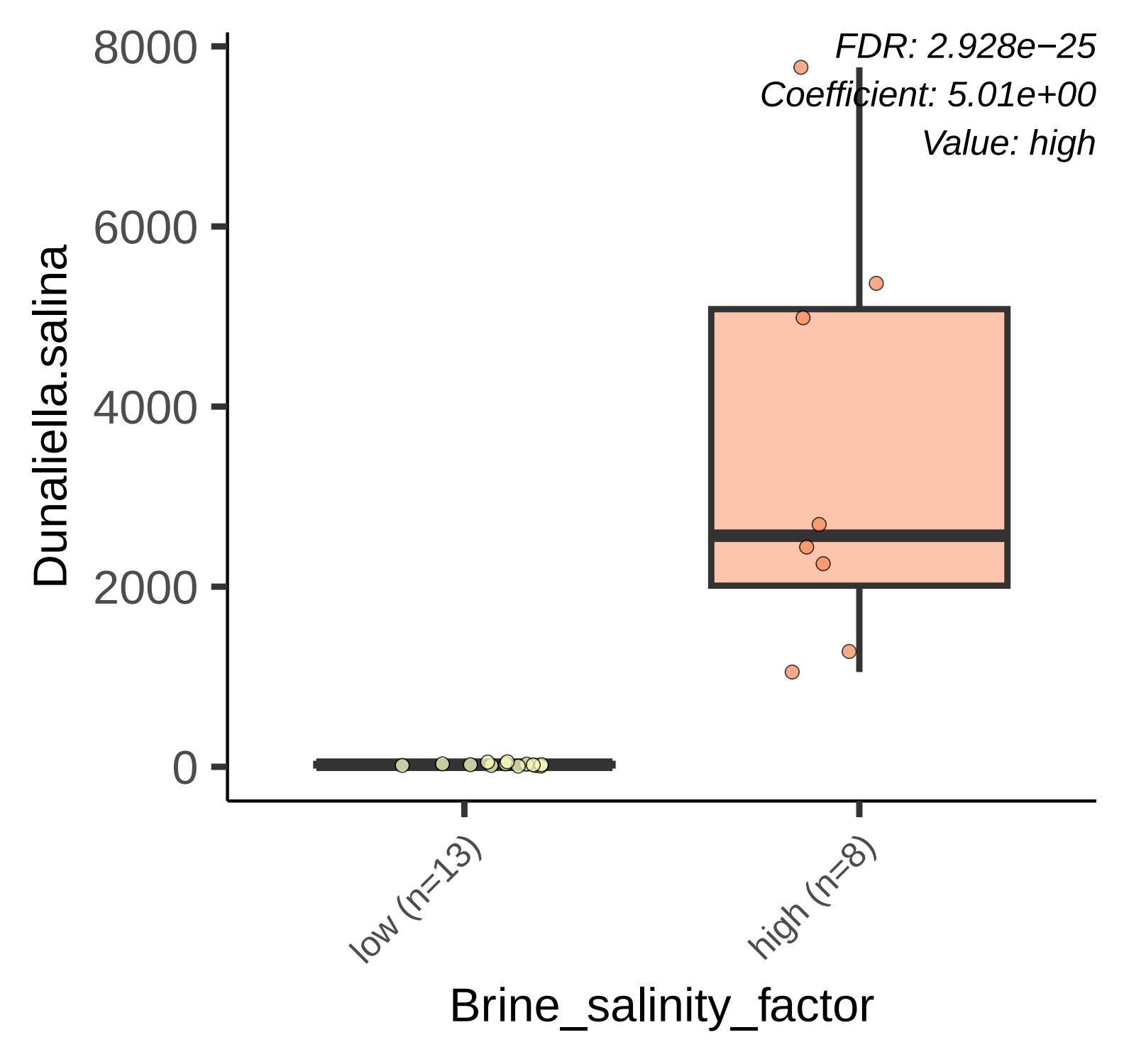
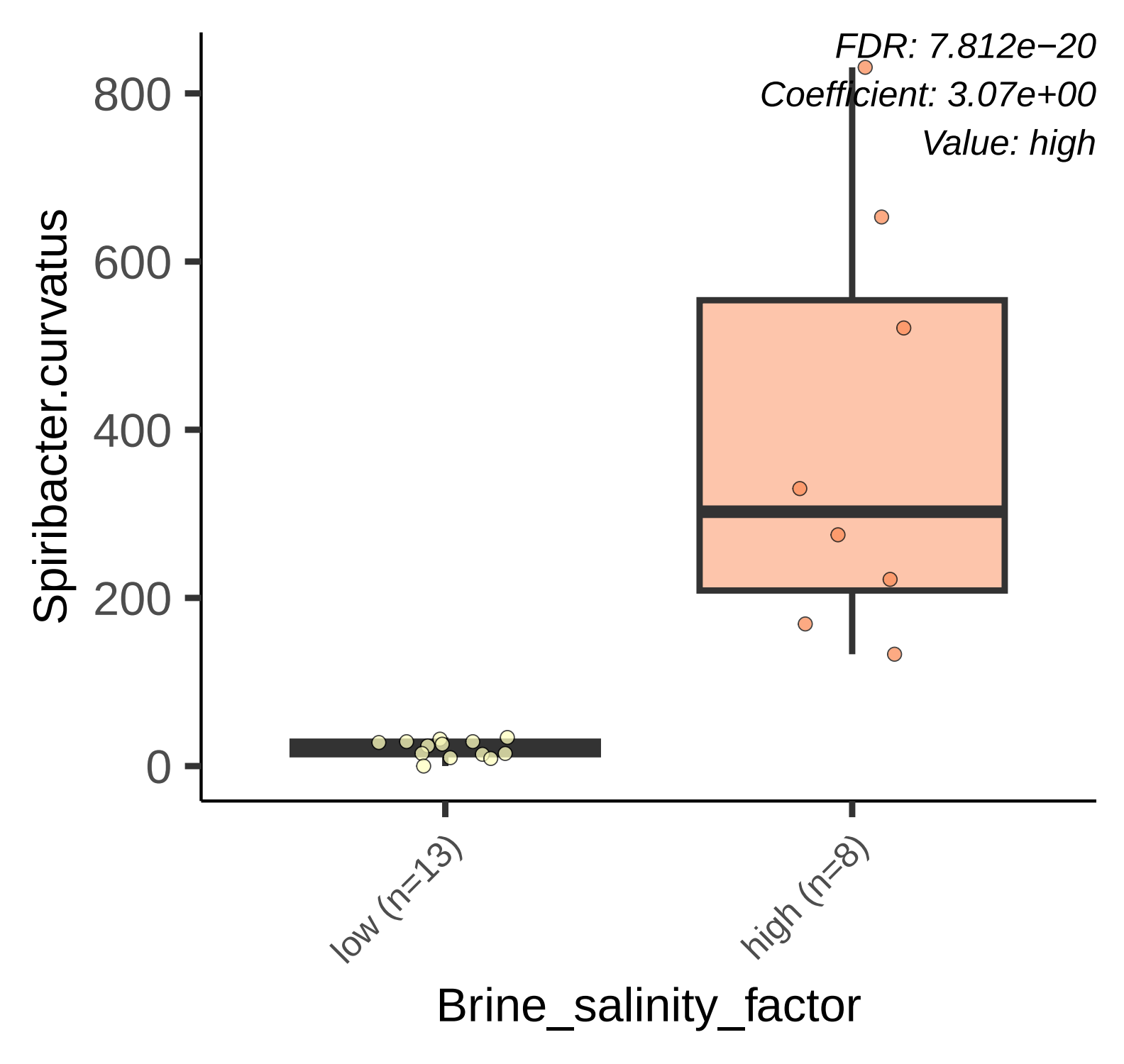
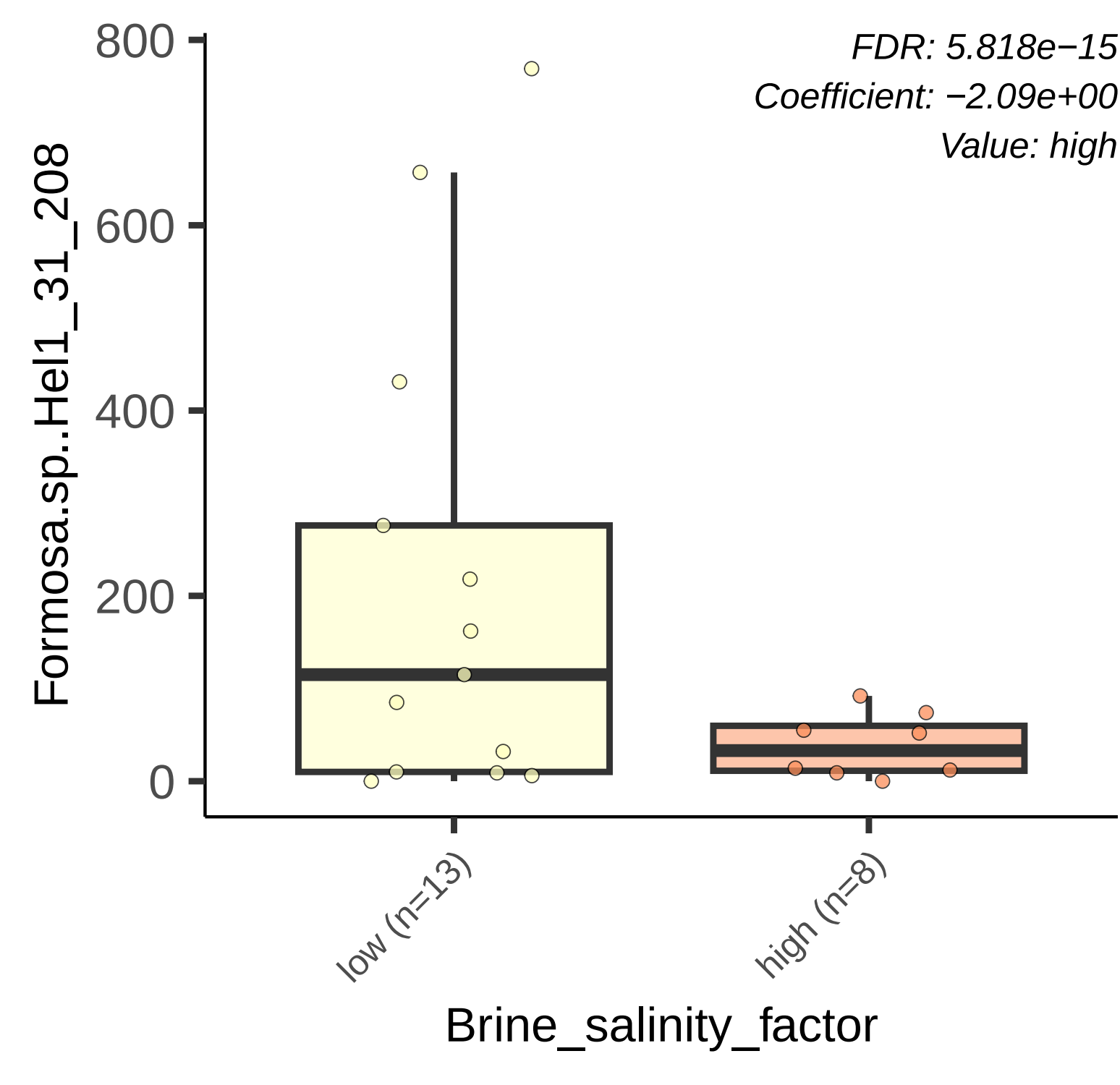
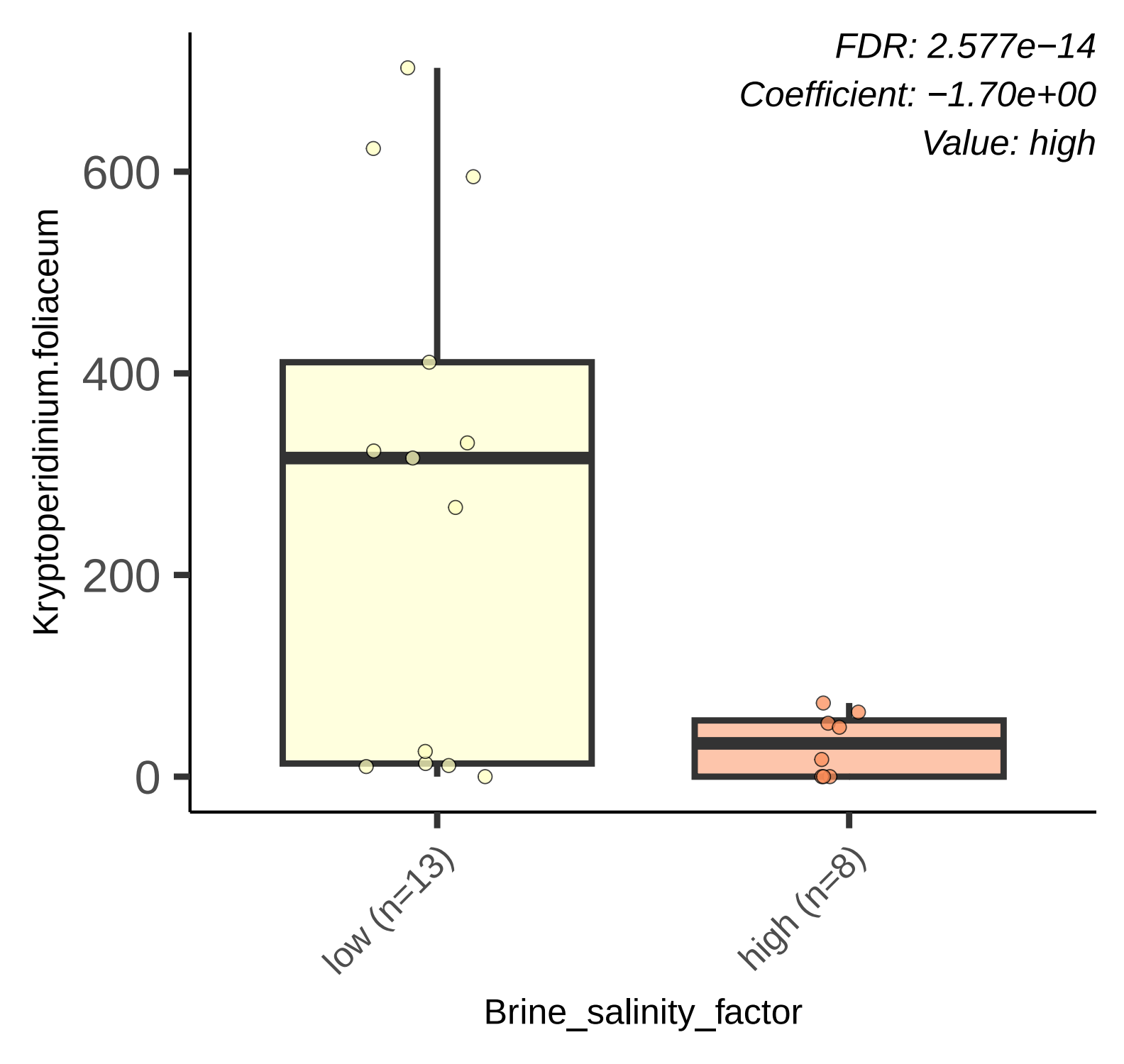
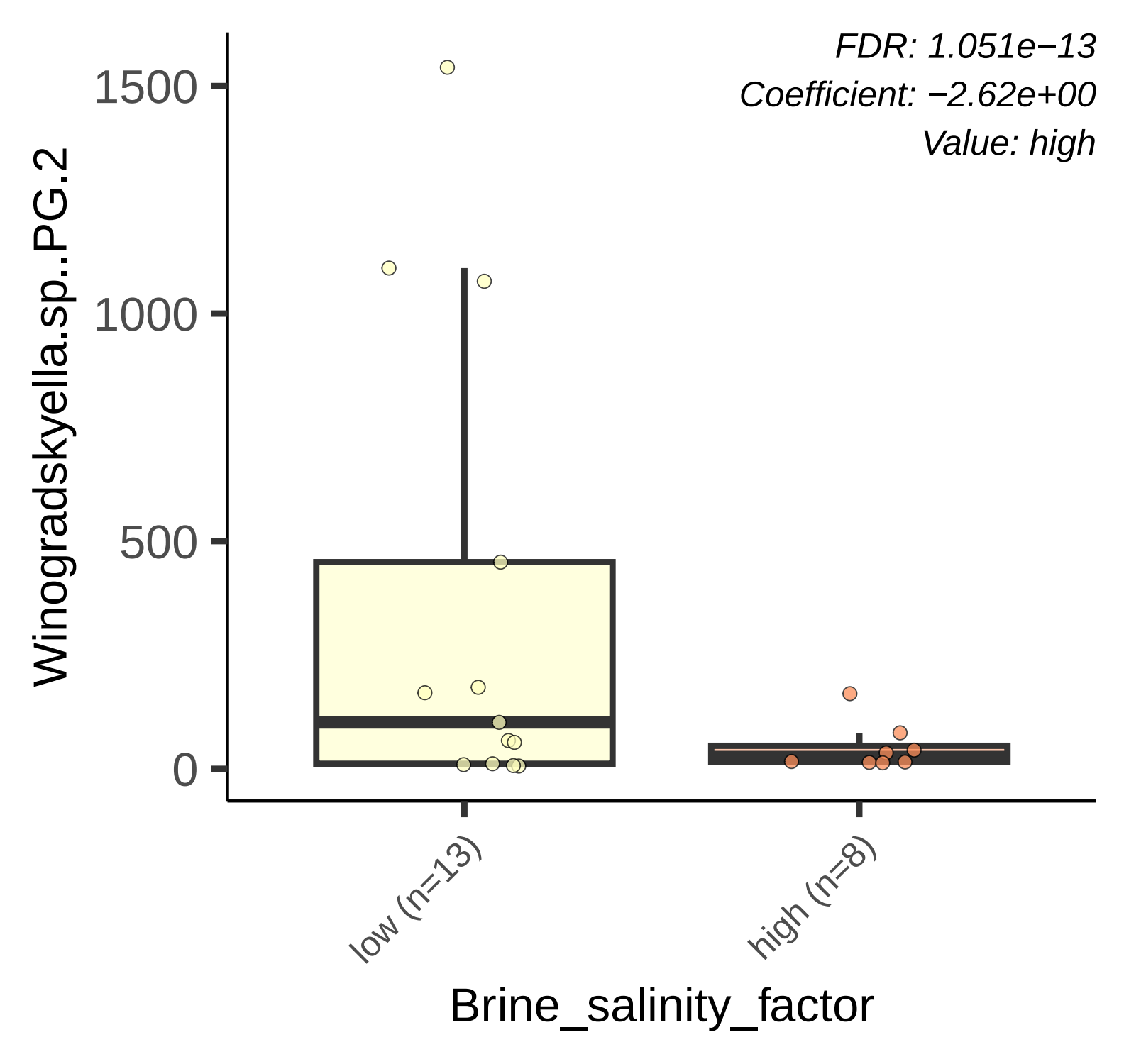
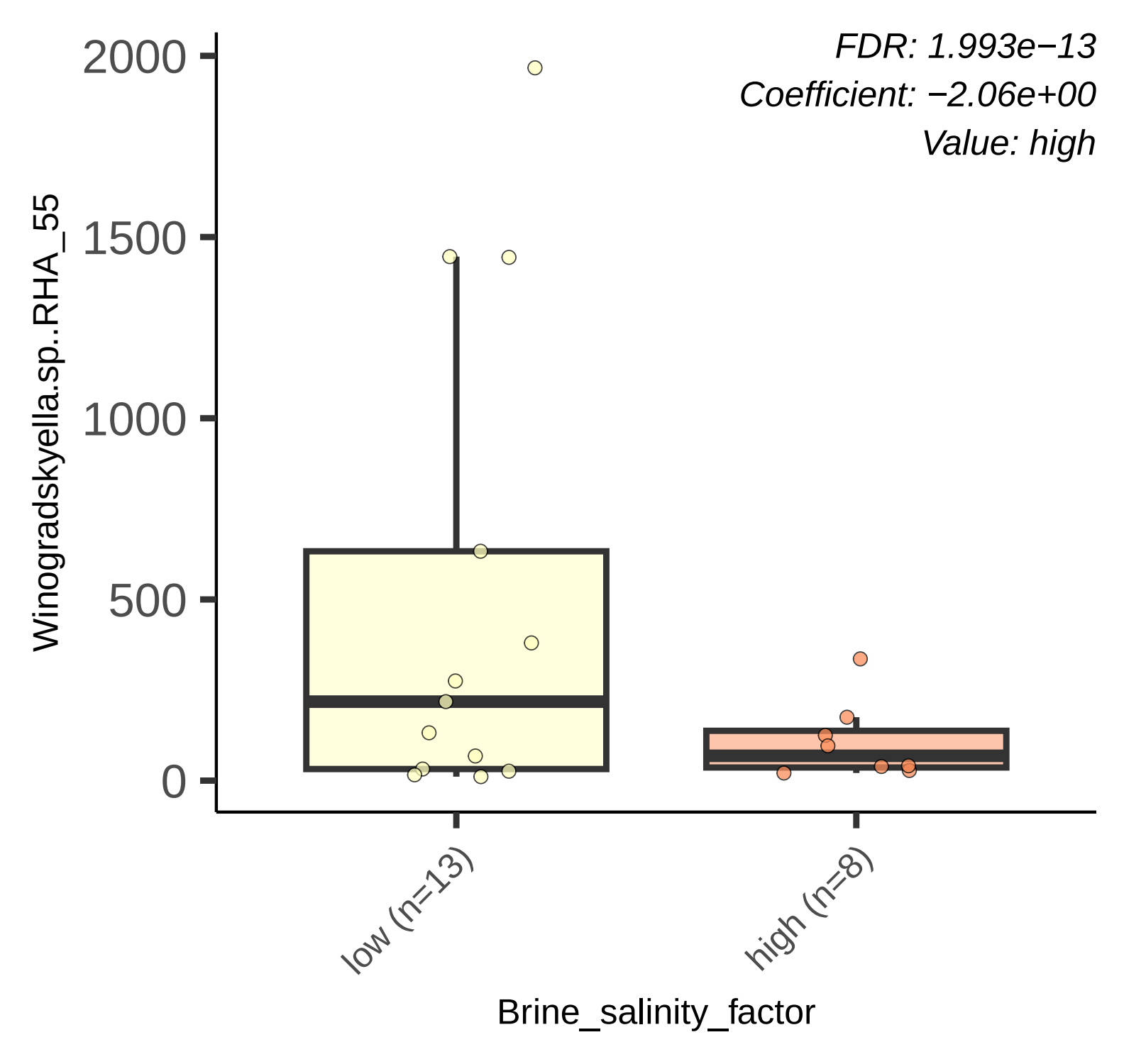

FDR: 2.928e−25
Coefficient: 5.01e+00
Value: high
8000
6000
4000
2000
0
Dunaliella.salina
low (n=13)
high (n=8)
Brine_salinity_factor

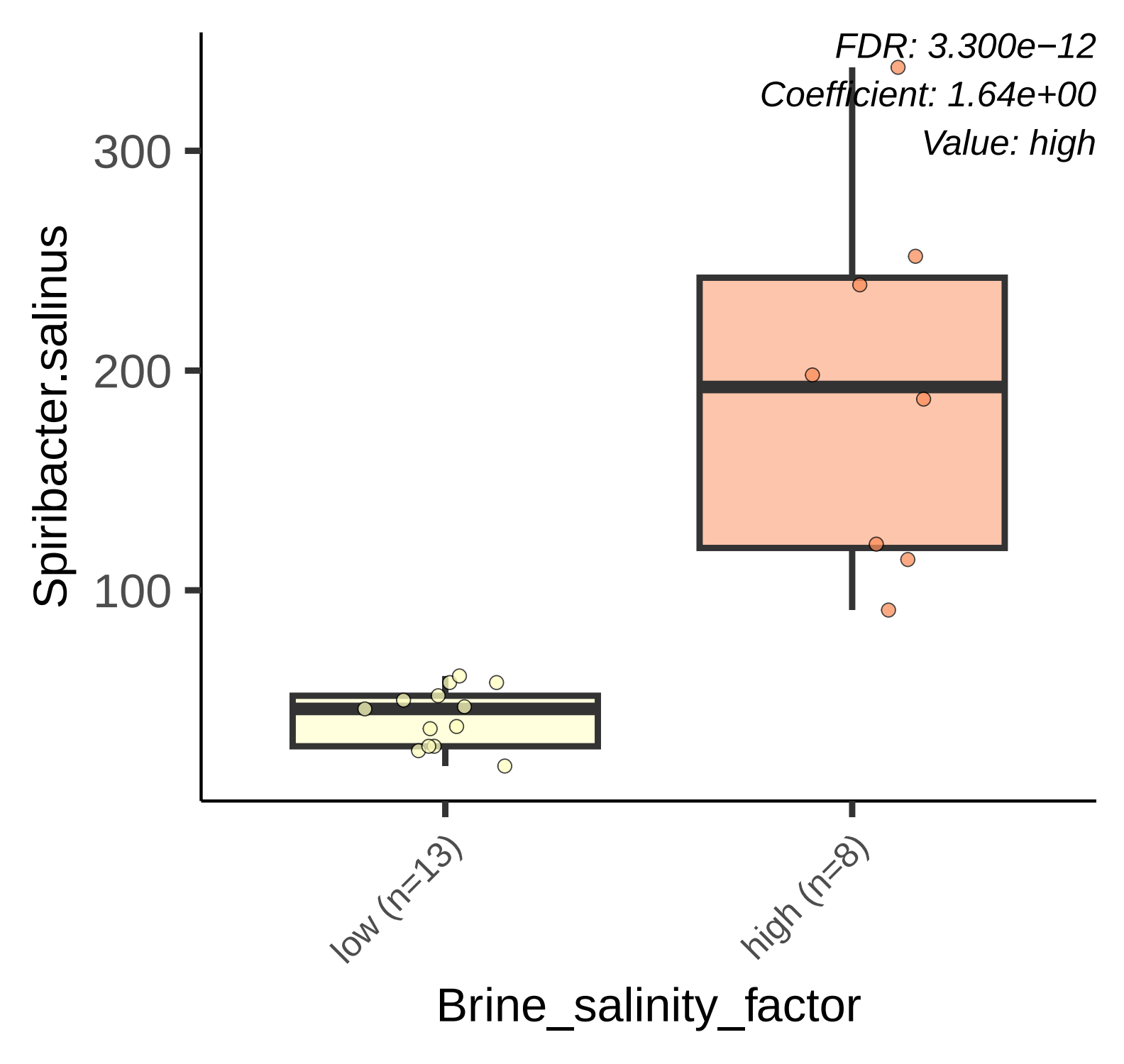

FDR: 7.812e−20
Coefficient: 3.07e+00
Value: high
800
600
400
200
0
Spiribacter.curvatus
low (n=13)
high (n=8)
Brine_salinity_factor

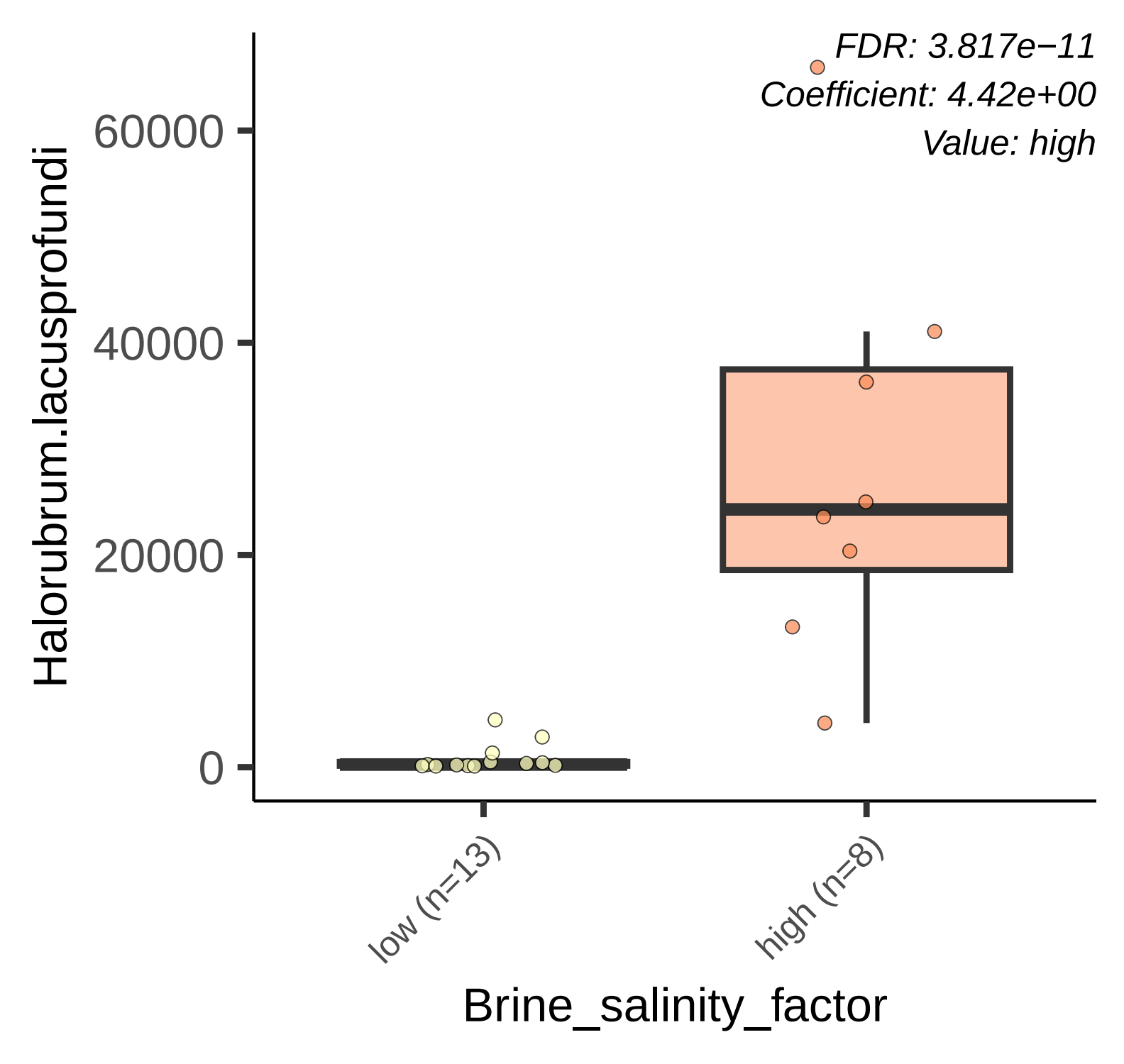

FDR: 5.818e−15
Coefficient: −2.09e+00
Value: high
800
600
400
200
0
Formosa.sp..Hel1_31_208
low (n=13)
high (n=8)
Brine_salinity_factor


FDR: 2.577e−14
Coefficient: −1.70e+00
Value: high
Kryptoperidinium.foliaceum
600
400
200
0
low (n=13)
high (n=8)
Brine_salinity_factor


FDR: 1.051e−13
Coefficient: −2.62e+00
Value: high
1500
1000
500
0
Winogradskyella.sp..PG.2
low (n=13)
high (n=8)
Brine_salinity_factor


FDR: 1.993e−13
Coefficient: −2.06e+00
Value: high
2000
1500
1000
500
0
Winogradskyella.sp..RHA_55
low (n=13)
high (n=8)
Brine_salinity_factor


FDR: 3.300e−12
Coefficient: 1.64e+00
Value: high
300
200
100
Spiribacter.salinus
low (n=13)
high (n=8)
Brine_salinity_factor


FDR: 3.817e−11
Coefficient: 4.42e+00
Value: high
60000
40000
20000
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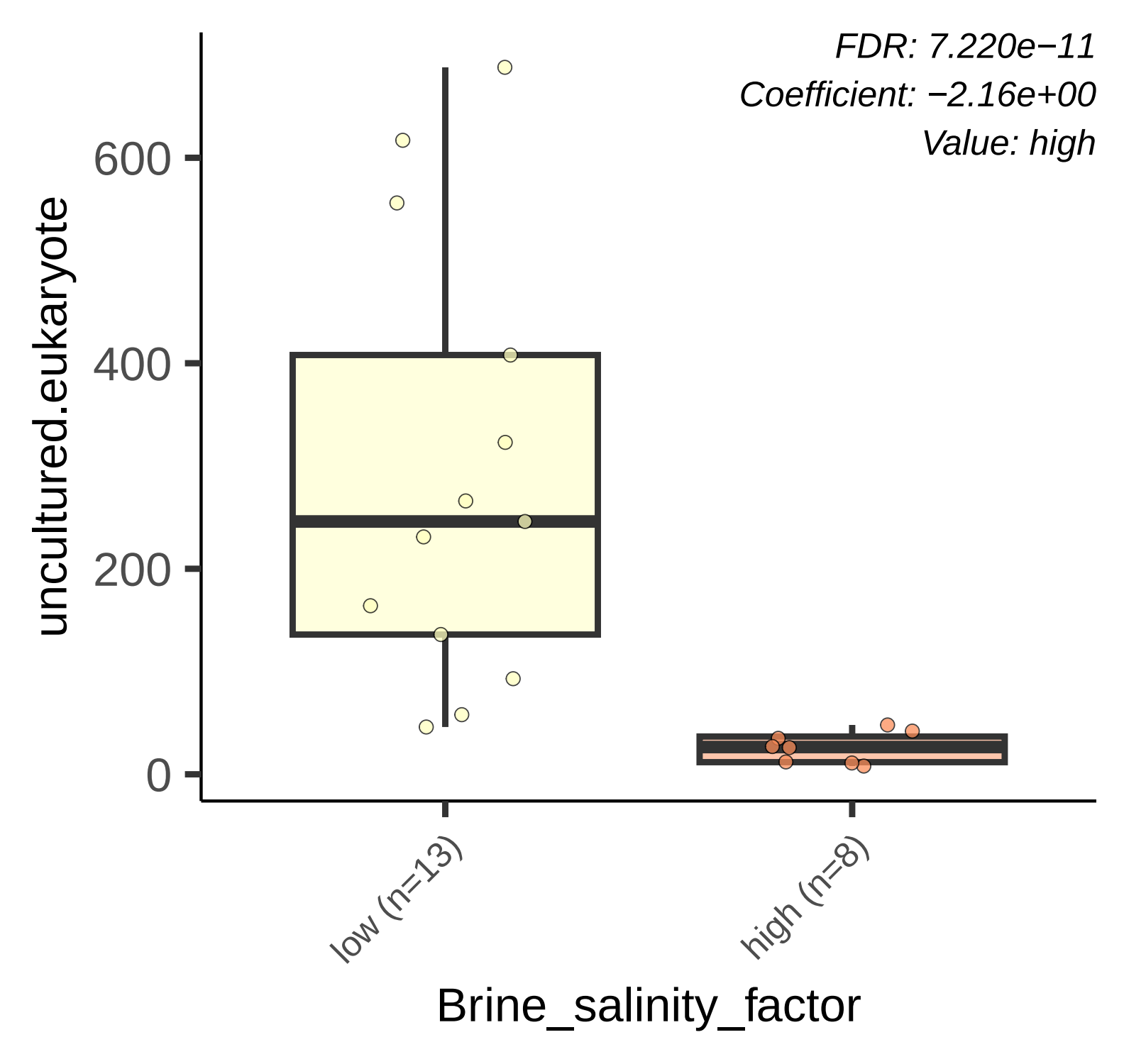
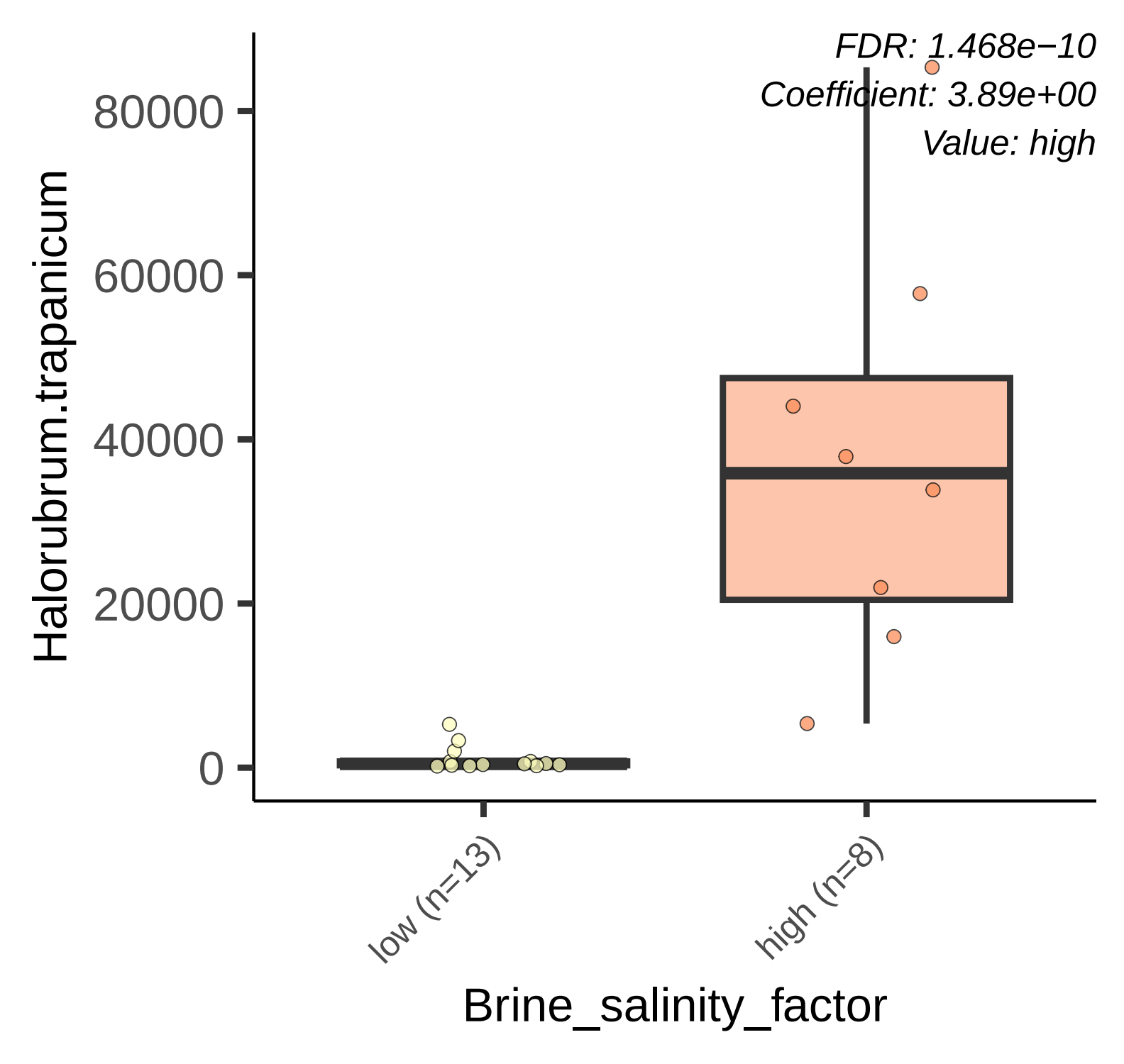
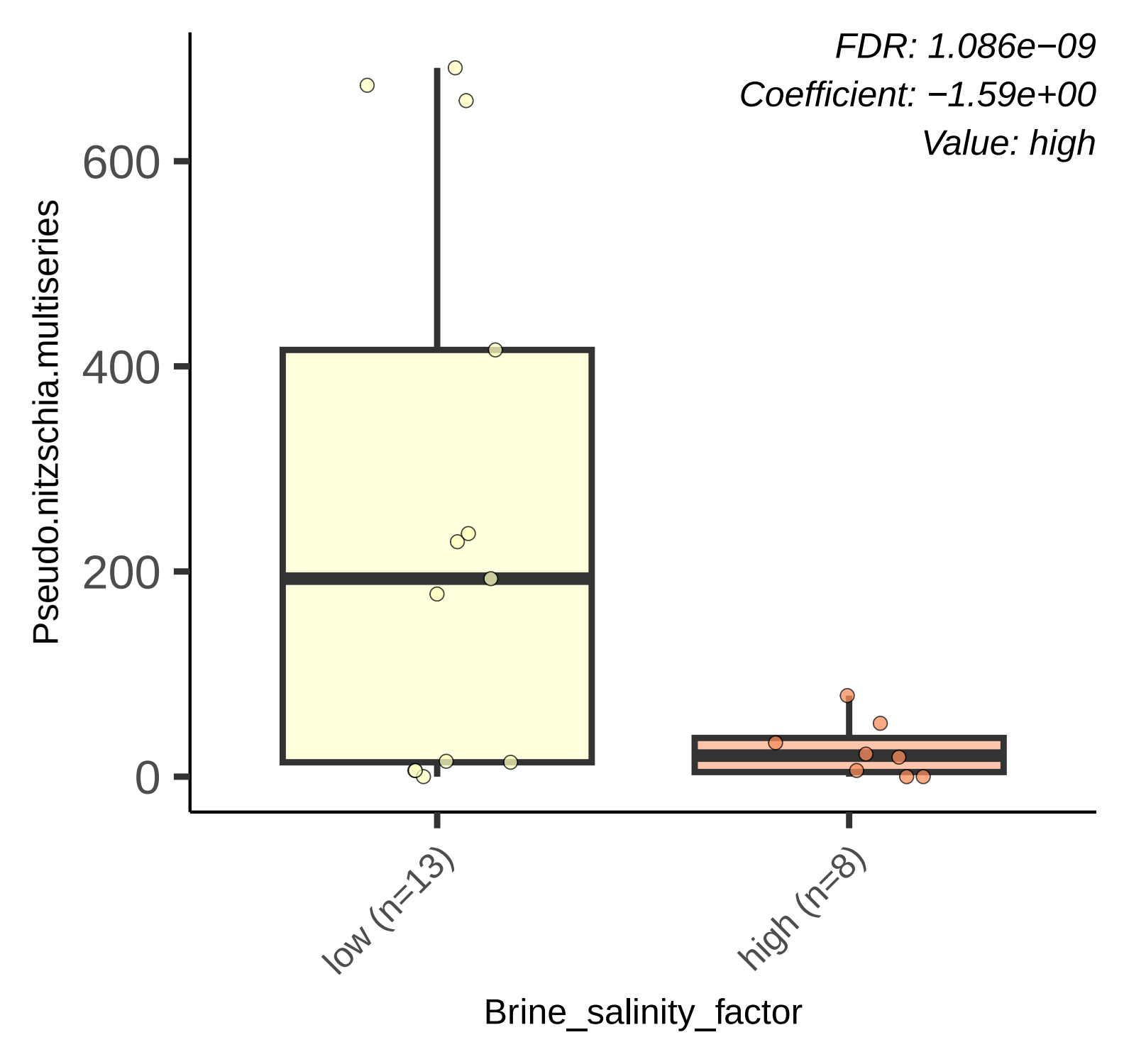
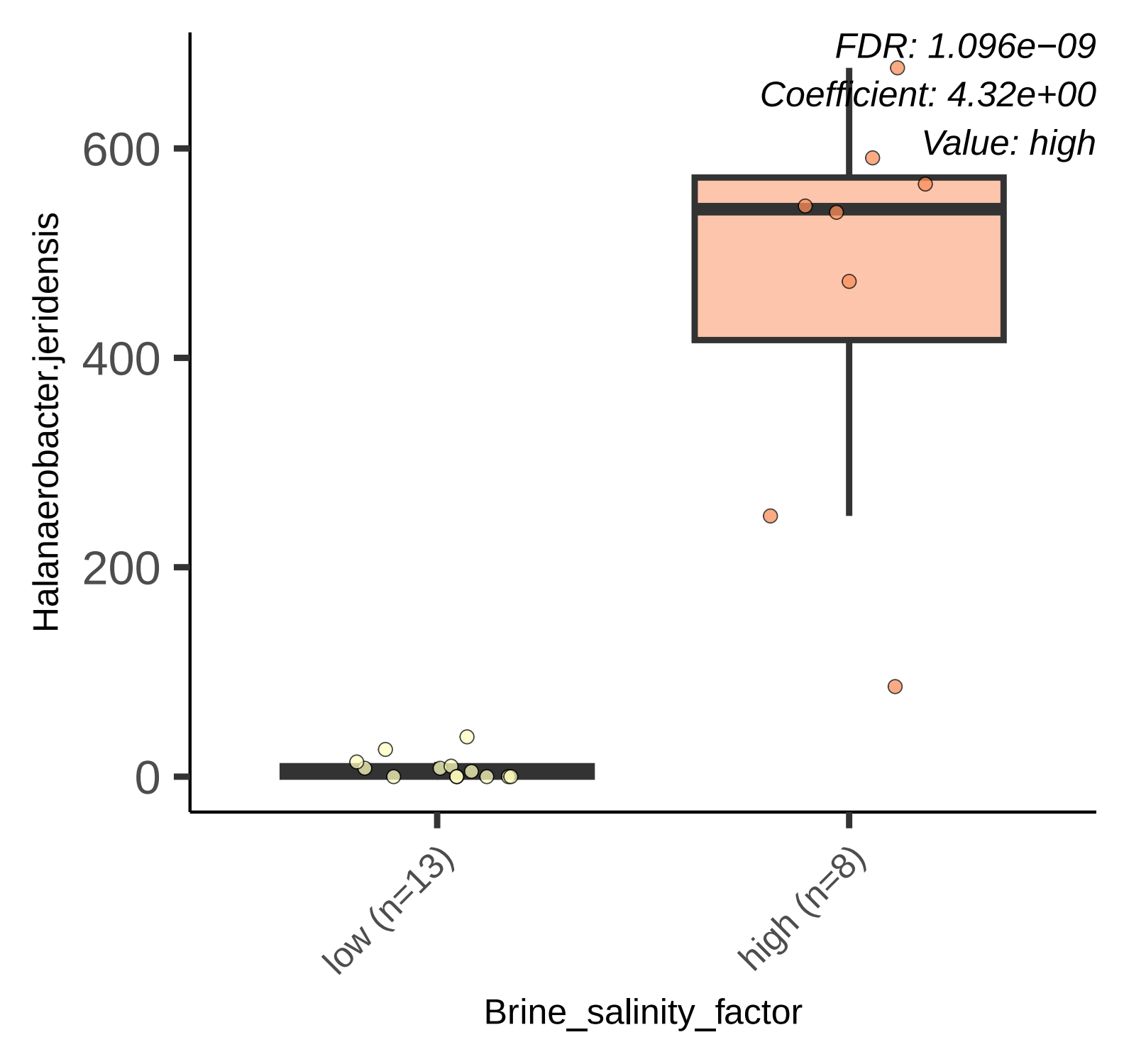
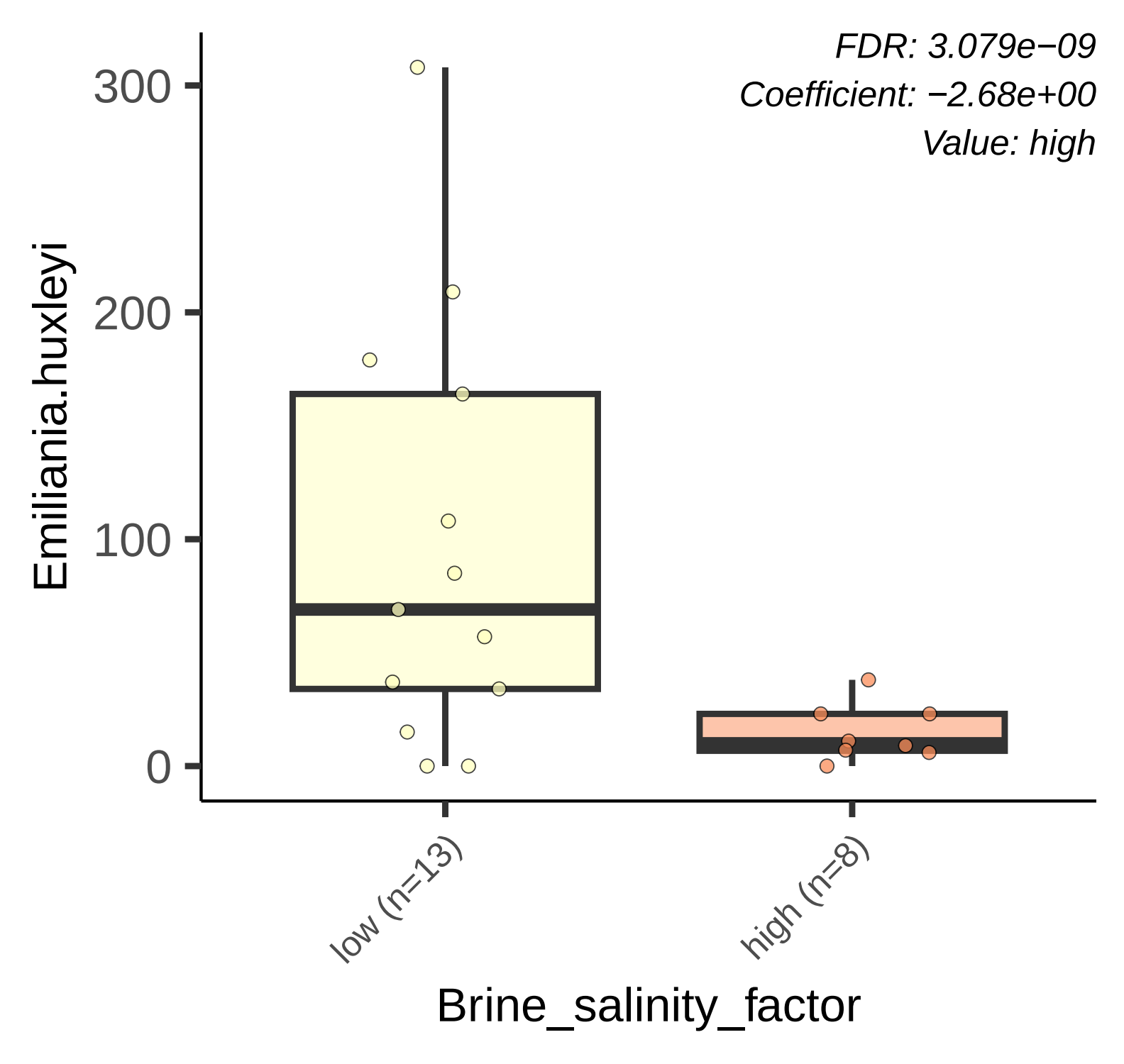
Halorubrum.lacusprofundi
low (n=13)
high (n=8)
Brine_salinity_factor

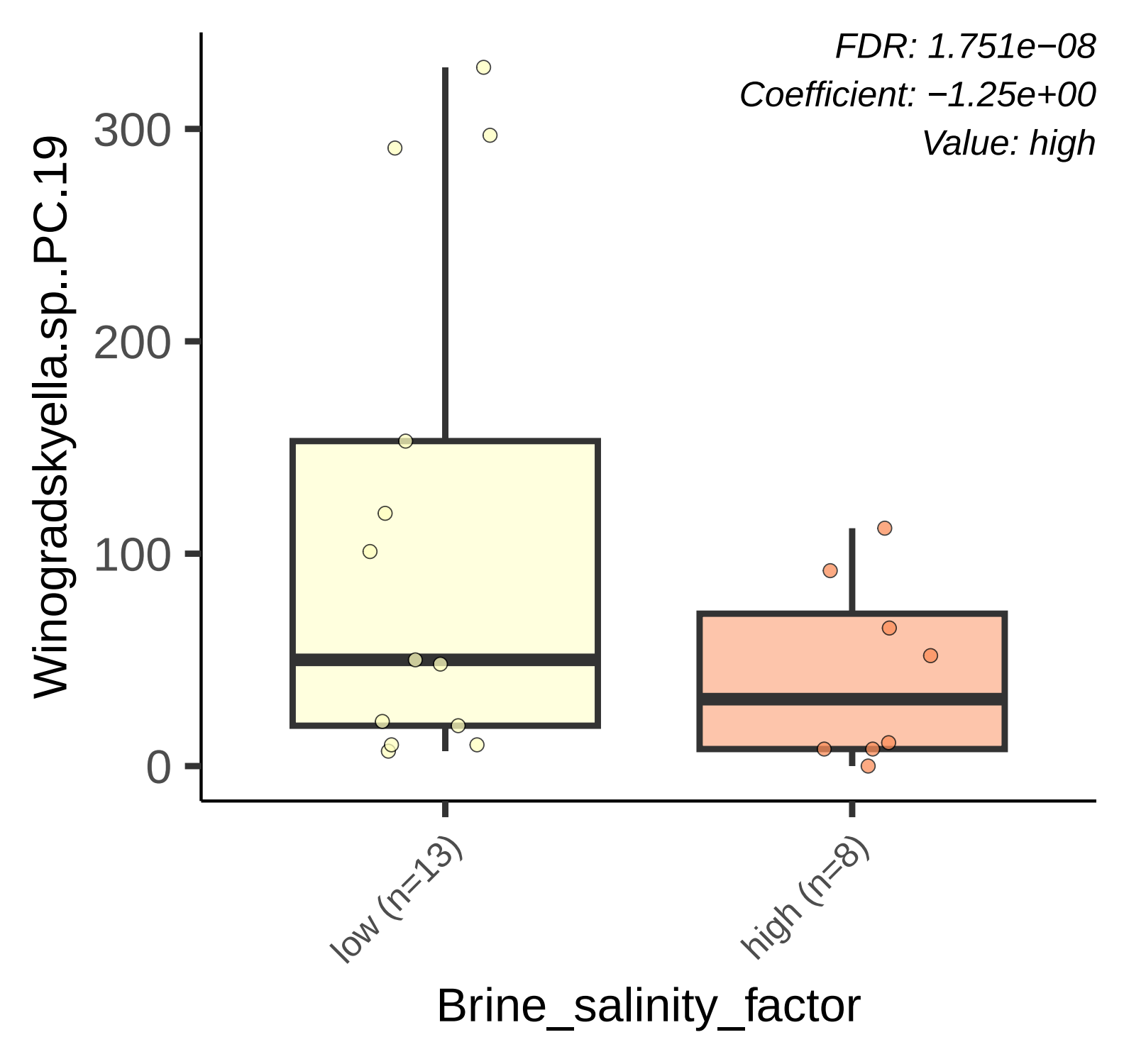

FDR: 7.220e−11
Coefficient: −2.16e+00
Value: high
uncultured.eukaryote
600
400
200
0
low (n=13)
high (n=8)
Brine_salinity_factor

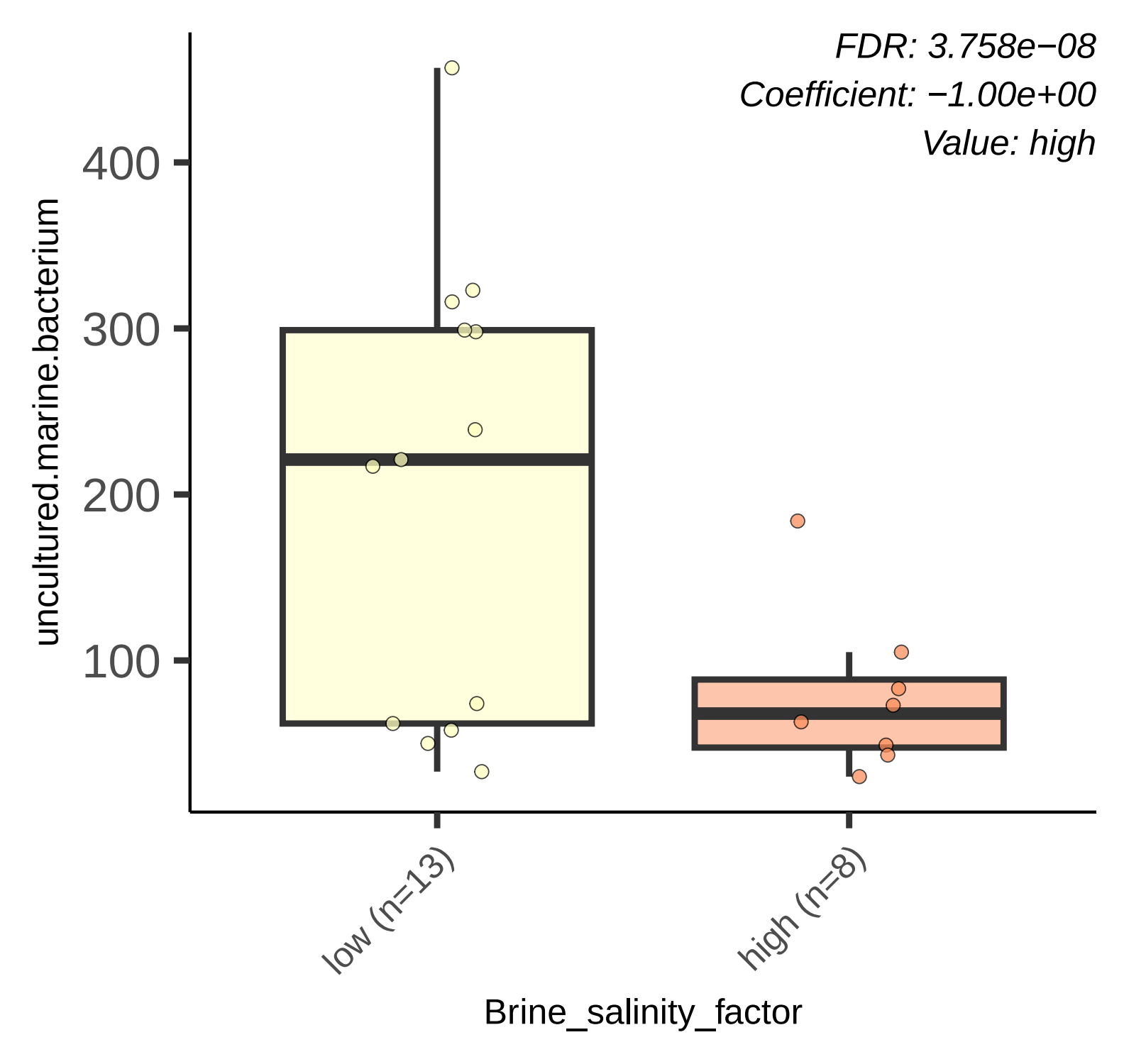

FDR: 1.468e−10
Coefficient: 3.89e+00
Value: high
80000
60000
40000
20000
0
Halorubrum.trapanicum
low (n=13)
high (n=8)
Brine_salinity_factor

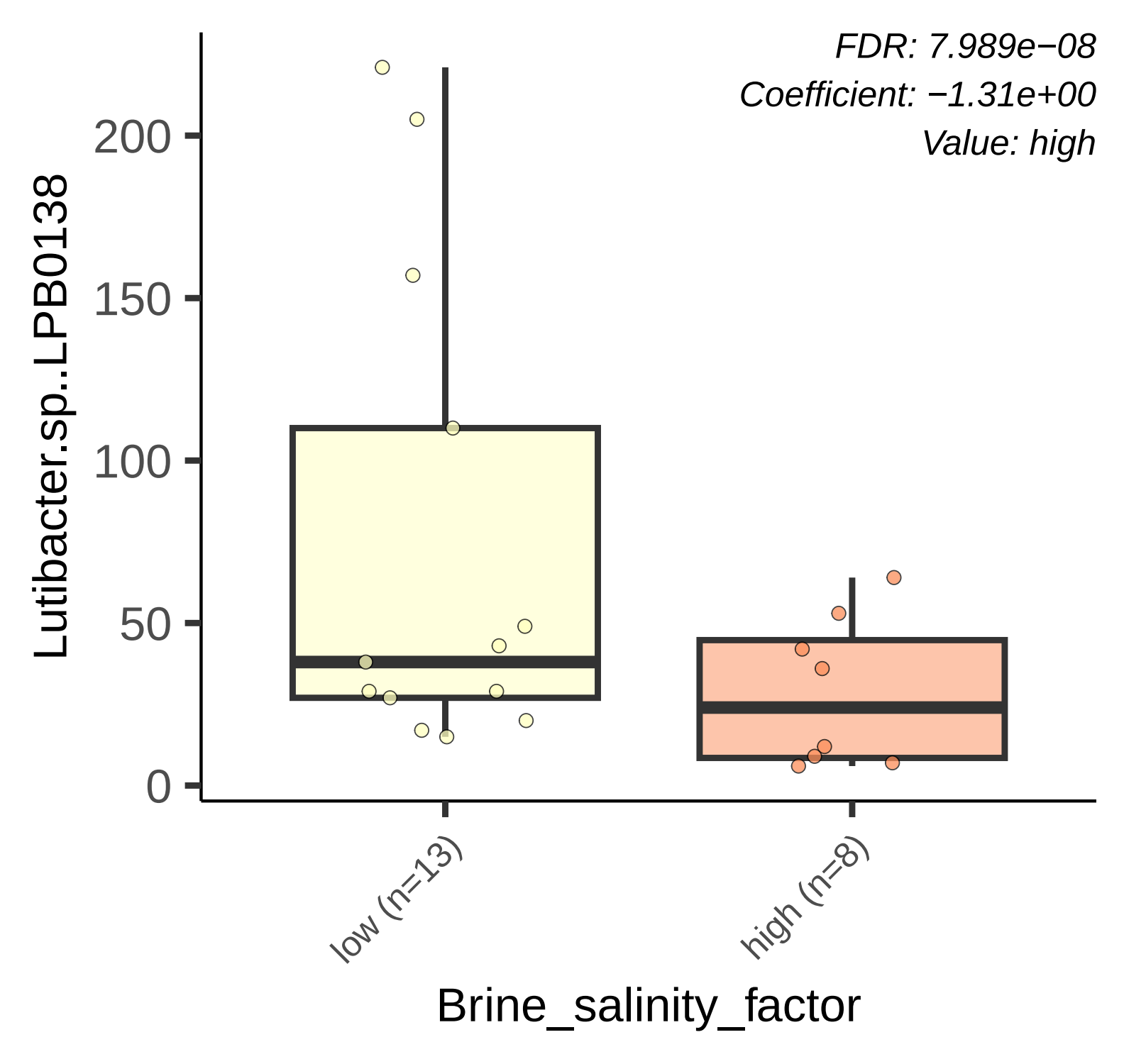

FDR: 1.086e−09
Coefficient: −1.59e+00
Value: high
Pseudo.nitzschia.multiseries
600
400
200
0
low (n=13)
high (n=8)
Brine_salinity_factor

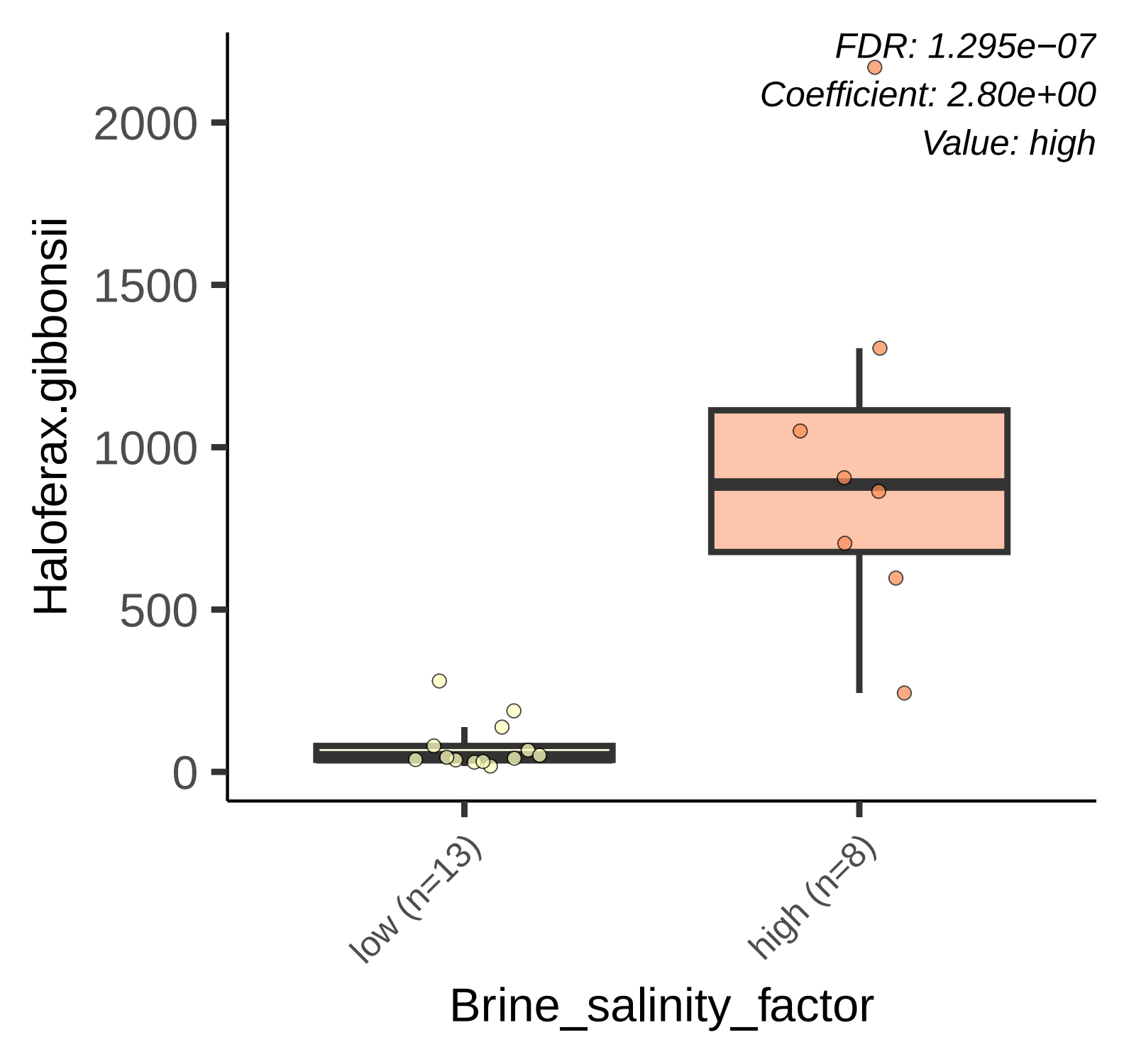

FDR: 1.096e−09
Coefficient: 4.32e+00
Value: high
600
400
200
0
Halanaerobacter.jeridensis
low (n=13)
high (n=8)
Brine_salinity_factor

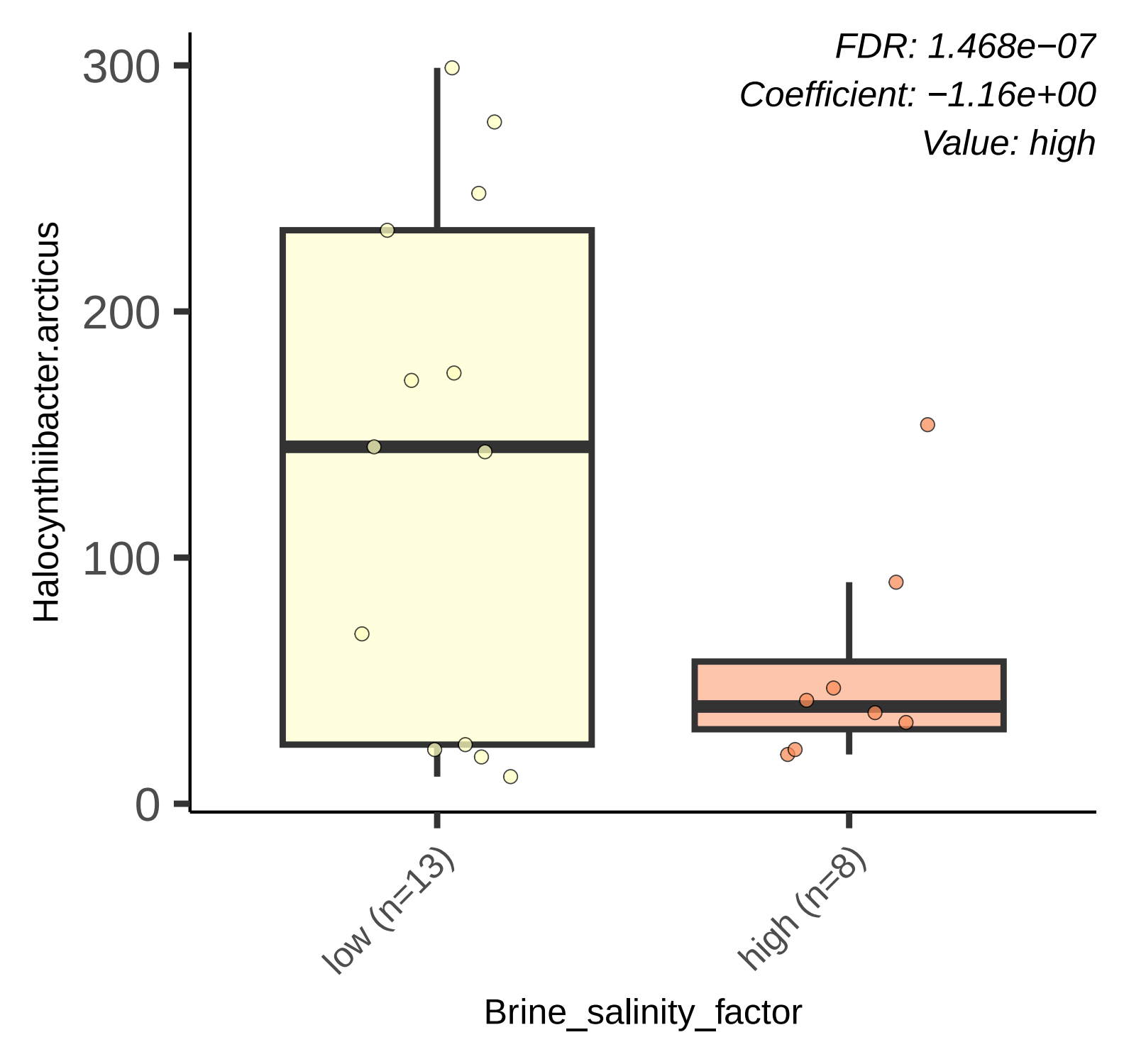

FDR: 3.079e−09
Coefficient: −2.68e+00
Value: high
300
200
100
0
Emiliania.huxleyi
low (n=13)
high (n=8)
Brine_salinity_factor

