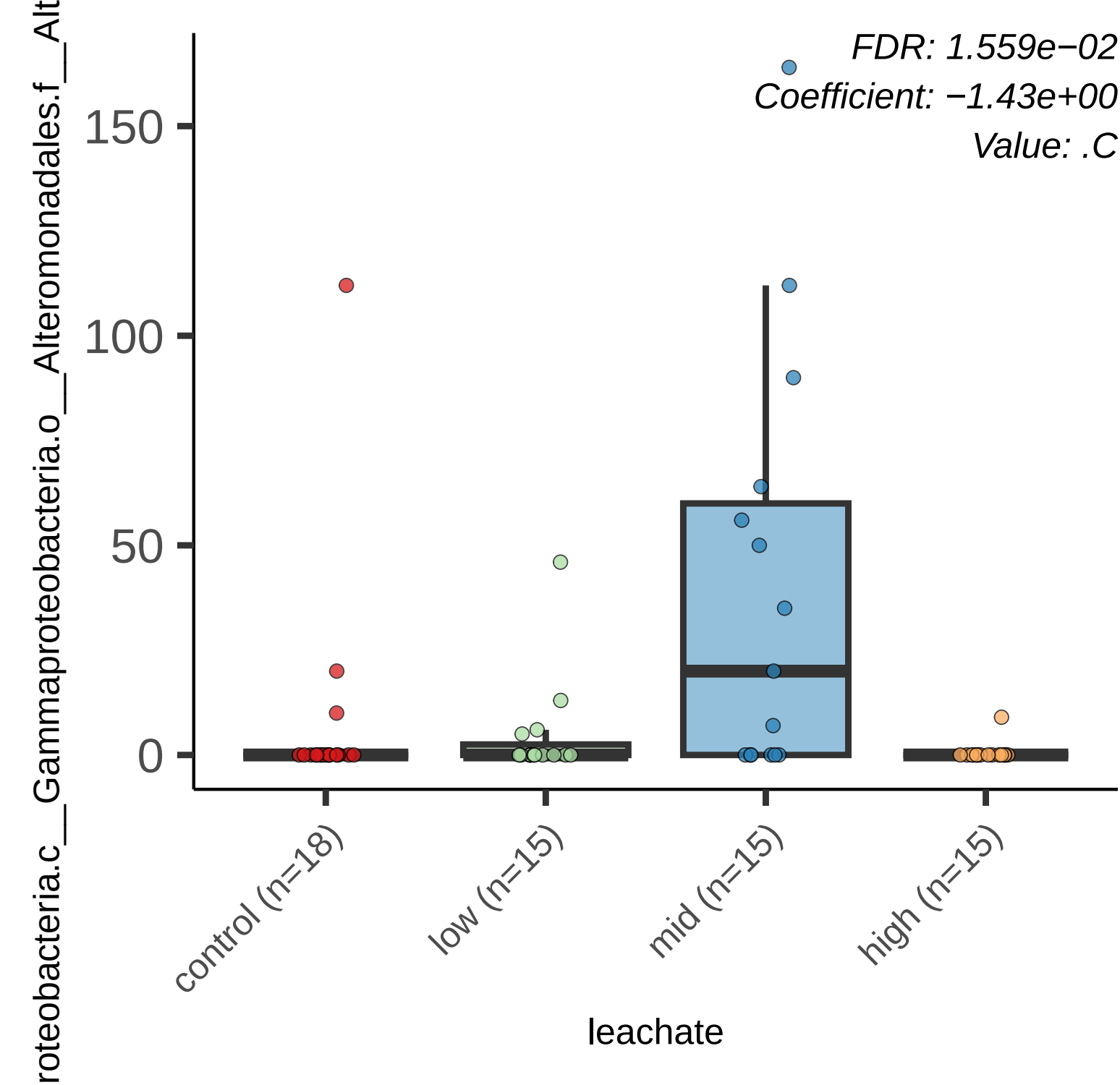
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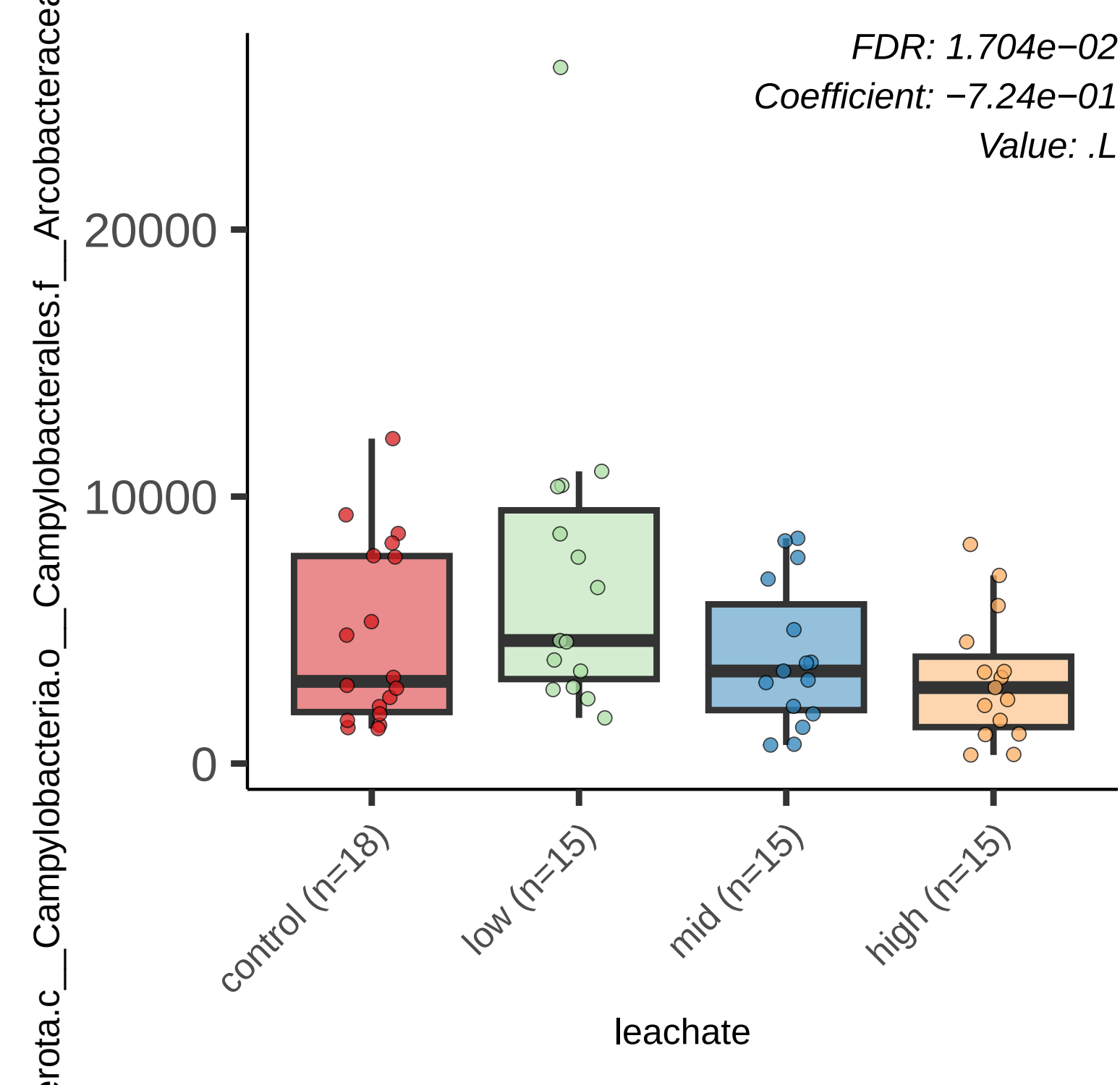
high (n=15)
leachate
roteobacteria.c__Gammaproteobacteria.o__Alteromonadales.f__Alt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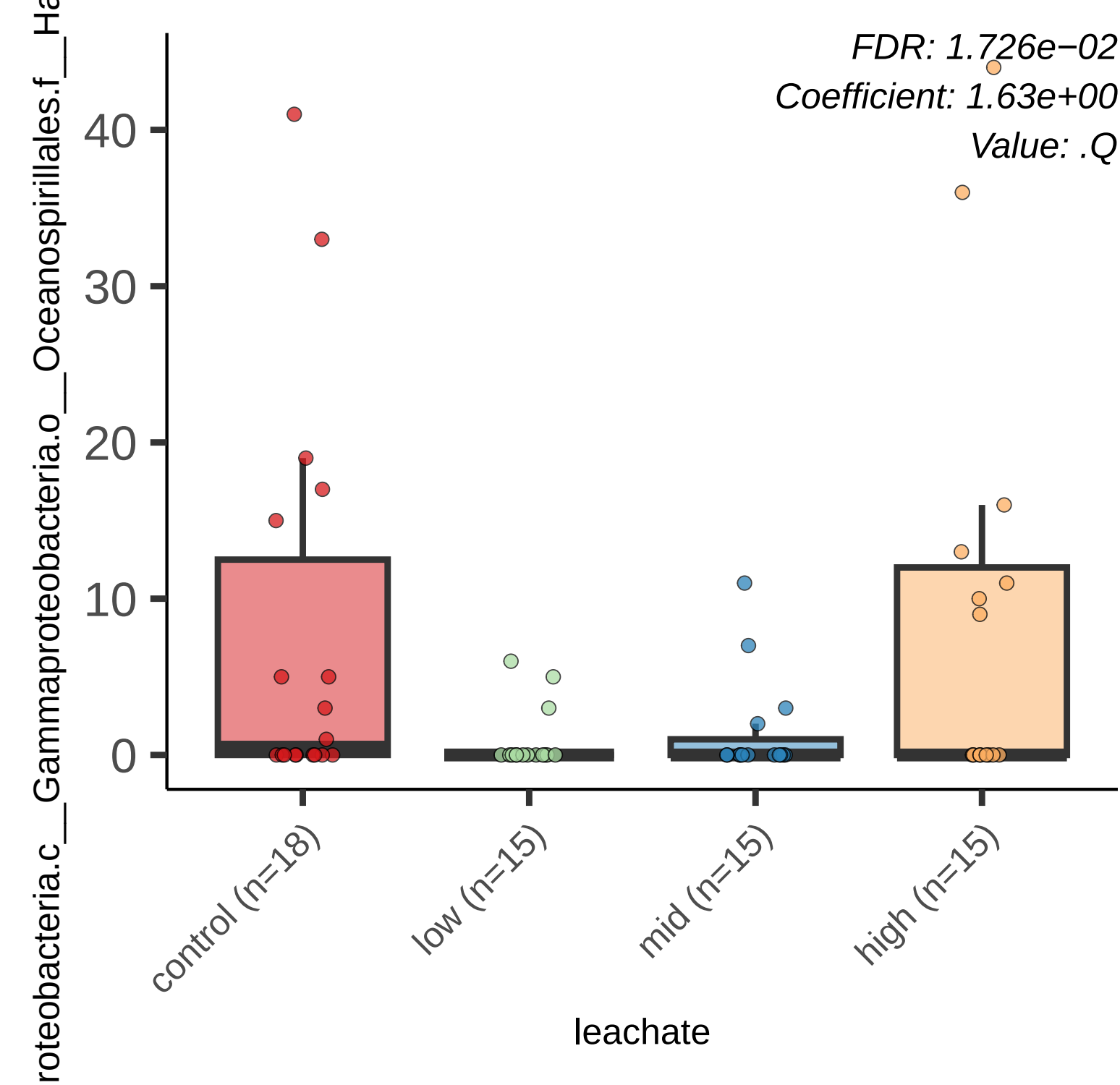
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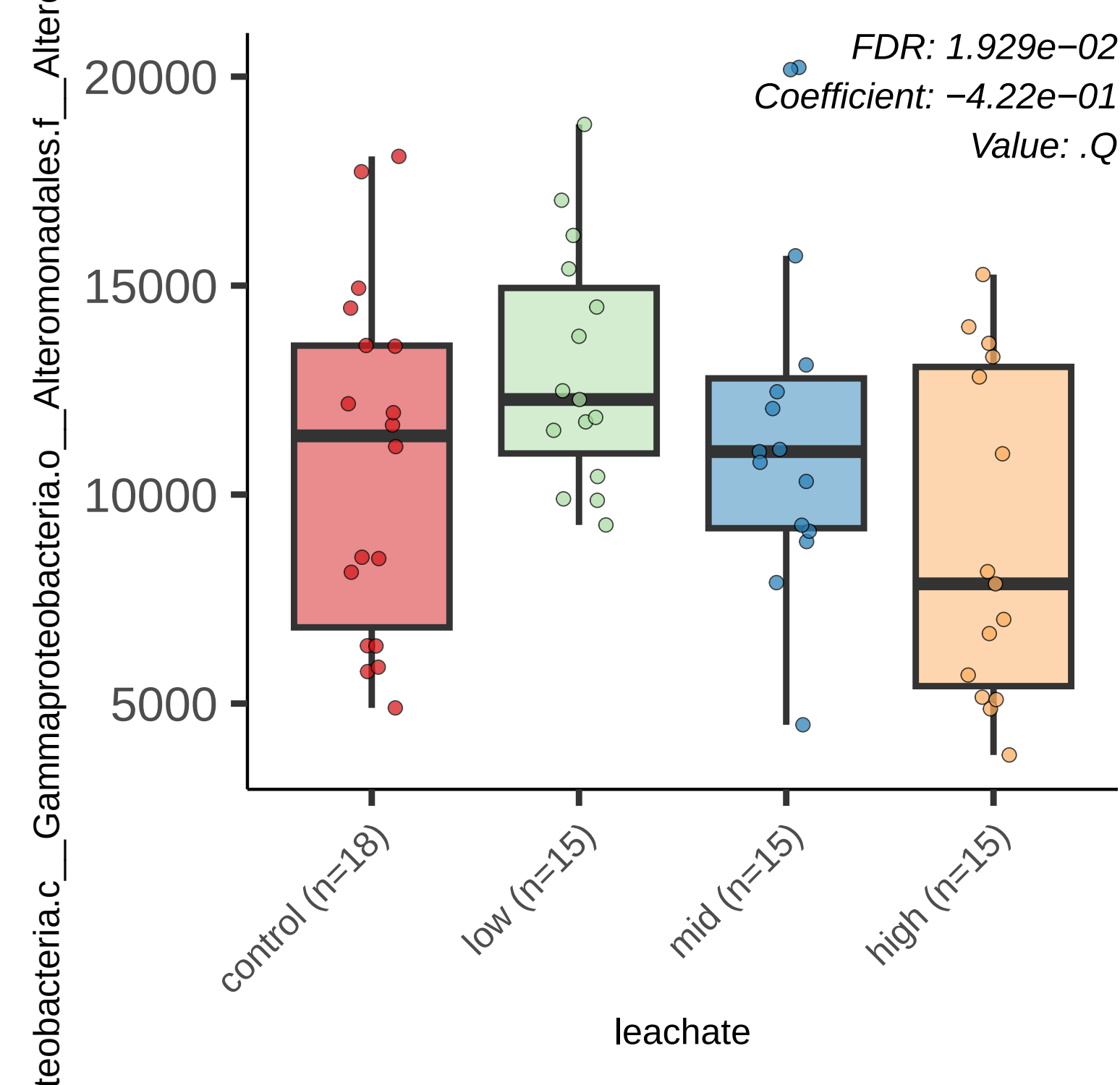
high (n=15)
leachate
roteobacteria.c__Gammaproteobacteria.o__Oceanospirillales.f__Ha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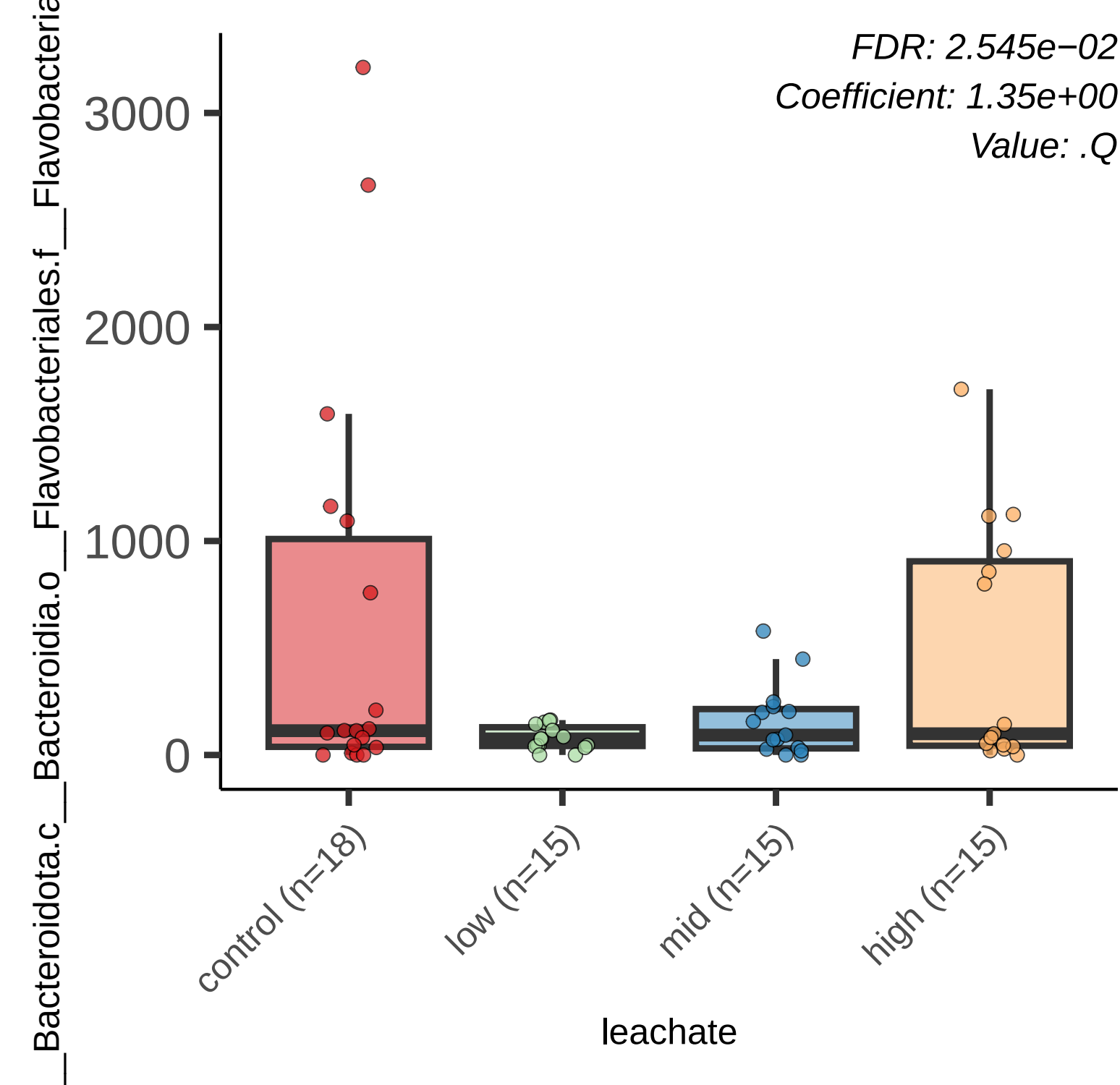
high (n=15)
leachate
teobacteria.c__Gammaproteobacteria.o__Alteromonadales.f__Altero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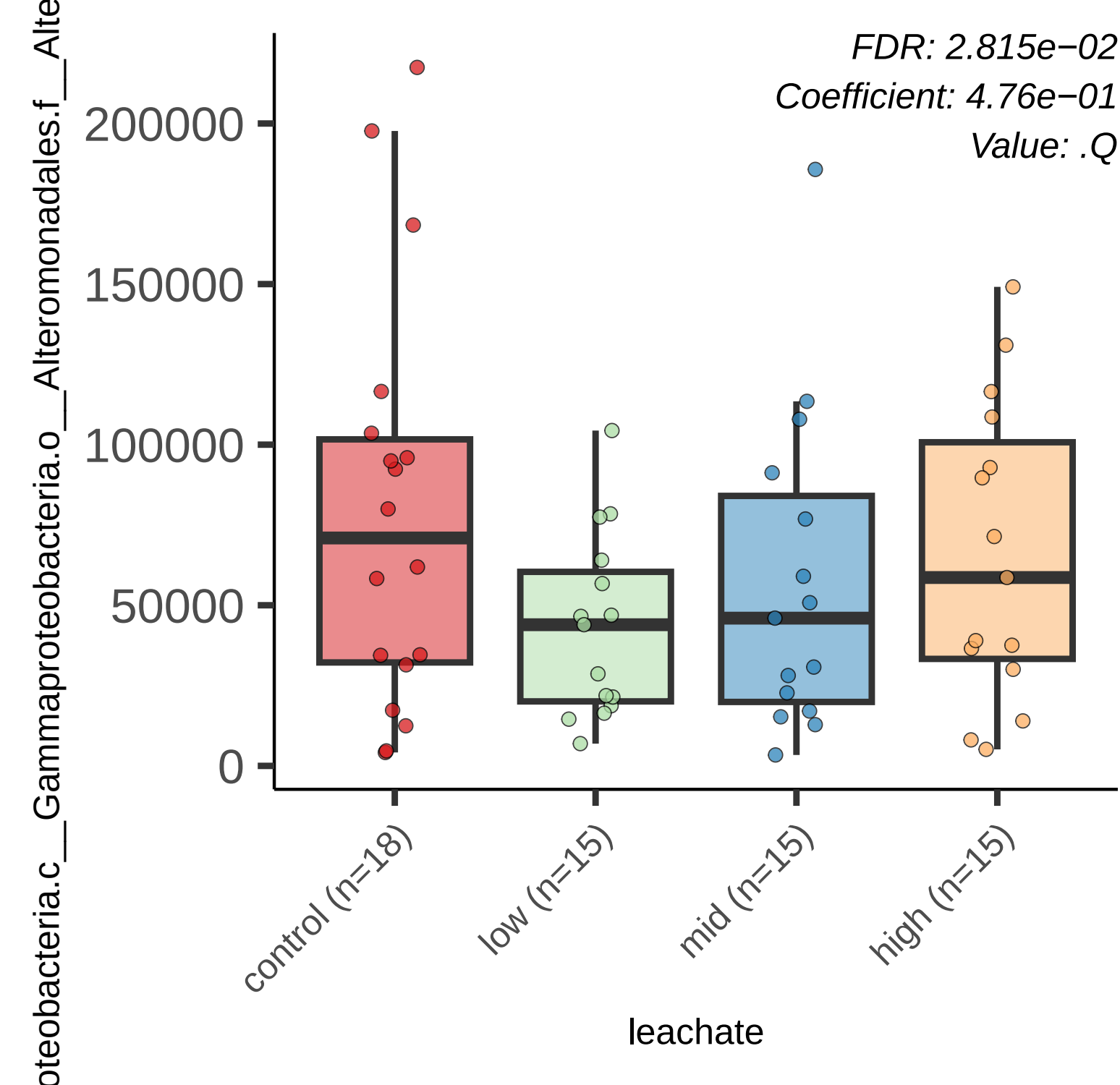
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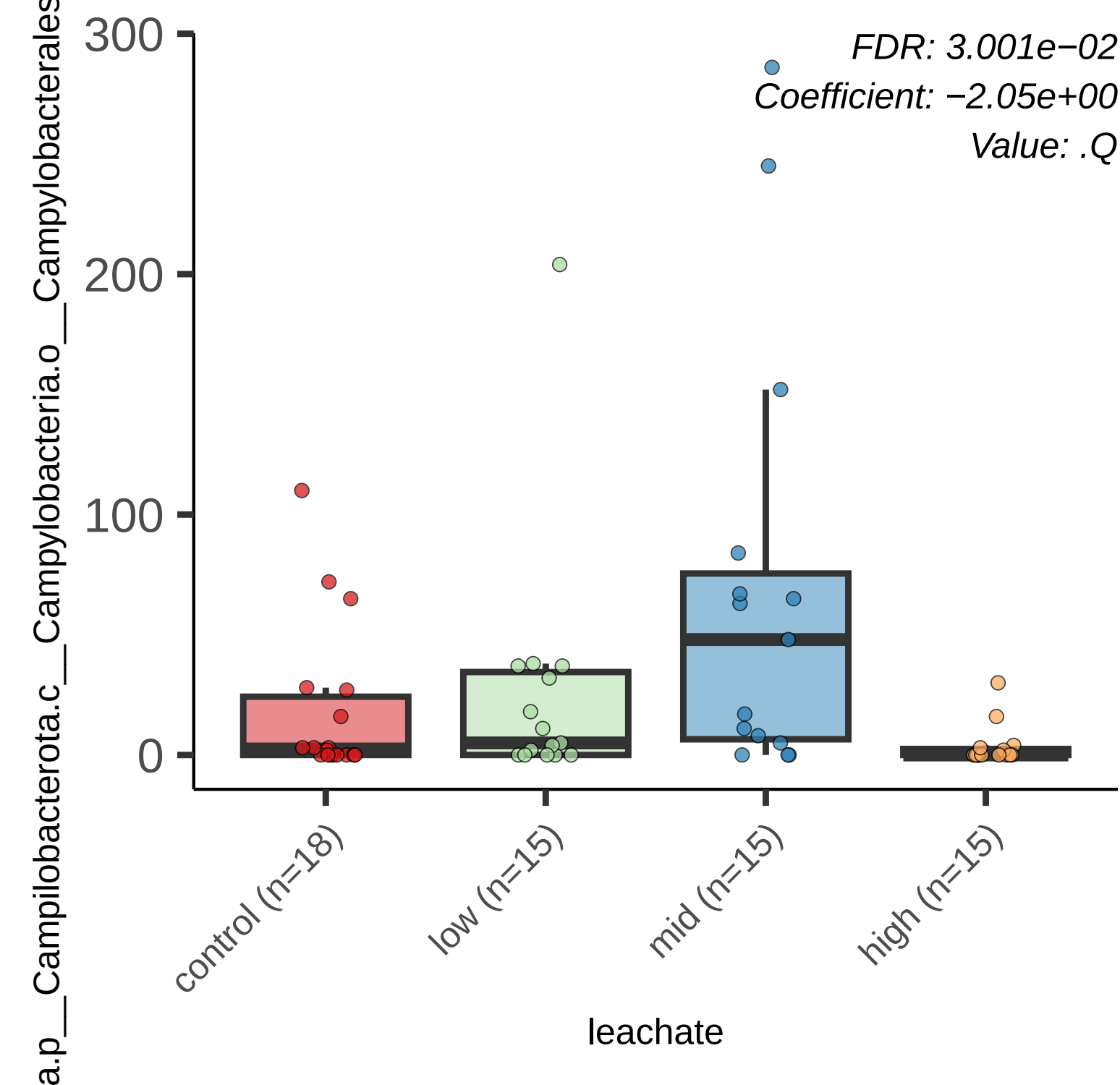
leachate
oteobacteria.c__Gammaproteobacteria.o__Alteromonadales.f__Alte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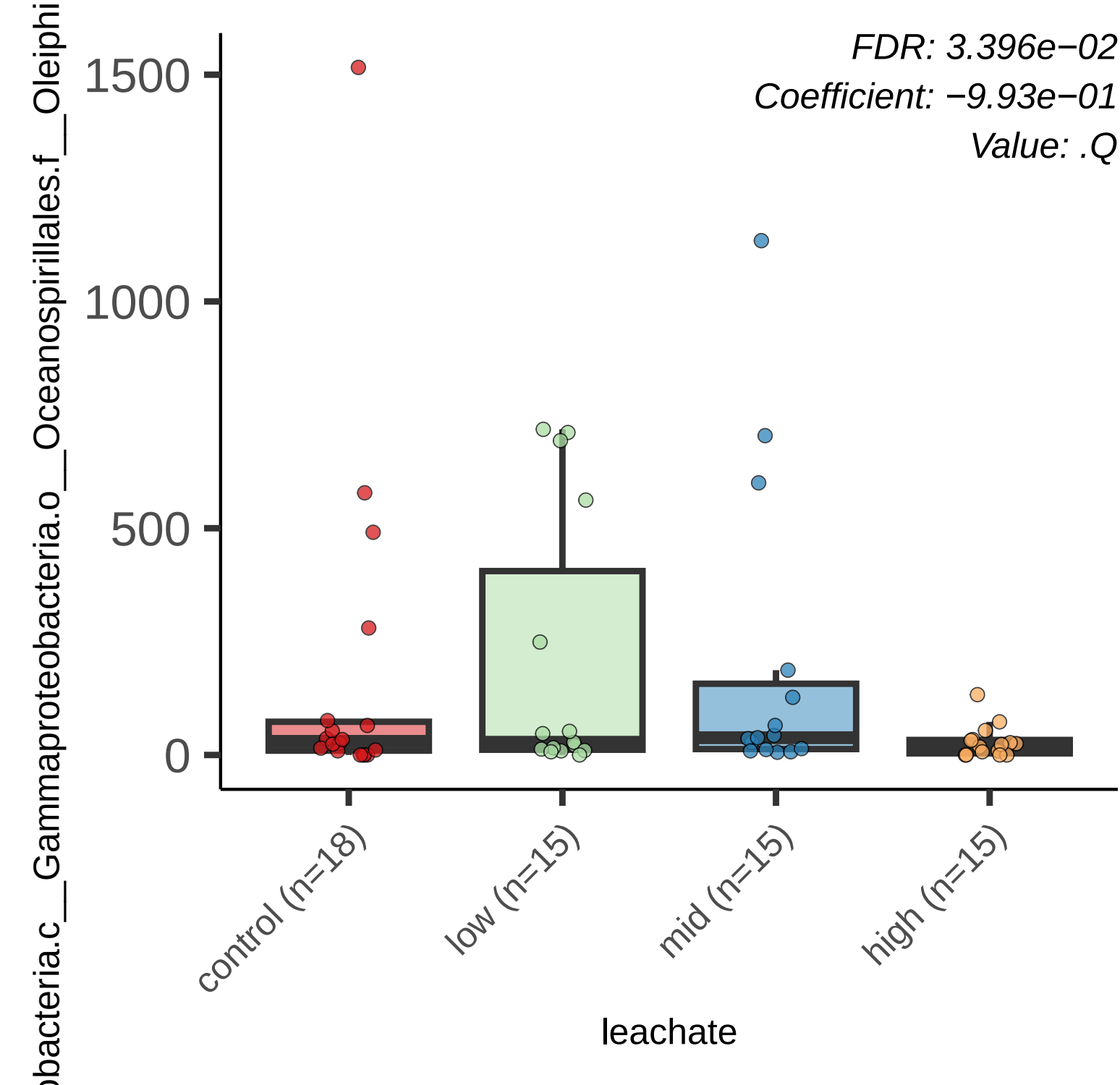
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leachate
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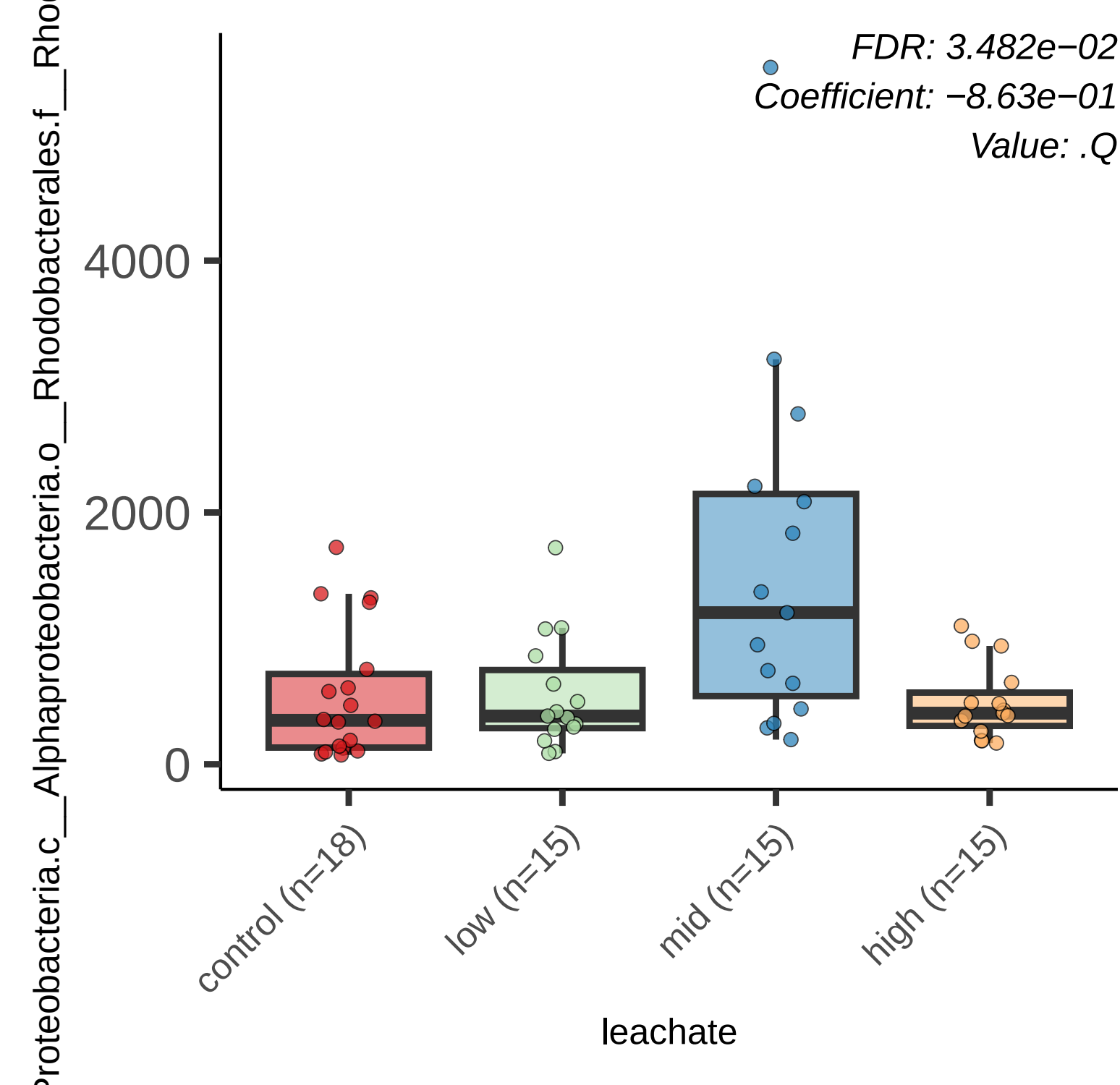
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leachate
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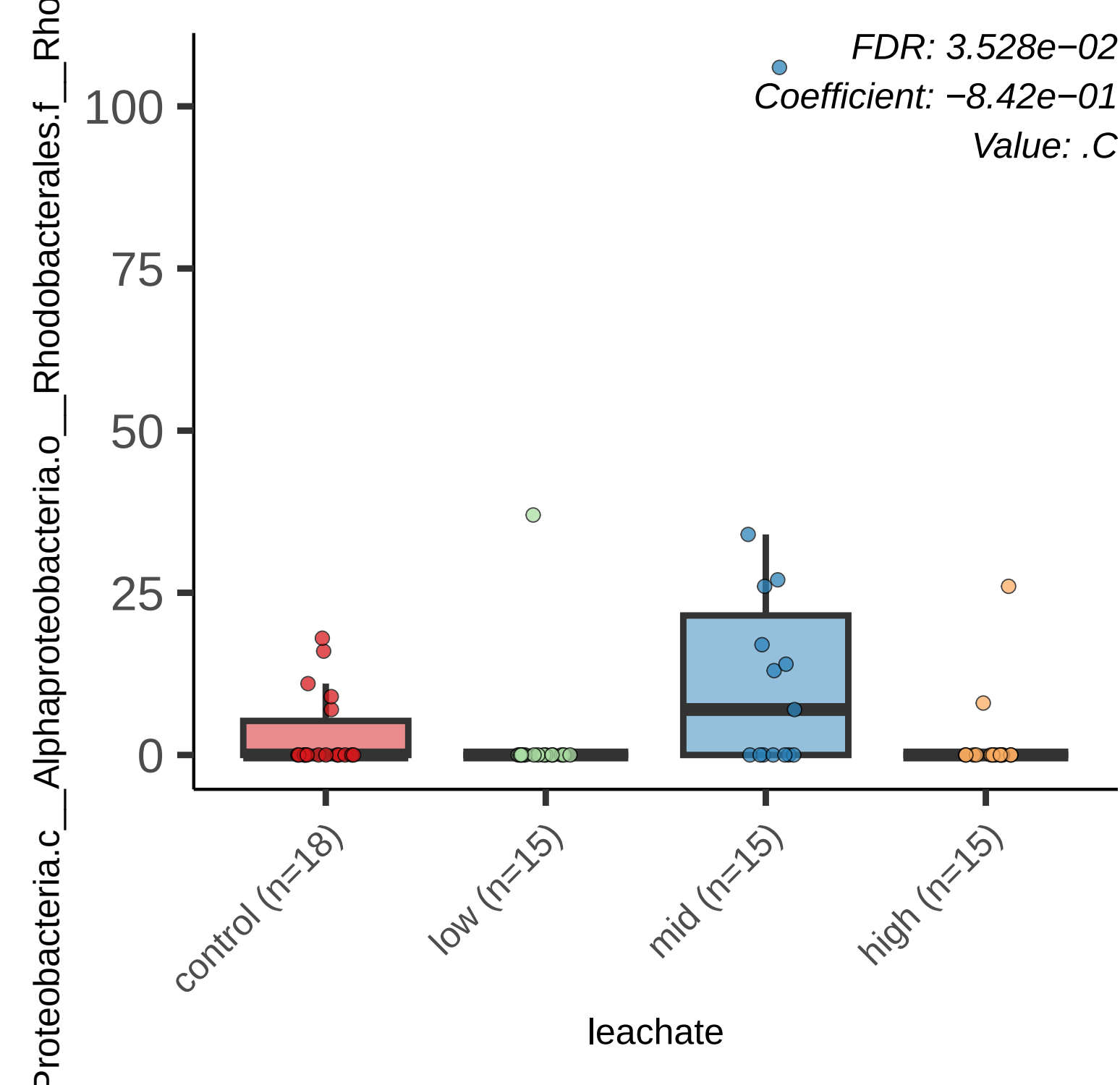
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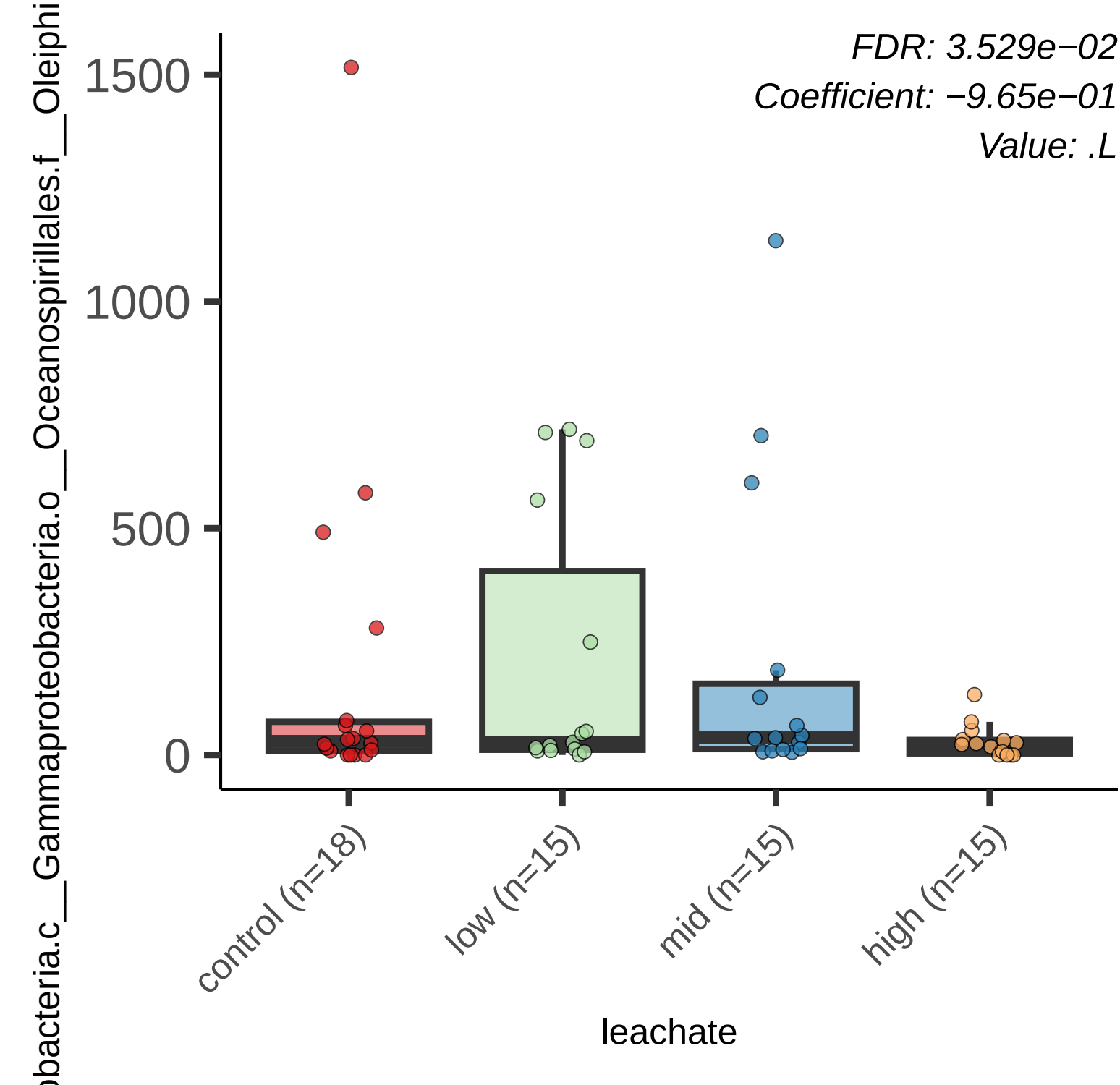
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leachate
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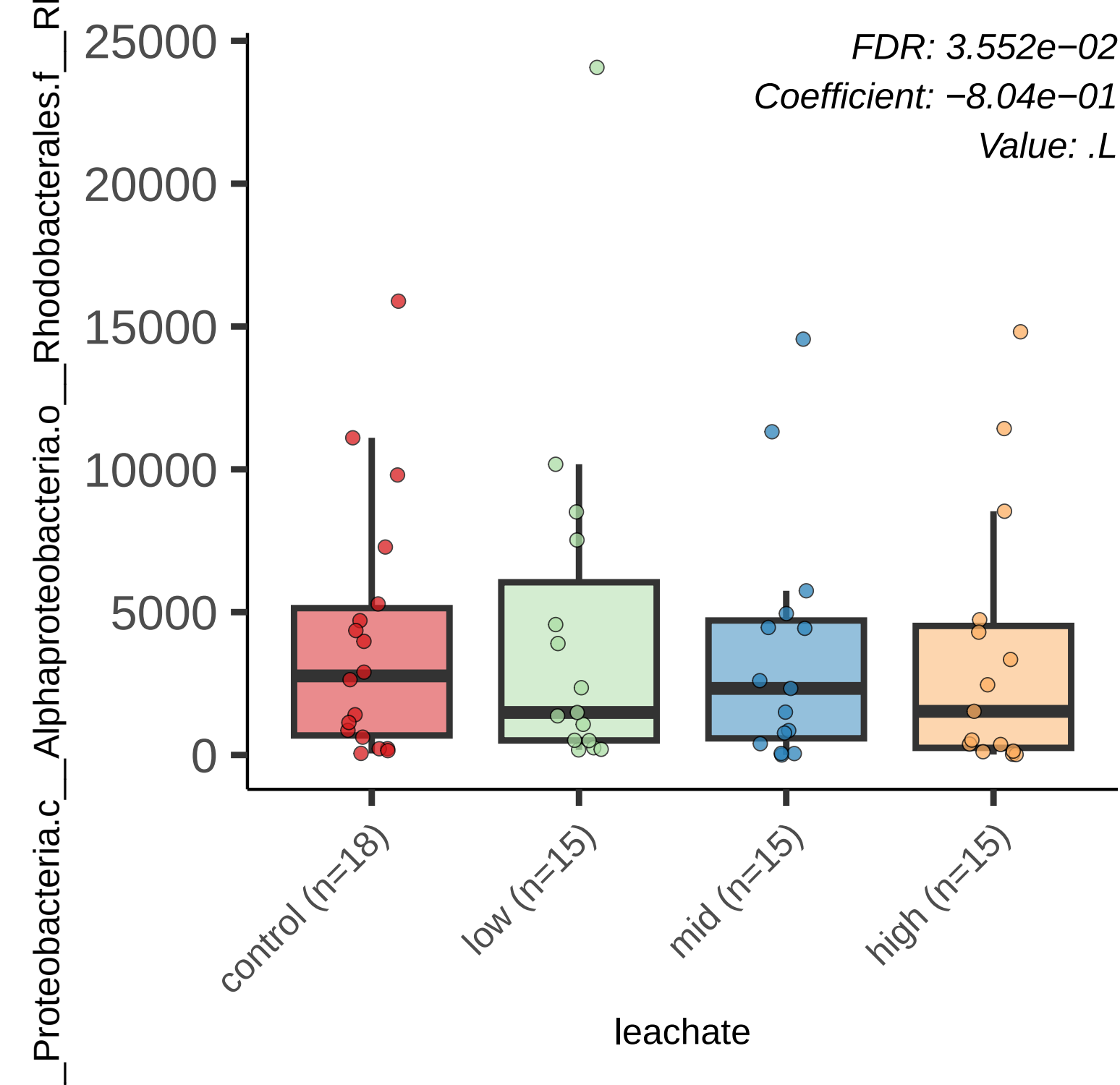
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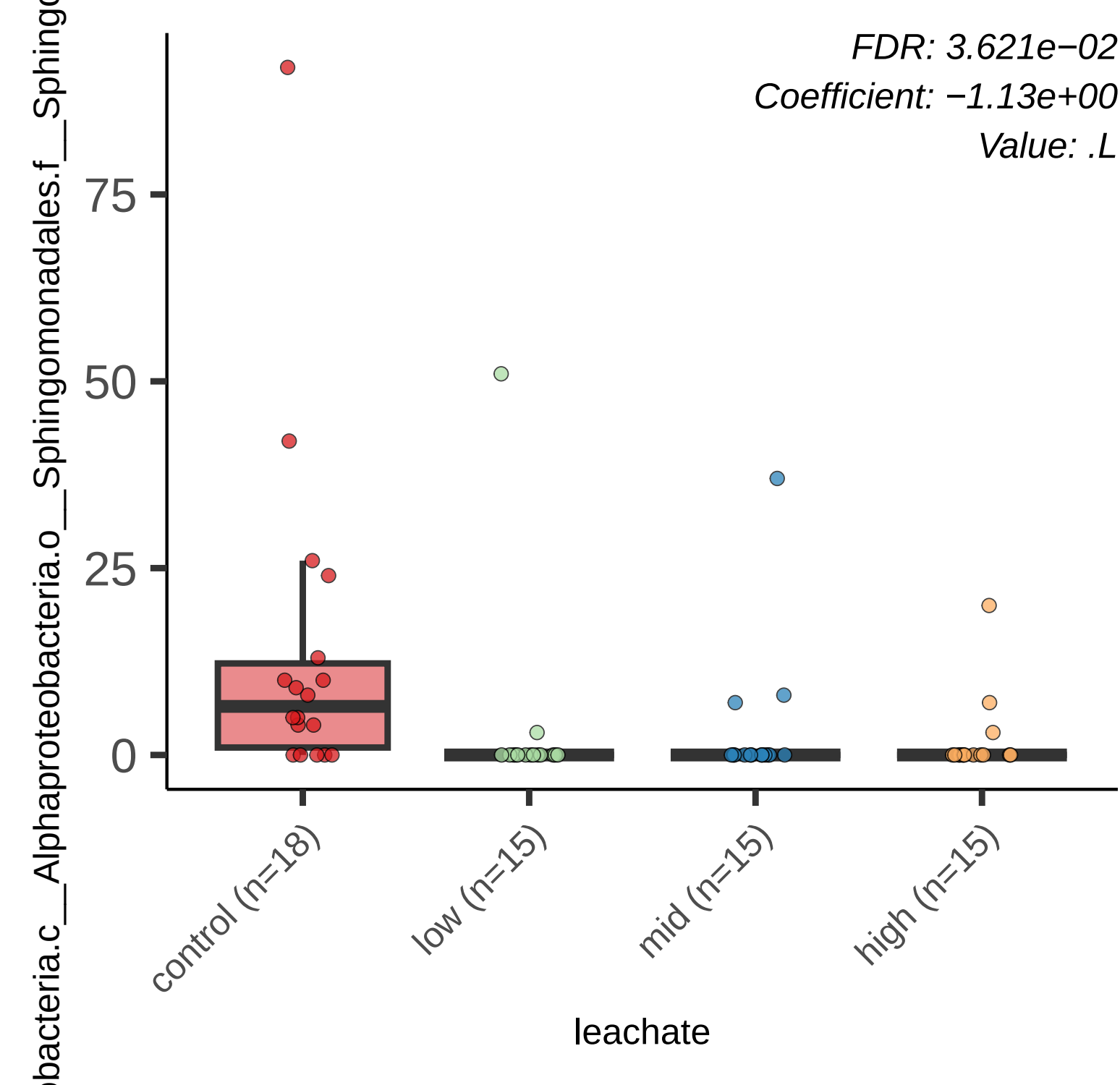
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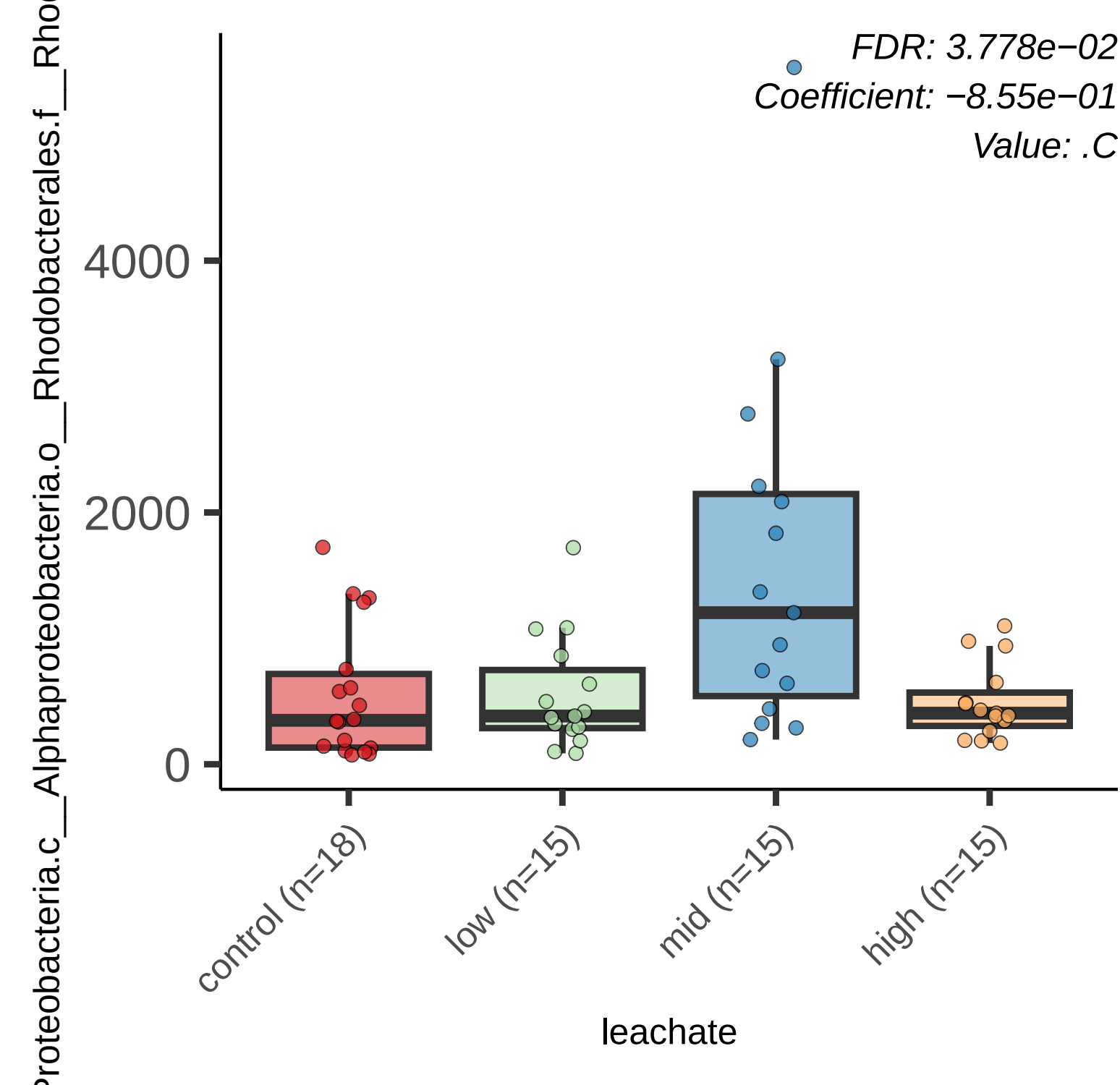