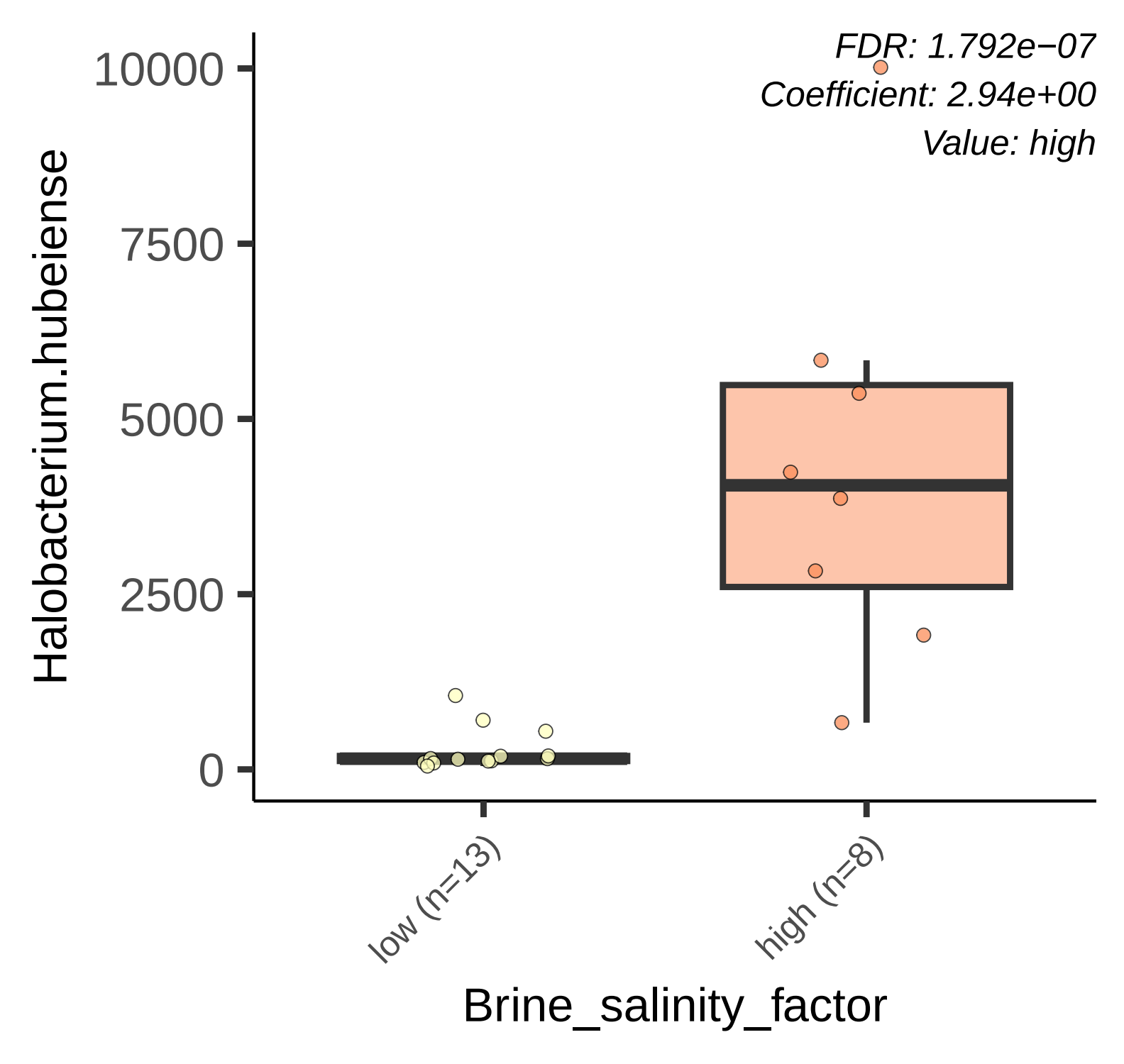

FDR: 1.751e−08
Coefficient: −1.25e+00
Value: high
Winogradskyella.sp..PC.19
300
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

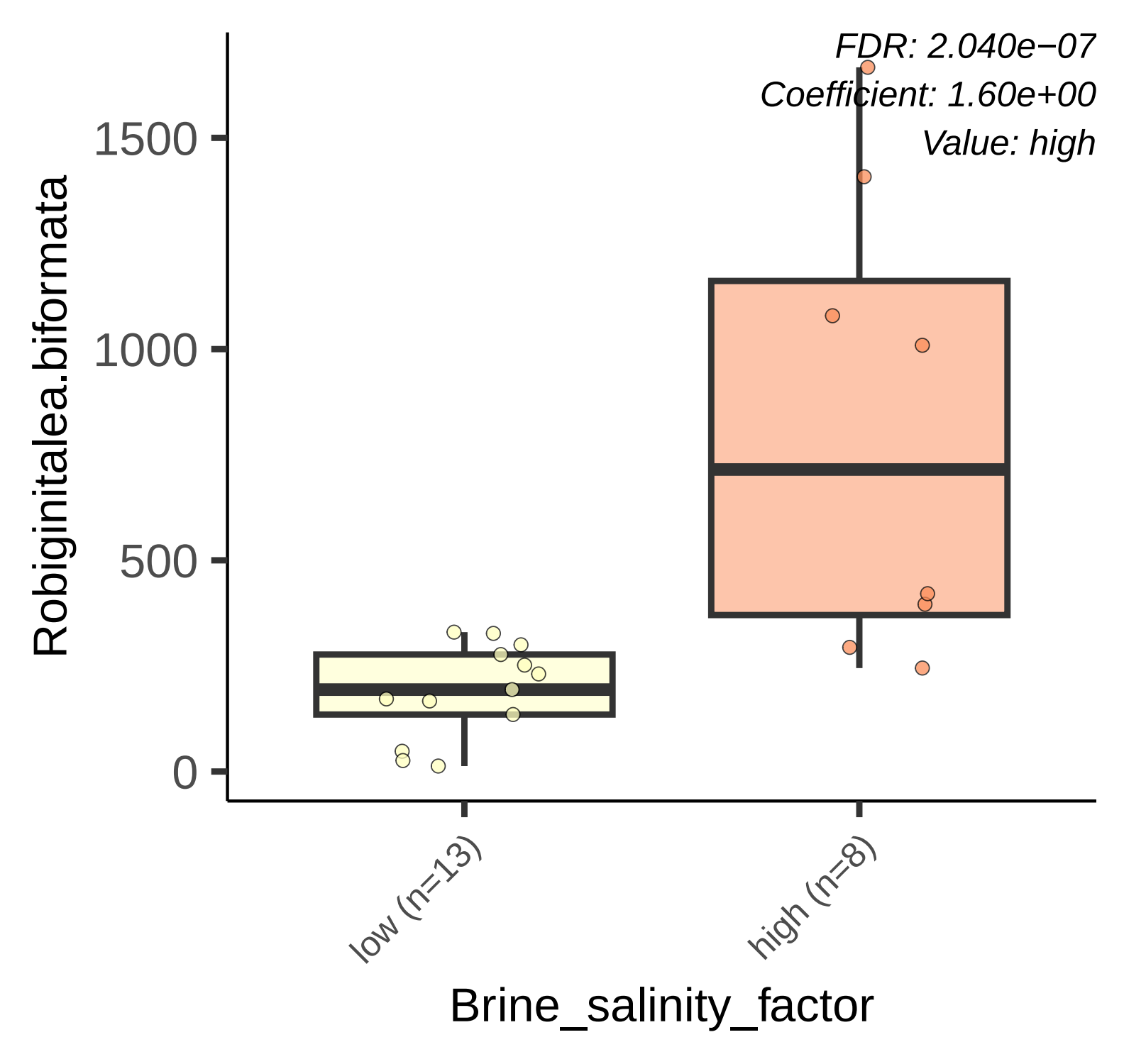

FDR: 3.758e−08
Coefficient: −1.00e+00
Value: high
uncultured.marine.bacterium
400
300
200
100
low (n=13)
high (n=8)
Brine_salinity_factor

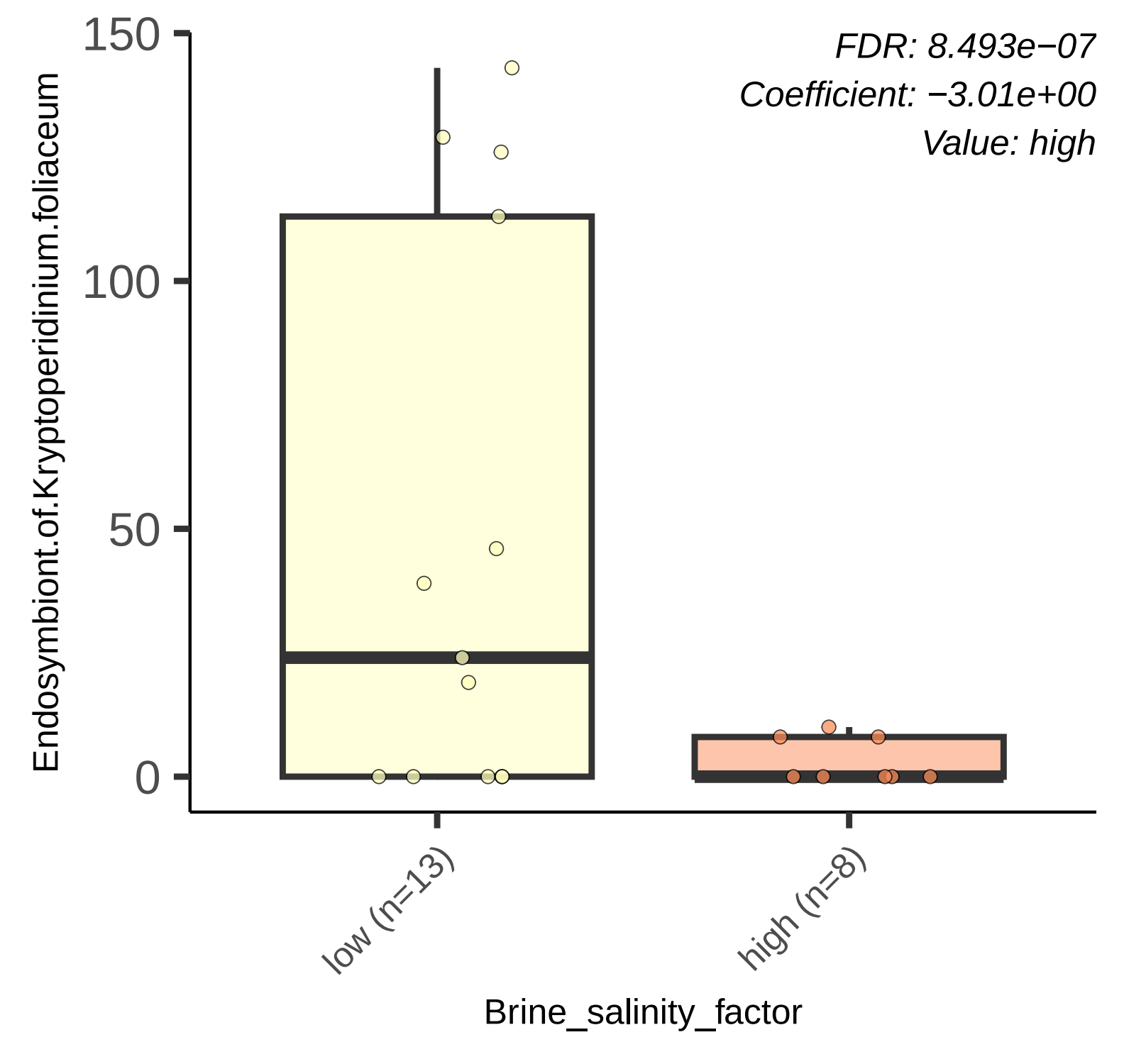

FDR: 7.989e−08
Coefficient: −1.31e+00
Value: high
Lutibacter.sp..LPB0138
200
150
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

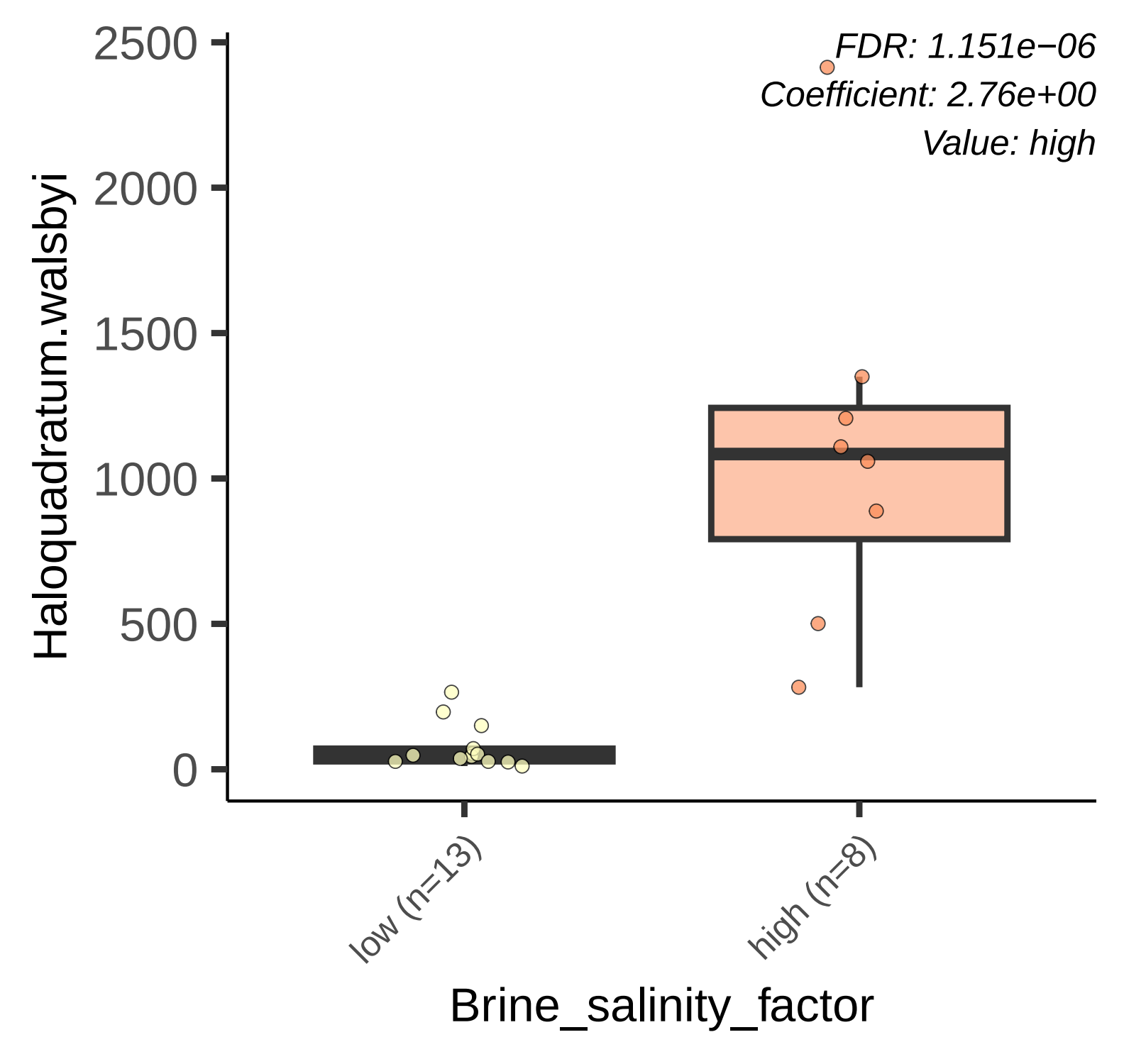

FDR: 1.295e−07
Coefficient: 2.80e+00
Value: high
Haloferax.gibbonsii
2000
1500
1000
500
0
low (n=13)
high (n=8)
Brine_salinity_factor

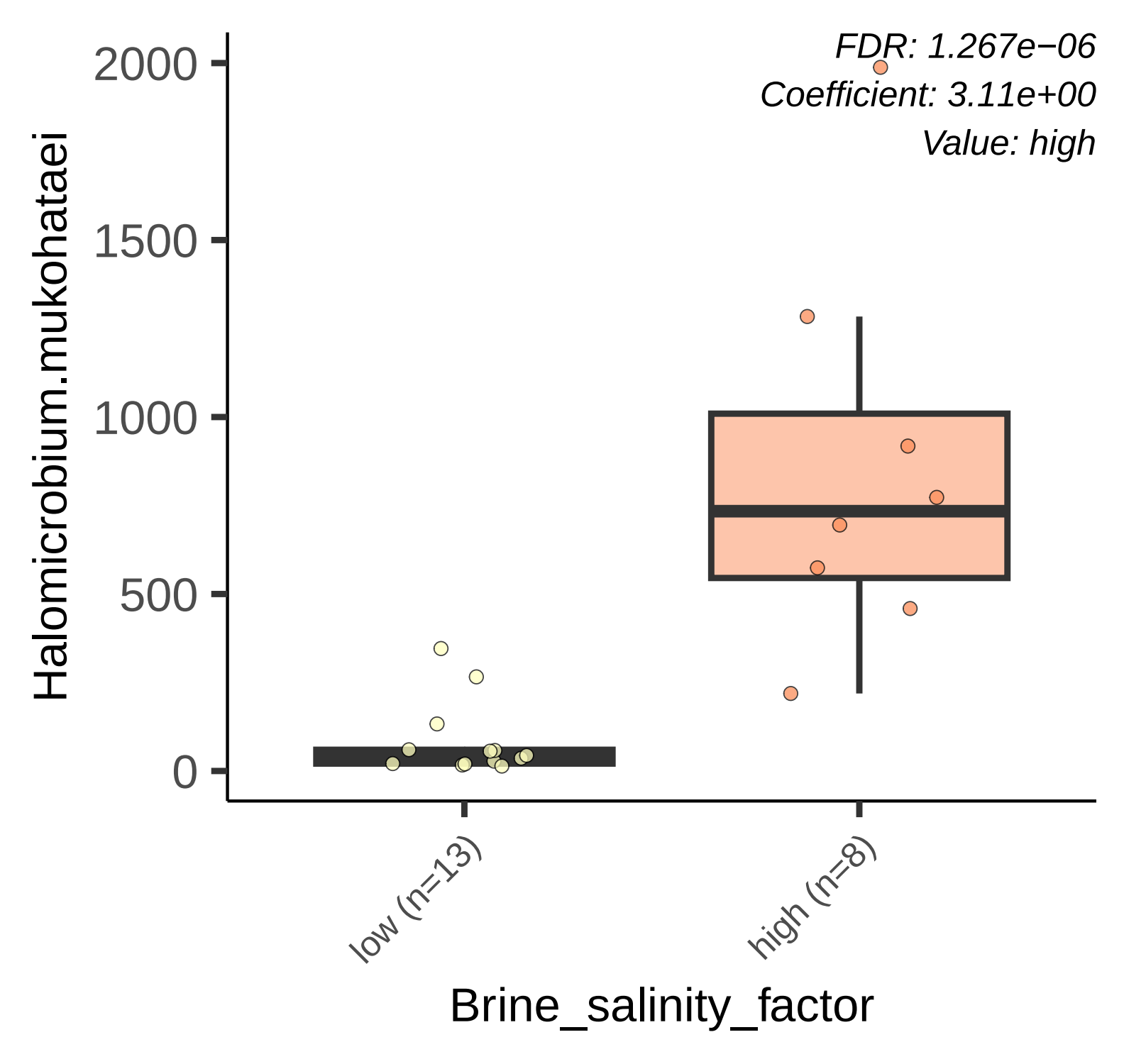

FDR: 1.468e−07
Coefficient: −1.16e+00
Value: high
Halocynthiibacter.arcticus
300
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

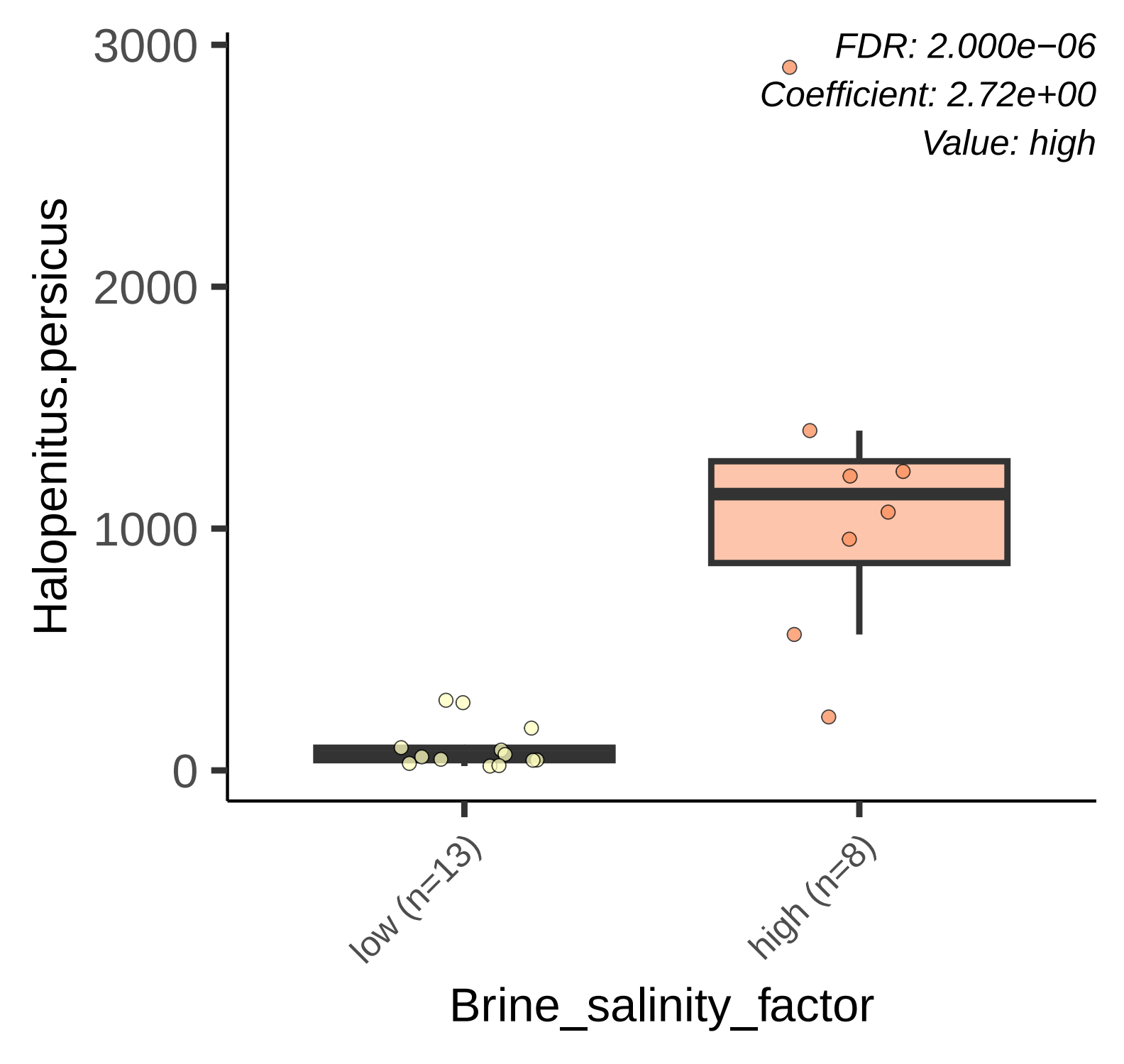

FDR: 1.792e−07
Coefficient: 2.94e+00
Value: high
10000
7500
5000
2500
0
Halobacterium.hubeiense
low (n=13)
high (n=8)
Brine_salinity_factor

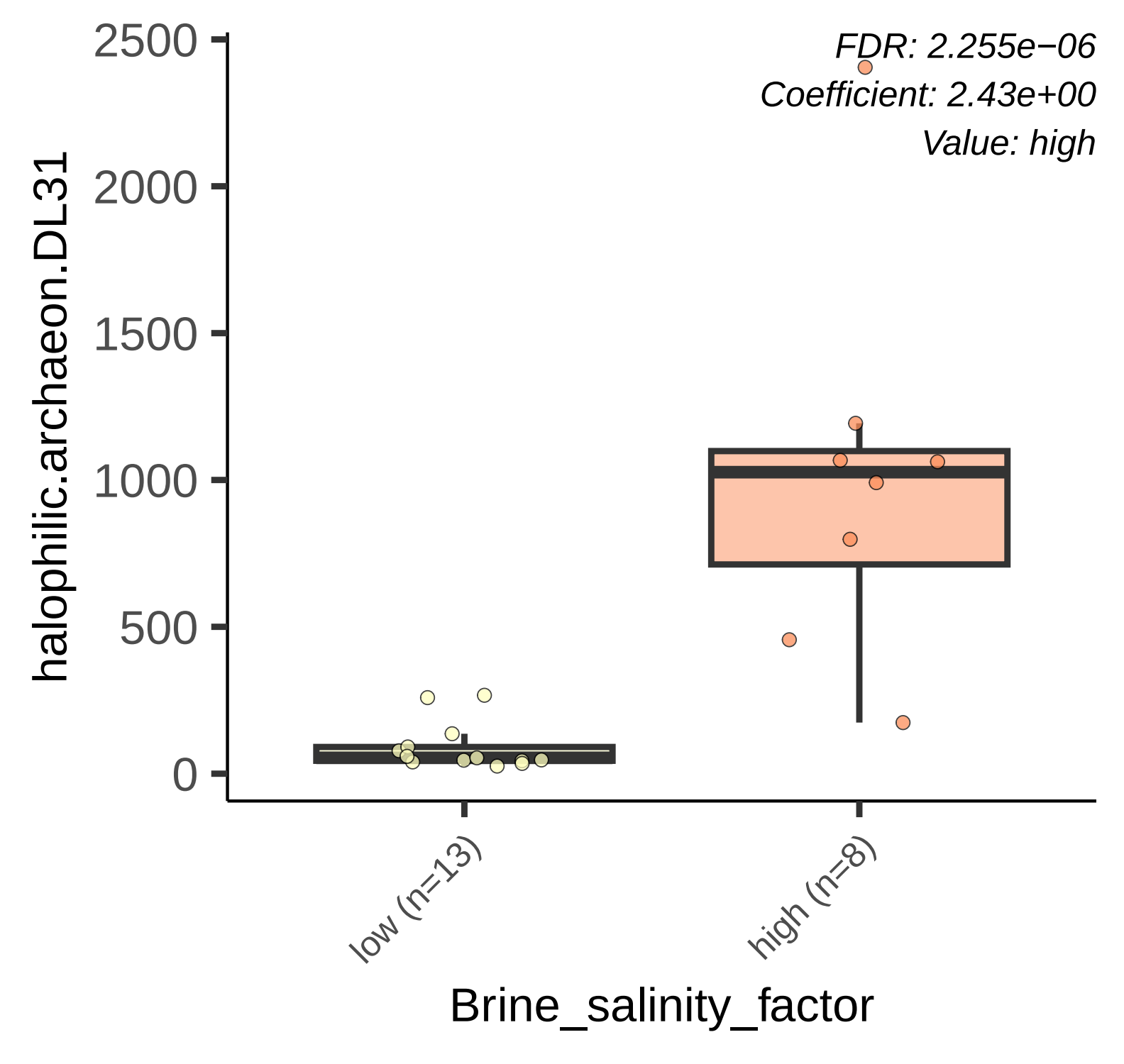

FDR: 2.040e−07
Coefficient: 1.60e+00
Value: high
1500
1000
500
0
Robiginitalea.biformata
low (n=13)
high (n=8)
Brine_salinity_factor

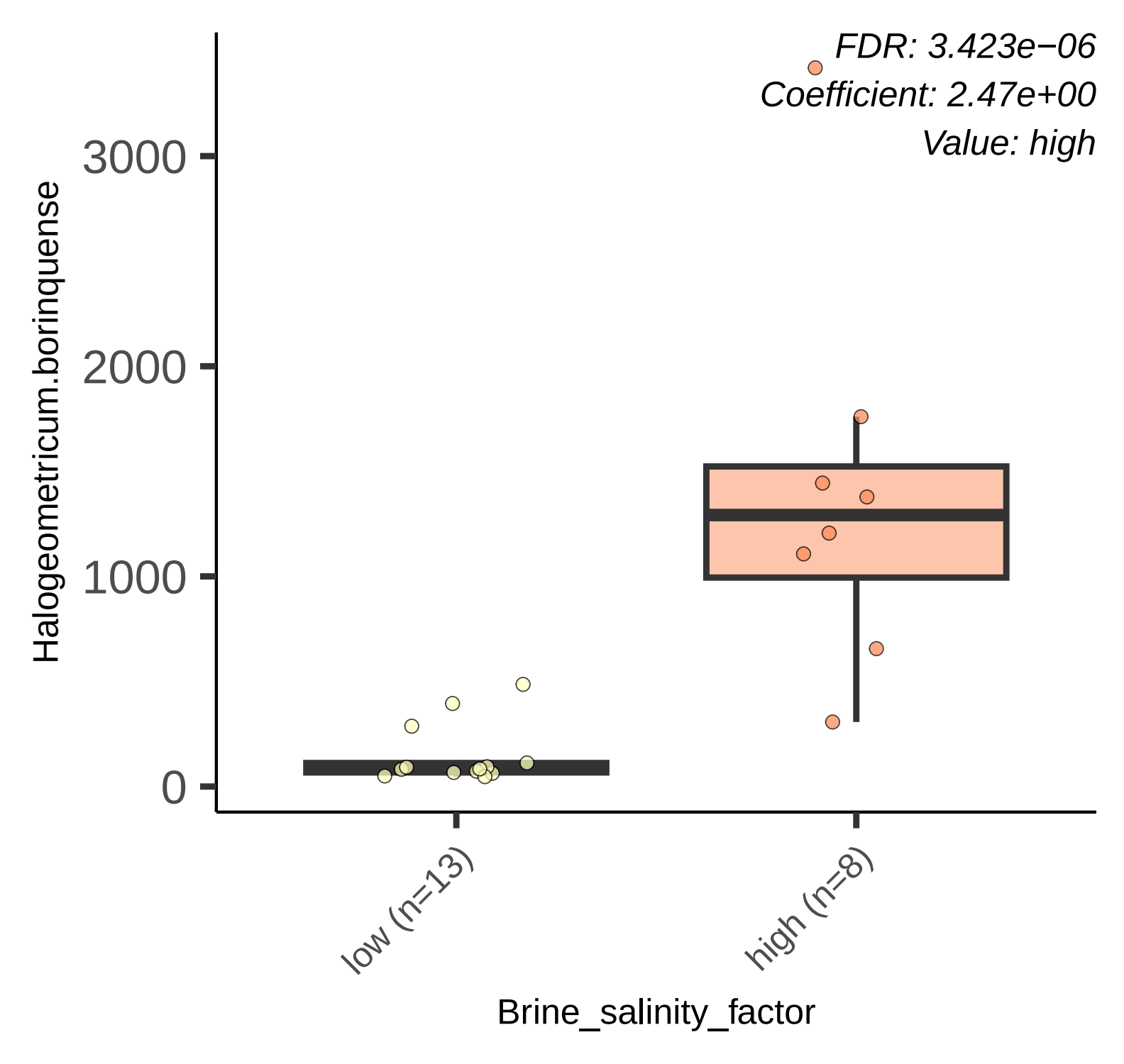

FDR: 8.493e−07
Coefficient: −3.01e+00
Value: high
Endosymbiont.of.Kryptoperidinium.foliaceum
150
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

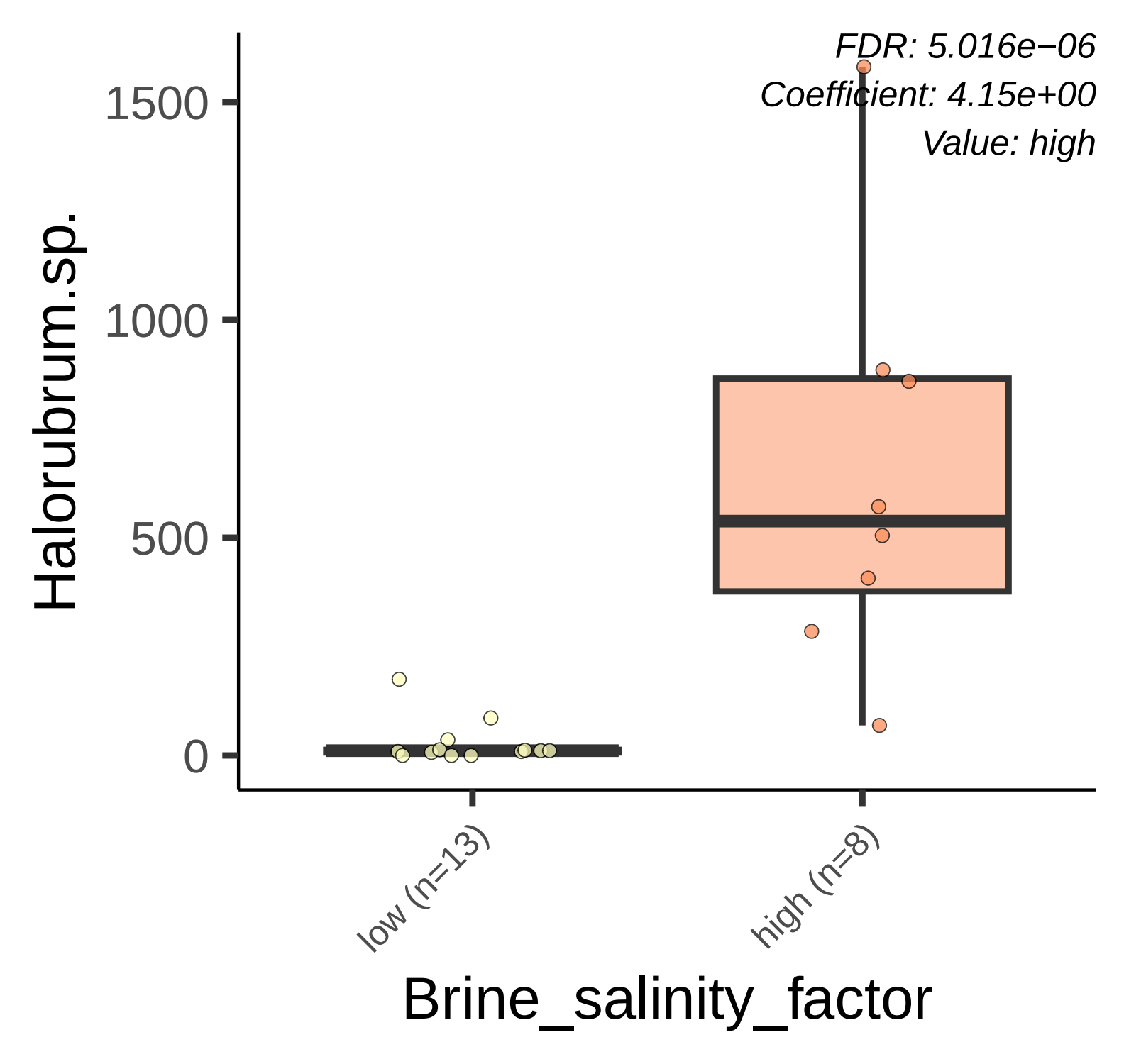

FDR: 1.151e−06
Coefficient: 2.76e+00
Value: high
Haloquadratum.walsbyi
2500
2000
1500
1000
500
0
low (n=13)
high (n=8)
Brine_salinity_factor

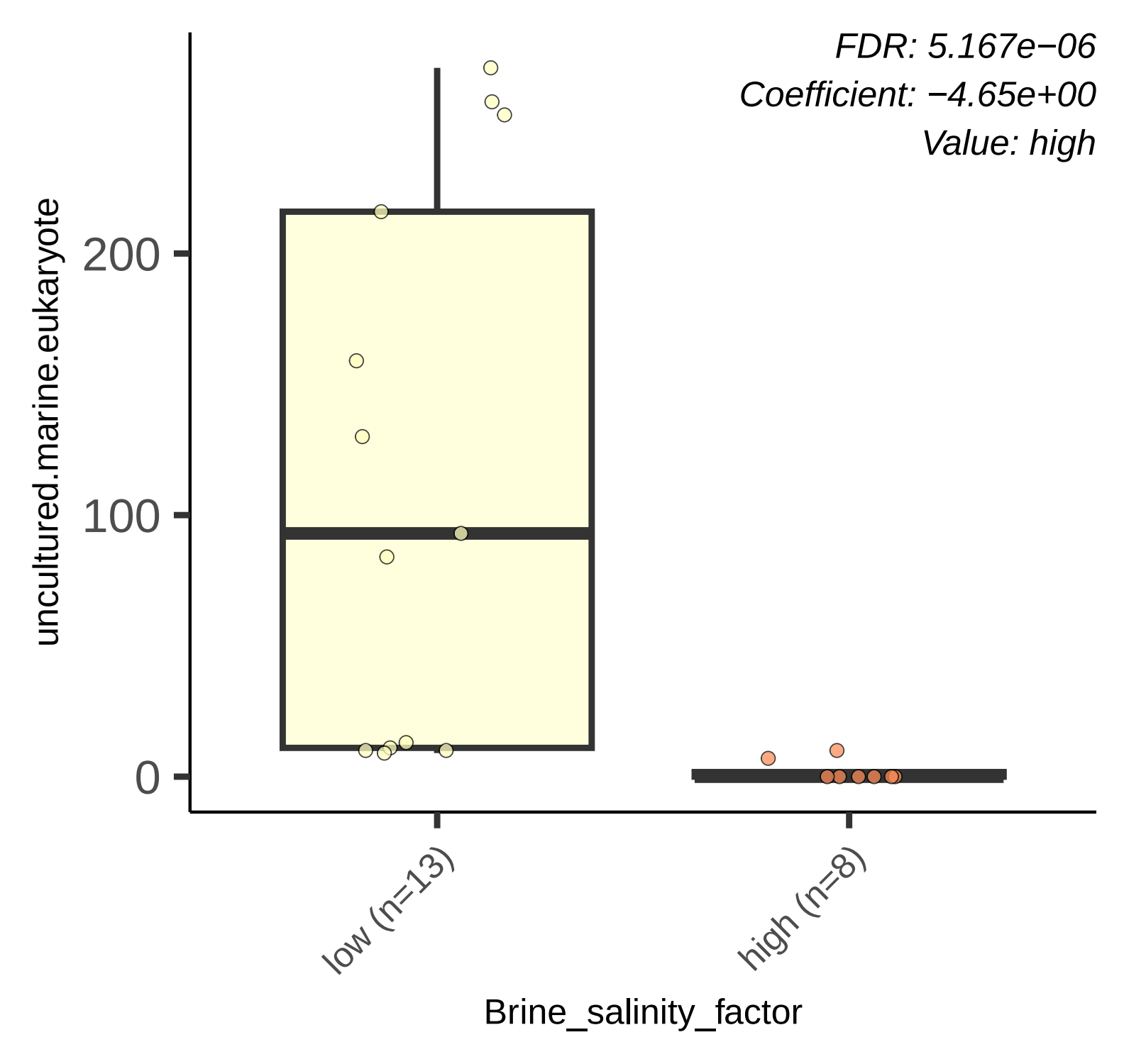

FDR: 1.267e−06
Coefficient: 3.11e+00
Value: high
2000
1500
1000
500
0
Halomicrobium.mukohataei
low (n=13)
high (n=8)
Brine_salinity_factor

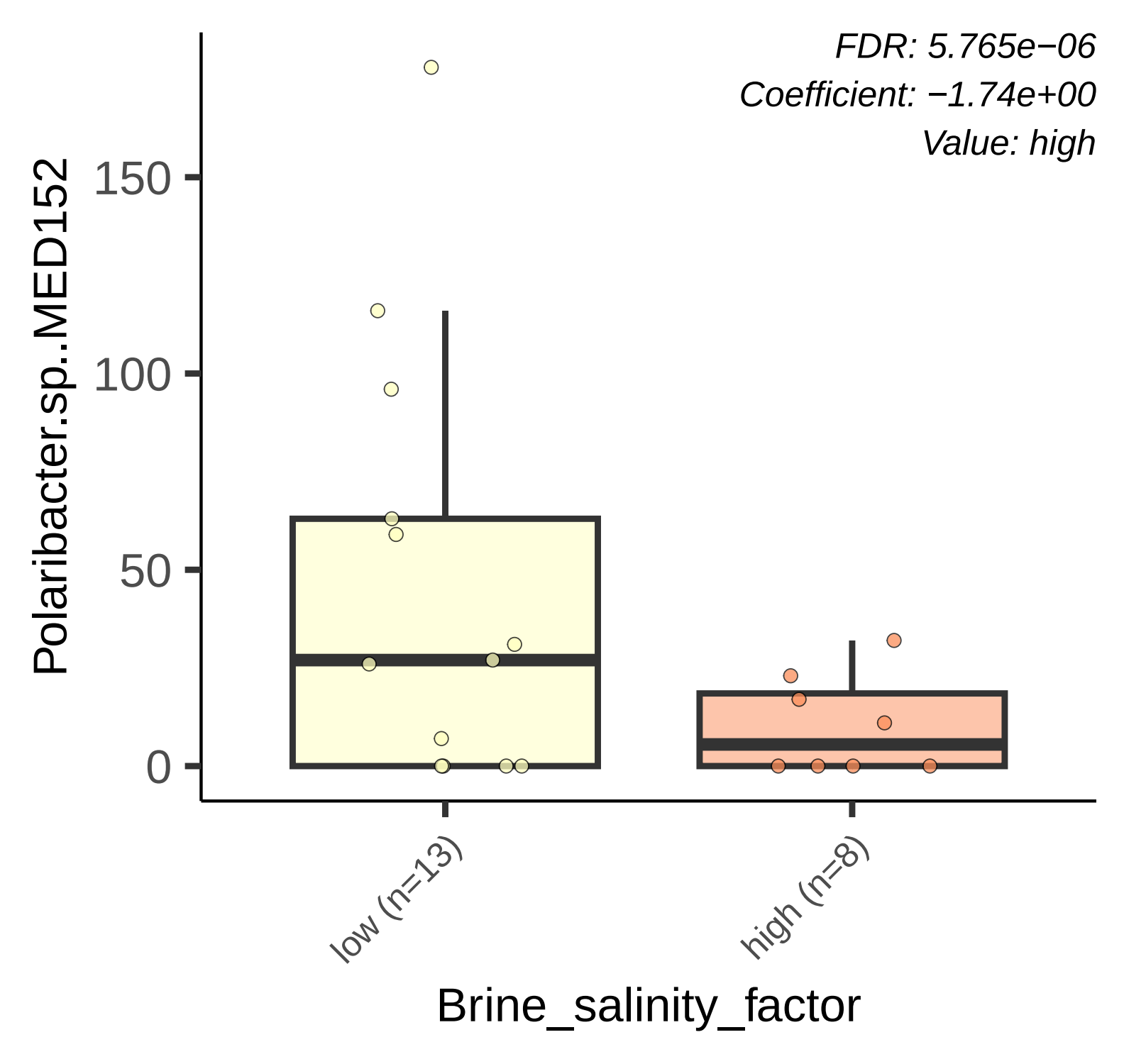

FDR: 2.000e−06
Coefficient: 2.72e+00
Value: high
3000
2000
1000
0
Halopenitus.persicus
low (n=13)
high (n=8)
Brine_salinity_factor

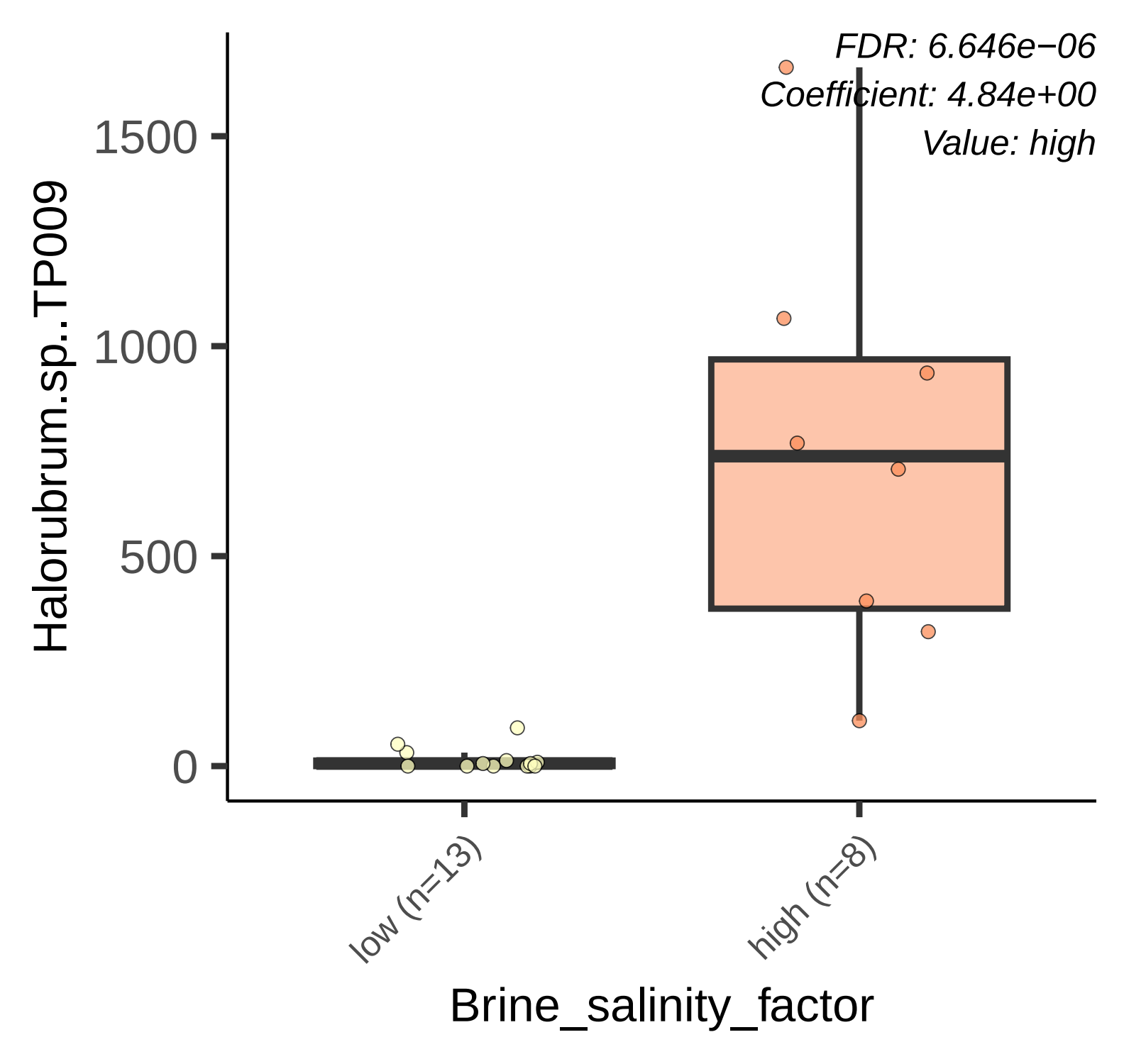

FDR: 2.255e−06
Coefficient: 2.43e+00
Value: high
2500
2000
1500
1000
500
0
halophilic.archaeon.DL31
low (n=13)
high (n=8)
Brine_salinity_factor

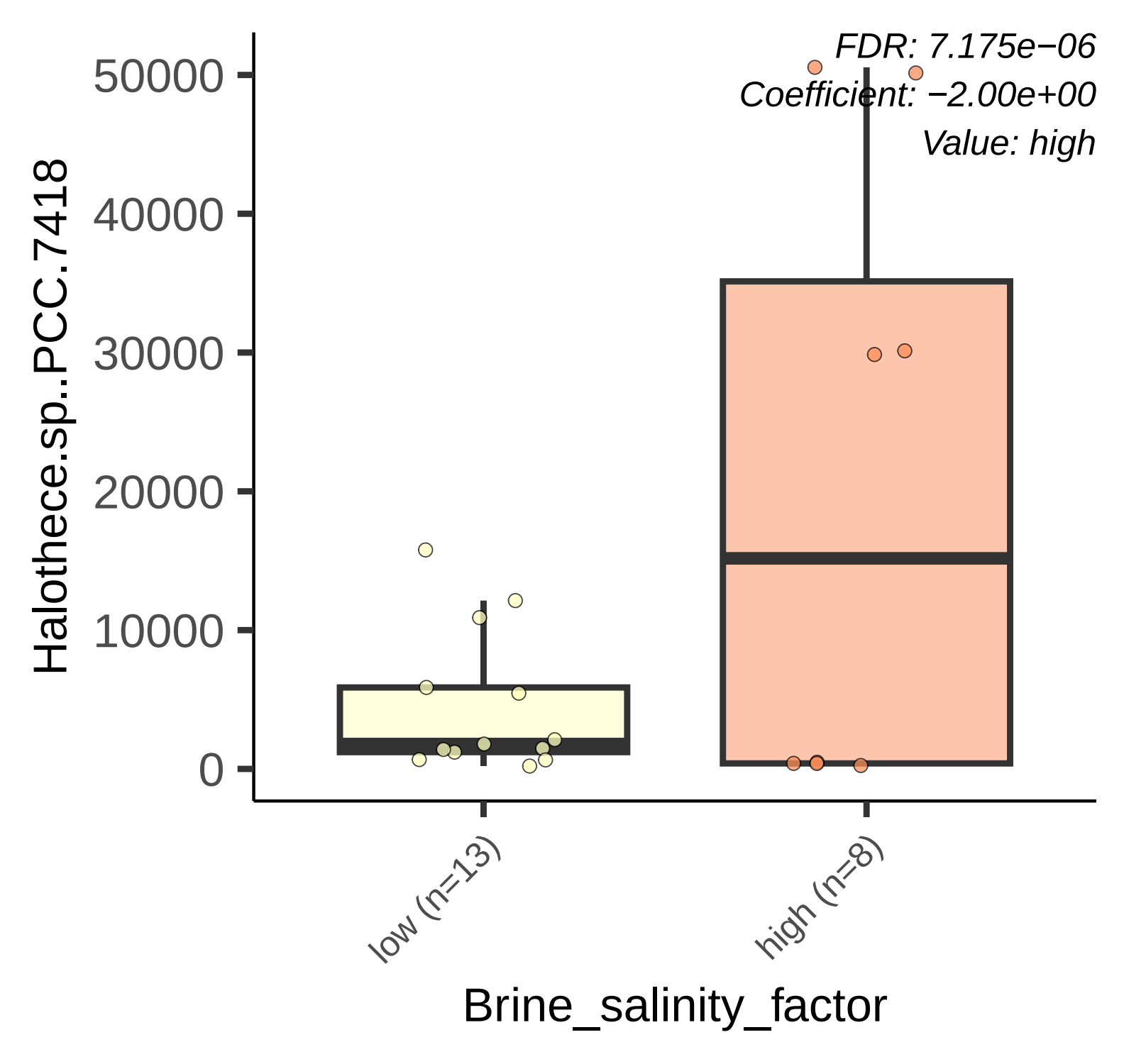

FDR: 3.423e−06
Coefficient: 2.47e+00
Value: high
Halogeometricum.borinquense
3000
2000
1000
0
low (n=13)
high (n=8)
Brine_salinity_factor

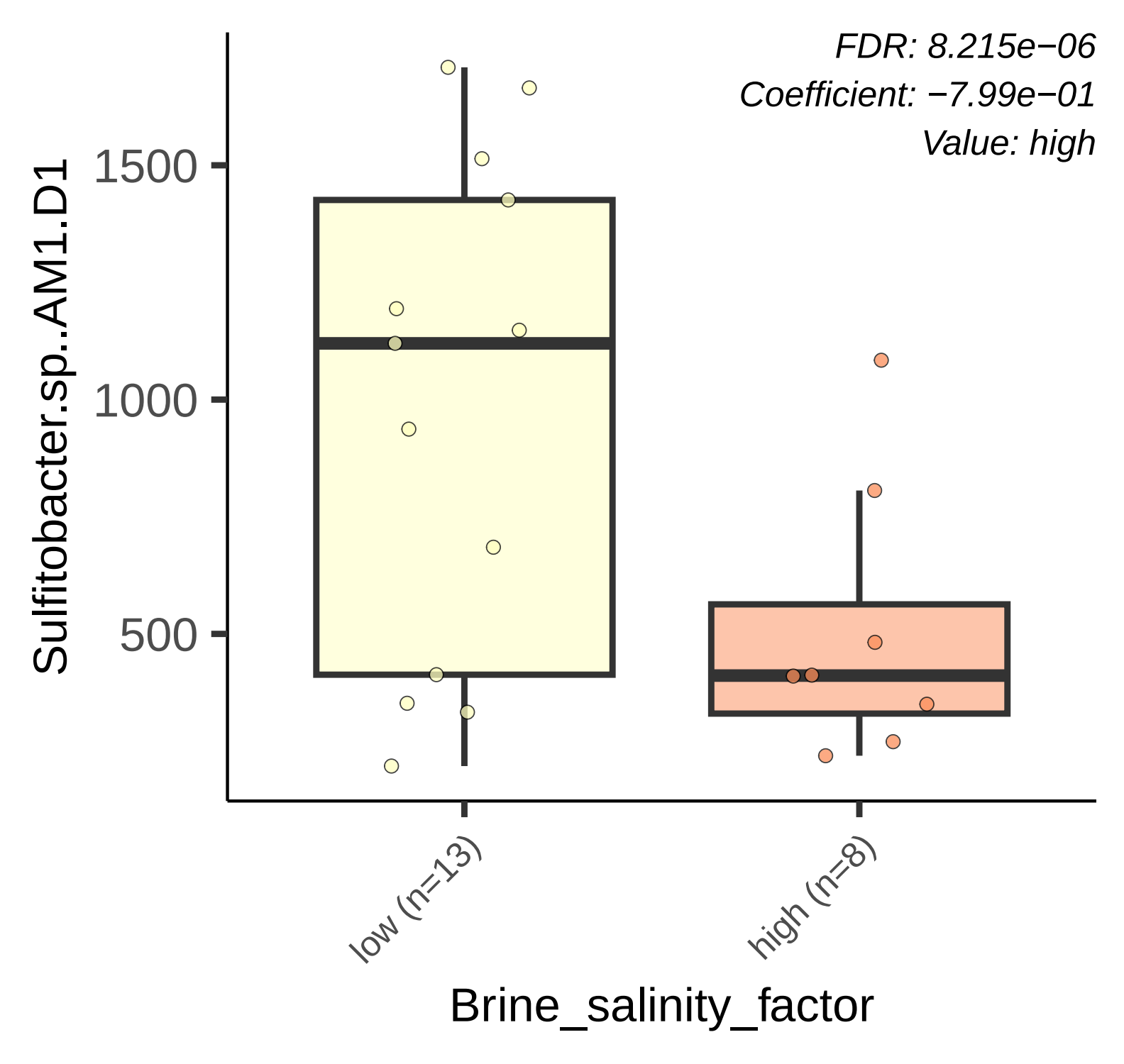

FDR: 5.016e−06
Coefficient: 4.15e+00
Value: high
Halorubrum.sp.
1500
1000
500
0
low (n=13)
high (n=8)
Brine_salinity_factor

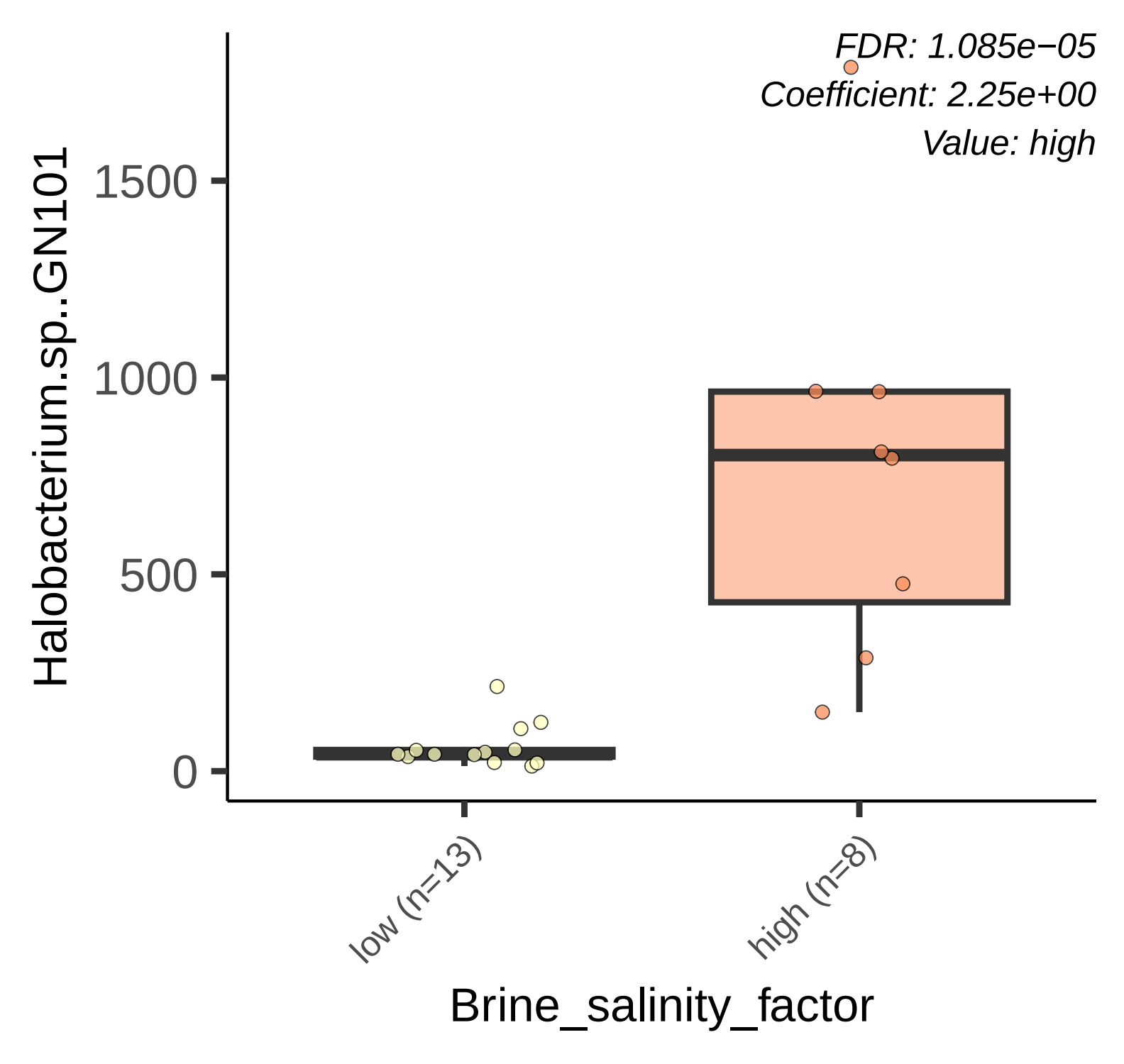

FDR: 5.167e−06
Coefficient: −4.65e+00
Value: high
uncultured.marine.eukaryote
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

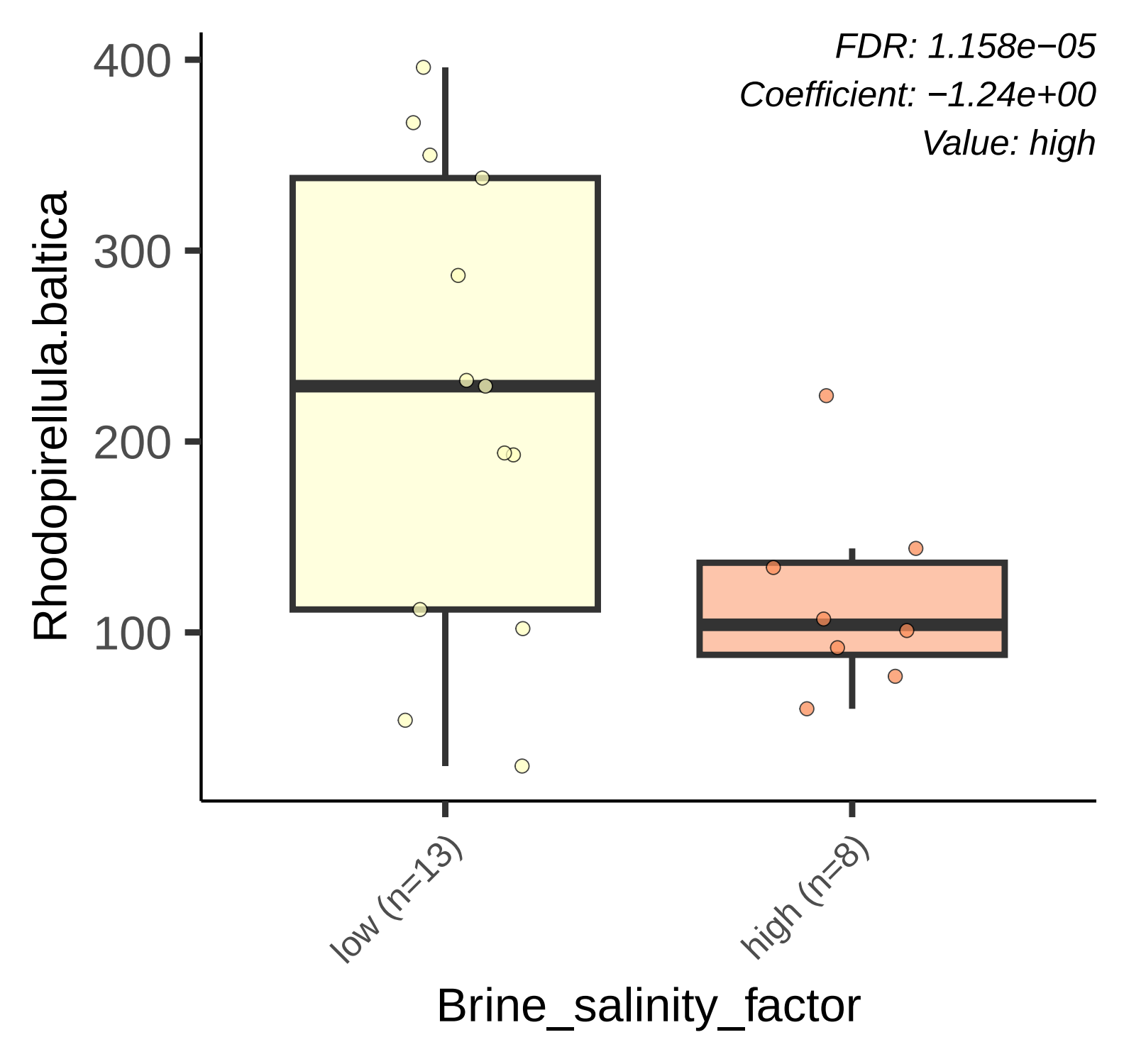

FDR: 5.765e−06
Coefficient: −1.74e+00
Value: high
Polaribacter.sp..MED152
150
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

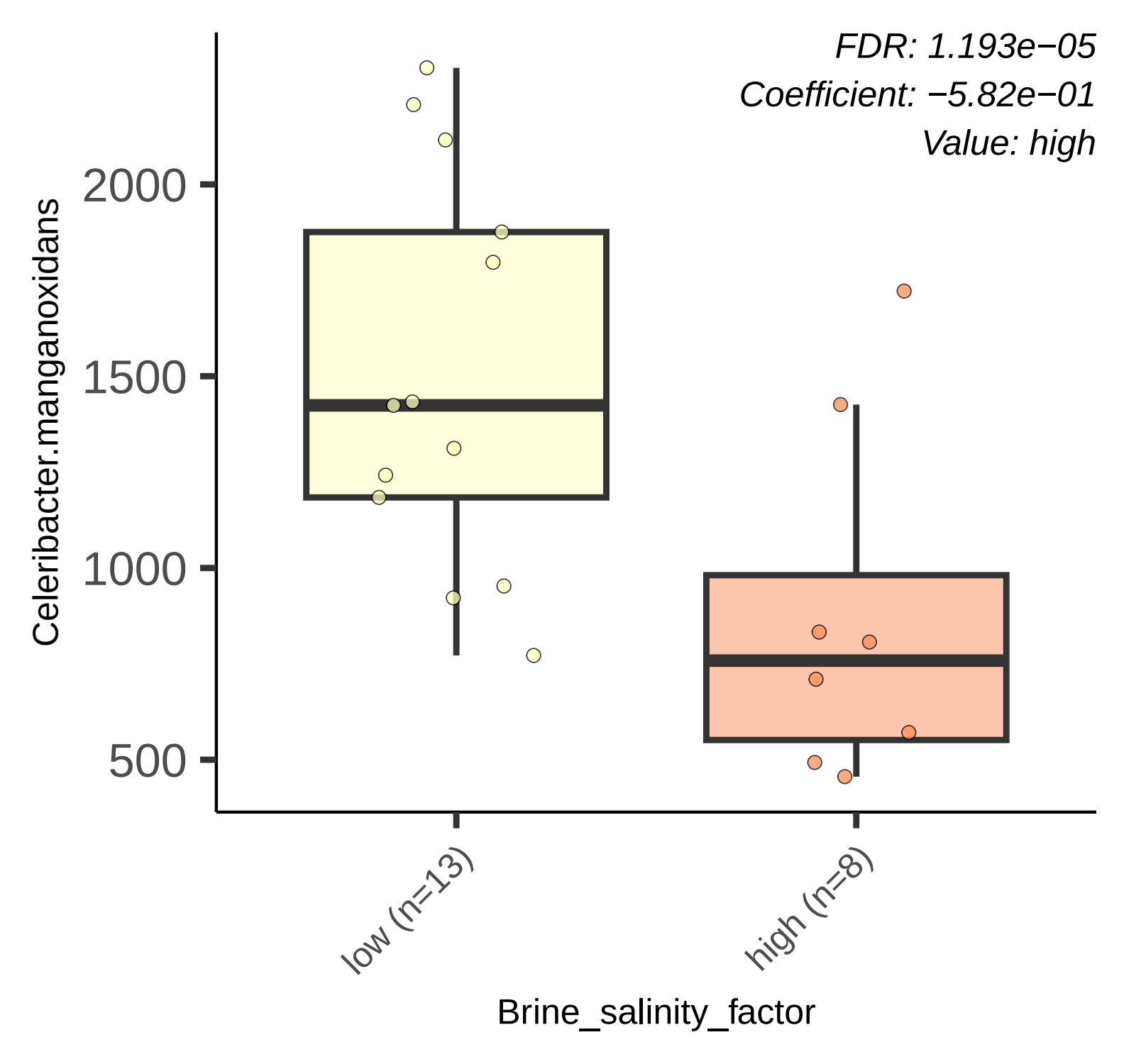

FDR: 6.646e−06
Coefficient: 4.84e+00
Value: high
Halorubrum.sp..TP009
1500
1000
500
0
low (n=13)
high (n=8)
Brine_salinity_factor

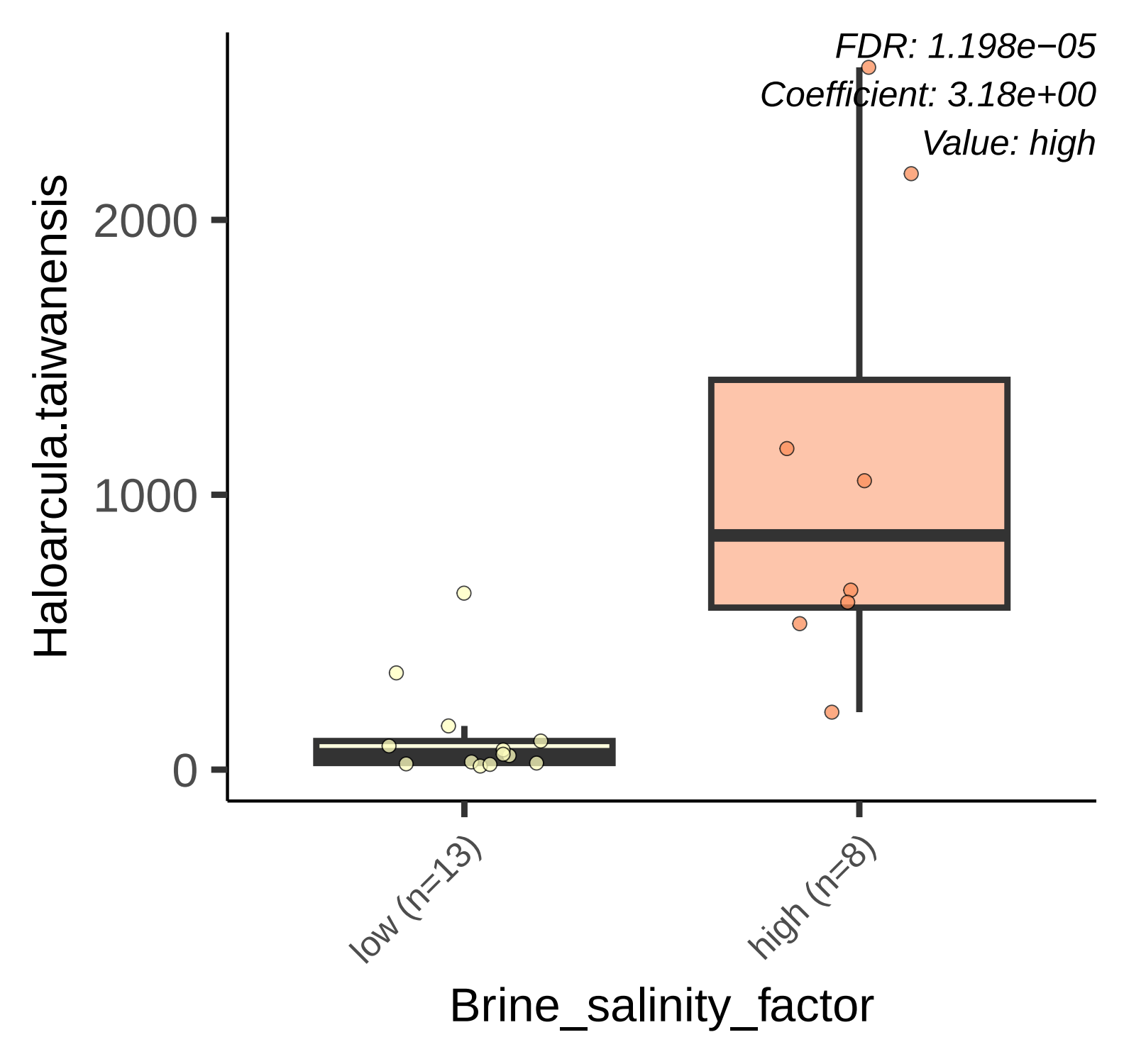

FDR: 7.175e−06
Coefficient: −2.00e+00
Value: high
50000
40000
30000
20000
10000
0
Halothece.sp..PCC.7418
low (n=13)
high (n=8)
Brine_salinity_factor

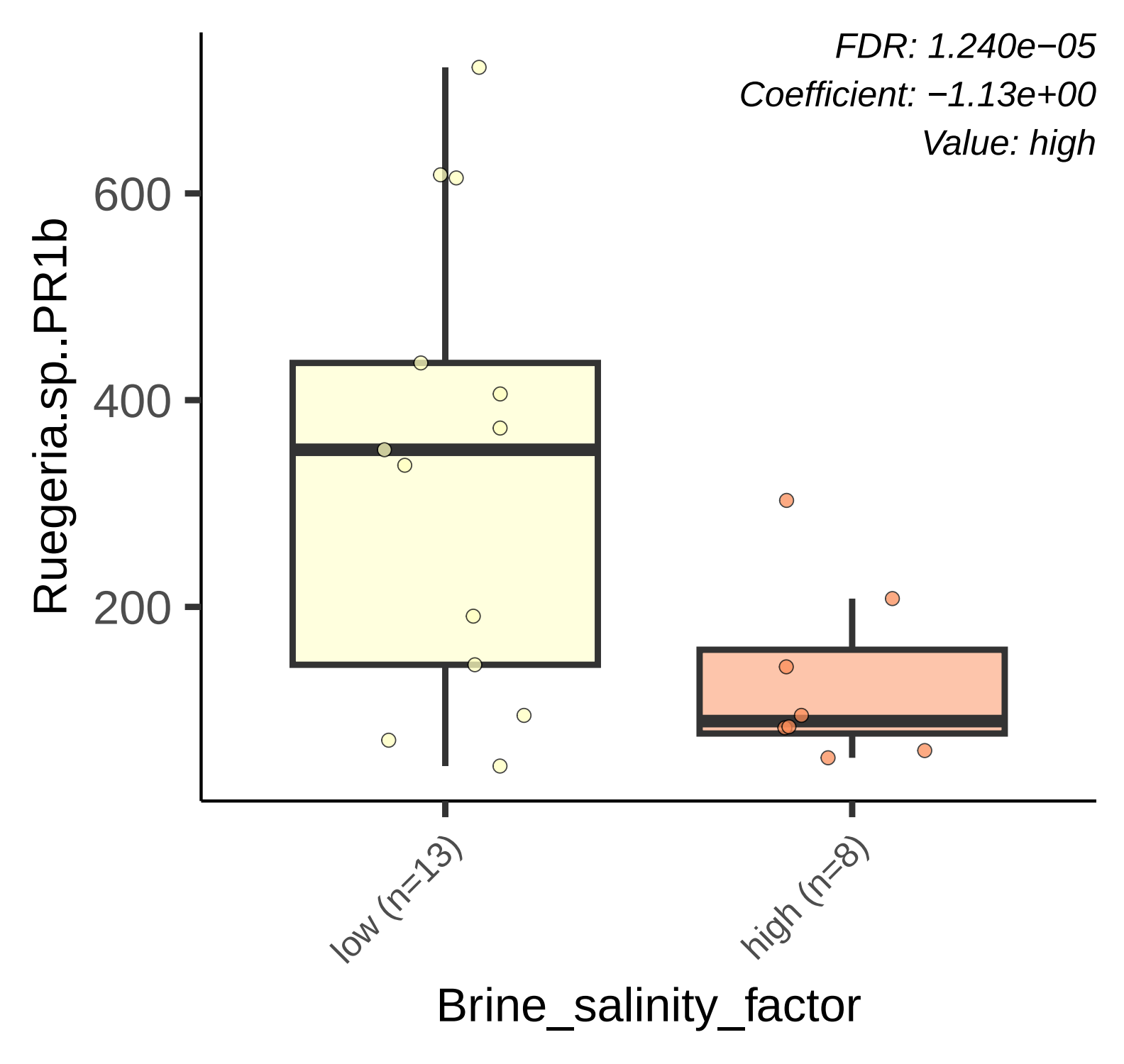

FDR: 8.215e−06
Coefficient: −7.99e−01
Value: high
Sulfitobacter.sp..AM1.D1
1500
1000
500
low (n=13)
high (n=8)
Brine_salinity_factor

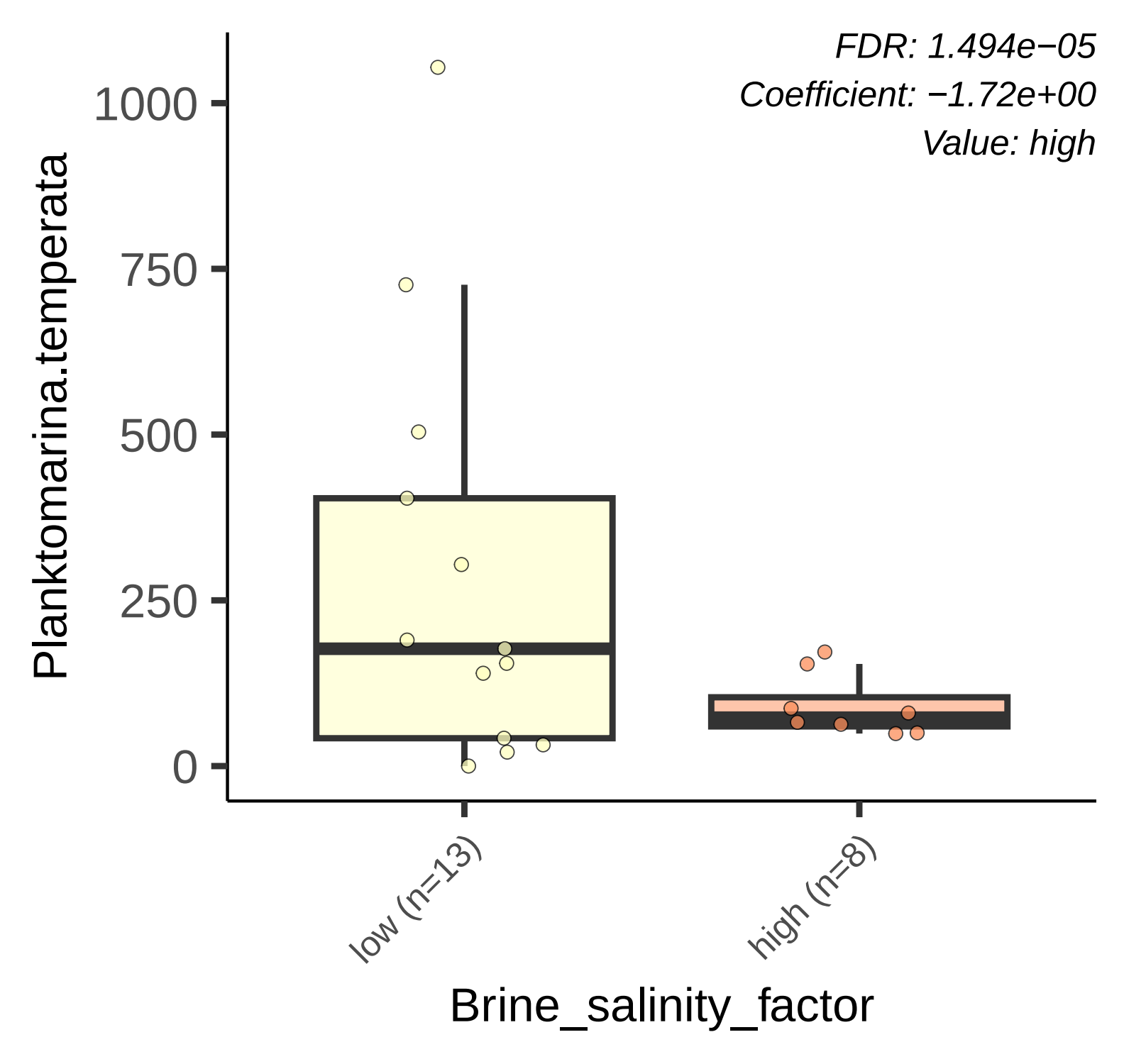

FDR: 1.085e−05
Coefficient: 2.25e+00
Value: high
Halobacterium.sp..GN101
1500
1000
500
0
low (n=13)
high (n=8)
Brine_salinity_factor

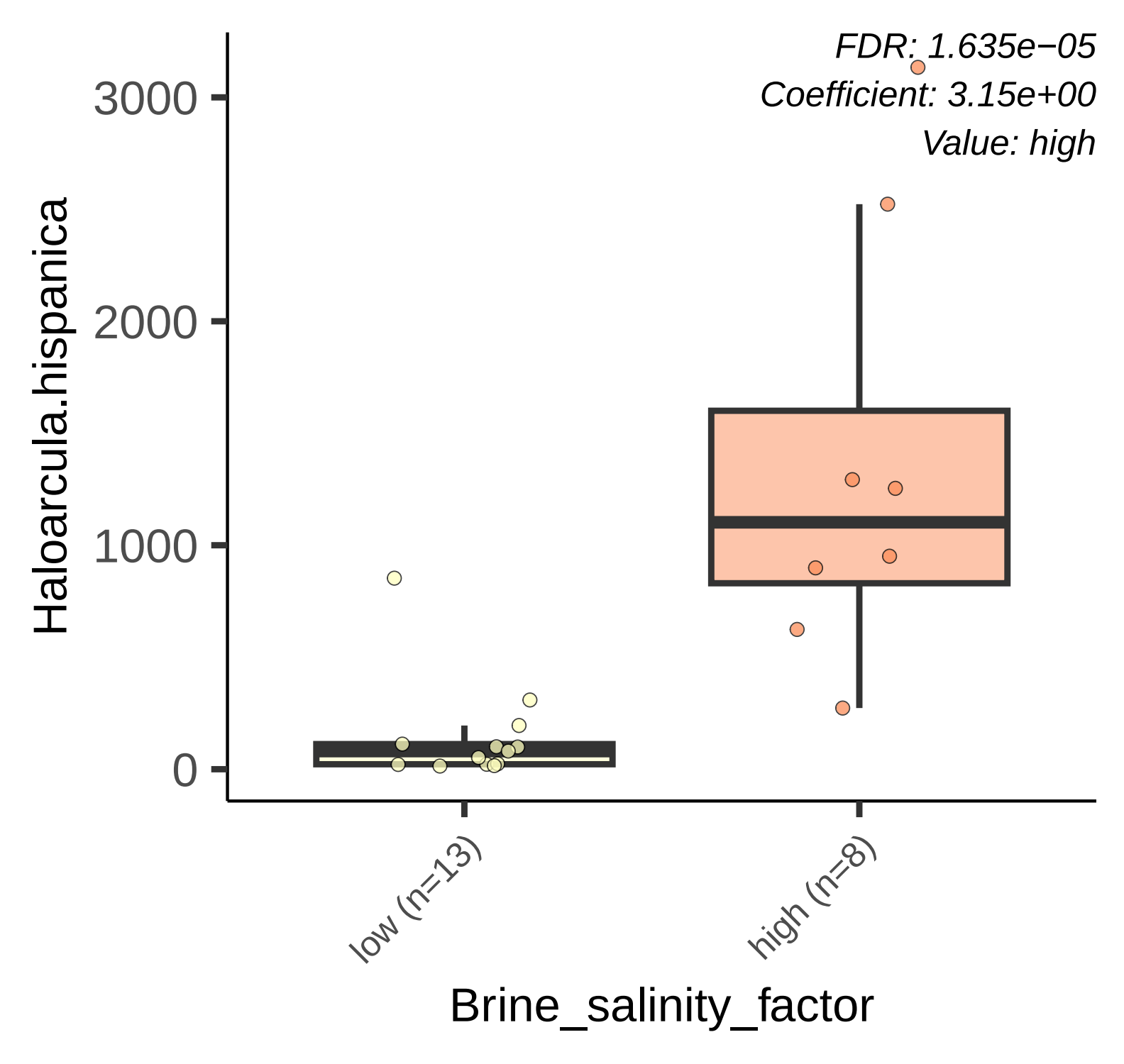

FDR: 1.158e−05
Coefficient: −1.24e+00
Value: high
Rhodopirellula.baltica
400
300
200
100
low (n=13)
high (n=8)
Brine_salinity_factor

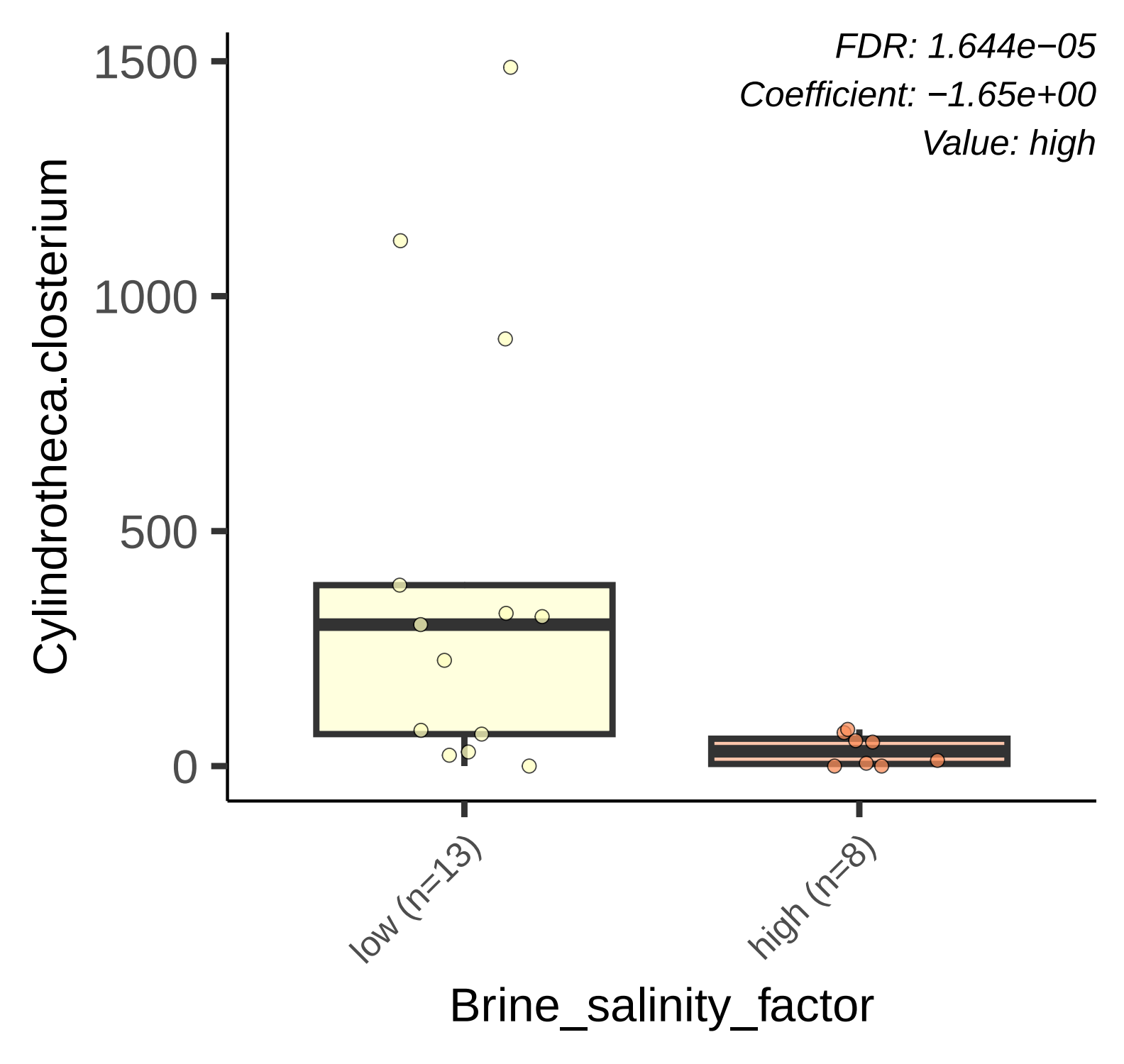

FDR: 1.193e−05
Coefficient: −5.82e−01
Value: high
Celeribacter.manganoxidans
2000
1500
1000
500
low (n=13)
high (n=8)
Brine_salinity_factor

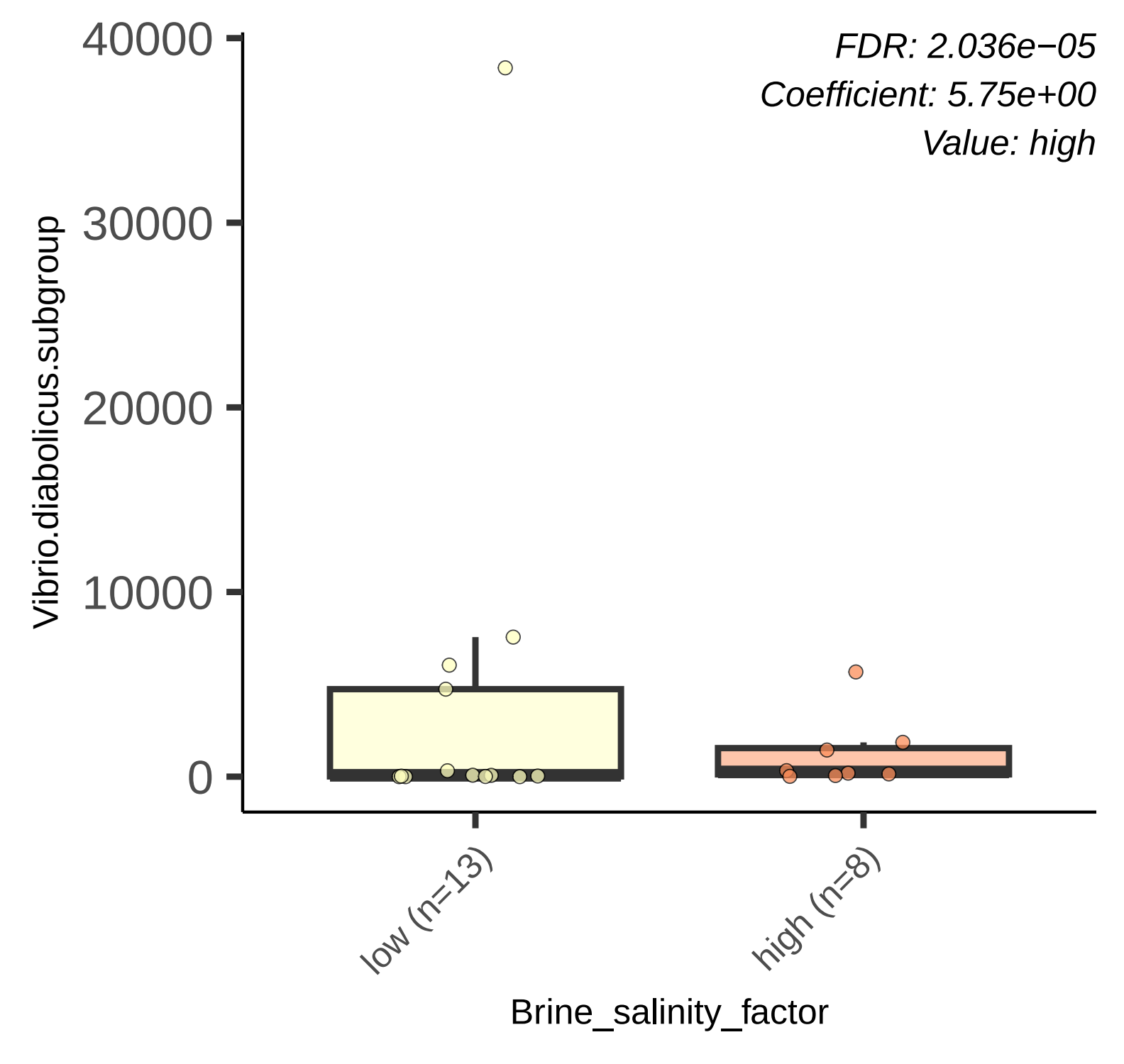

FDR: 1.198e−05
Coefficient: 3.18e+00
Value: high
Haloarcula.taiwanensis
2000
1000
0
low (n=13)
high (n=8)
Brine_salinity_factor

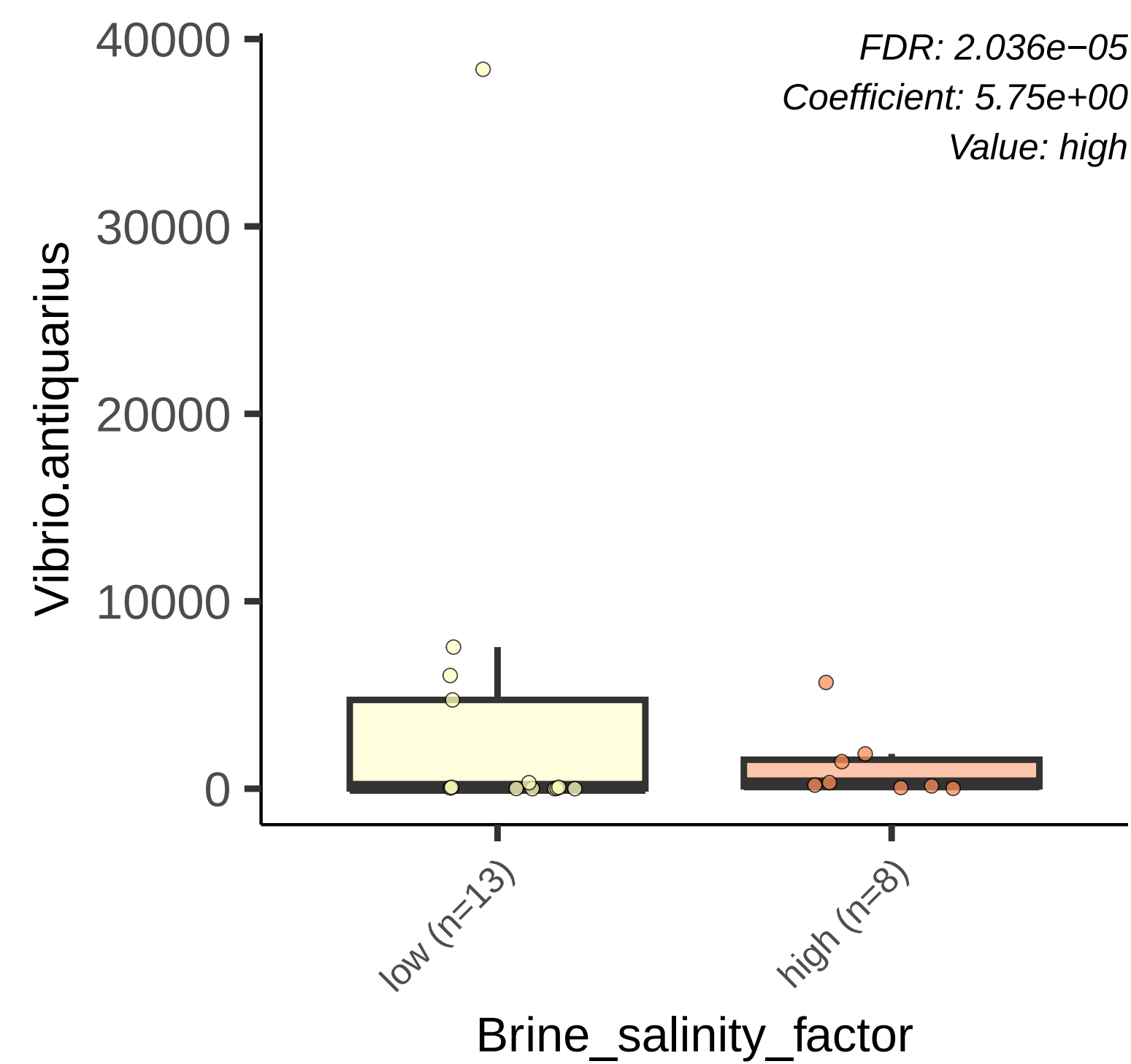

FDR: 1.240e−05
Coefficient: −1.13e+00
Value: high
Ruegeria.sp..PR1b
600
400
200
low (n=13)
high (n=8)
Brine_salinity_factor

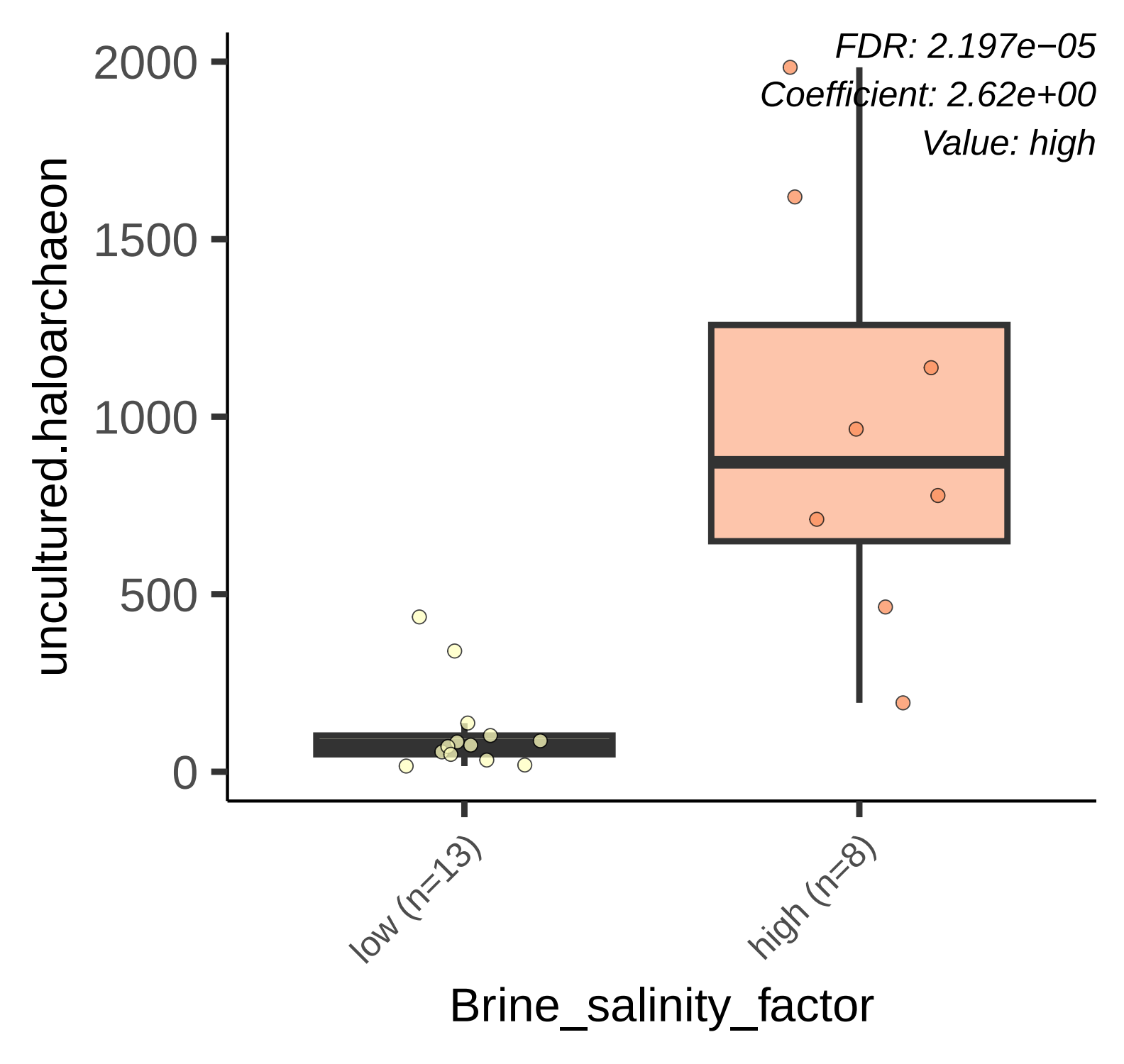

FDR: 1.494e−05
Coefficient: −1.72e+00
Value: high
Planktomarina.temperata
1000
750
500
250
0
low (n=13)
high (n=8)
Brine_salinity_factor

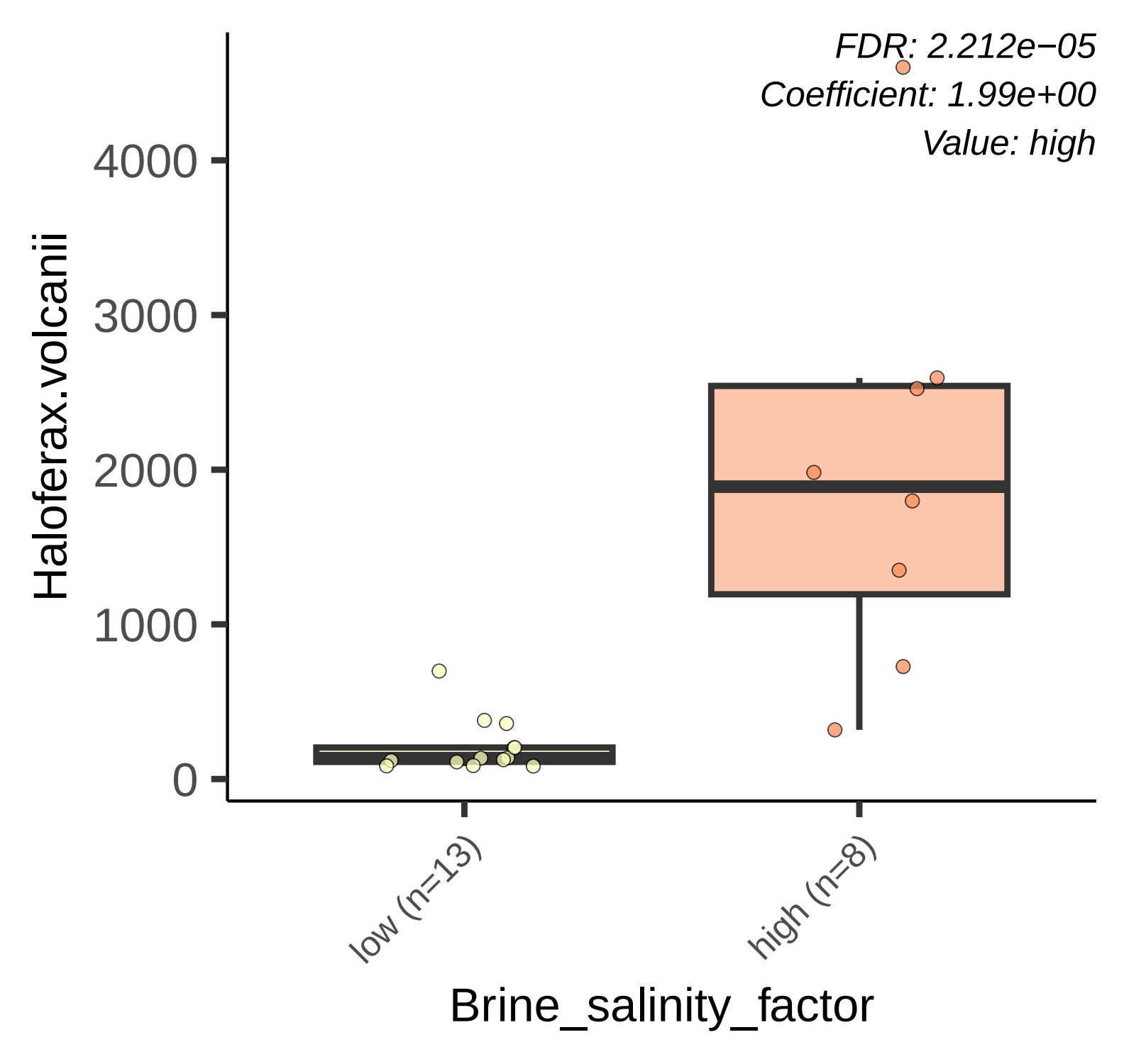

FDR: 1.635e−05
Coefficient: 3.15e+00
Value: high
3000
2000
1000
0
Haloarcula.hispanica
low (n=13)
high (n=8)
Brine_salinity_factor

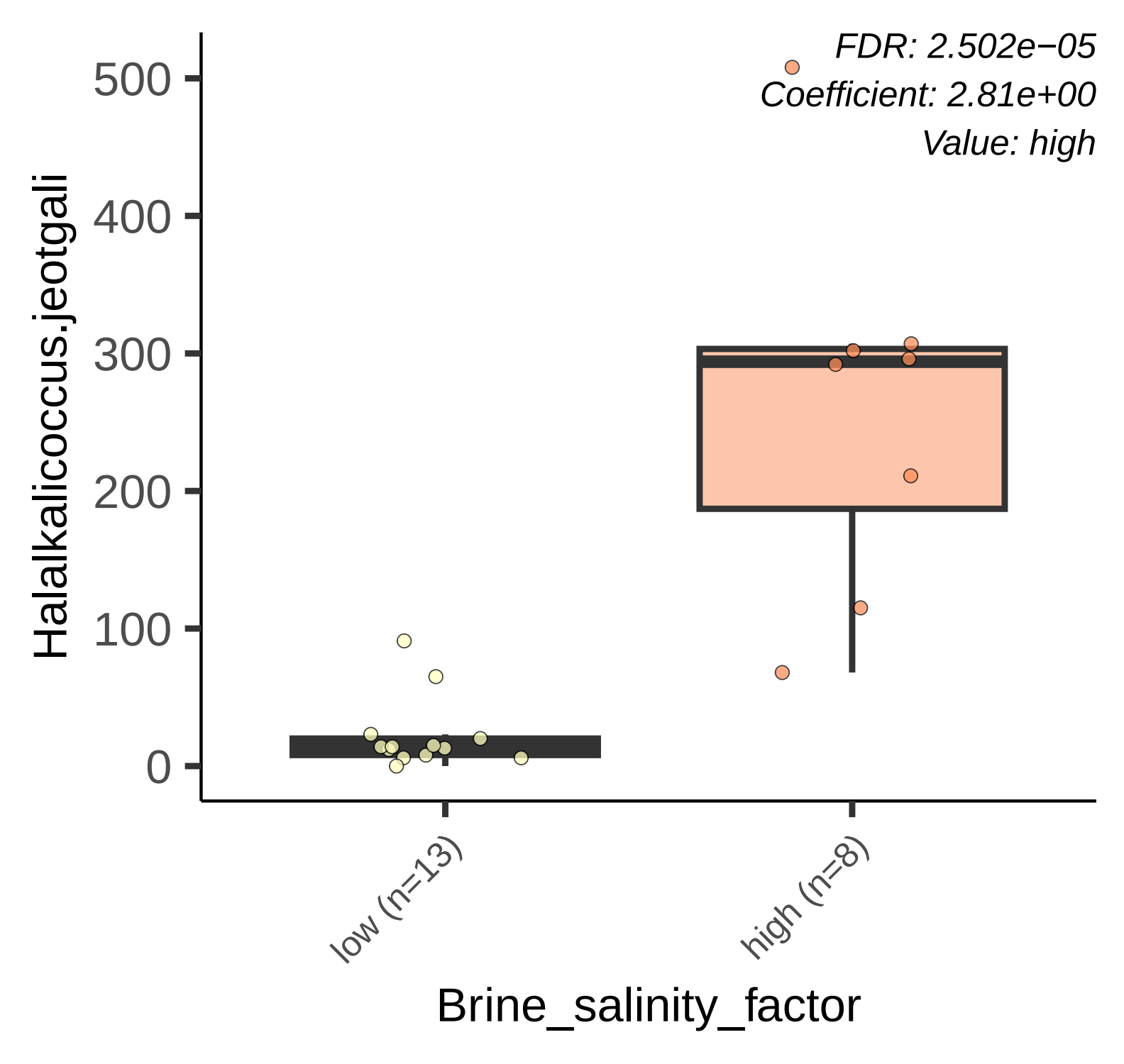

FDR: 1.644e−05
Coefficient: −1.65e+00
Value: high
1500
1000
500
0
Cylindrotheca.closterium
low (n=13)
high (n=8)
Brine_salinity_factor

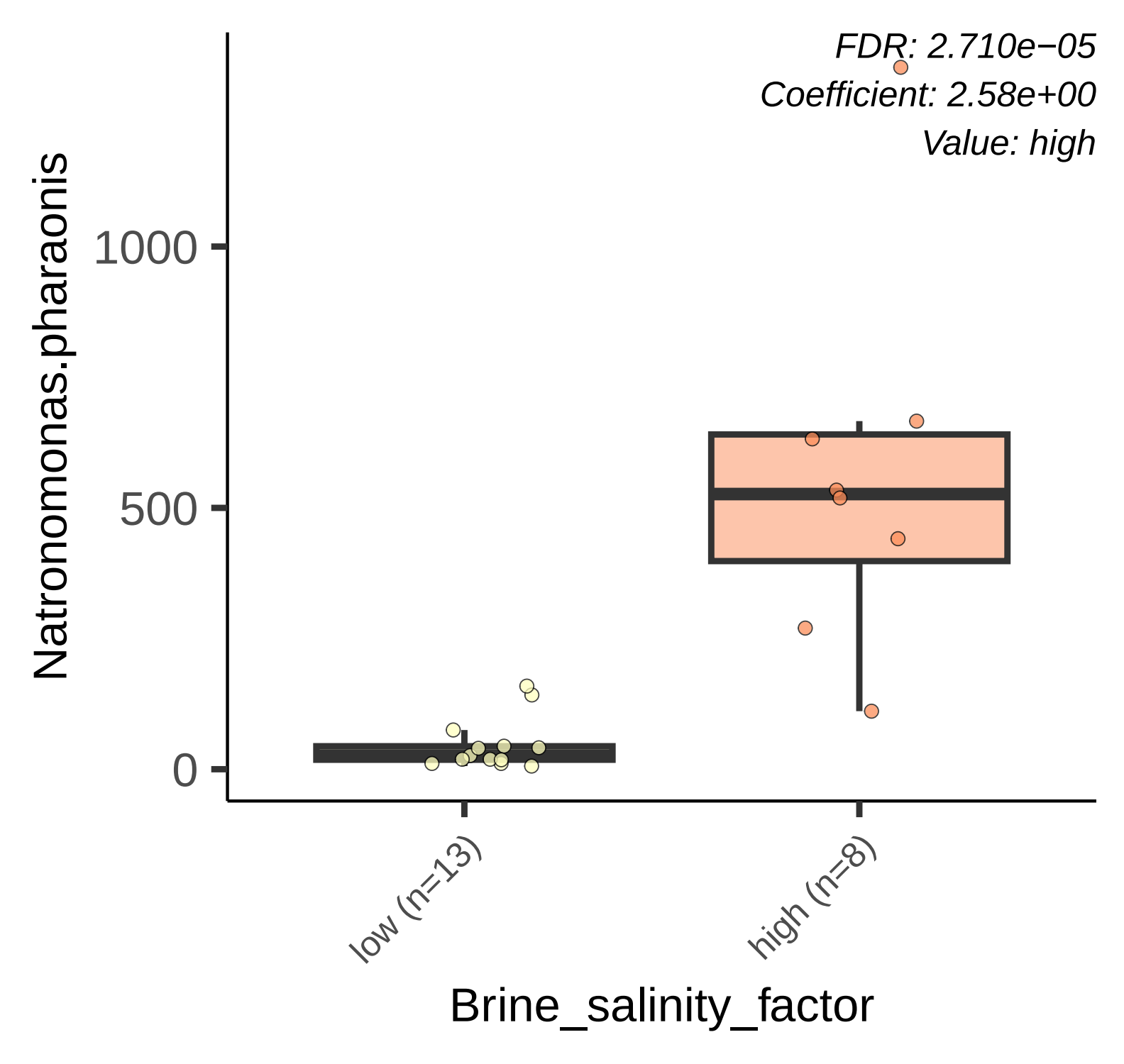

FDR: 2.036e−05
Coefficient: 5.75e+00
Value: high
40000
30000
20000
10000
0
Vibrio.diabolicus.subgroup
low (n=13)
high (n=8)
Brine_salinity_factor

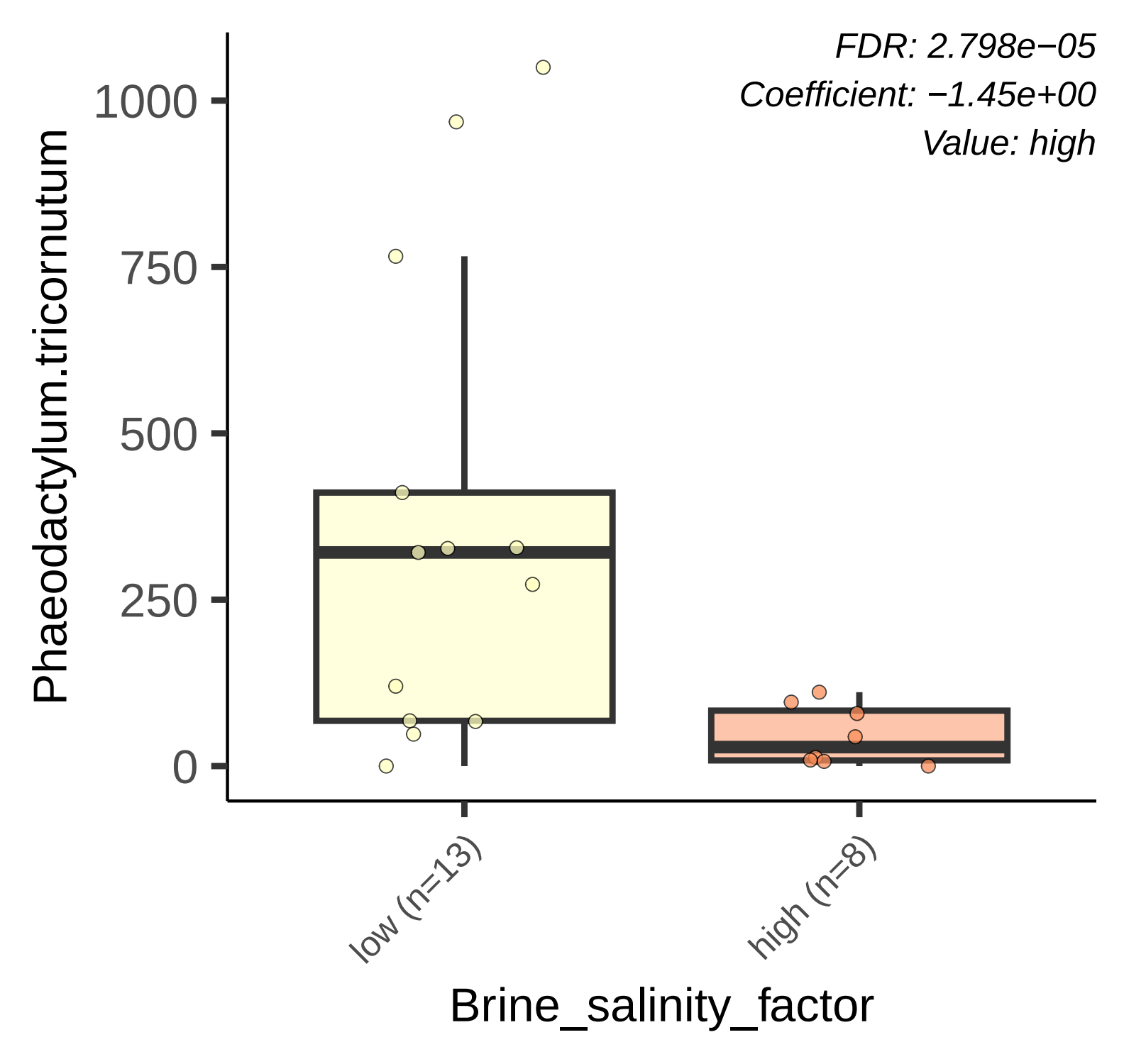

FDR: 2.036e−05
Coefficient: 5.75e+00
Value: high
Vibrio.antiquarius
40000
30000
20000
10000
0
low (n=13)
high (n=8)
Brine_salinity_factor

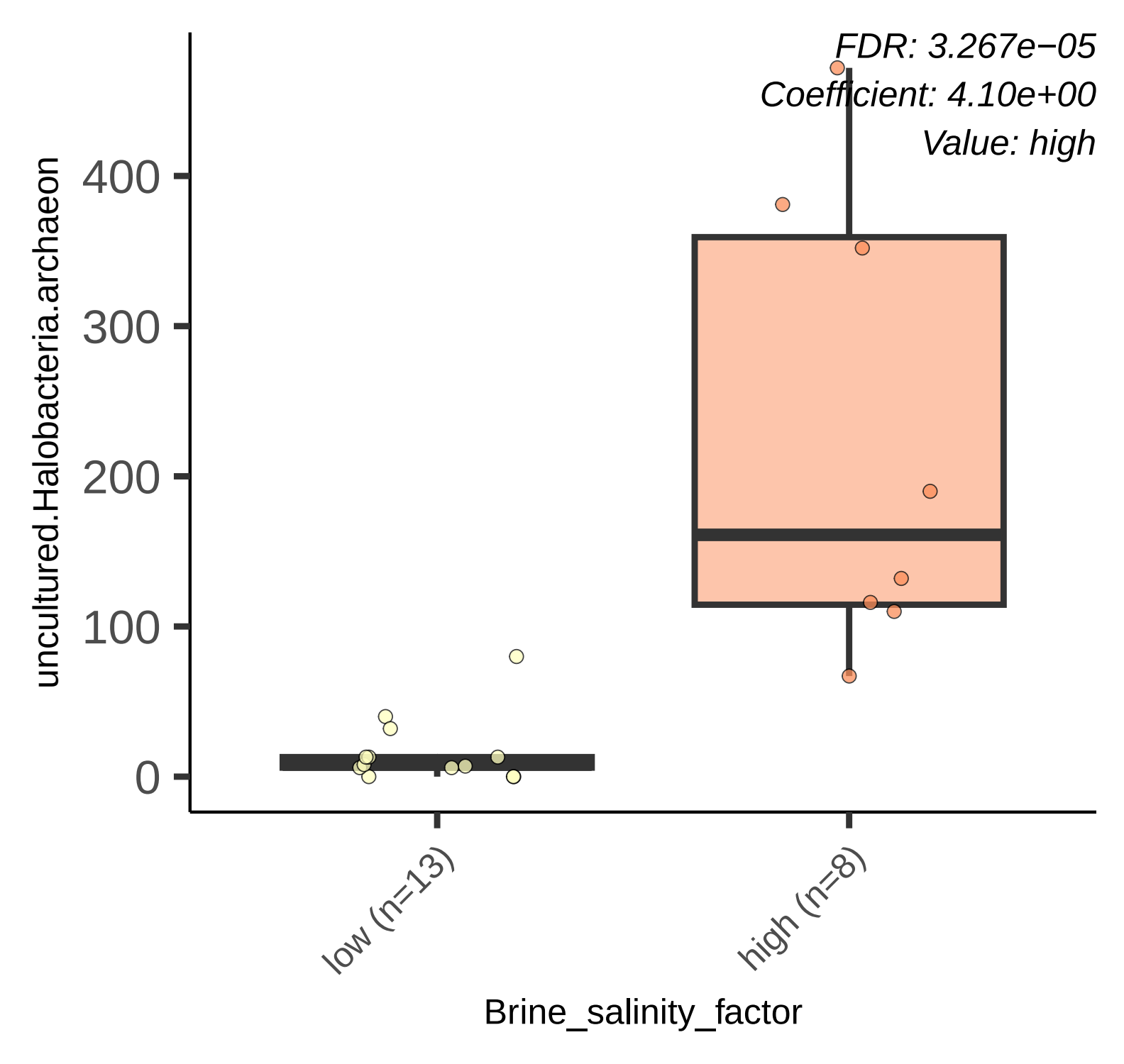

FDR: 2.197e−05
Coefficient: 2.62e+00
Value: high
2000
1500
1000
500
0
uncultured.haloarchaeon
low (n=13)
high (n=8)
Brine_salinity_factor

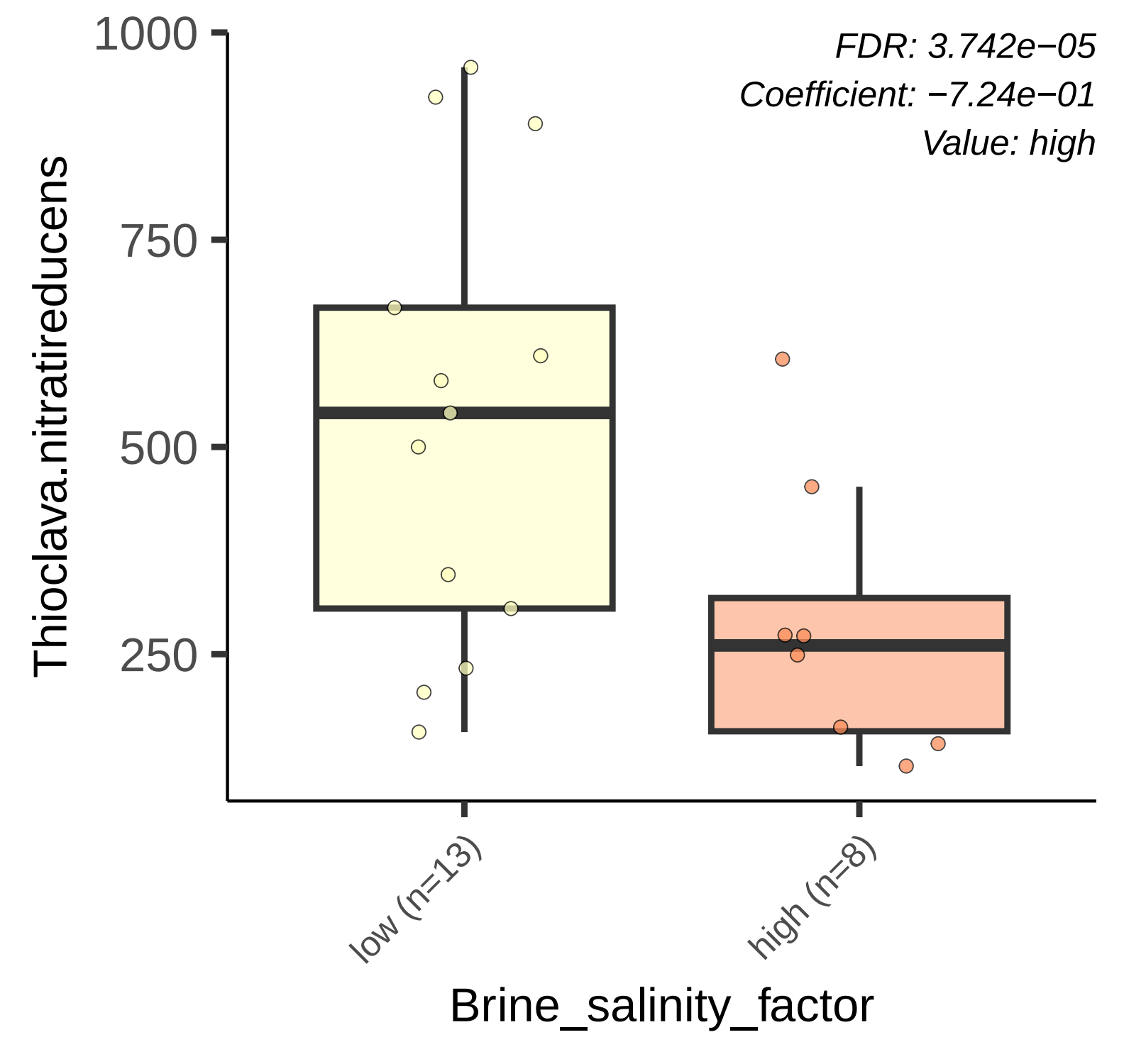

FDR: 2.212e−05
Coefficient: 1.99e+00
Value: high
Haloferax.volcanii
4000
3000
2000
1000
0
low (n=13)
high (n=8)
Brine_salinity_factor

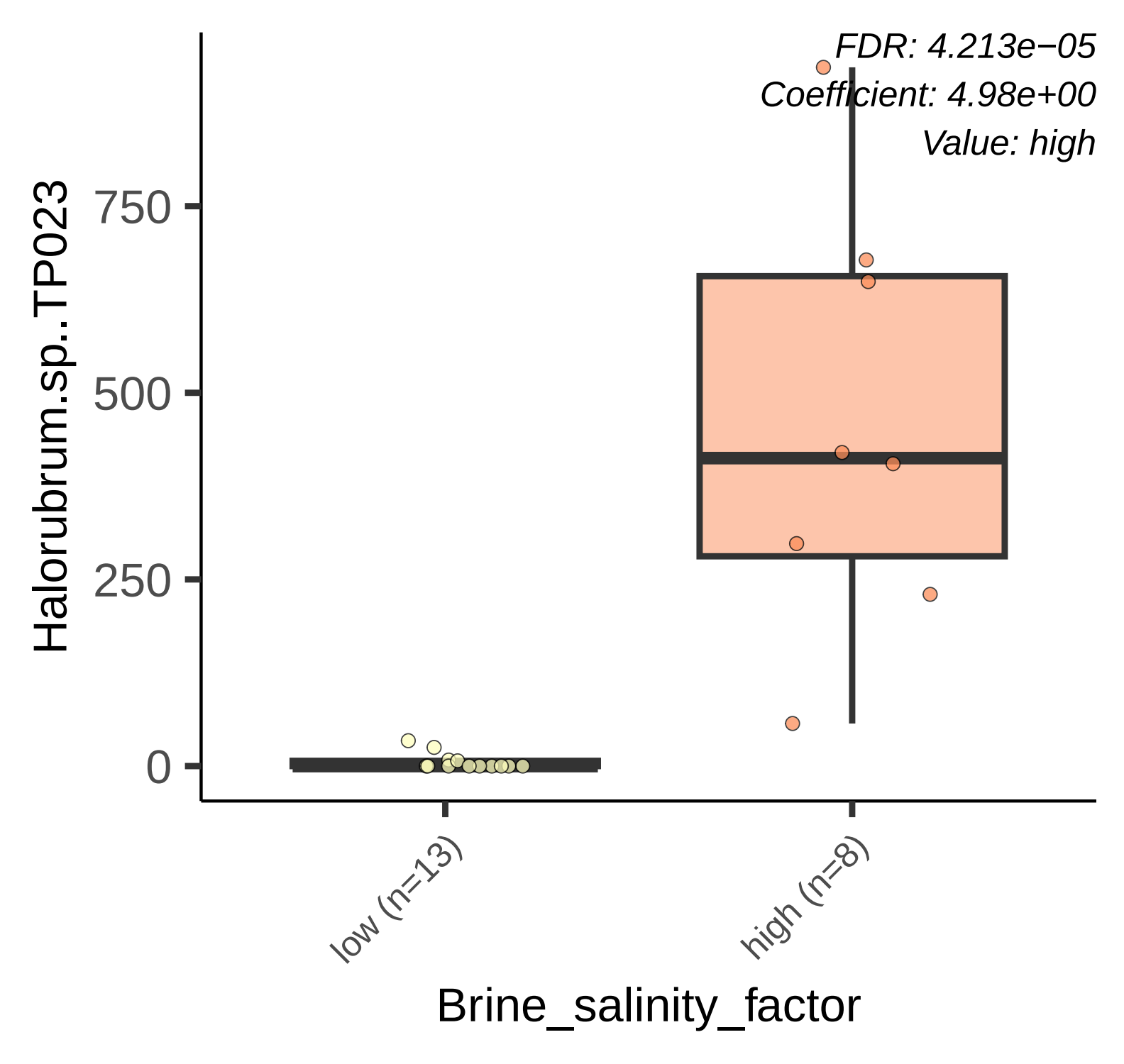

FDR: 2.502e−05
Coefficient: 2.81e+00
Value: high
Halalkalicoccus.jeotgali
500
400
300
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

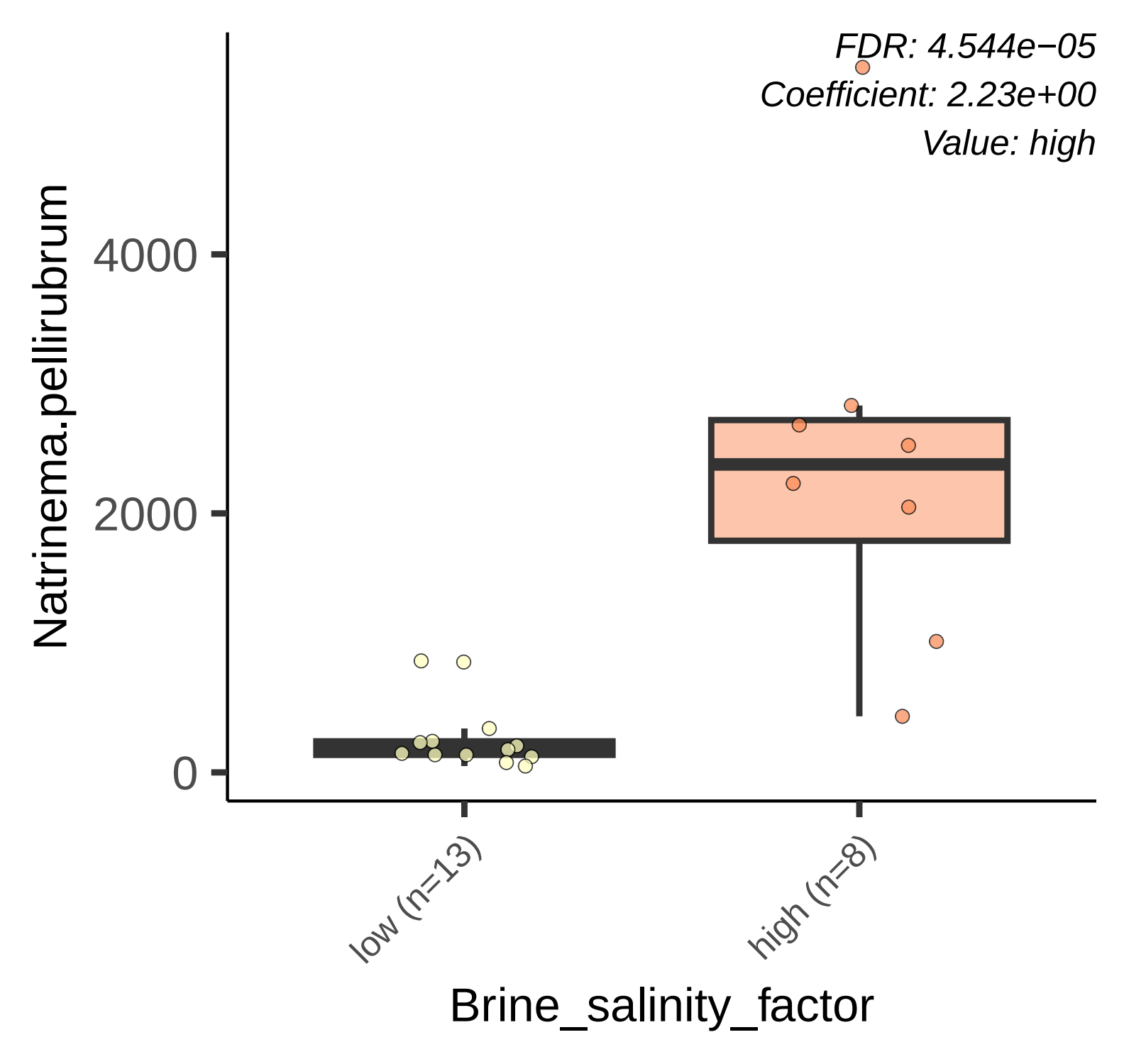

FDR: 2.710e−05
Coefficient: 2.58e+00
Value: high
Natronomonas.pharaonis
1000
500
0
low (n=13)
high (n=8)
Brine_salinity_factor

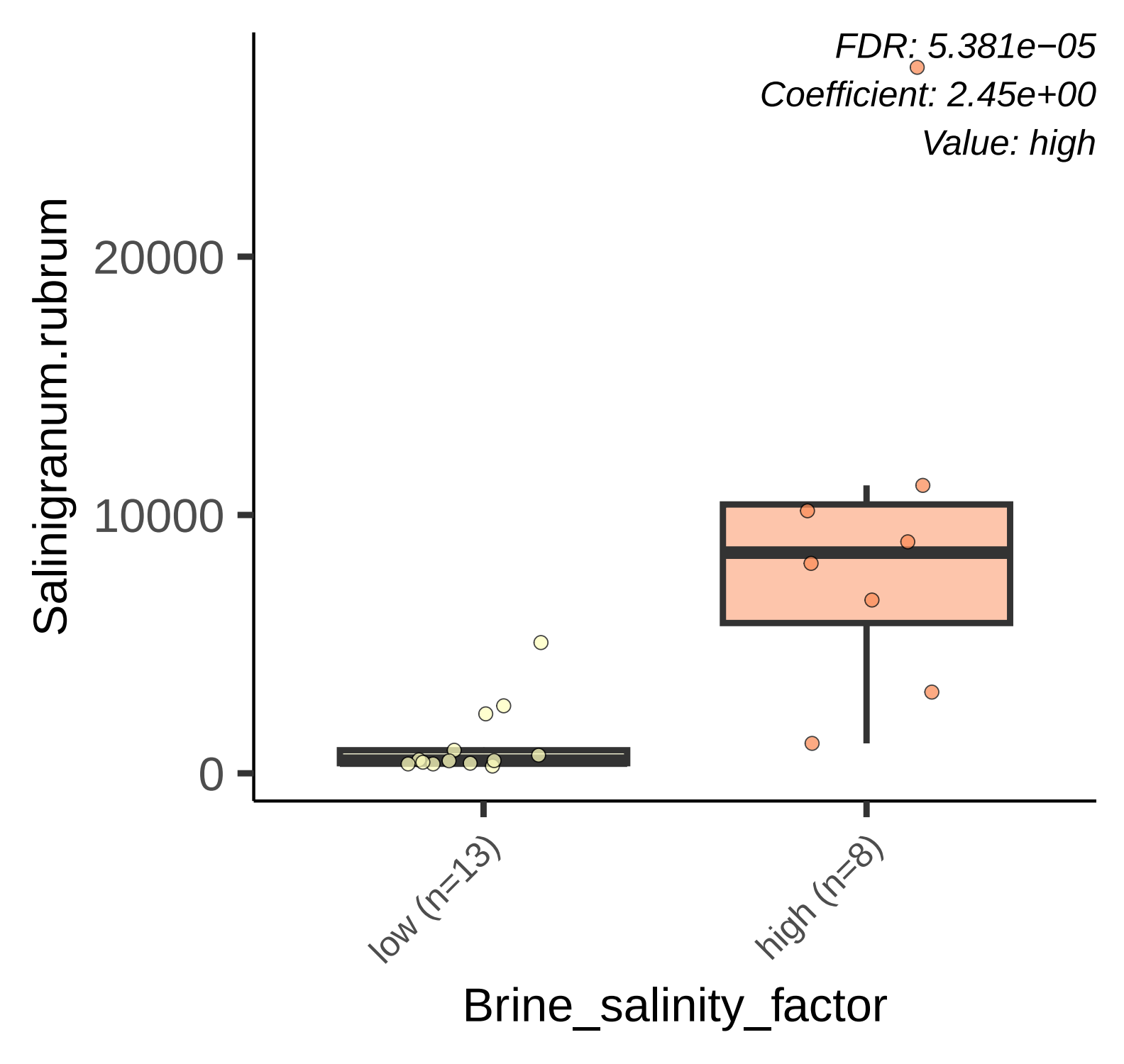

FDR: 2.798e−05
Coefficient: −1.45e+00
Value: high
1000
750
500
250
0
Phaeodactylum.tricornutum
low (n=13)
high (n=8)
Brine_salinity_factor

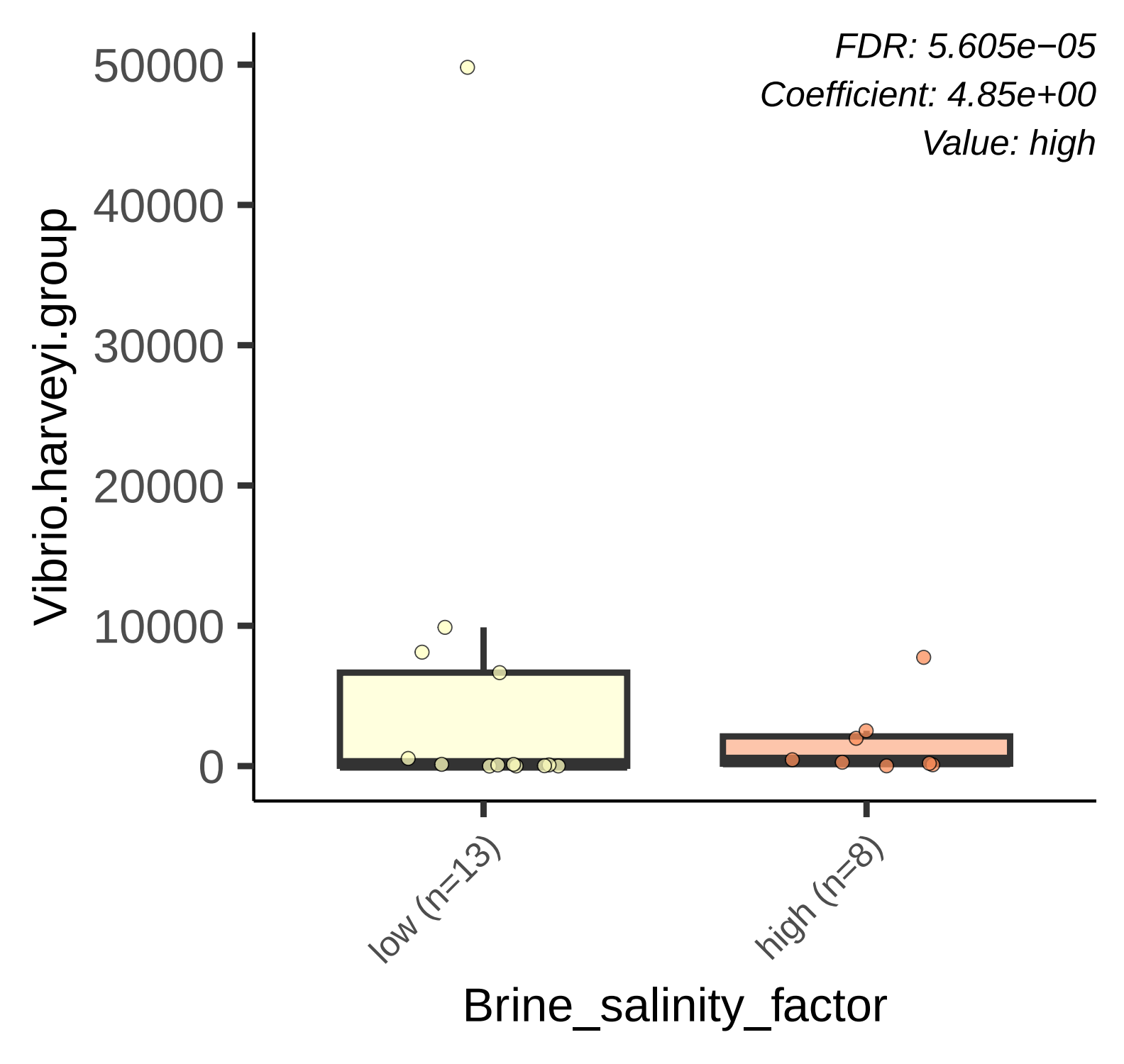

FDR: 3.267e−05
Coefficient: 4.10e+00
Value: high
uncultured.Halobacteria.archaeon
400
300
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

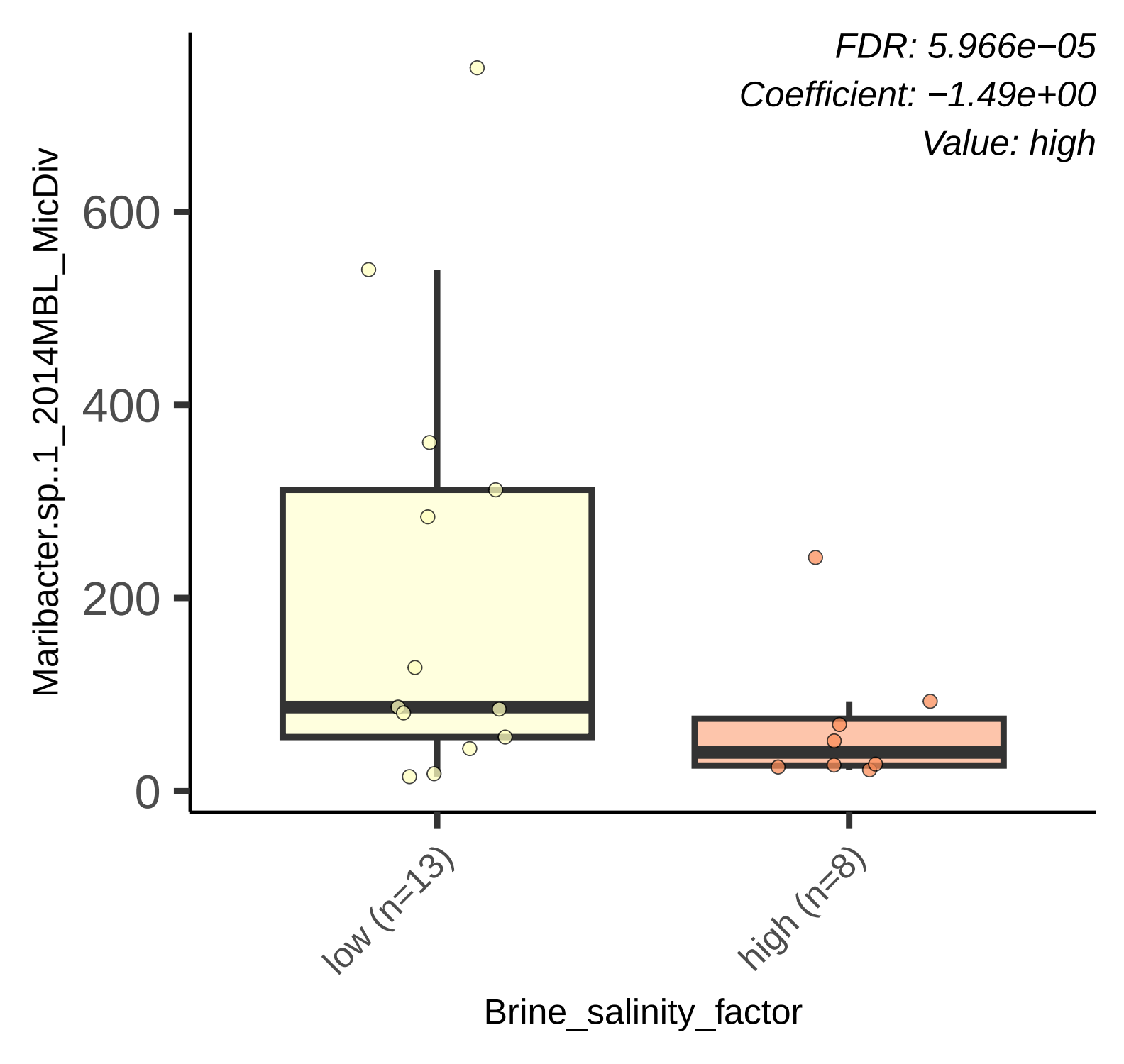

FDR: 3.742e−05
Coefficient: −7.24e−01
Value: high
1000
750
500
250
Thioclava.nitratireducens
low (n=13)
high (n=8)
Brine_salinity_factor