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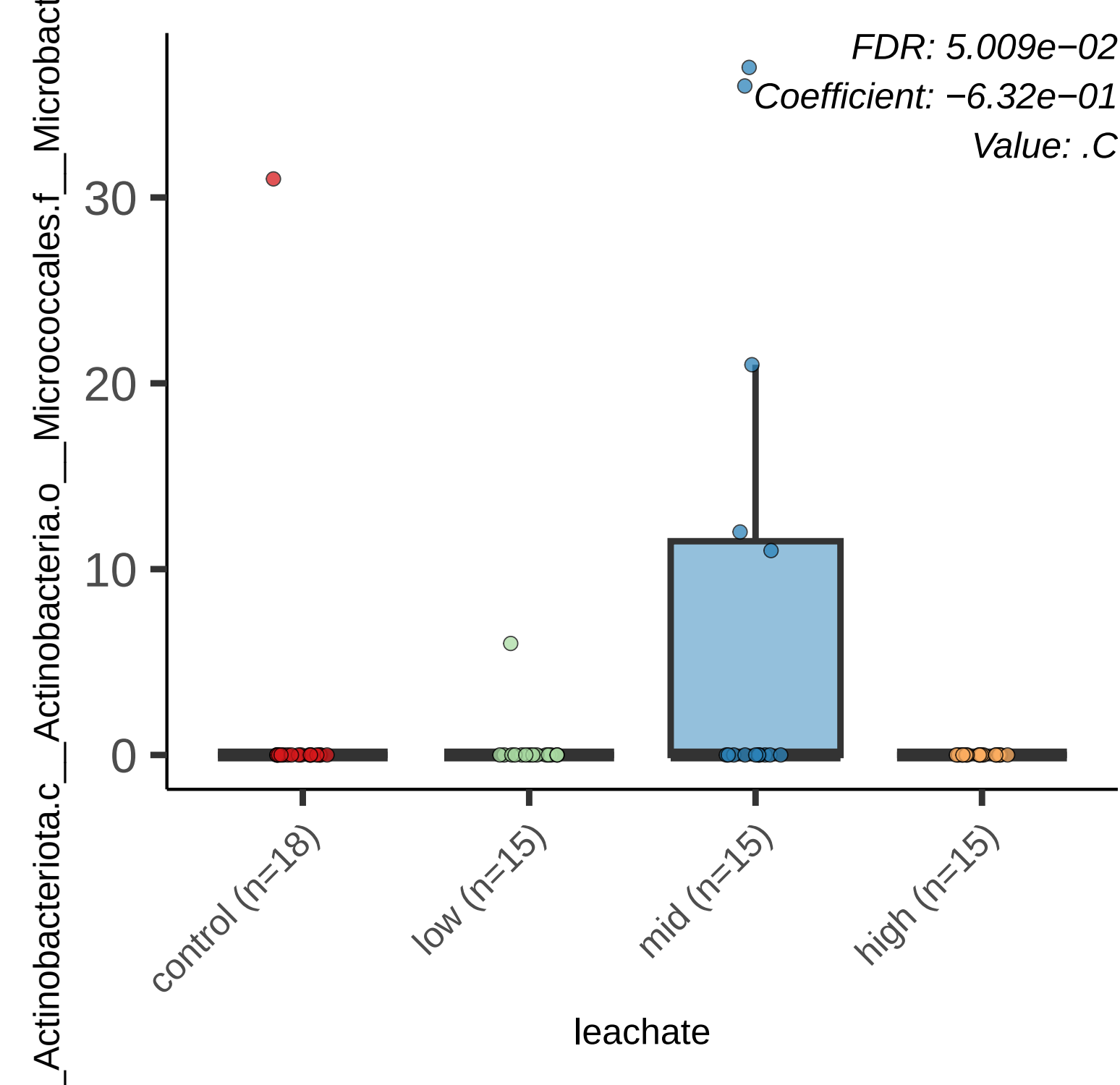
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high (n=15)
leachate
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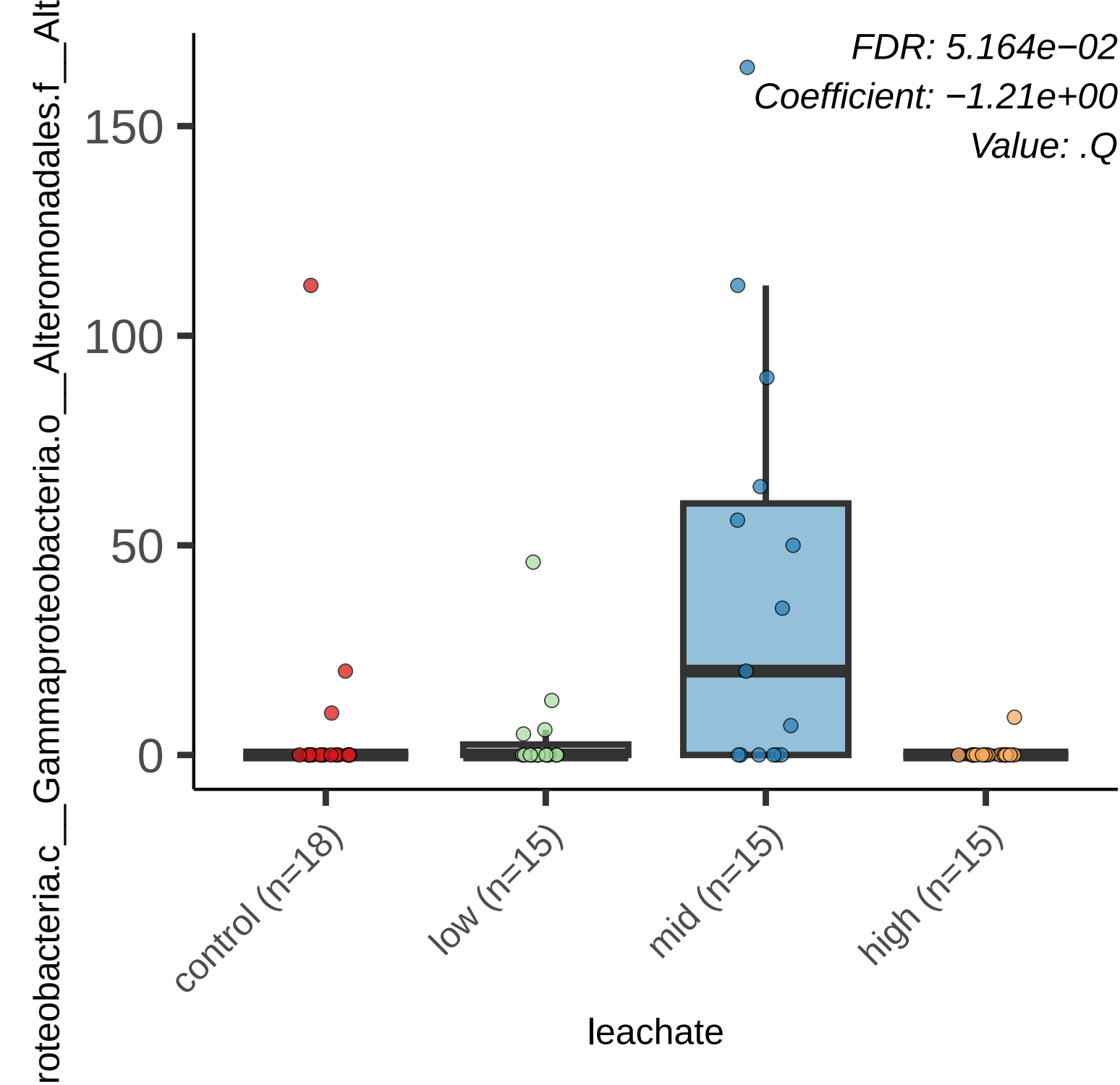
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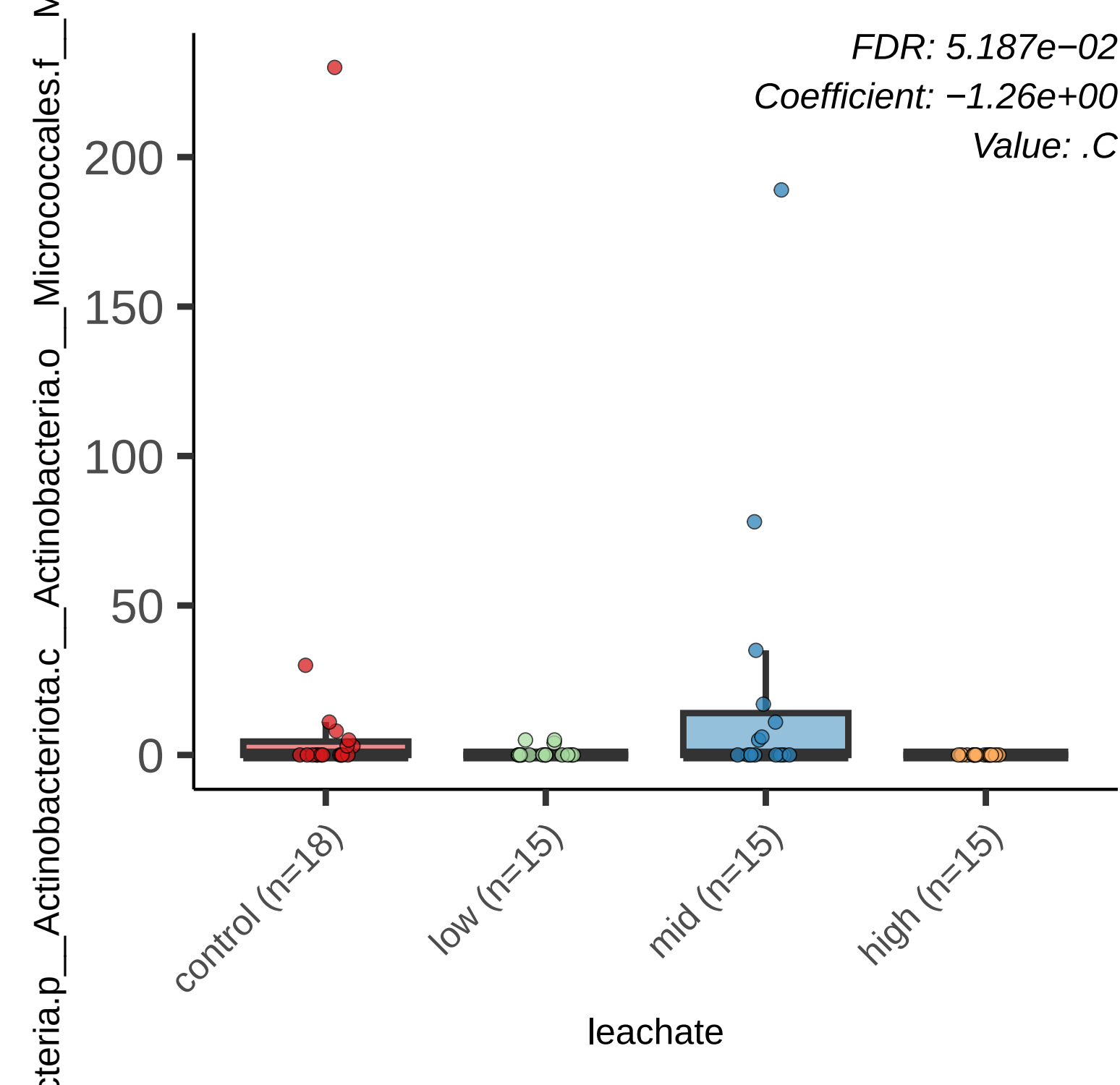
leachate
roteobacteria.c__Gammaproteobacteria.o__Alteromonadales.f__Alt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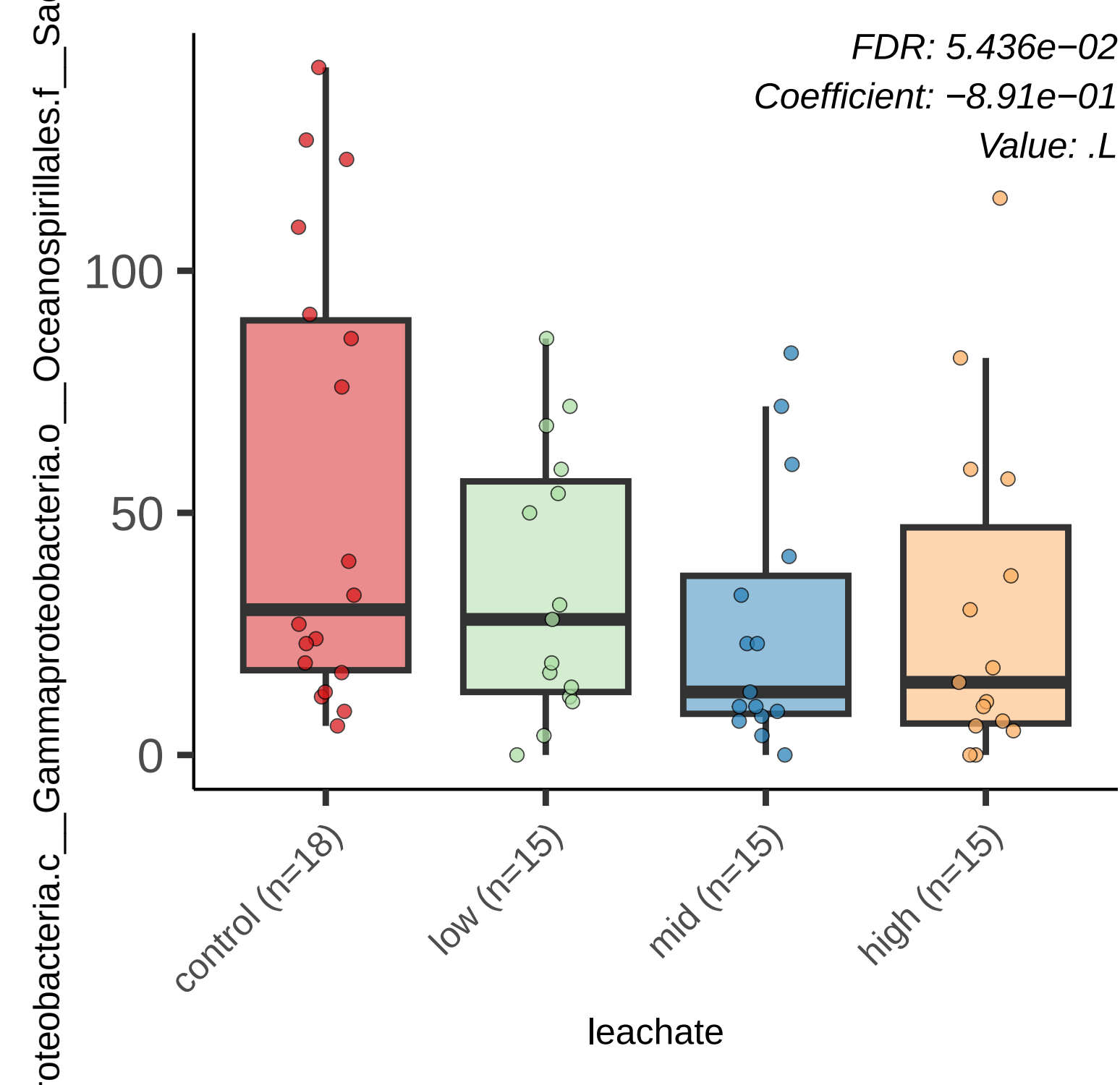
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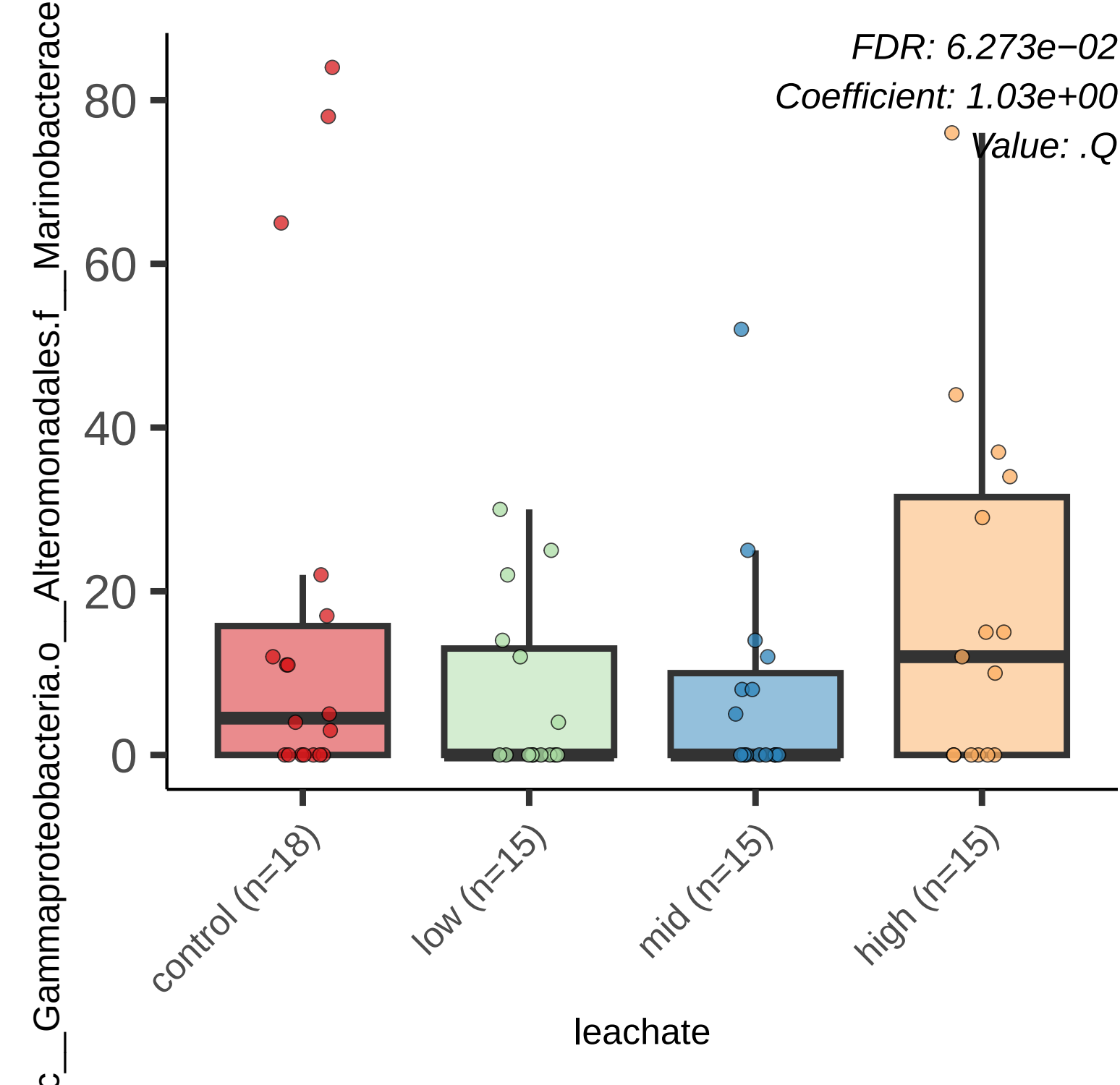
roteobacteria.c__Gammaproteobacteria.o__Oceanospirillales.f__Sa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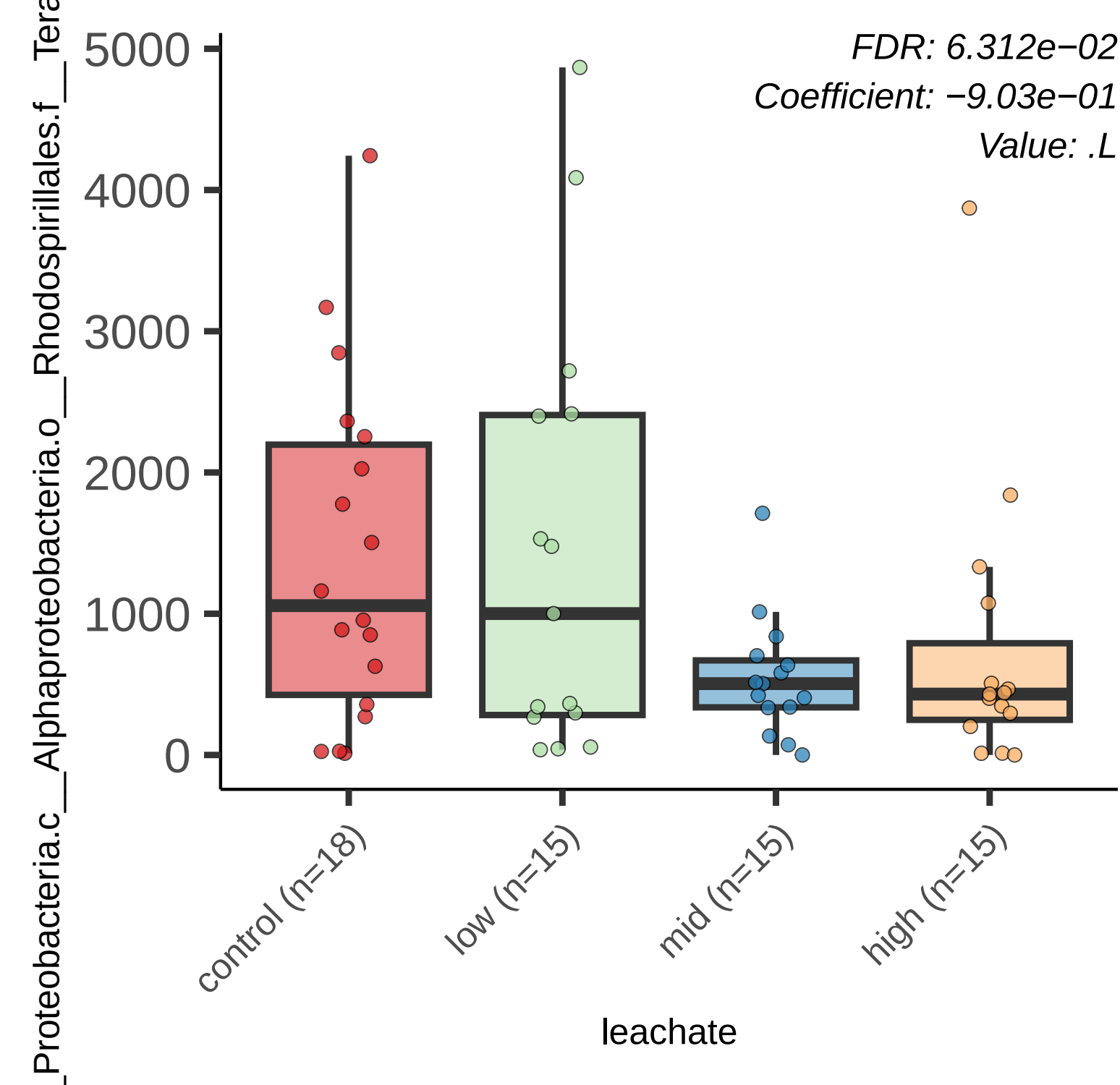
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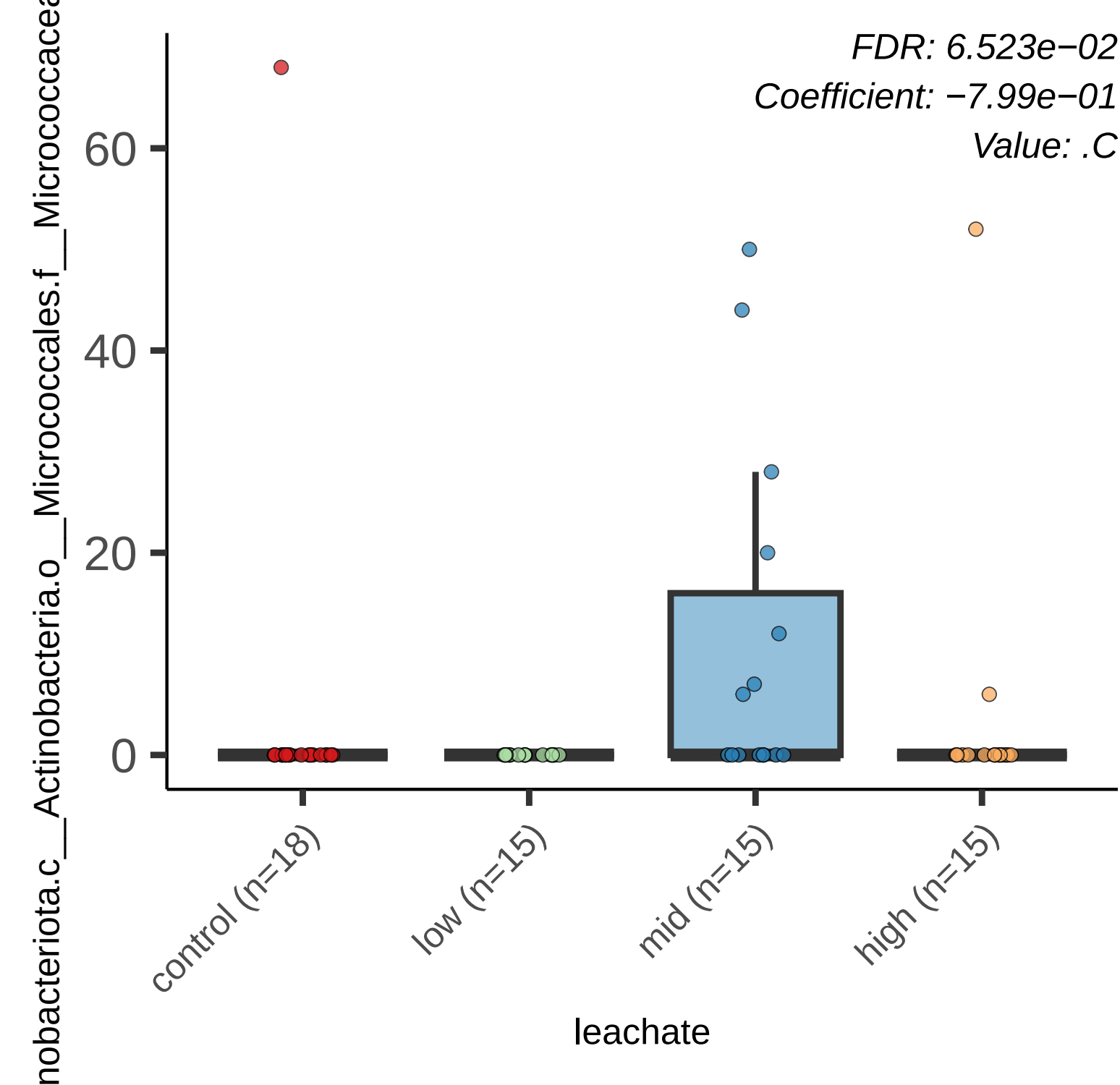
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leachate
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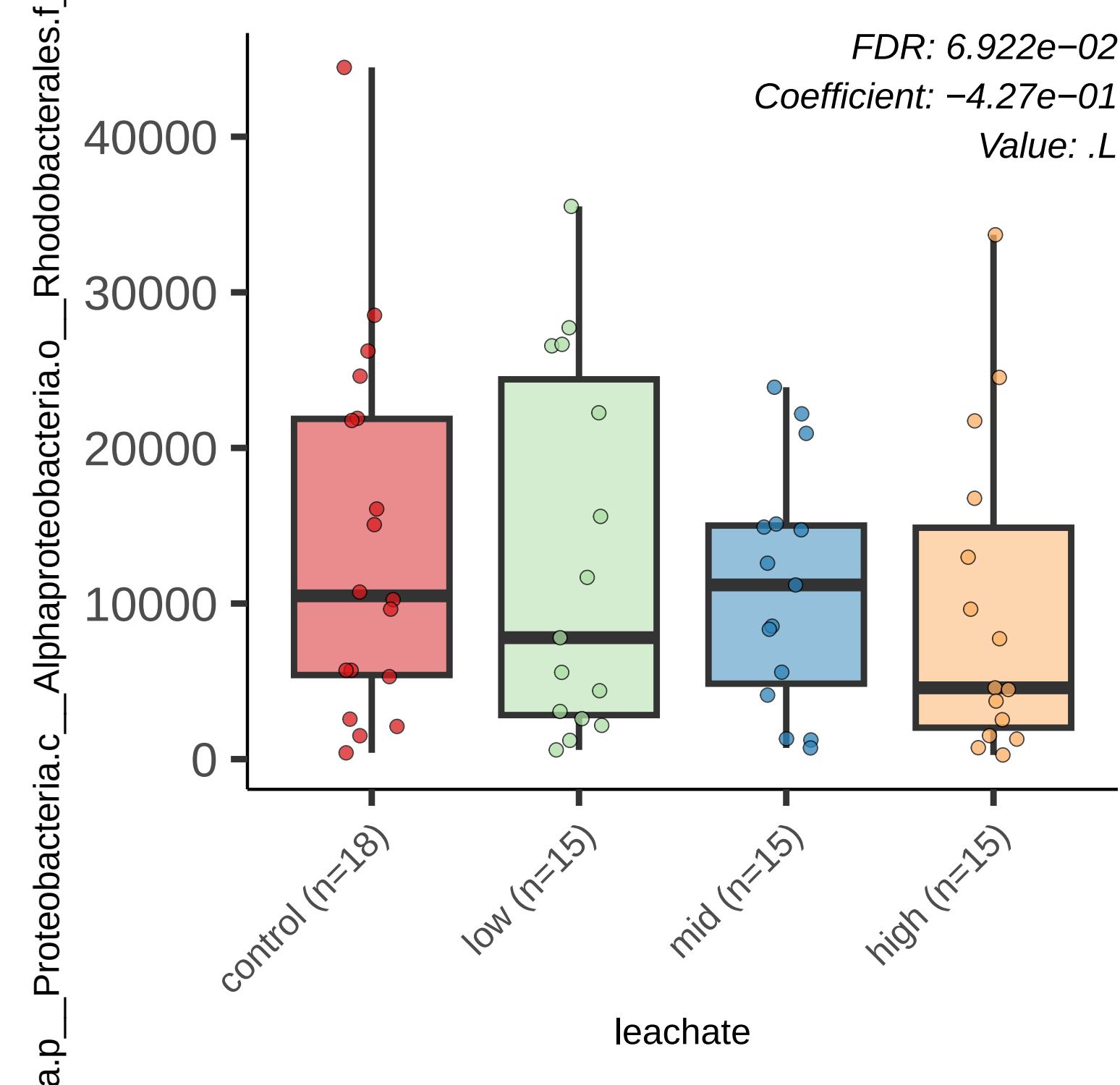
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leachate
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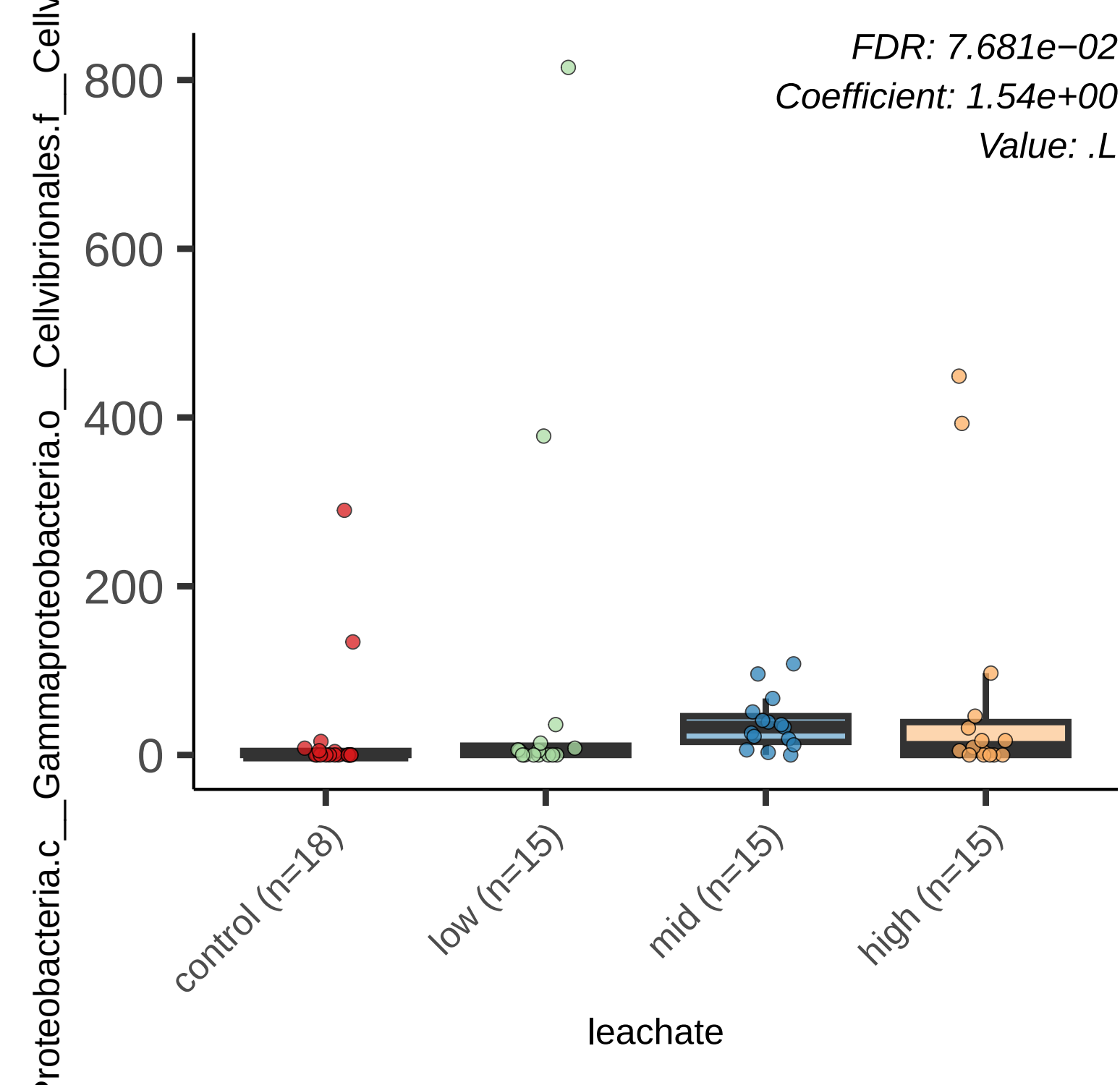
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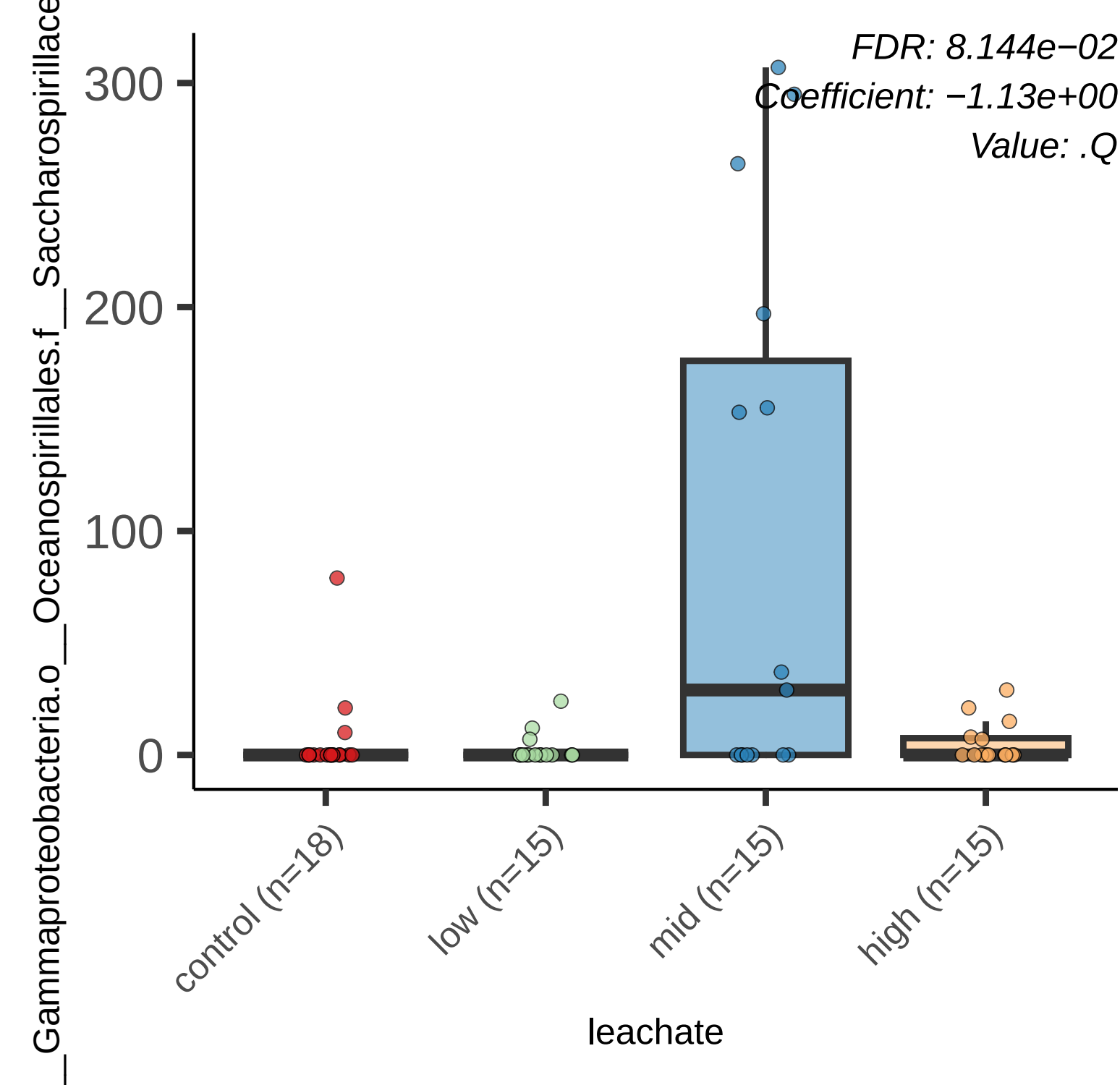
leachate
roteobacteria.c__Gammaproteobacteria.o__Cellvibrionales.f__Cellv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Coefficient: −1.13e+00
Value: .Q
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200
100
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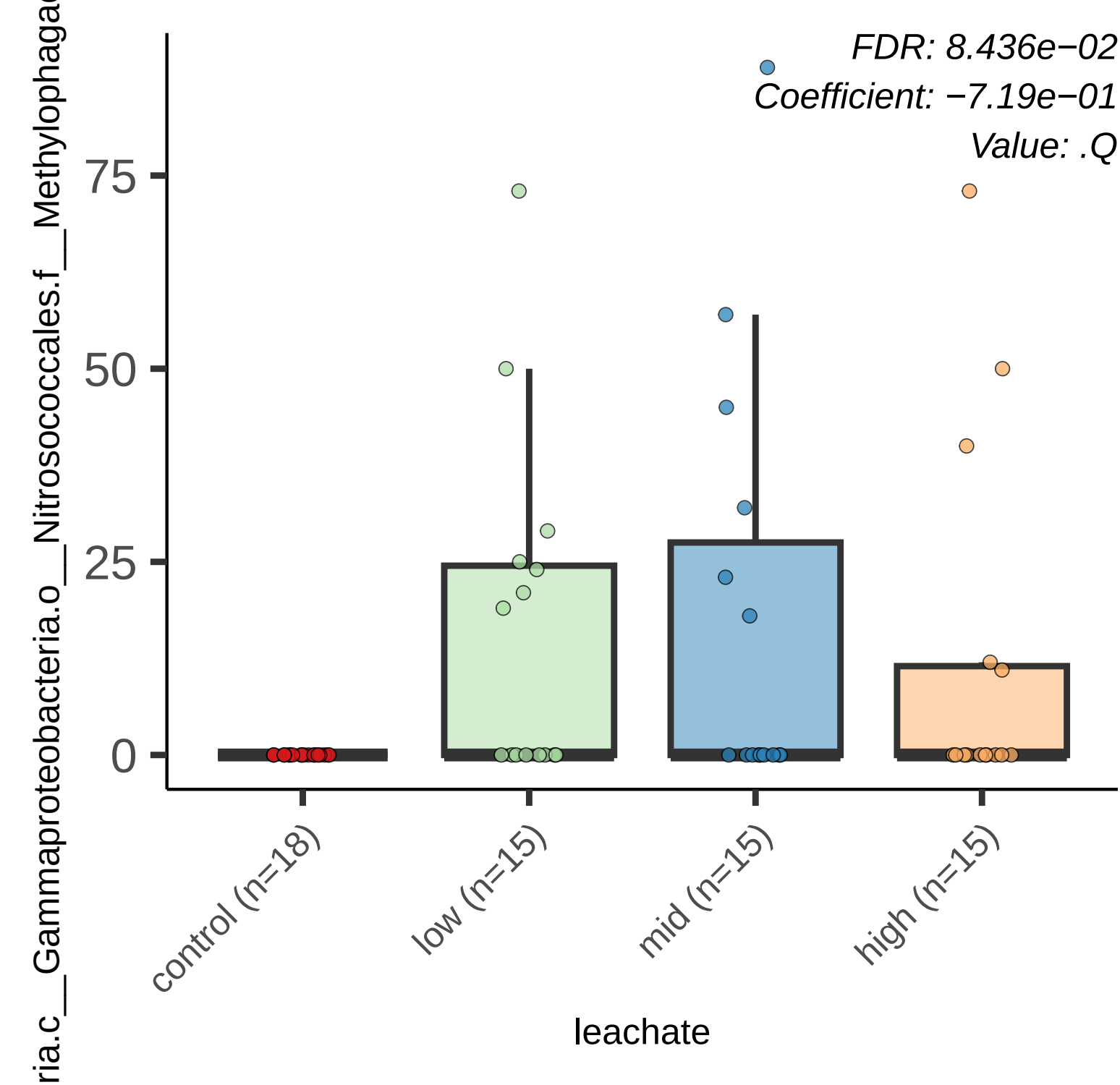
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
__Gammaproteobacteria.o__Oceanospirillales.f__Saccharospirillace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Value: .Q
75
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25