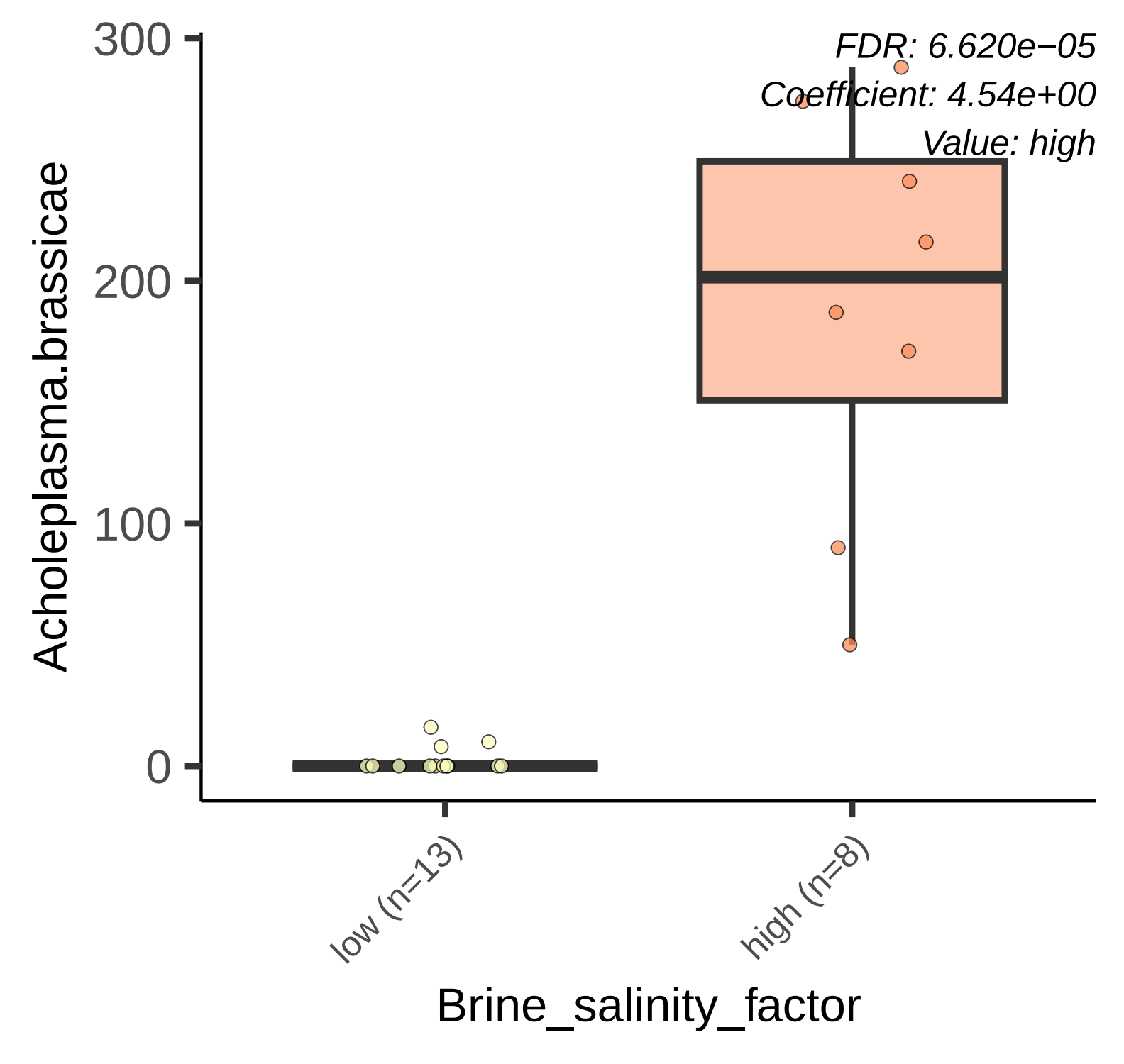

FDR: 4.213e−05
Coefficient: 4.98e+00
Value: high
Halorubrum.sp..TP023
750
500
250
0
low (n=13)
high (n=8)
Brine_salinity_factor

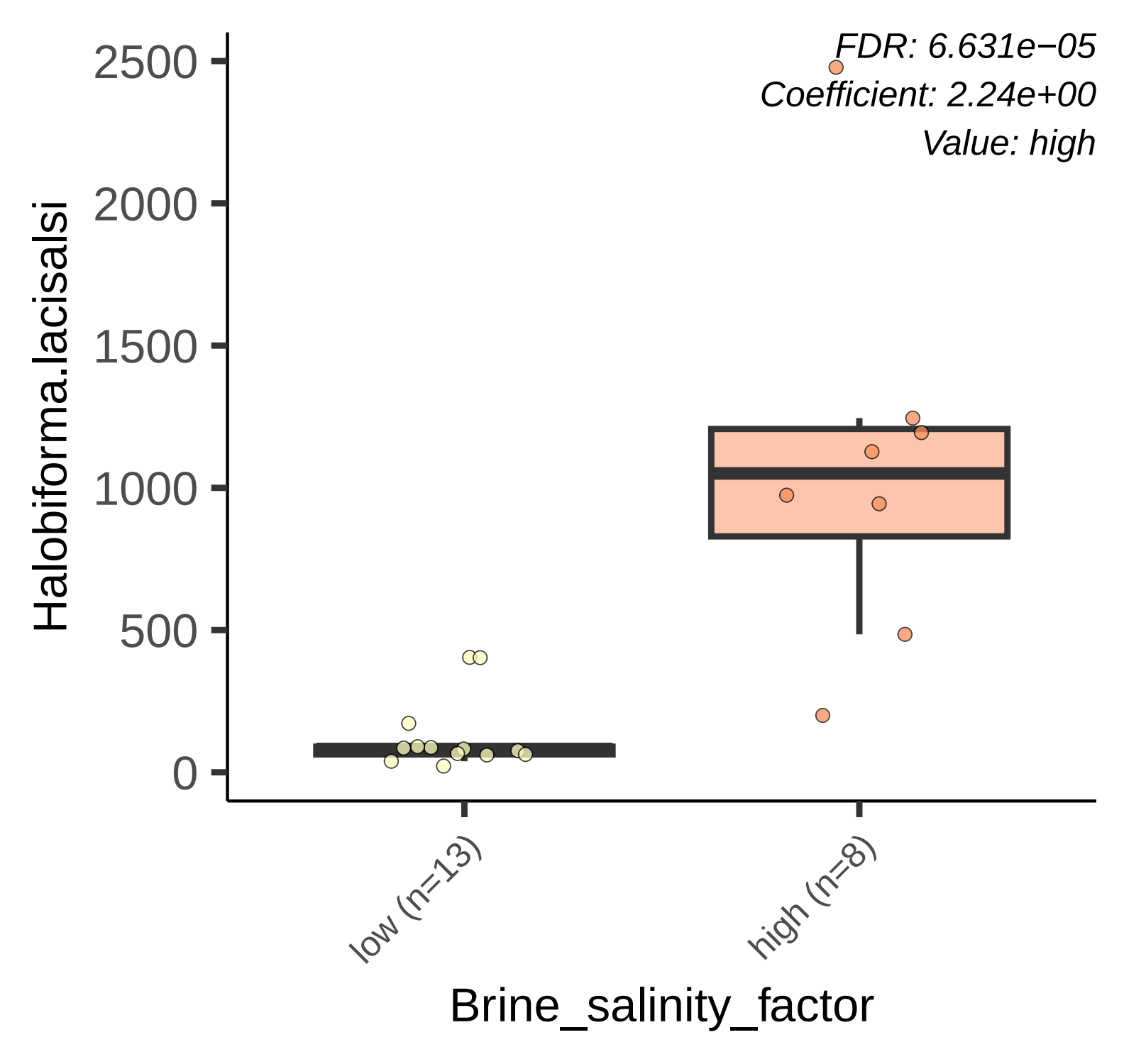

FDR: 4.544e−05
Coefficient: 2.23e+00
Value: high
Natrinema.pellirubrum
4000
2000
0
low (n=13)
high (n=8)
Brine_salinity_factor

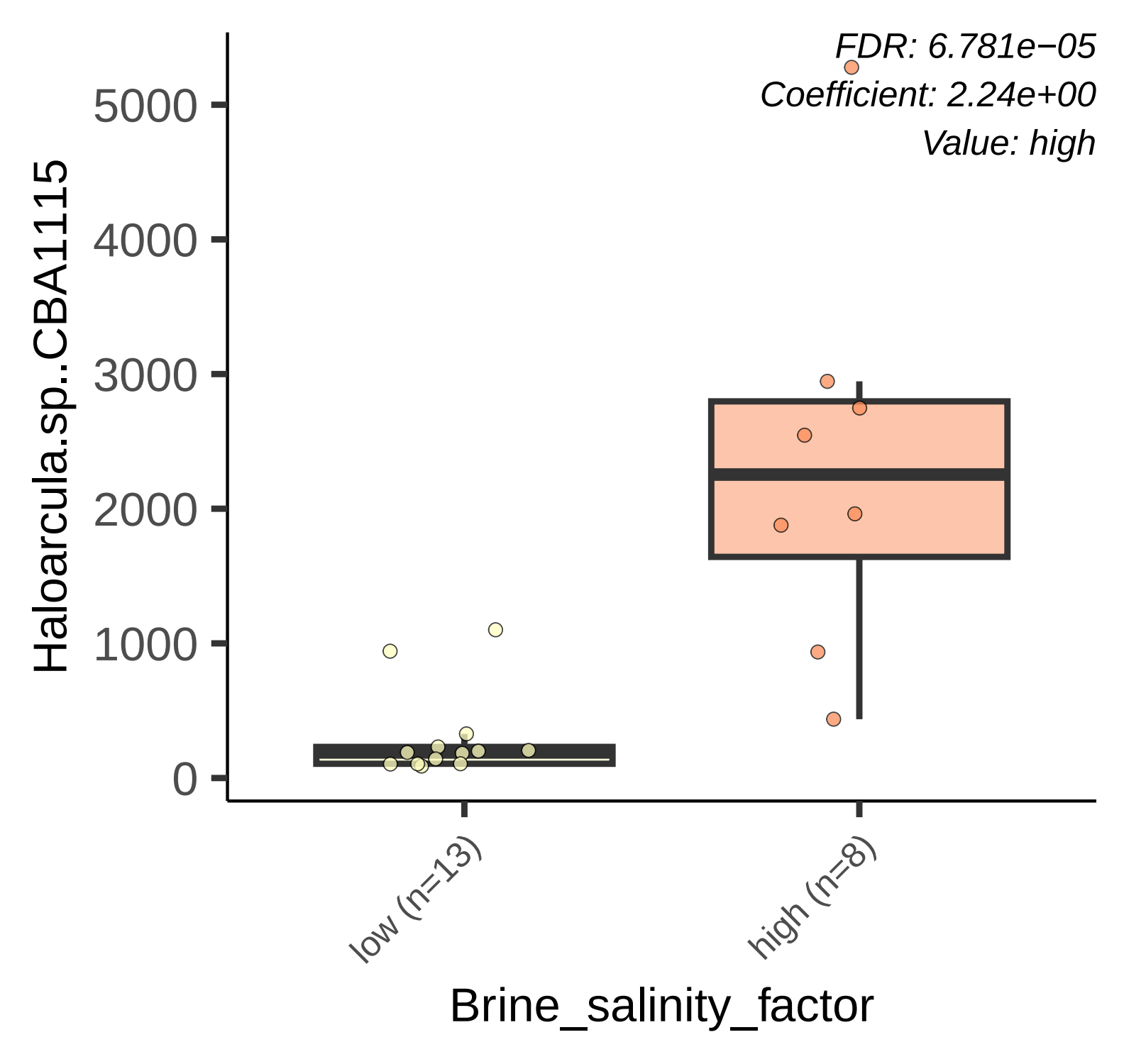

FDR: 5.381e−05
Coefficient: 2.45e+00
Value: high
Salinigranum.rubrum
20000
10000
0
low (n=13)
high (n=8)
Brine_salinity_factor

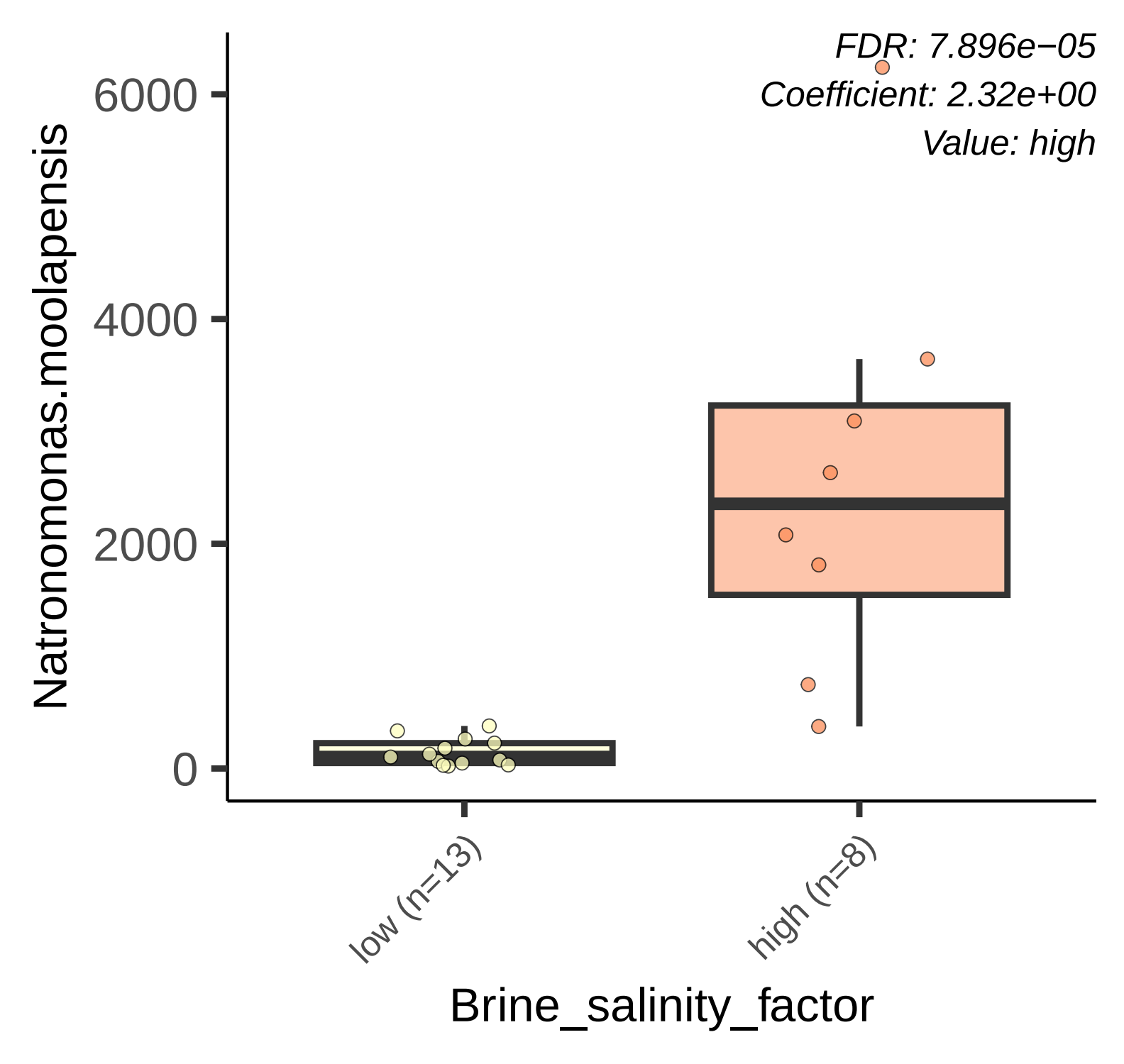

FDR: 5.605e−05
Coefficient: 4.85e+00
Value: high
50000
40000
30000
20000
10000
0
Vibrio.harveyi.group
low (n=13)
high (n=8)
Brine_salinity_factor

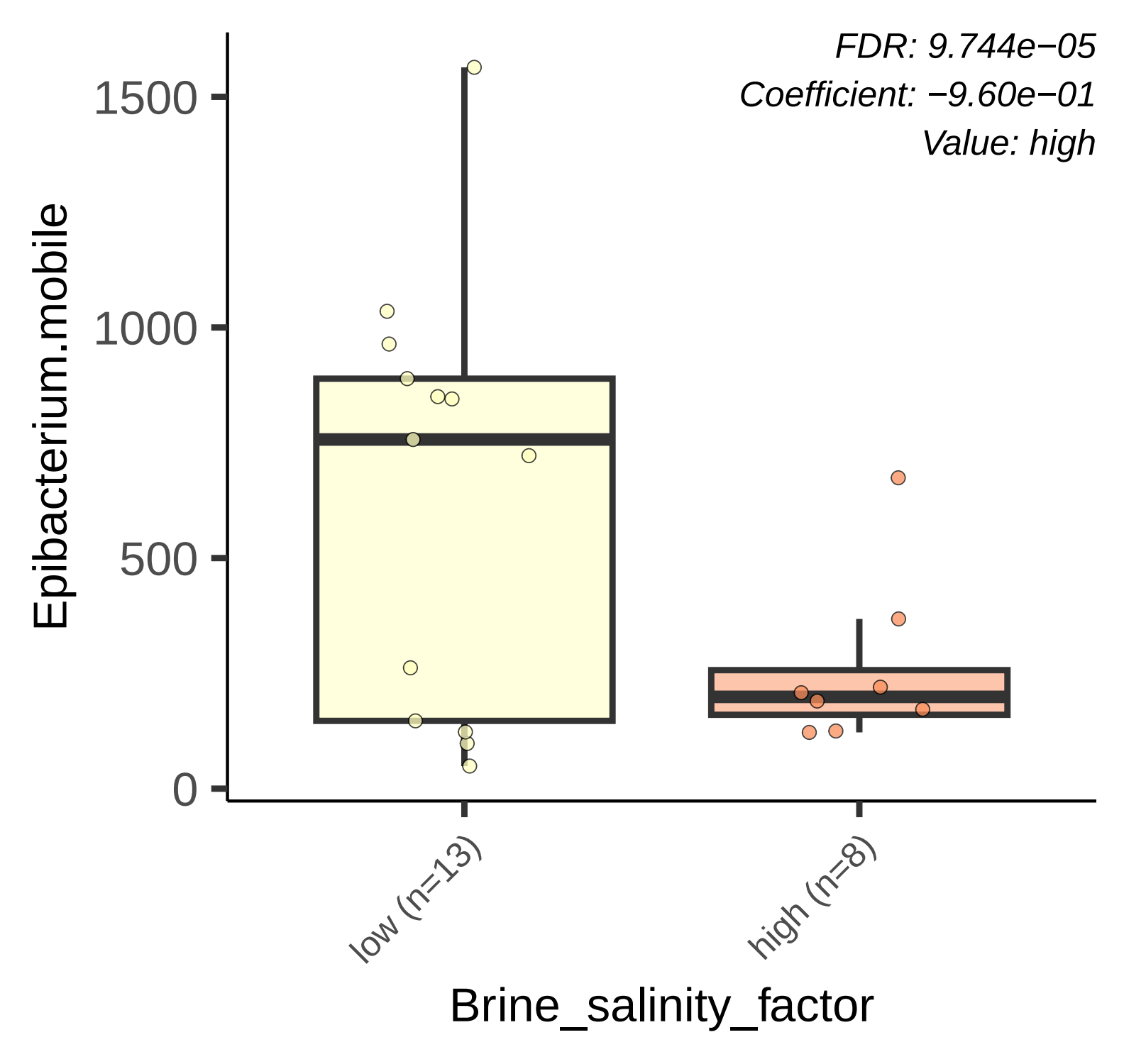

FDR: 5.966e−05
Coefficient: −1.49e+00
Value: high
Maribacter.sp..1_2014MBL_MicDiv
600
400
200
0
low (n=13)
high (n=8)
Brine_salinity_factor

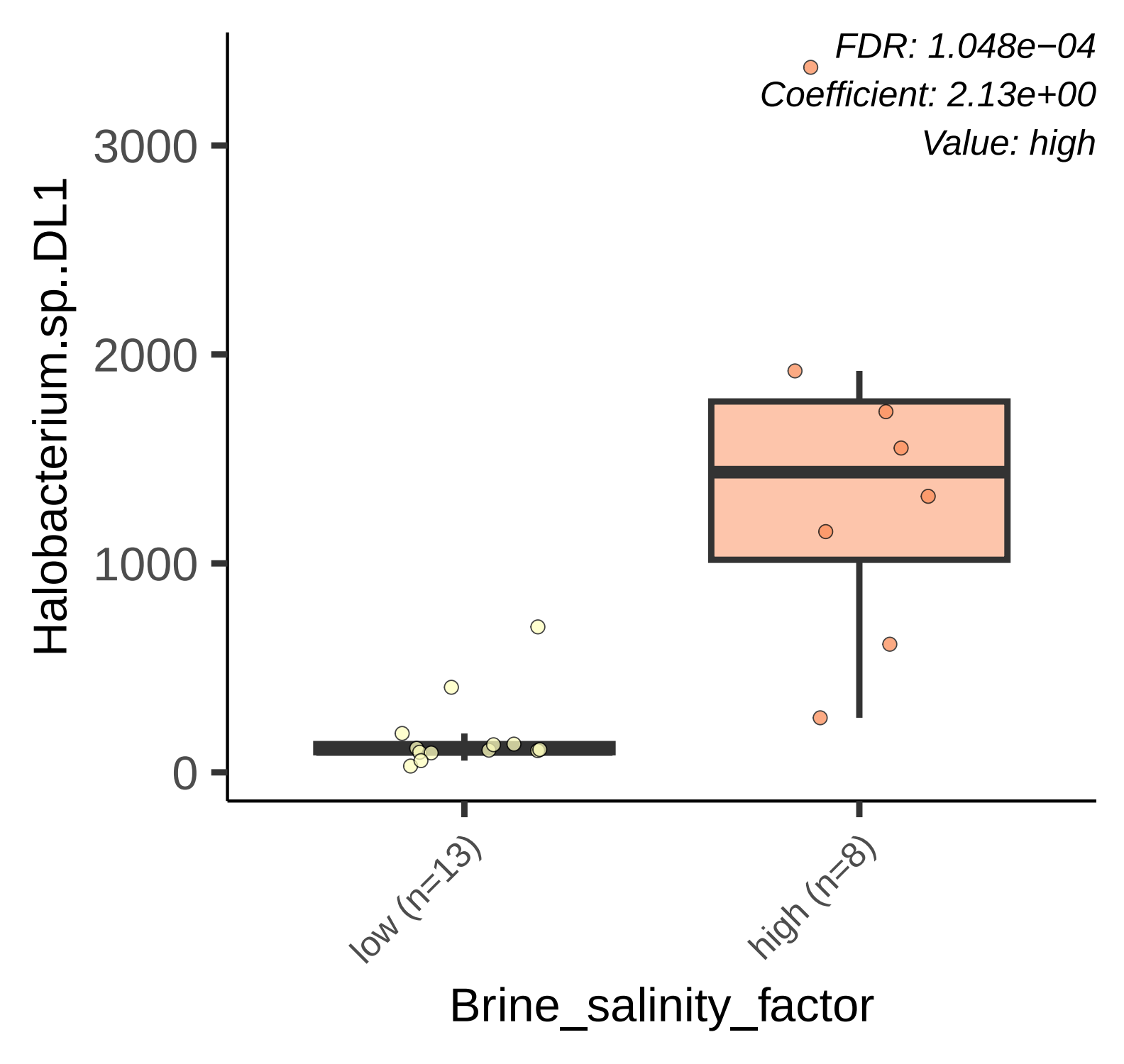

FDR: 6.620e−05
Coefficient: 4.54e+00
Value: high
300
200
100
0
Acholeplasma.brassicae
low (n=13)
high (n=8)
Brine_salinity_factor

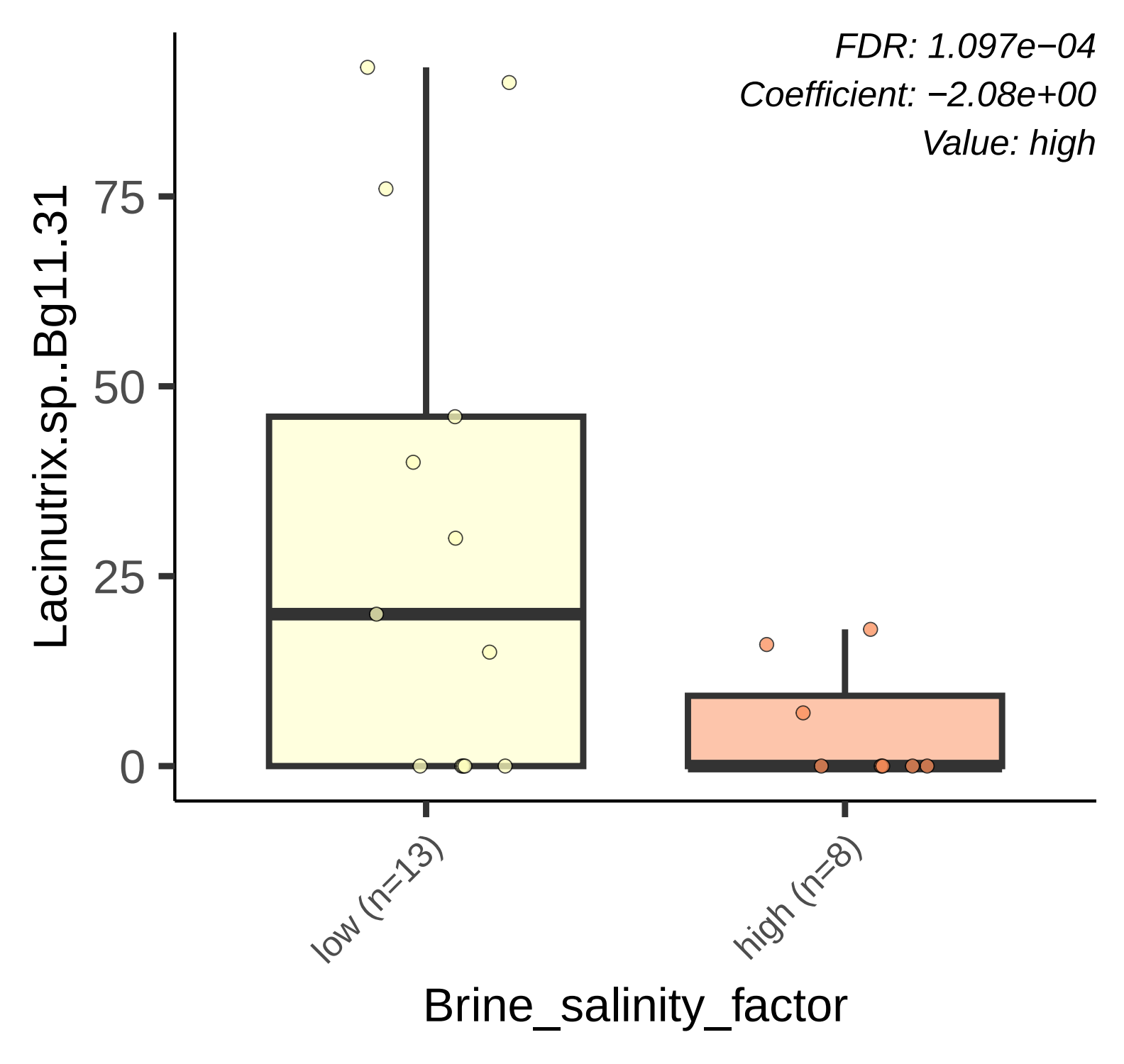

FDR: 6.631e−05
Coefficient: 2.24e+00
Value: high
2500
2000
1500
1000
500
0
Halobiforma.lacisalsi
low (n=13)
high (n=8)
Brine_salinity_factor

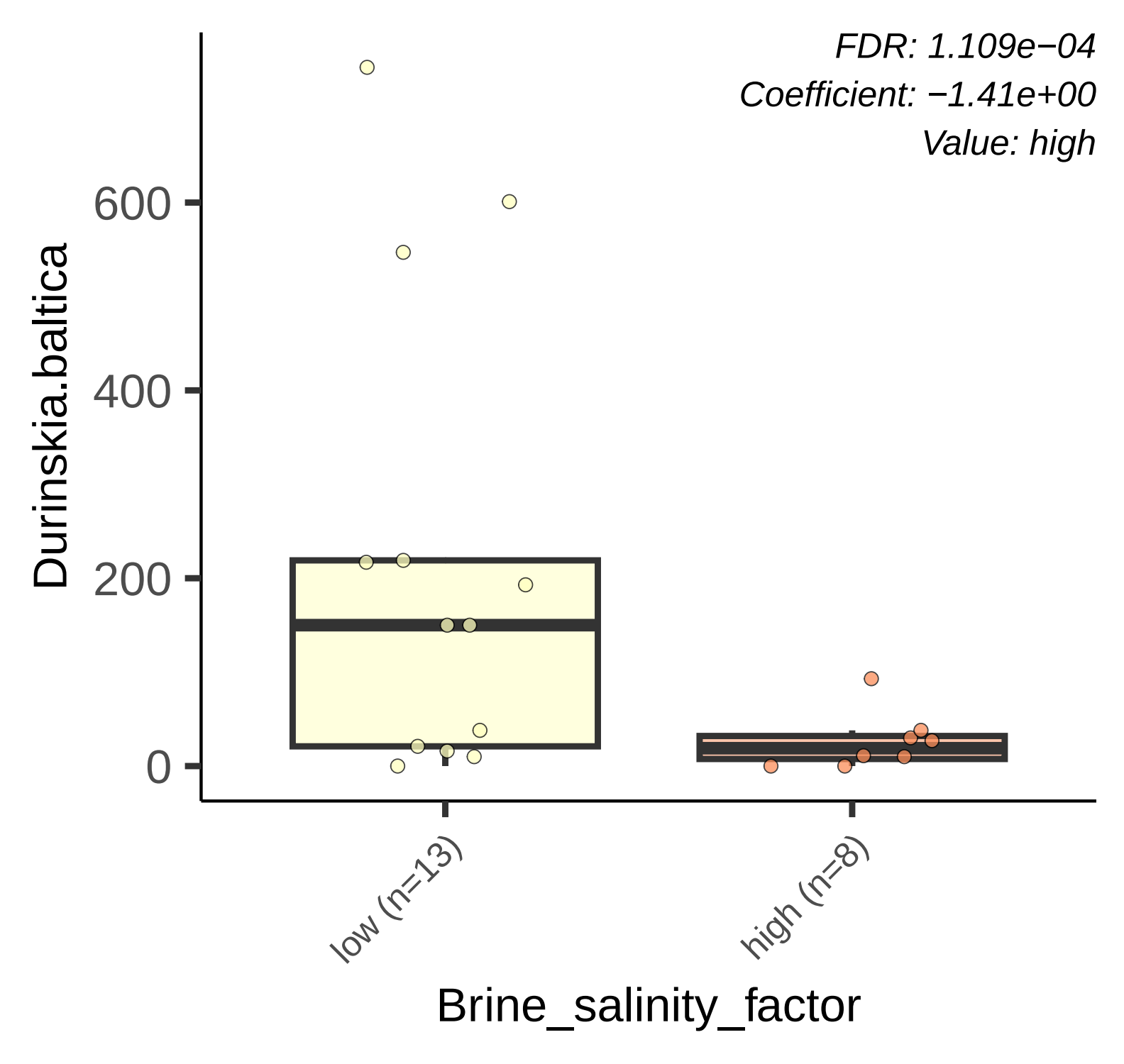

FDR: 6.781e−05
Coefficient: 2.24e+00
Value: high
Haloarcula.sp..CBA1115
5000
4000
3000
2000
1000
0
low (n=13)
high (n=8)
Brine_salinity_factor

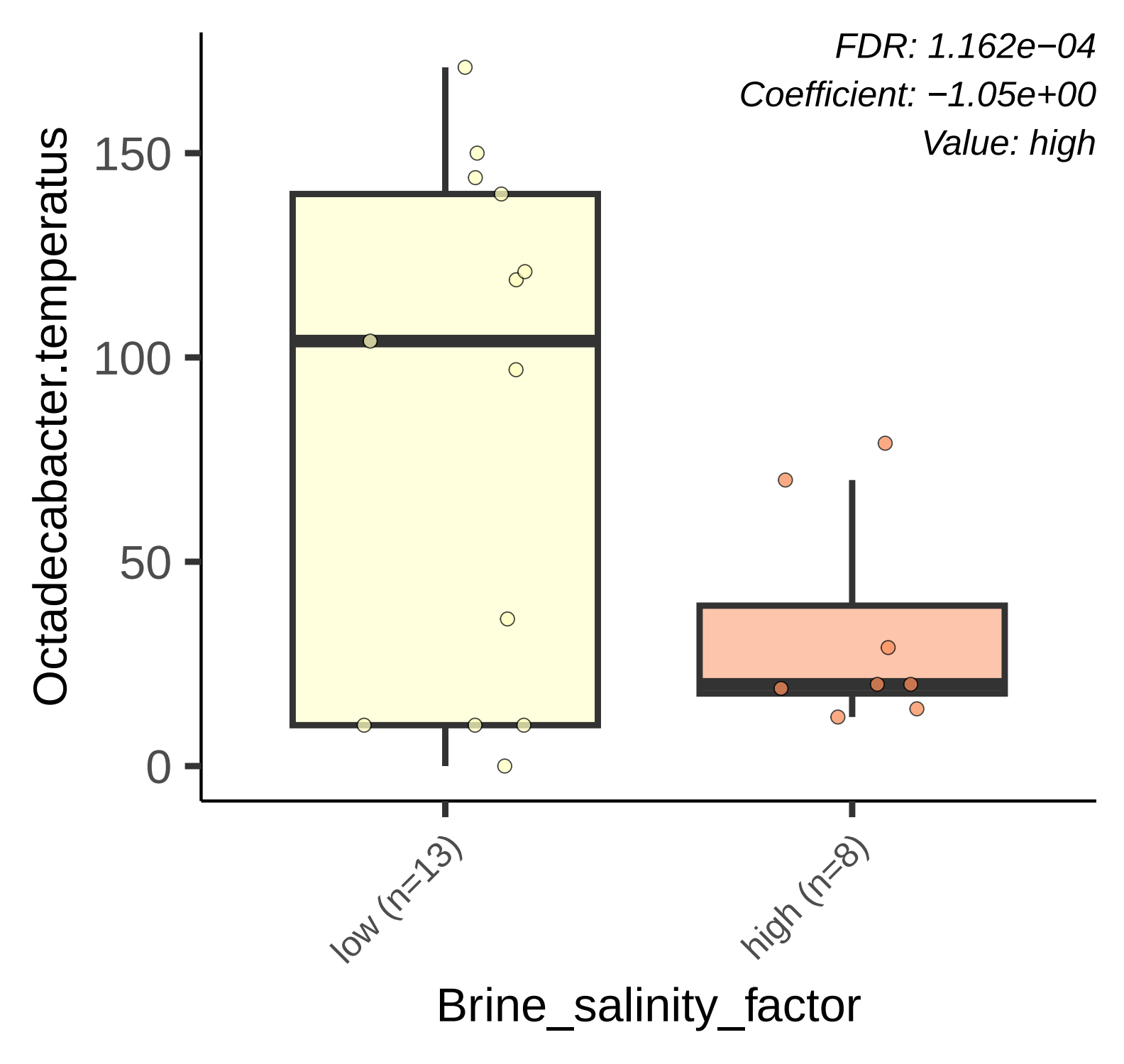

FDR: 7.896e−05
Coefficient: 2.32e+00
Value: high
Natronomonas.moolapensis
6000
4000
2000
0
low (n=13)
high (n=8)
Brine_salinity_factor

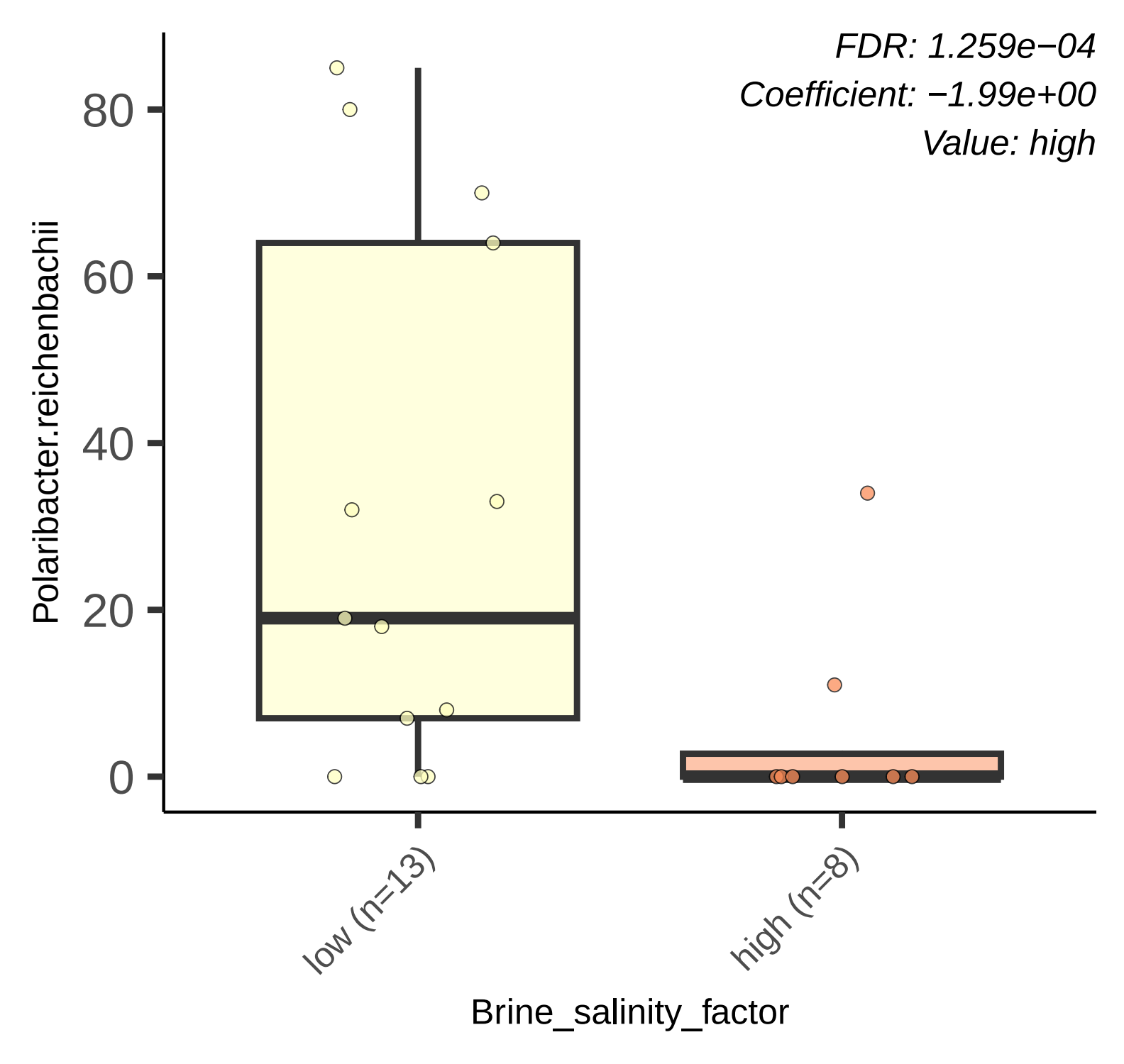

FDR: 9.744e−05
Coefficient: −9.60e−01
Value: high
1500
1000
500
0
Epibacterium.mobile
low (n=13)
high (n=8)
Brine_salinity_factor

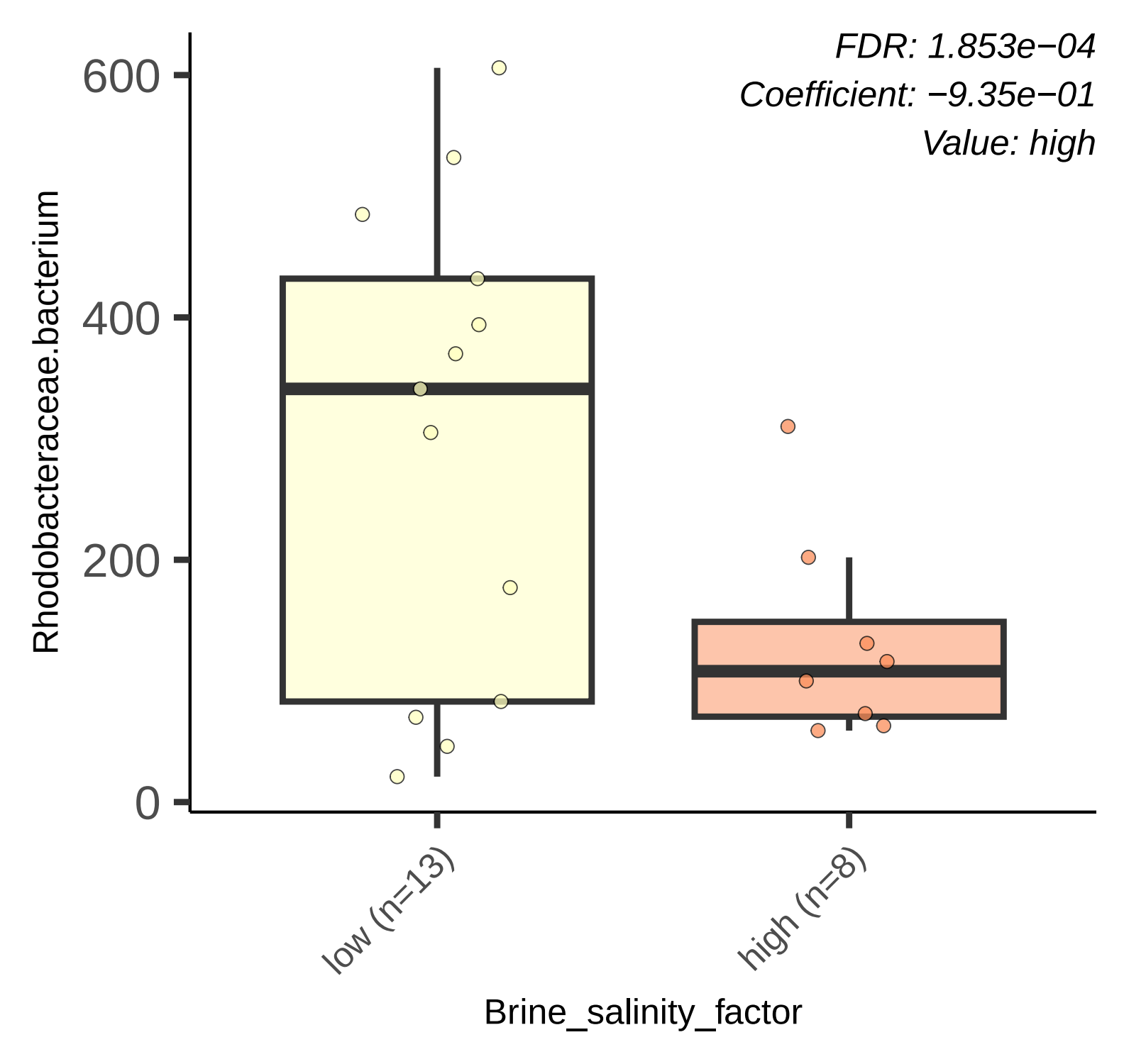

FDR: 1.048e−04
Coefficient: 2.13e+00
Value: high
3000
2000
1000
0
Halobacterium.sp..DL1
low (n=13)
high (n=8)
Brine_salinity_factor

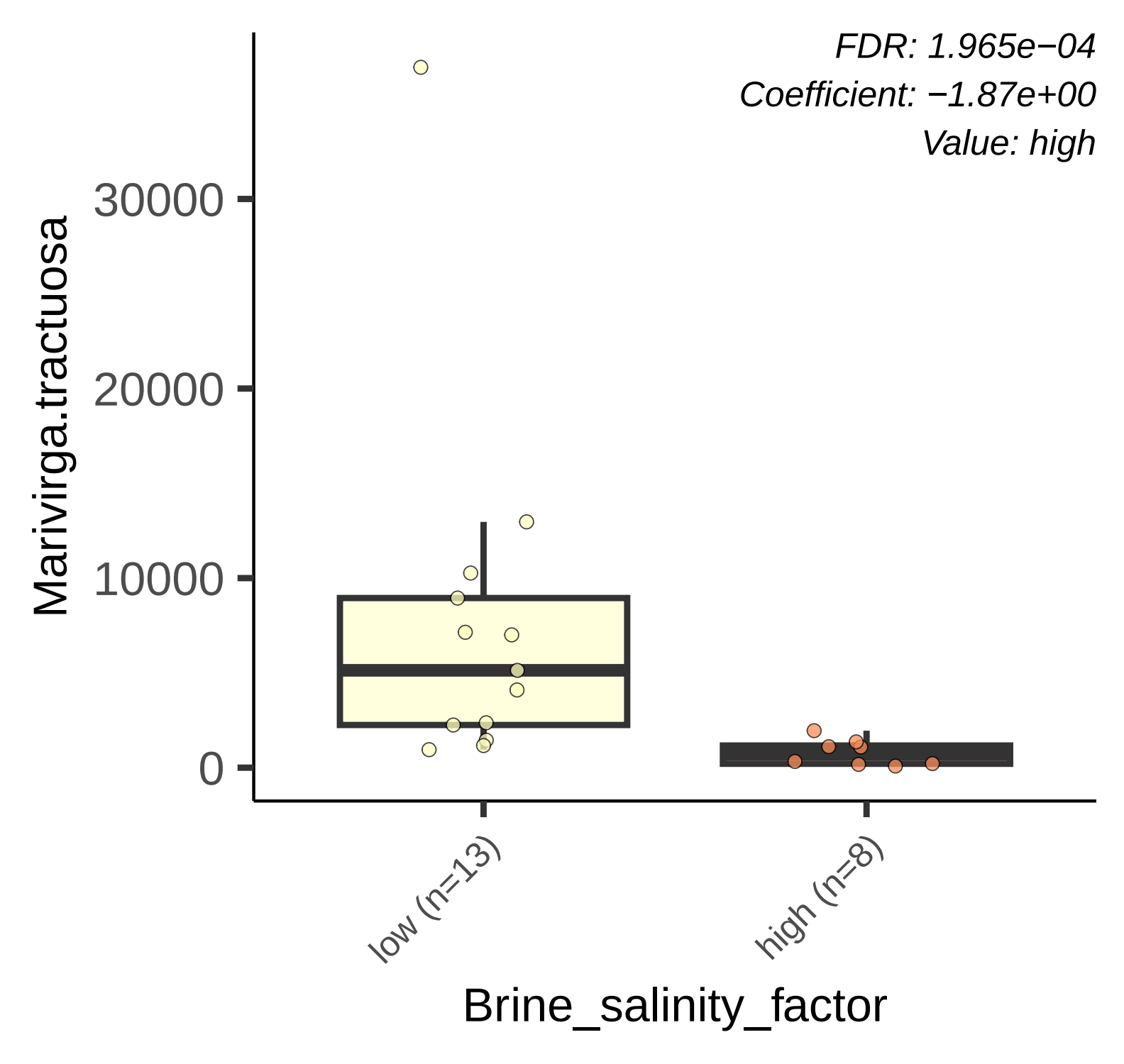

FDR: 1.097e−04
Coefficient: −2.08e+00
Value: high
Lacinutrix.sp..Bg11.31
75
50
25
0
low (n=13)
high (n=8)
Brine_salinity_factor

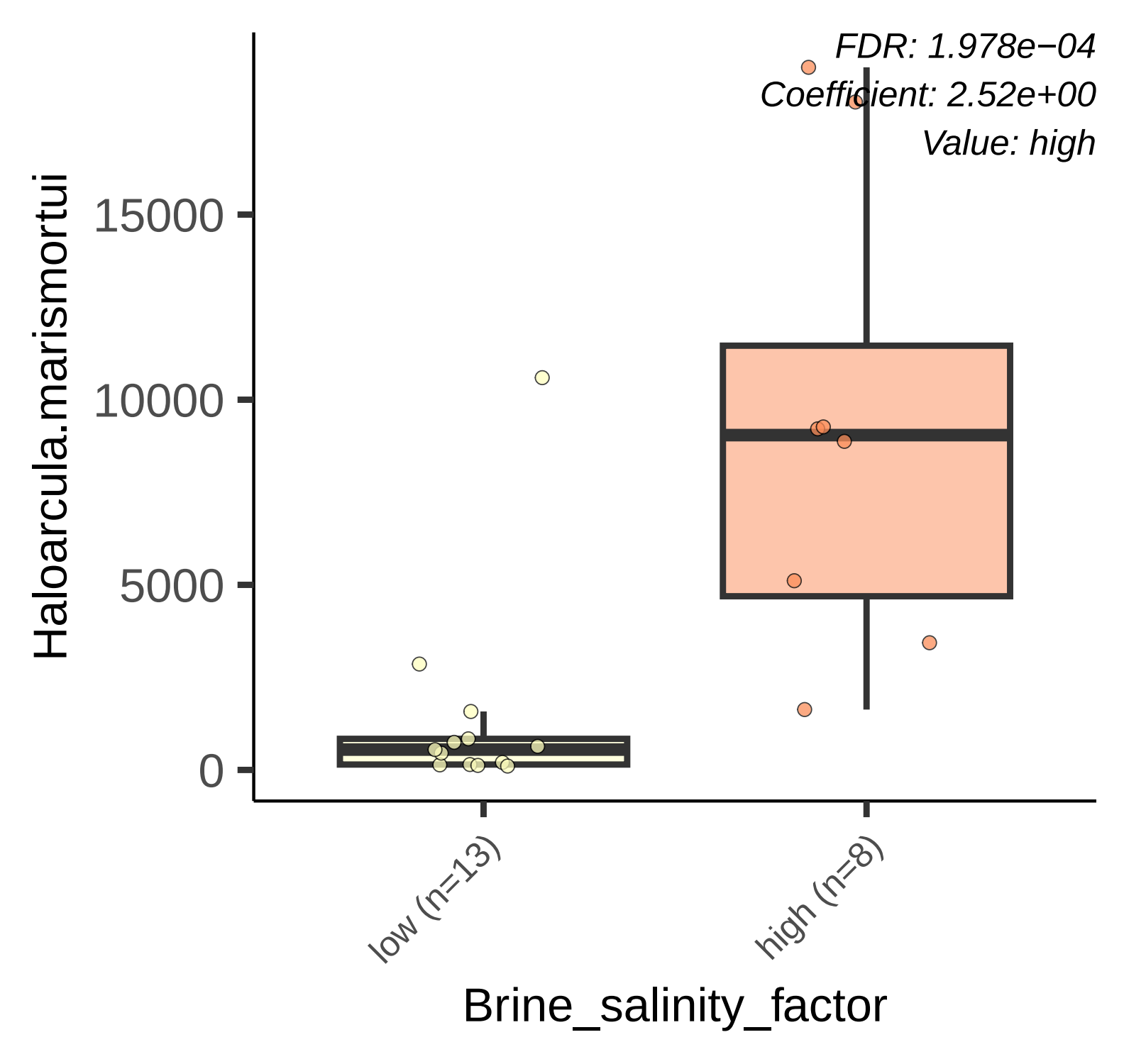

FDR: 1.109e−04
Coefficient: −1.41e+00
Value: high
Durinskia.baltica
600
400
200
0
low (n=13)
high (n=8)
Brine_salinity_factor

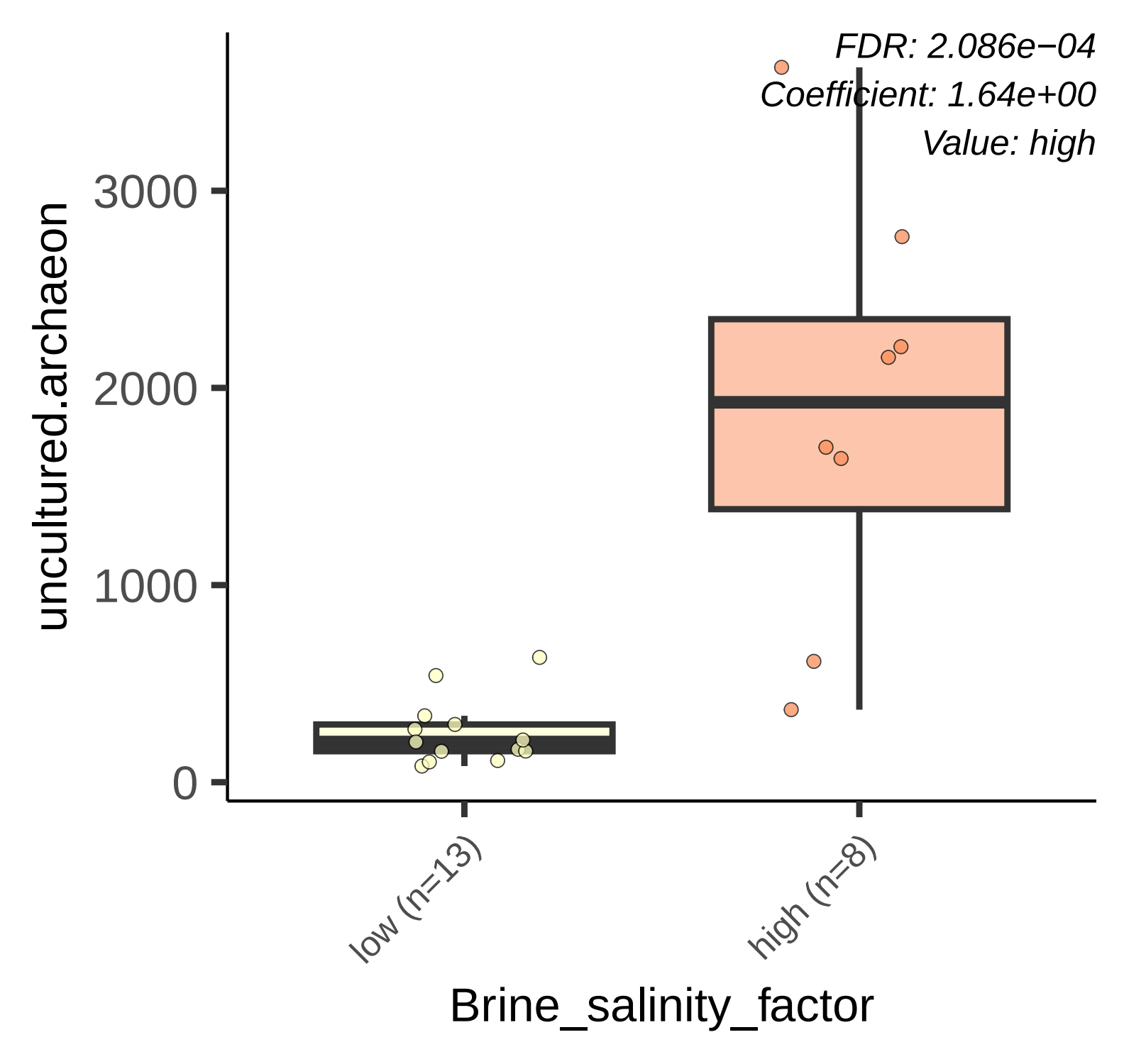

FDR: 1.162e−04
Coefficient: −1.05e+00
Value: high
Octadecabacter.temperatus
150
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

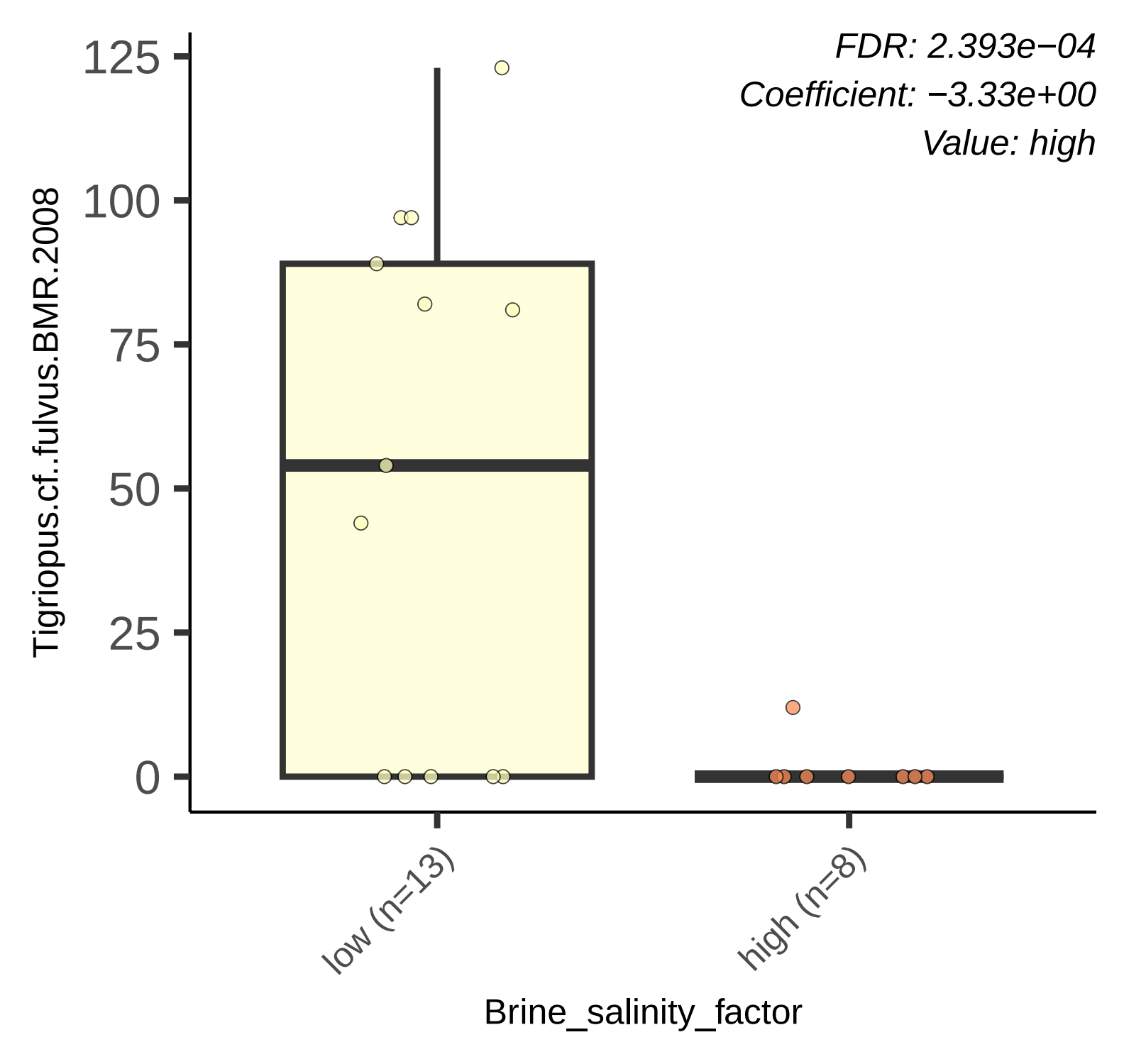

FDR: 1.259e−04
Coefficient: −1.99e+00
Value: high
Polaribacter.reichenbachii
80
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

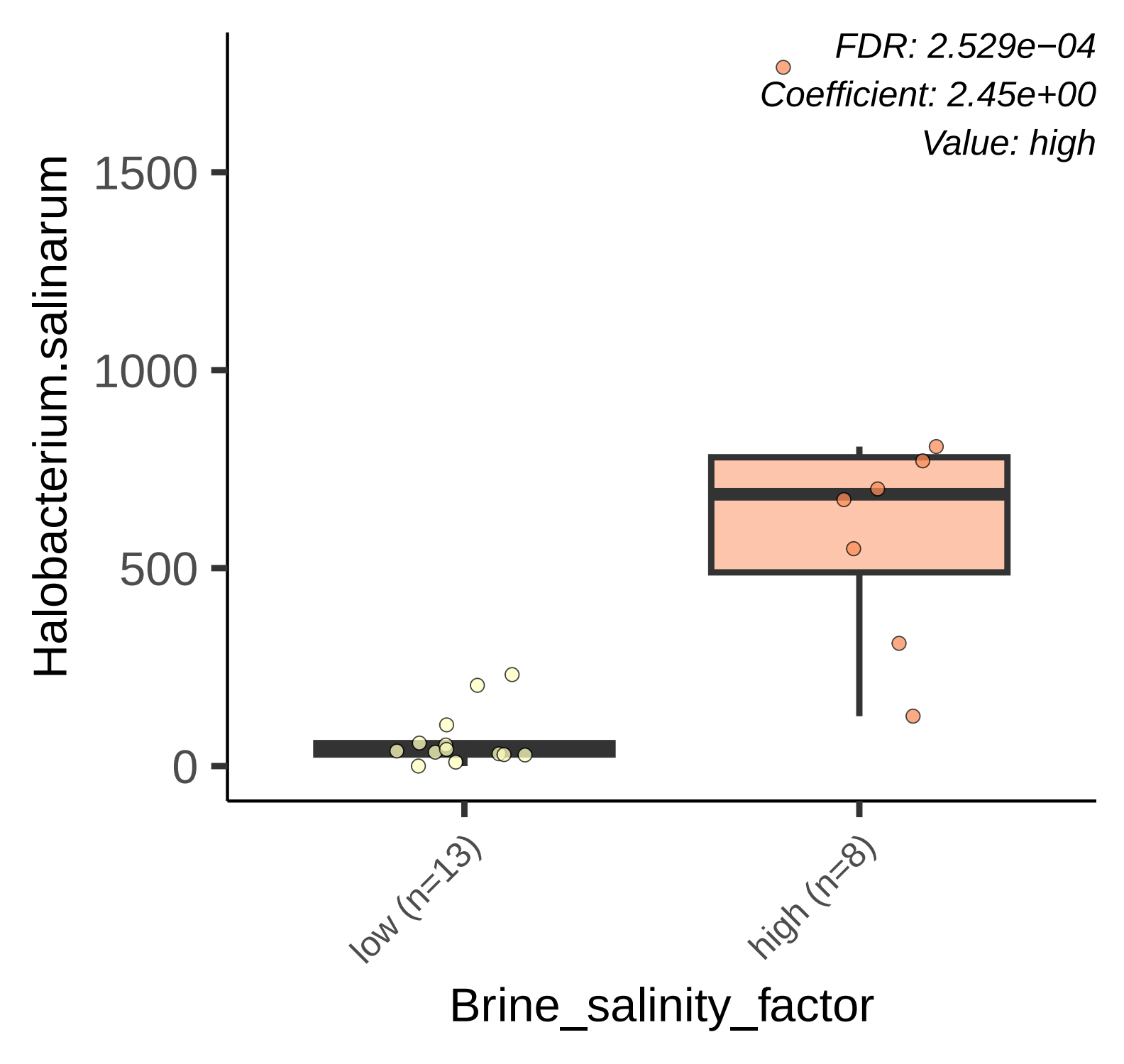

FDR: 1.853e−04
Coefficient: −9.35e−01
Value: high
600
400
200
0
Rhodobacteraceae.bacterium
low (n=13)
high (n=8)
Brine_salinity_factor

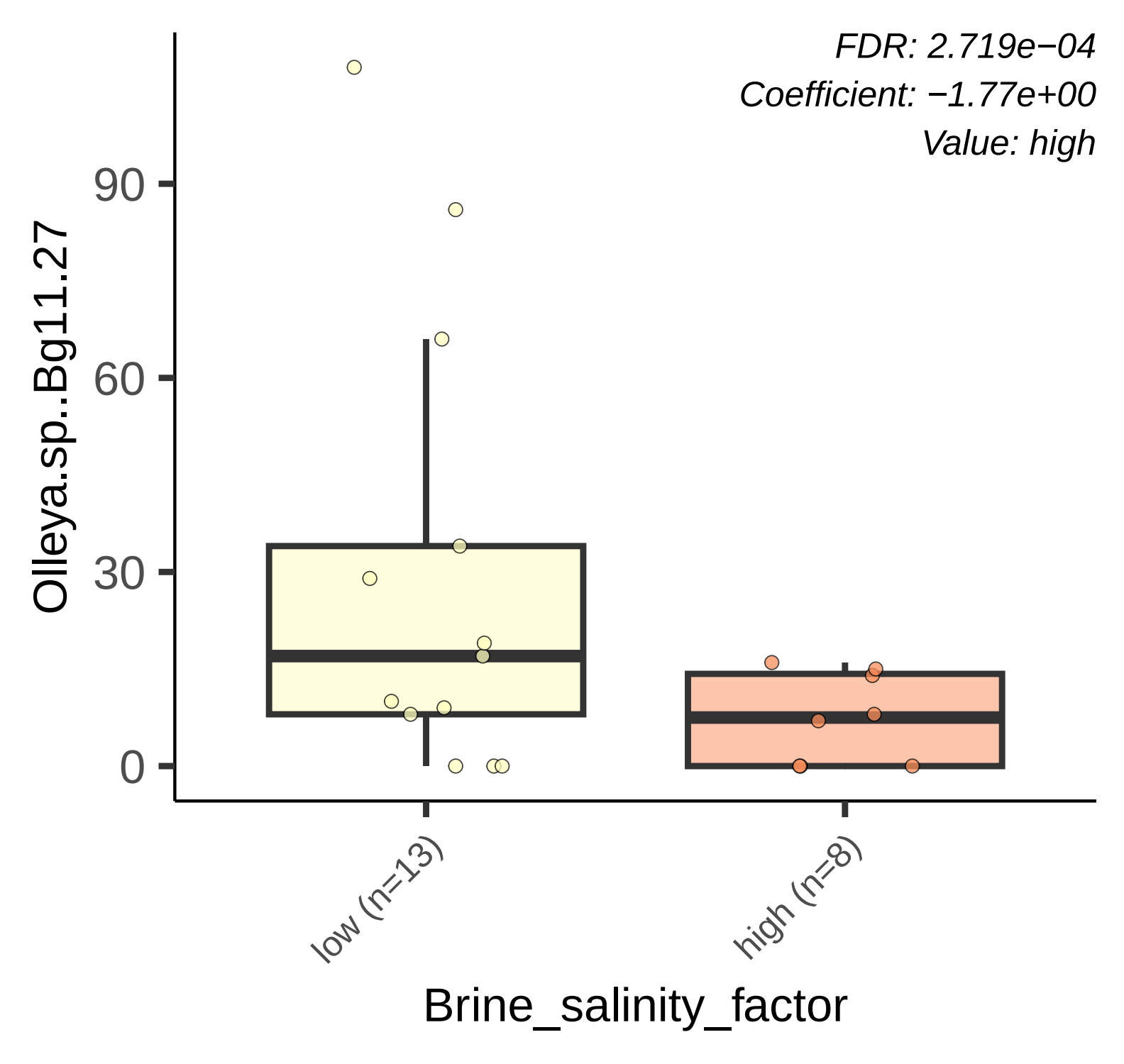

FDR: 1.965e−04
Coefficient: −1.87e+00
Value: high
Marivirga.tractuosa
30000
20000
10000
0
low (n=13)
high (n=8)
Brine_salinity_factor

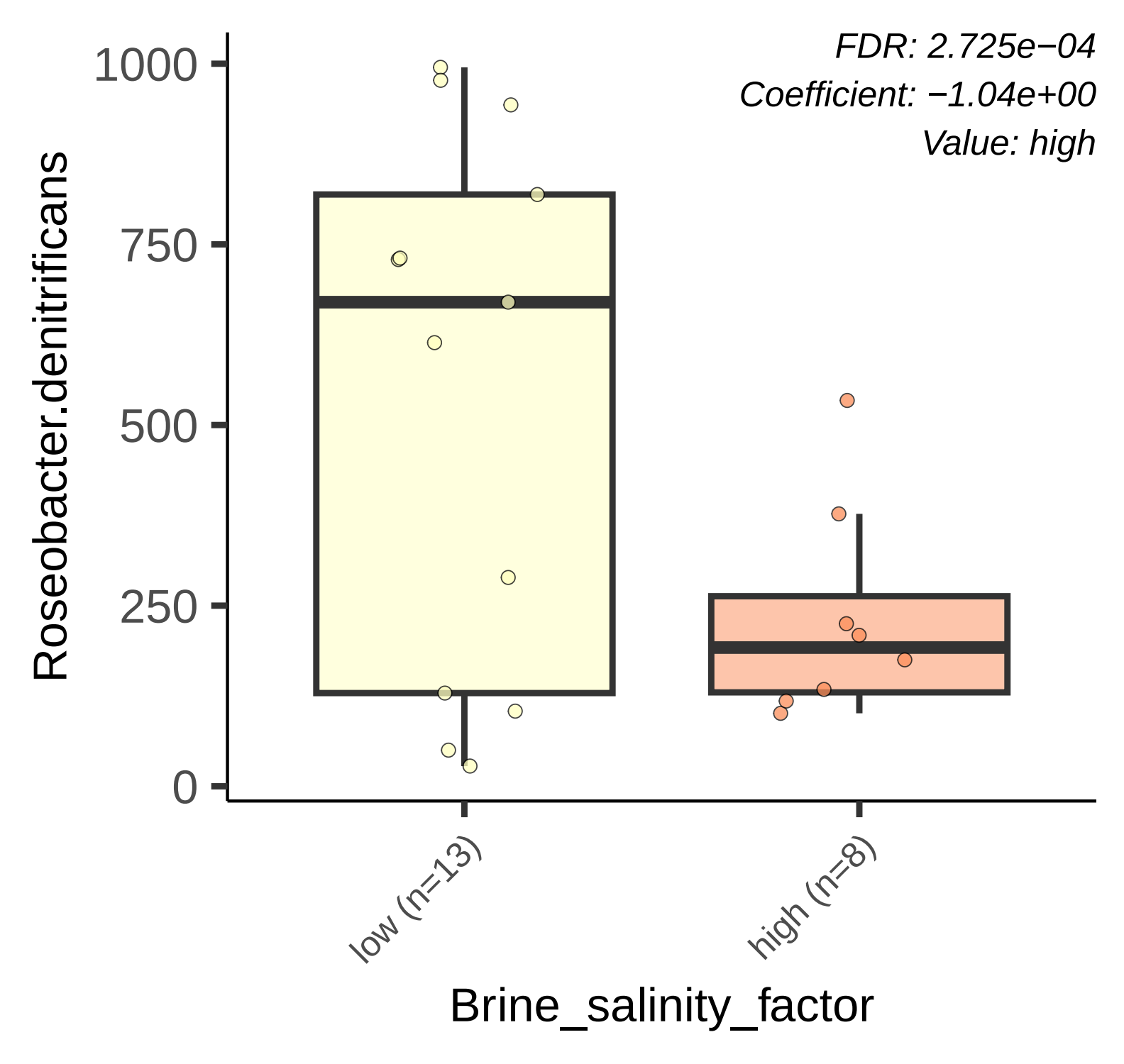

FDR: 1.978e−04
Coefficient: 2.52e+00
Value: high
Haloarcula.marismortui
15000
10000
5000
0
low (n=13)
high (n=8)
Brine_salinity_factor

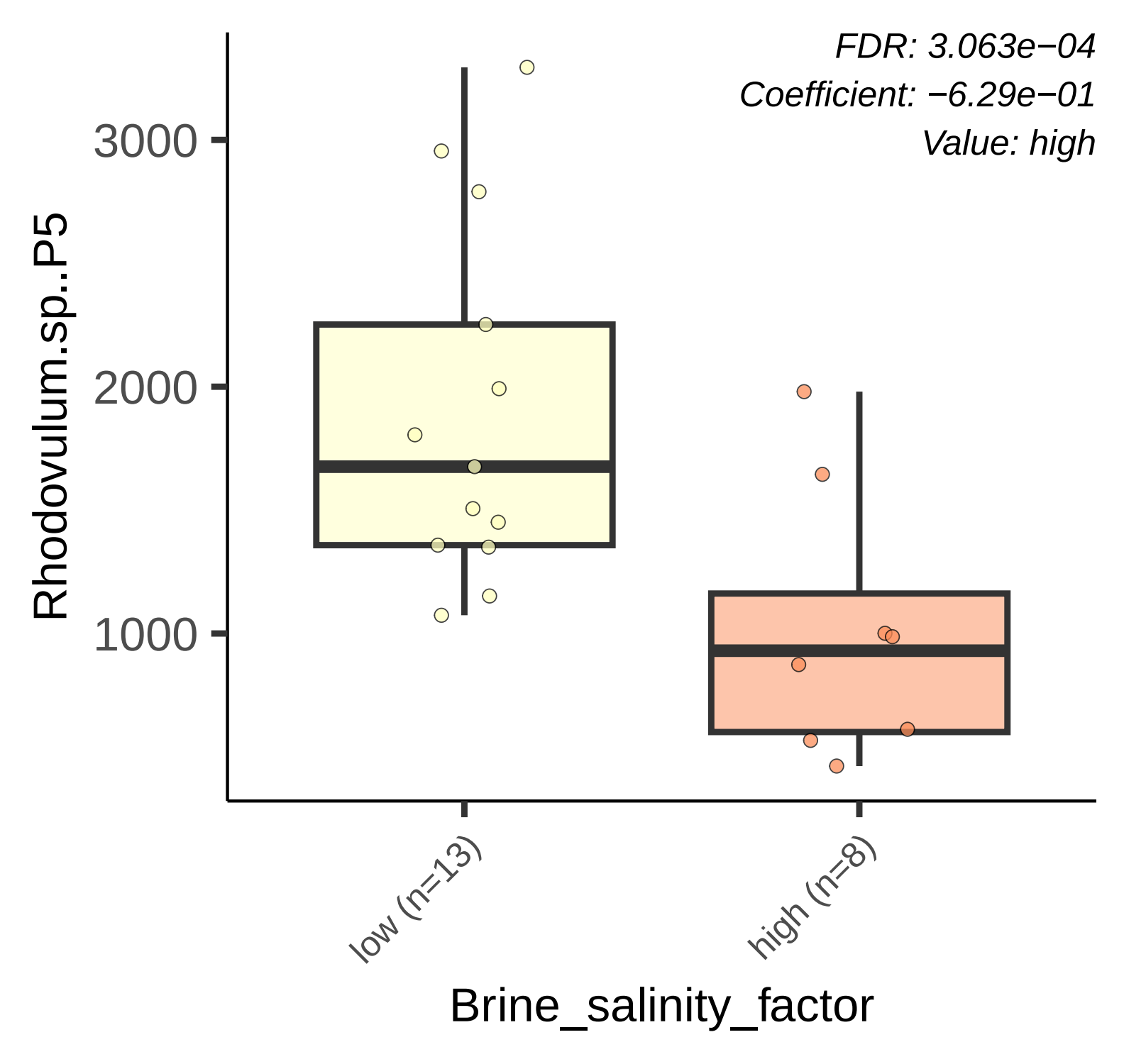

FDR: 2.086e−04
Coefficient: 1.64e+00
Value: high
uncultured.archaeon
3000
2000
1000
0
low (n=13)
high (n=8)
Brine_salinity_factor

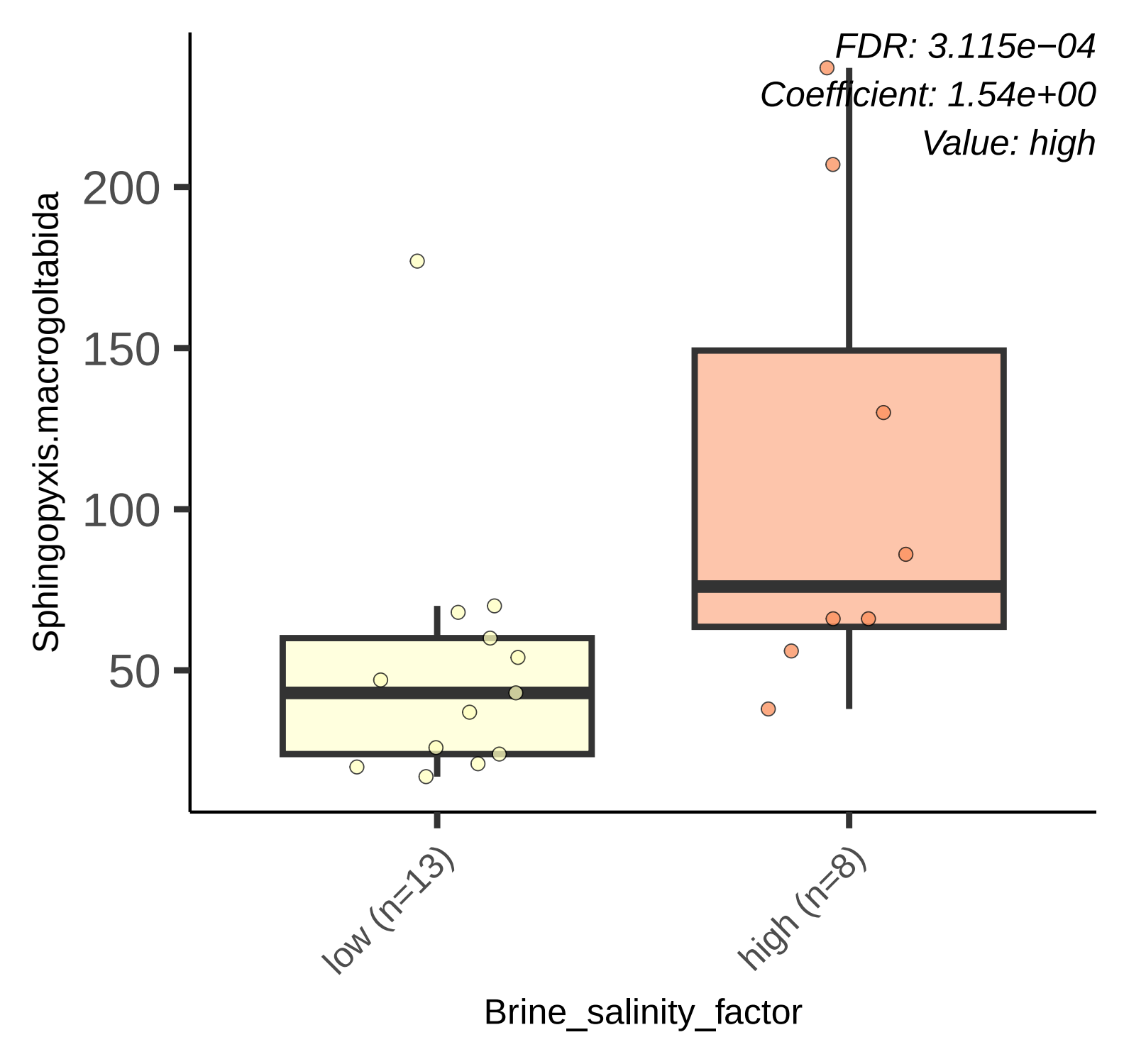

FDR: 2.393e−04
Coefficient: −3.33e+00
Value: high
125
100
75
50
25
0
Tigriopus.cf..fulvus.BMR.2008
low (n=13)
high (n=8)
Brine_salinity_factor

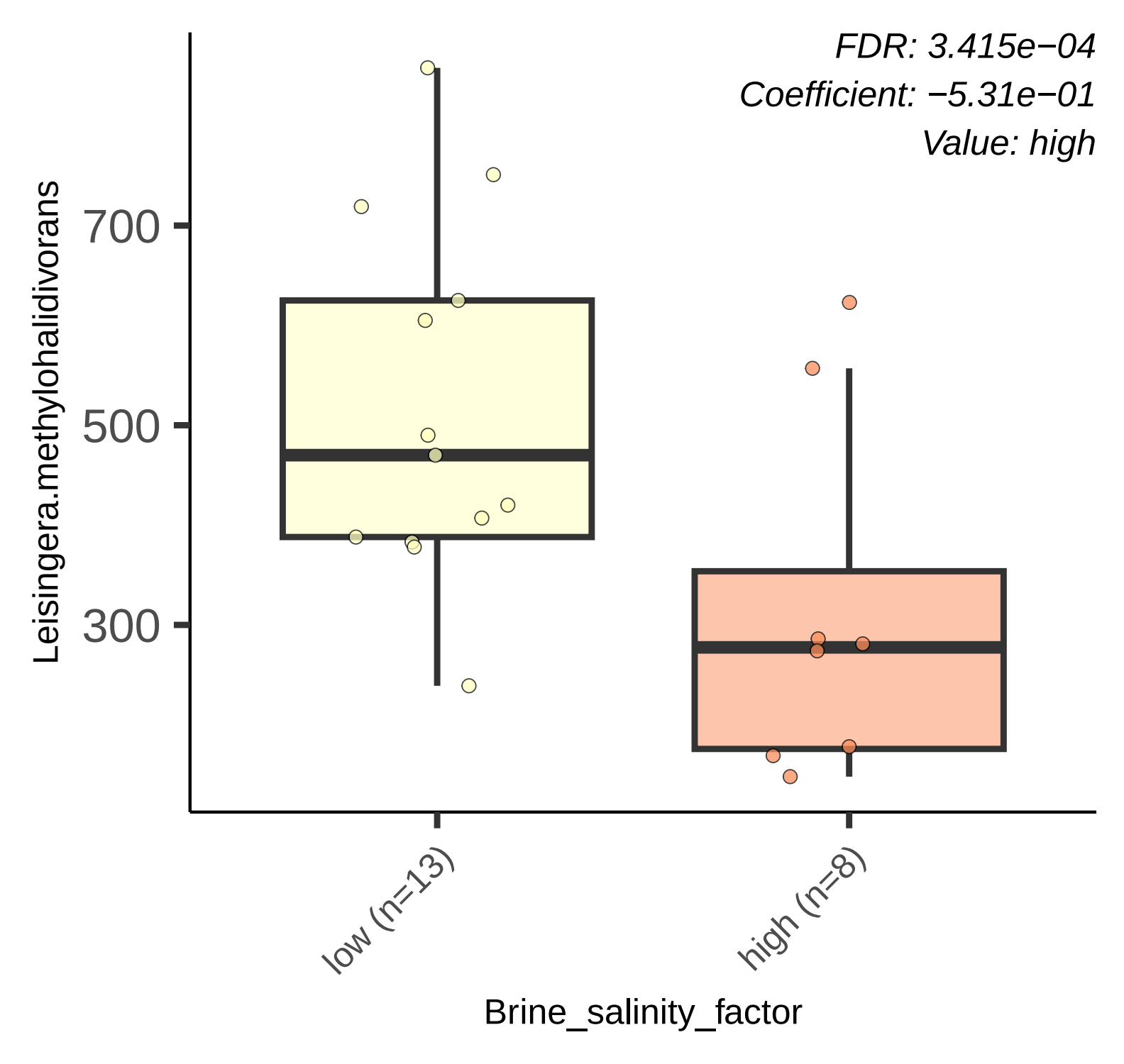

FDR: 2.529e−04
Coefficient: 2.45e+00
Value: high
Halobacterium.salinarum
1500
1000
500
0
low (n=13)
high (n=8)
Brine_salinity_factor

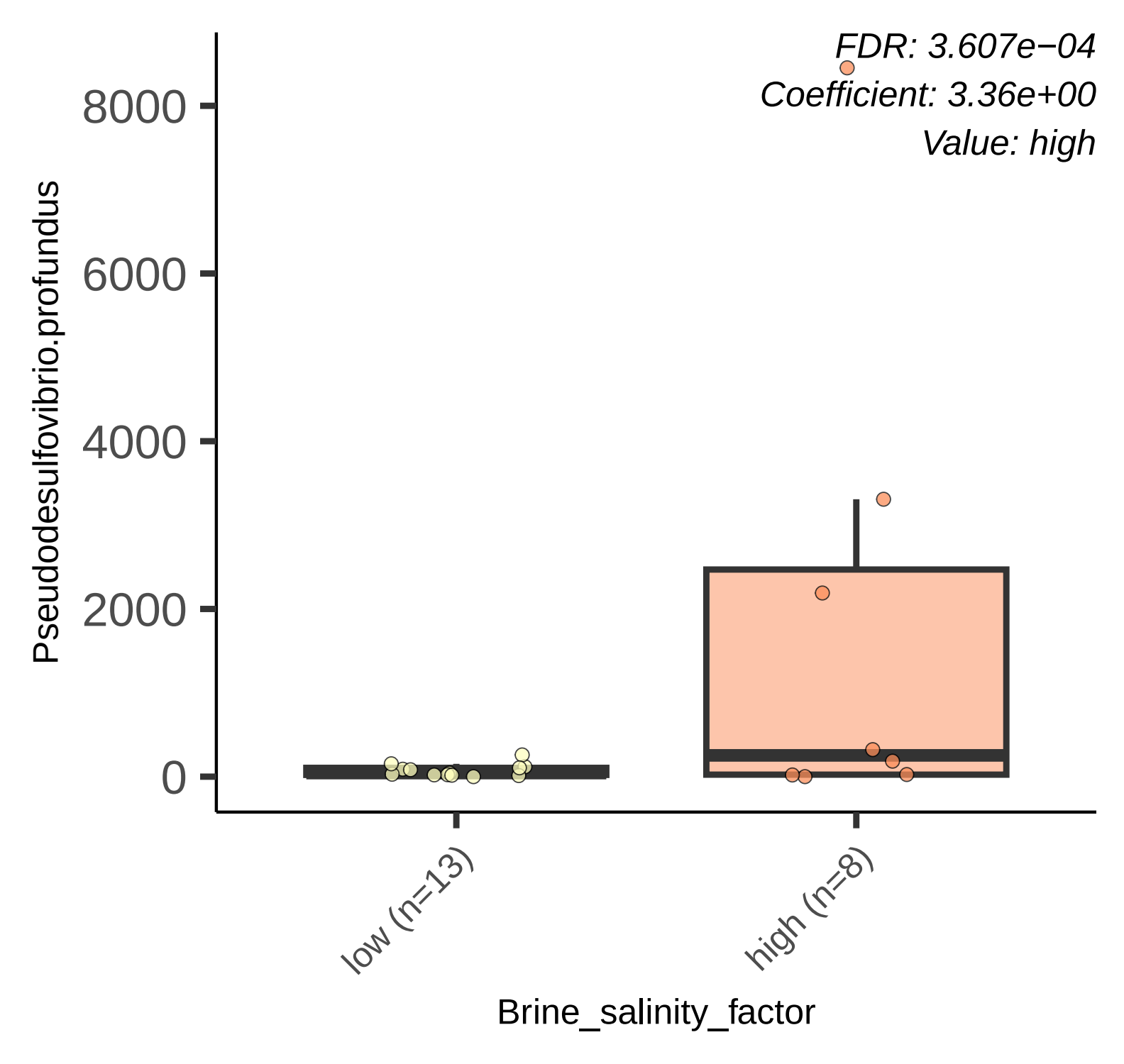

FDR: 2.719e−04
Coefficient: −1.77e+00
Value: high
Olleya.sp..Bg11.27
90
60
30
0
low (n=13)
high (n=8)
Brine_salinity_factor

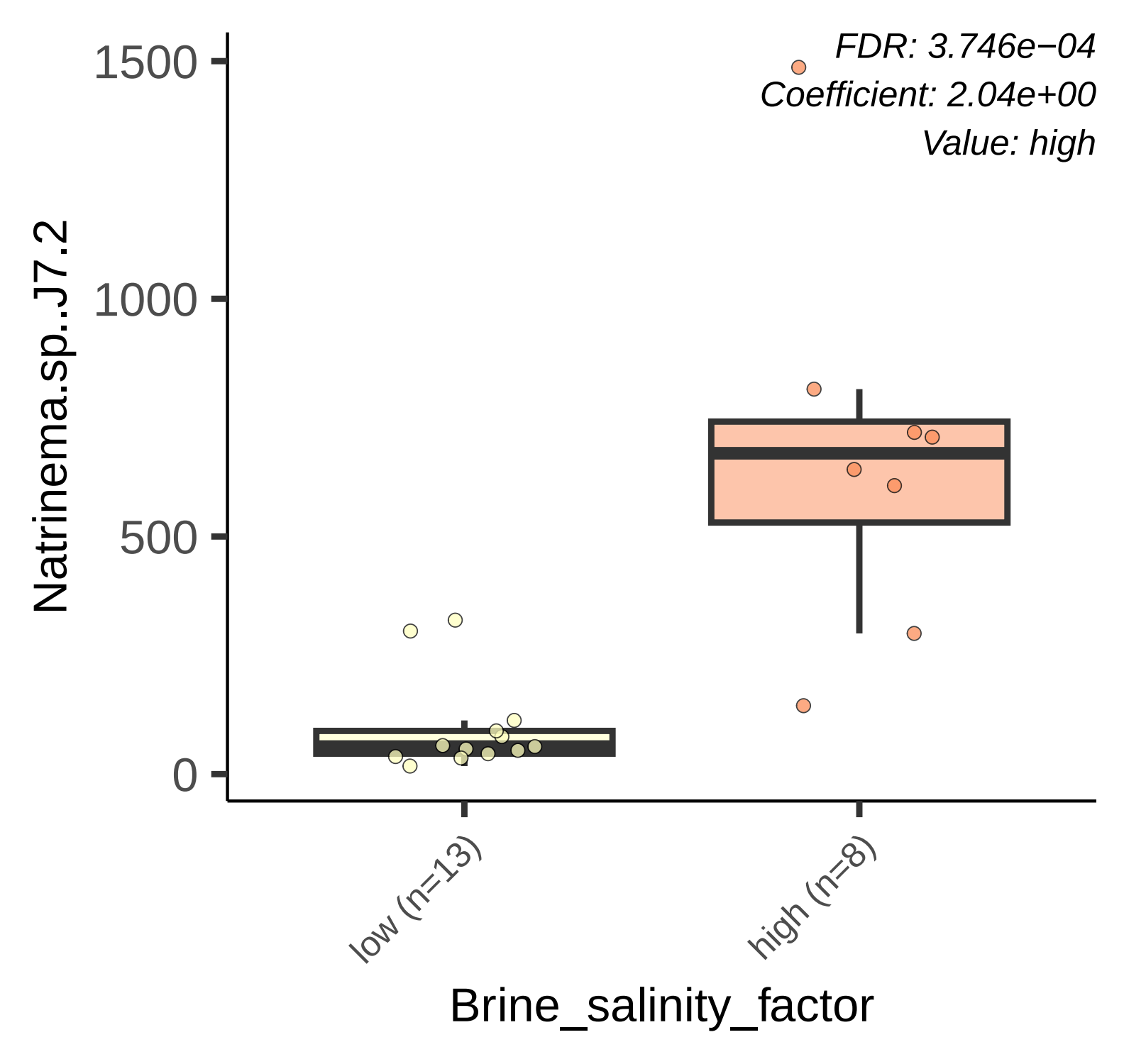

FDR: 2.725e−04
Coefficient: −1.04e+00
Value: high
1000
750
500
250
0
Roseobacter.denitrificans
low (n=13)
high (n=8)
Brine_salinity_factor

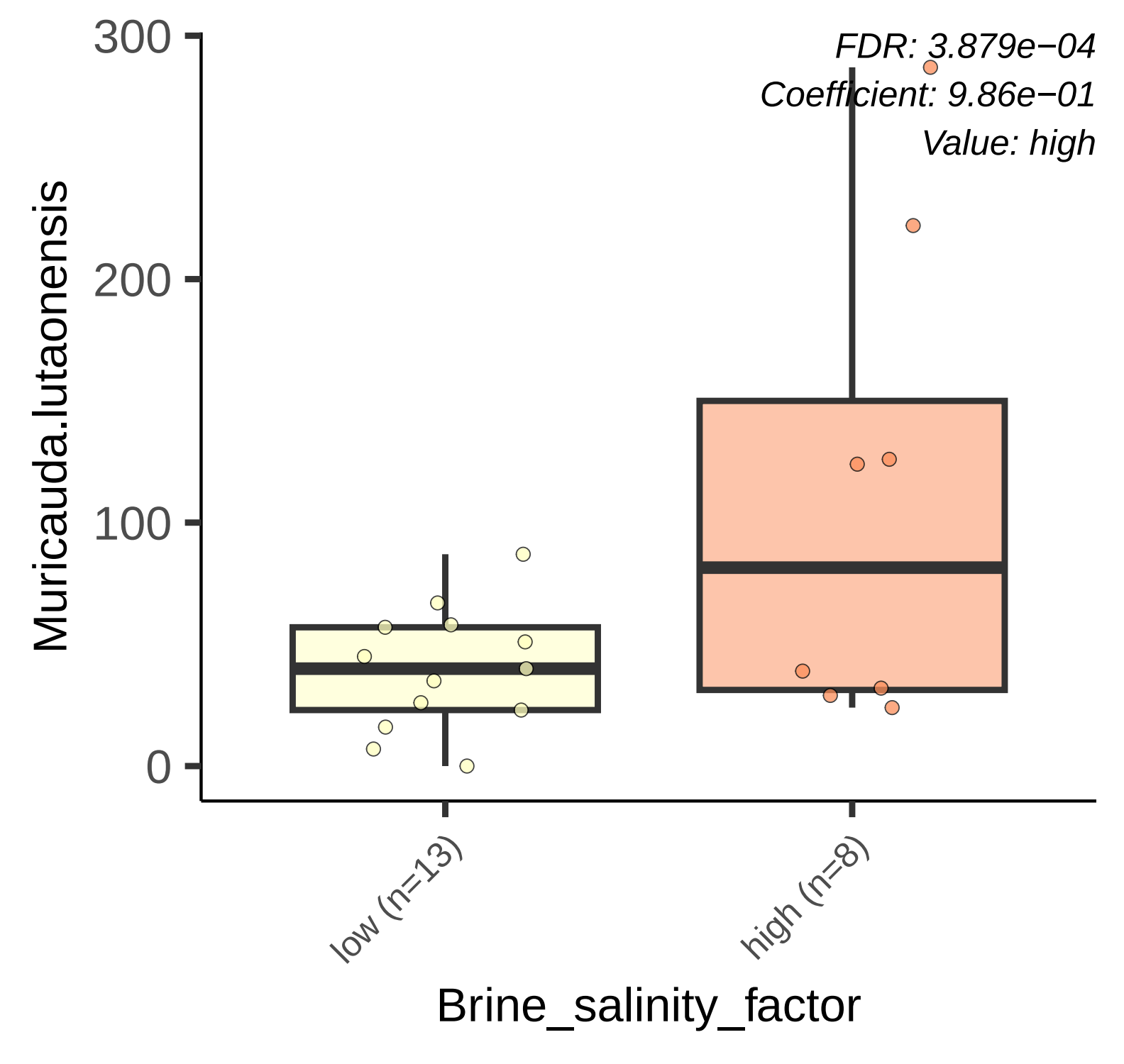

FDR: 3.063e−04
Coefficient: −6.29e−01
Value: high
3000
2000
1000
Rhodovulum.sp..P5
low (n=13)
high (n=8)
Brine_salinity_factor

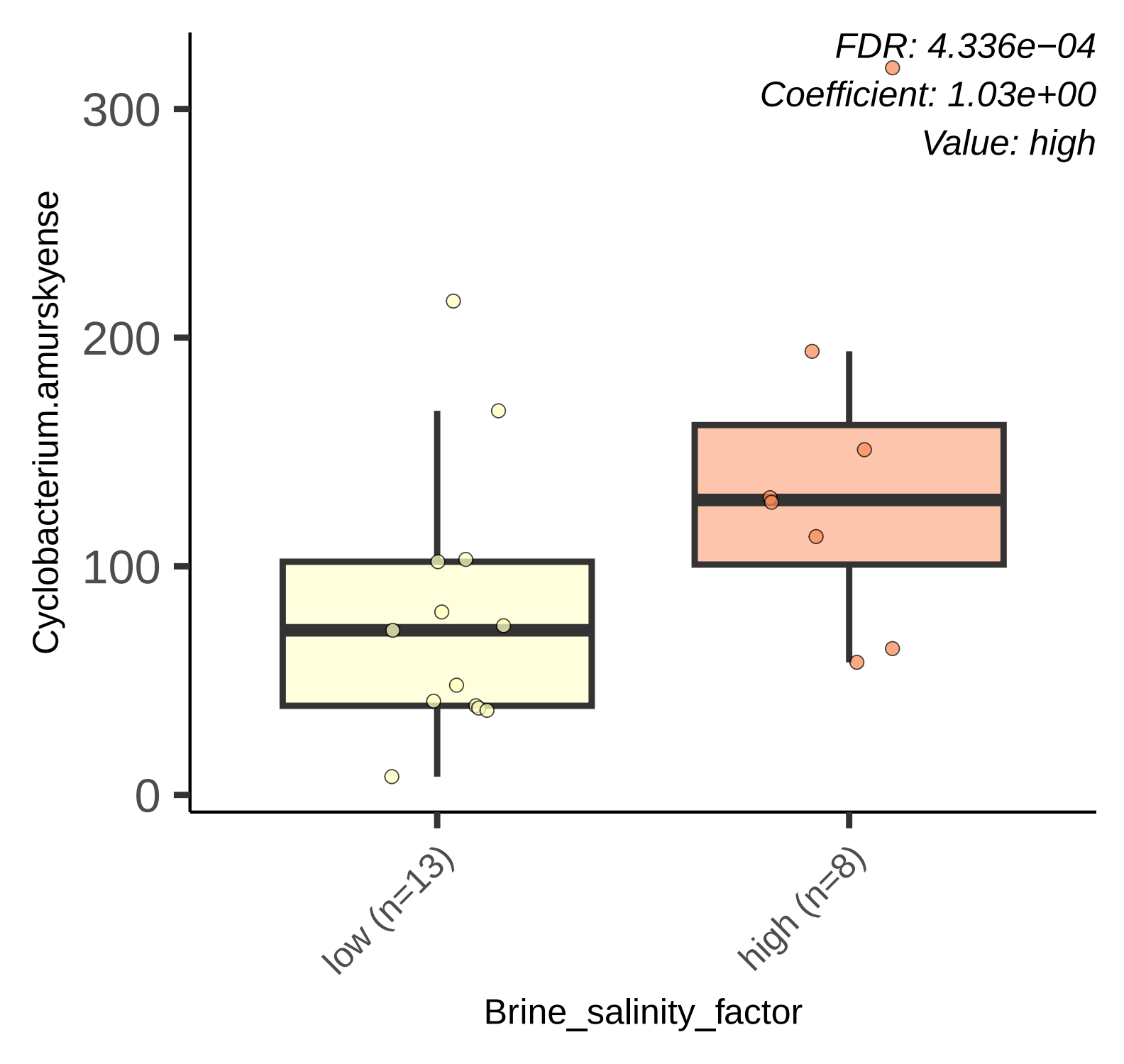

FDR: 3.115e−04
Coefficient: 1.54e+00
Value: high
Sphingopyxis.macrogoltabida
200
150
100
50
low (n=13)
high (n=8)
Brine_salinity_factor

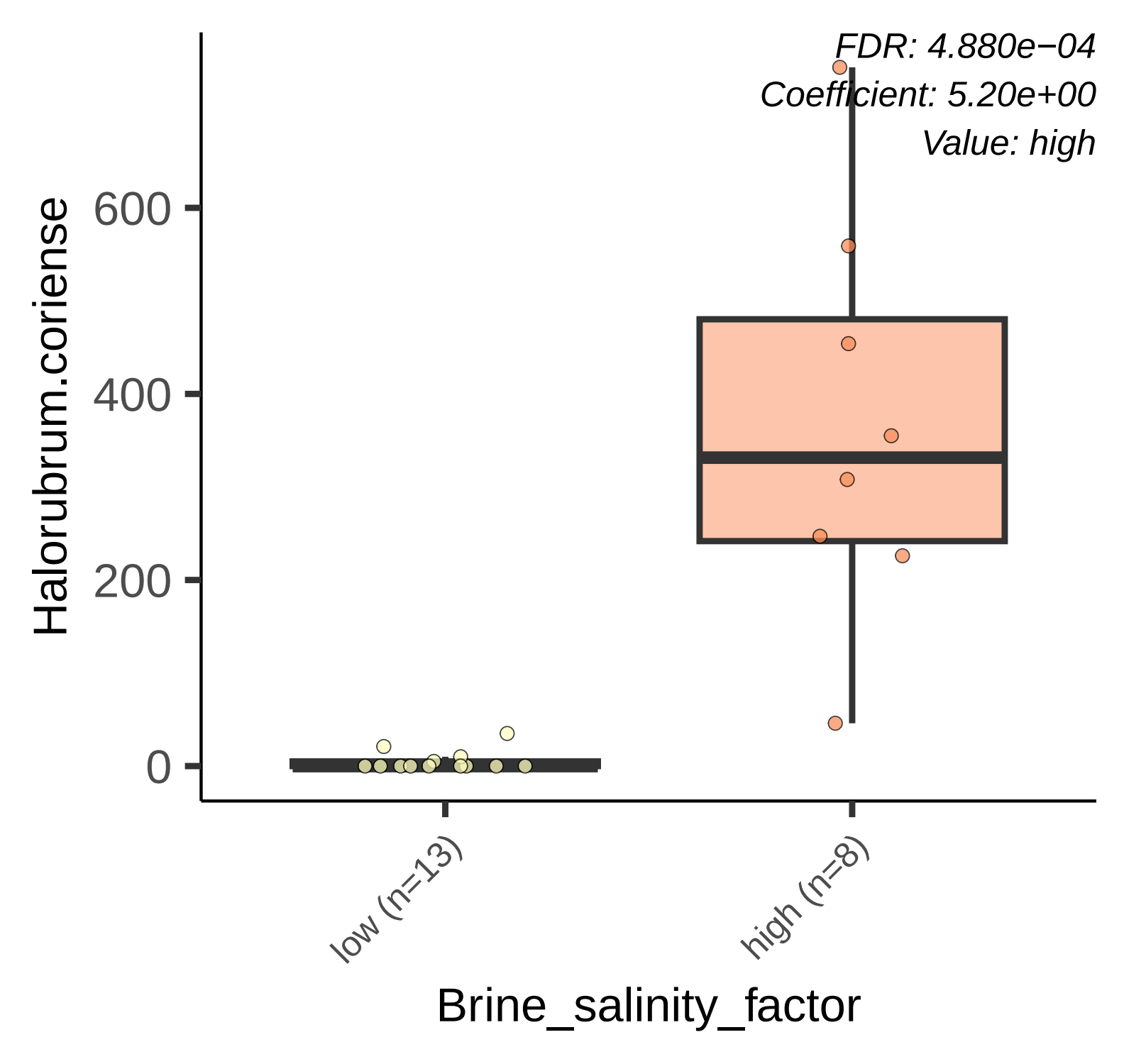

FDR: 3.415e−04
Coefficient: −5.31e−01
Value: high
Leisingera.methylohalidivorans
700
500
300
low (n=13)
high (n=8)
Brine_salinity_factor

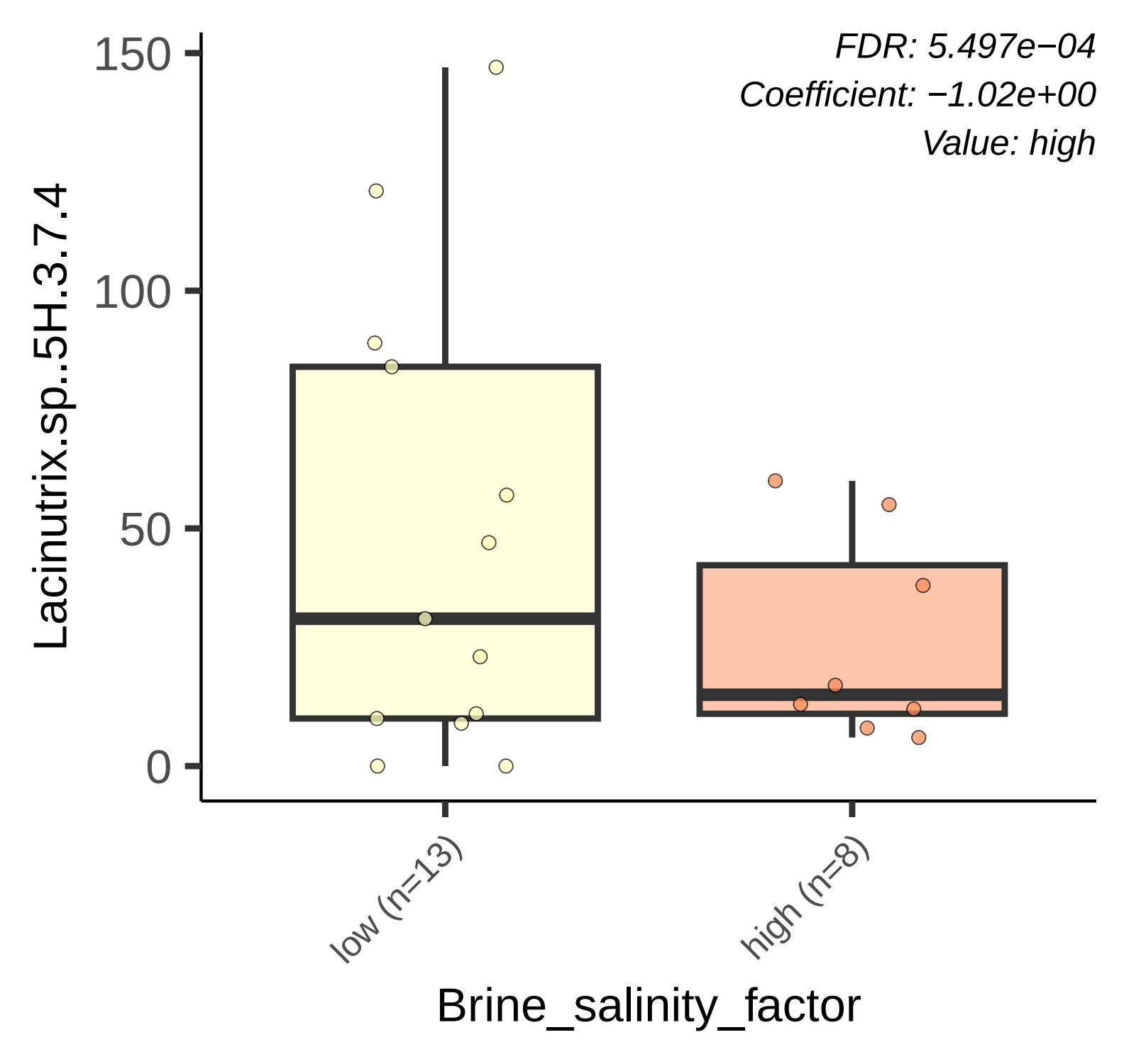

FDR: 3.607e−04
Coefficient: 3.36e+00
Value: high
8000
6000
4000
2000
0
Pseudodesulfovibrio.profundus
low (n=13)
high (n=8)
Brine_salinity_factor

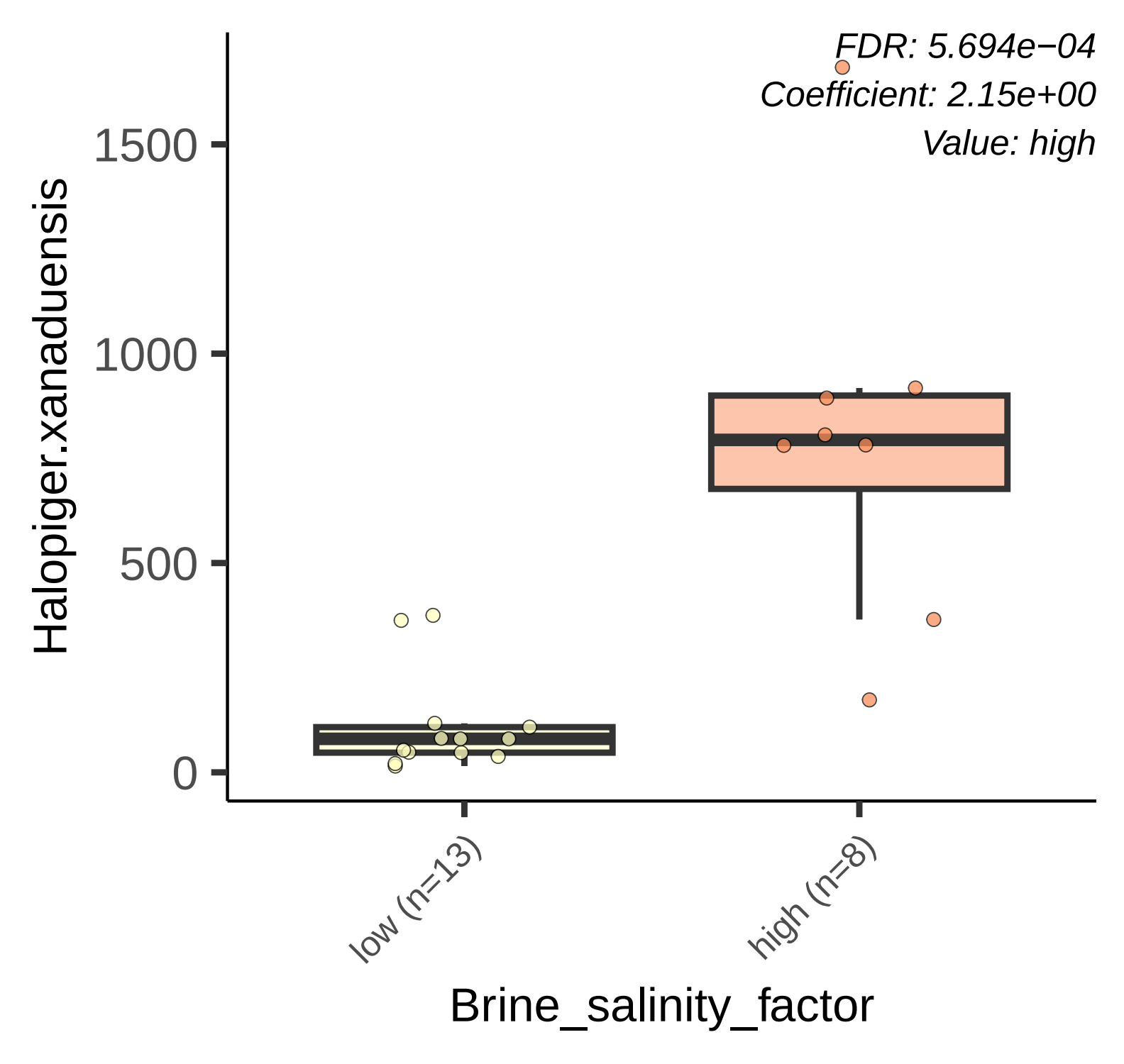

FDR: 3.746e−04
Coefficient: 2.04e+00
Value: high
1500
1000
500
0
Natrinema.sp..J7.2
low (n=13)
high (n=8)
Brine_salinity_factor

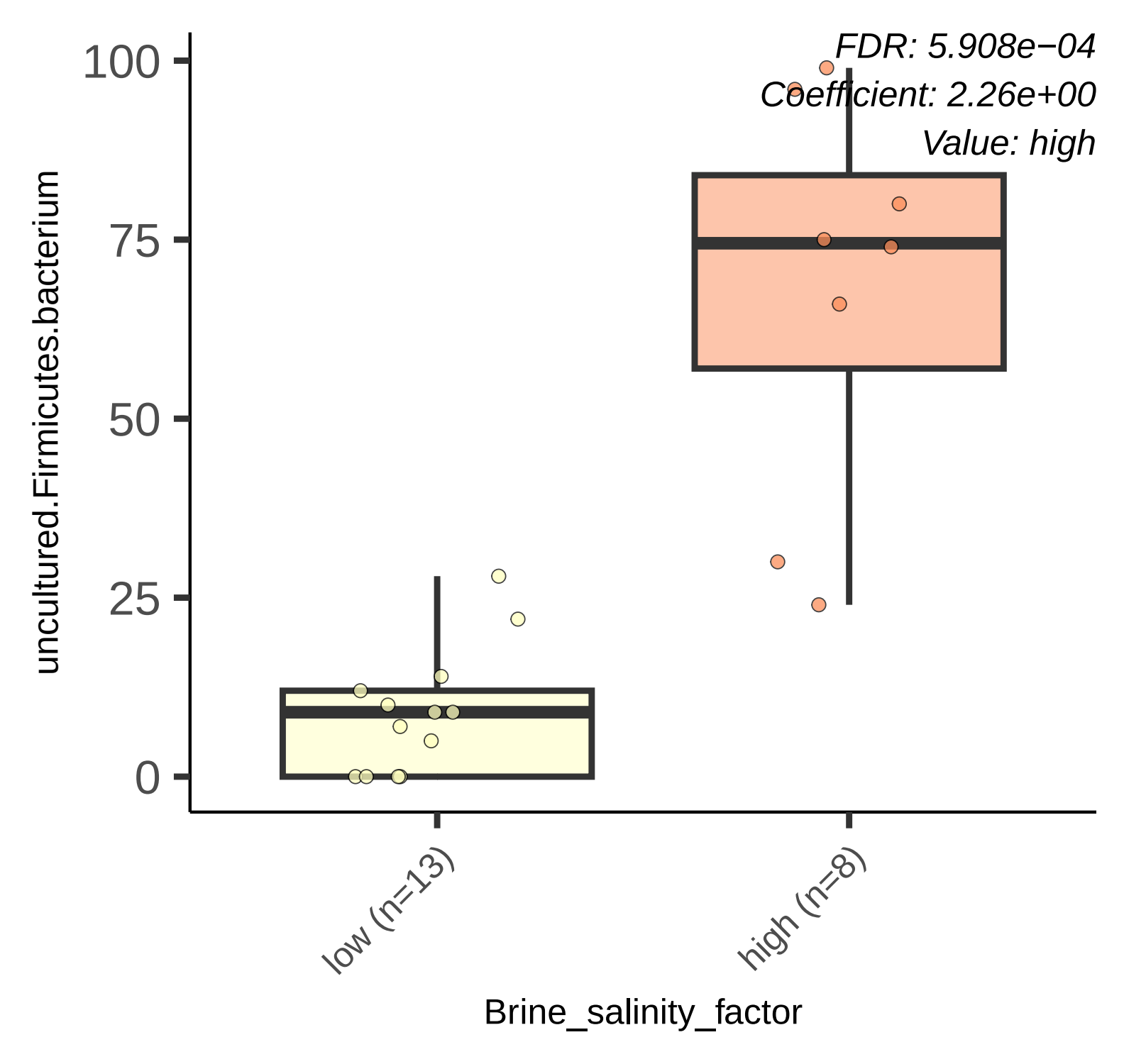

FDR: 3.879e−04
Coefficient: 9.86e−01
Value: high
Muricauda.lutaonensis
300
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

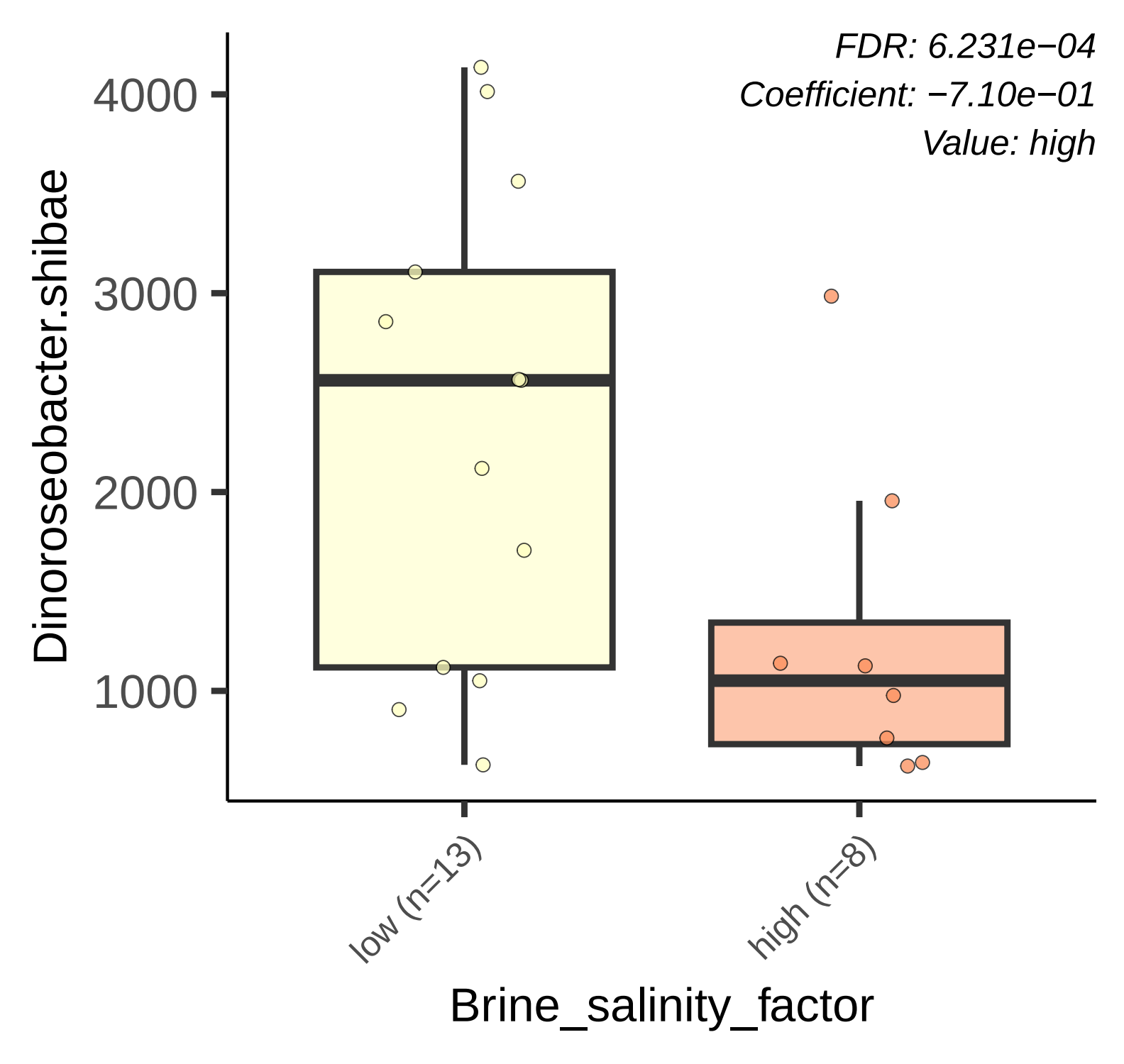

FDR: 4.336e−04
Coefficient: 1.03e+00
Value: high
300
200
100
0
Cyclobacterium.amurskyense
low (n=13)
high (n=8)
Brine_salinity_factor

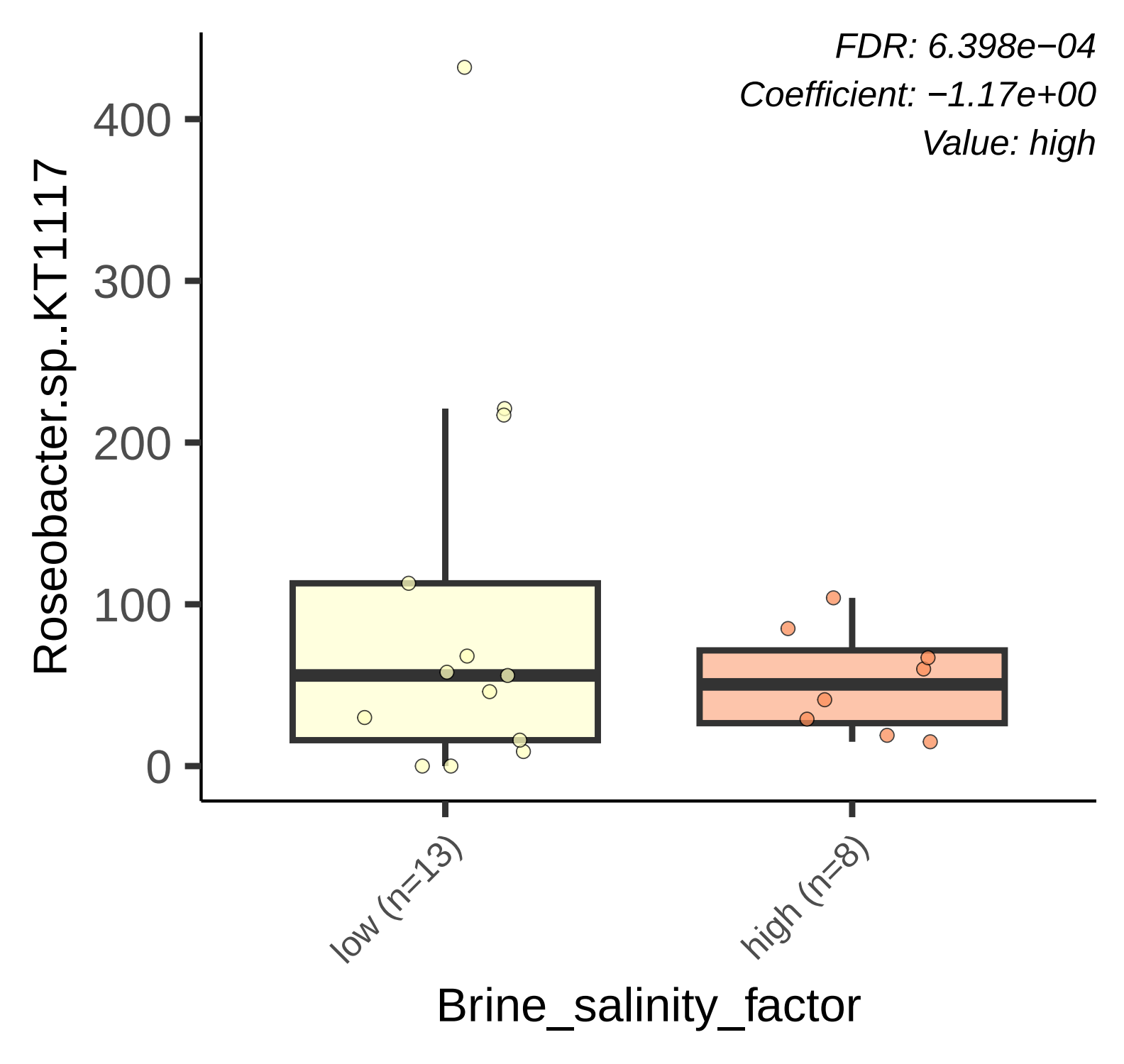

FDR: 4.880e−04
Coefficient: 5.20e+00
Value: high
Halorubrum.coriense
600
400
200
0
low (n=13)
high (n=8)
Brine_salinity_factor

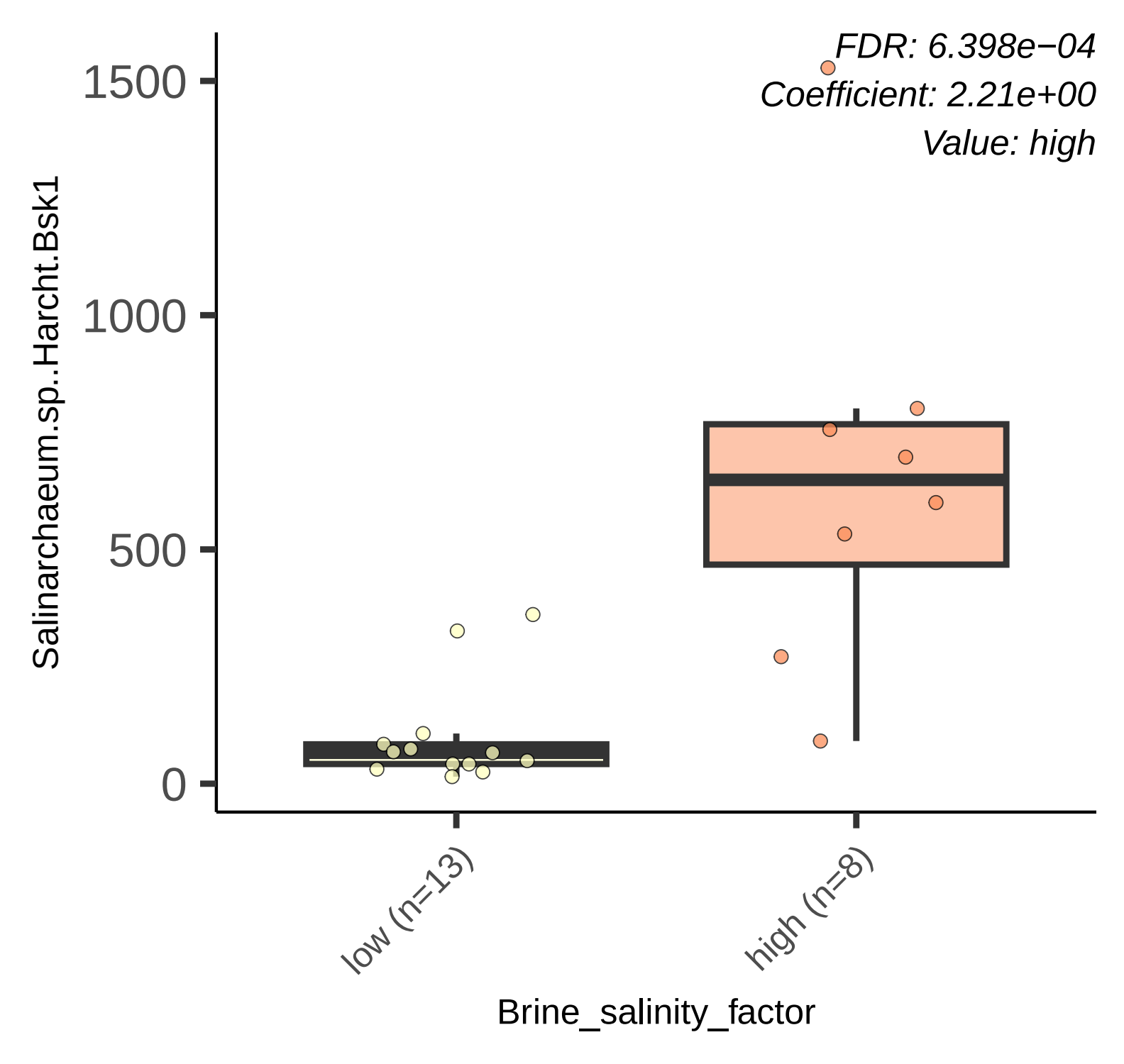

FDR: 5.497e−04
Coefficient: −1.02e+00
Value: high
Lacinutrix.sp..5H.3.7.4
150
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

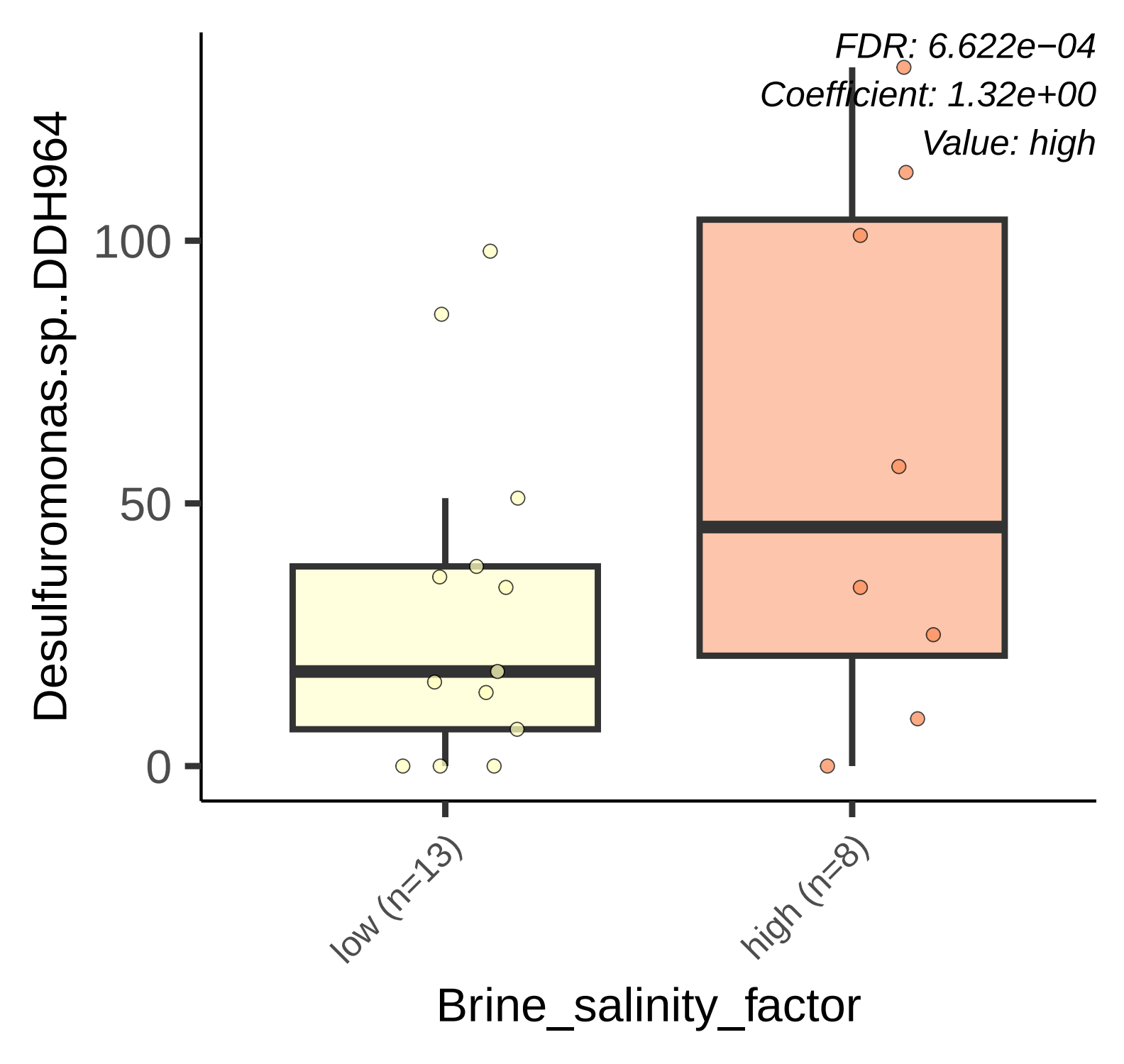

FDR: 5.694e−04
Coefficient: 2.15e+00
Value: high
1500
1000
500
0
Halopiger.xanaduensis
low (n=13)
high (n=8)
Brine_salinity_factor

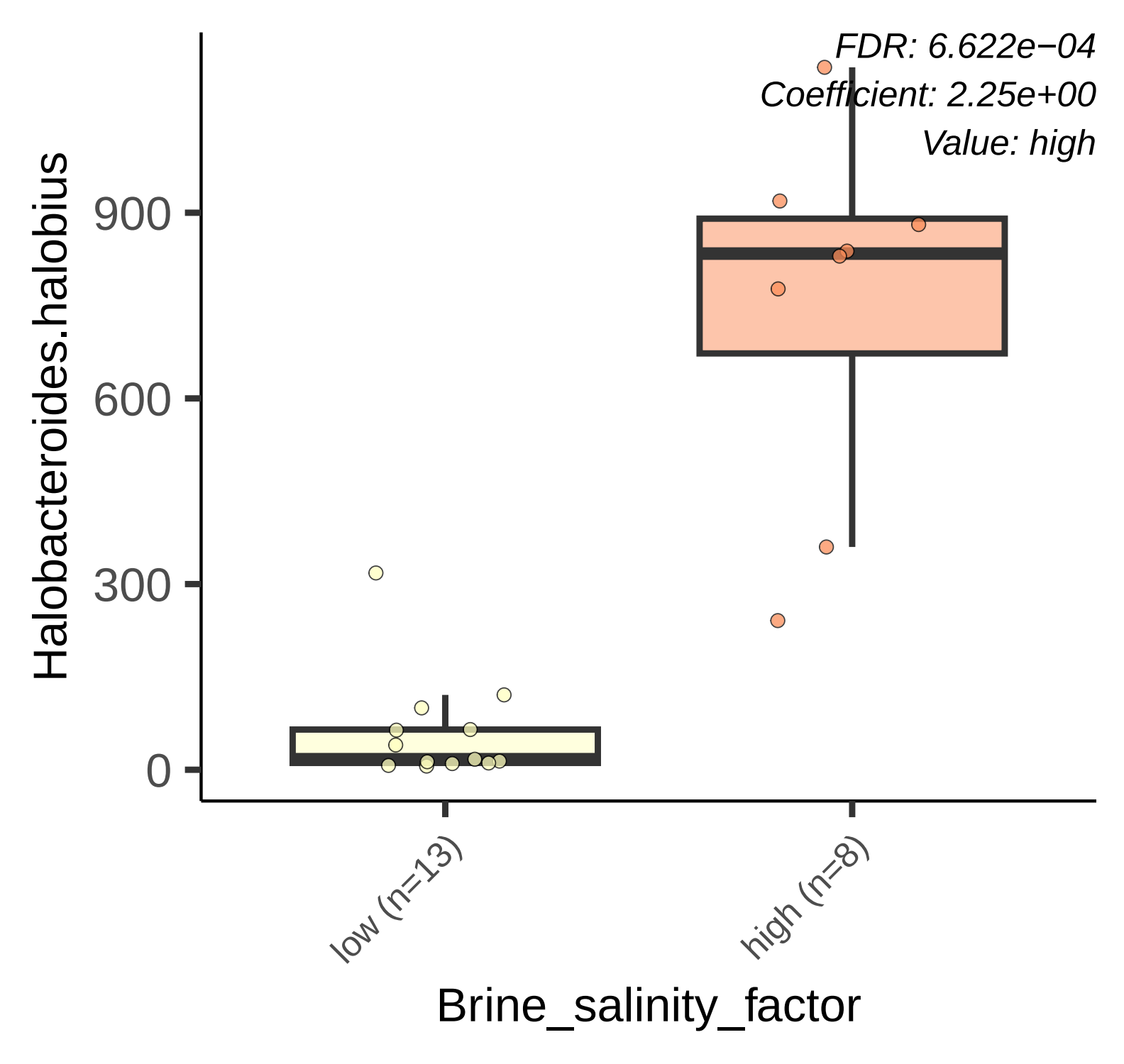

FDR: 5.908e−04
Coefficient: 2.26e+00
Value: high
100
75
50
25
0
uncultured.Firmicutes.bacterium
low (n=13)
high (n=8)
Brine_salinity_factor

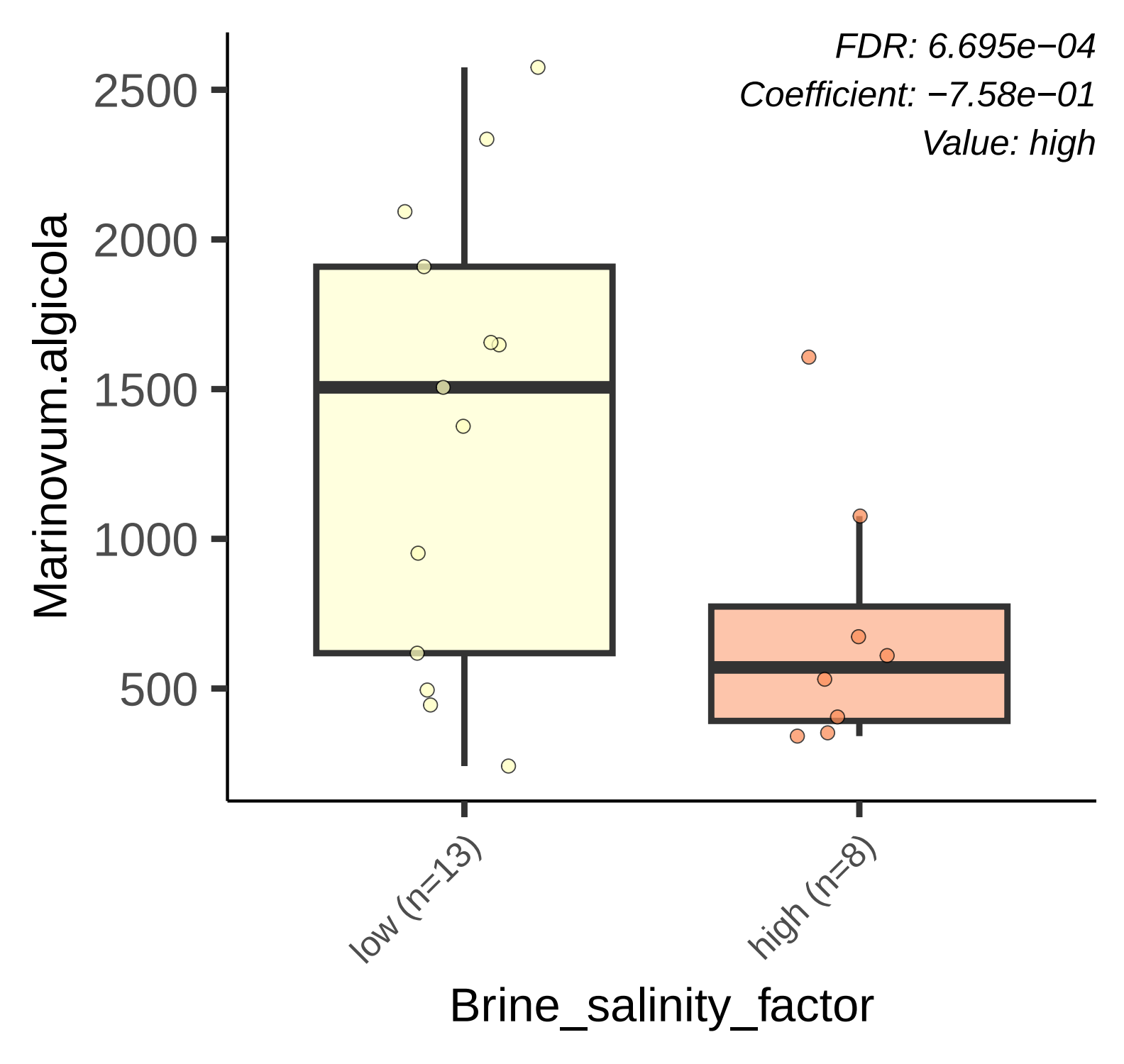

FDR: 6.231e−04
Coefficient: −7.10e−01
Value: high
4000
3000
2000
1000
Dinoroseobacter.shibae
low (n=13)
high (n=8)
Brine_salinity_factor