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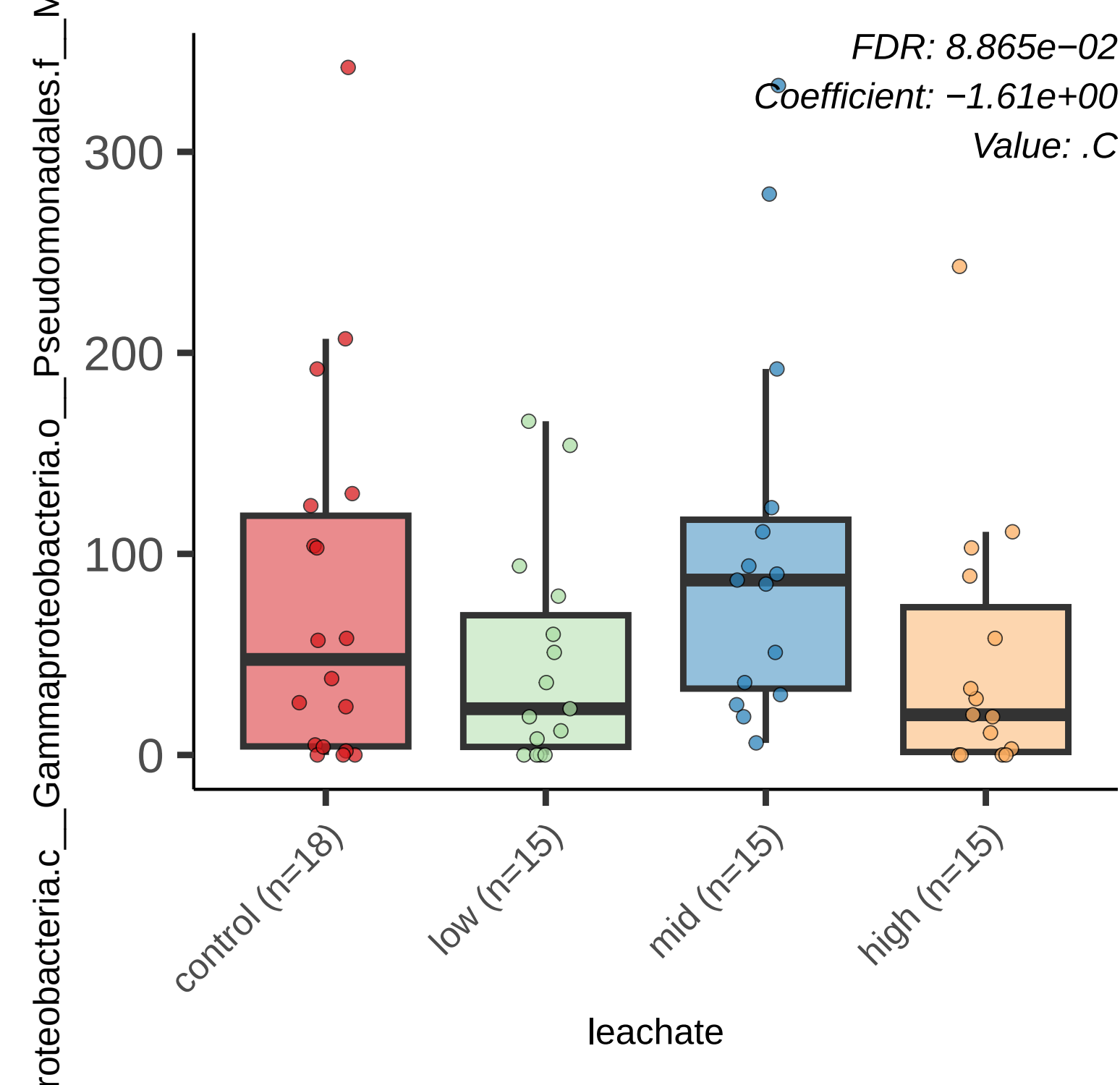
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
ria.c__Gammaproteobacteria.o__Nitrosococcales.f__Methylophaga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Coefficient: −1.61e+00
Value: .C
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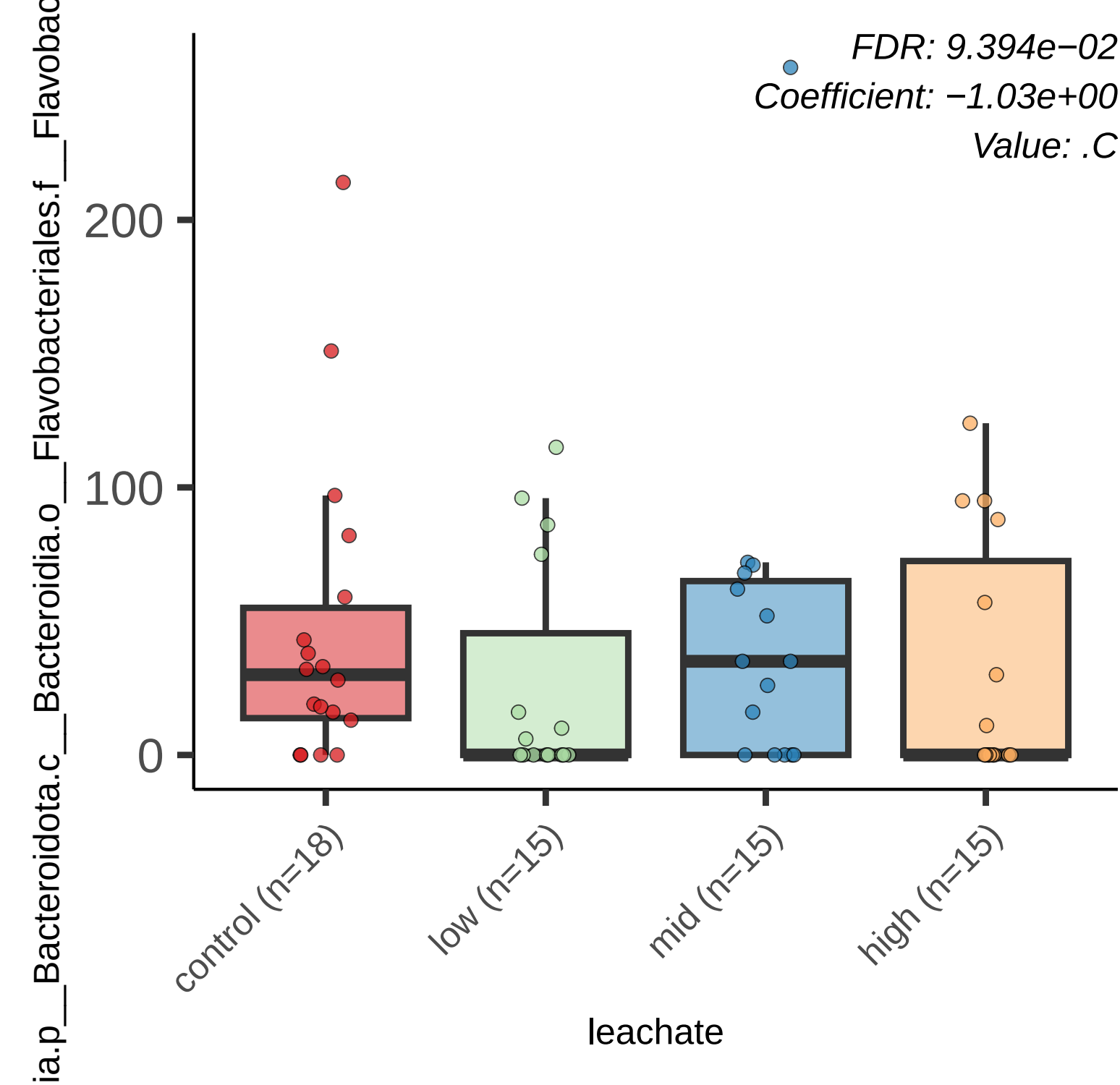
200
100
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
roteobacteria.c__Gammaproteobacteria.o__Pseudomonadales.f__M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Value: .C
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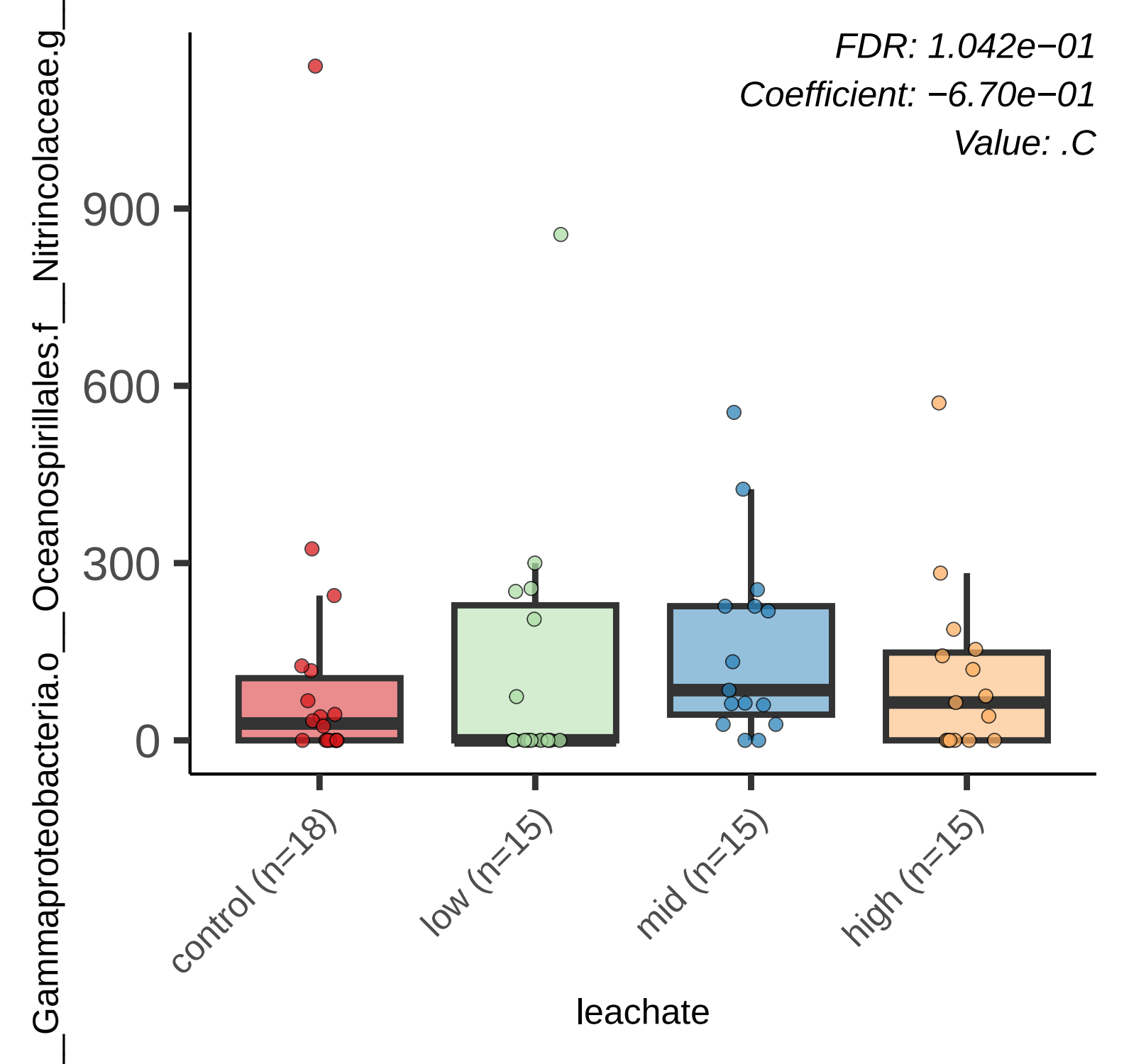
100
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
ia.p__Bacteroidota.c__Bacteroidia.o__Flavobacteriales.f__Flavobac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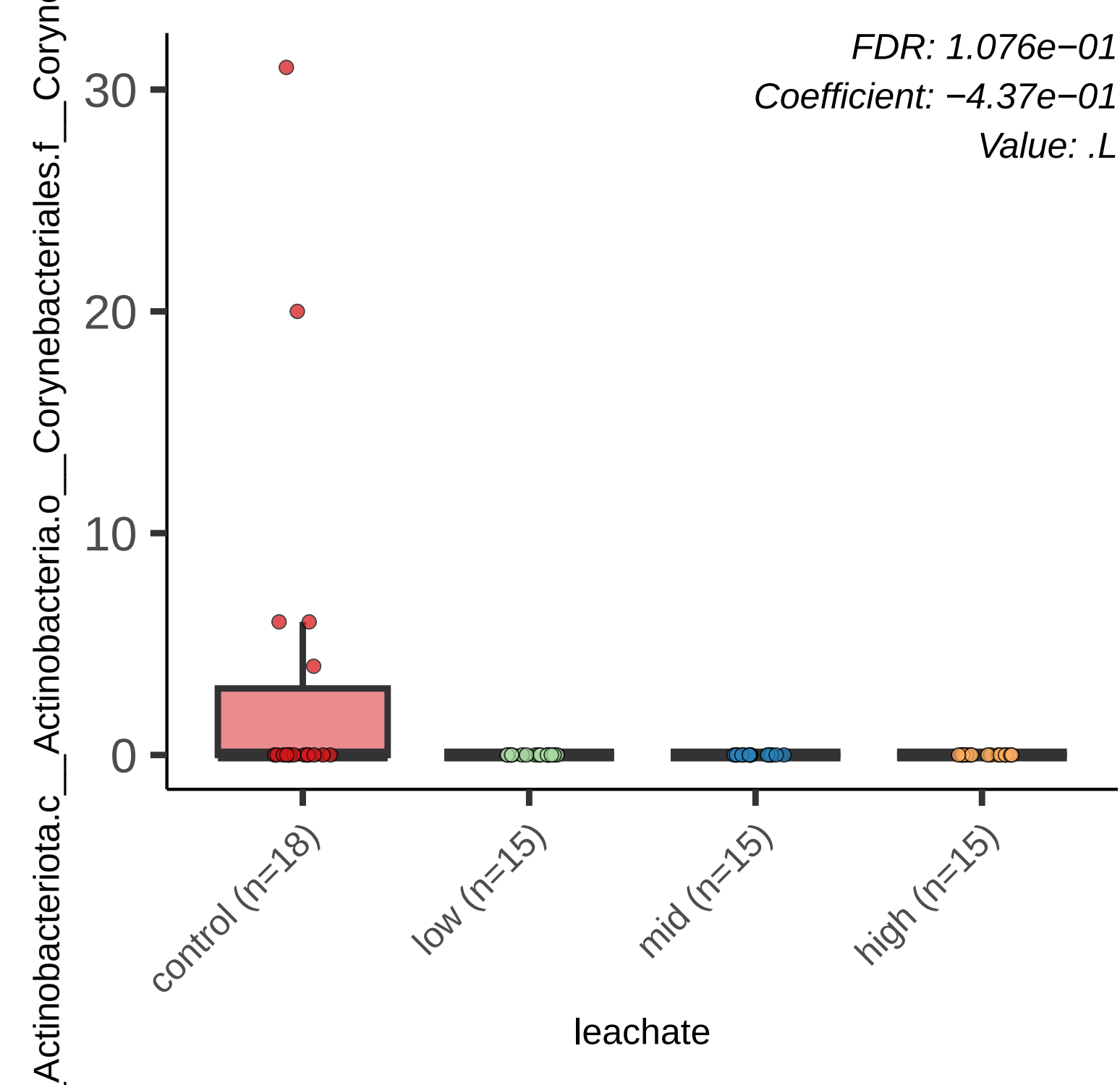
Value: .C
900
600
300
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
__Gammaproteobacteria.o__Oceanospirillales.f__Nitrincolaceae.g__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10
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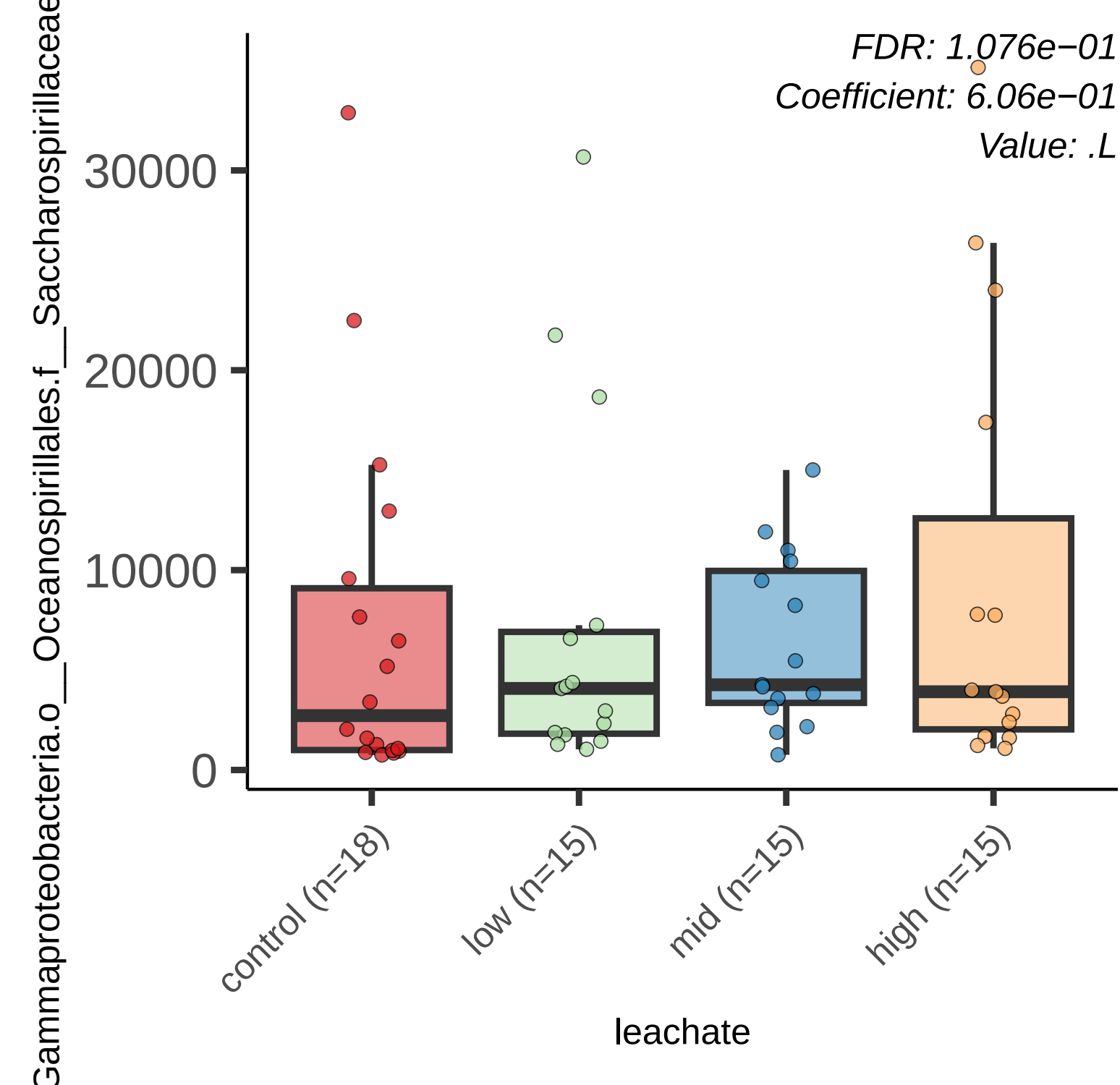
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
Actinobacteriota.c__Actinobacteria.o__Corynebacteriales.f__Coryne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Value: .L
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20000
10000
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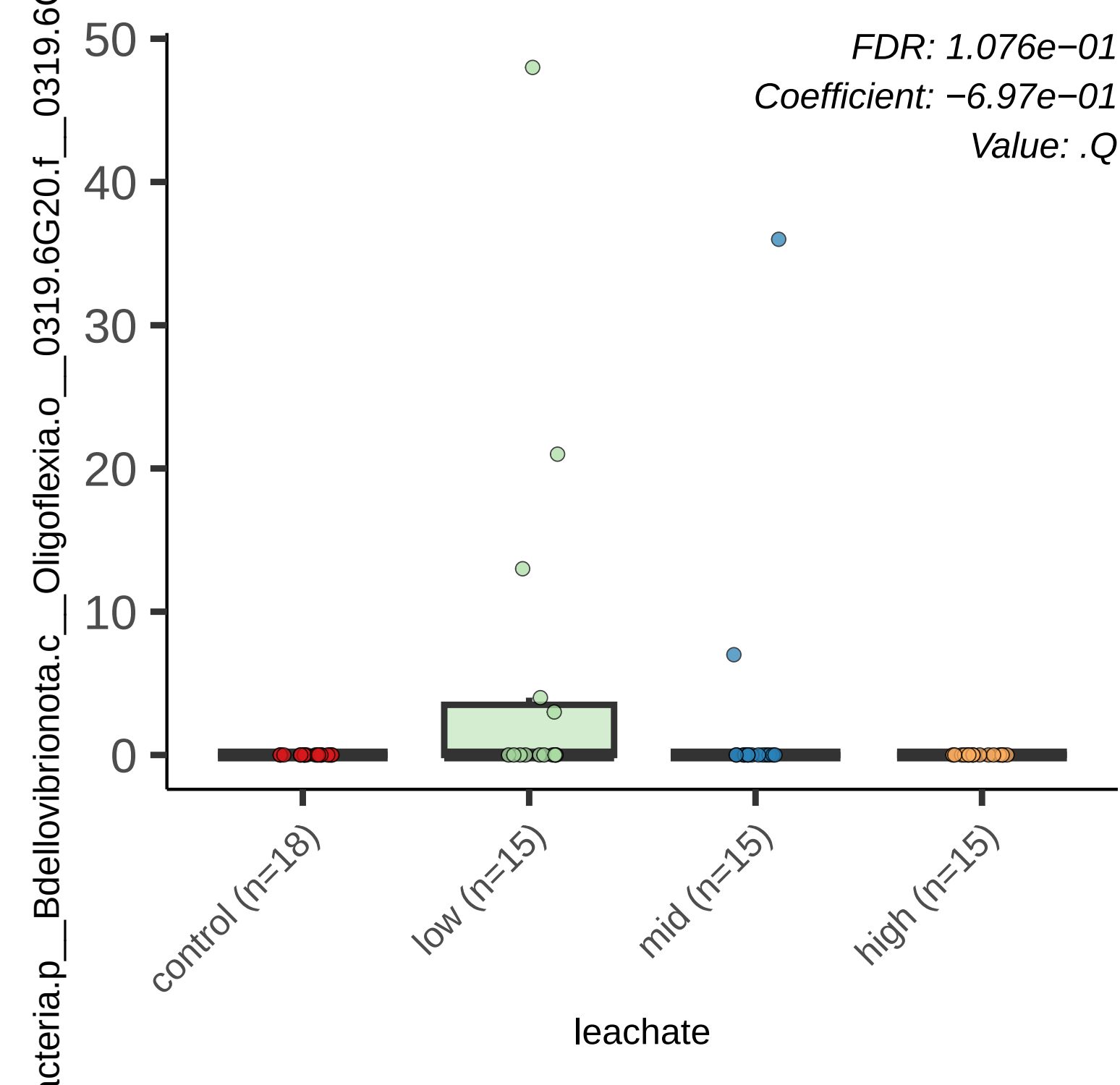
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate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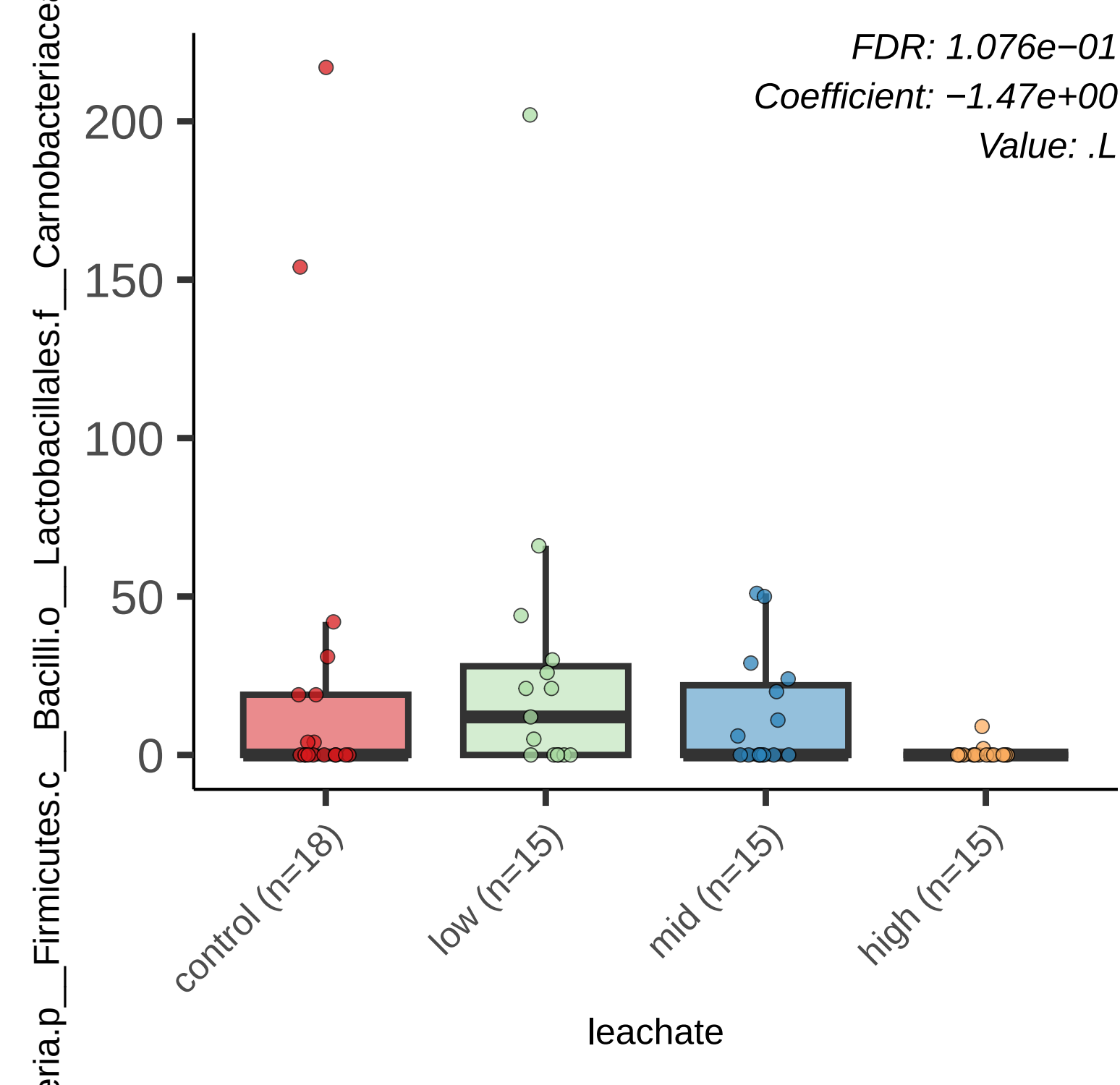
40
30
20
10
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
cteria.p__Bdellovibrionota.c__Oligoflexia.o__0319.6G20.f__0319.6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Value: .L