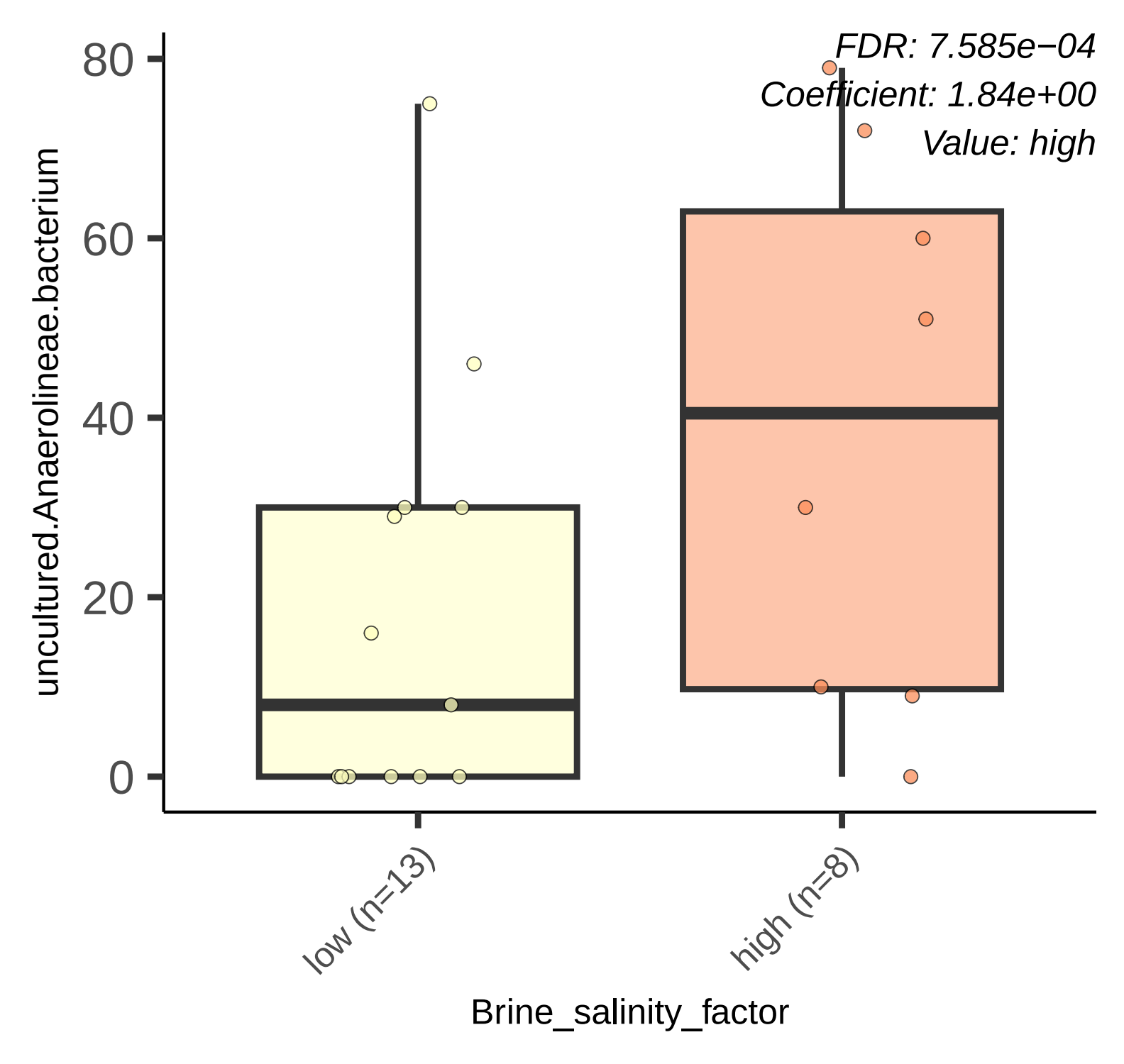

FDR: 6.398e−04
Coefficient: −1.17e+00
Value: high
Roseobacter.sp..KT1117
400
300
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

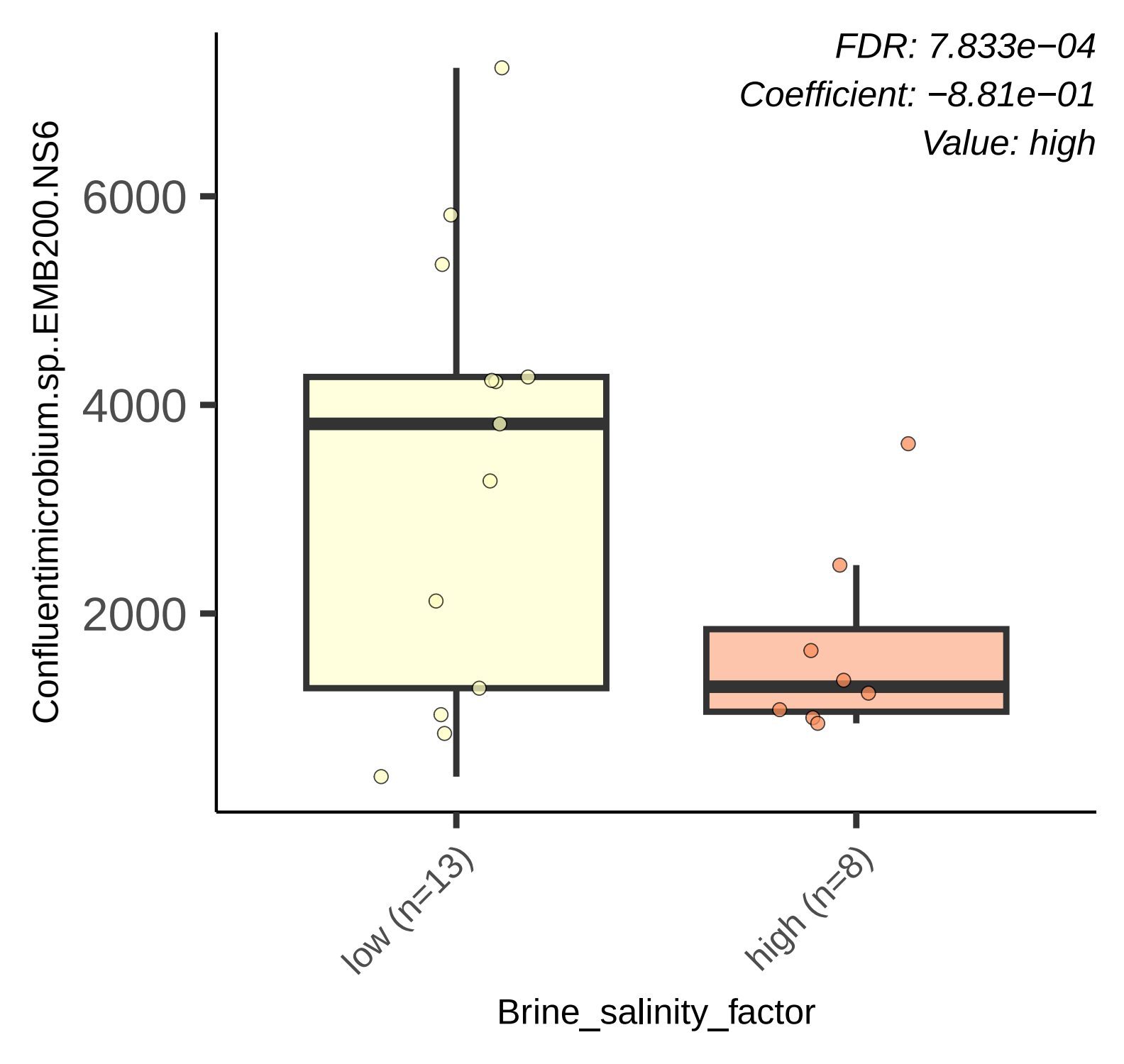

FDR: 6.398e−04
Coefficient: 2.21e+00
Value: high
1500
1000
500
0
Salinarchaeum.sp..Harcht.Bsk1
low (n=13)
high (n=8)
Brine_salinity_factor

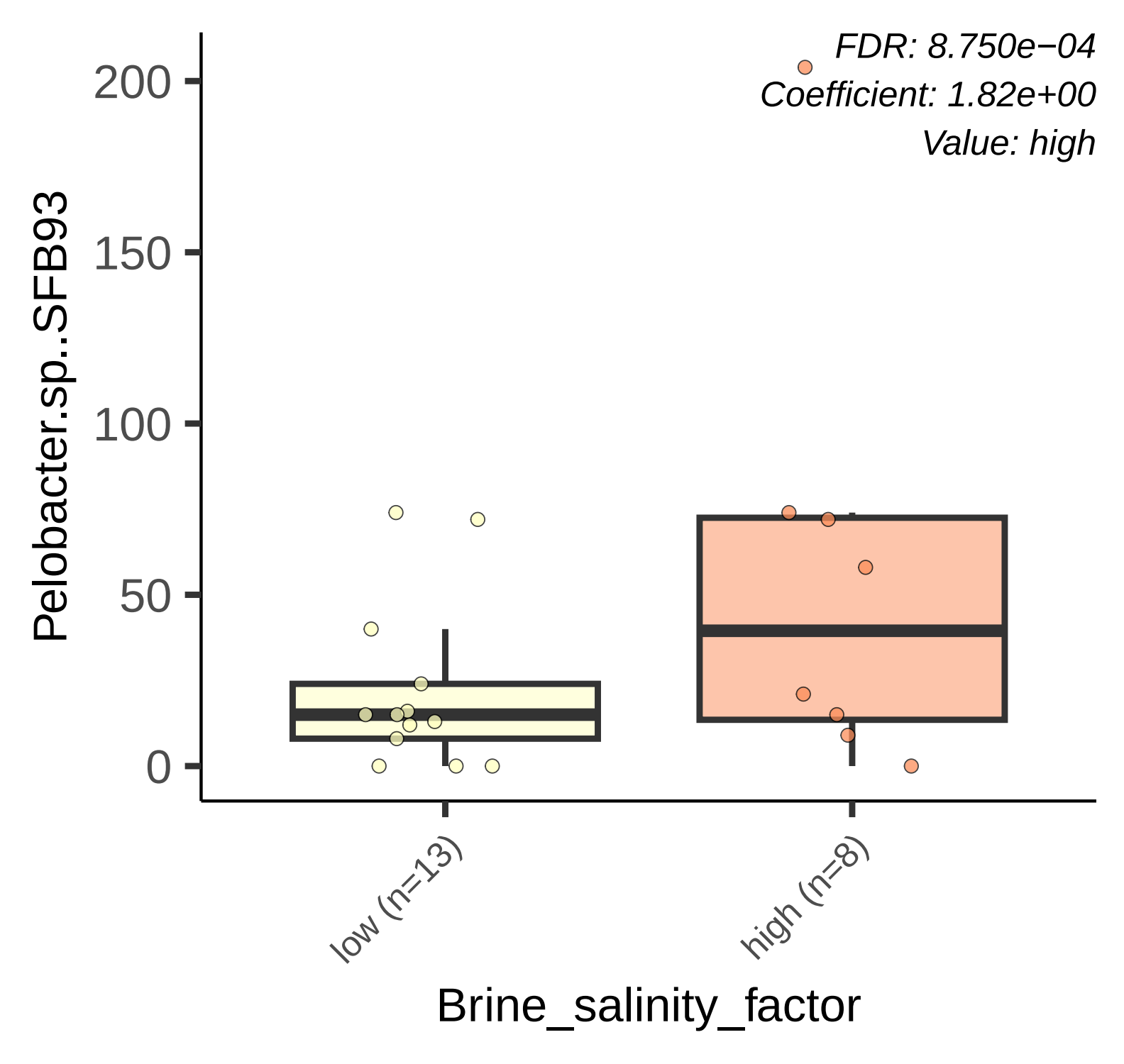

FDR: 6.622e−04
Coefficient: 1.32e+00
Value: high
Desulfuromonas.sp..DDH964
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

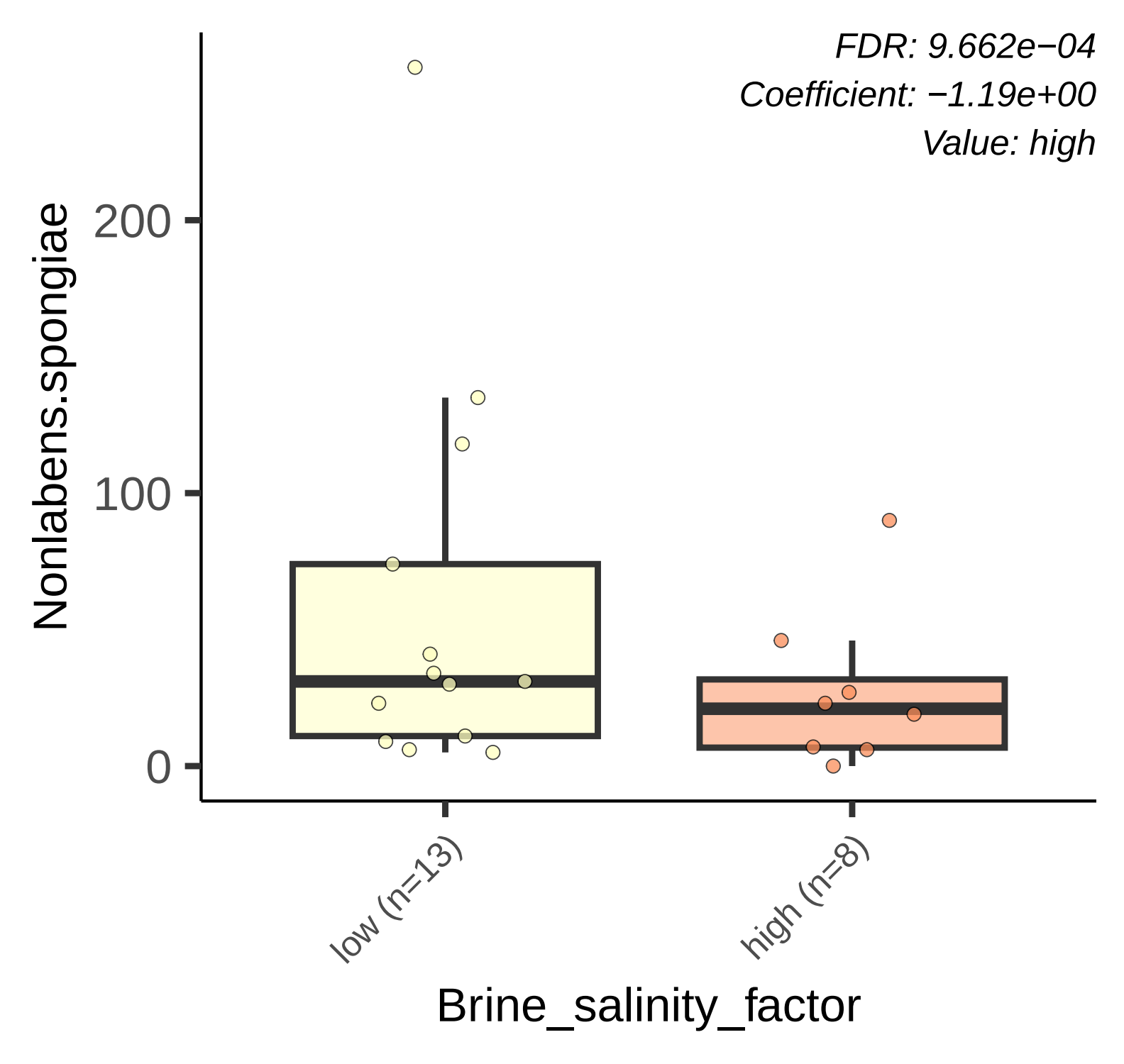

FDR: 6.622e−04
Coefficient: 2.25e+00
Value: high
Halobacteroides.halobius
900
600
300
0
low (n=13)
high (n=8)
Brine_salinity_factor

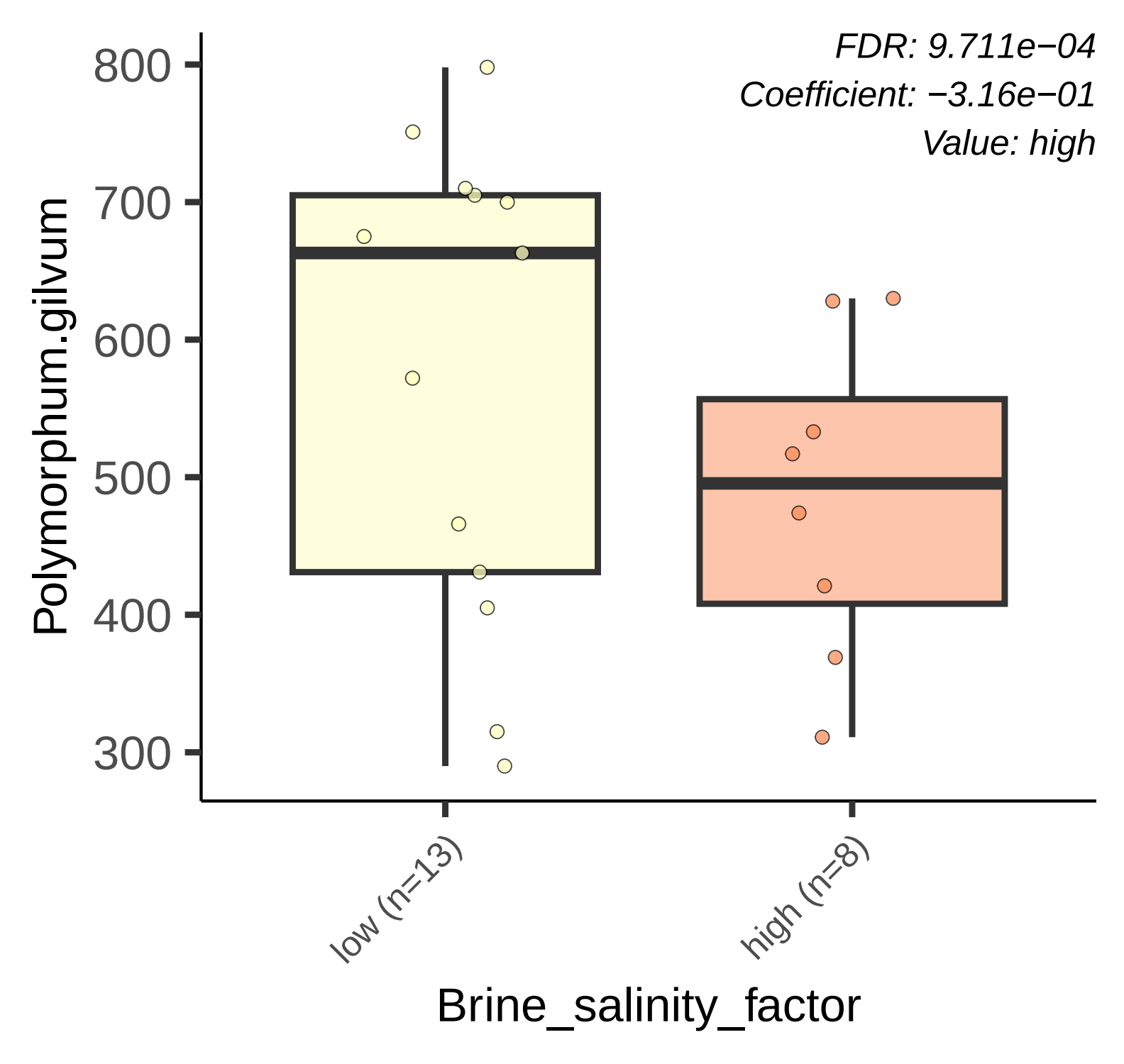

FDR: 6.695e−04
Coefficient: −7.58e−01
Value: high
Marinovum.algicola
2500
2000
1500
1000
500
low (n=13)
high (n=8)
Brine_salinity_factor

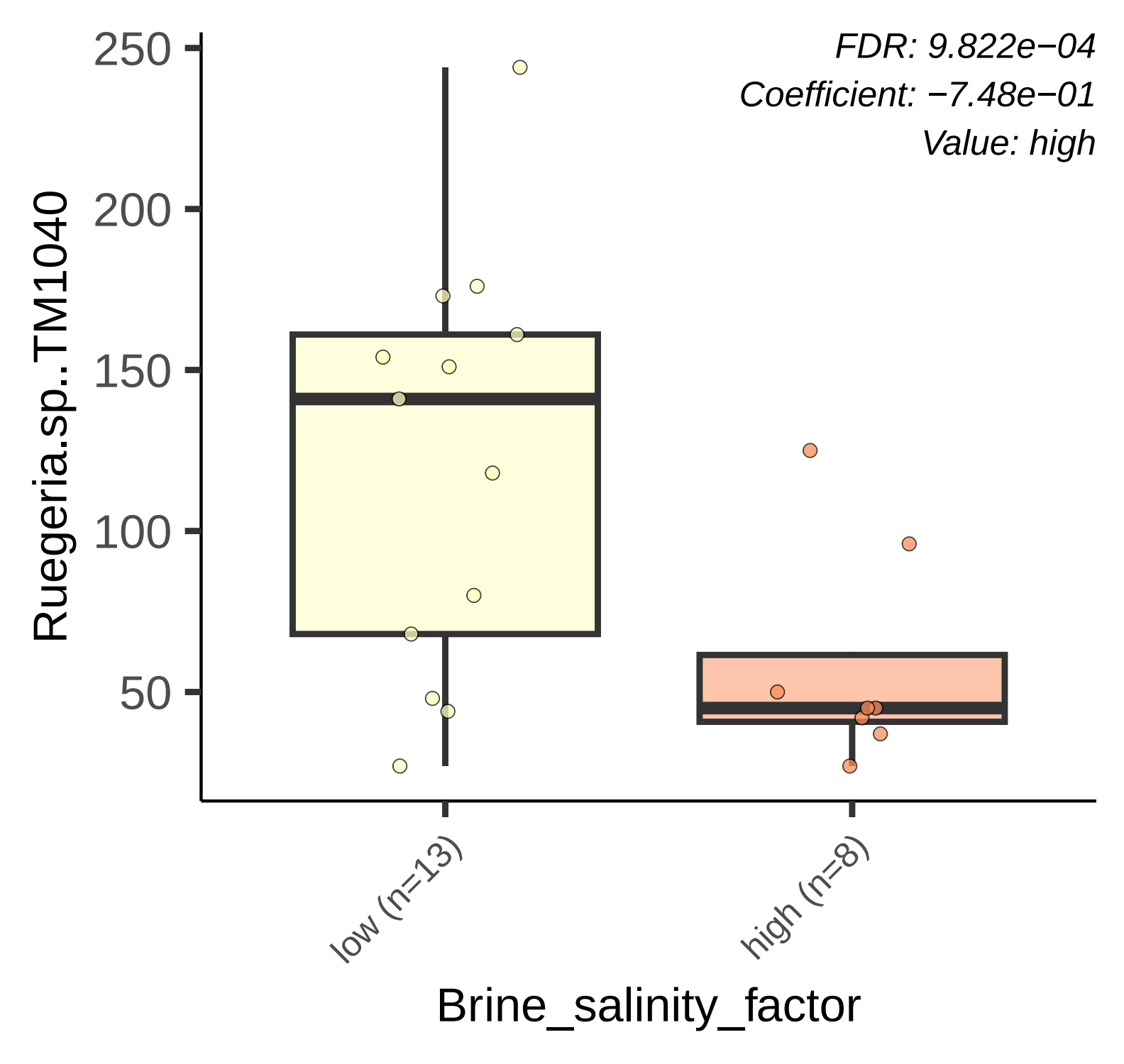

FDR: 7.585e−04
Coefficient: 1.84e+00
Value: high
uncultured.Anaerolineae.bacterium
80
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

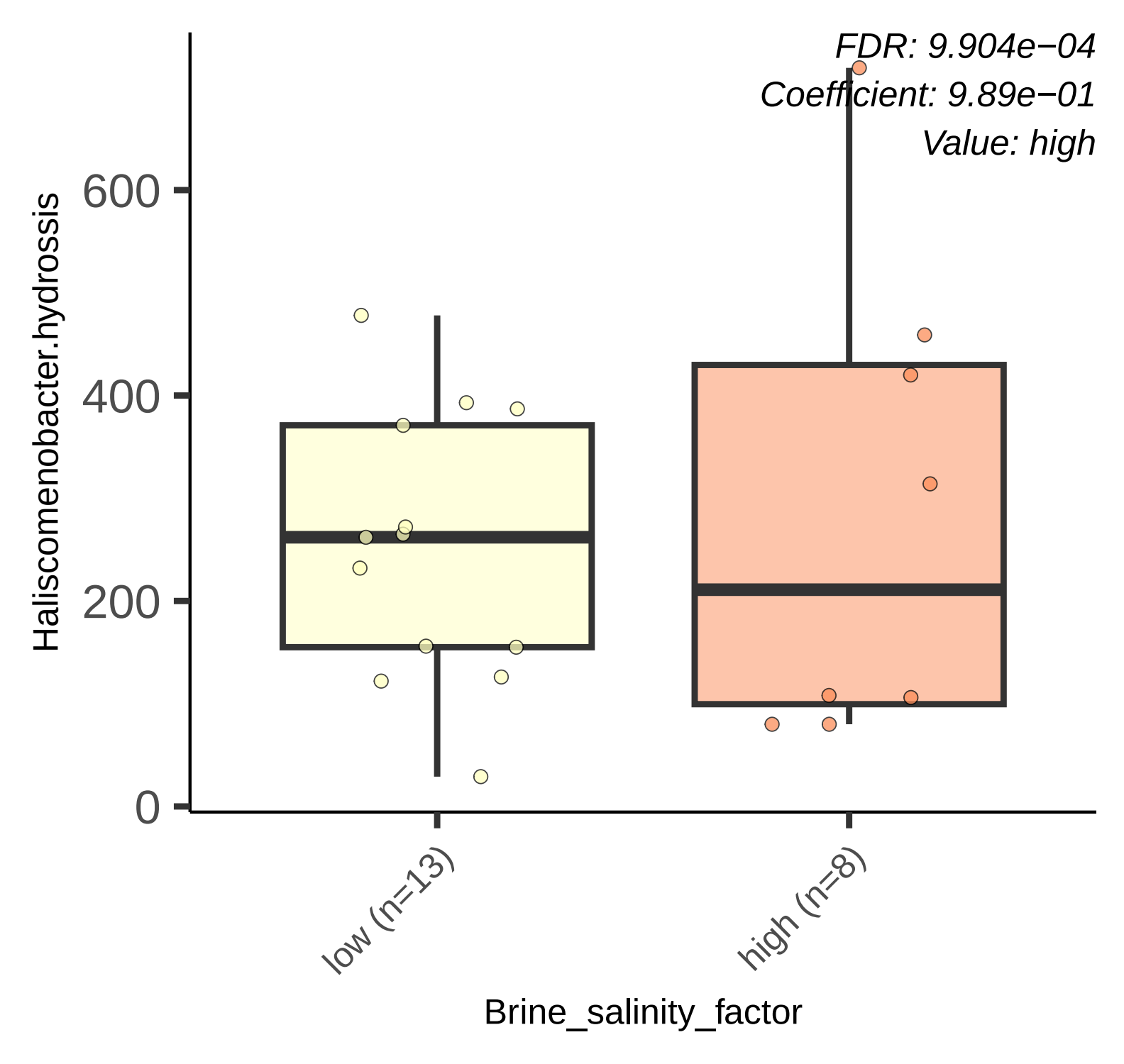

FDR: 7.833e−04
Coefficient: −8.81e−01
Value: high
Confluentimicrobium.sp..EMB200.NS6
6000
4000
2000
low (n=13)
high (n=8)
Brine_salinity_factor

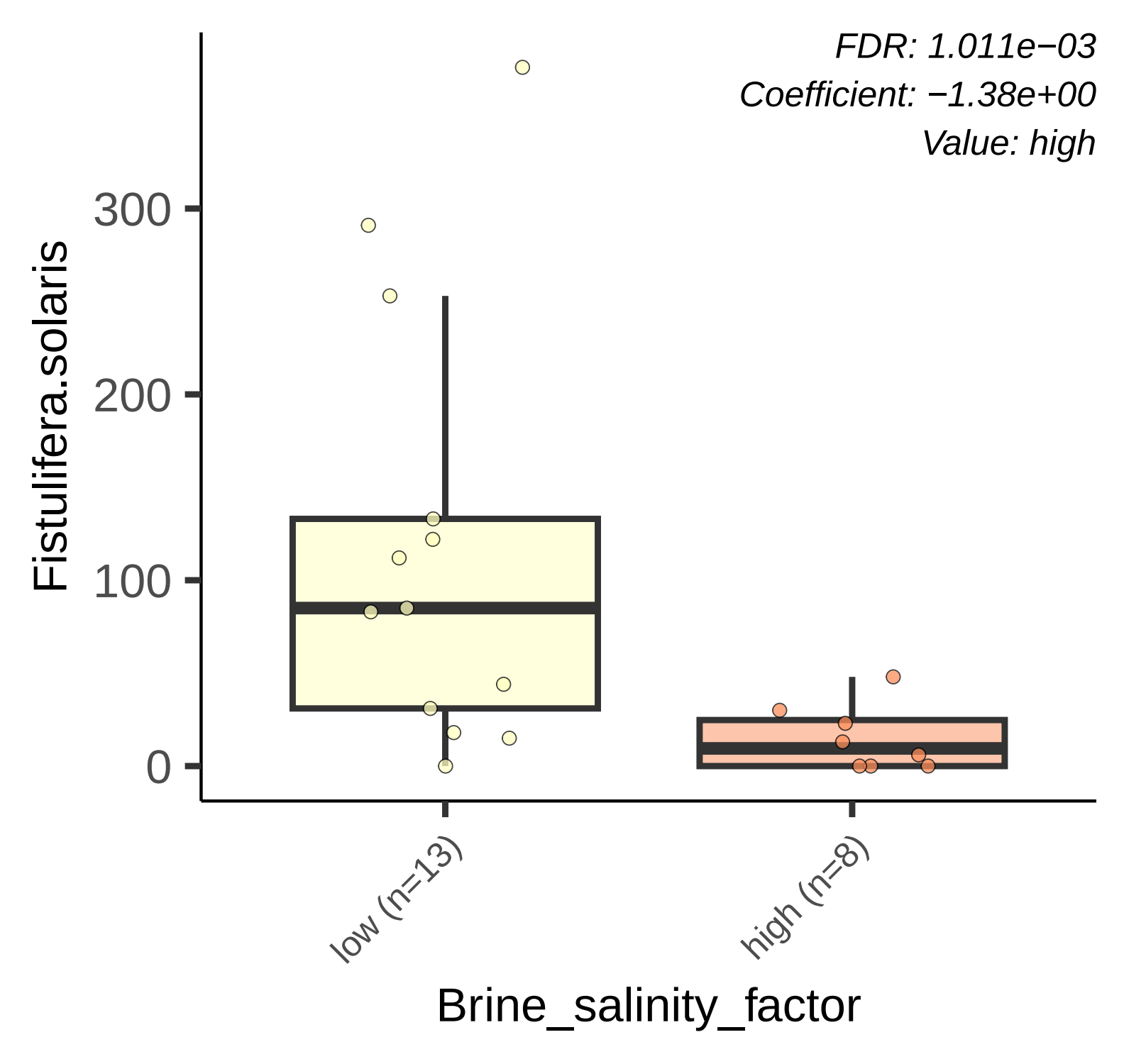

FDR: 8.750e−04
Coefficient: 1.82e+00
Value: high
Pelobacter.sp..SFB93
200
150
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

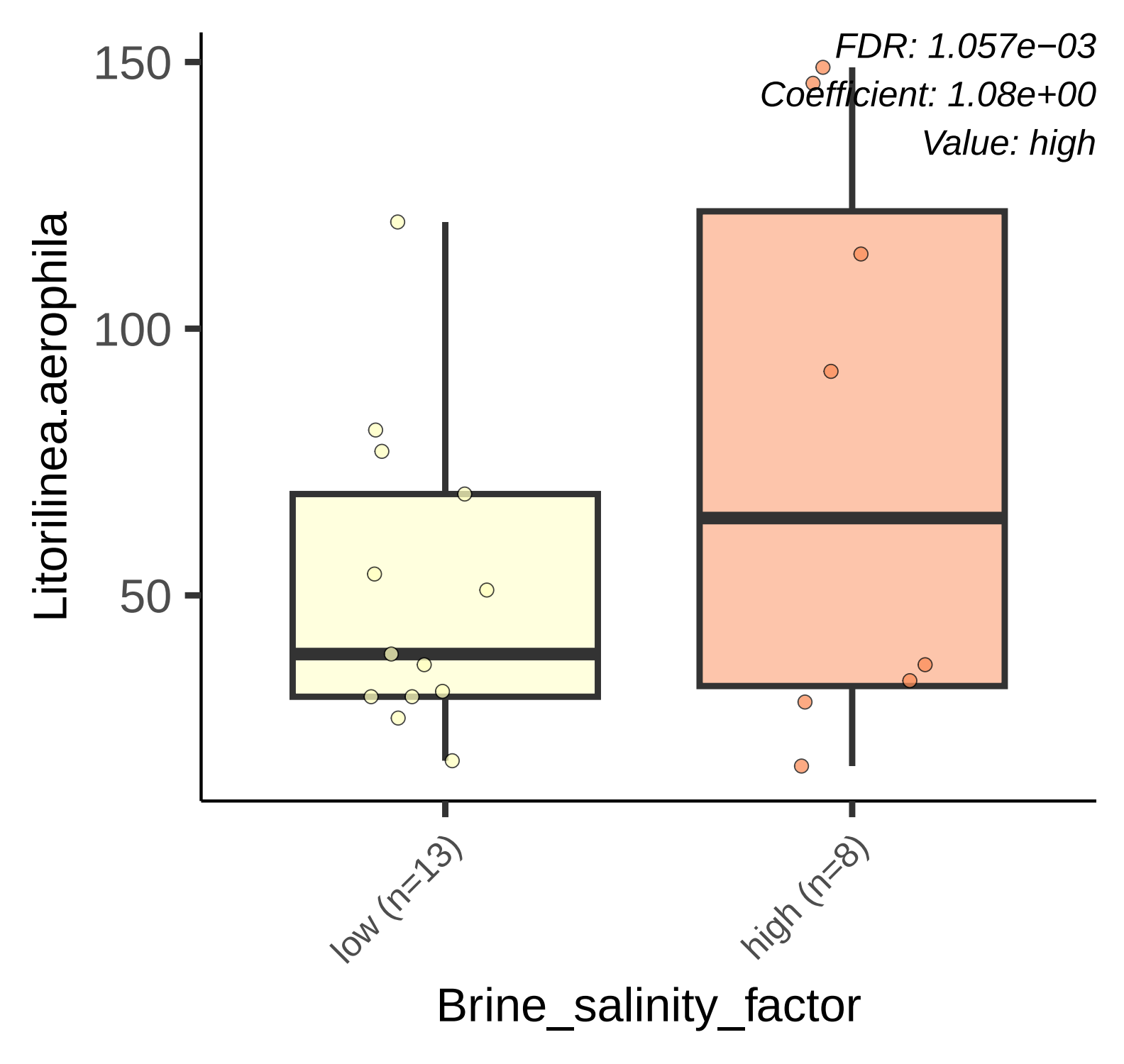

FDR: 9.662e−04
Coefficient: −1.19e+00
Value: high
Nonlabens.spongiae
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

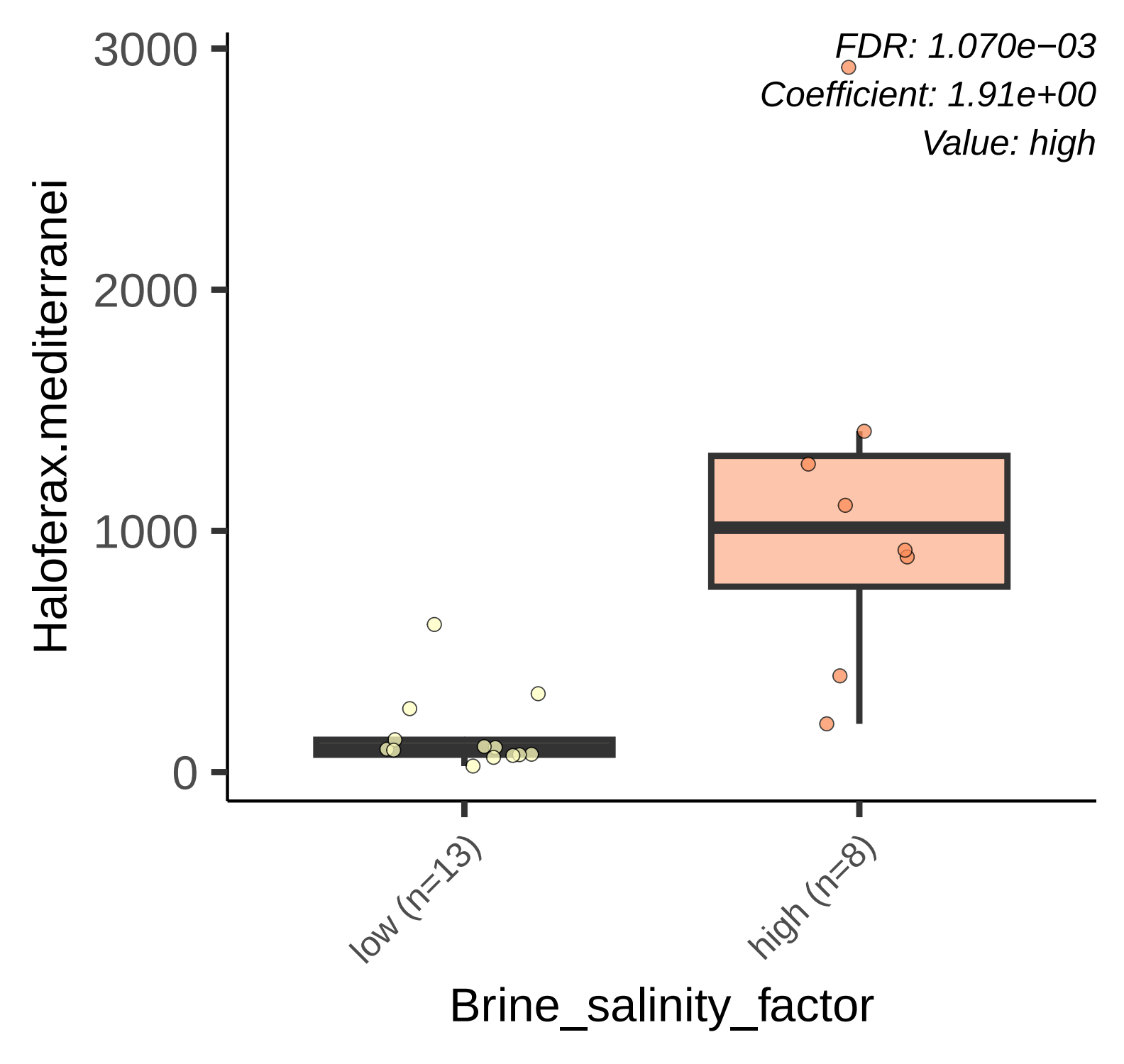

FDR: 9.711e−04
Coefficient: −3.16e−01
Value: high
Polymorphum.gilvum
800
700
600
500
400
300
low (n=13)
high (n=8)
Brine_salinity_factor

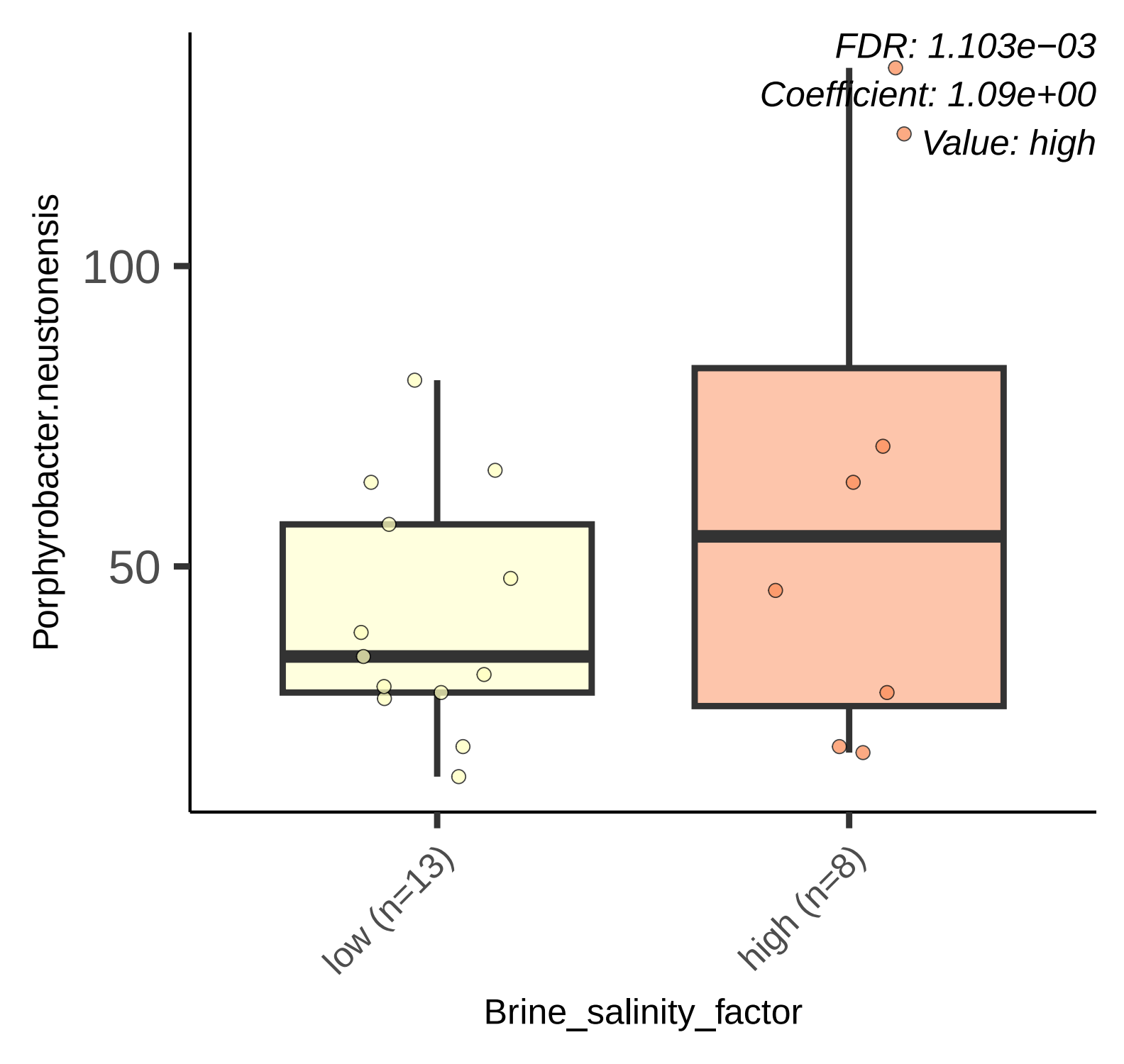

FDR: 9.822e−04
Coefficient: −7.48e−01
Value: high
250
200
150
100
50
Ruegeria.sp..TM1040
low (n=13)
high (n=8)
Brine_salinity_factor

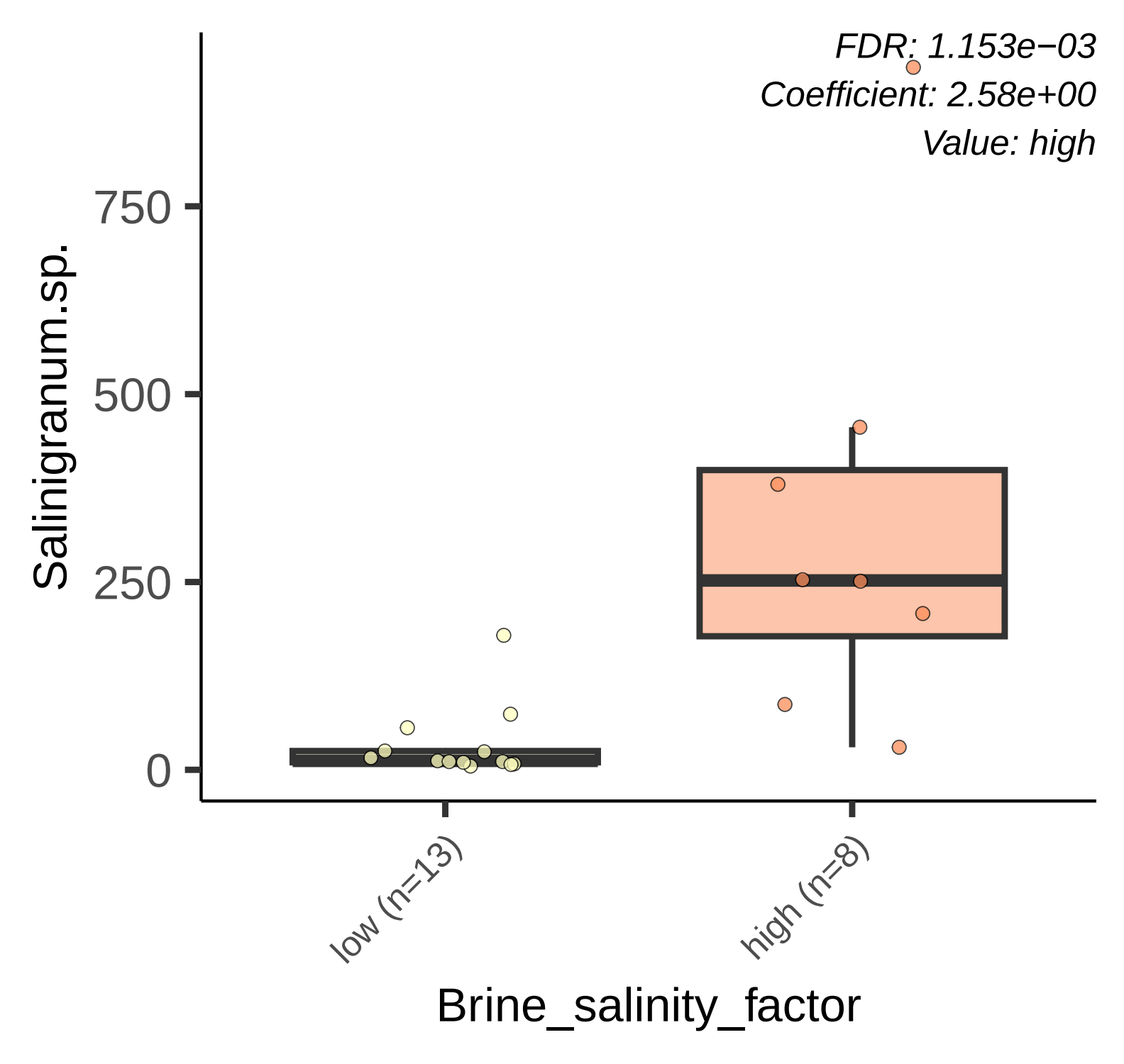

FDR: 9.904e−04
Coefficient: 9.89e−01
Value: high
Haliscomenobacter.hydrossis
600
400
200
0
low (n=13)
high (n=8)
Brine_salinity_factor

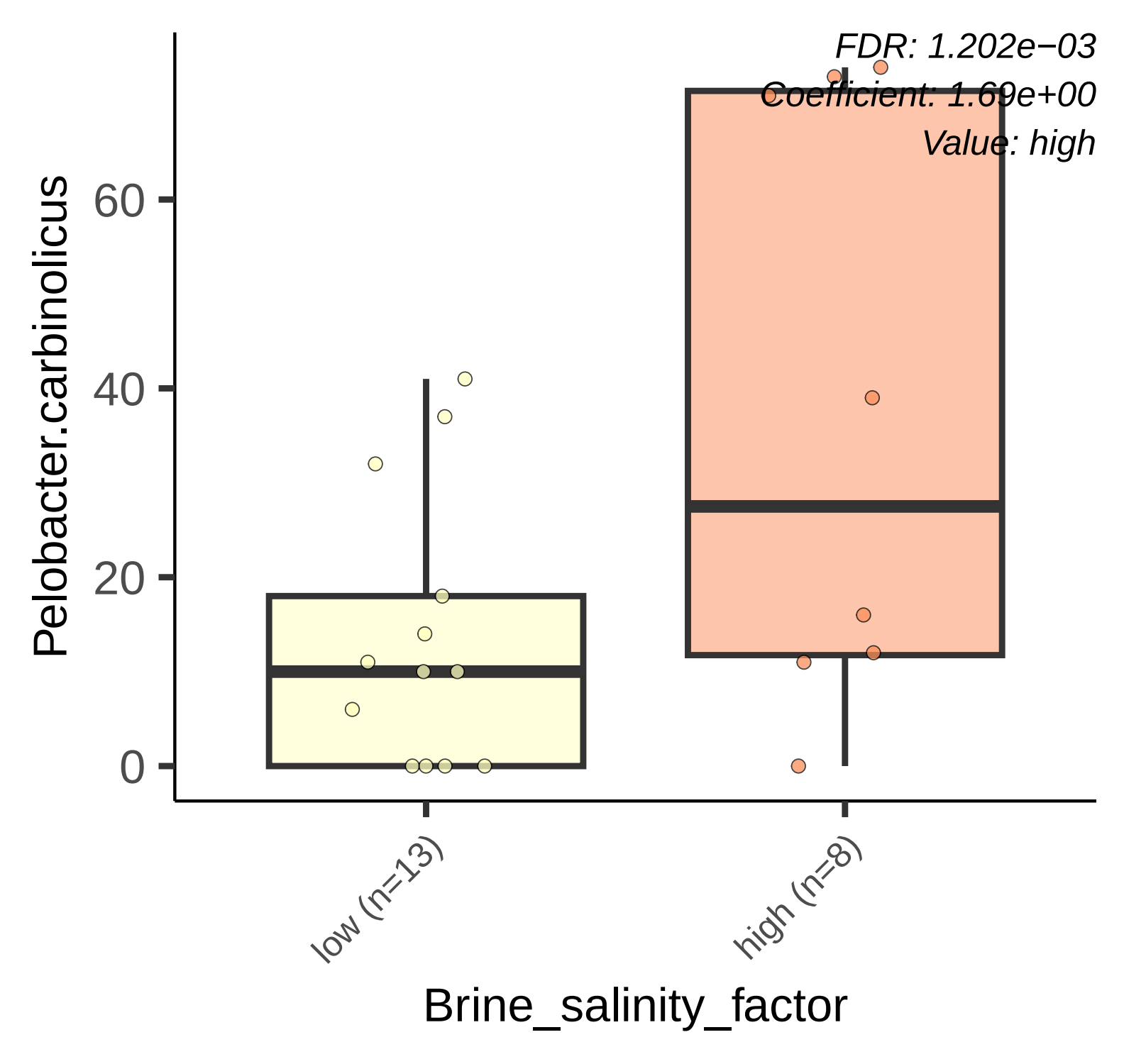

FDR: 1.011e−03
Coefficient: −1.38e+00
Value: high
Fistulifera.solaris
300
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

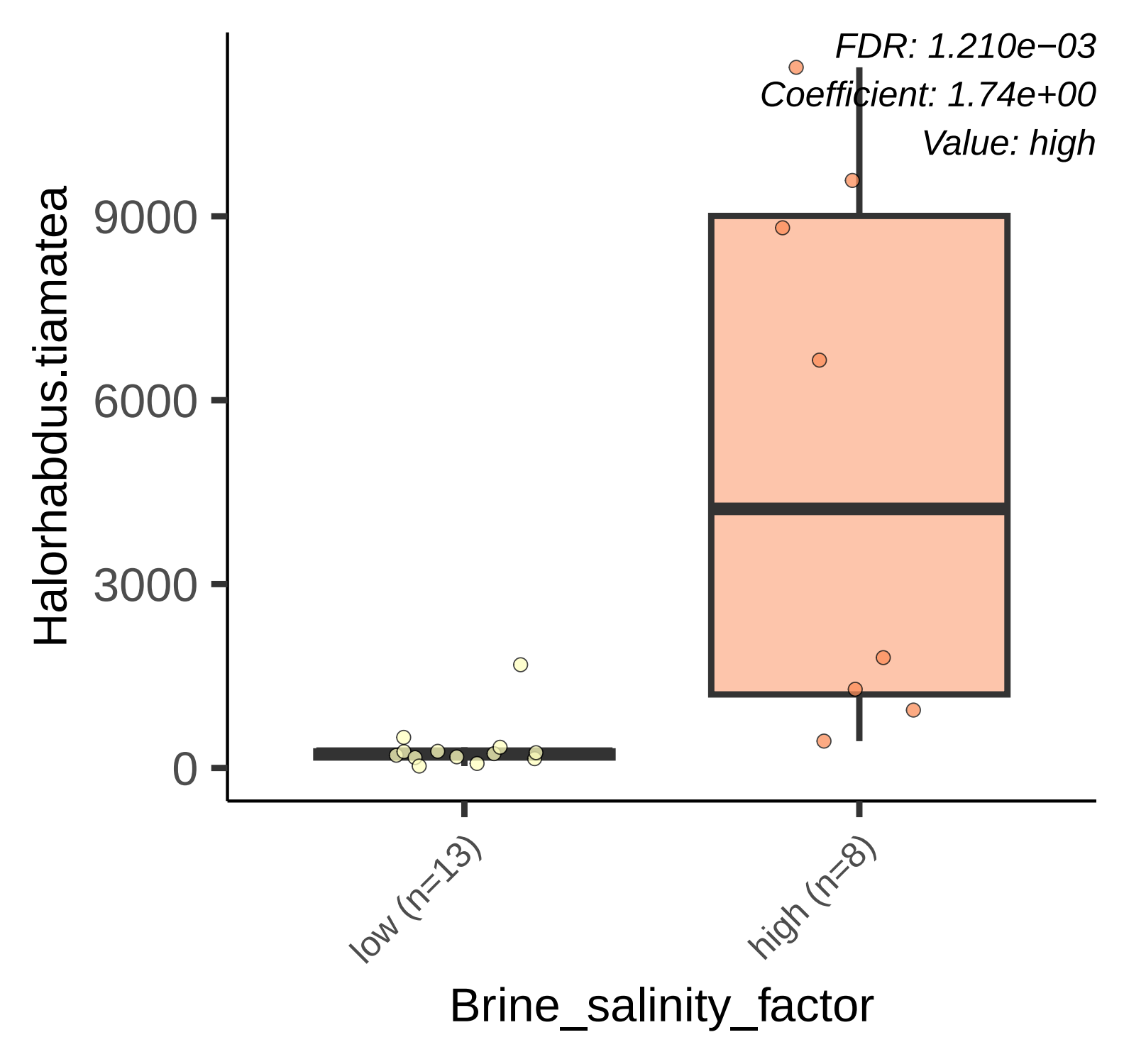

FDR: 1.057e−03
Coefficient: 1.08e+00
Value: high
150
100
50
Litorilinea.aerophila
low (n=13)
high (n=8)
Brine_salinity_factor

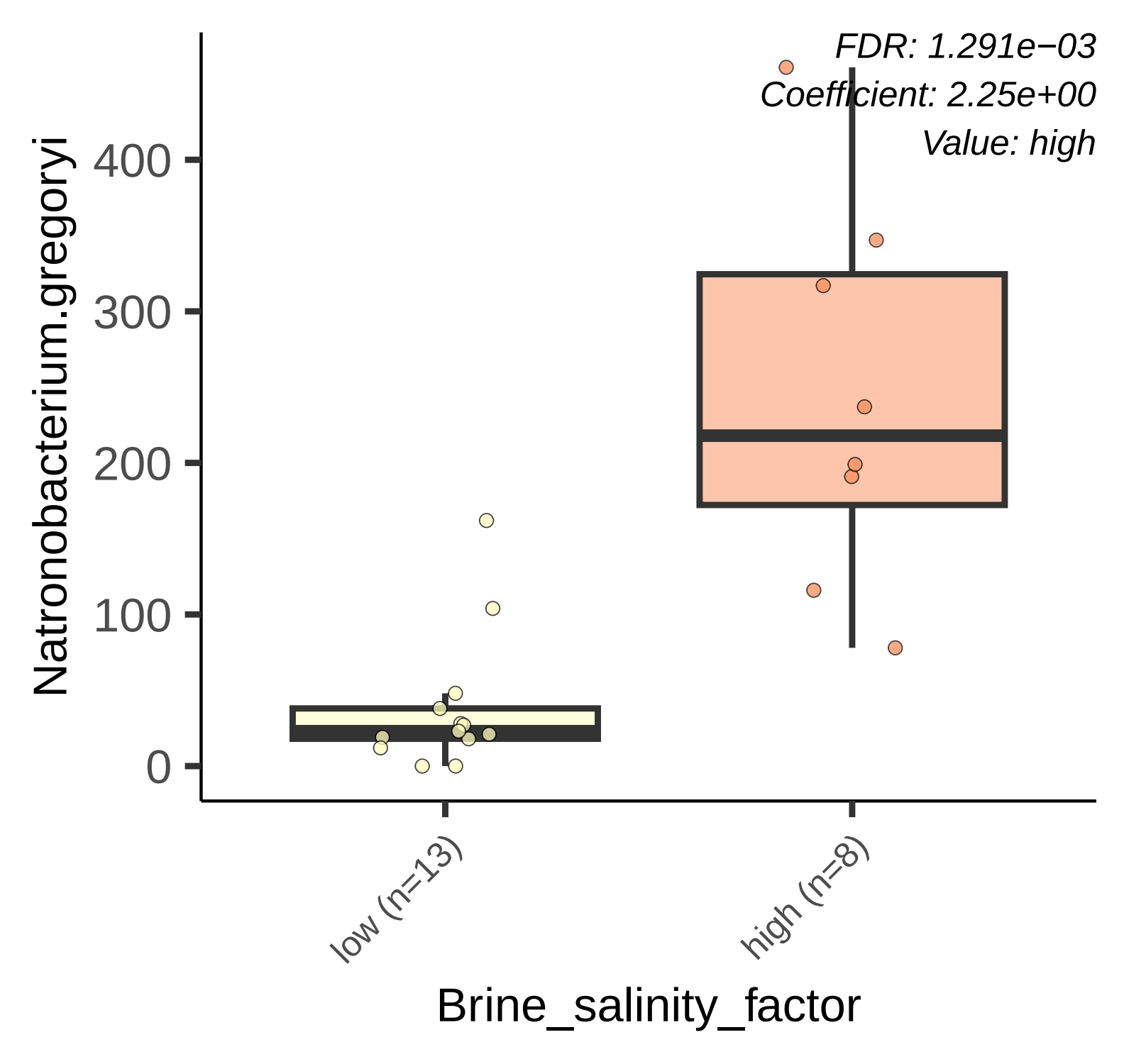

FDR: 1.070e−03
Coefficient: 1.91e+00
Value: high
3000
2000
1000
0
Haloferax.mediterranei
low (n=13)
high (n=8)
Brine_salinity_factor

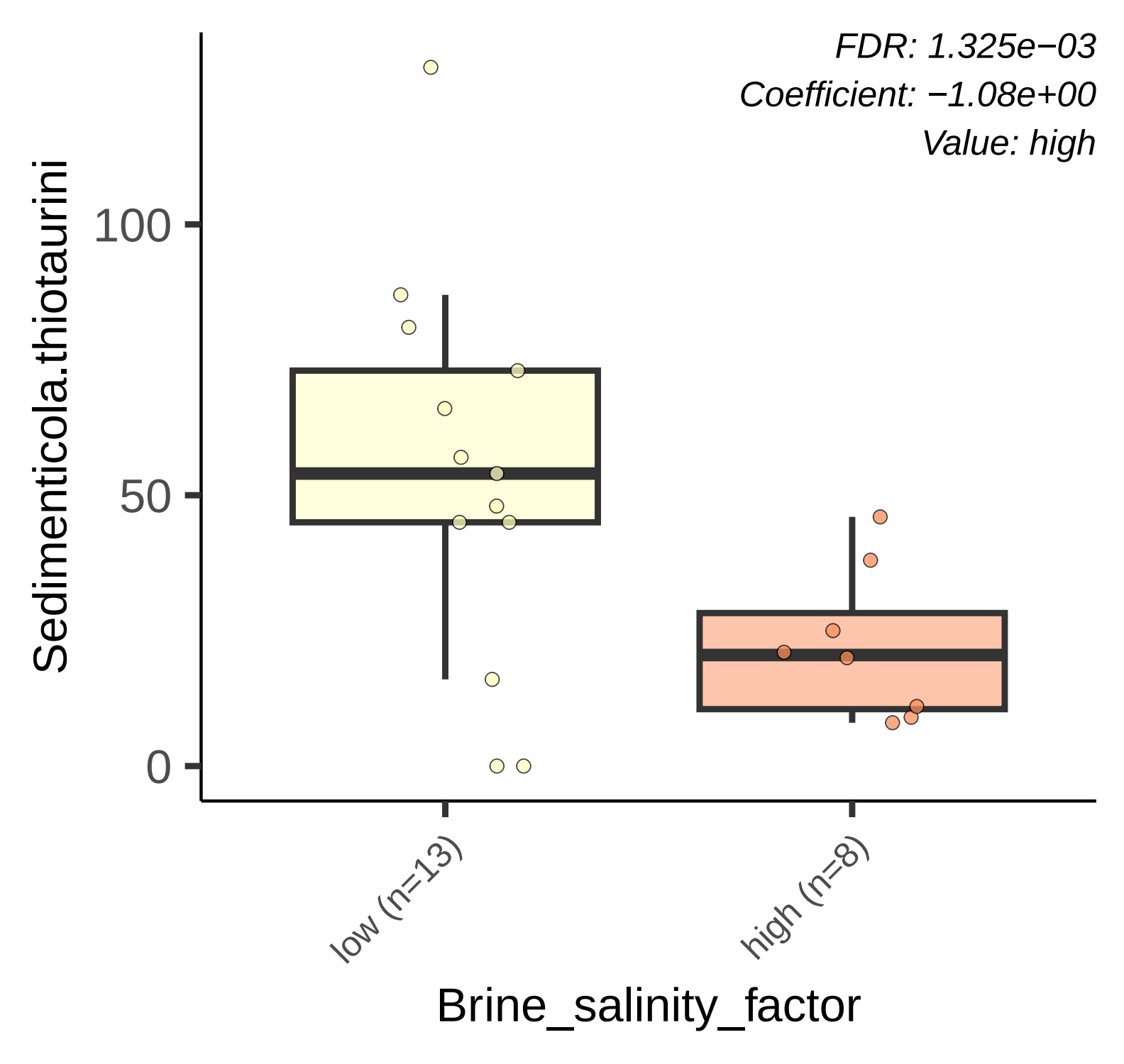

FDR: 1.103e−03
Coefficient: 1.09e+00
Value: high
Porphyrobacter.neustonensis
100
50
low (n=13)
high (n=8)
Brine_salinity_factor

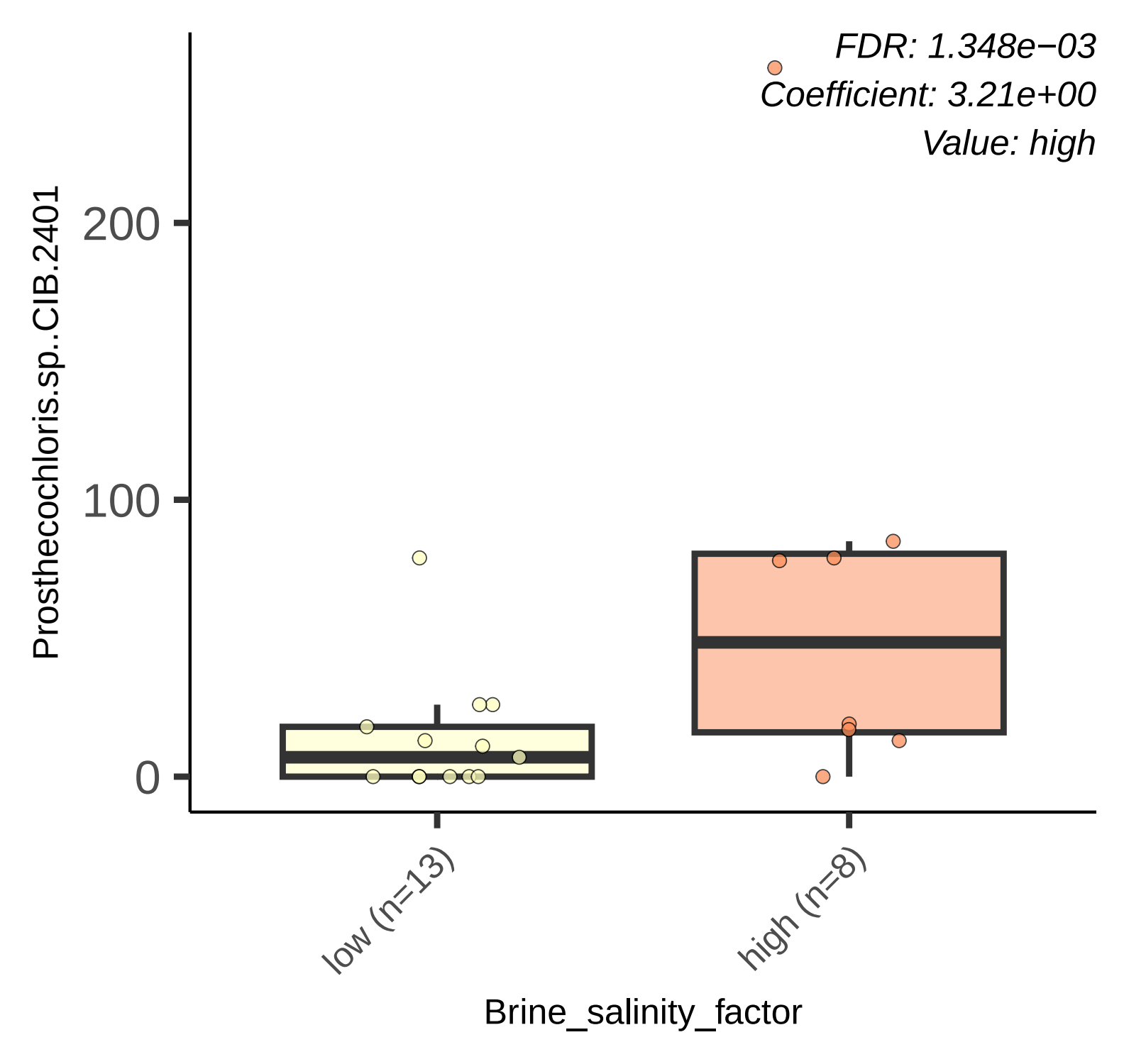

FDR: 1.153e−03
Coefficient: 2.58e+00
Value: high
Salinigranum.sp.
750
500
250
0
low (n=13)
high (n=8)
Brine_salinity_factor

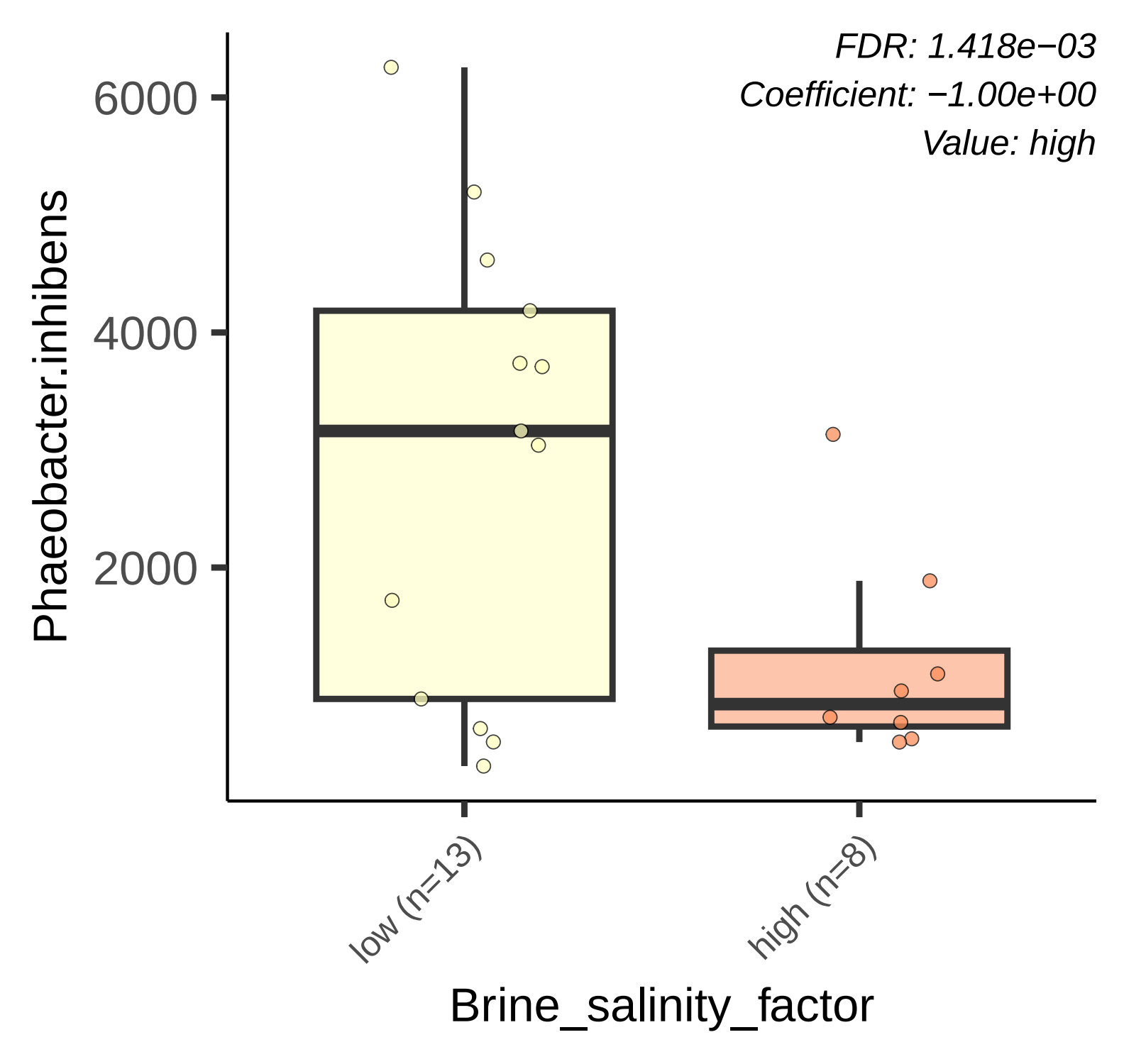

FDR: 1.202e−03
Coefficient: 1.69e+00
Value: high
Pelobacter.carbinolicus
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

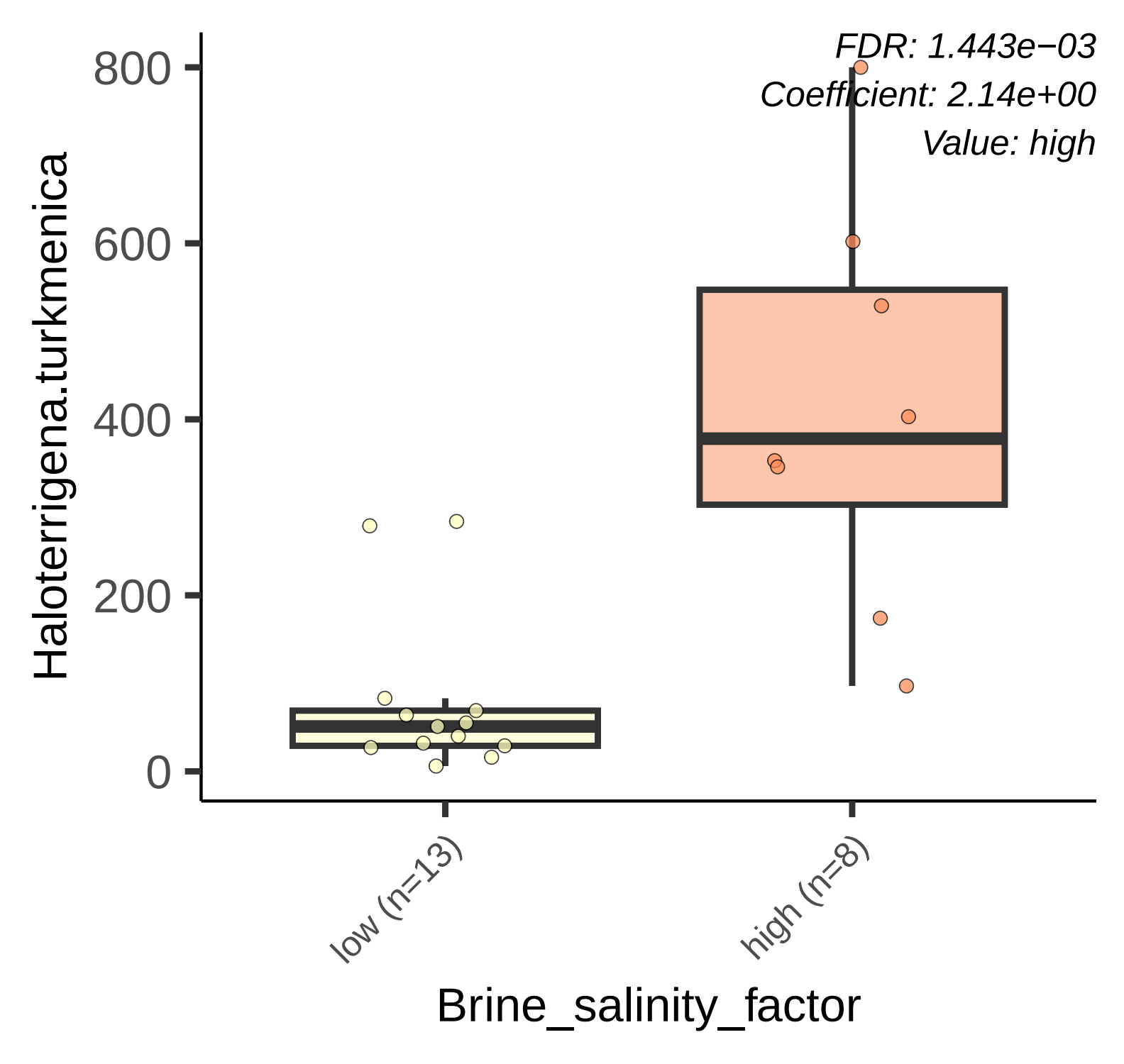

FDR: 1.210e−03
Coefficient: 1.74e+00
Value: high
Halorhabdus.tiamatea
9000
6000
3000
0
low (n=13)
high (n=8)
Brine_salinity_factor

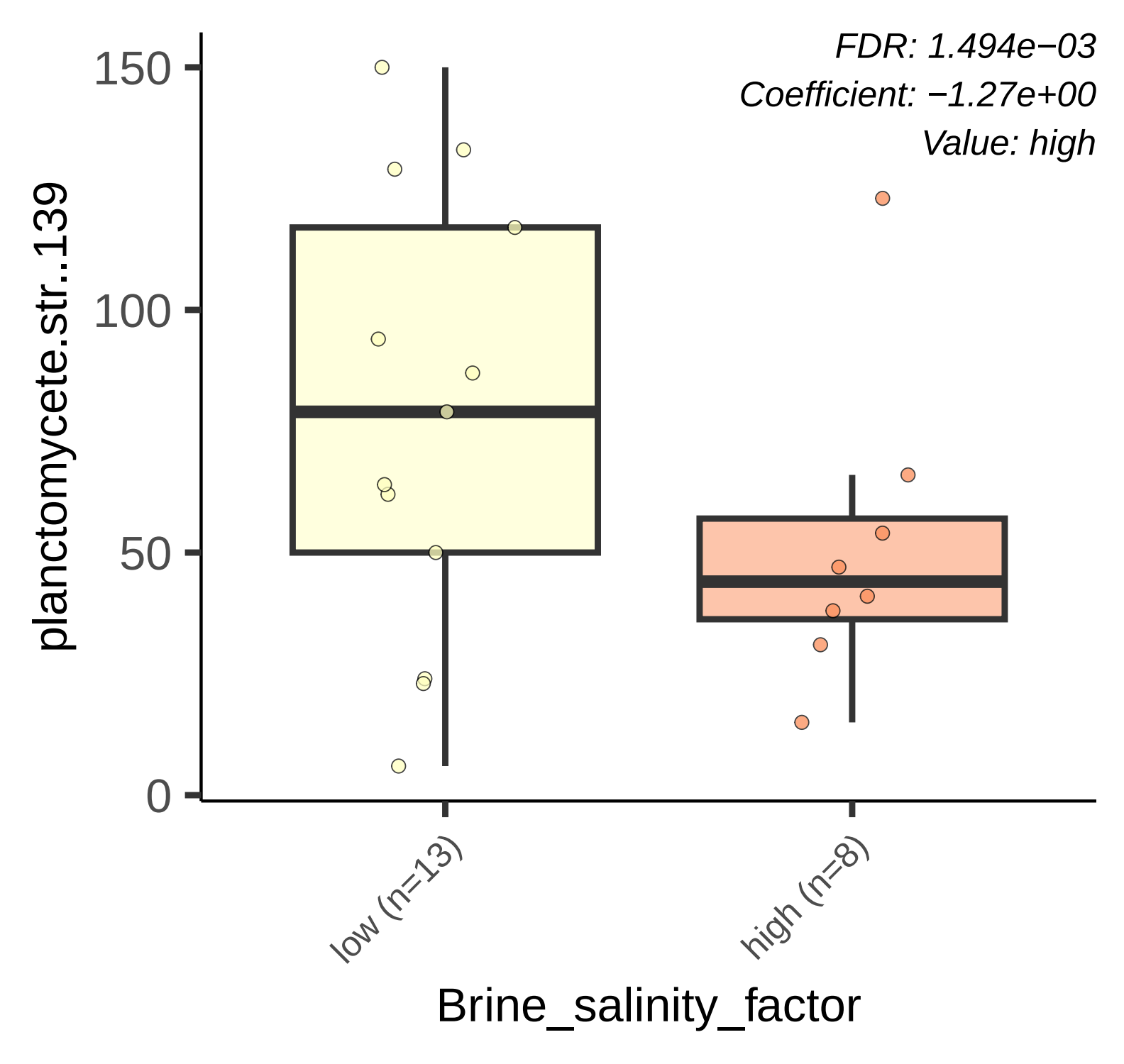

FDR: 1.291e−03
Coefficient: 2.25e+00
Value: high
Natronobacterium.gregoryi
400
300
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

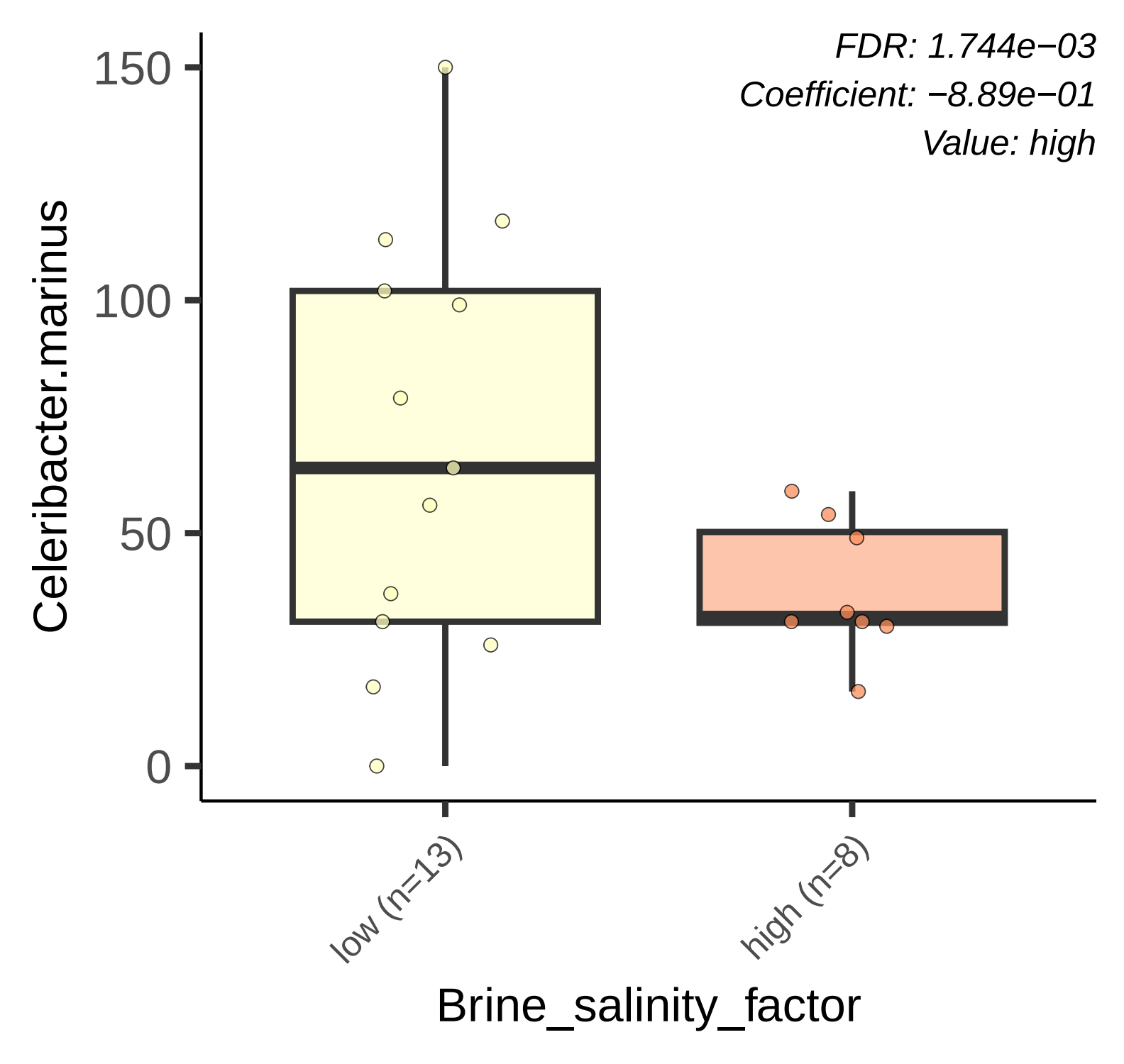

FDR: 1.325e−03
Coefficient: −1.08e+00
Value: high
Sedimenticola.thiotaurini
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

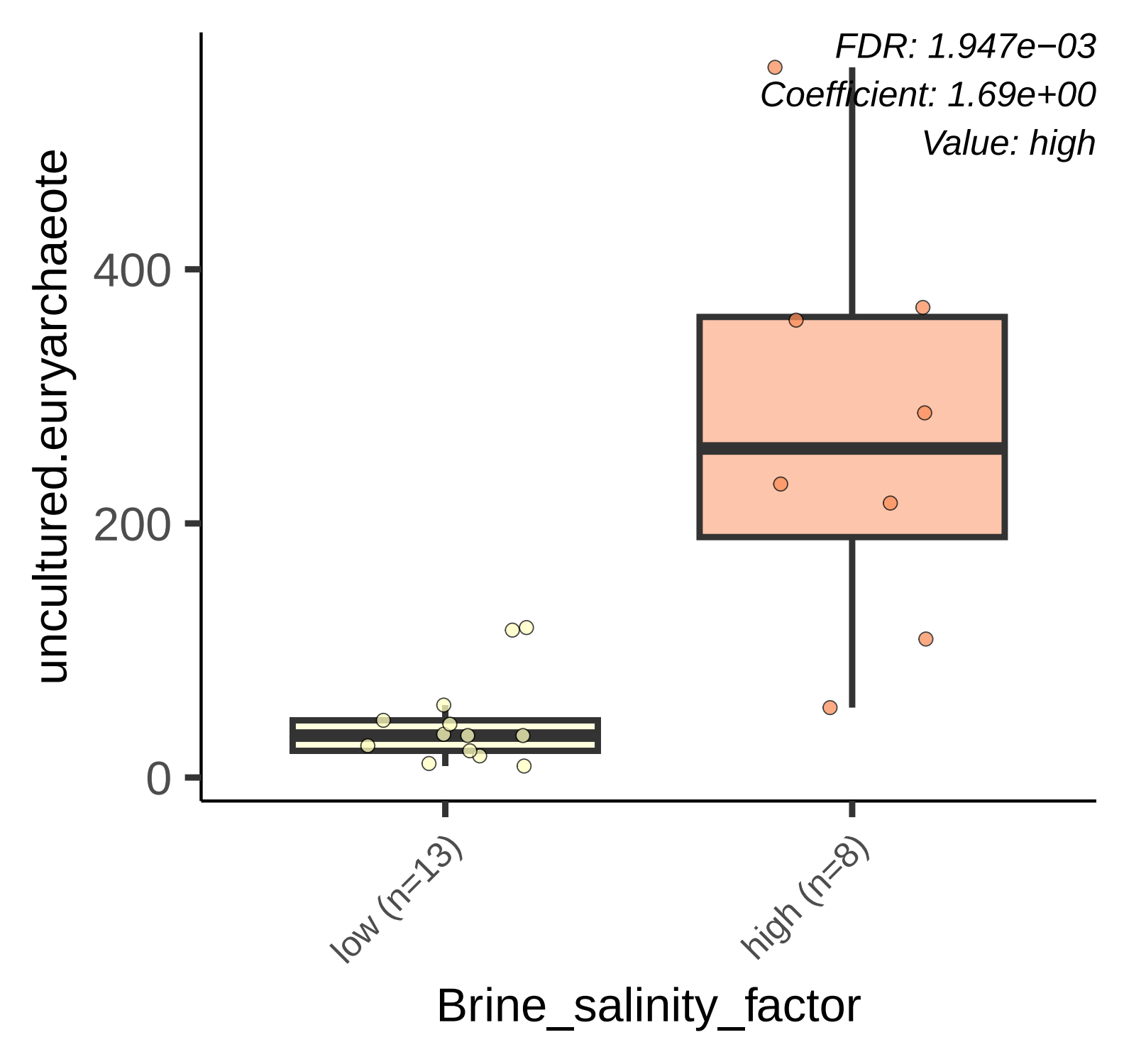

FDR: 1.348e−03
Coefficient: 3.21e+00
Value: high
Prosthecochloris.sp..CIB.2401
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

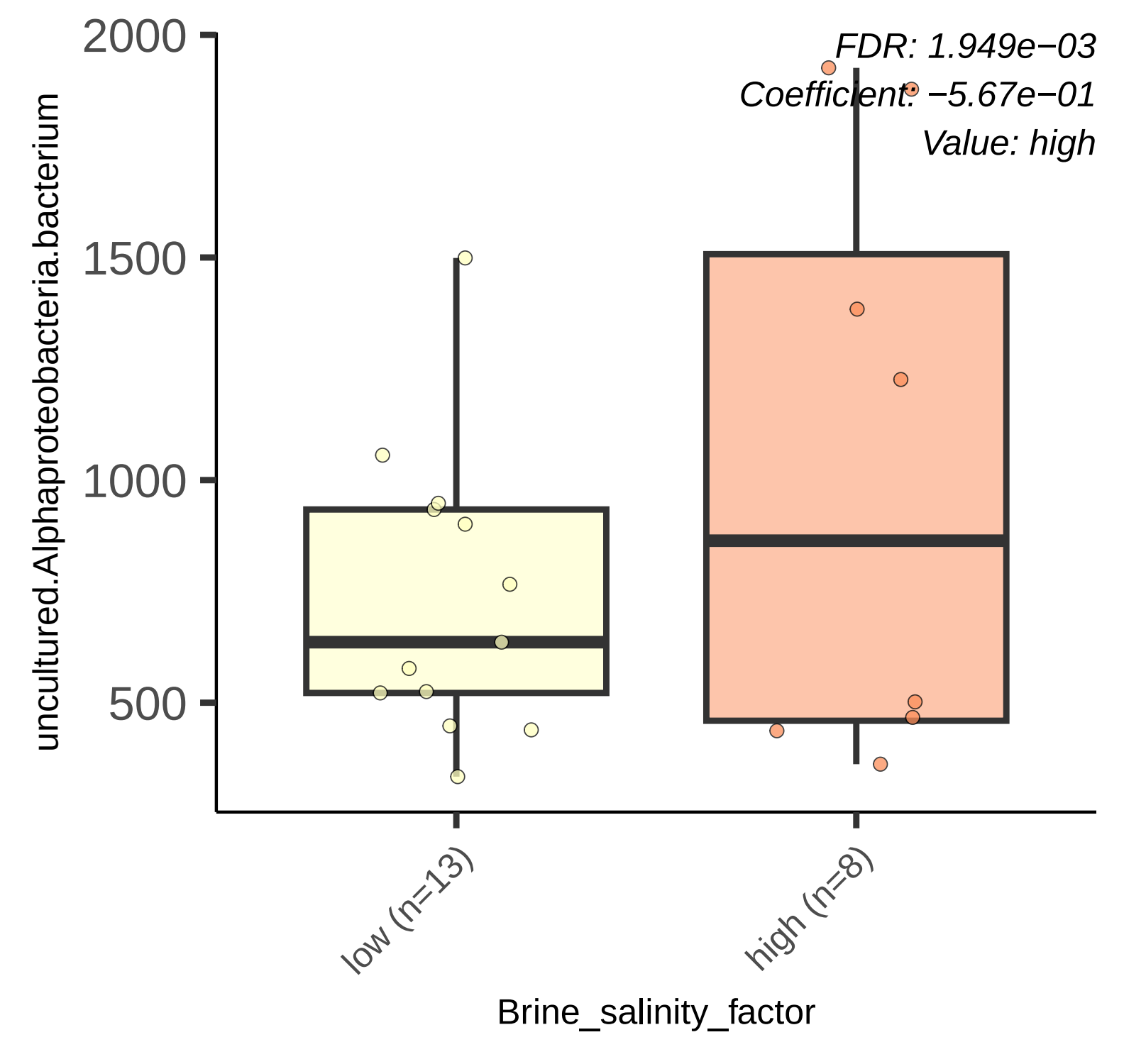

FDR: 1.418e−03
Coefficient: −1.00e+00
Value: high
6000
4000
2000
Phaeobacter.inhibens
low (n=13)
high (n=8)
Brine_salinity_factor

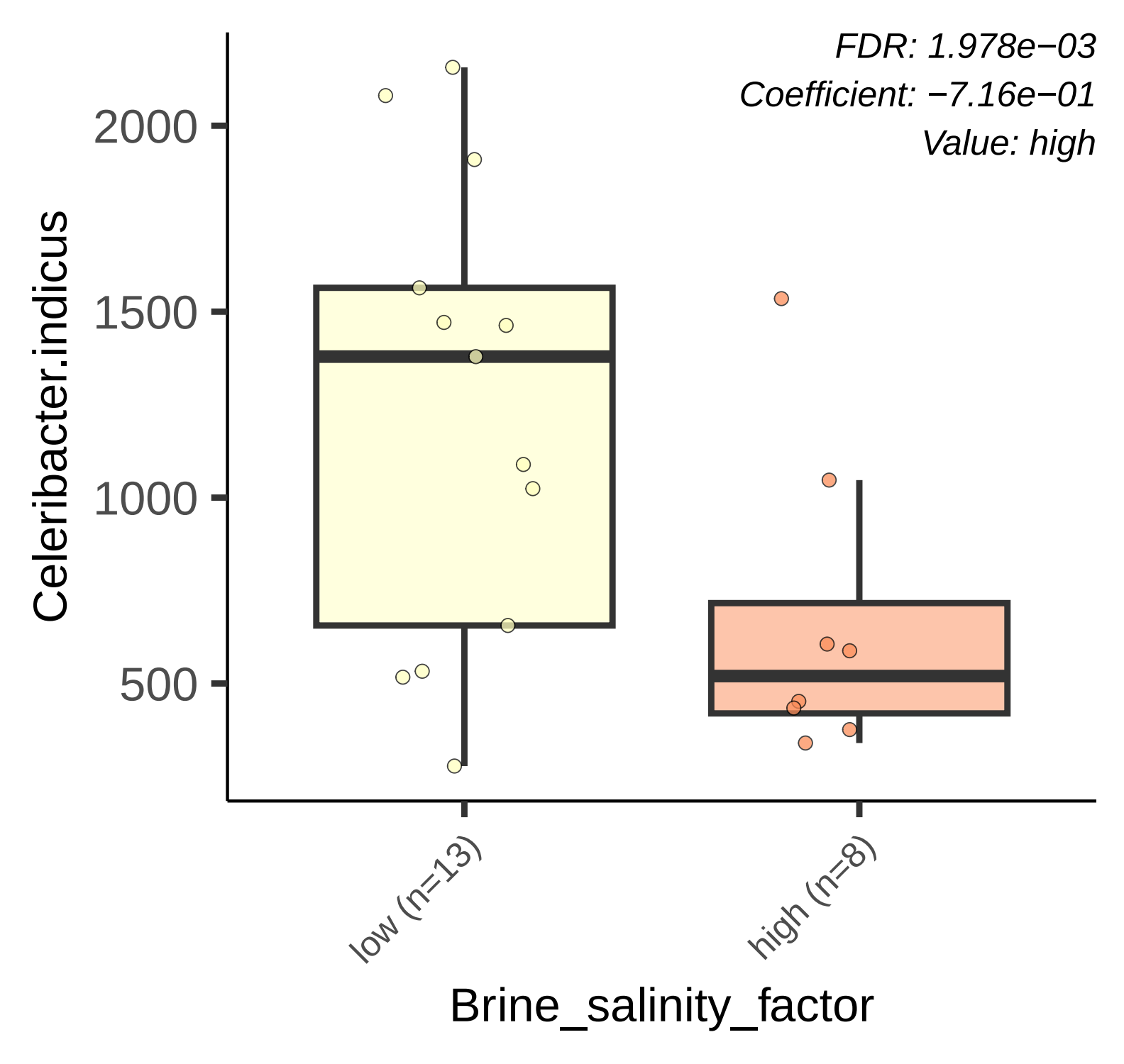

FDR: 1.443e−03
Coefficient: 2.14e+00
Value: high
800
600
400
200
0
Haloterrigena.turkmenica
low (n=13)
high (n=8)
Brine_salinity_factor

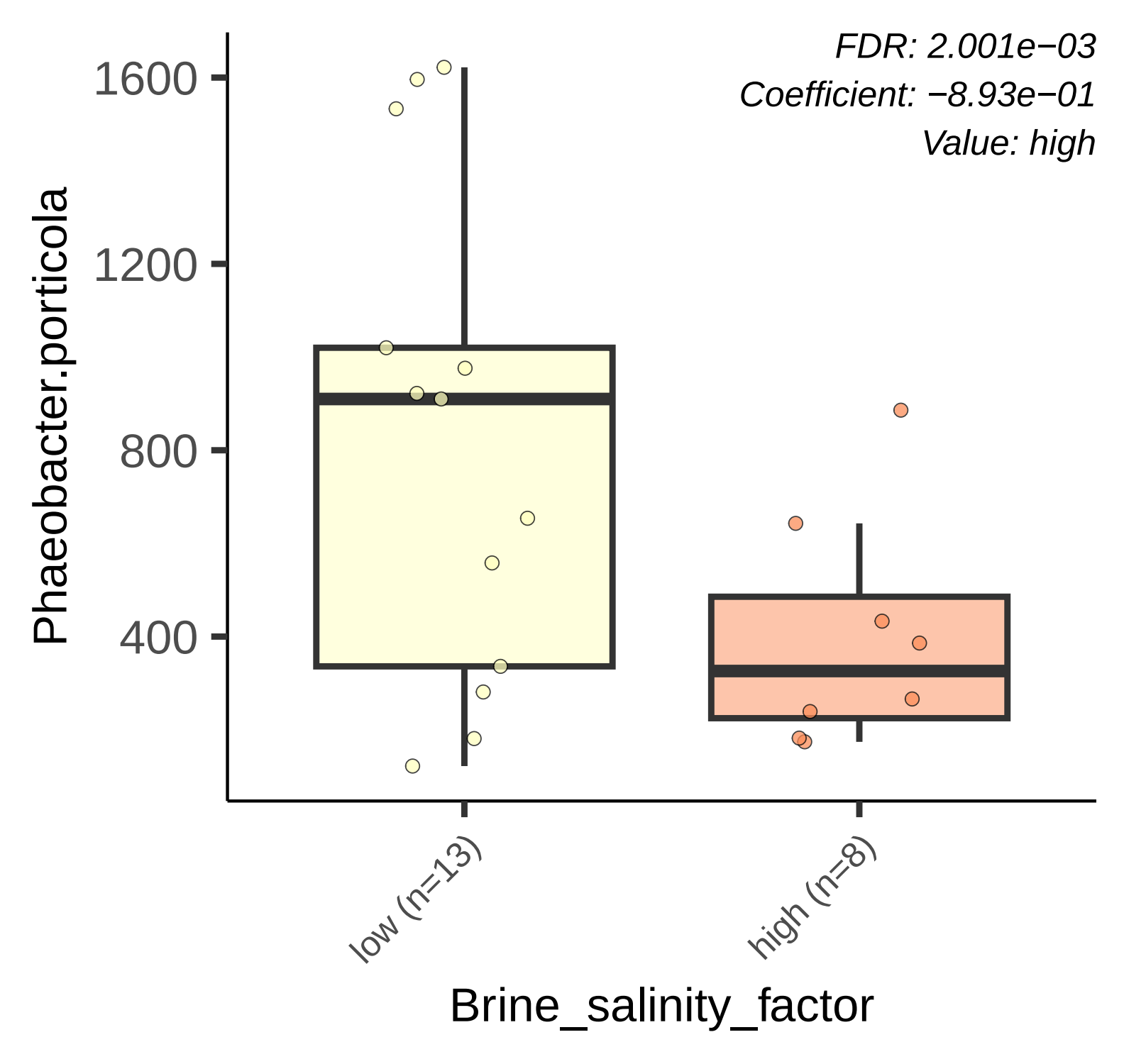

FDR: 1.494e−03
Coefficient: −1.27e+00
Value: high
150
100
50
0
planctomycete.str..139
low (n=13)
high (n=8)
Brine_salinity_factor

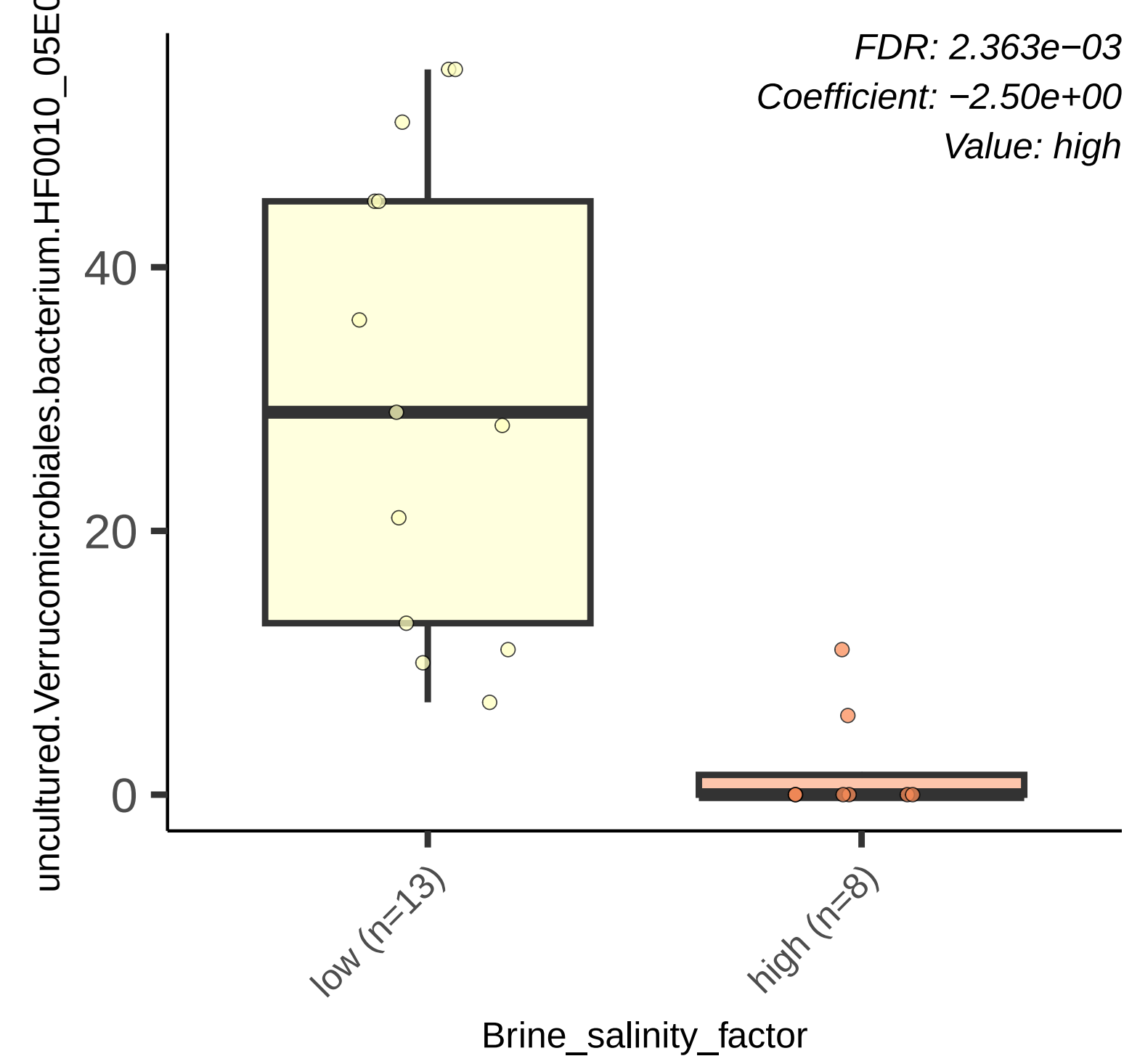

FDR: 1.744e−03
Coefficient: −8.89e−01
Value: high
Celeribacter.marinus
150
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

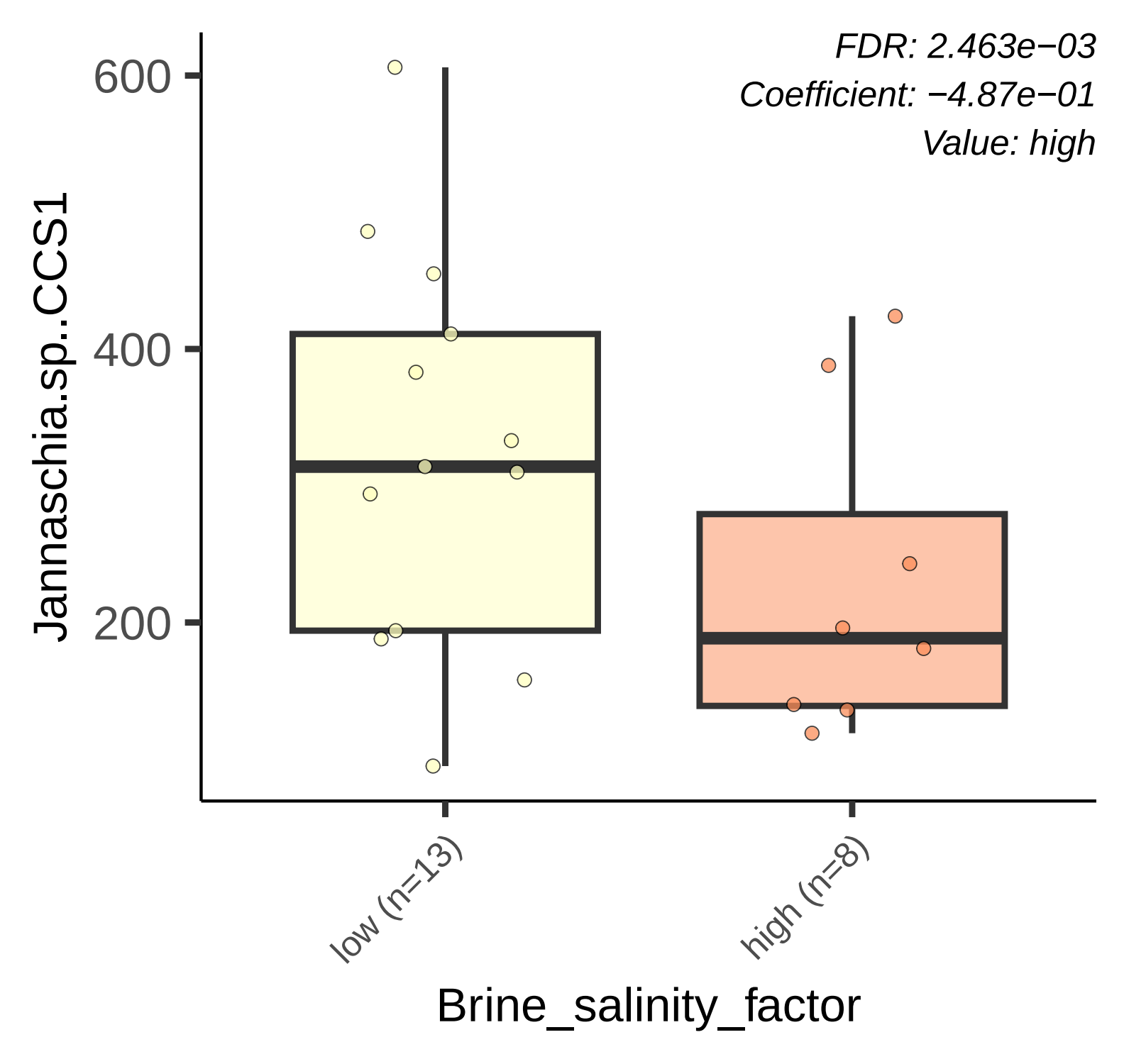

FDR: 1.947e−03
Coefficient: 1.69e+00
Value: high
uncultured.euryarchaeote
400
200
0
low (n=13)
high (n=8)
Brine_salinity_factor

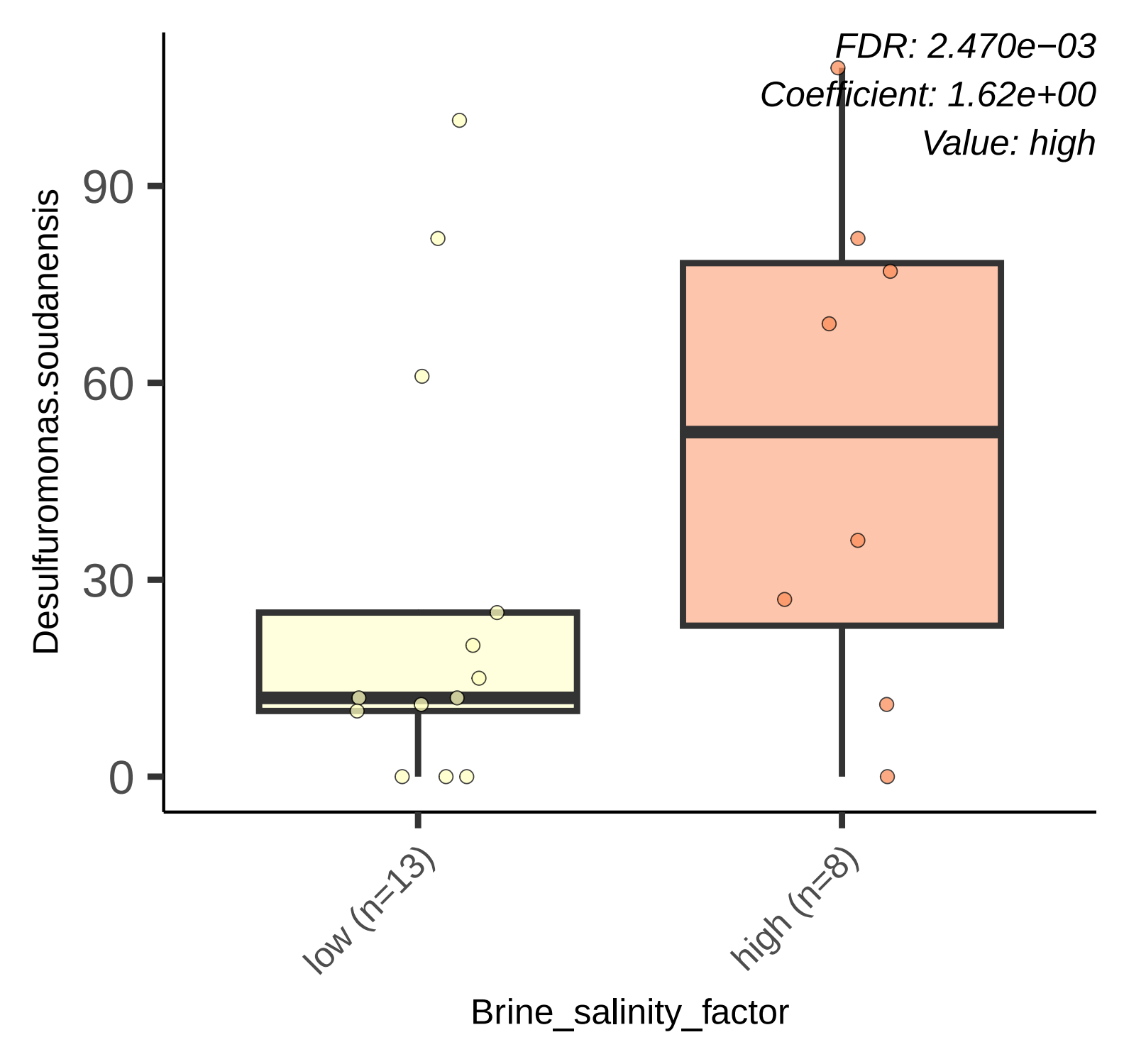

FDR: 1.949e−03
Coefficient: −5.67e−01
Value: high
2000
1500
1000
500
uncultured.Alphaproteobacteria.bacterium
low (n=13)
high (n=8)
Brine_salinity_factor

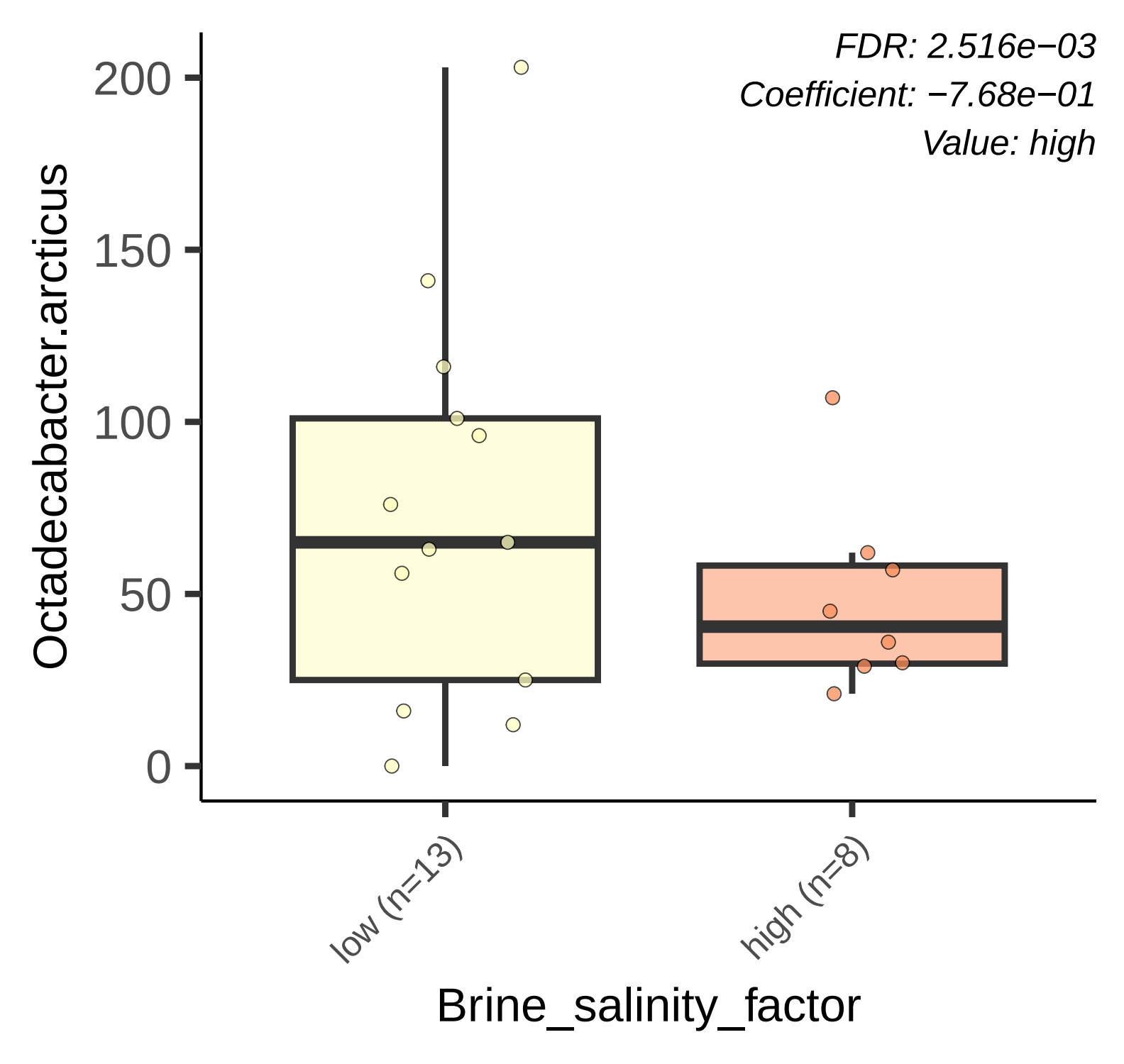

FDR: 1.978e−03
Coefficient: −7.16e−01
Value: high
2000
1500
1000
500
Celeribacter.indicus
low (n=13)
high (n=8)
Brine_salinity_factor

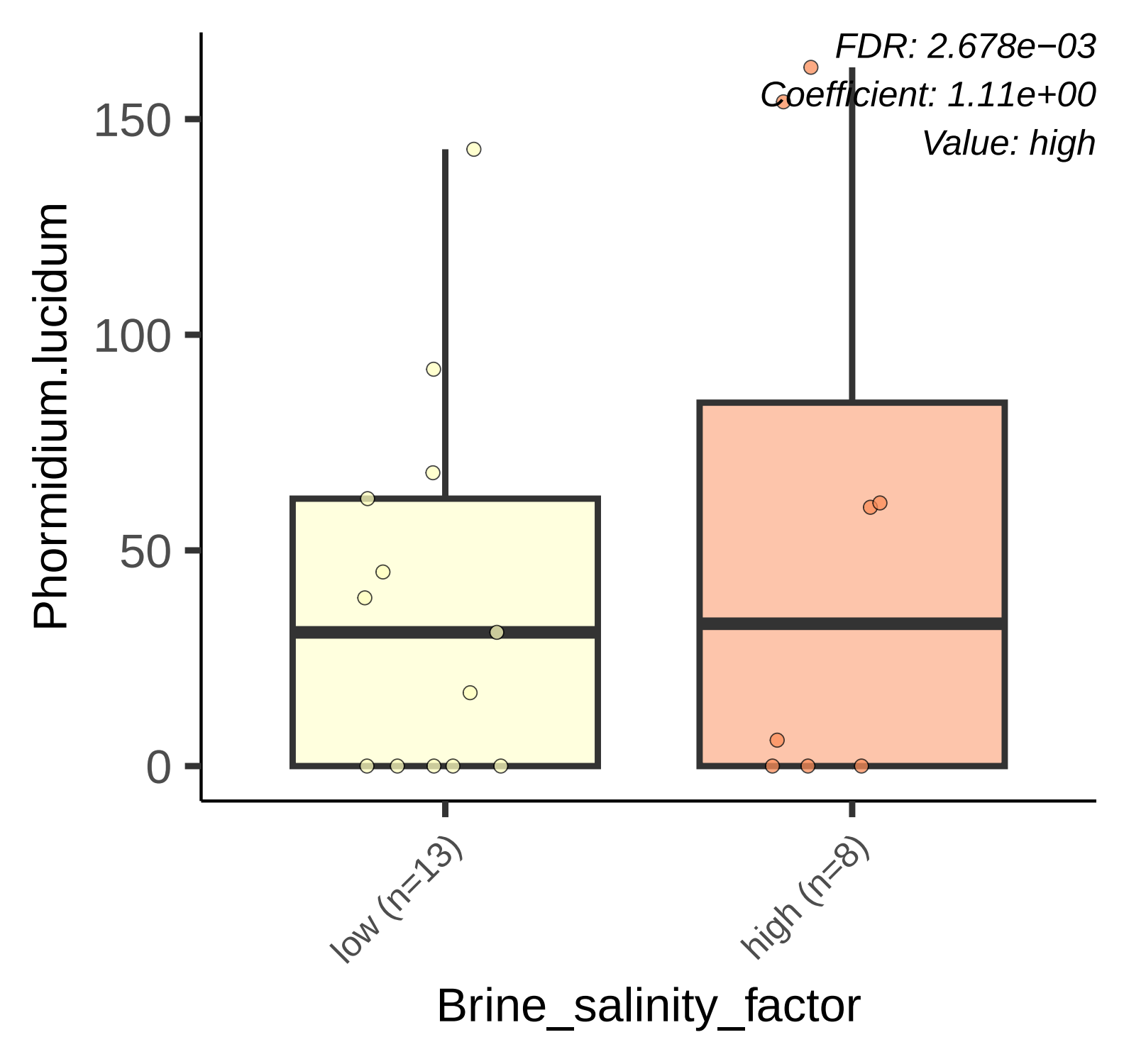

FDR: 2.001e−03
Coefficient: −8.93e−01
Value: high
1600
1200
800
400
Phaeobacter.porticola
low (n=13)
high (n=8)
Brine_salinity_factor

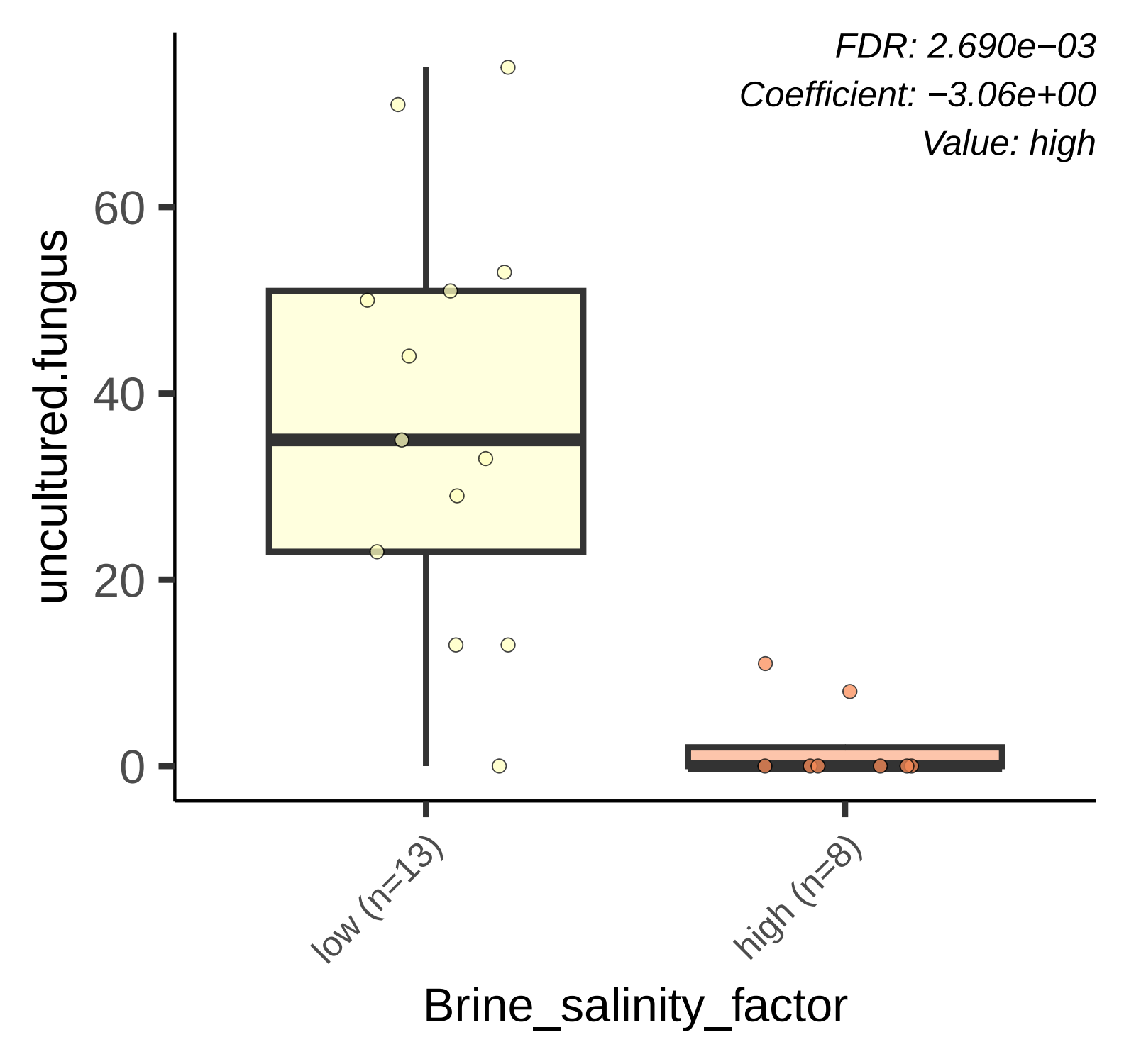

FDR: 2.363e−03
Coefficient: −2.50e+00
Value: high
uncultured.Verrucomicrobiales.bacterium.HF0010_05E0
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

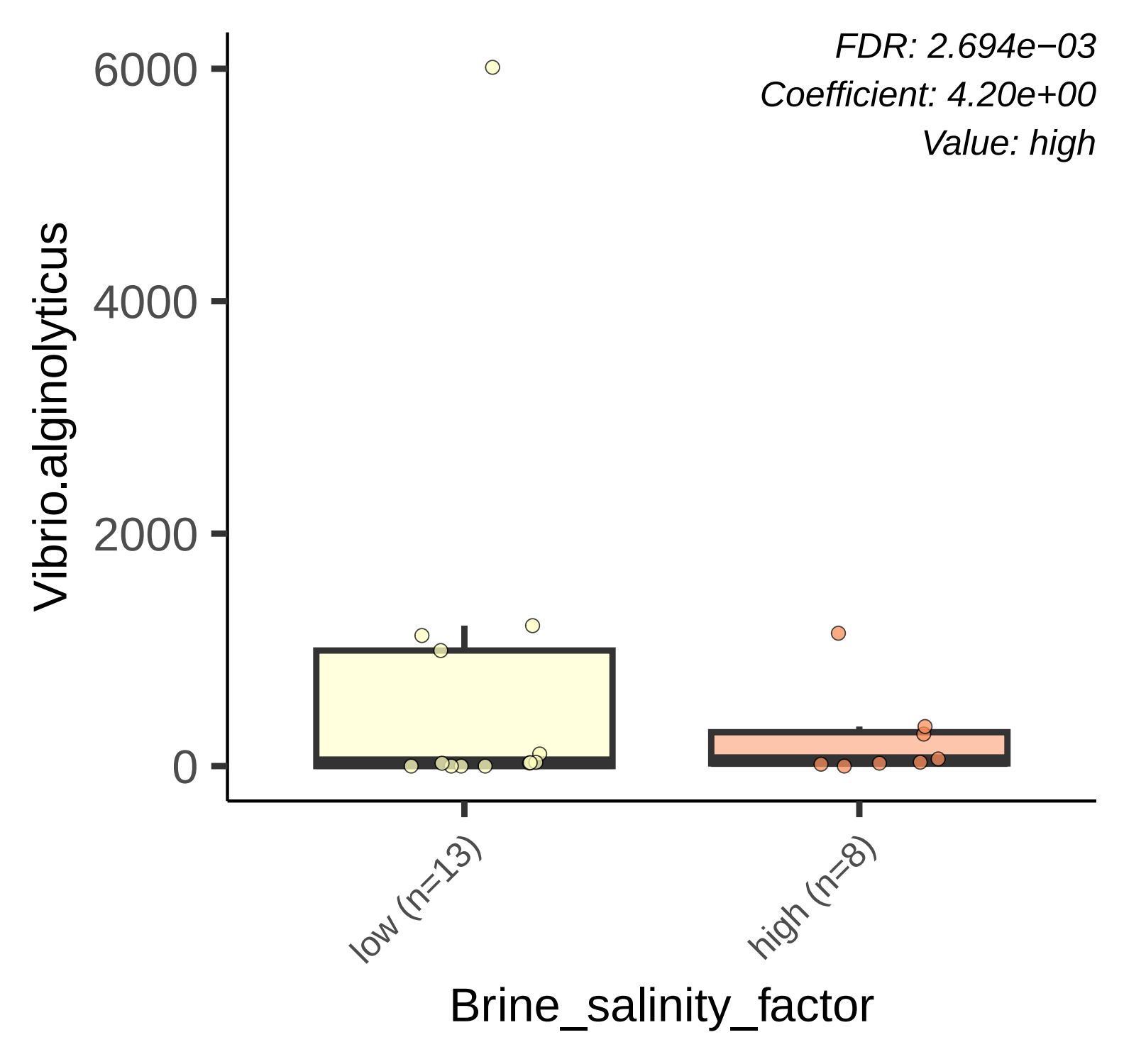

FDR: 2.463e−03
Coefficient: −4.87e−01
Value: high
600
400
200
Jannaschia.sp..CCS1
low (n=13)
high (n=8)
Brine_salinity_factor

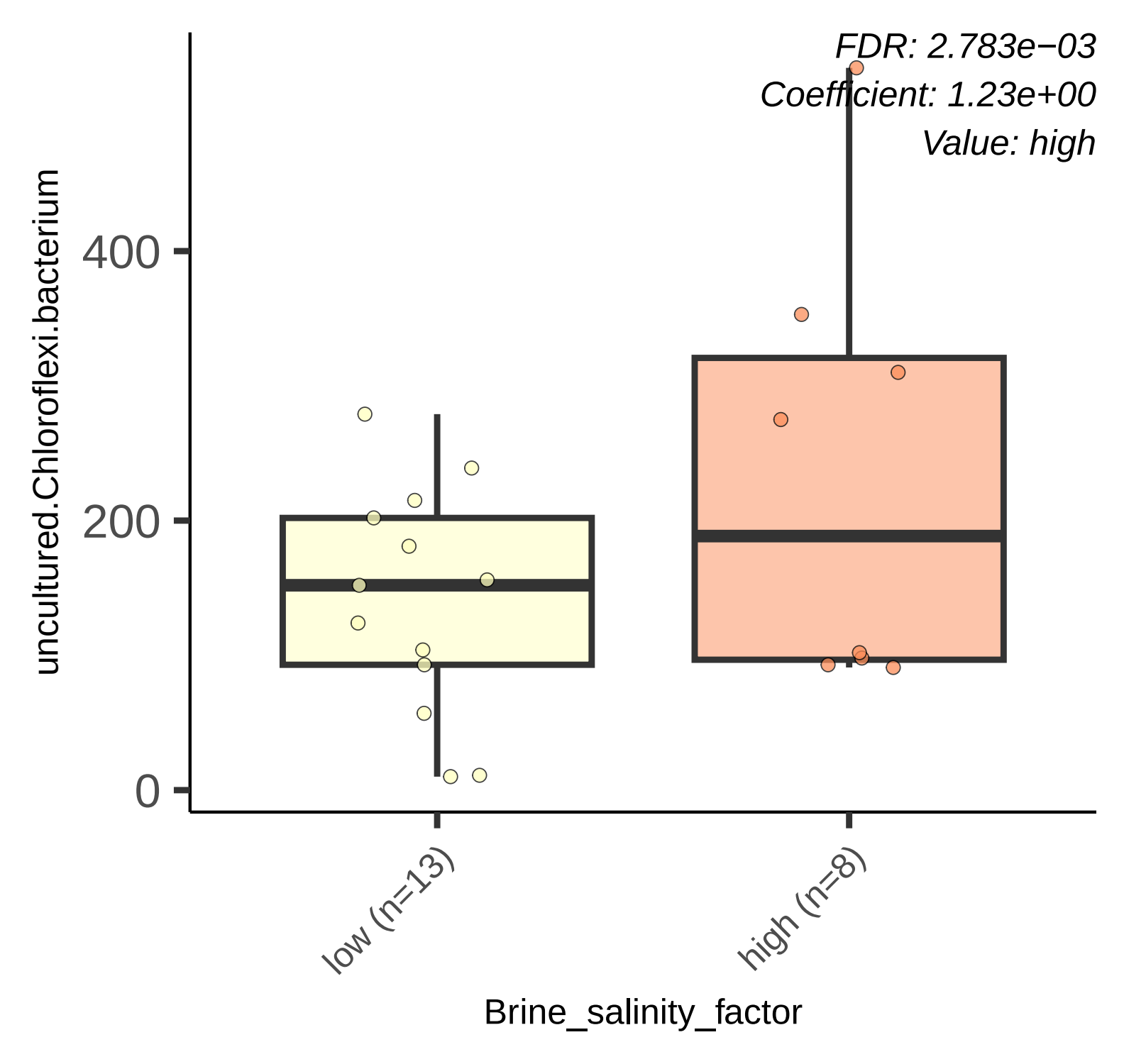

FDR: 2.470e−03
Coefficient: 1.62e+00
Value: high
Desulfuromonas.soudanensis
90
60
30
0
low (n=13)
high (n=8)
Brine_salinity_factor

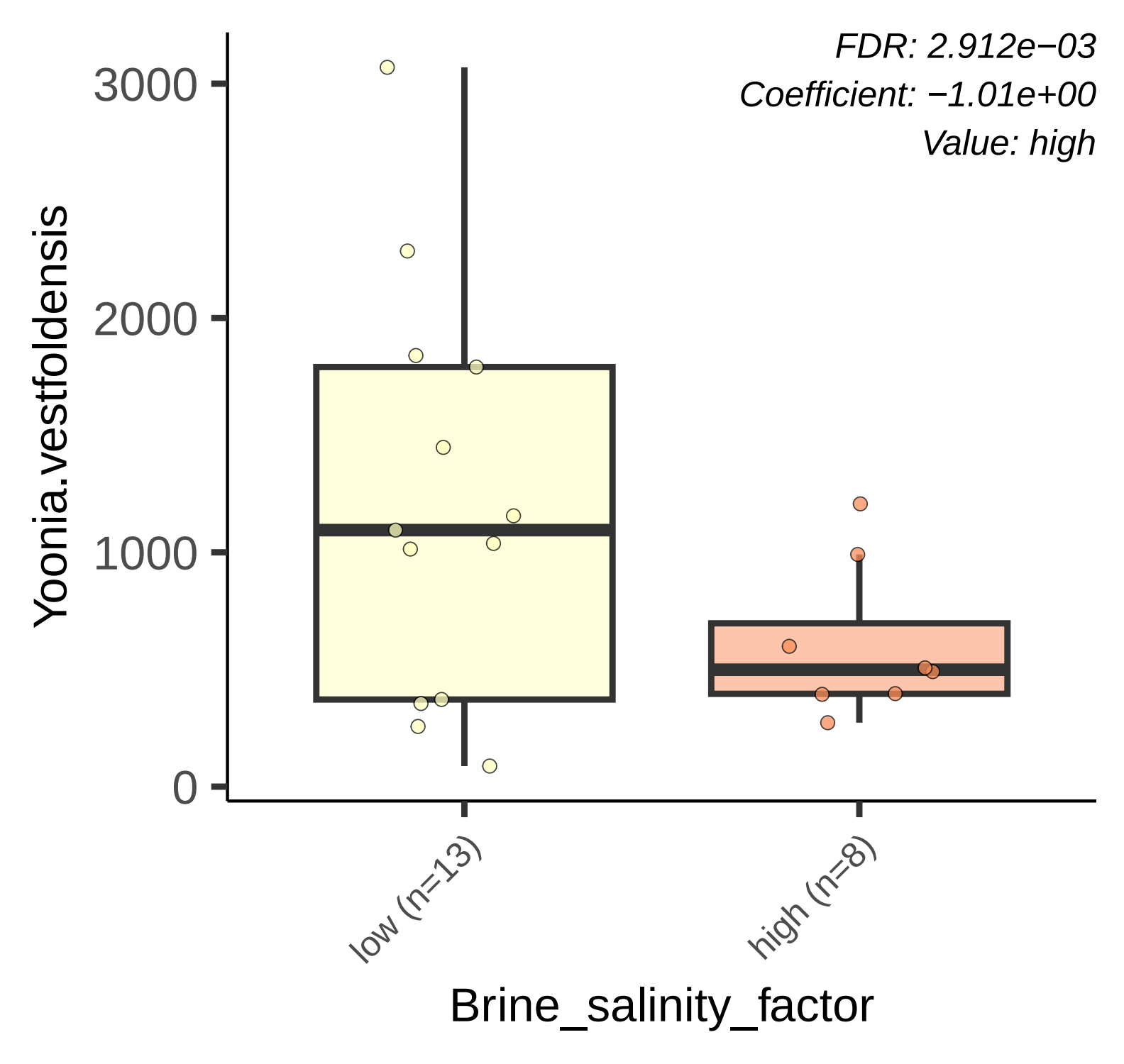

FDR: 2.516e−03
Coefficient: −7.68e−01
Value: high
Octadecabacter.arcticus
200
150
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

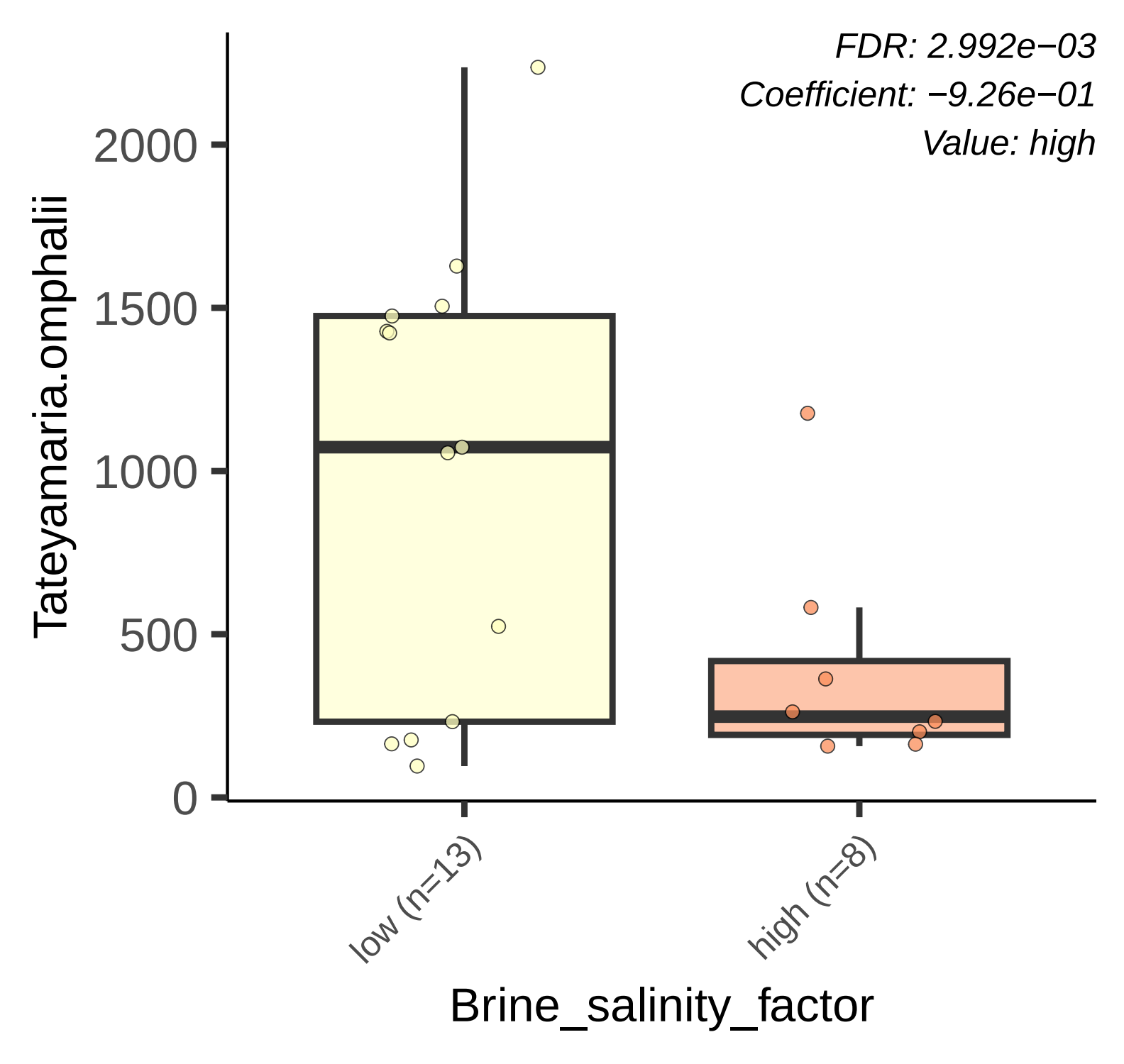

FDR: 2.678e−03
Coefficient: 1.11e+00
Value: high
Phormidium.lucidum
150
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

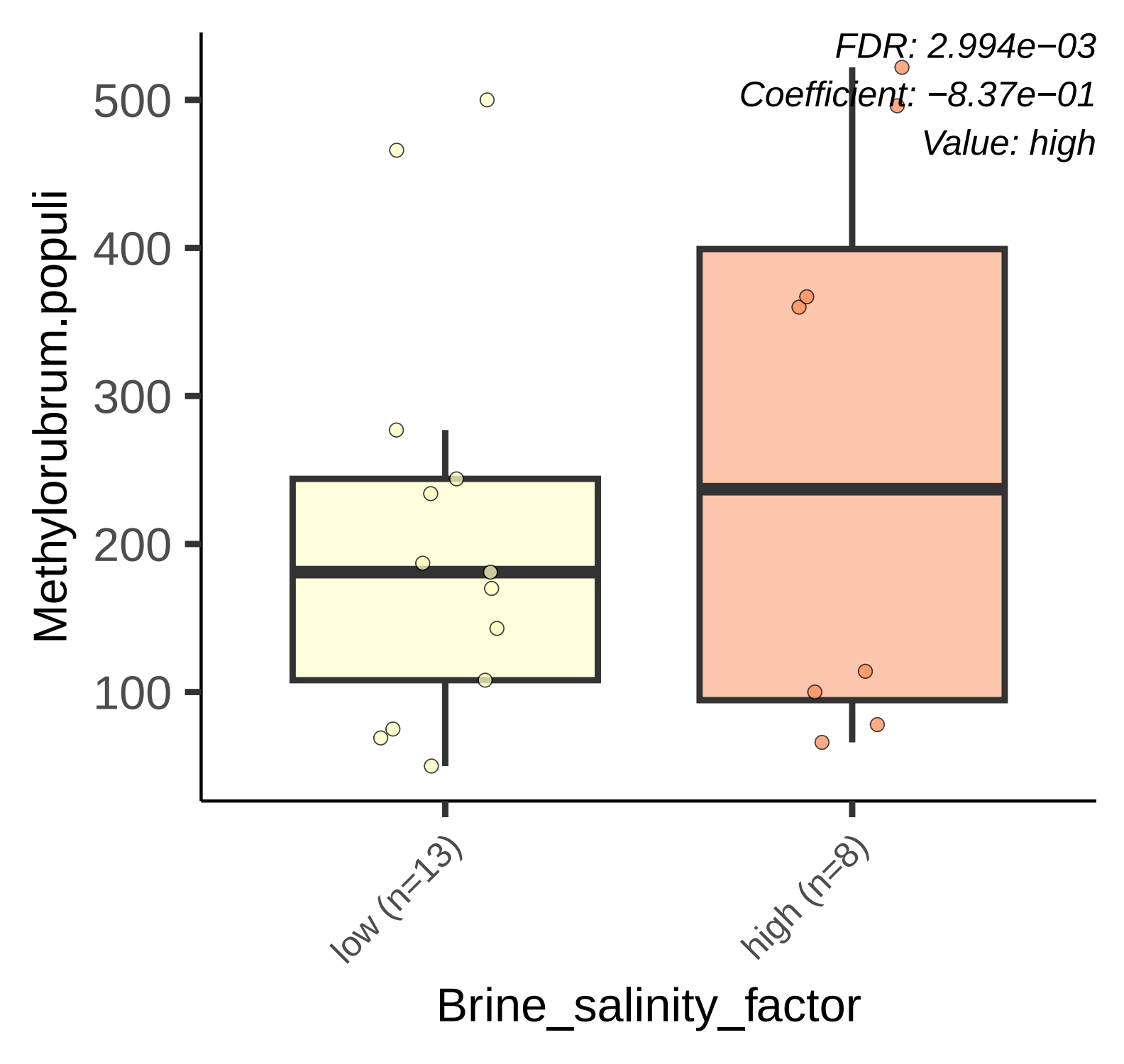

FDR: 2.690e−03
Coefficient: −3.06e+00
Value: high
uncultured.fungus
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