200
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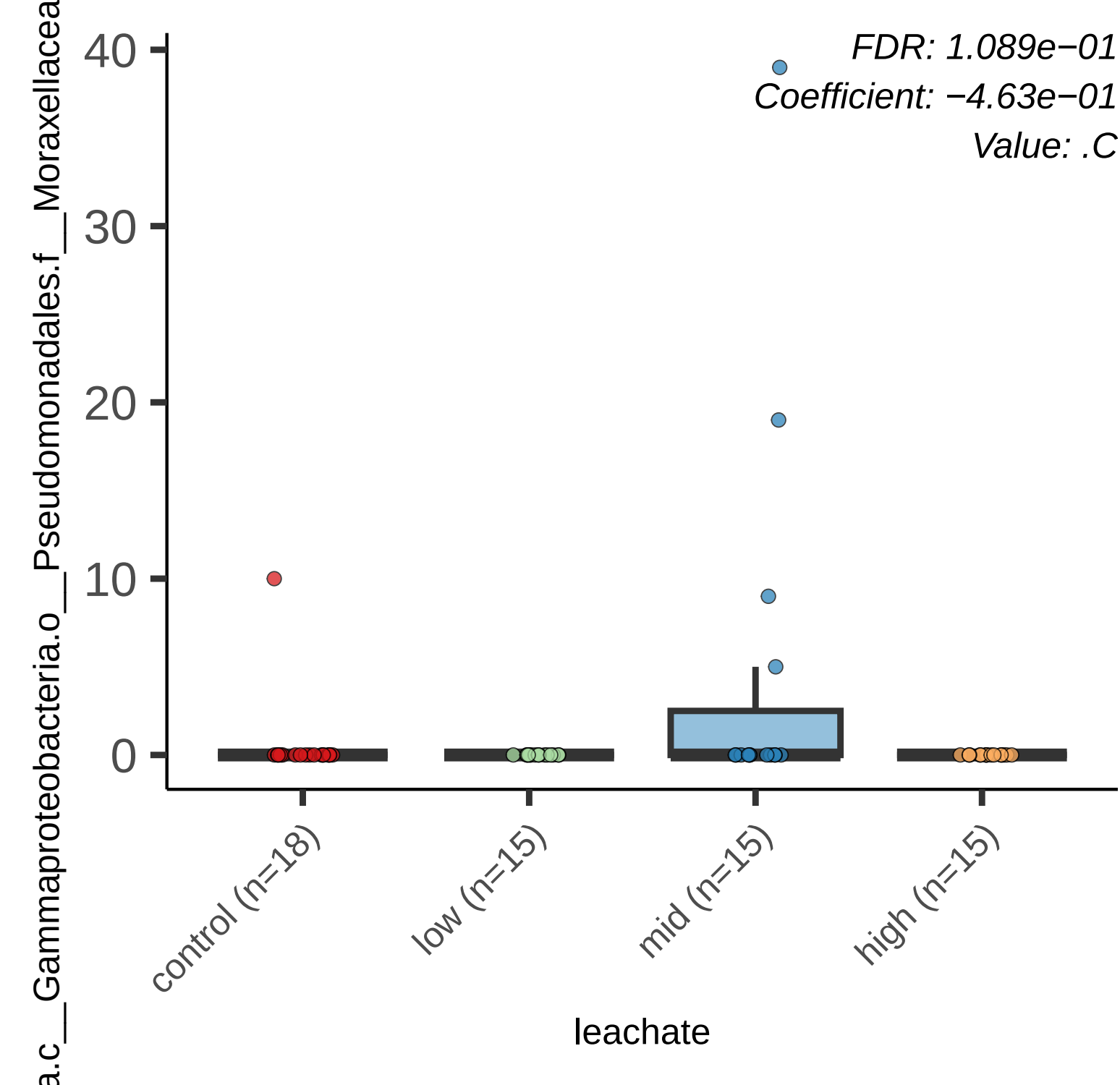
100
50
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
eria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Carnobacteriace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Coefficient: −4.63e−01
Value: .C
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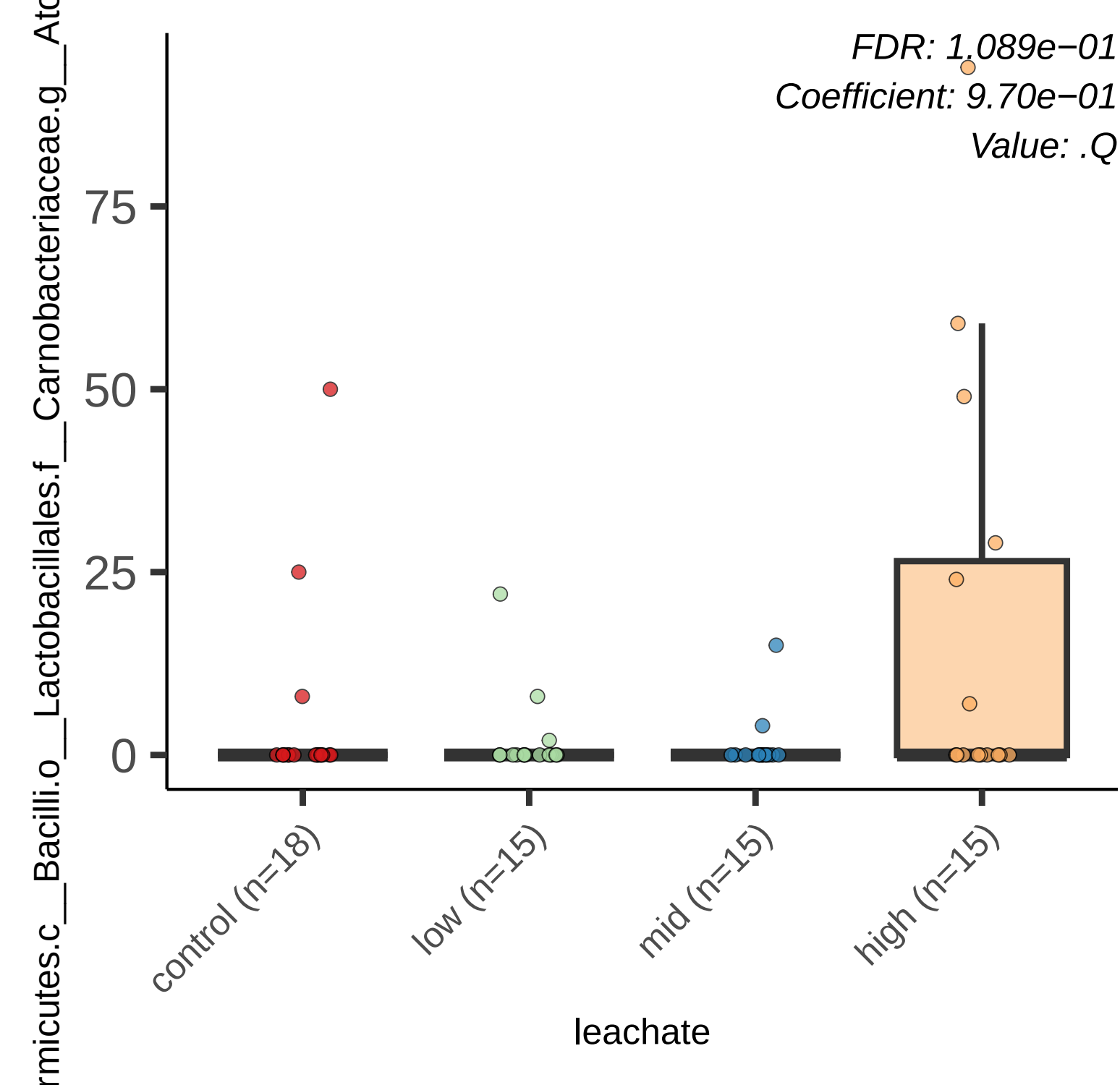
30
20
10
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
a.c__Gammaproteobacteria.o__Pseudomonadales.f__Moraxellacea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Coefficient: 9.70e−01
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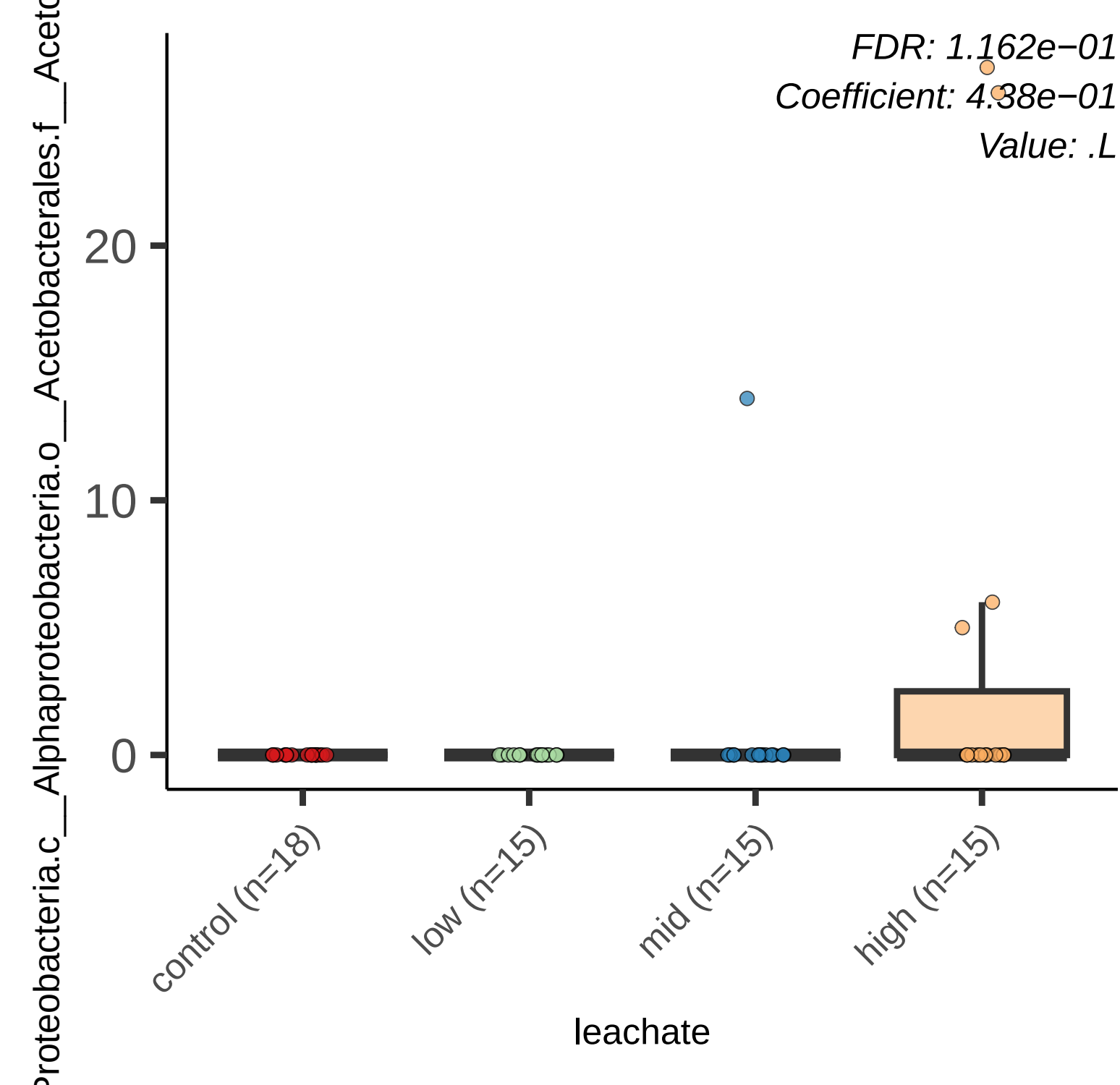
25
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
rmicutes.c__Bacilli.o__Lactobacillales.f__Carnobacteriaceae.g__Ato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Coefficient: 4.38e−01
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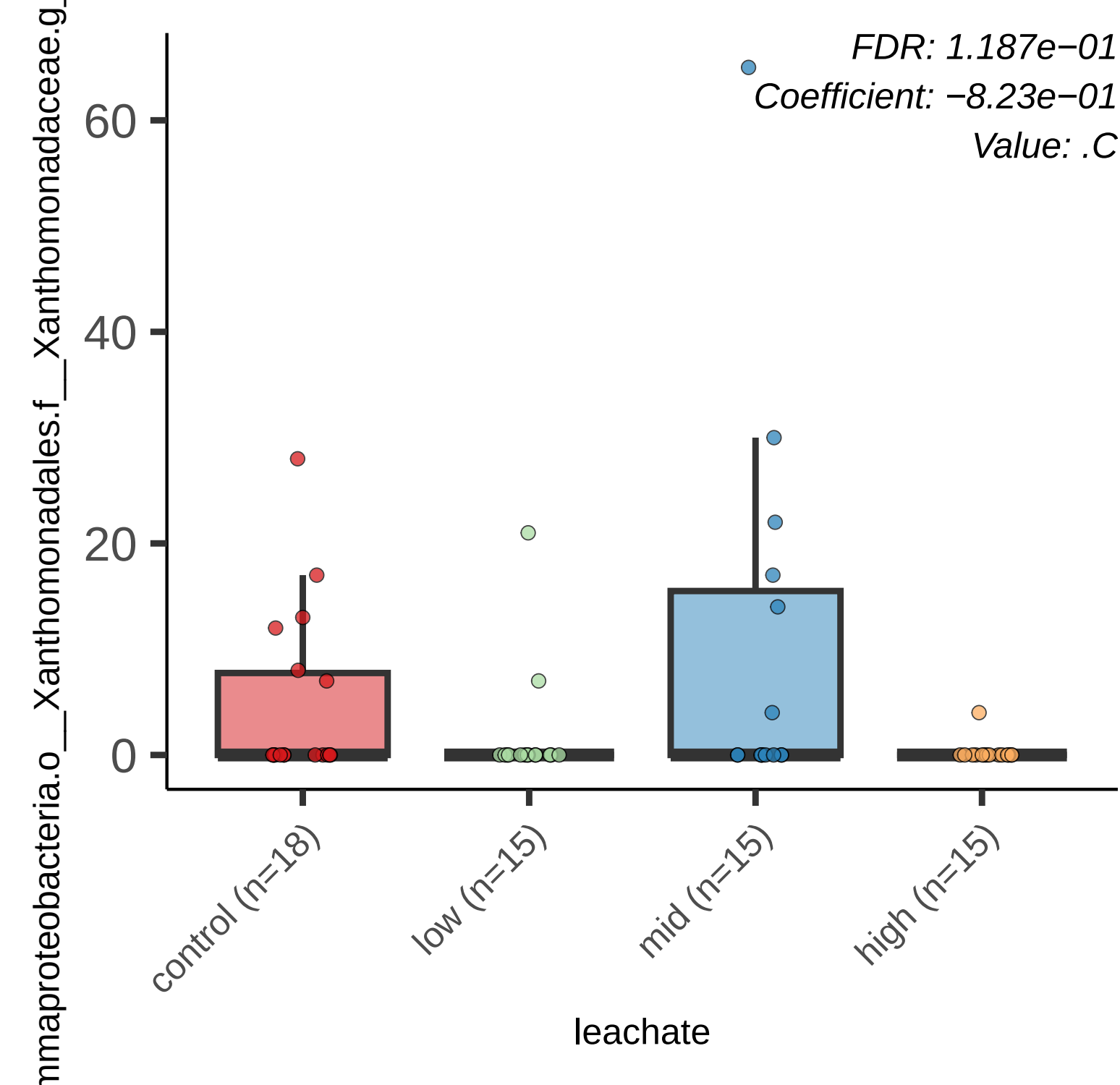
10
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
Proteobacteria.c__Alphaproteobacteria.o__Acetobacterales.f__Aceto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Value: .C
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20
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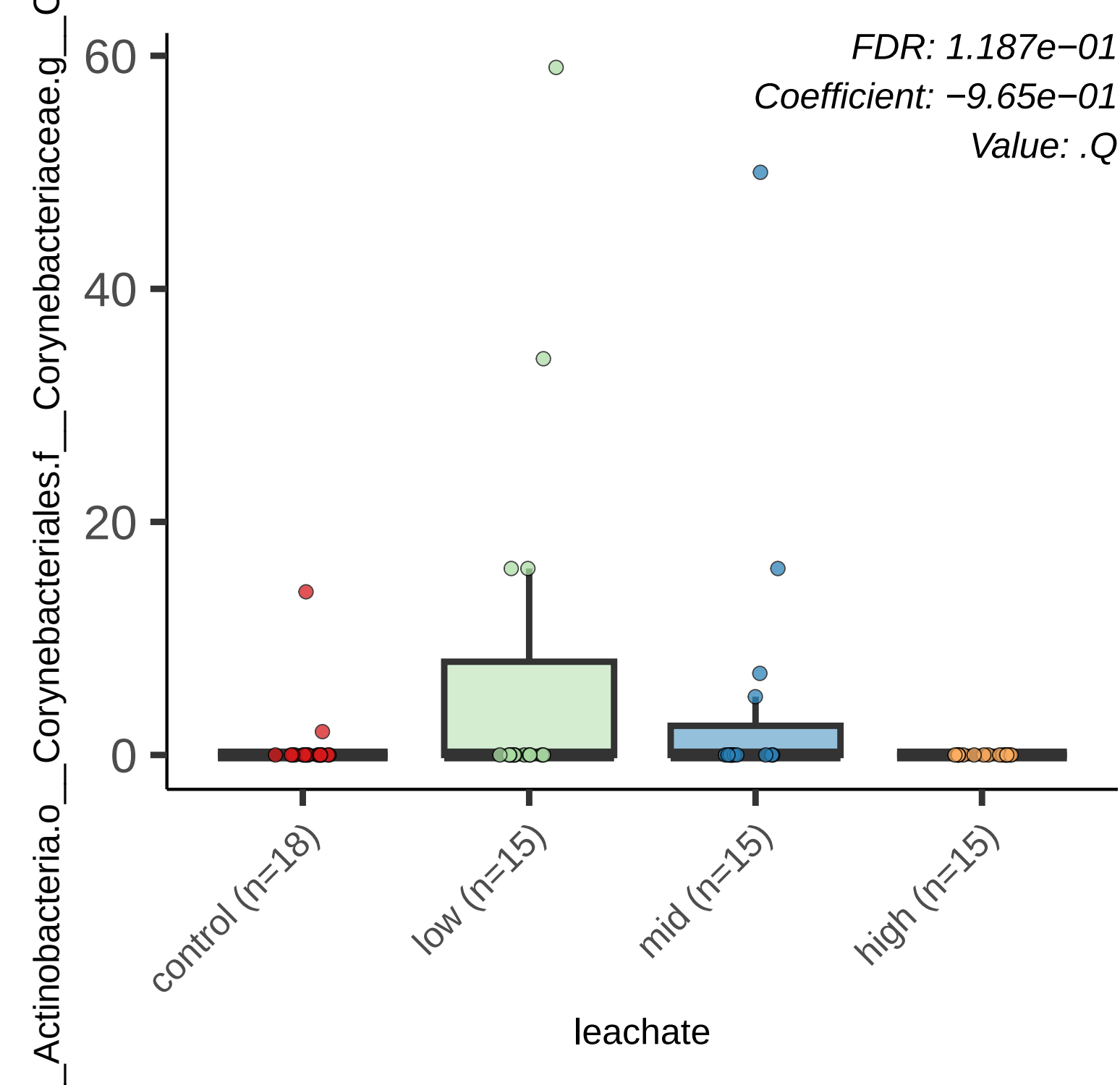
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
nmaproteobacteria.o__Xanthomonadales.f__Xanthomonadaceae.g_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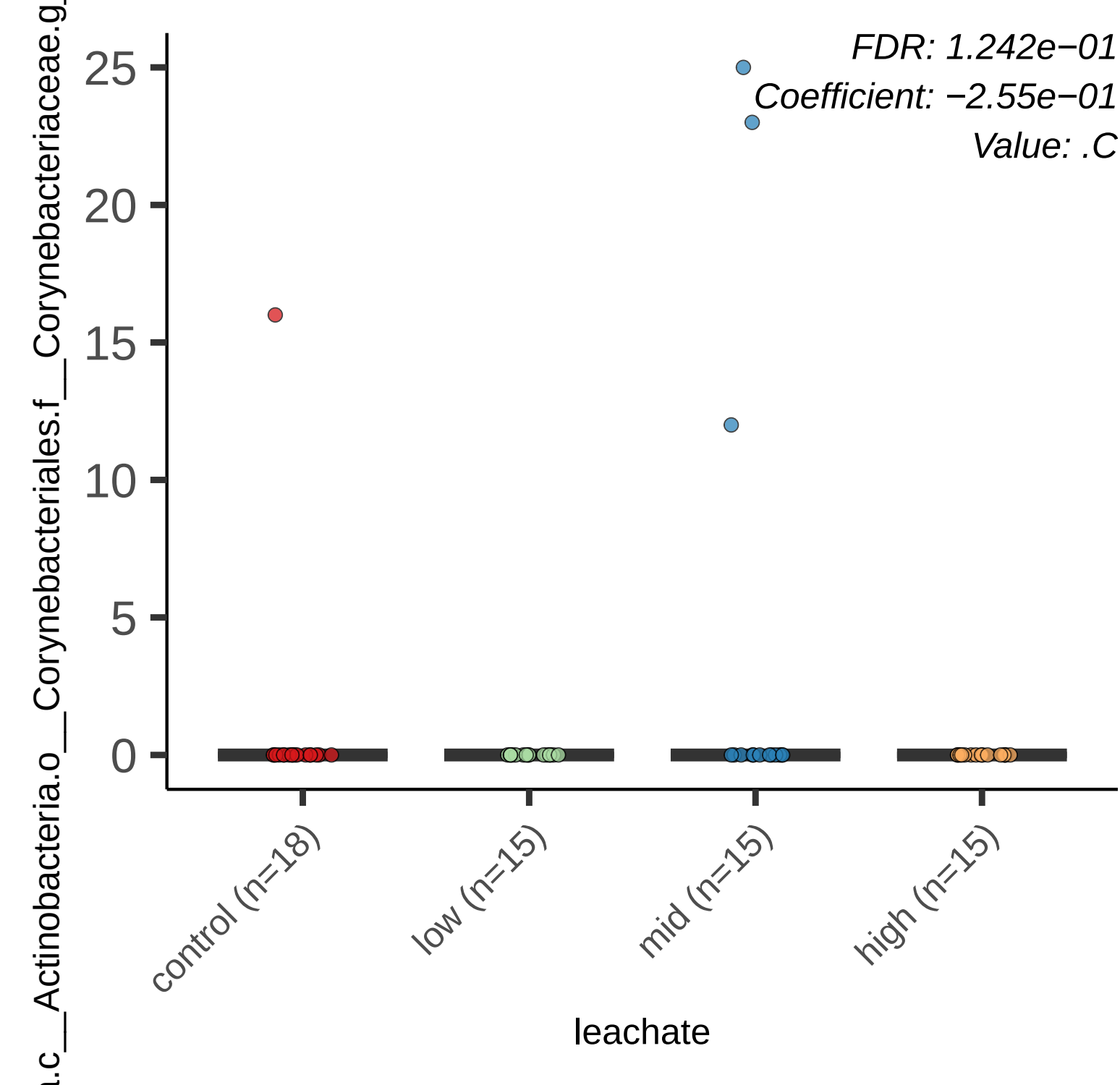
40
20
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
_Actinobacteria.o__Corynebacteriales.f__Corynebacteriaceae.g__C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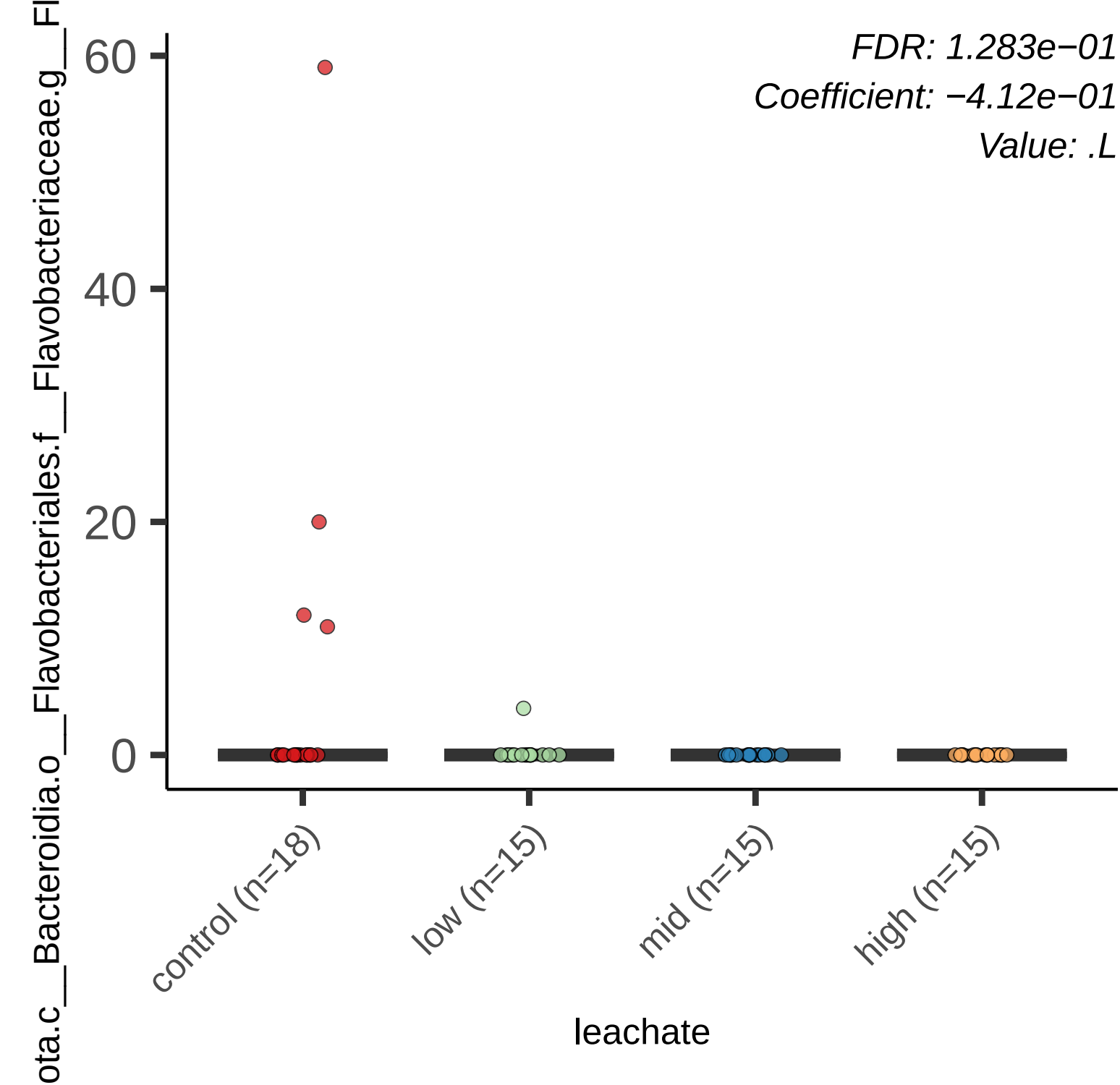
15
10
5
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
.c__Actinobacteria.o__Corynebacteriales.f__Corynebacteriaceae.g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Value: .L
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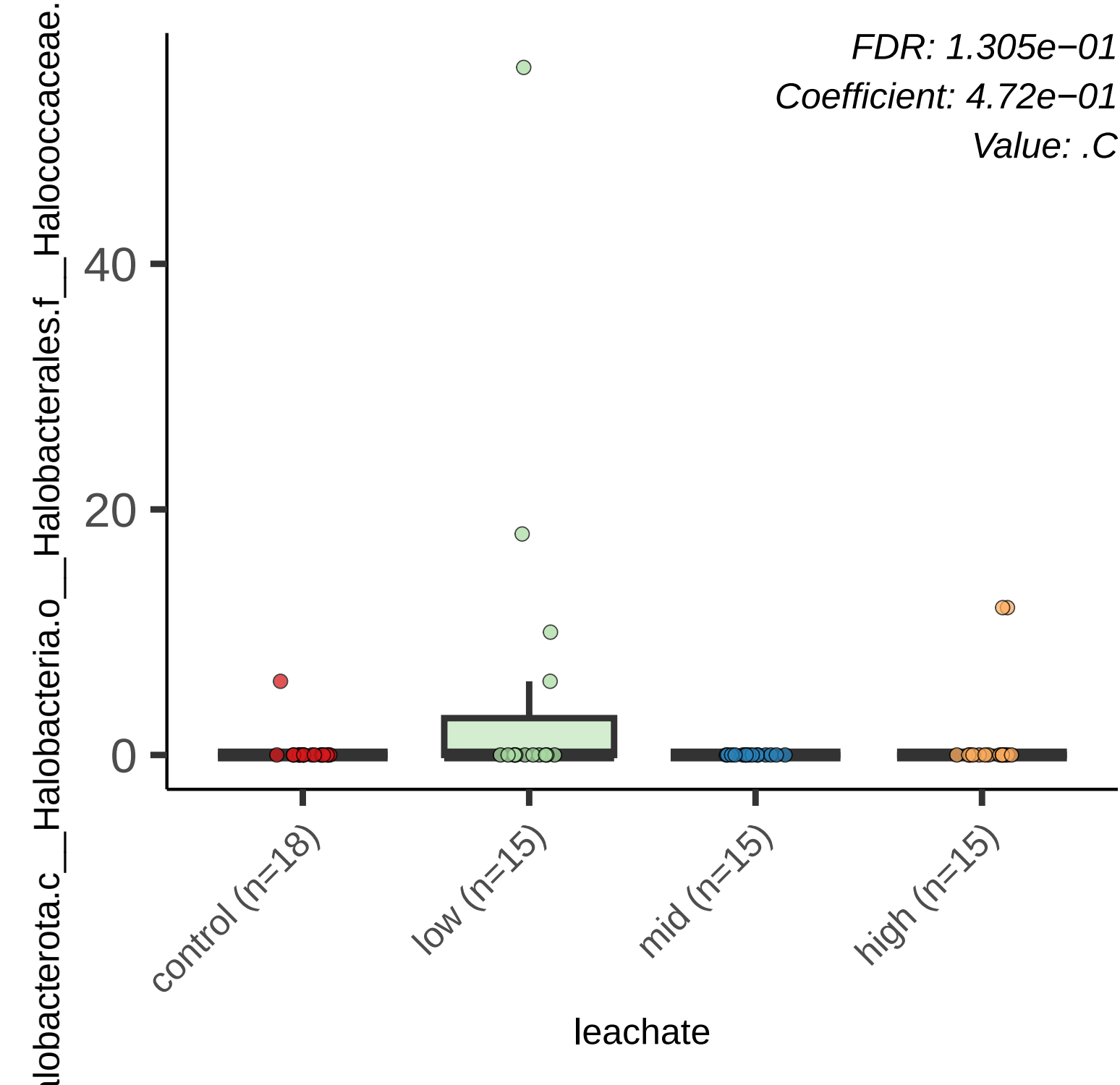
40
20
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
ota.c__Bacteroidia.o__Flavobacteriales.f__Flavobacteriaceae.g__Fl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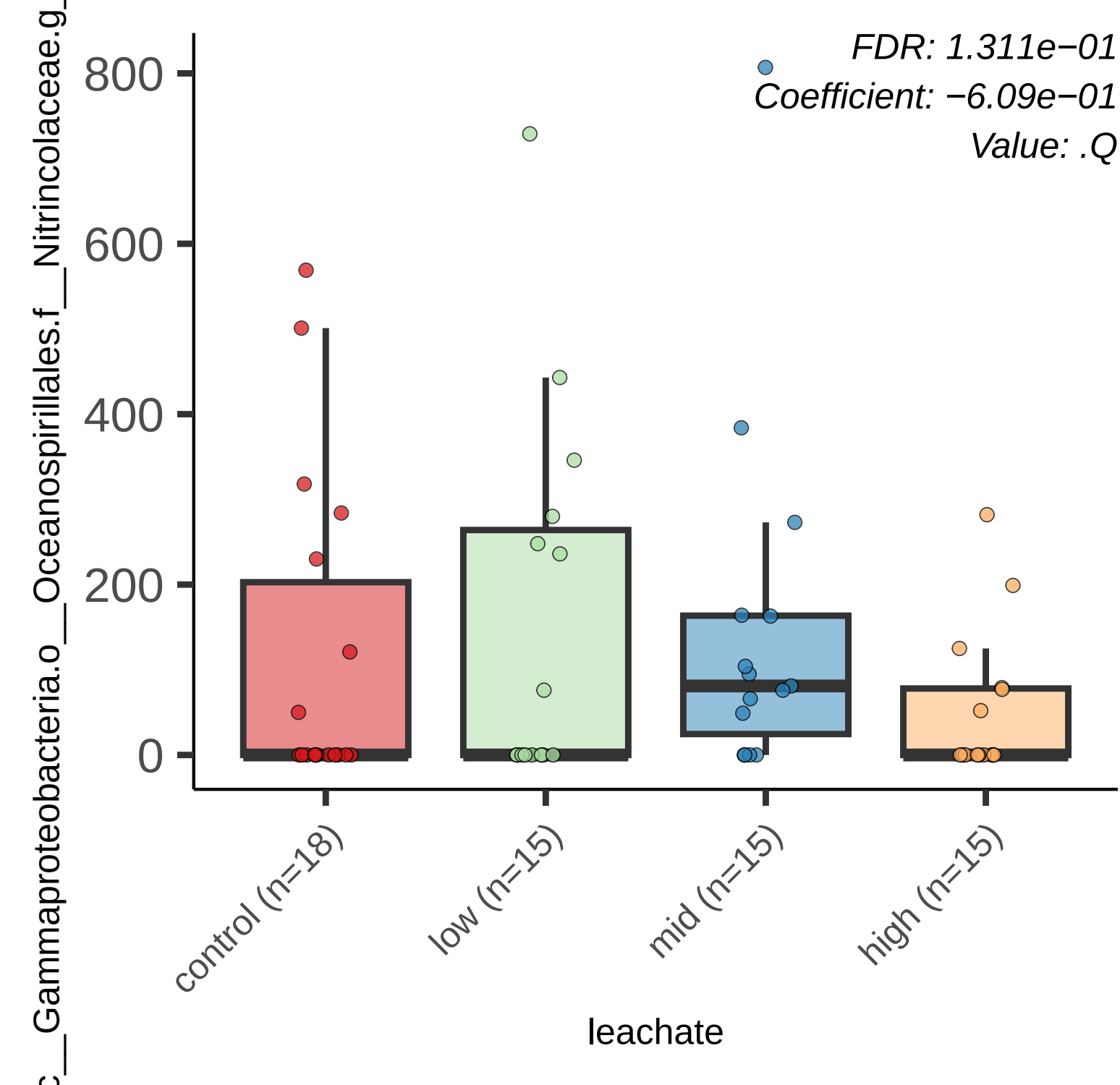
20
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
Halobacterota.c__Halobacteria.o__Halobacterales.f__Halococcaceae.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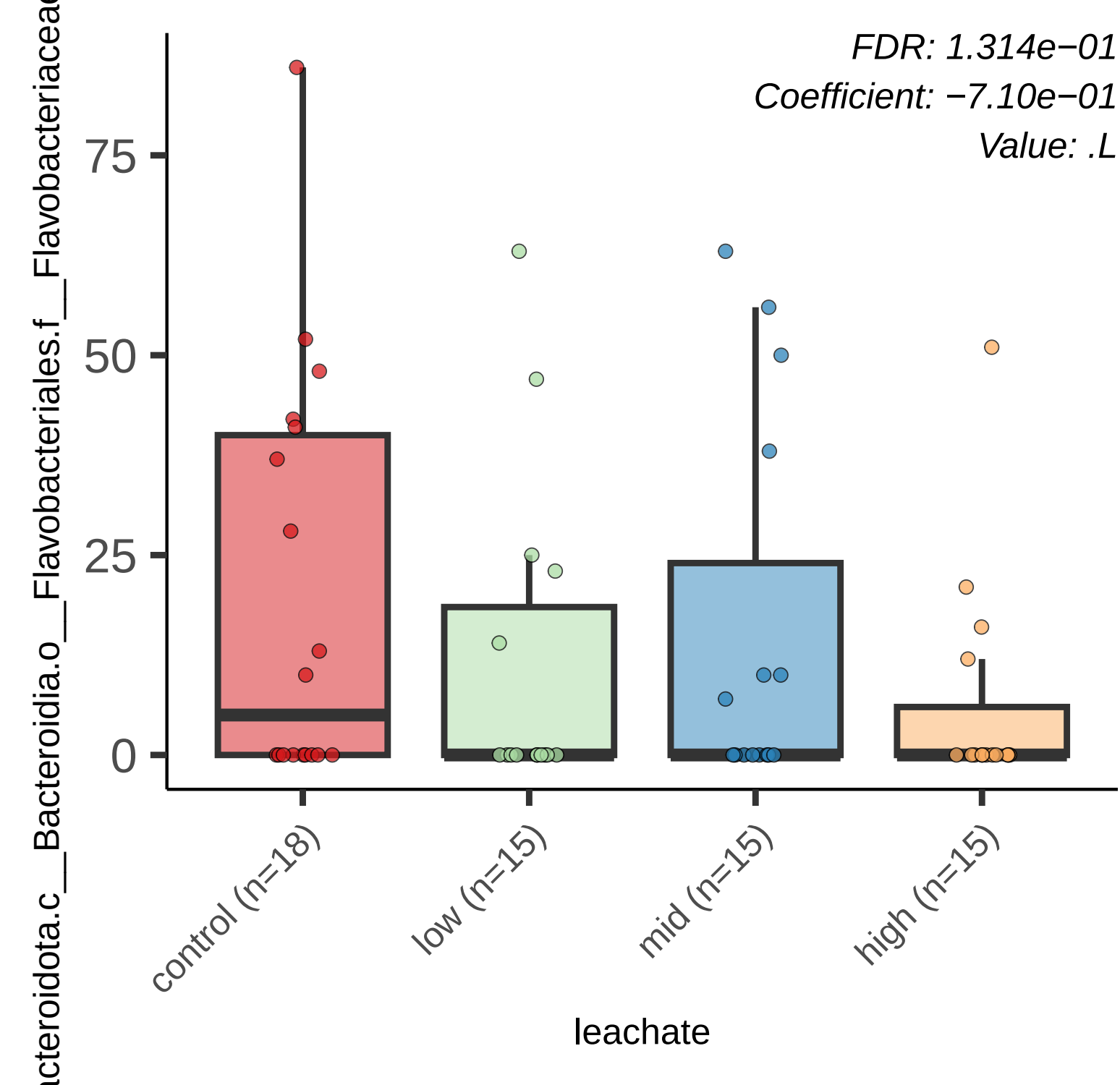
400
200
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
c__Gammaproteobacteria.o__Oceanospirillales.f__Nitrincolaceae.g_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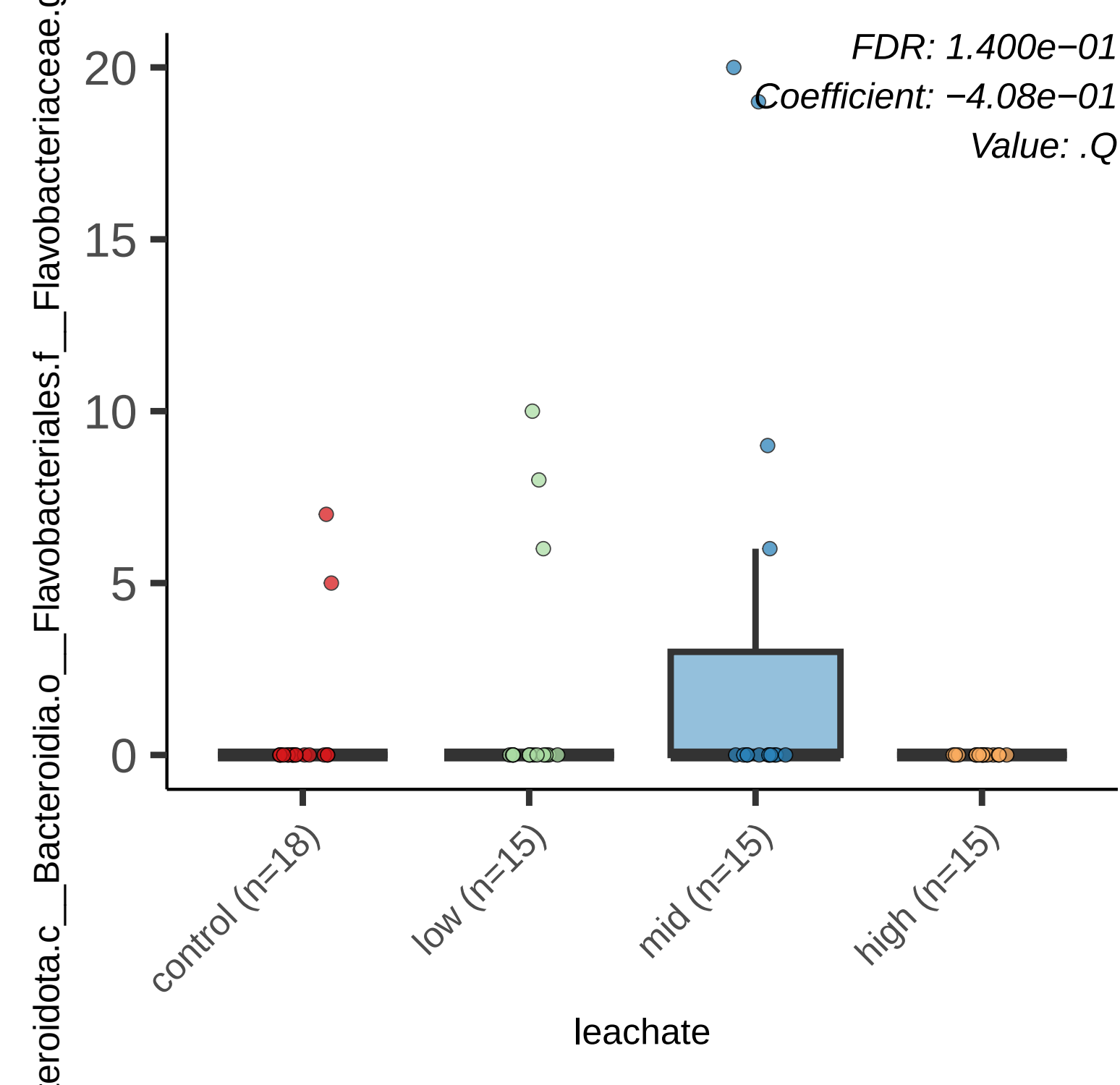
Coefficient: −7.10e−01
Value: .L
75
50
25
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
cteroidota.c__Bacteroidia.o__Flavobacteriales.f__Flavobacteriacea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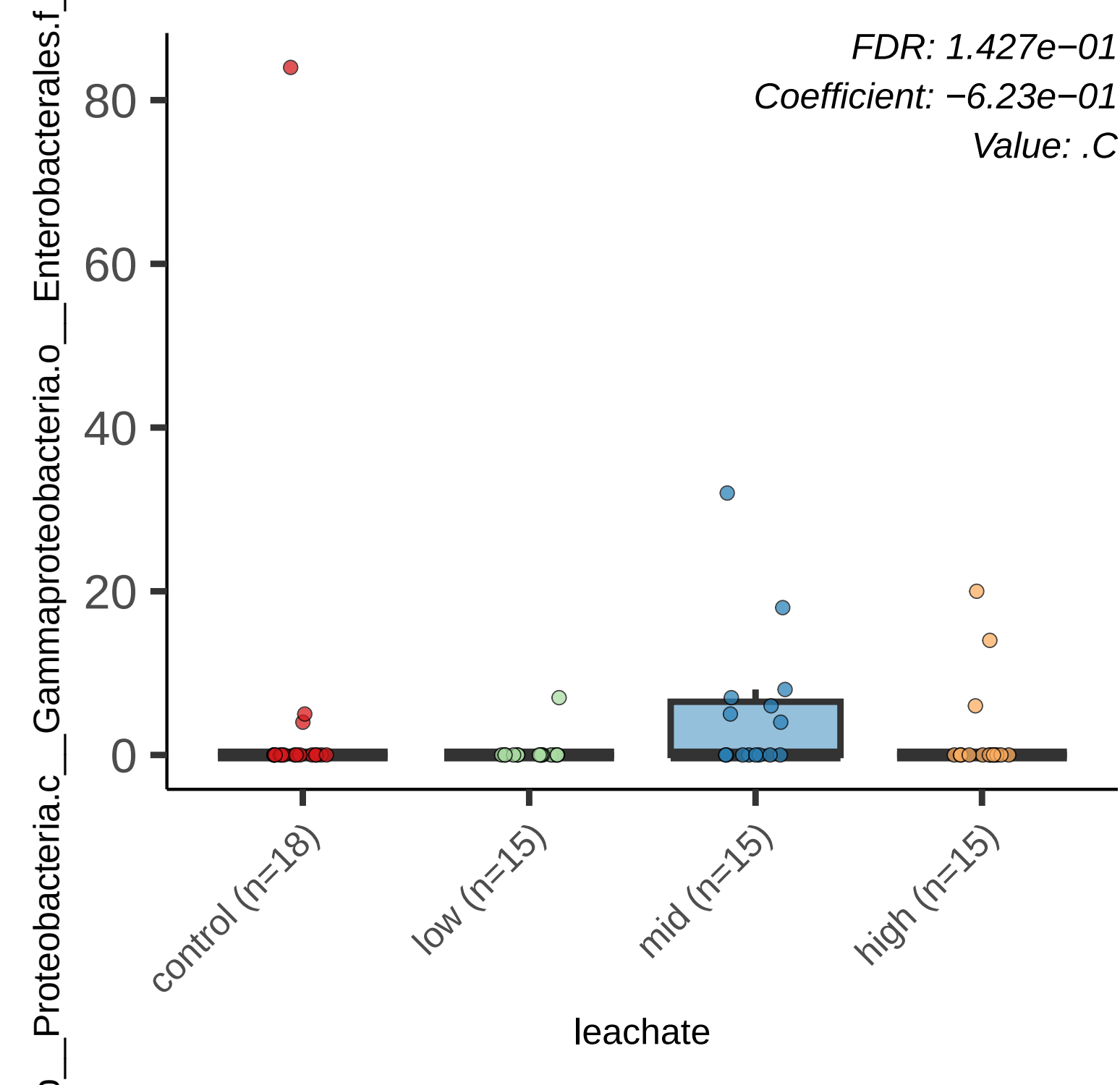
15
10
5
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
teroidota.c__Bacteroidia.o__Flavobacteriales.f__Flavobacteriaceae.g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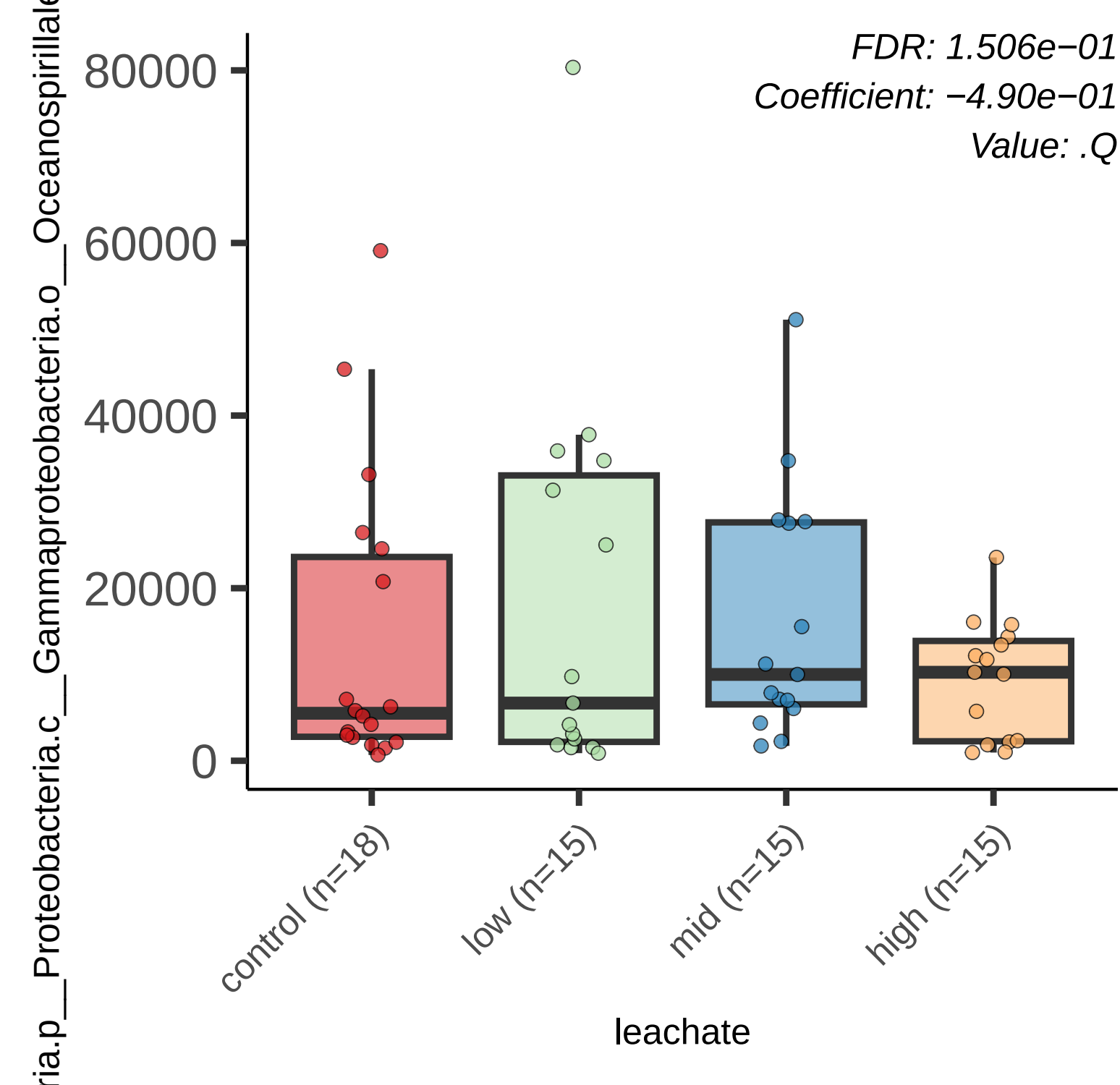
40
20
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
o__Proteobacteria.c__Gammaproteobacteria.o__Enterobacterales.f_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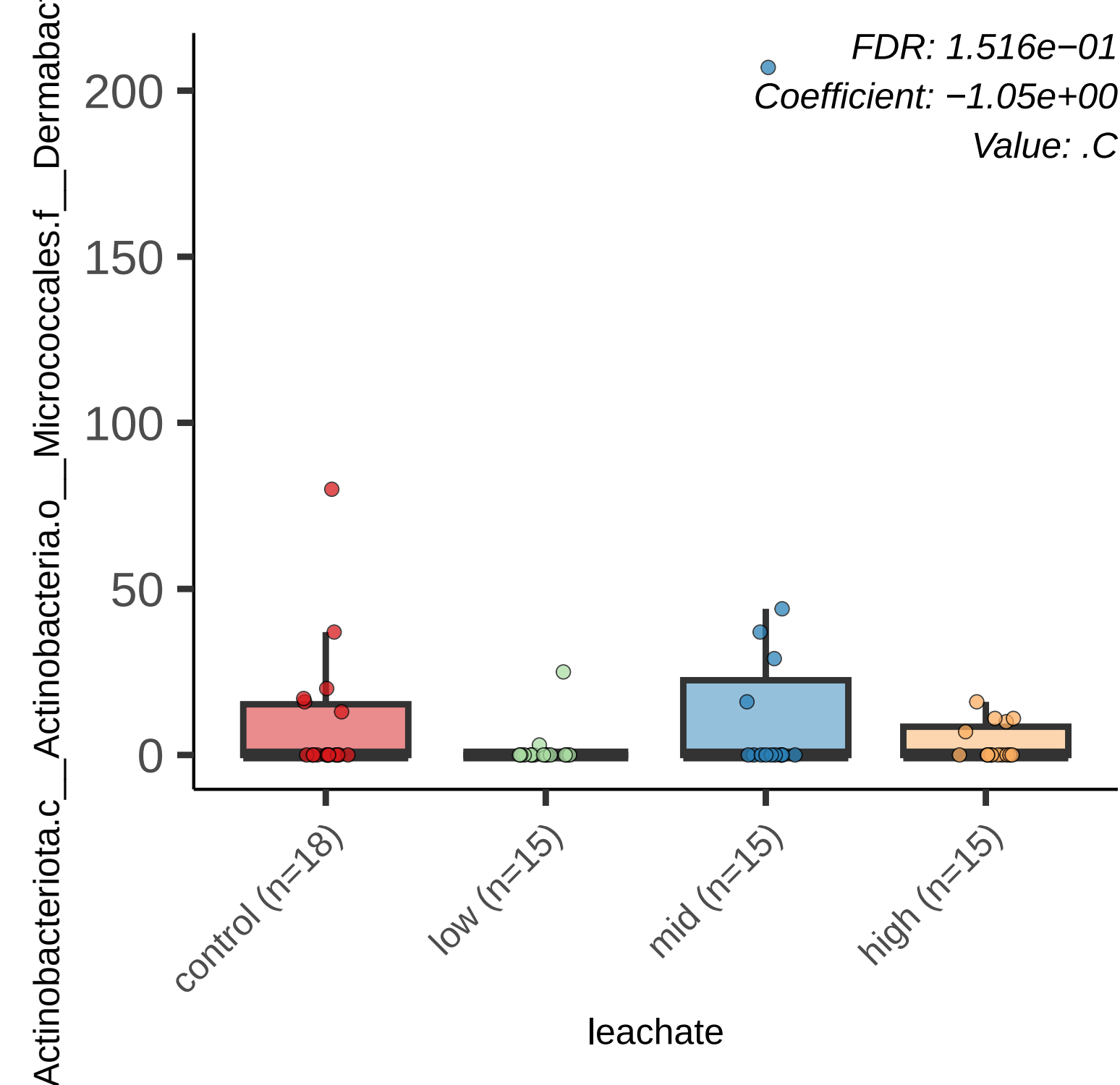
Value: .Q
80000
60000
40000
20000
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
ria.p__Proteobacteria.c__Gammaproteobacteria.o__Oceanospirillale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100
50
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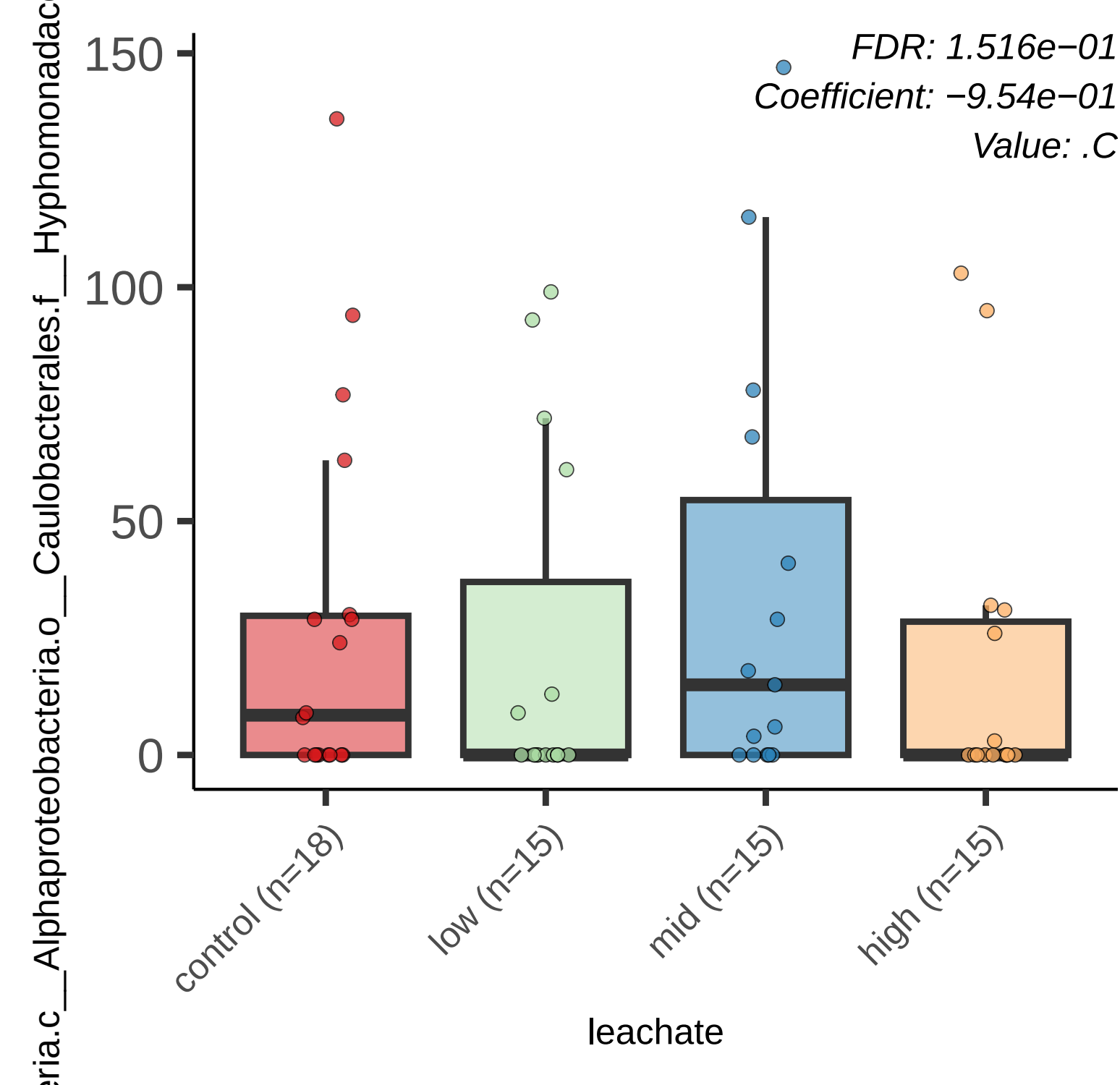
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
Actinobacteriota.c__Actinobacteria.o__Micrococcales.f__Dermabac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Coefficient: −9.54e−01
Value: .C
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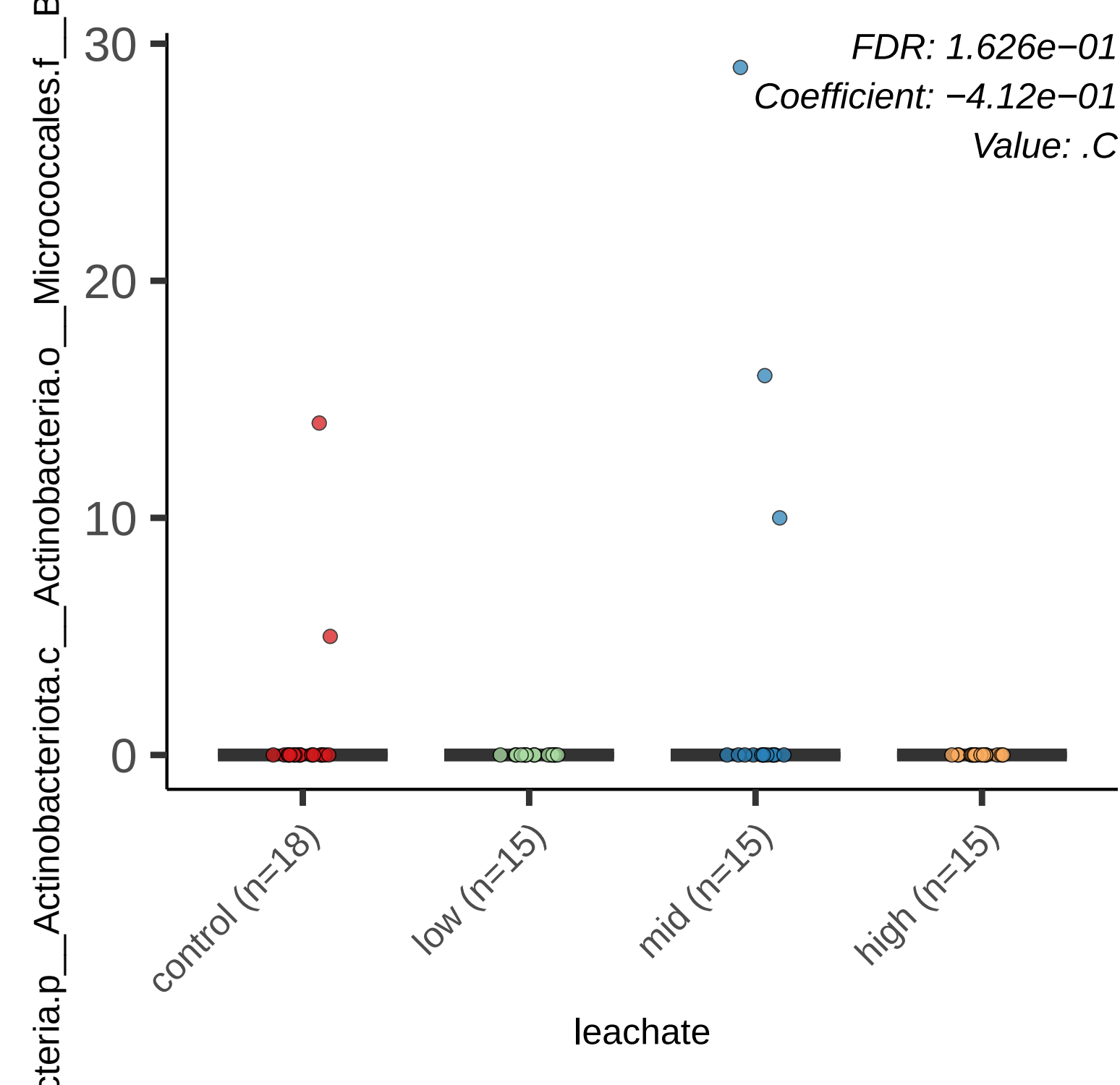
100
50
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
eria.c__Alphaproteobacteria.o__Caulobacterales.f__Hyphomonadac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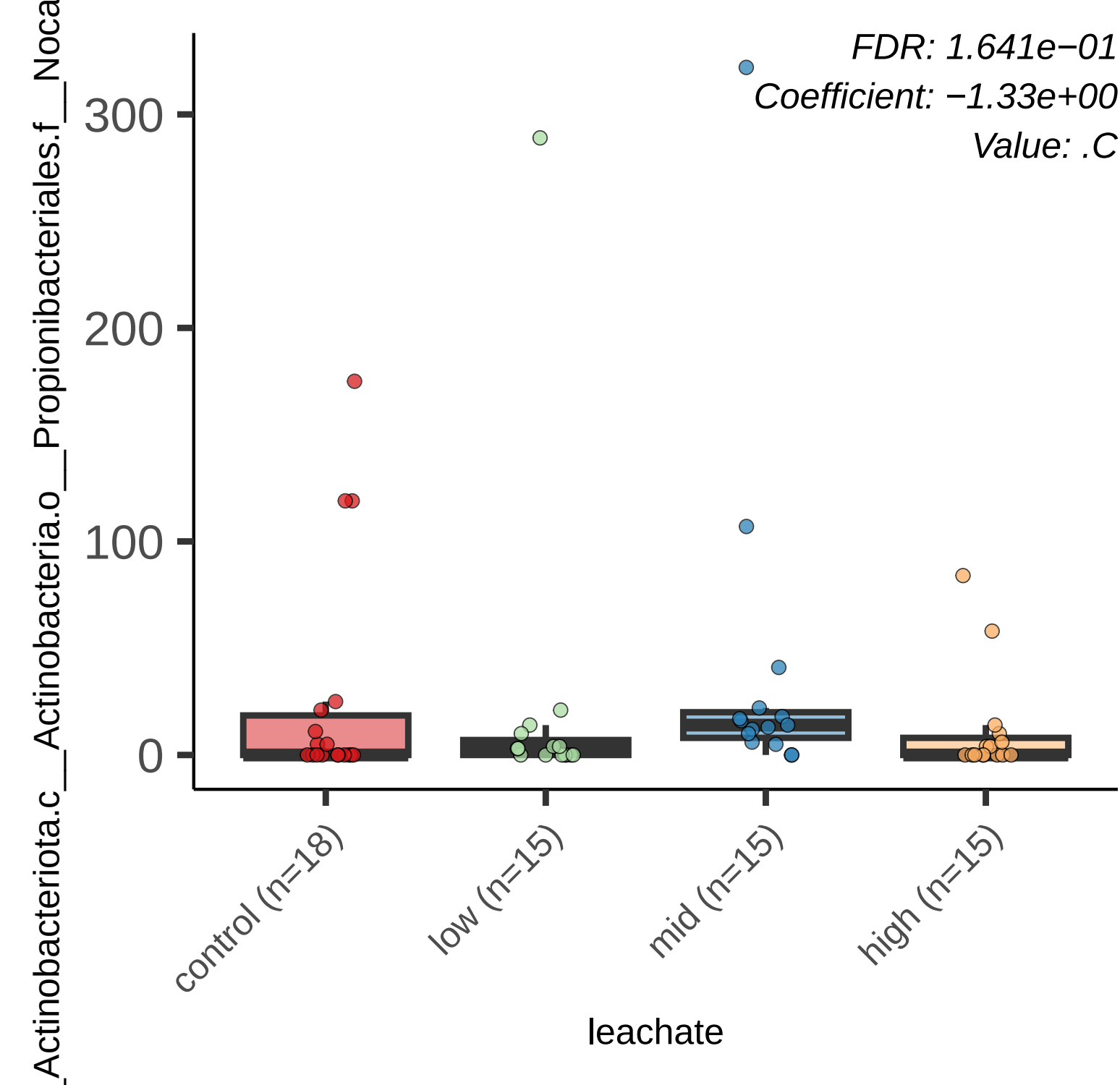
Value: .C
30
20
10
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
cteria.p__Actinobacteriota.c__Actinobacteria.o__Micrococcales.f__B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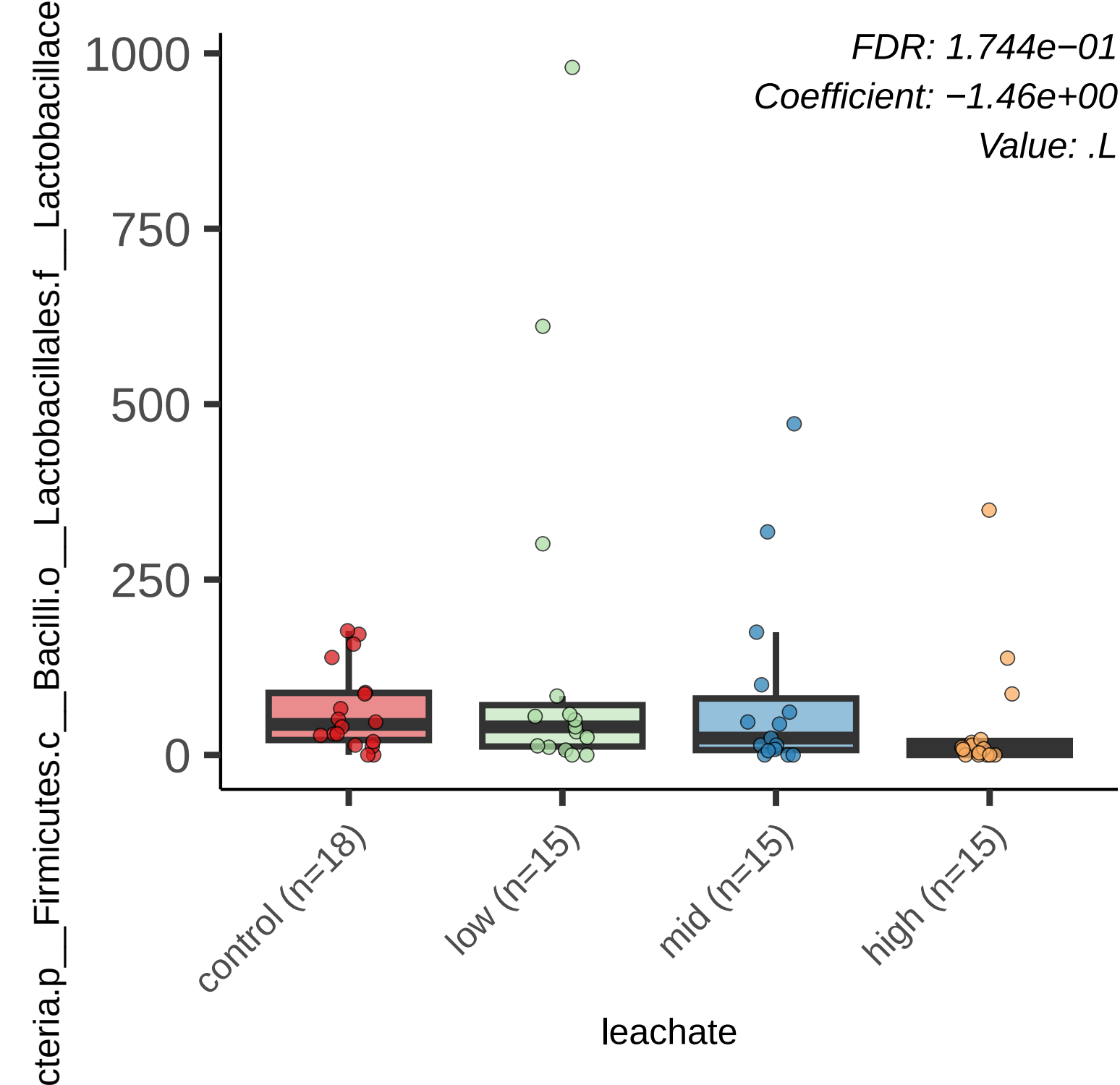
Coefficient: −1.33e+00
Value: .C
300
200
100
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
_Actinobacteriota.c__Actinobacteria.o__Propionibacteriales.f__Noca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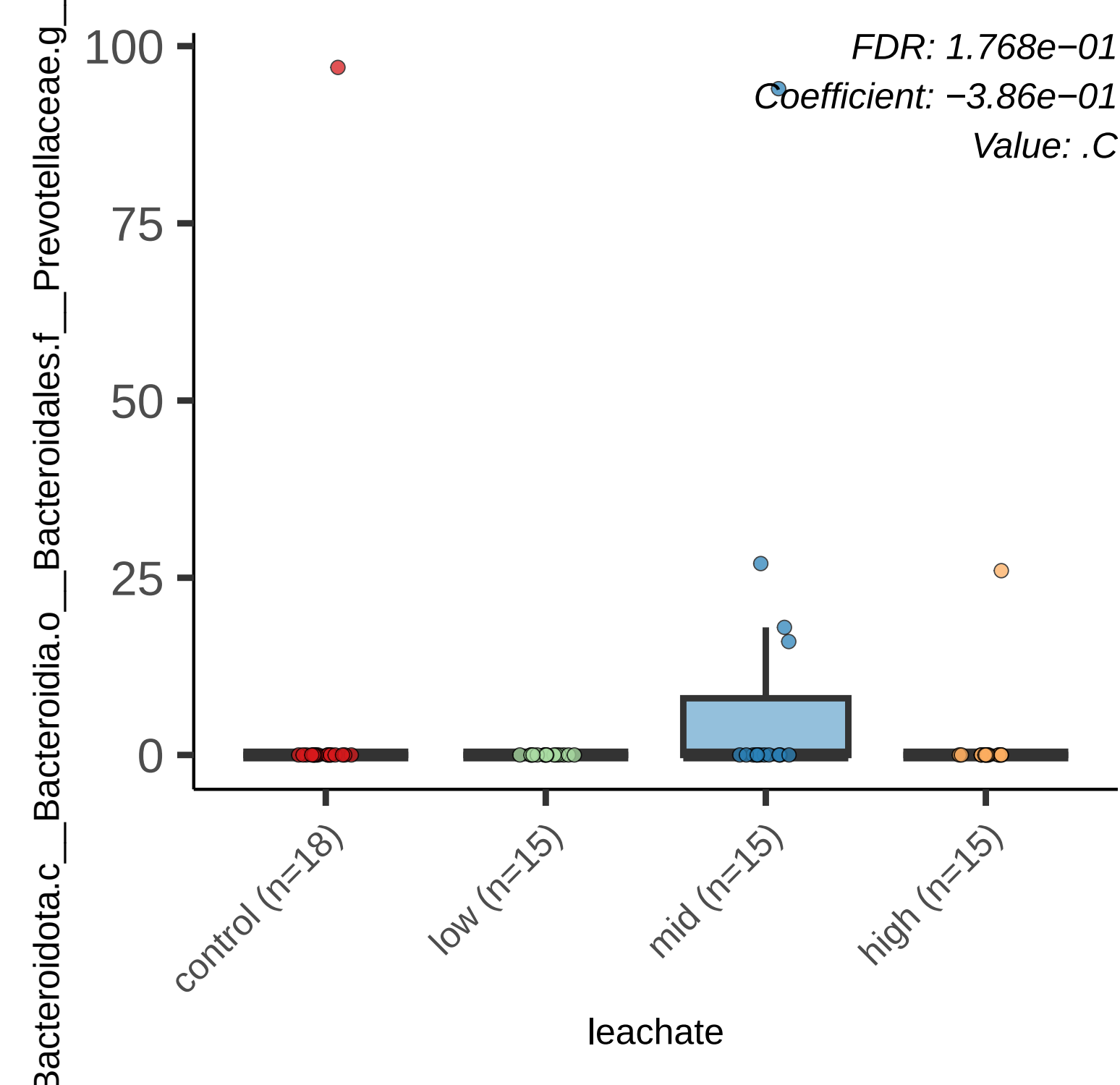
Coefficient: −1.46e+00
Value: .L
1000
750
500
250
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
cteria.p__Firmicutes.c__Bacilli.o__Lactobacillales.f__Lactobacillace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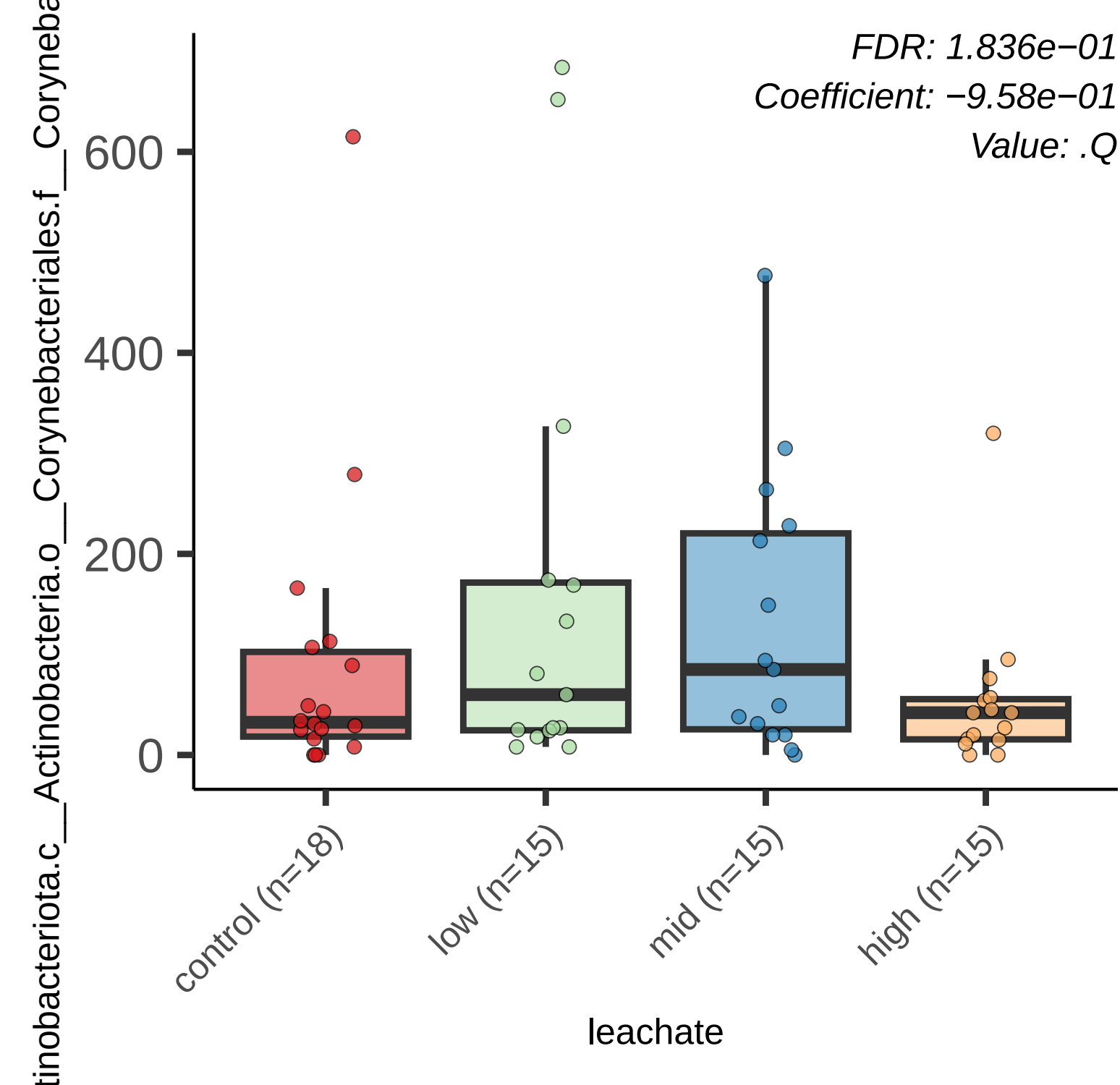
Coefficient: −3.86e−01
Value: .C
100
75
50
25
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
Bacteroidota.c__Bacteroidia.o__Bacteroidales.f__Prevotellaceae.g__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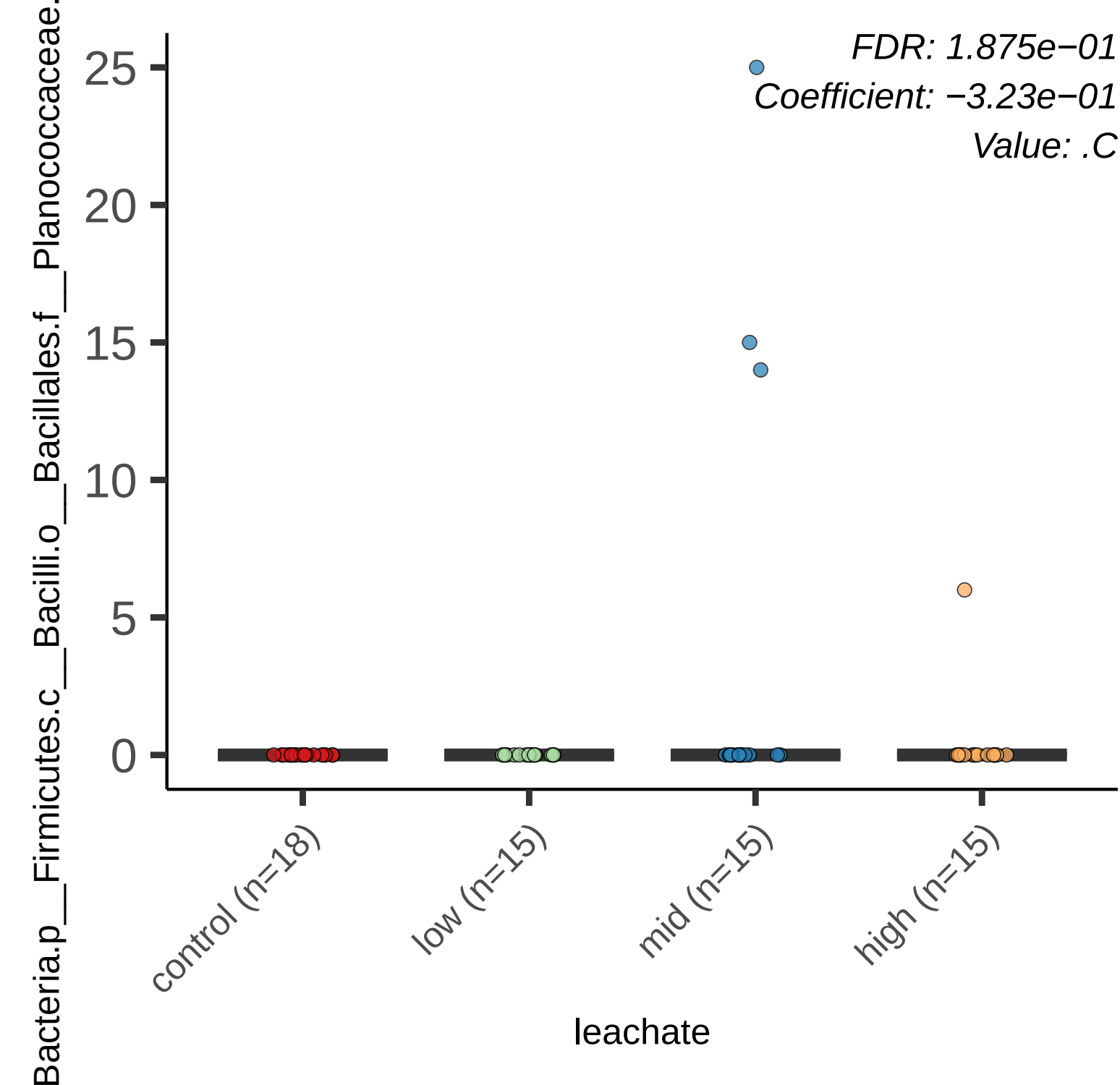
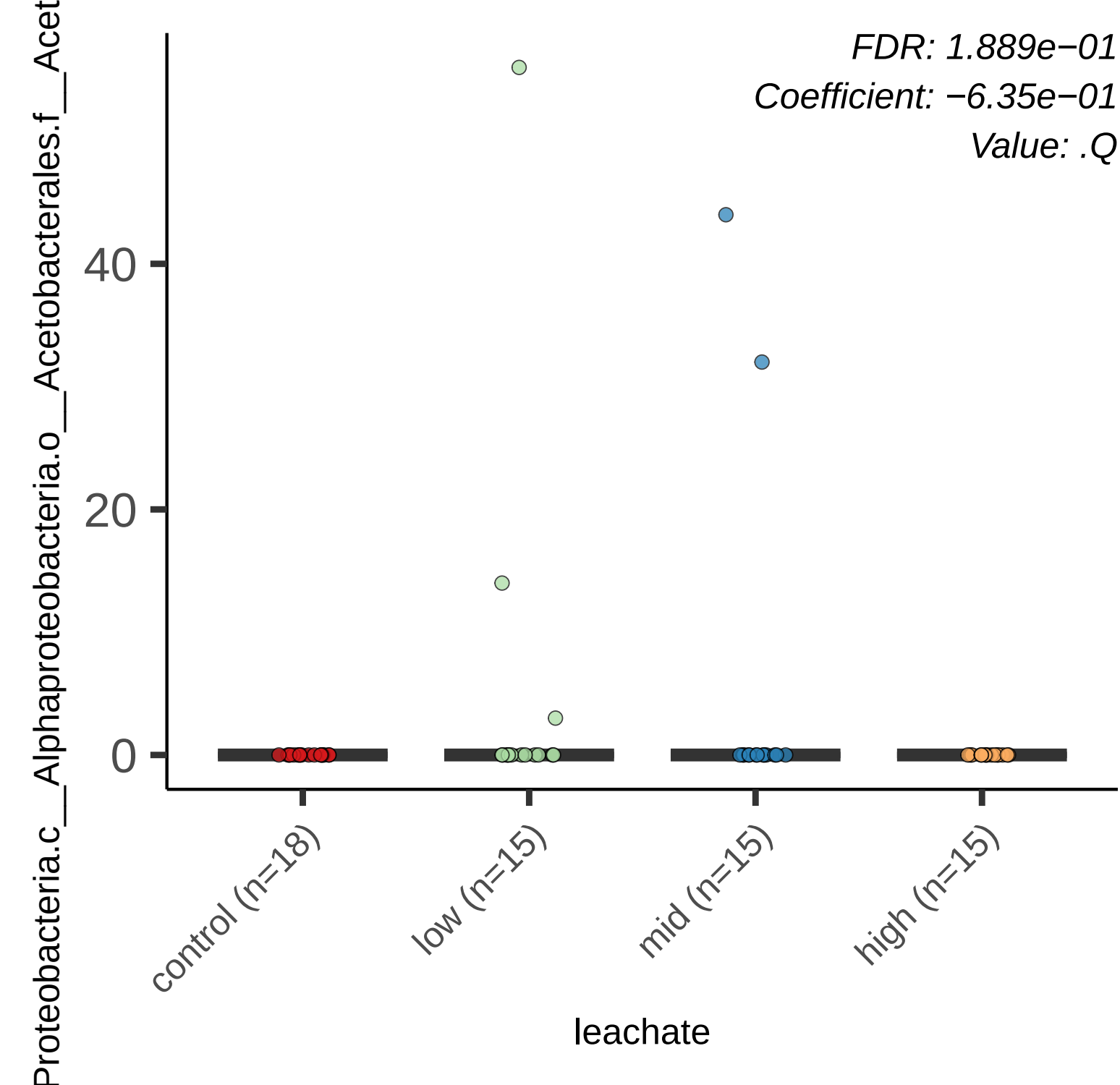
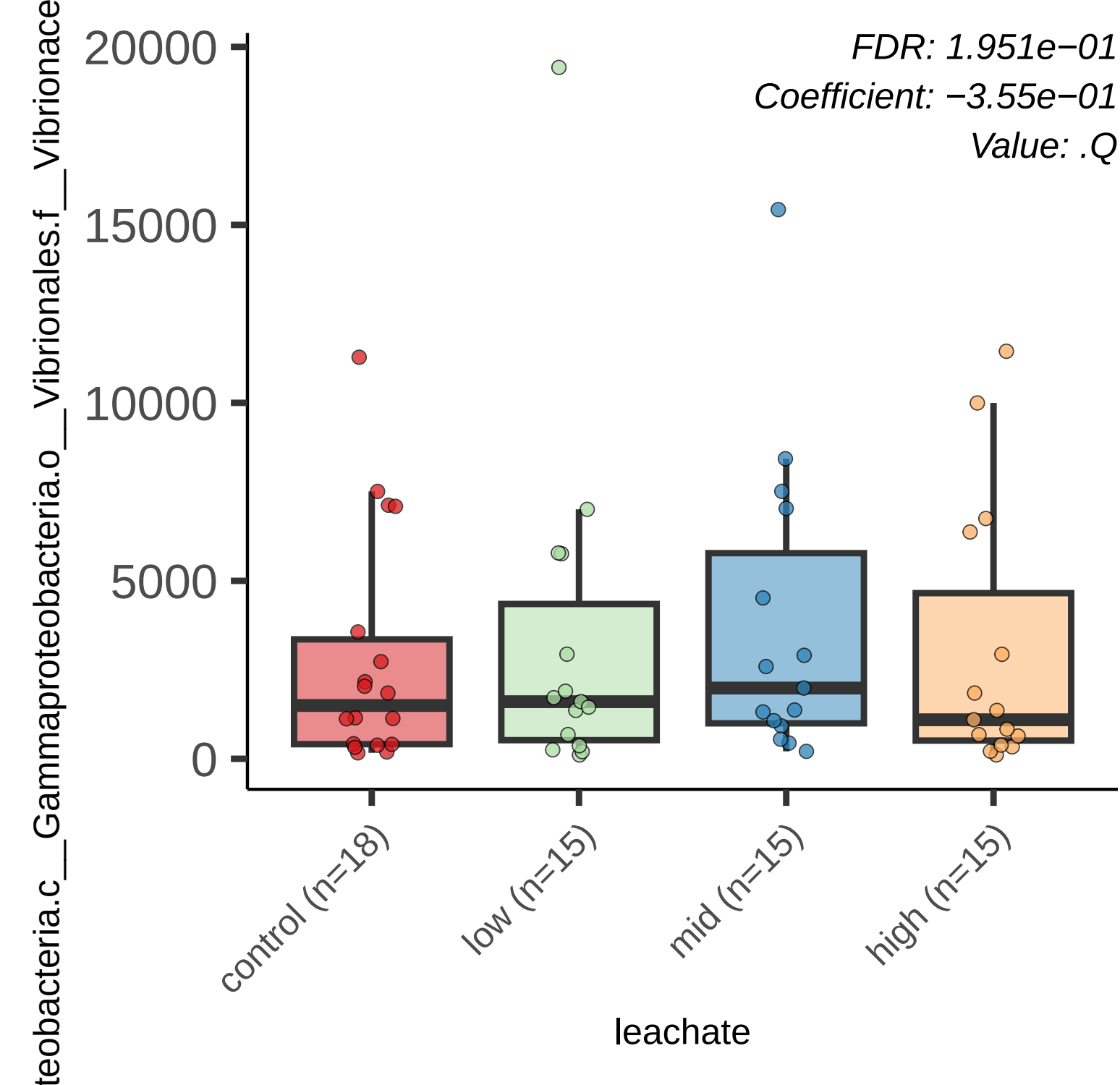
Coefficient: −9.58e−01
Value: .Q
600
400
200
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
tinobacteriota.c__Actinobacteria.o__Corynebacteriales.f__Coryneba


FDR: 1.875e−01
Coefficient: −3.23e−01
Value: .C
Bacteria.p__Firmicutes.c__Bacilli.o__Bacillales.f__Planococcaceae.
25
20
15
10
5
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate


FDR: 1.889e−01
Coefficient: −6.35e−01
Value: .Q
40
20
0
control (n=18)
low (n=15)
mid (n=15)
high (n=15)
leachate
Proteobacteria.c__Alphaproteobacteria.o__Acetobacterales.f__Acet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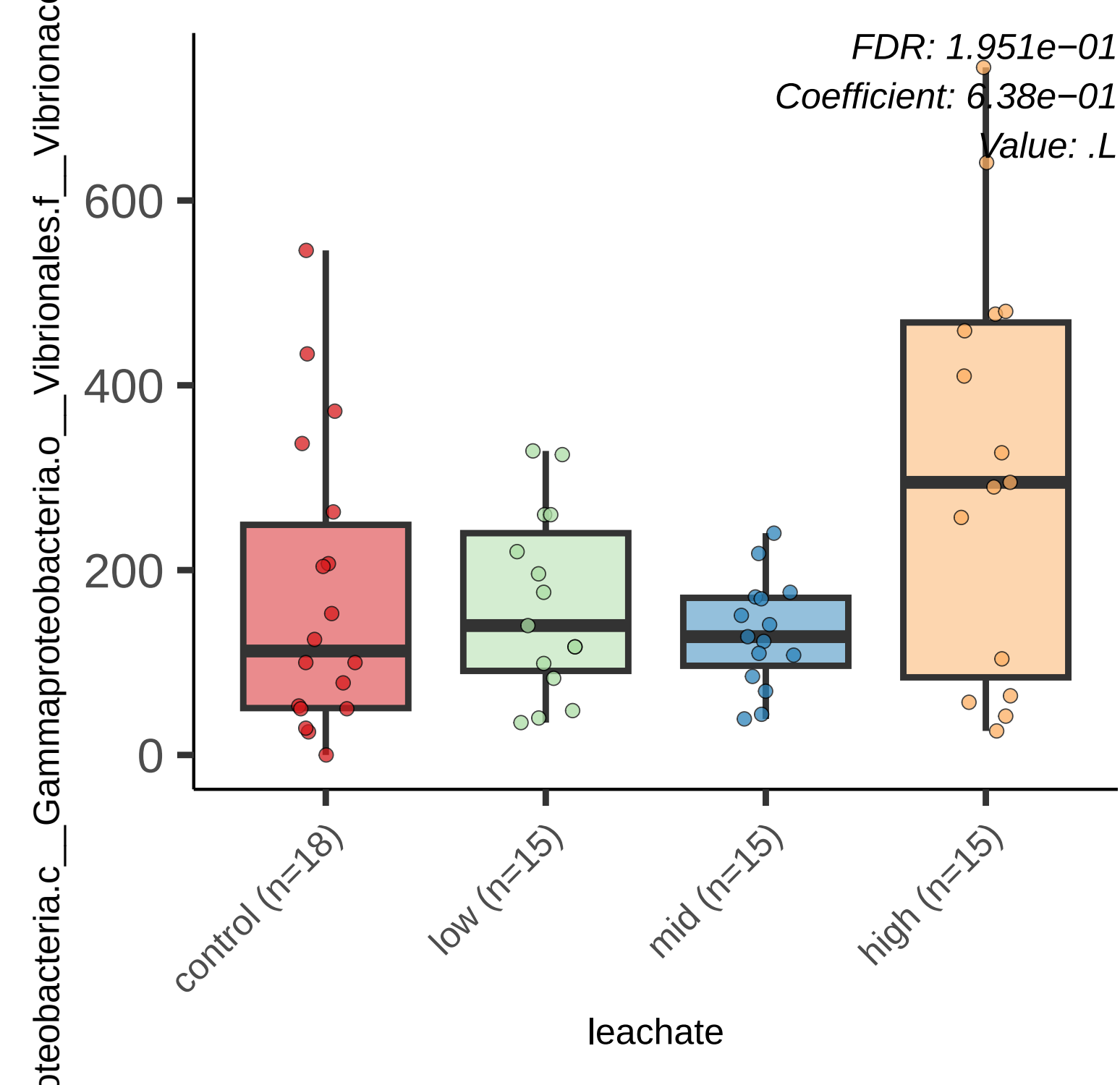
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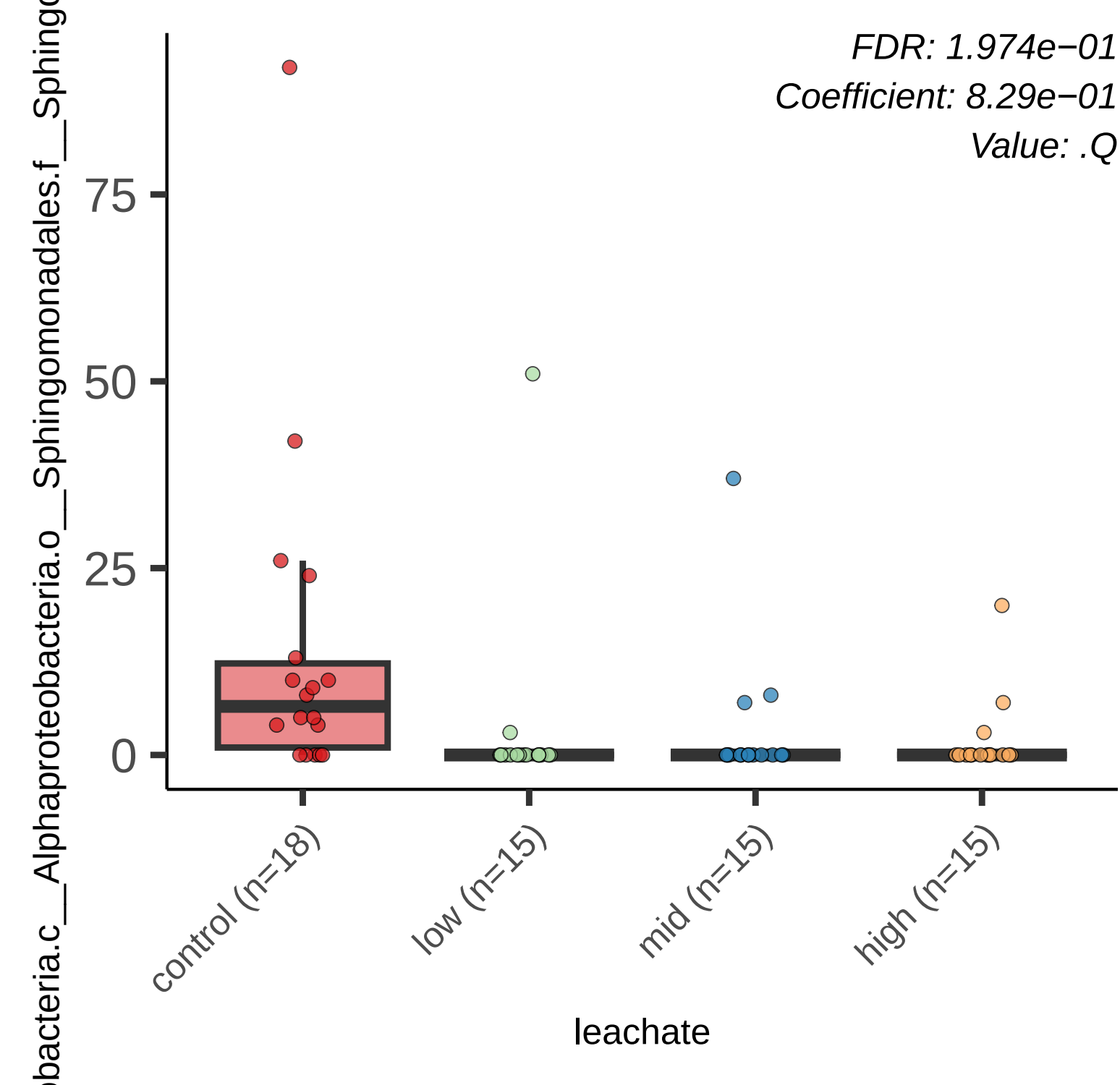
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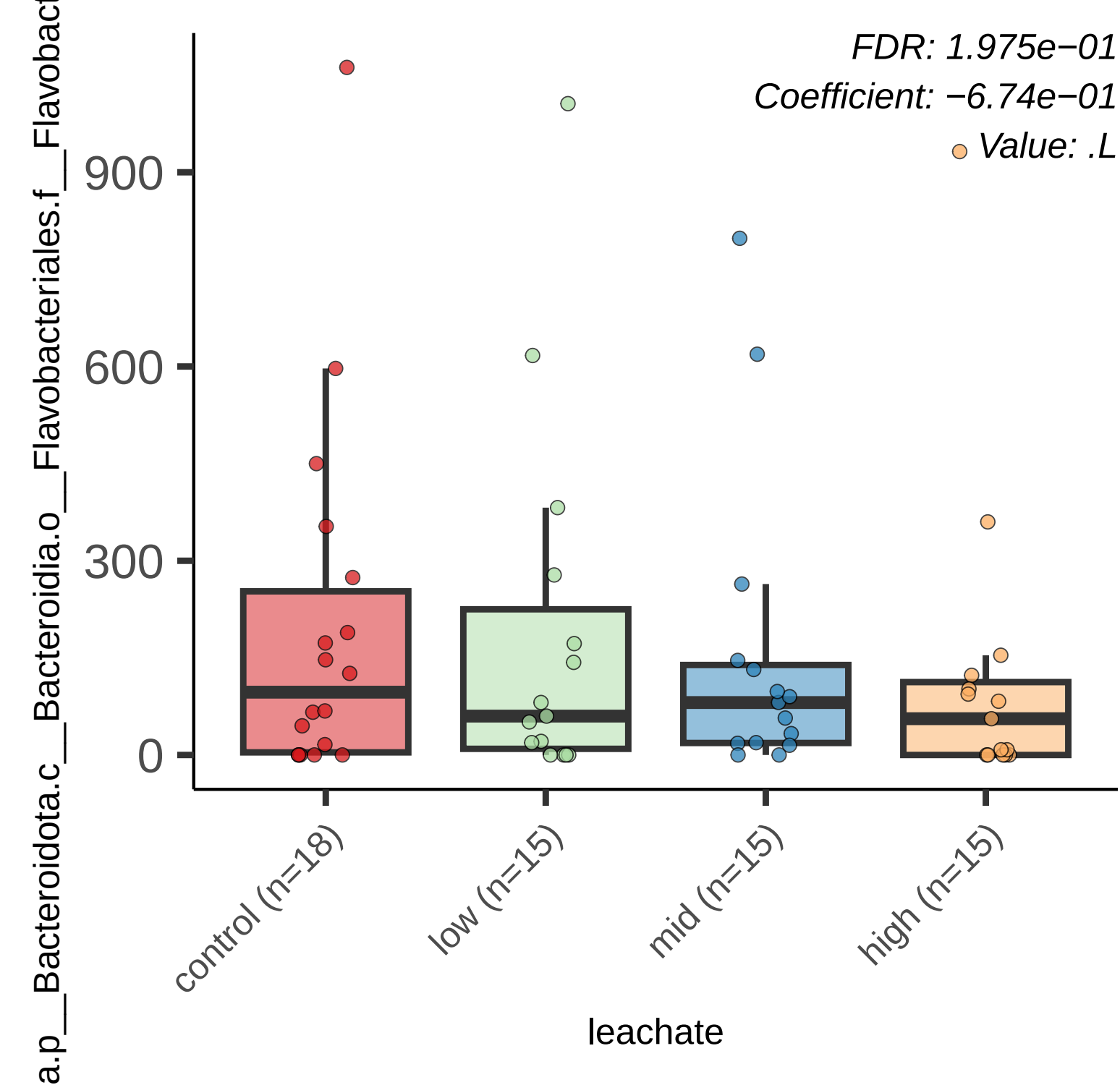
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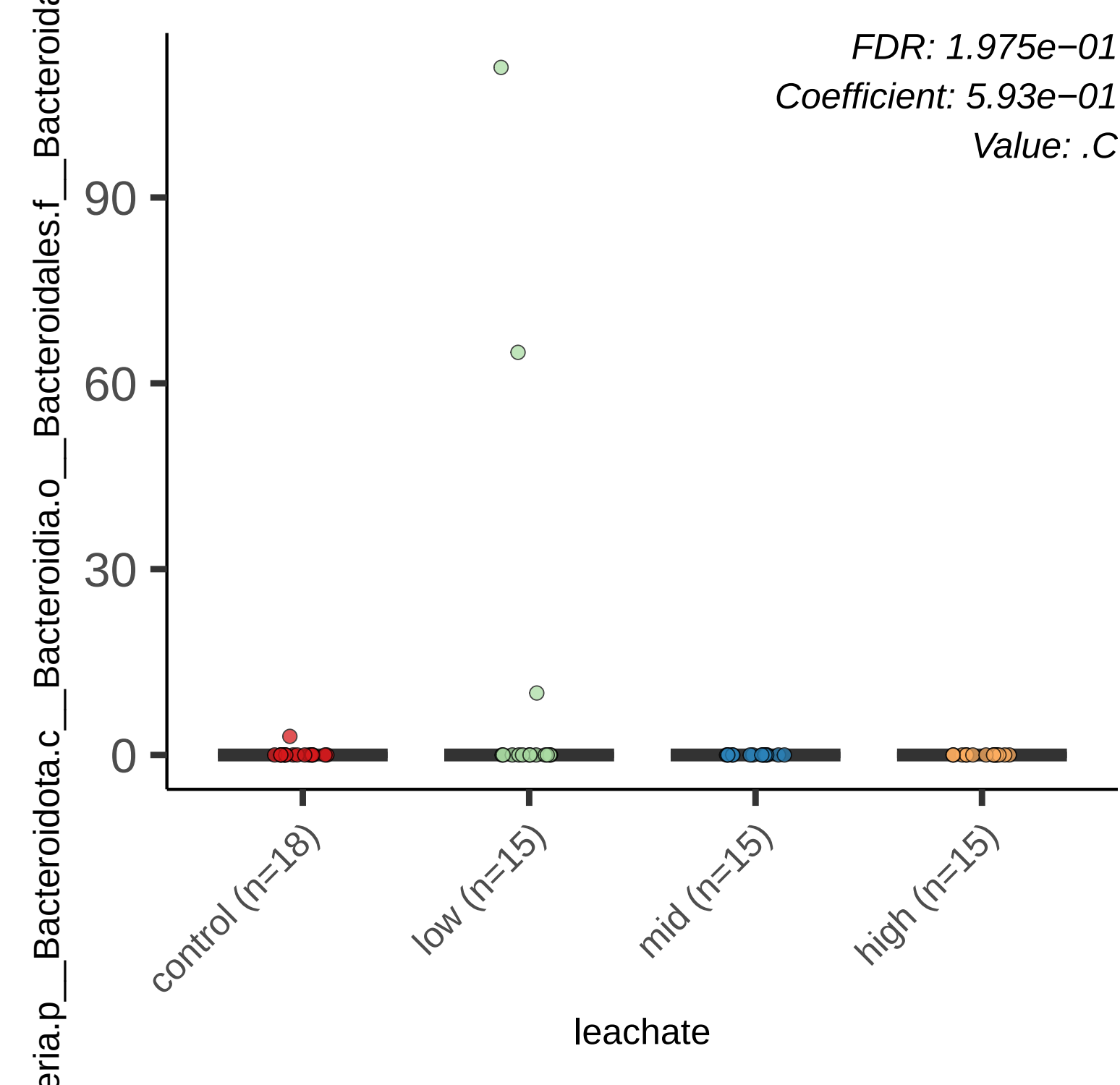
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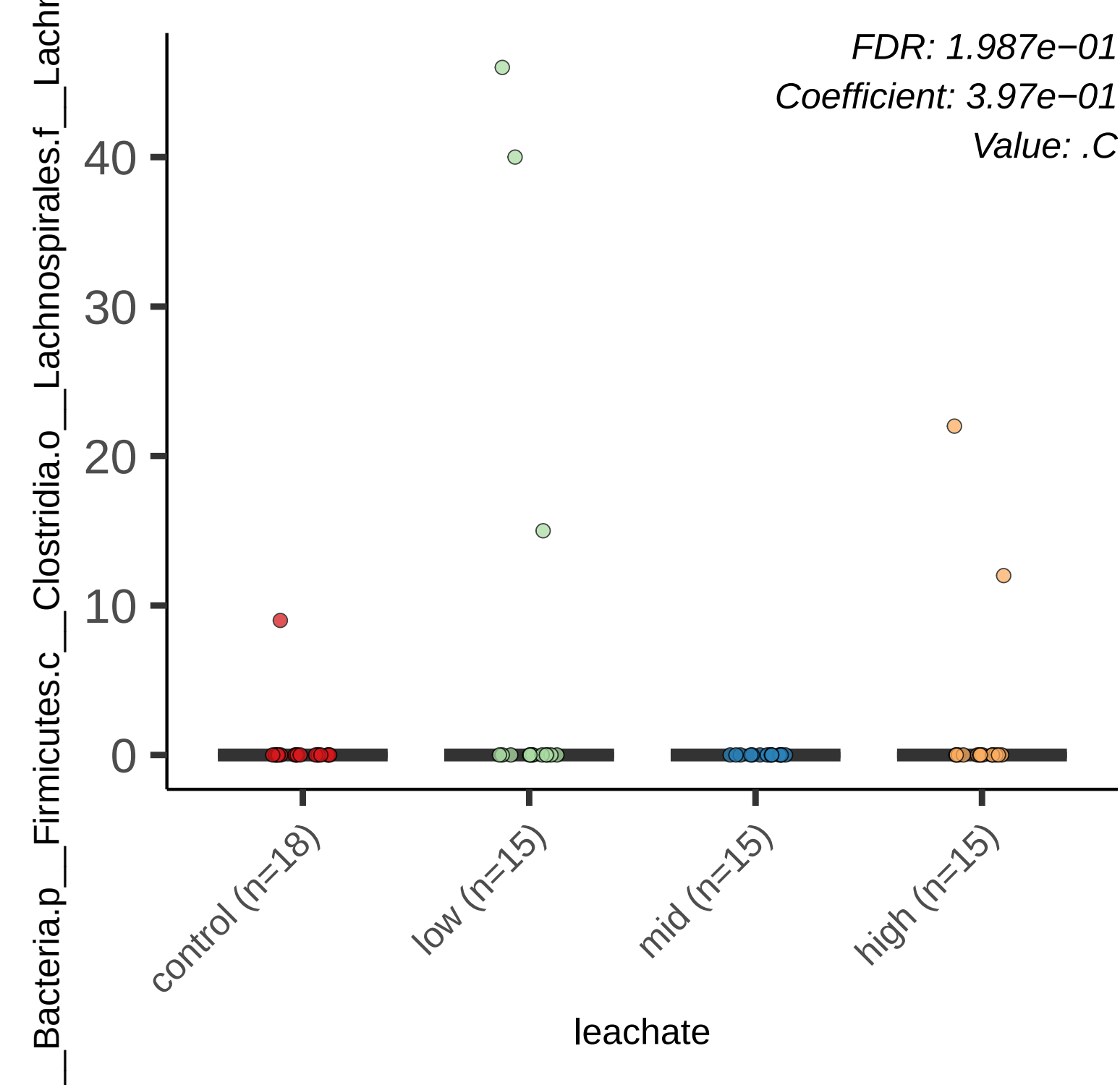
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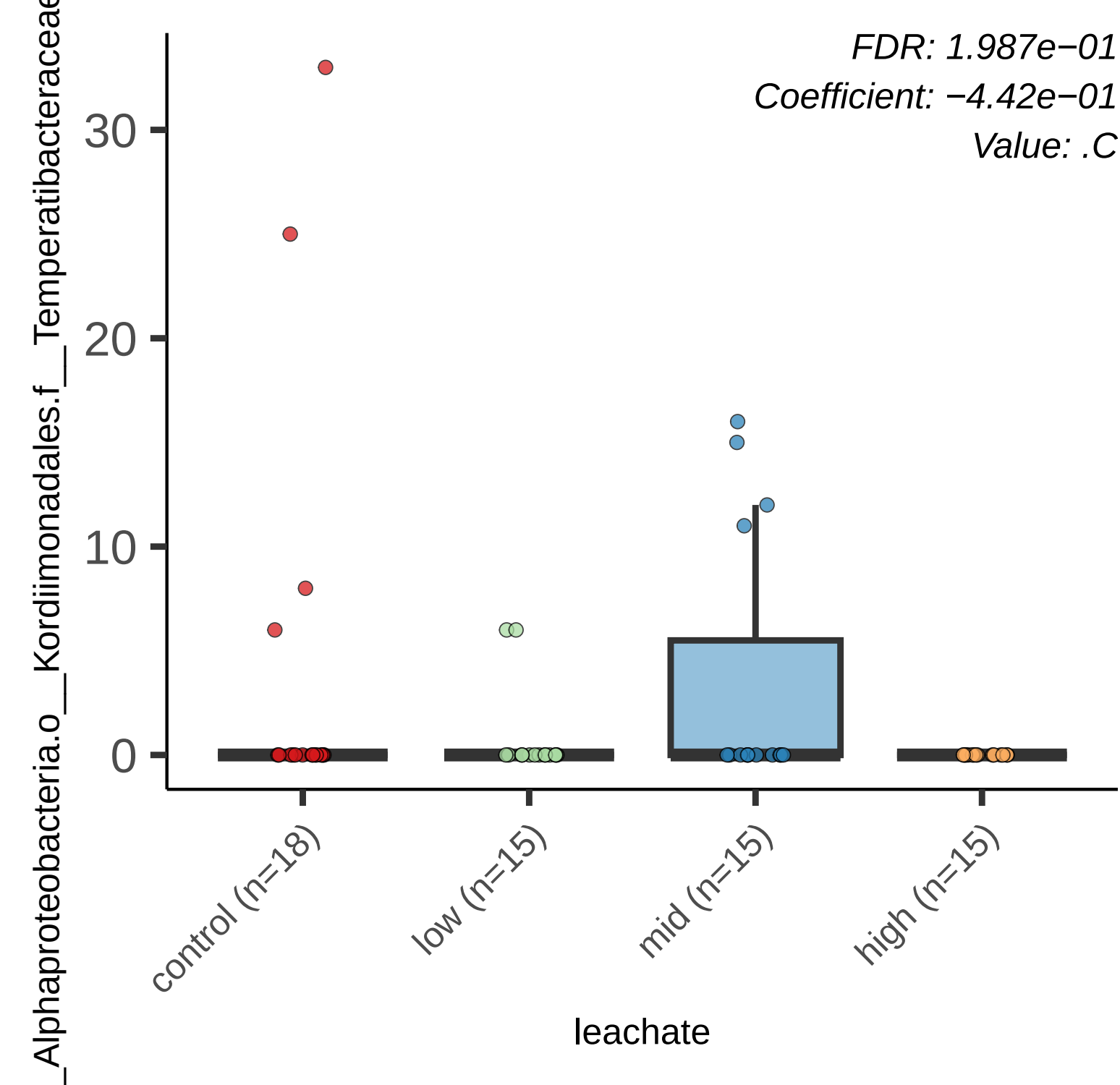
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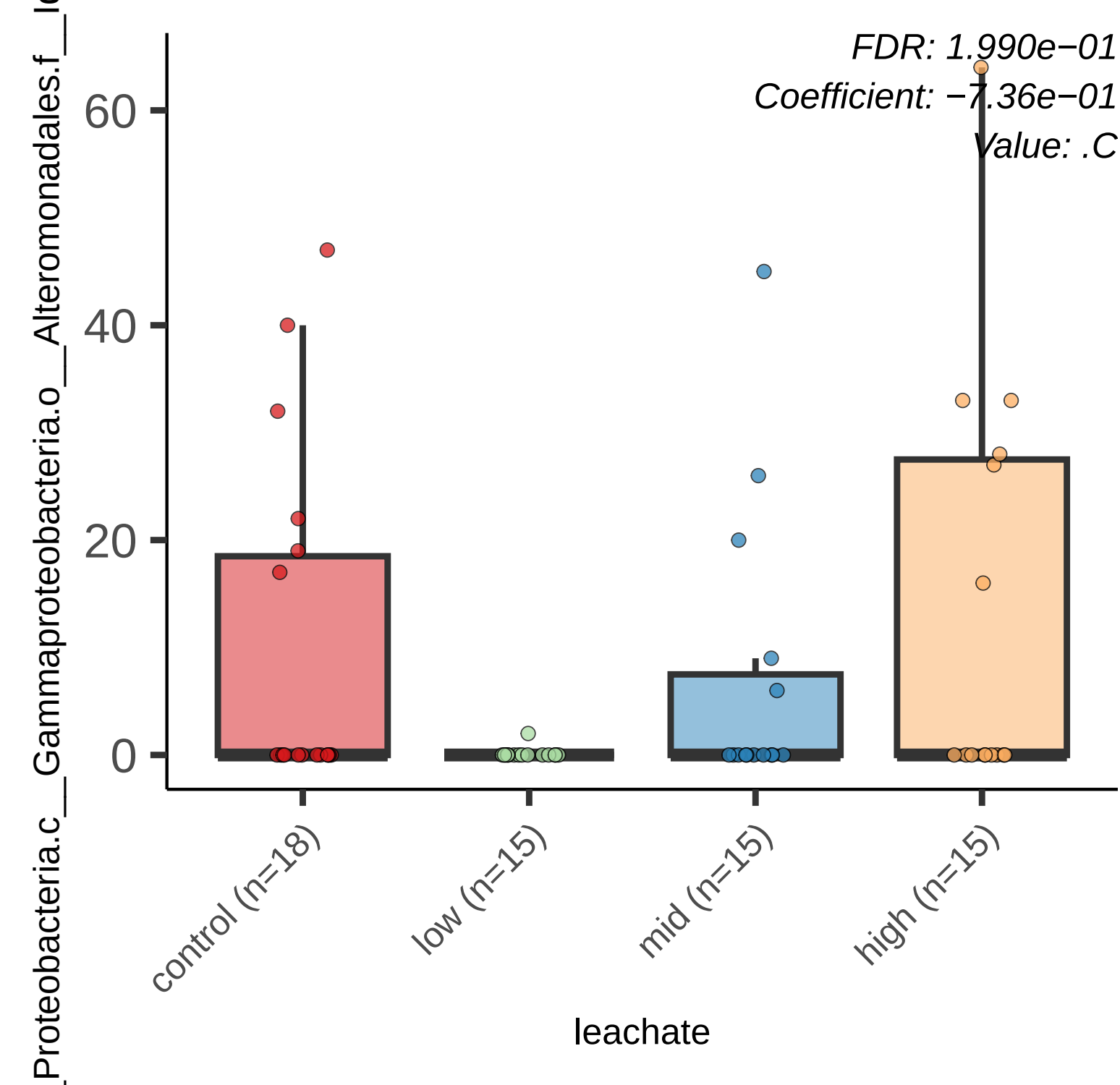
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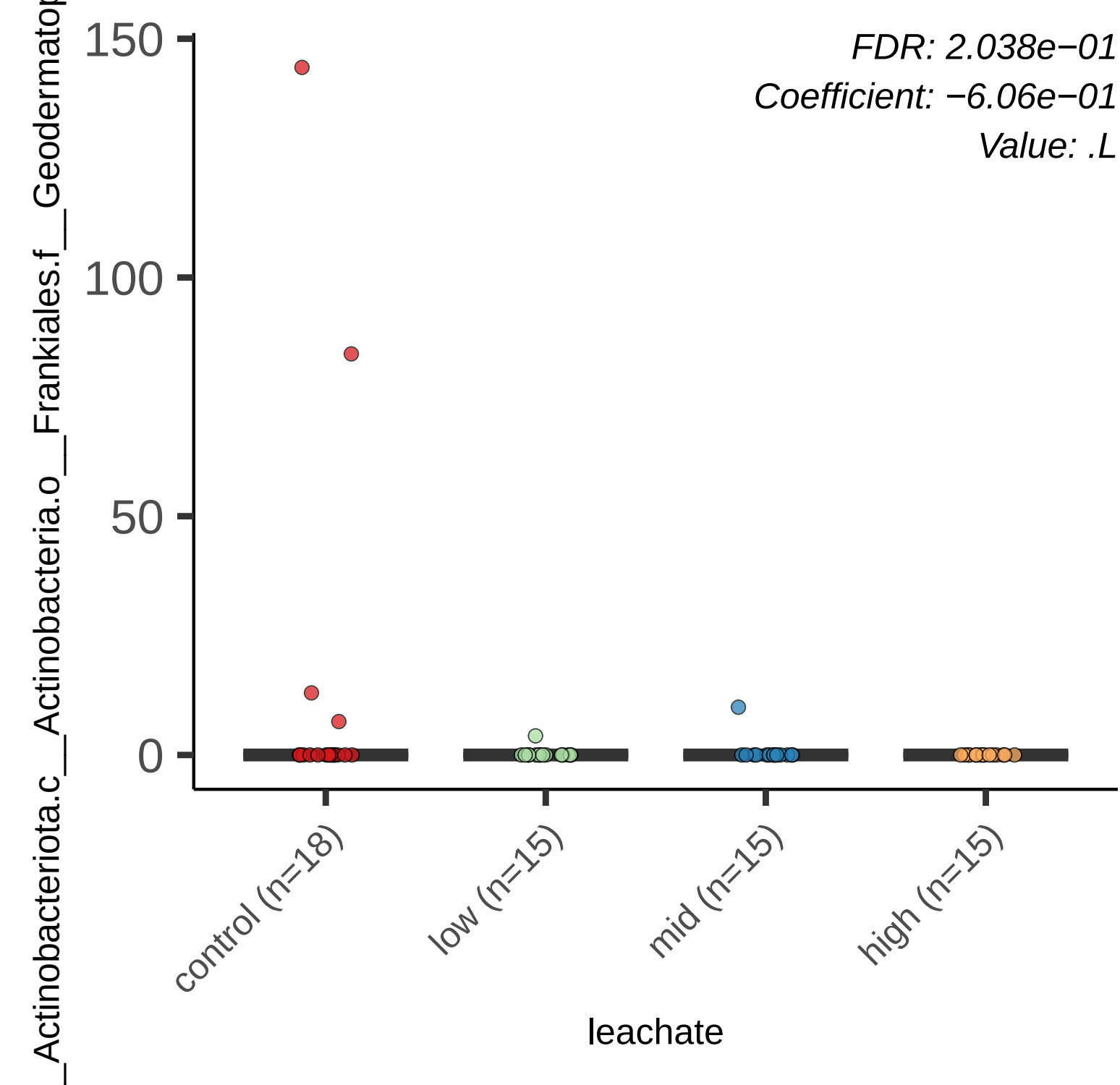
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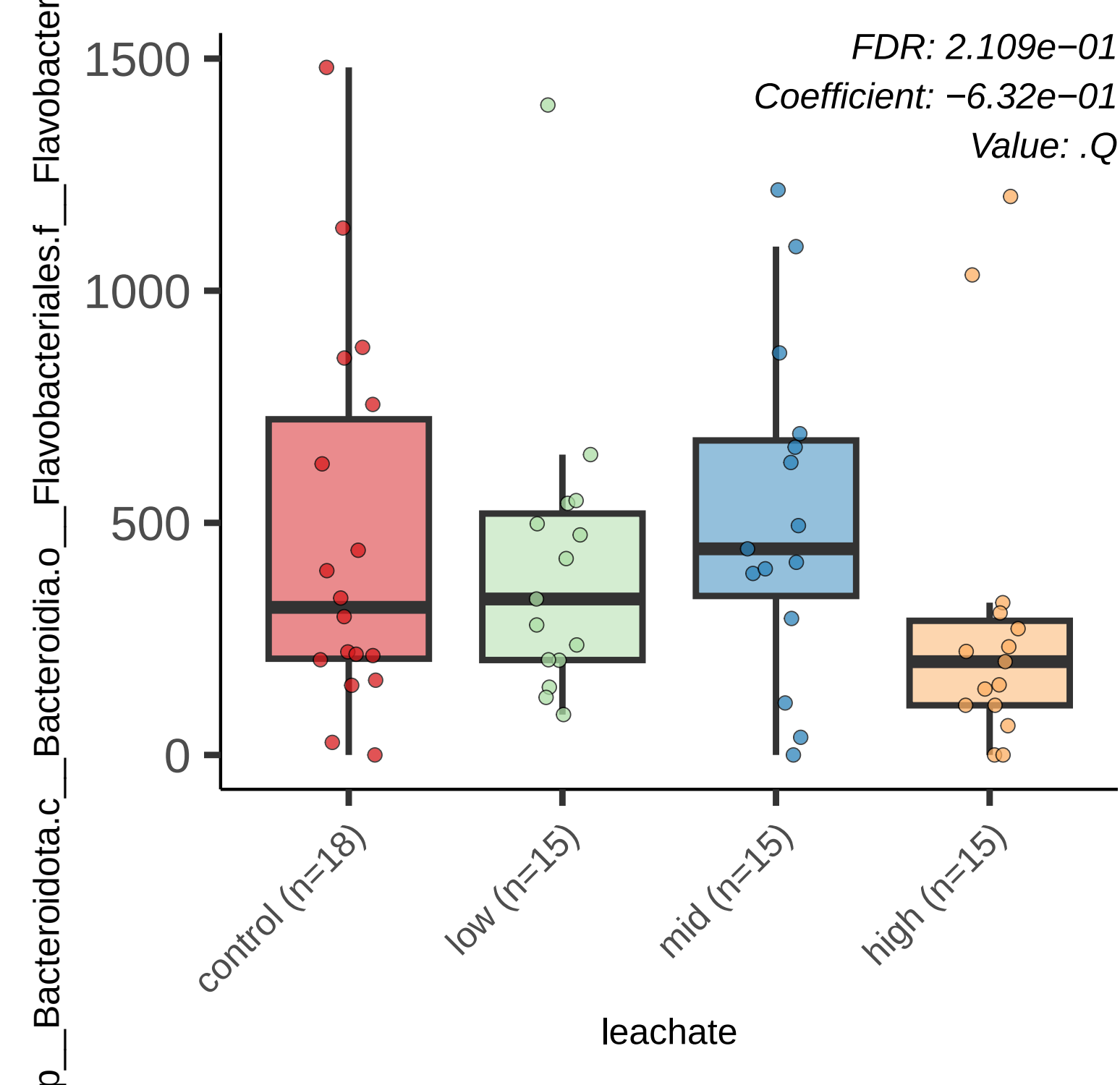
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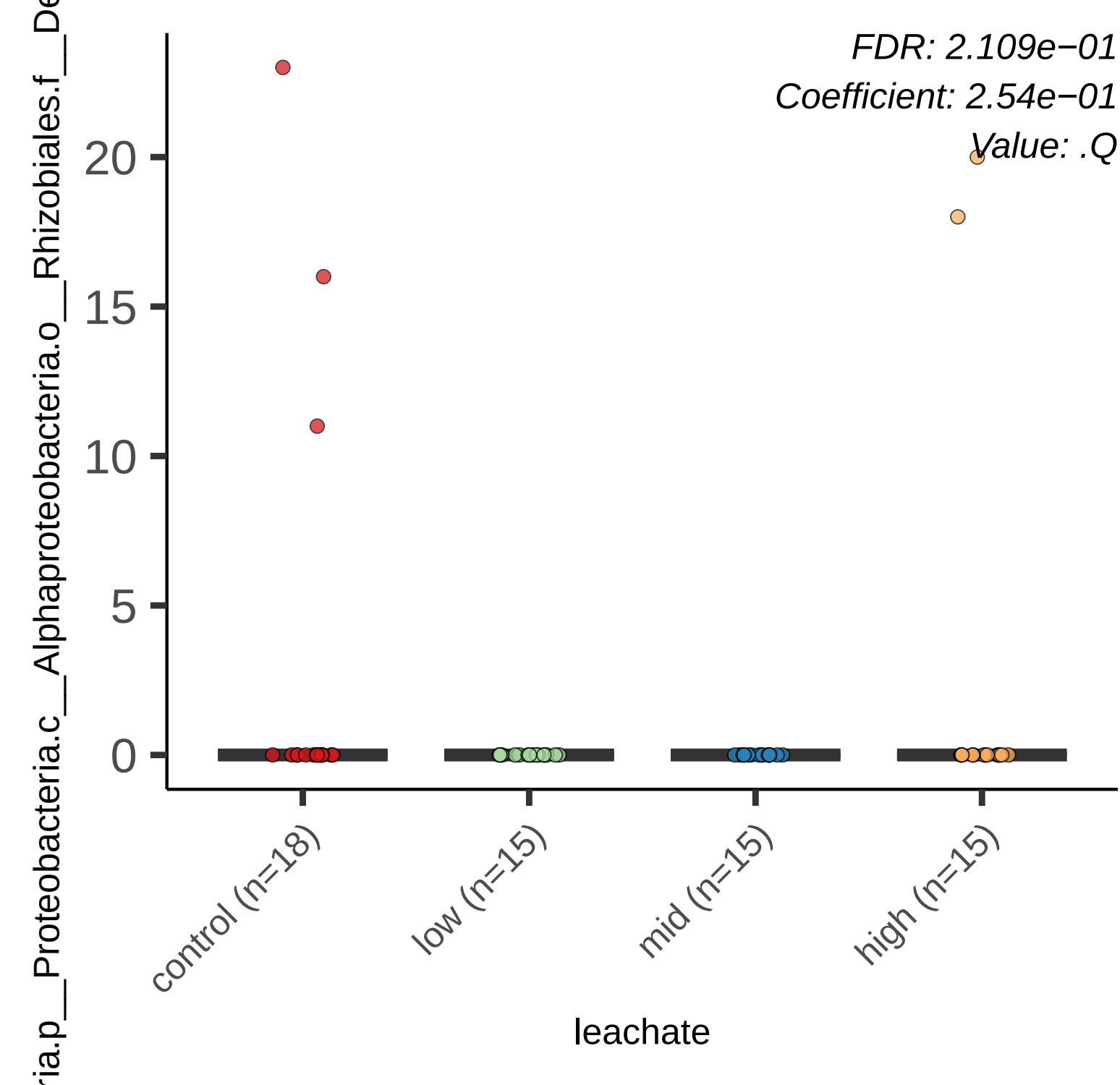
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control (n=18)
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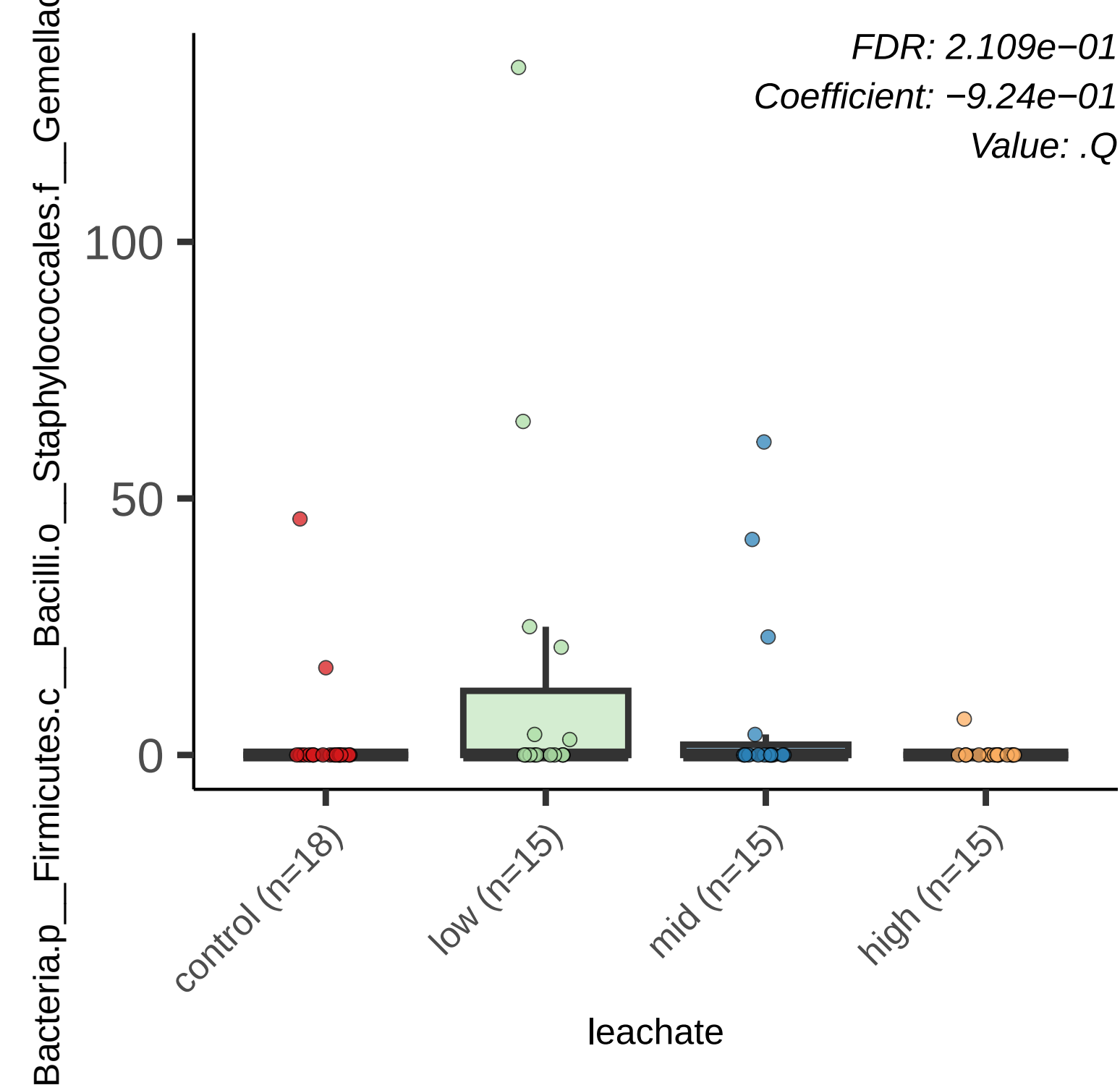
leachate
ria.p__Proteobacteria.c__Alphaproteobacteria.o__Rhizobiales.f__De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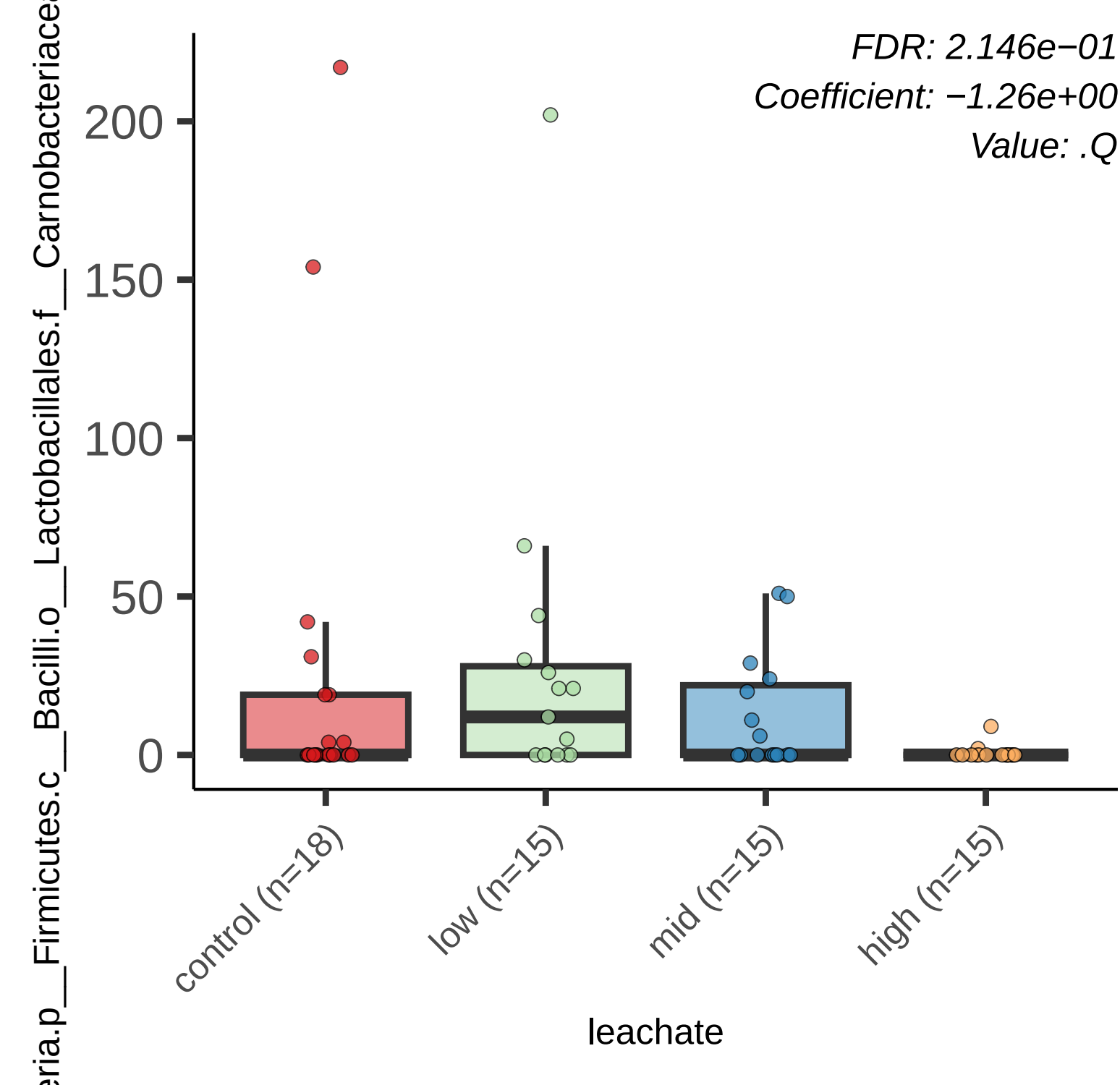
high (n=15)
leachate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high (n=15)
leachate
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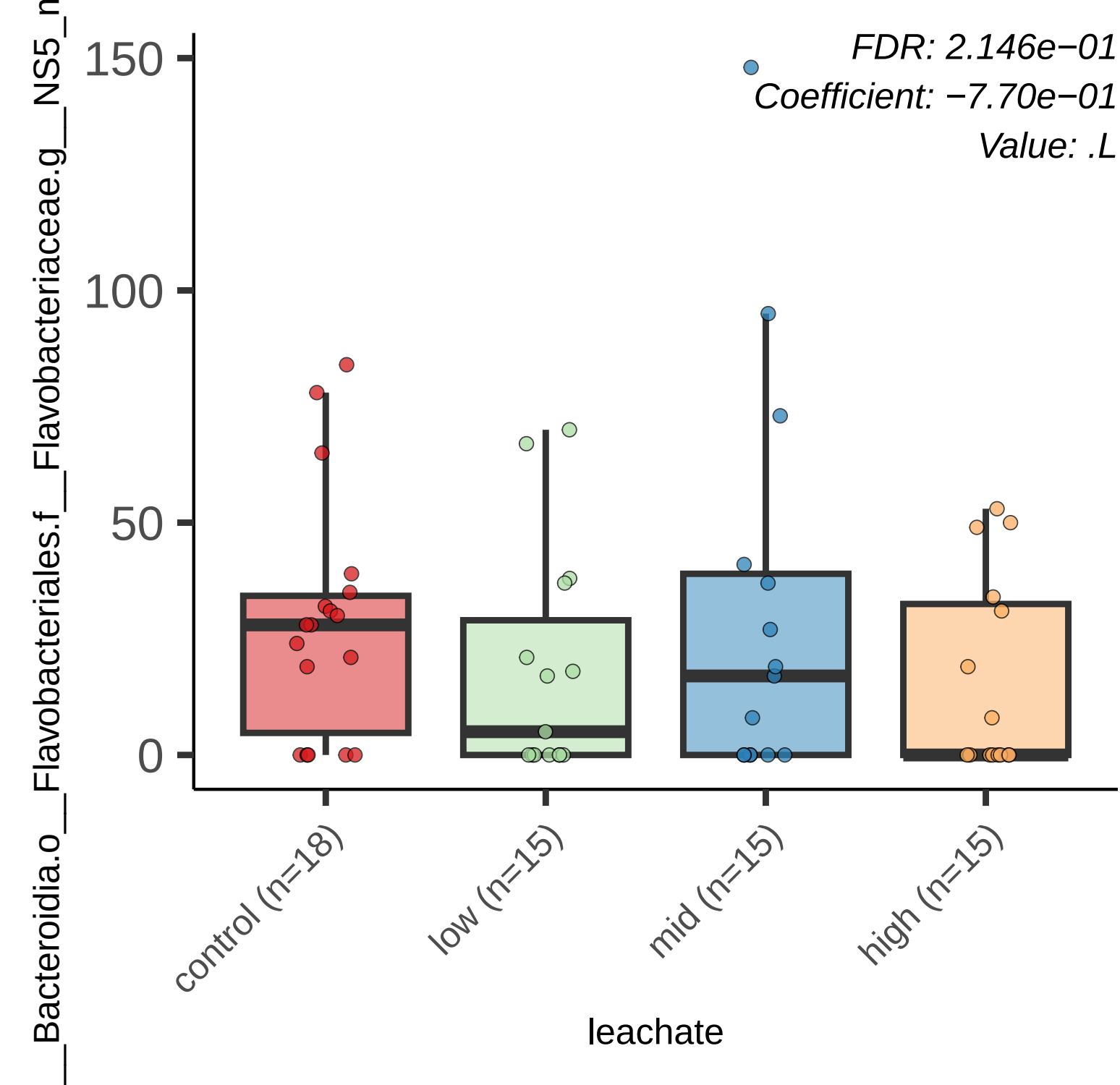
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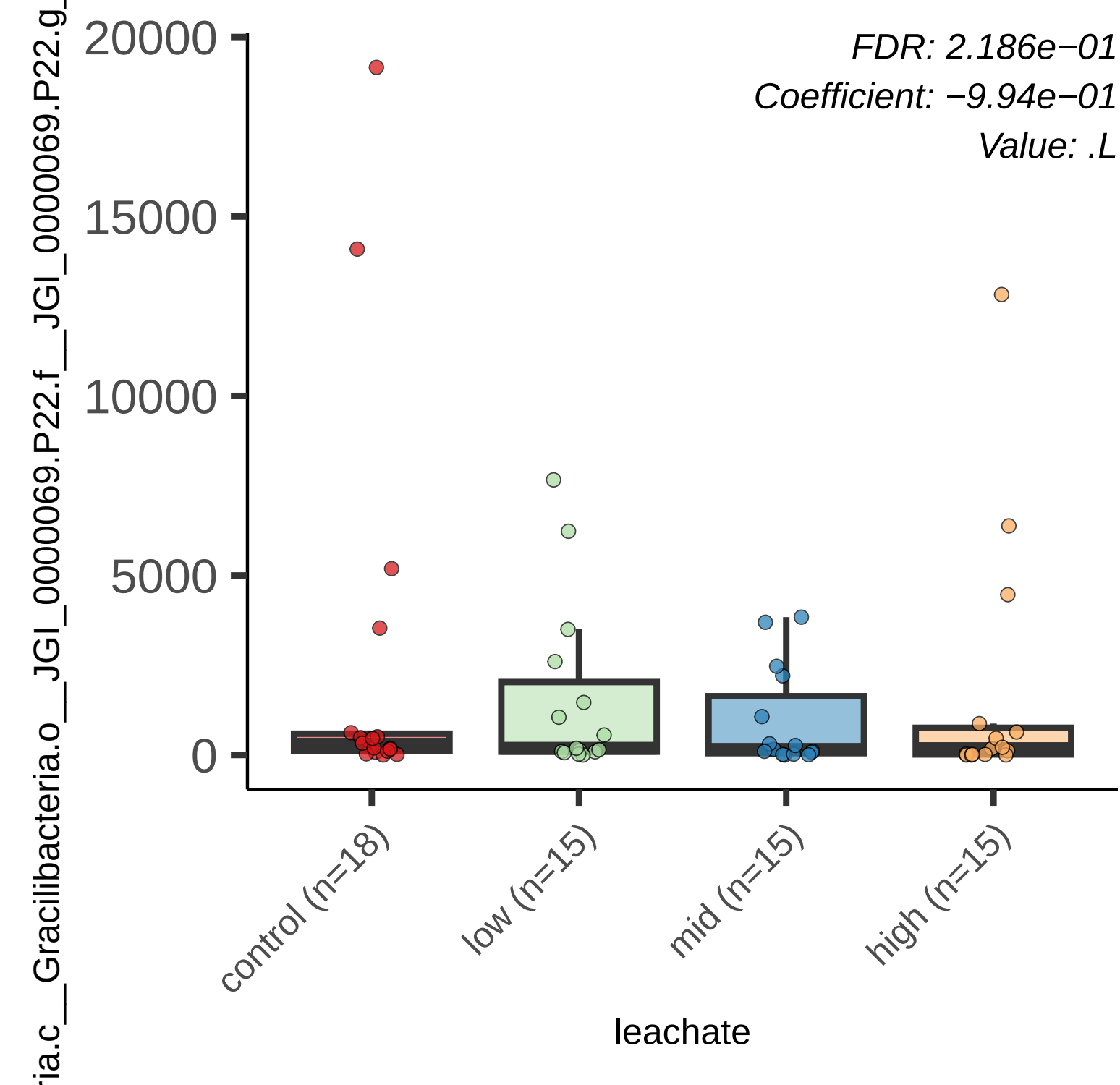
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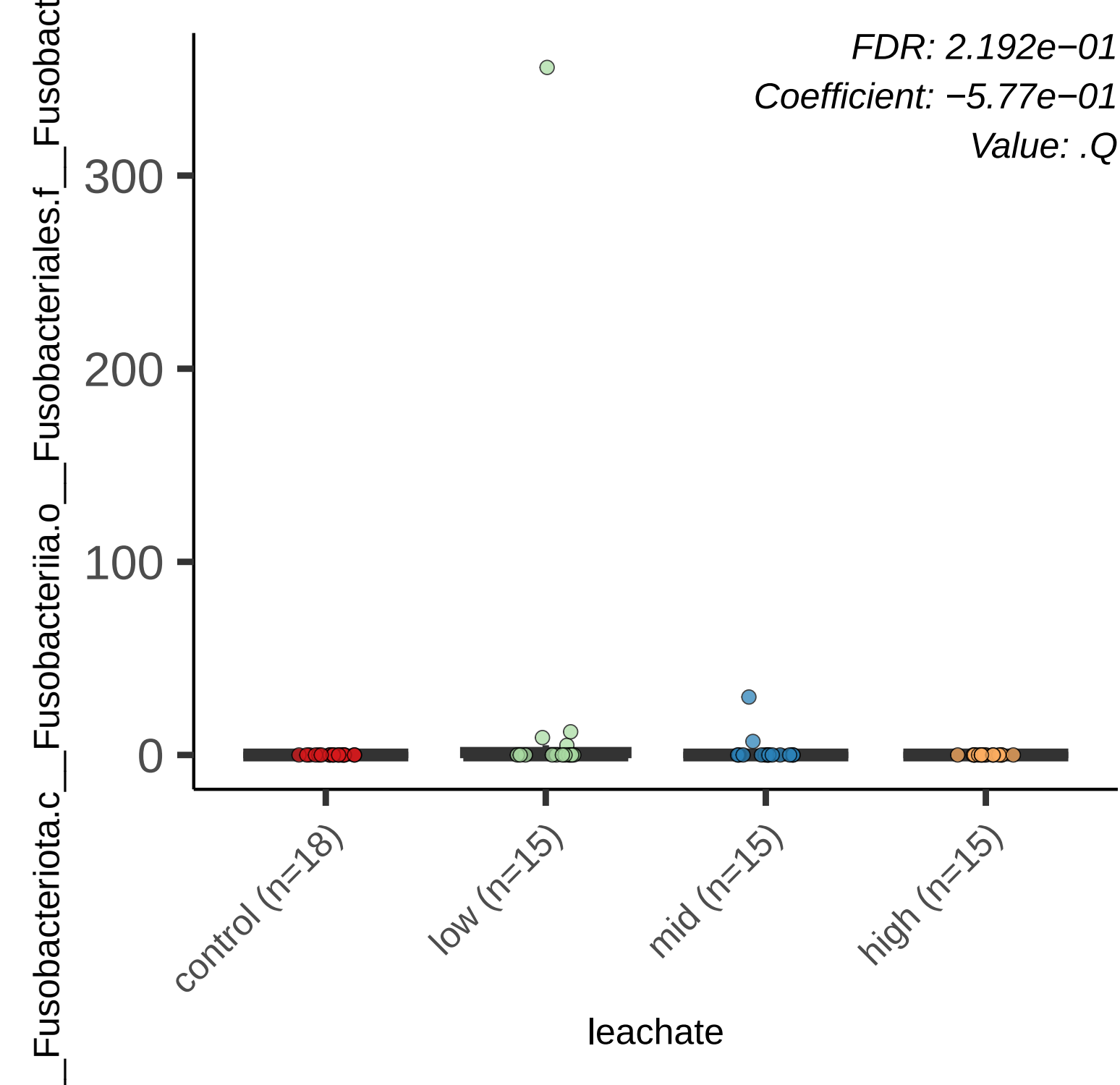
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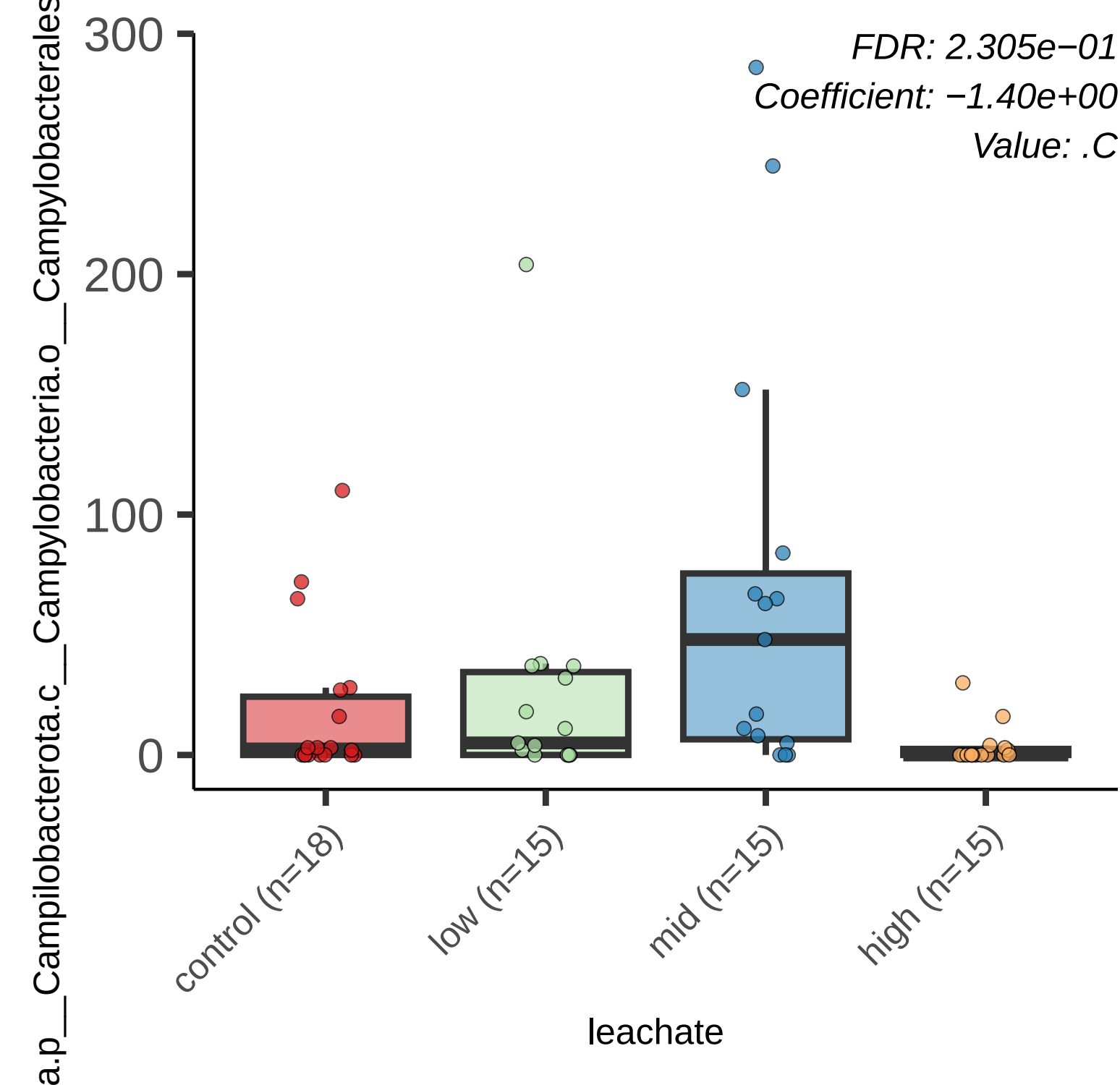
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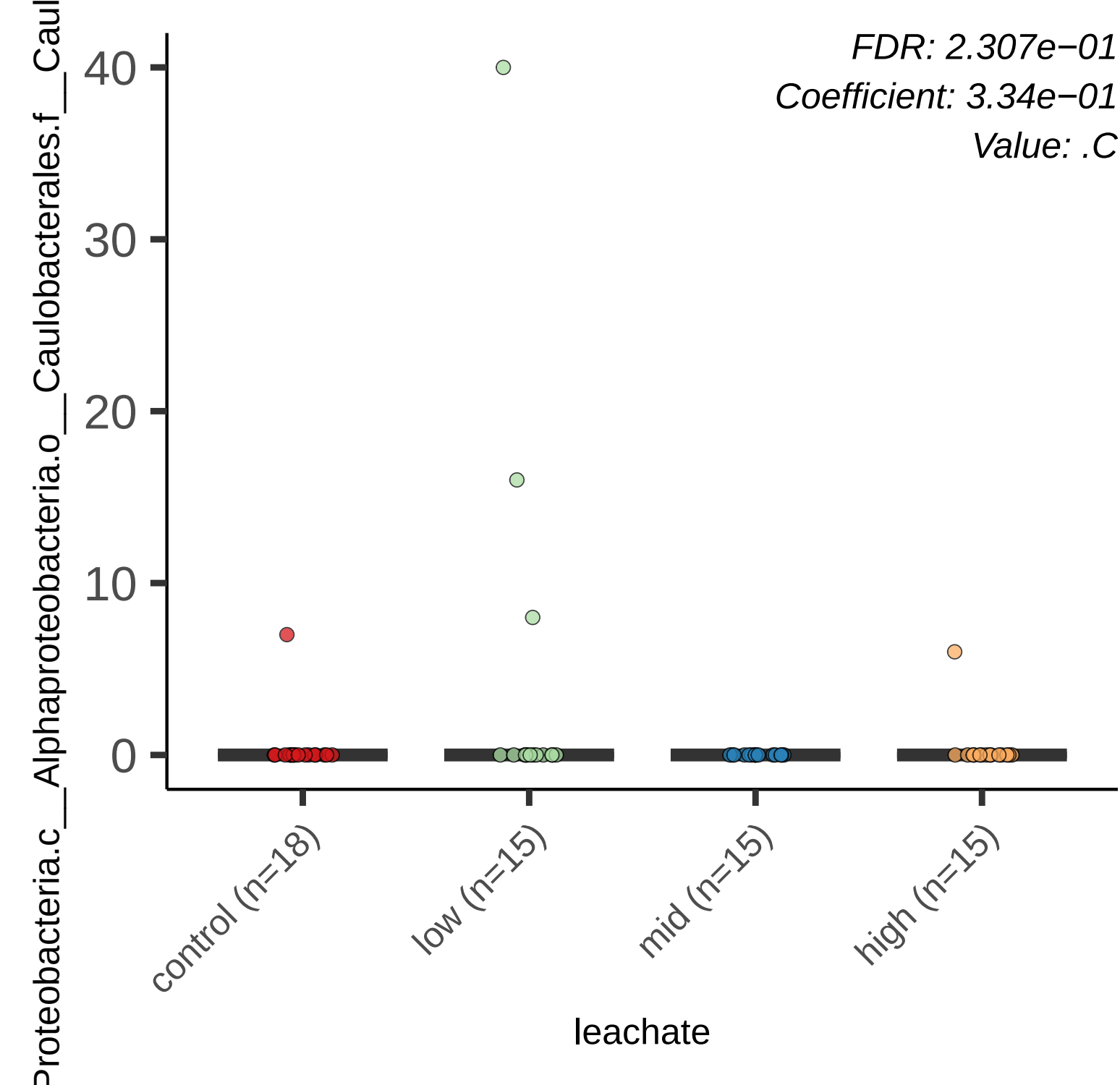
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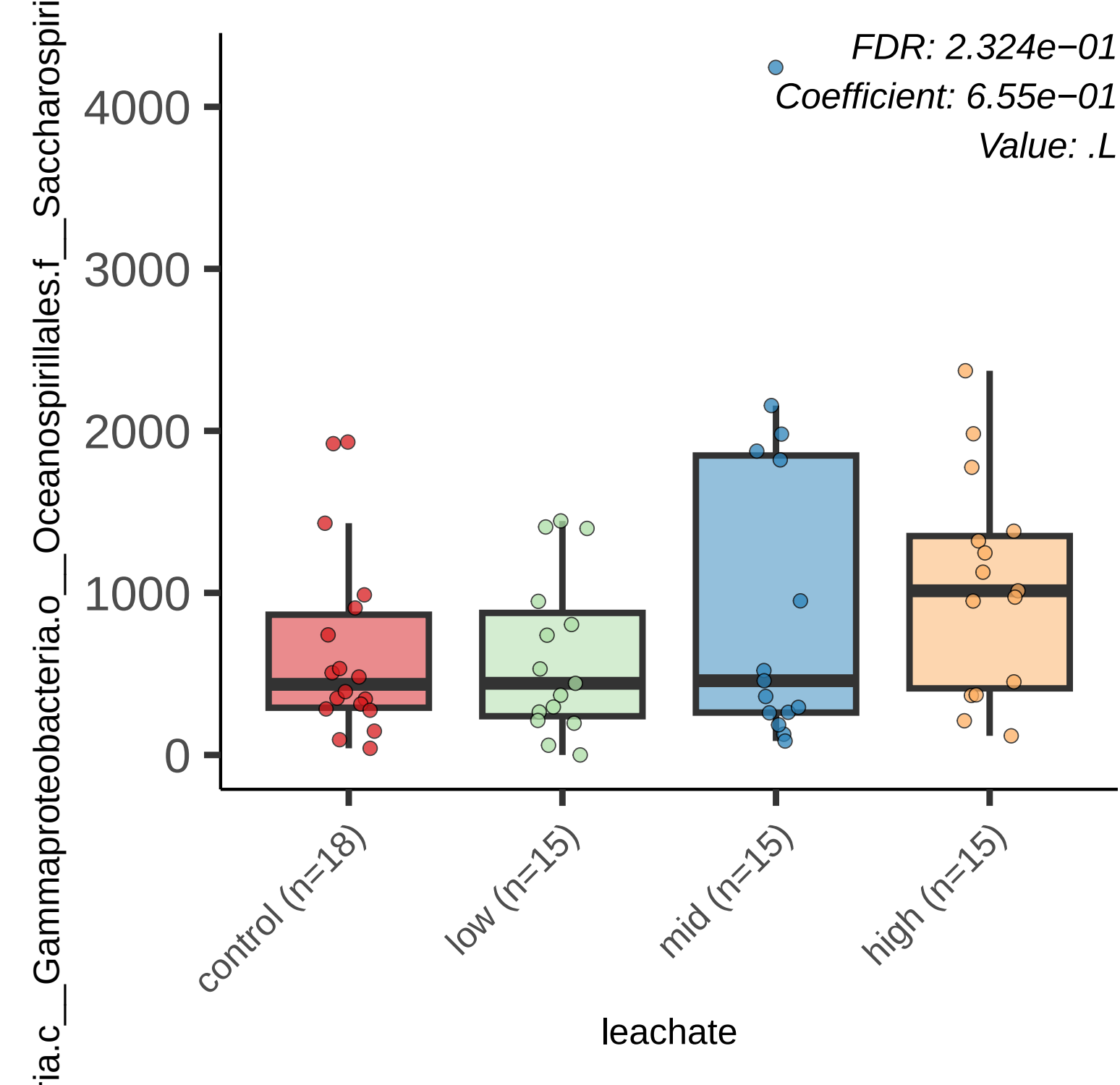
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leachate
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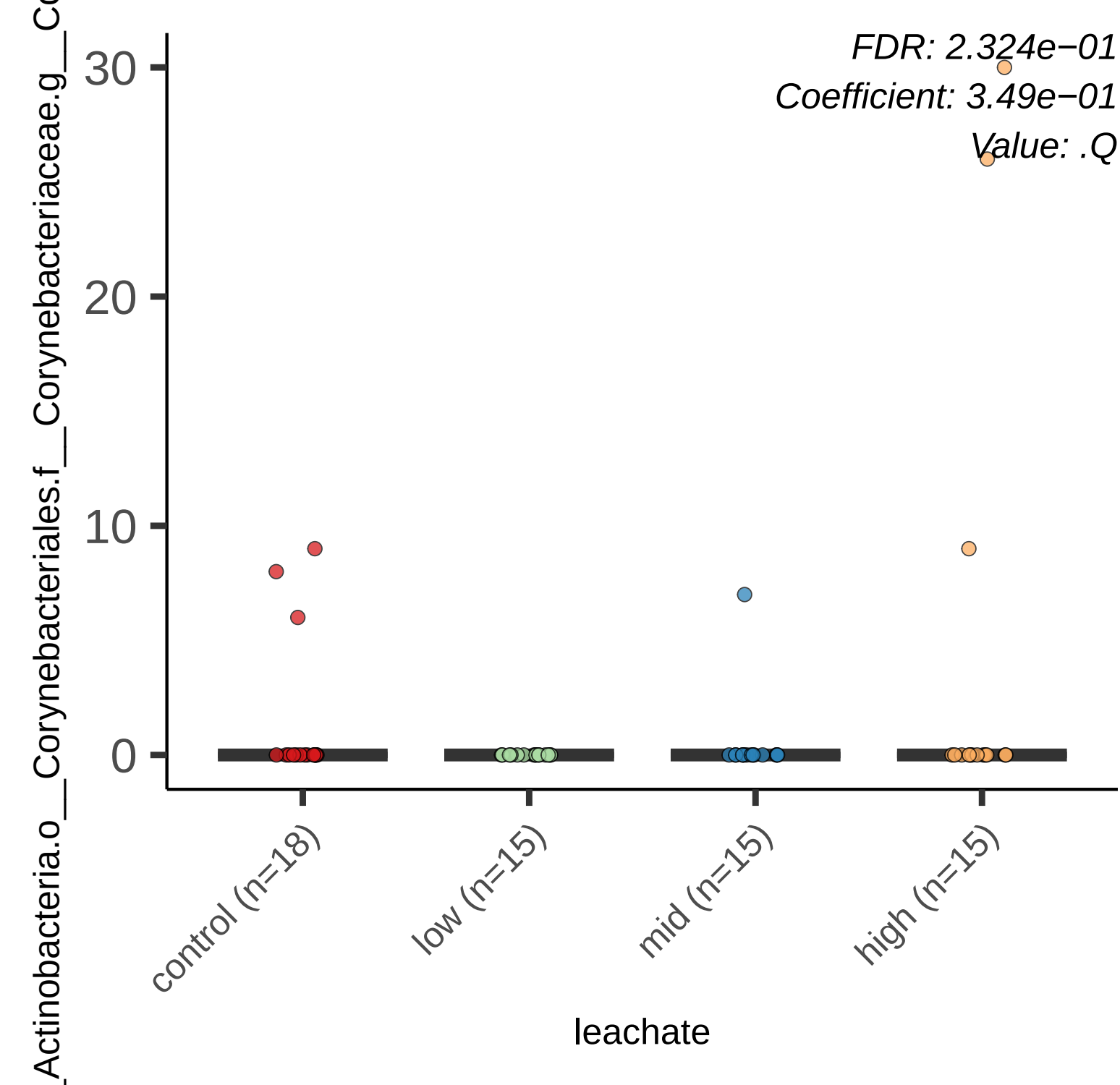
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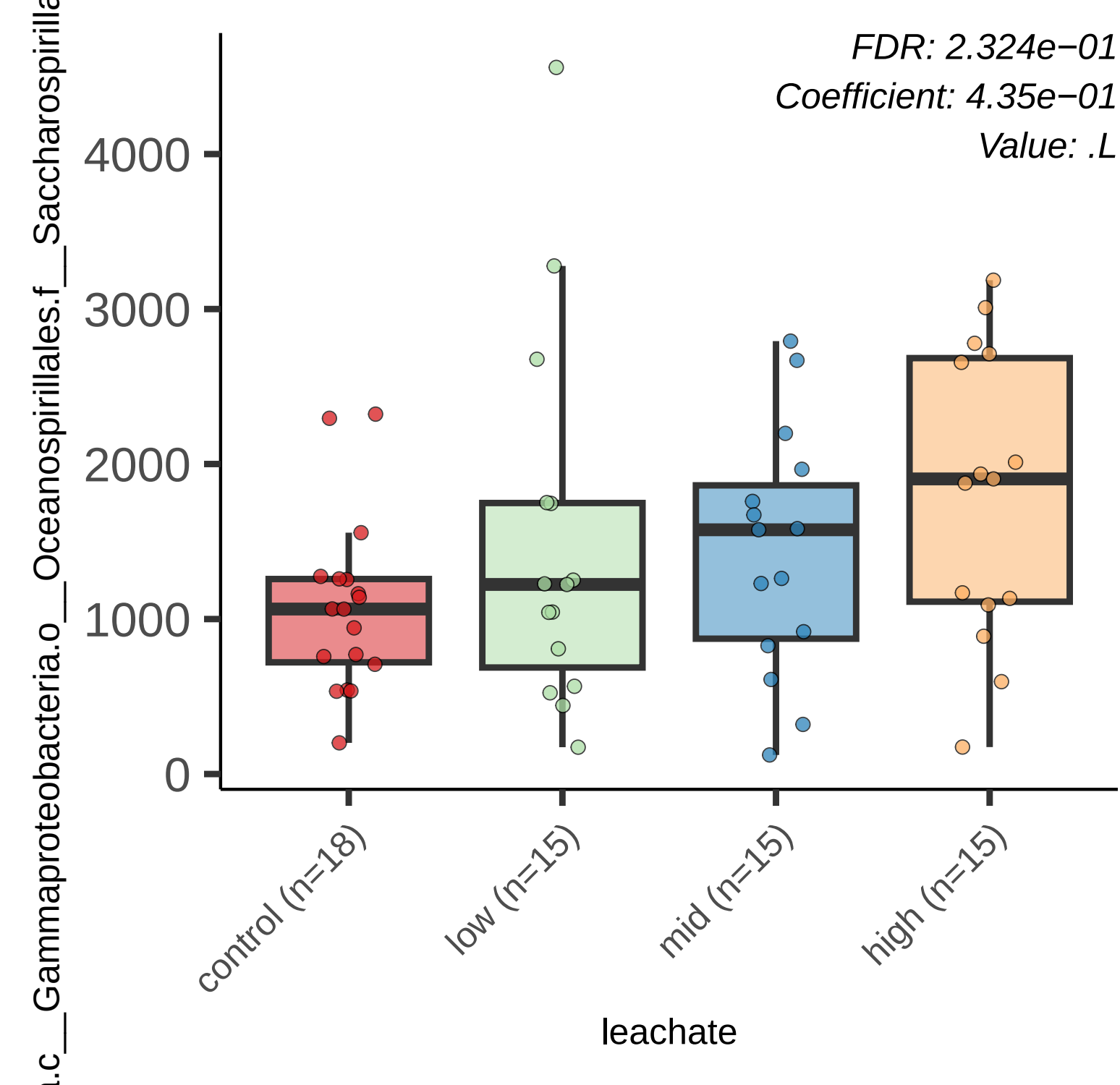
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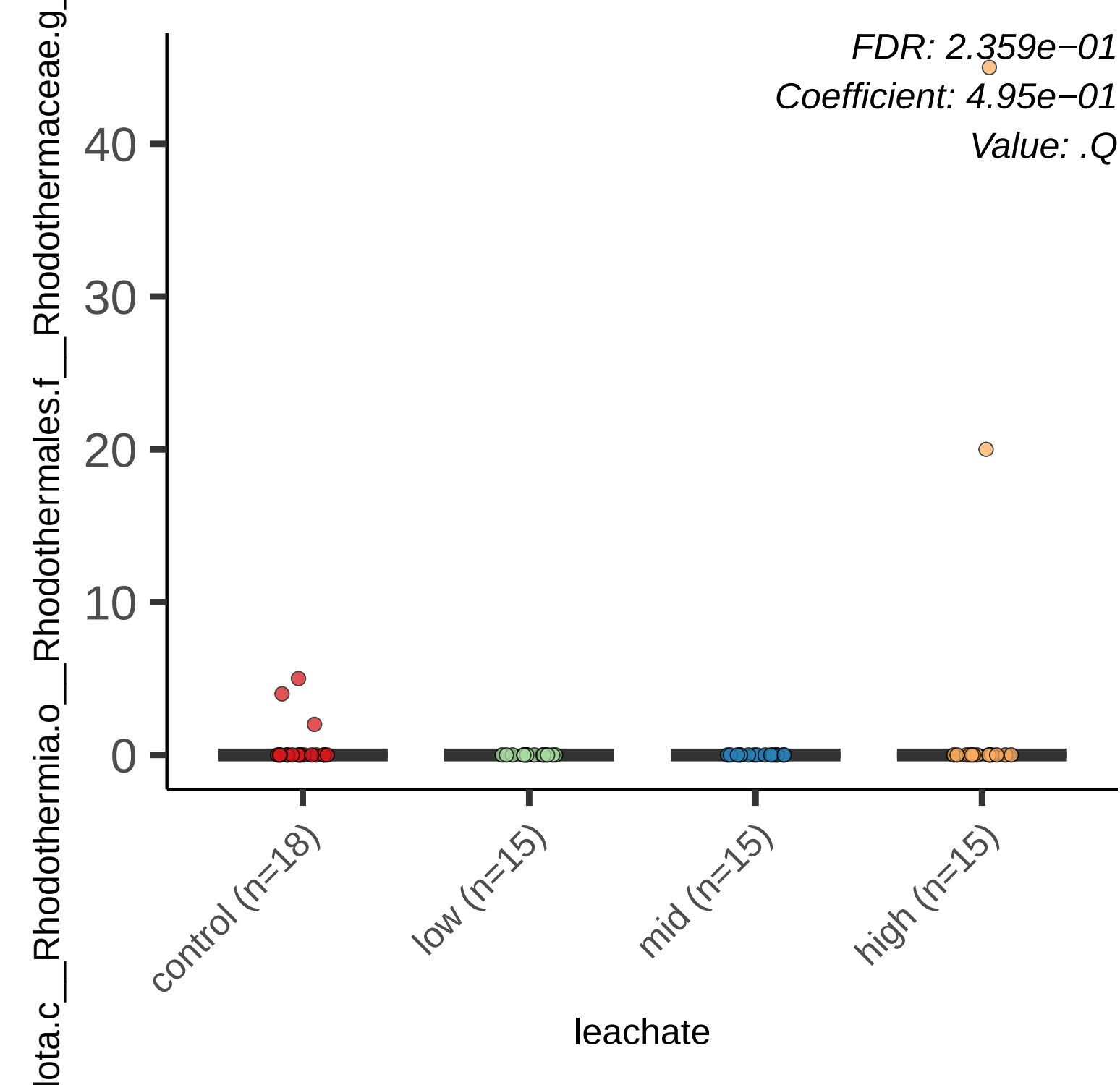
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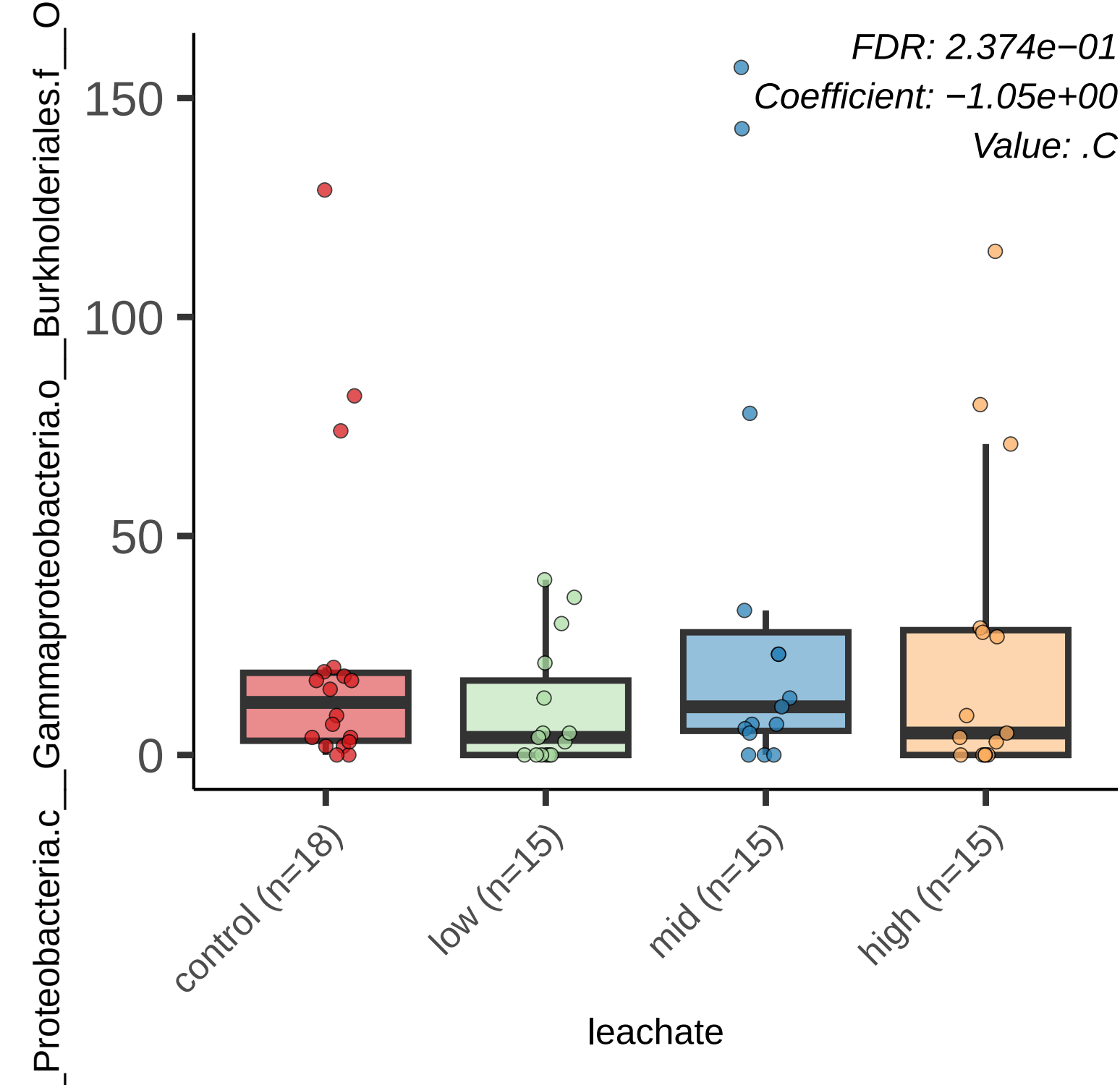
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high (n=15)
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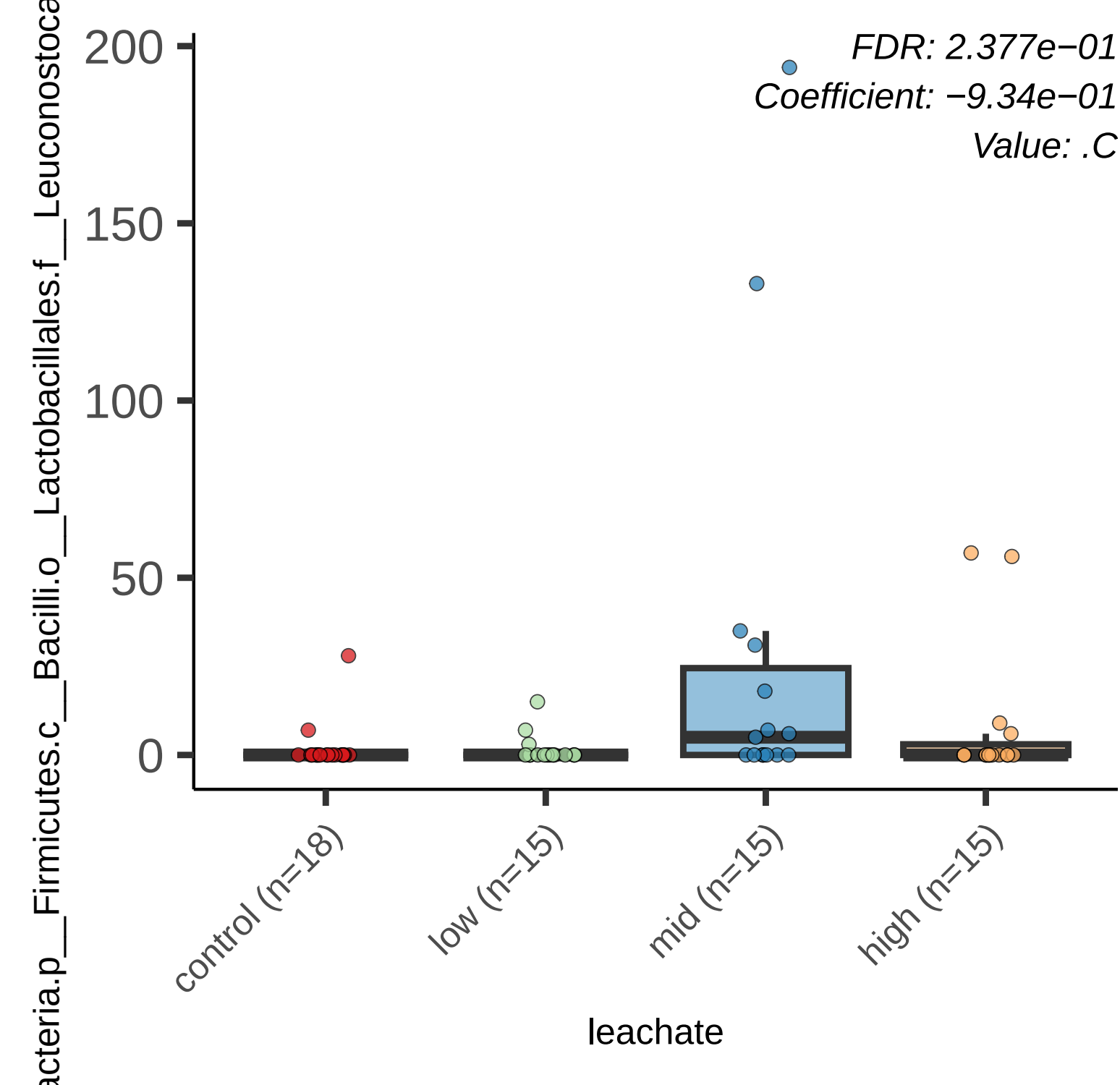
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leachate
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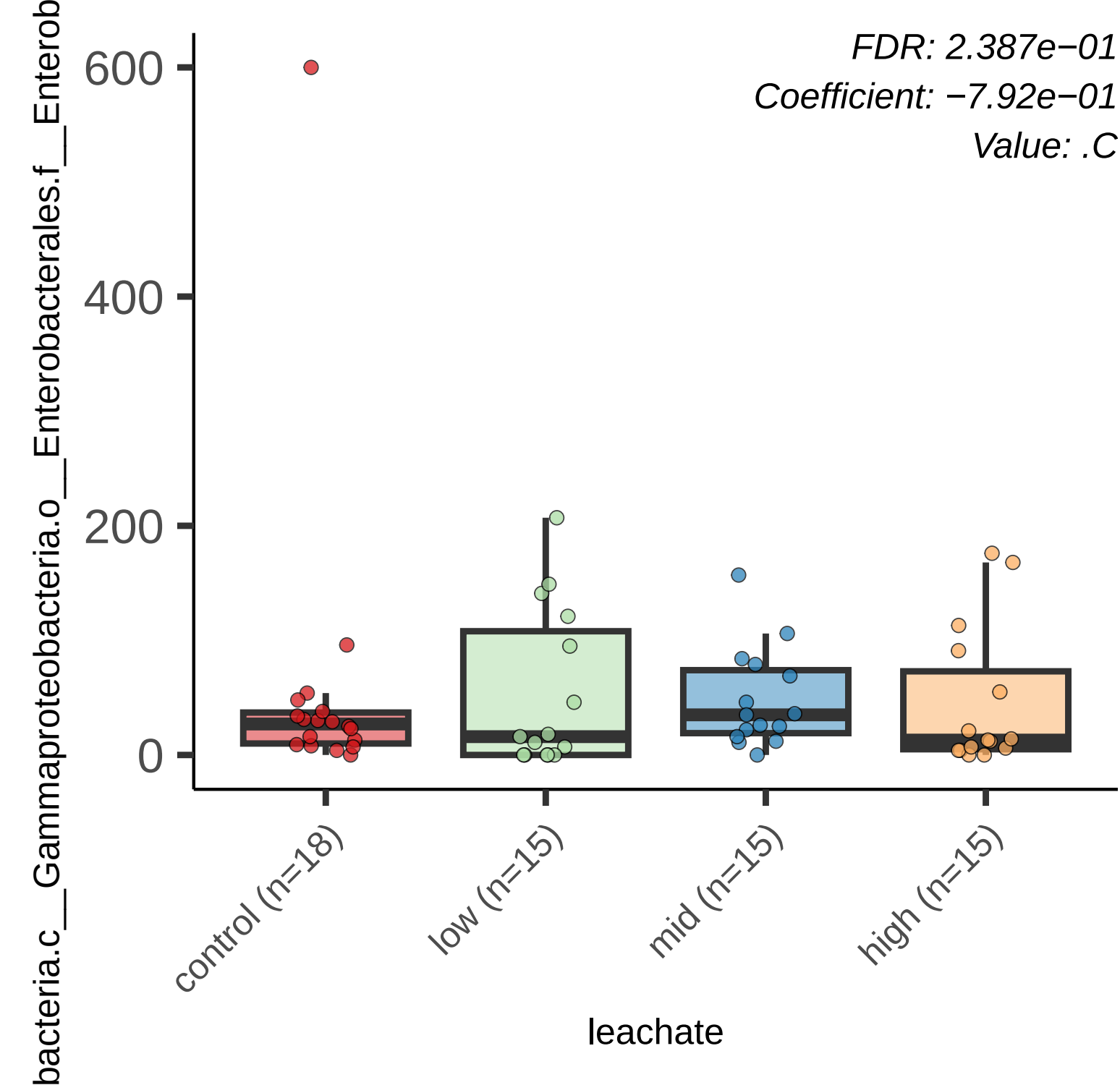
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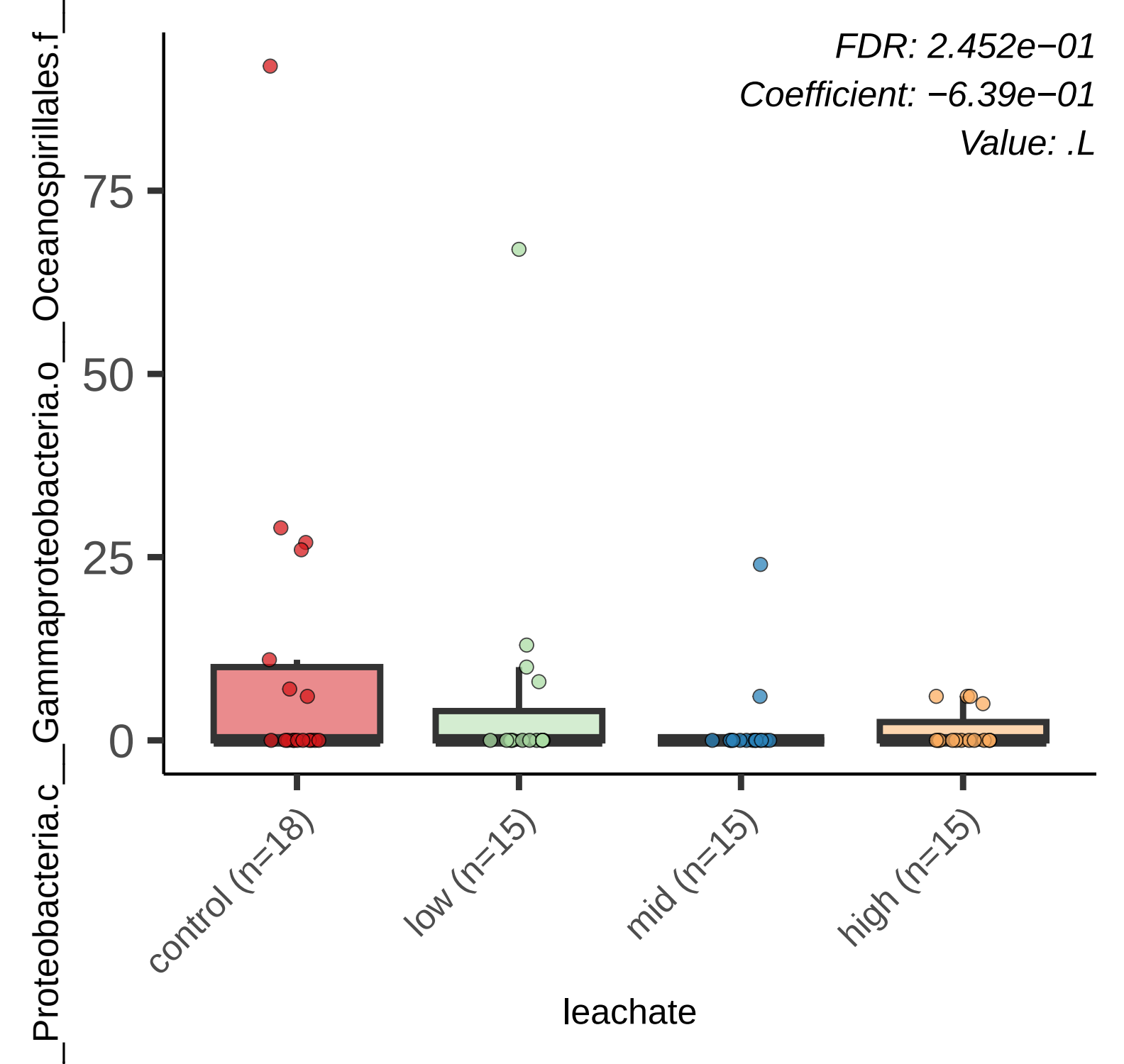
high (n=15)
leachate
bacteria.c__Gammaproteobacteria.o__Enterobacterales.f__Enterob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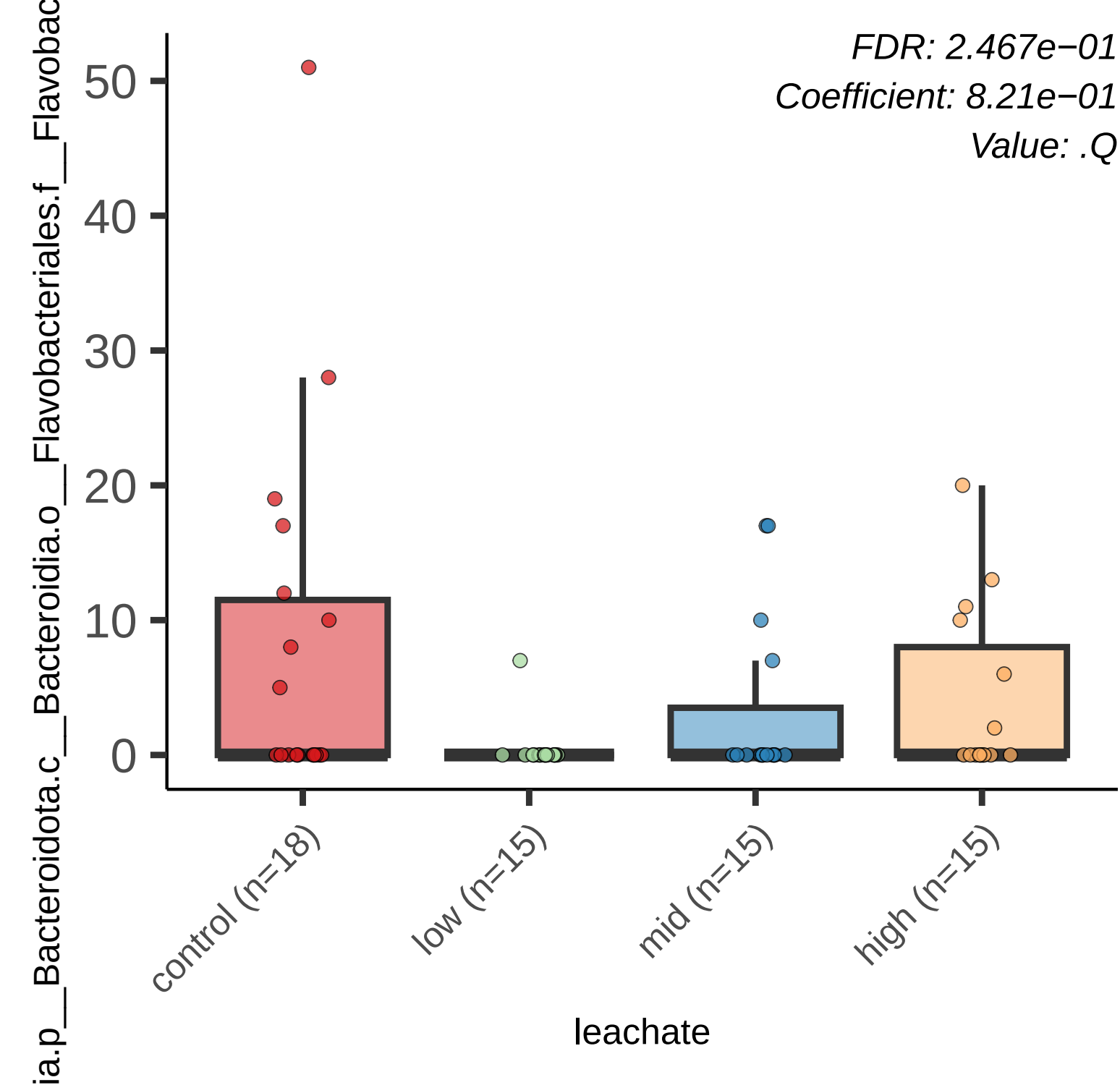
high (n=15)
leachate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high (n=15)
leachate
ia.p__Bacteroidota.c__Bacteroidia.o__Flavobacteriales.f__Flavobac