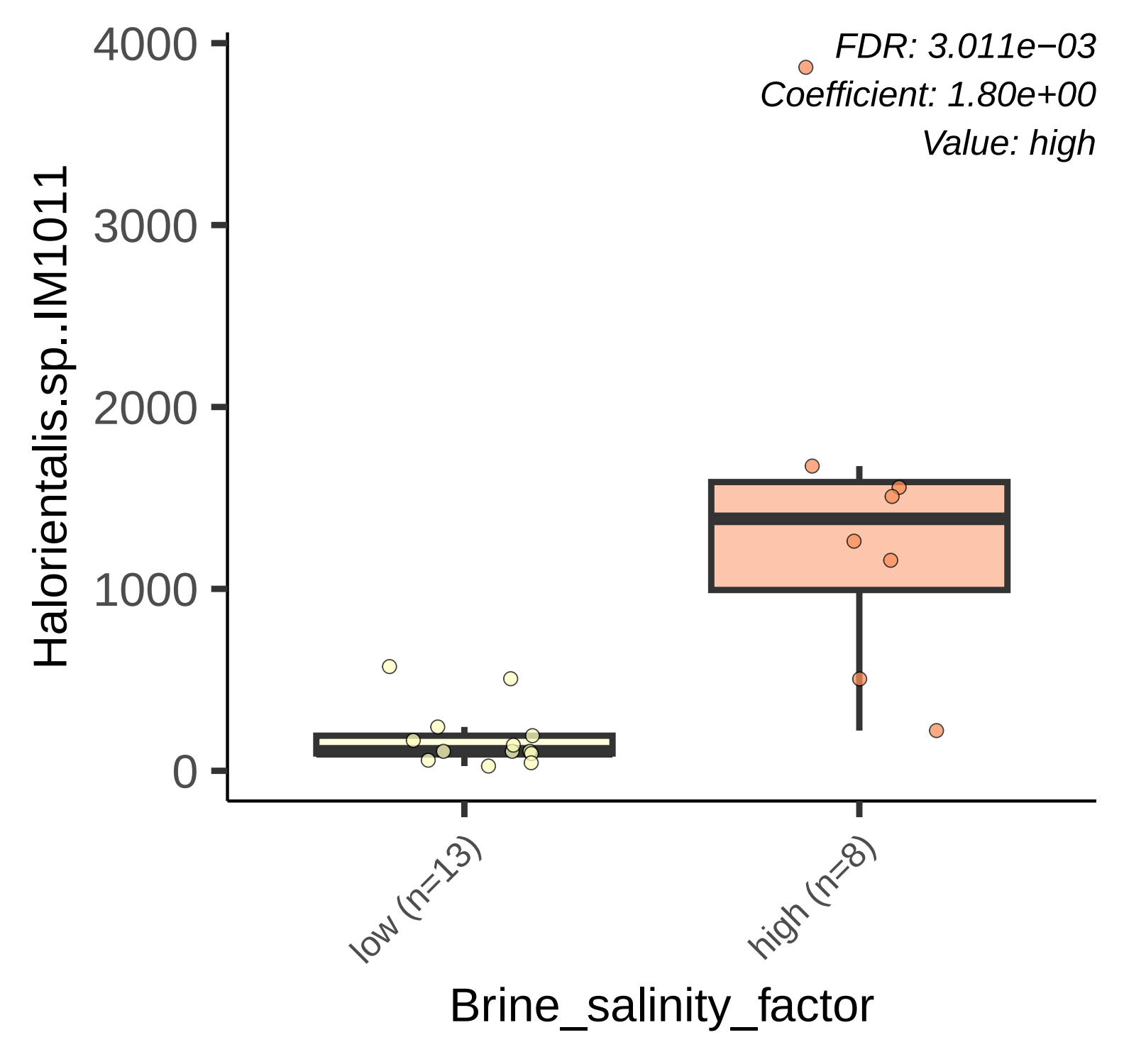

FDR: 2.694e−03
Coefficient: 4.20e+00
Value: high
6000
4000
2000
0
Vibrio.alginolyticus
low (n=13)
high (n=8)
Brine_salinity_factor

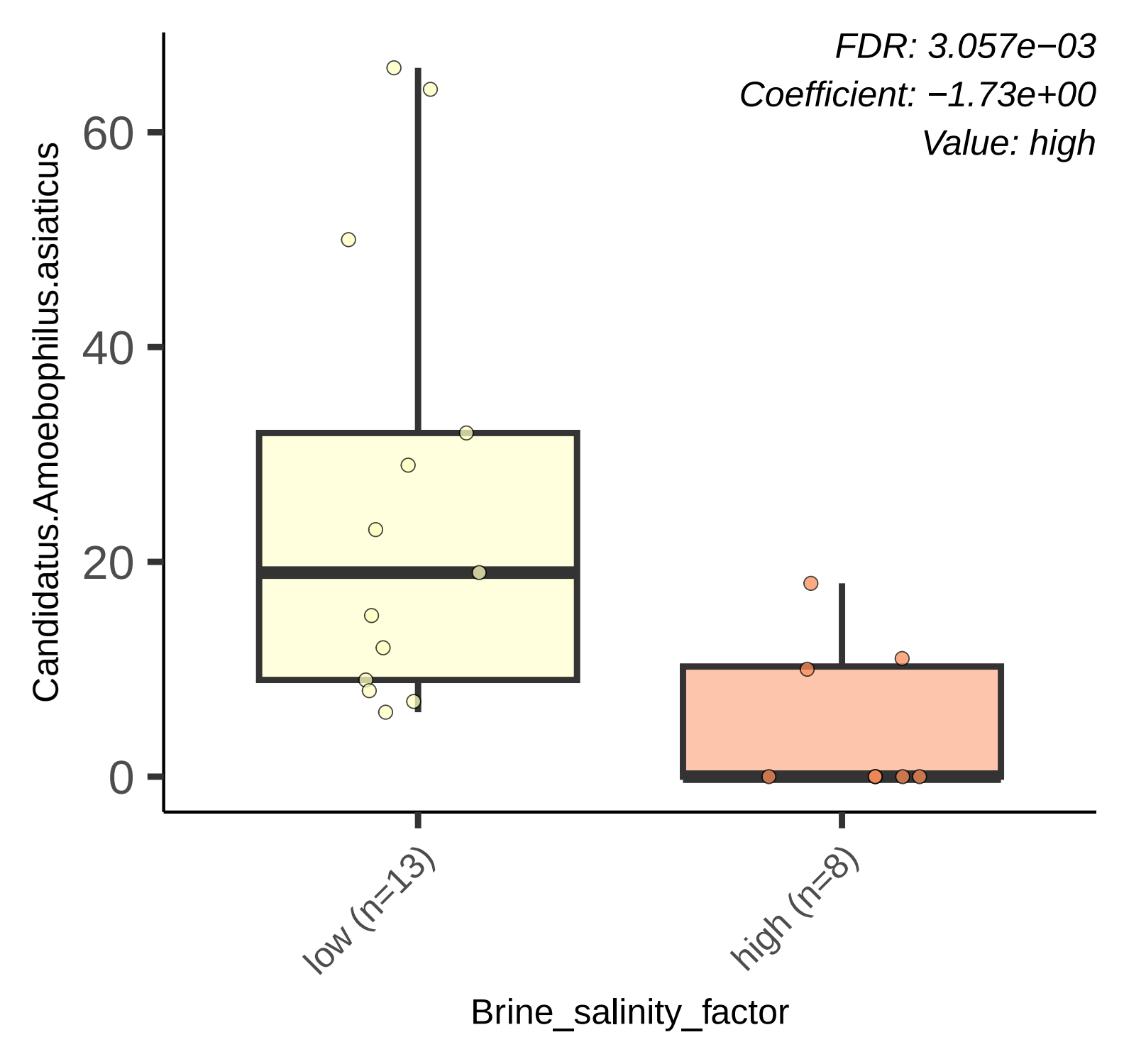

FDR: 2.783e−03
Coefficient: 1.23e+00
Value: high
uncultured.Chloroflexi.bacterium
400
200
0
low (n=13)
high (n=8)
Brine_salinity_factor

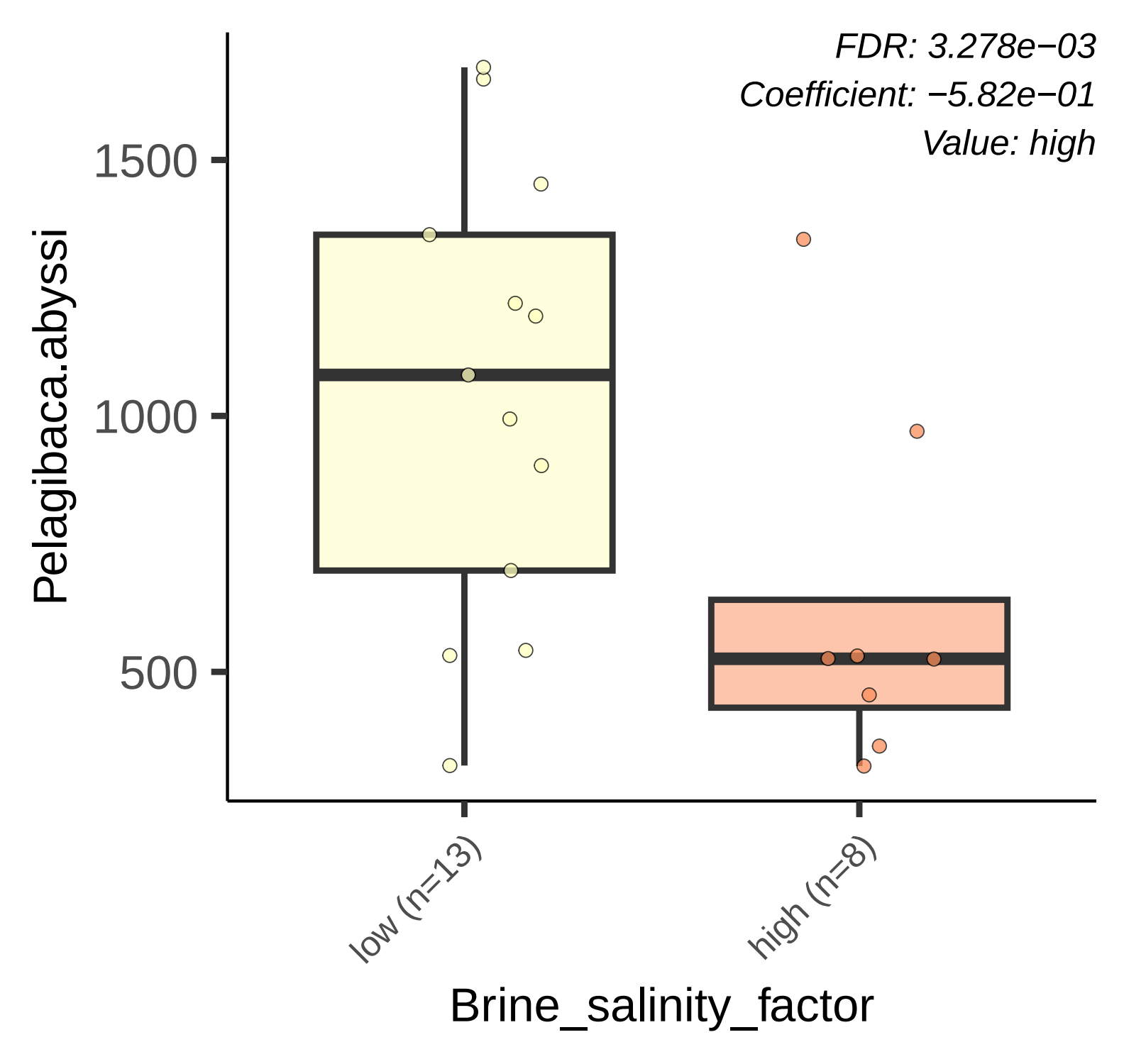

FDR: 2.912e−03
Coefficient: −1.01e+00
Value: high
3000
2000
1000
0
Yoonia.vestfoldensis
low (n=13)
high (n=8)
Brine_salinity_factor

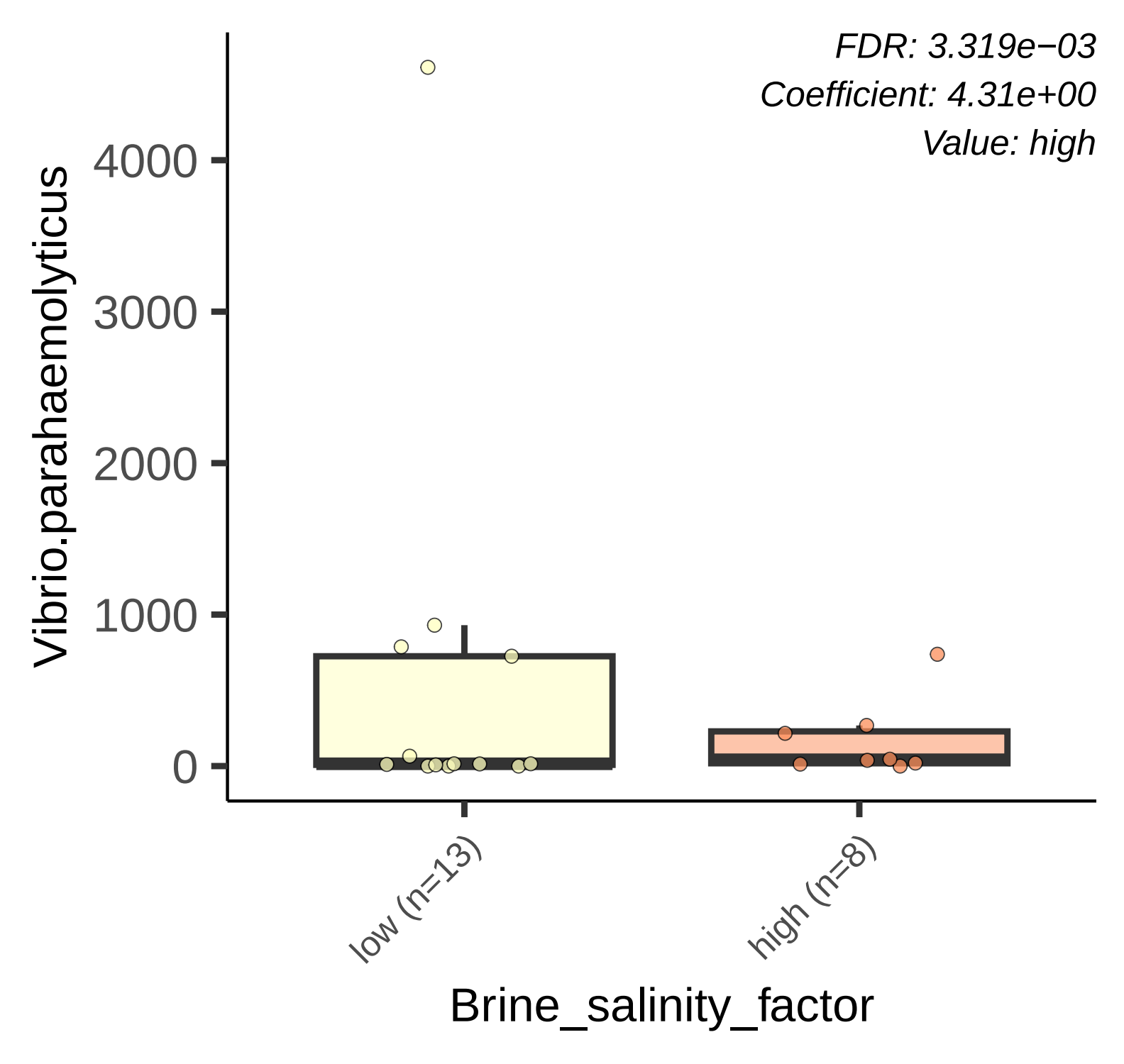

FDR: 2.992e−03
Coefficient: −9.26e−01
Value: high
Tateyamaria.omphalii
2000
1500
1000
500
0
low (n=13)
high (n=8)
Brine_salinity_factor

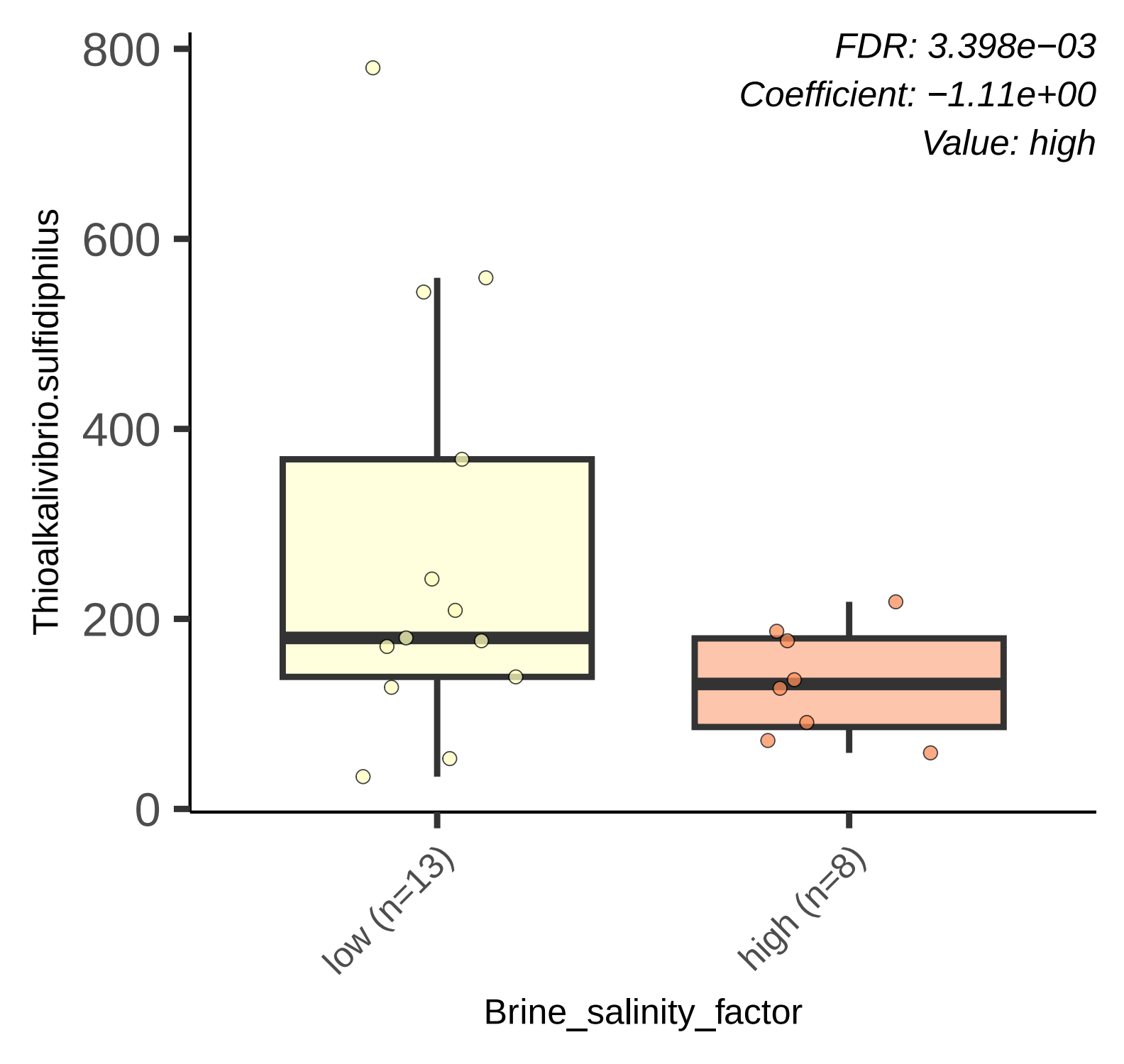

FDR: 2.994e−03
Coefficient: −8.37e−01
Value: high
Methylorubrum.populi
500
400
300
200
100
low (n=13)
high (n=8)
Brine_salinity_factor

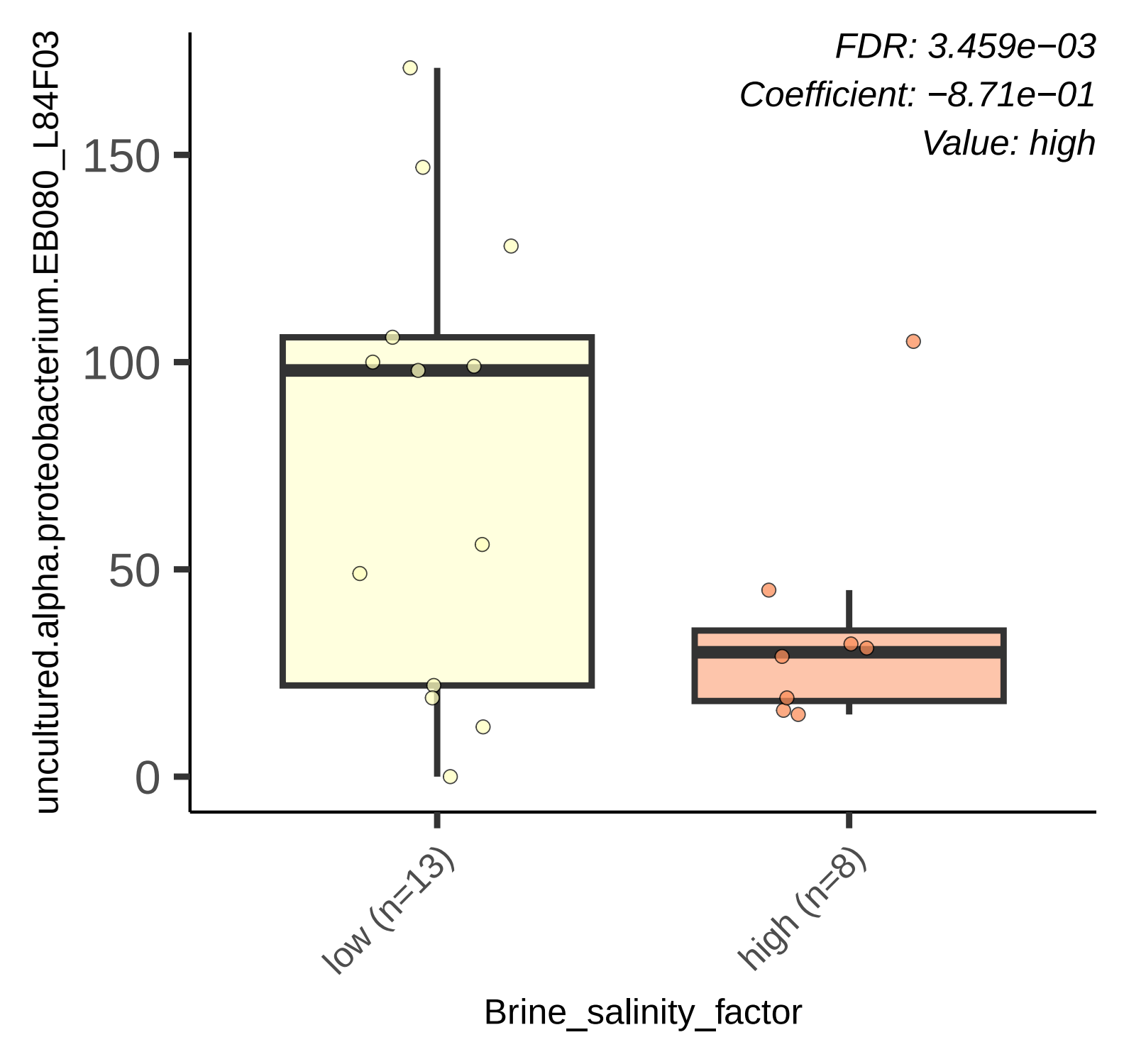

FDR: 3.011e−03
Coefficient: 1.80e+00
Value: high
Halorientalis.sp..IM1011
4000
3000
2000
1000
0
low (n=13)
high (n=8)
Brine_salinity_factor

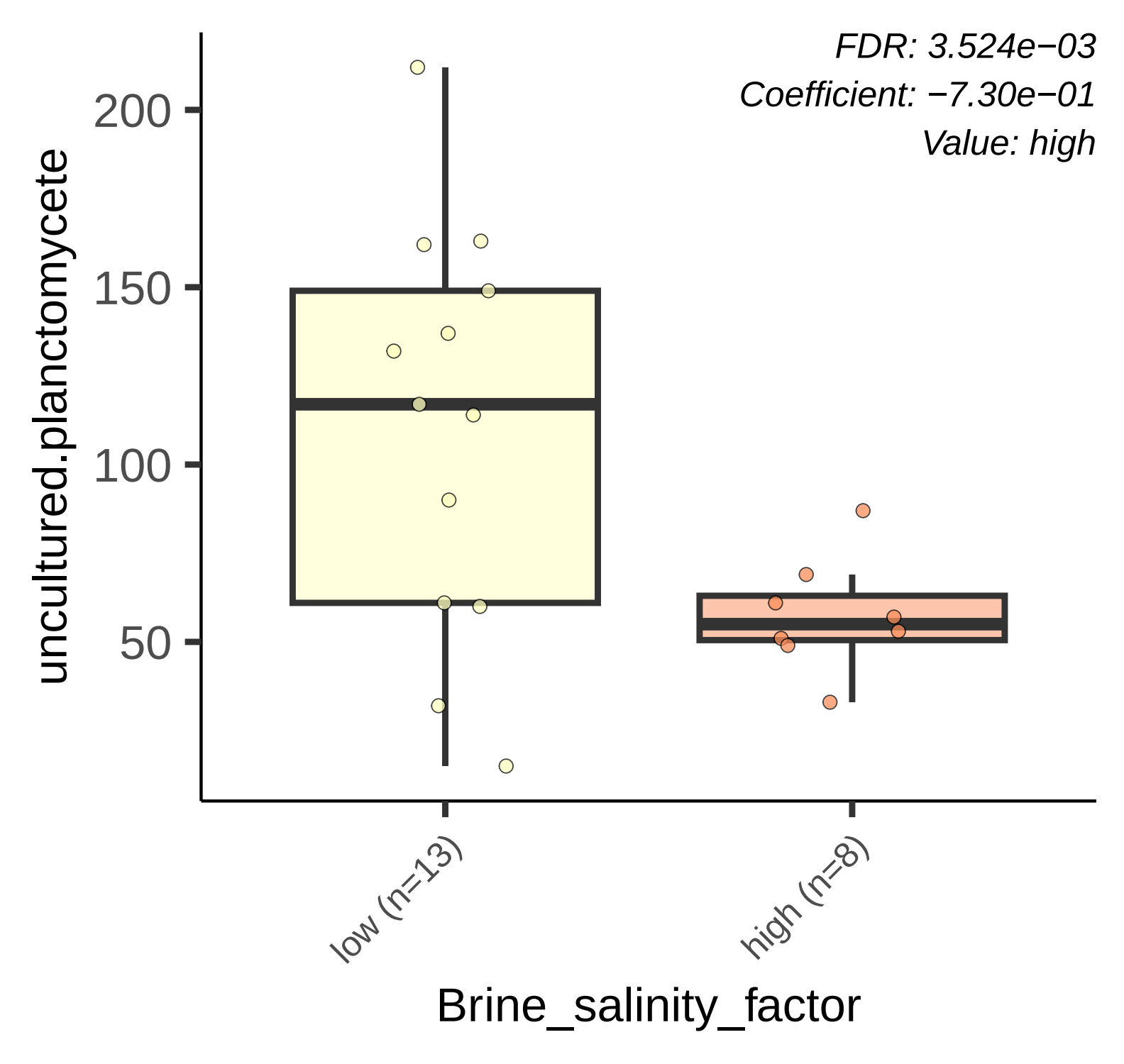

FDR: 3.057e−03
Coefficient: −1.73e+00
Value: high
Candidatus.Amoebophilus.asiaticus
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

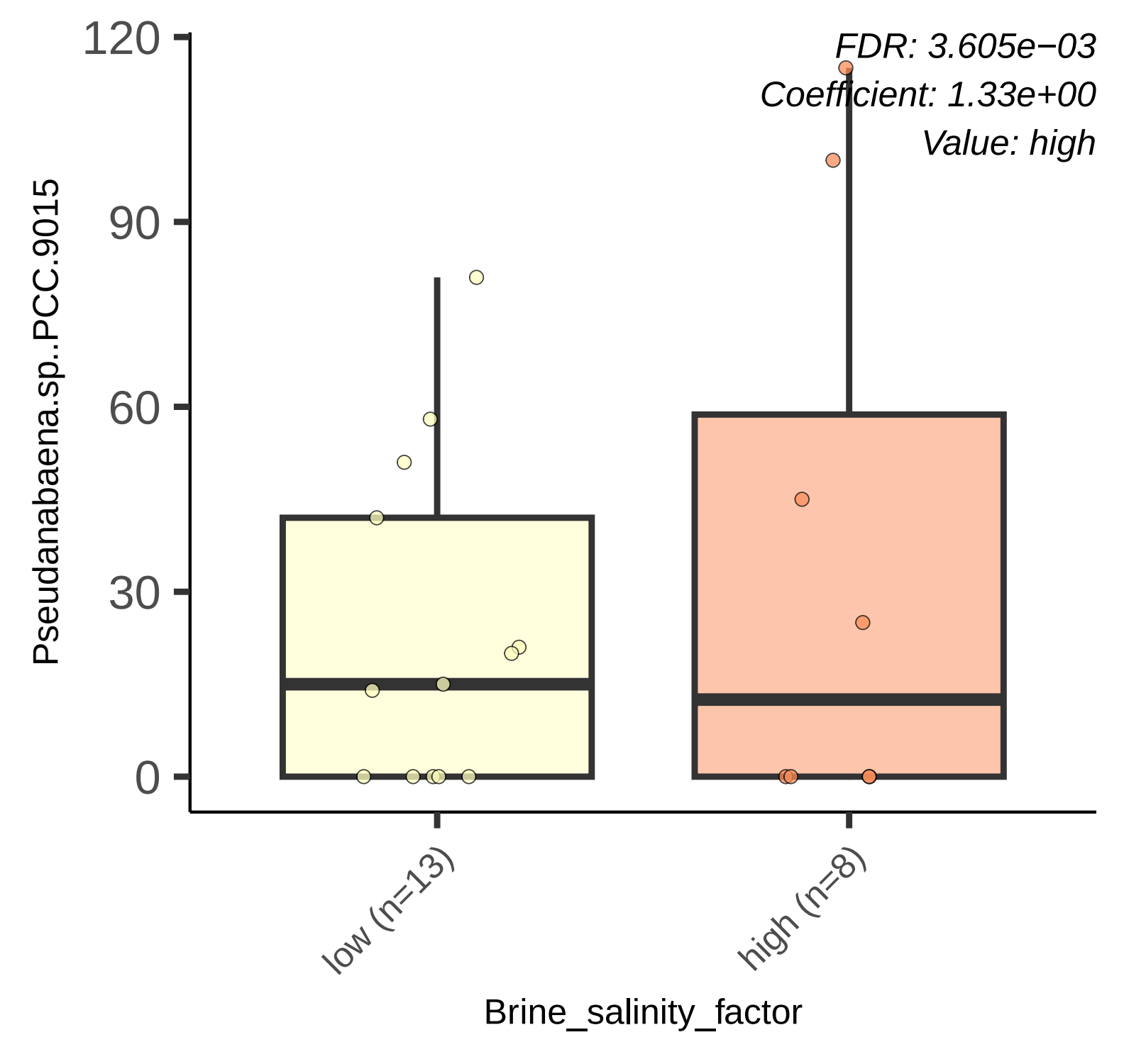

FDR: 3.278e−03
Coefficient: −5.82e−01
Value: high
1500
1000
500
Pelagibaca.abyssi
low (n=13)
high (n=8)
Brine_salinity_factor

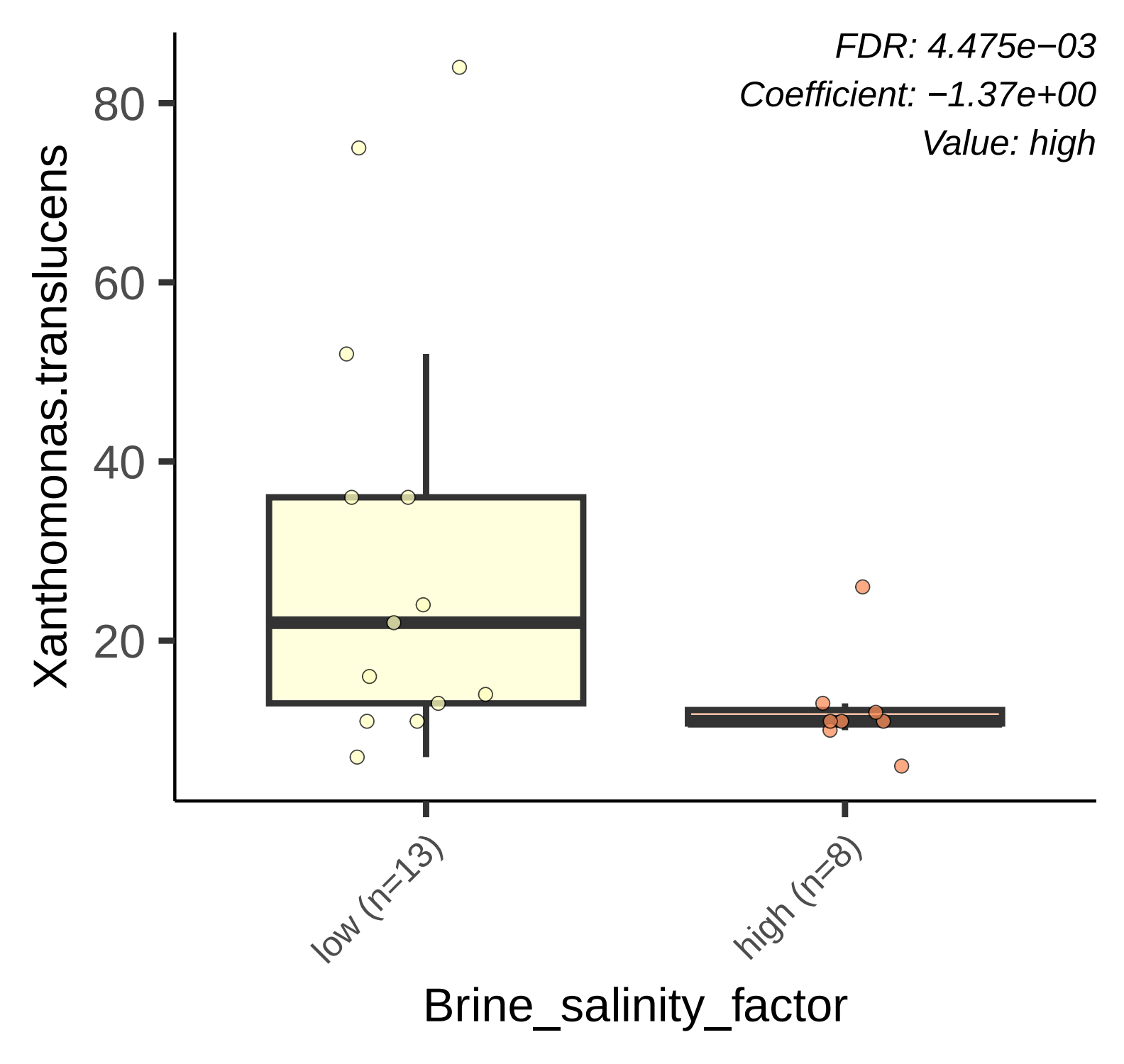

FDR: 3.319e−03
Coefficient: 4.31e+00
Value: high
Vibrio.parahaemolyticus
4000
3000
2000
1000
0
low (n=13)
high (n=8)
Brine_salinity_factor

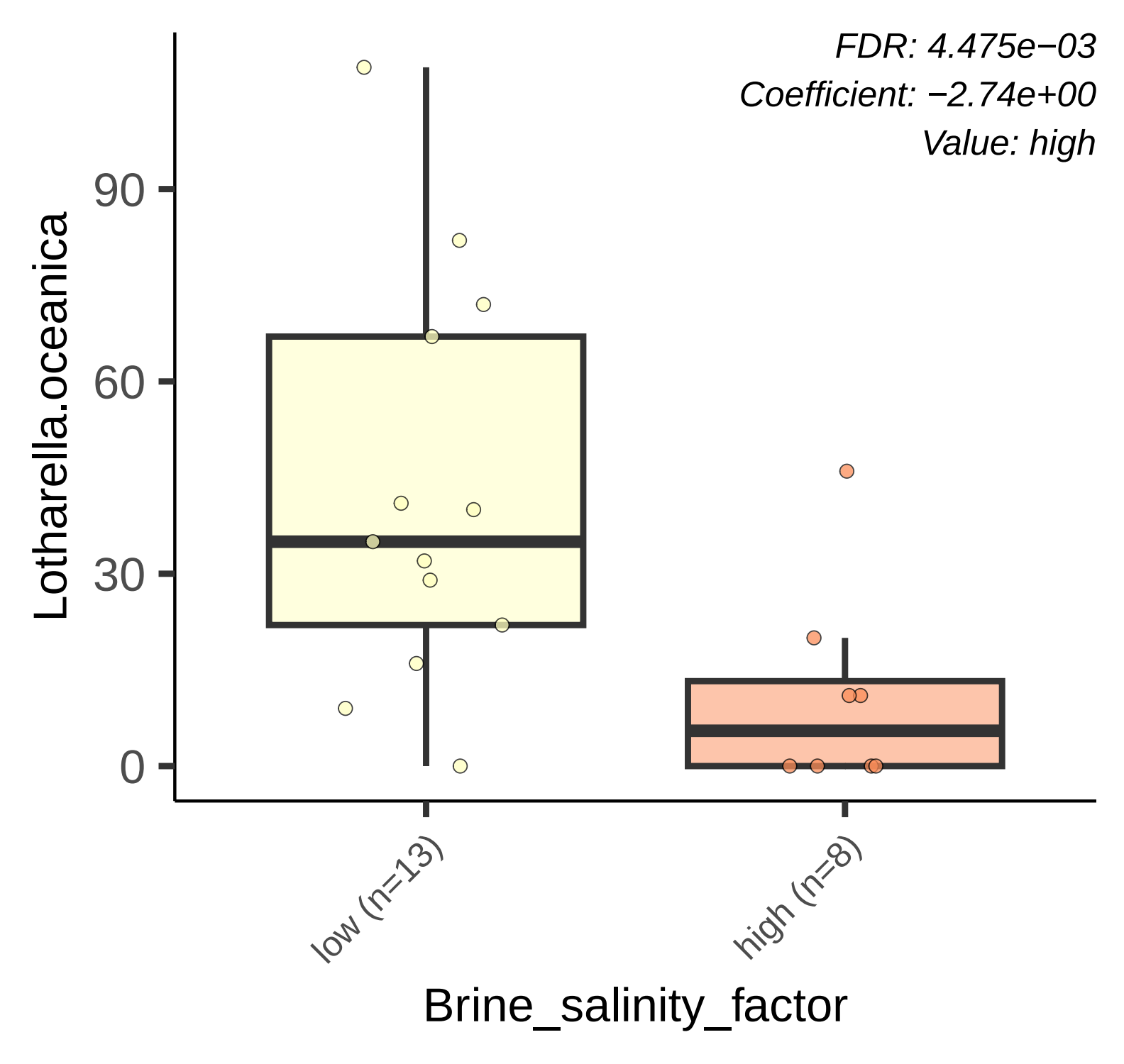

FDR: 3.398e−03
Coefficient: −1.11e+00
Value: high
Thioalkalivibrio.sulfidiphilus
800
600
400
200
0
low (n=13)
high (n=8)
Brine_salinity_factor

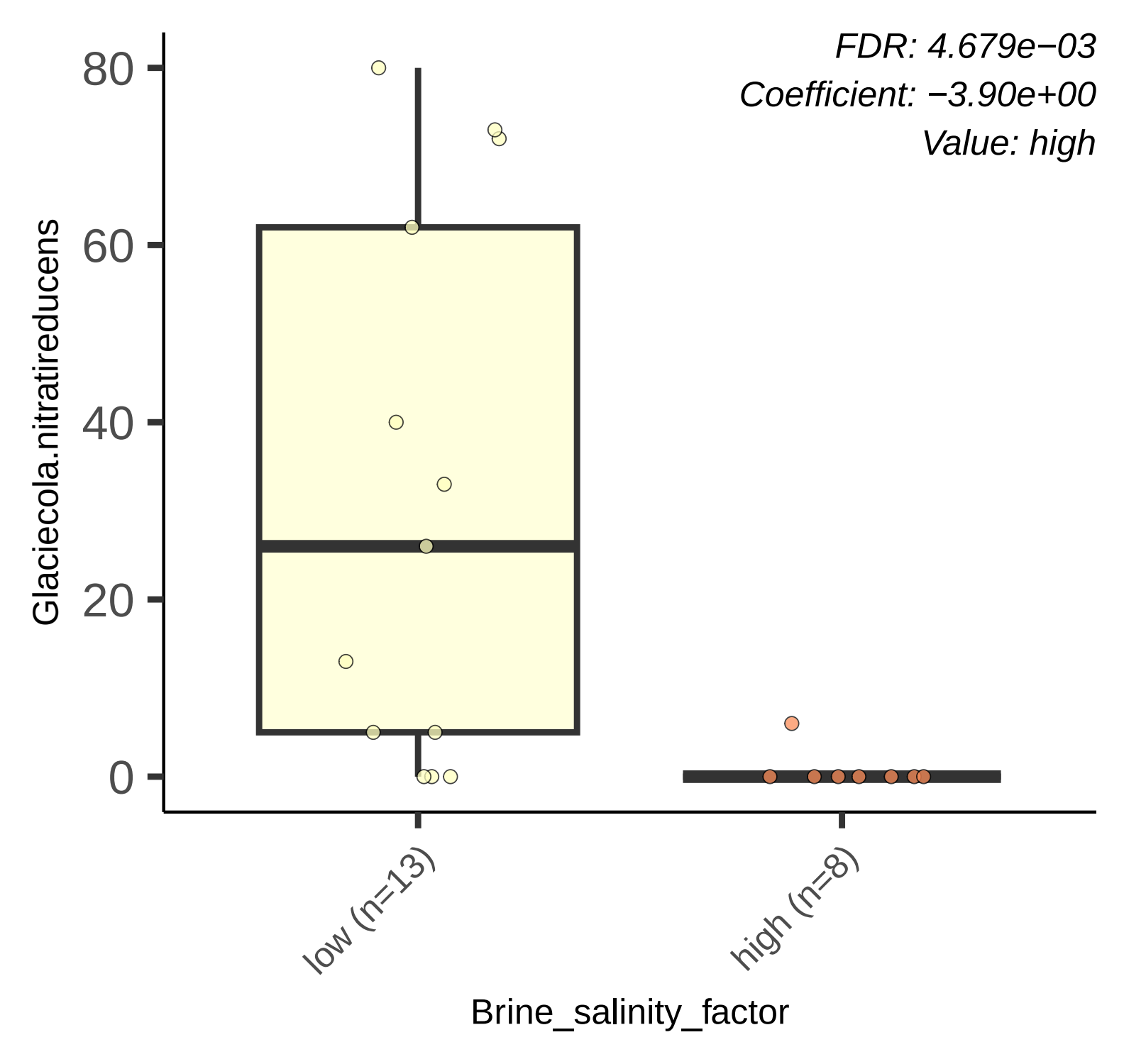

FDR: 3.459e−03
Coefficient: −8.71e−01
Value: high
uncultured.alpha.proteobacterium.EB080_L84F03
150
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

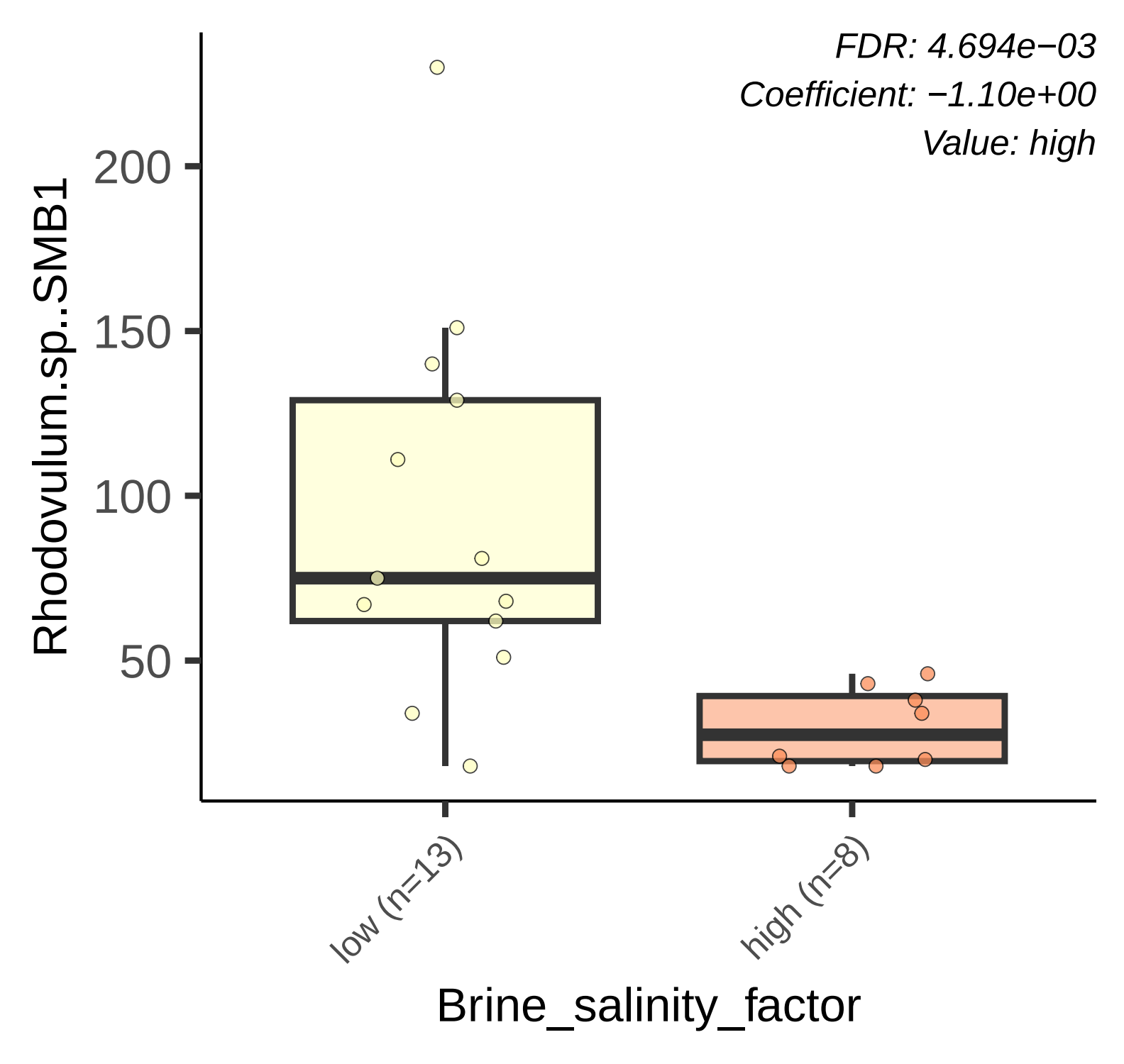

FDR: 3.524e−03
Coefficient: −7.30e−01
Value: high
uncultured.planctomycete
200
150
100
50
low (n=13)
high (n=8)
Brine_salinity_factor

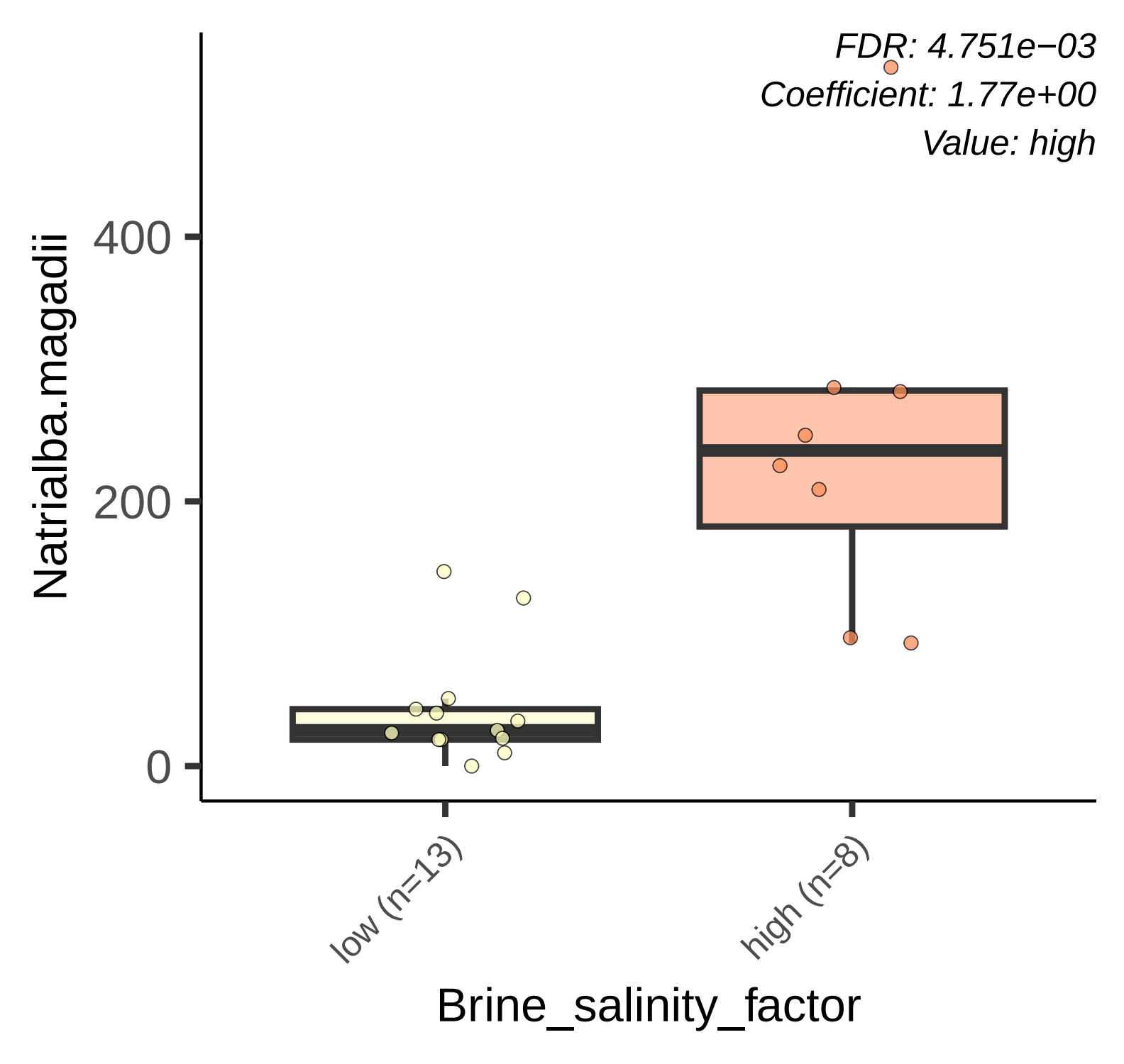

FDR: 3.605e−03
Coefficient: 1.33e+00
Value: high
120
90
60
30
0
Pseudanabaena.sp..PCC.9015
low (n=13)
high (n=8)
Brine_salinity_factor

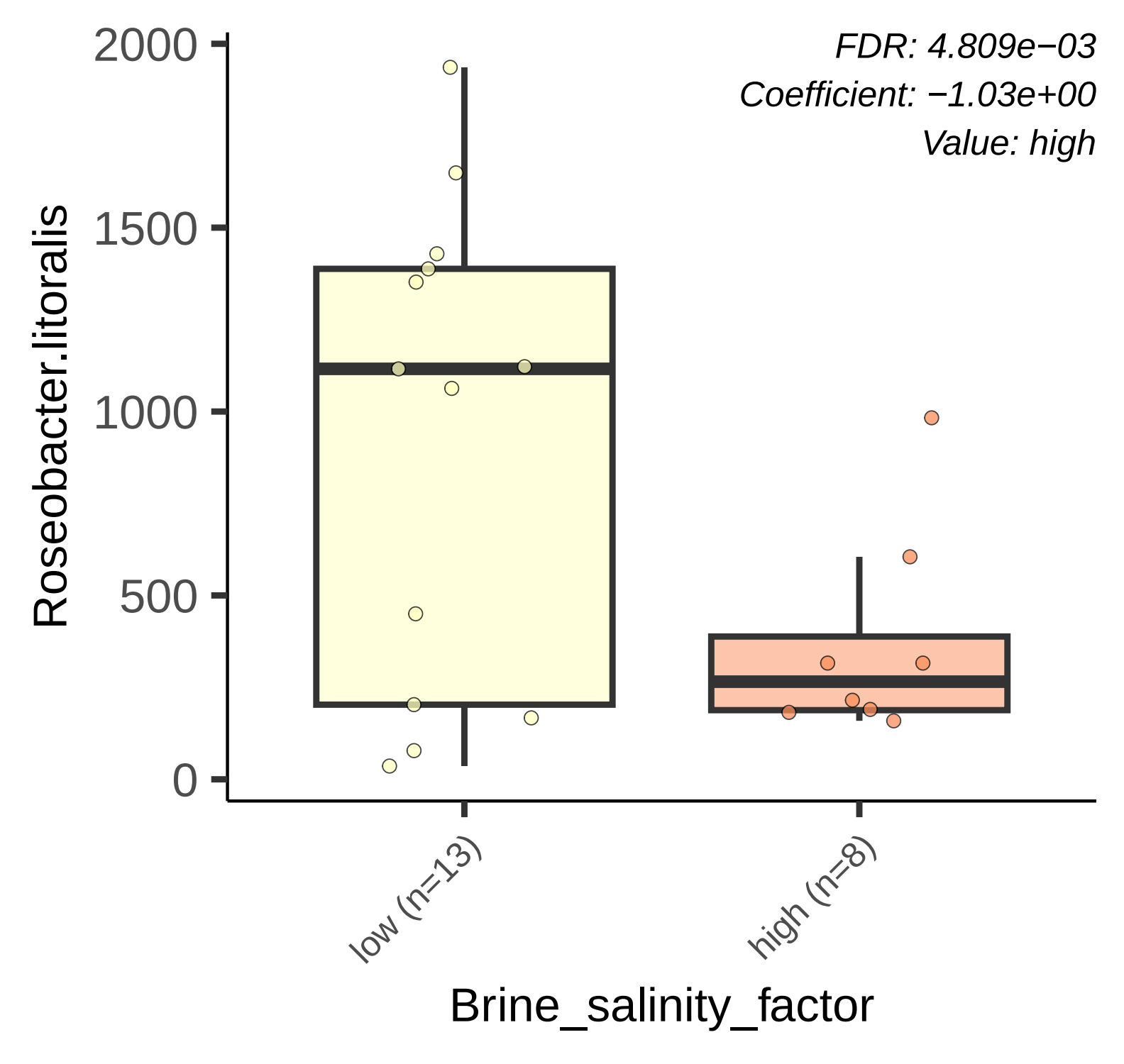

FDR: 4.475e−03
Coefficient: −1.37e+00
Value: high
Xanthomonas.translucens
80
60
40
20
low (n=13)
high (n=8)
Brine_salinity_factor

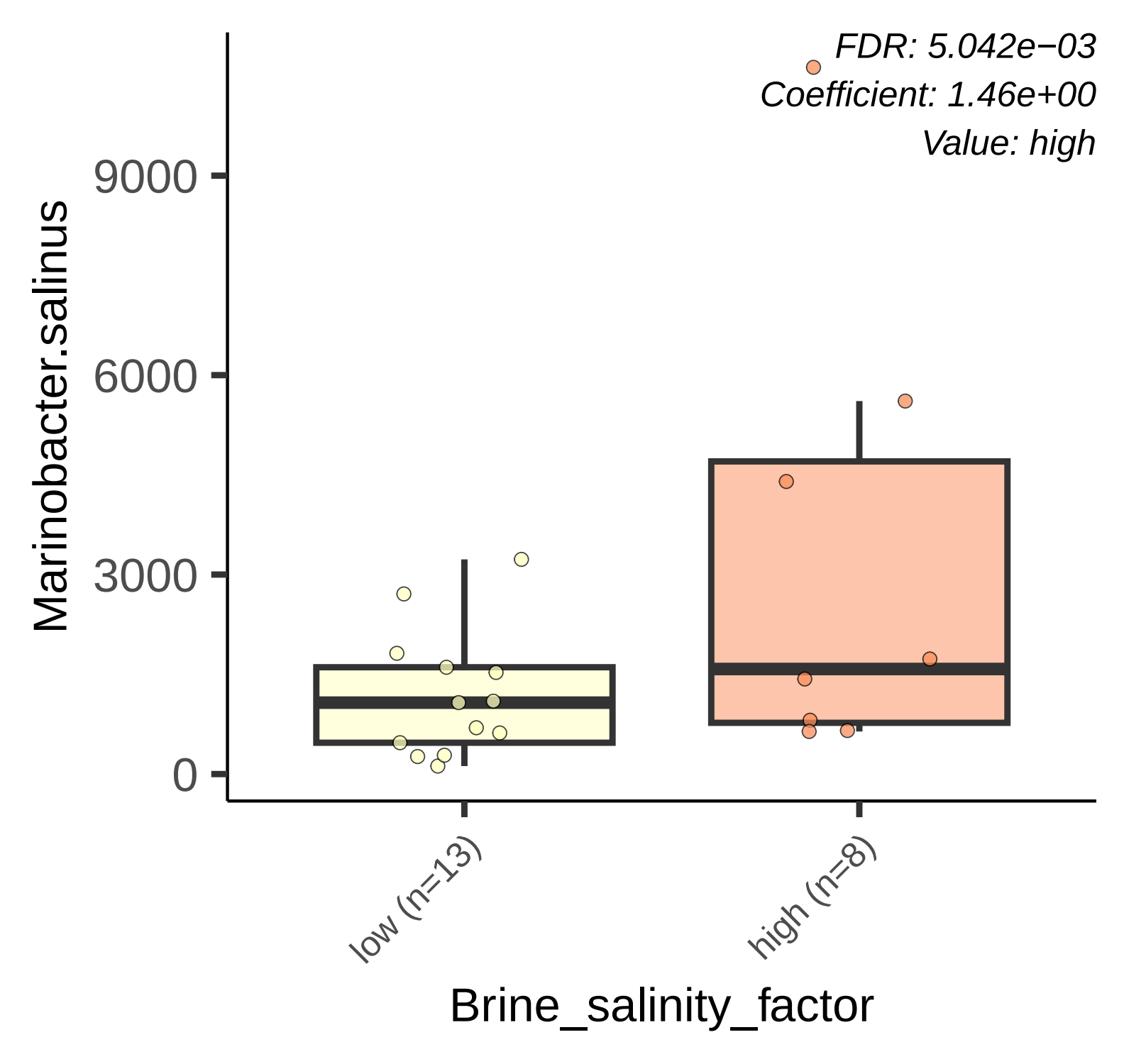

FDR: 4.475e−03
Coefficient: −2.74e+00
Value: high
Lotharella.oceanica
90
60
30
0
low (n=13)
high (n=8)
Brine_salinity_factor

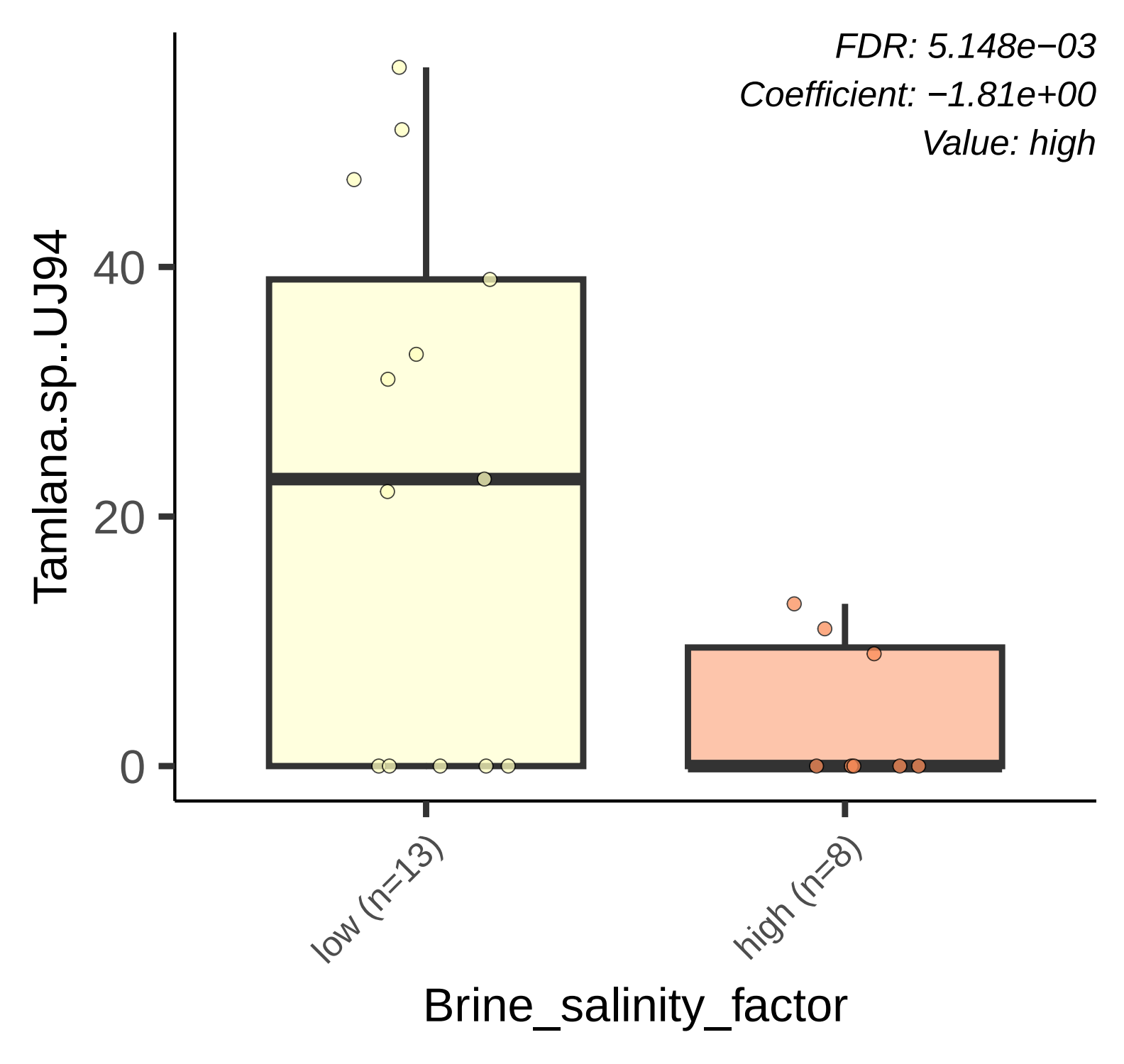

FDR: 4.679e−03
Coefficient: −3.90e+00
Value: high
Glaciecola.nitratireducens
80
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

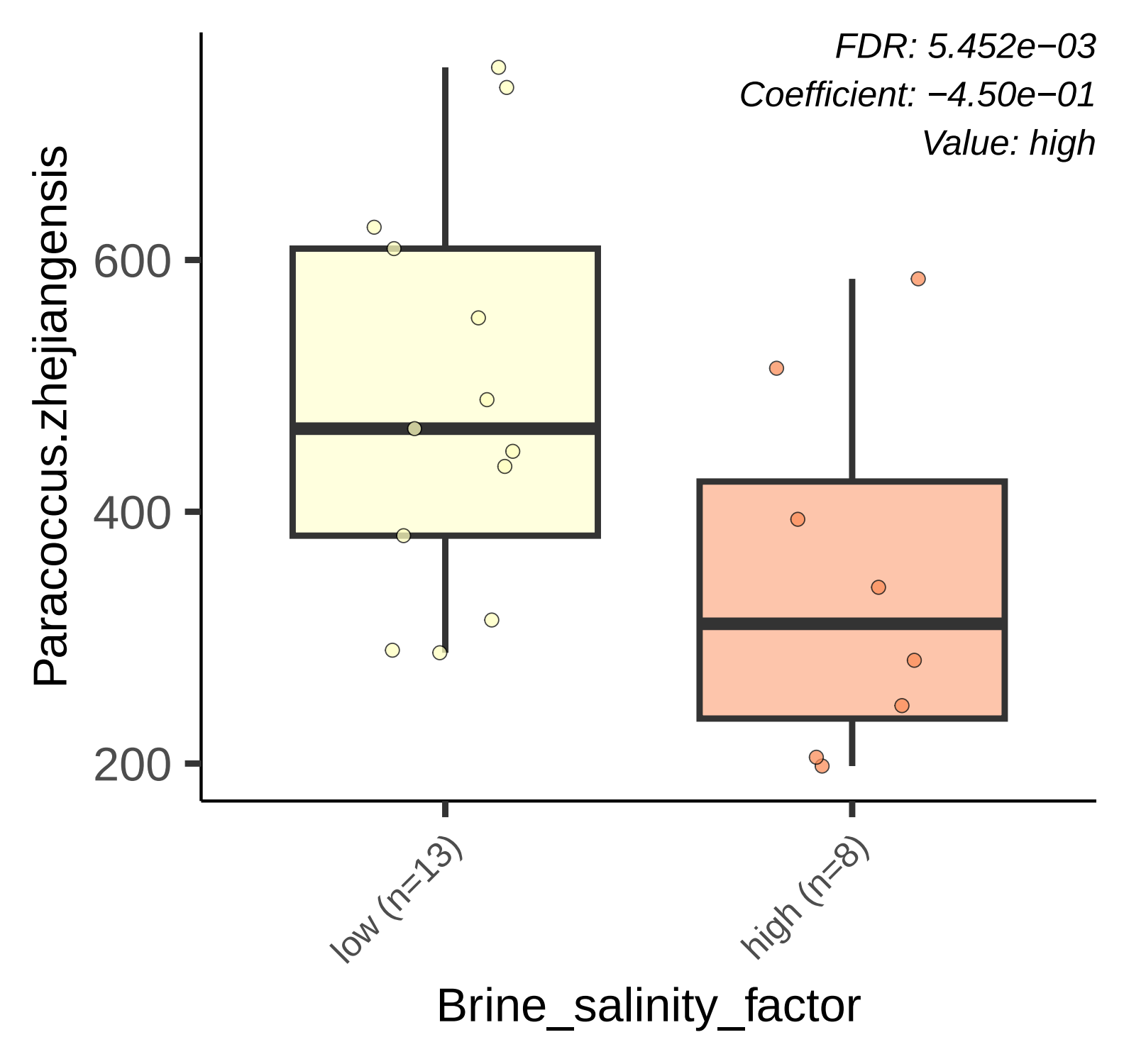

FDR: 4.694e−03
Coefficient: −1.10e+00
Value: high
Rhodovulum.sp..SMB1
200
150
100
50
low (n=13)
high (n=8)
Brine_salinity_factor

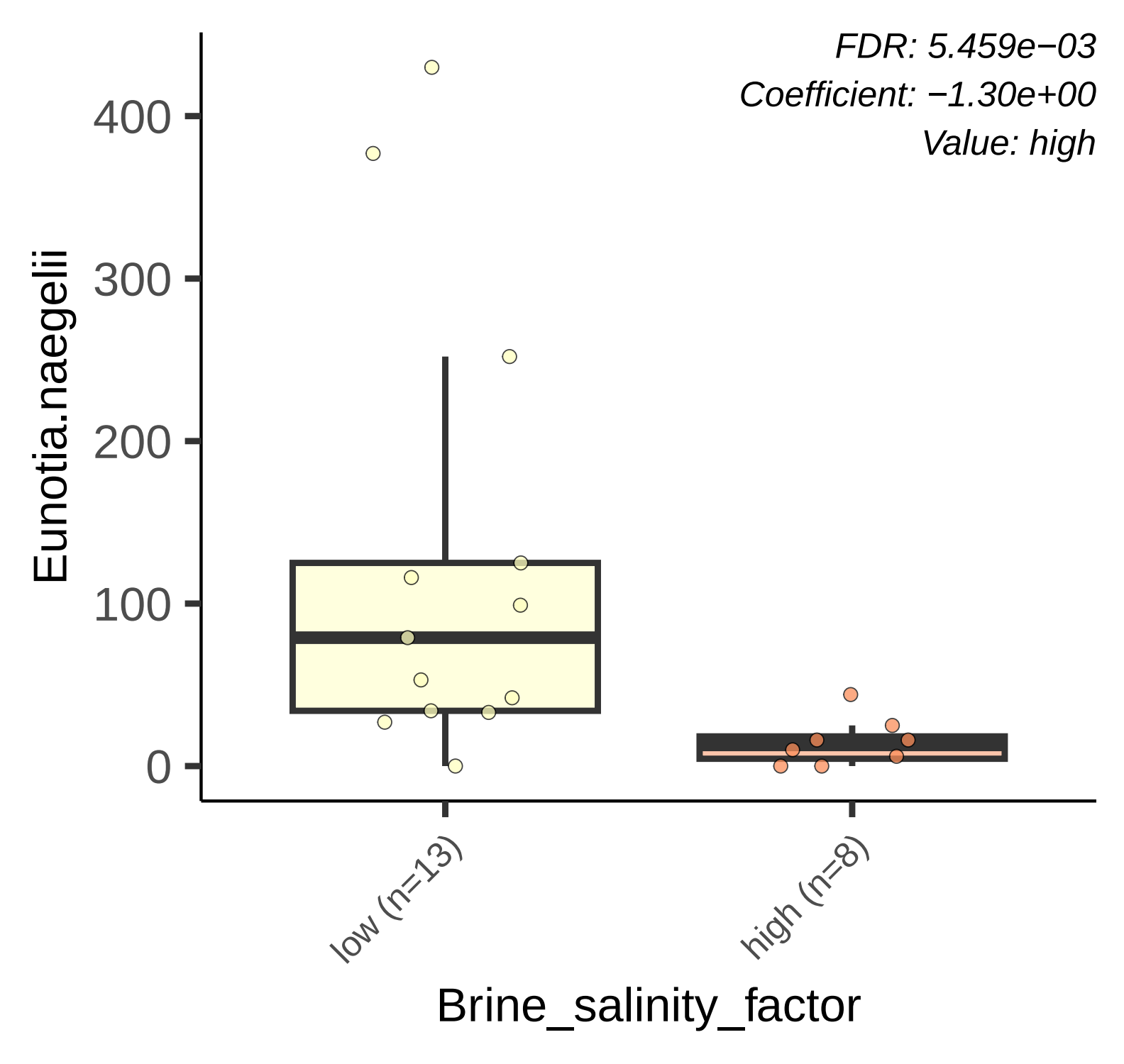

FDR: 4.751e−03
Coefficient: 1.77e+00
Value: high
Natrialba.magadii
400
200
0
low (n=13)
high (n=8)
Brine_salinity_factor

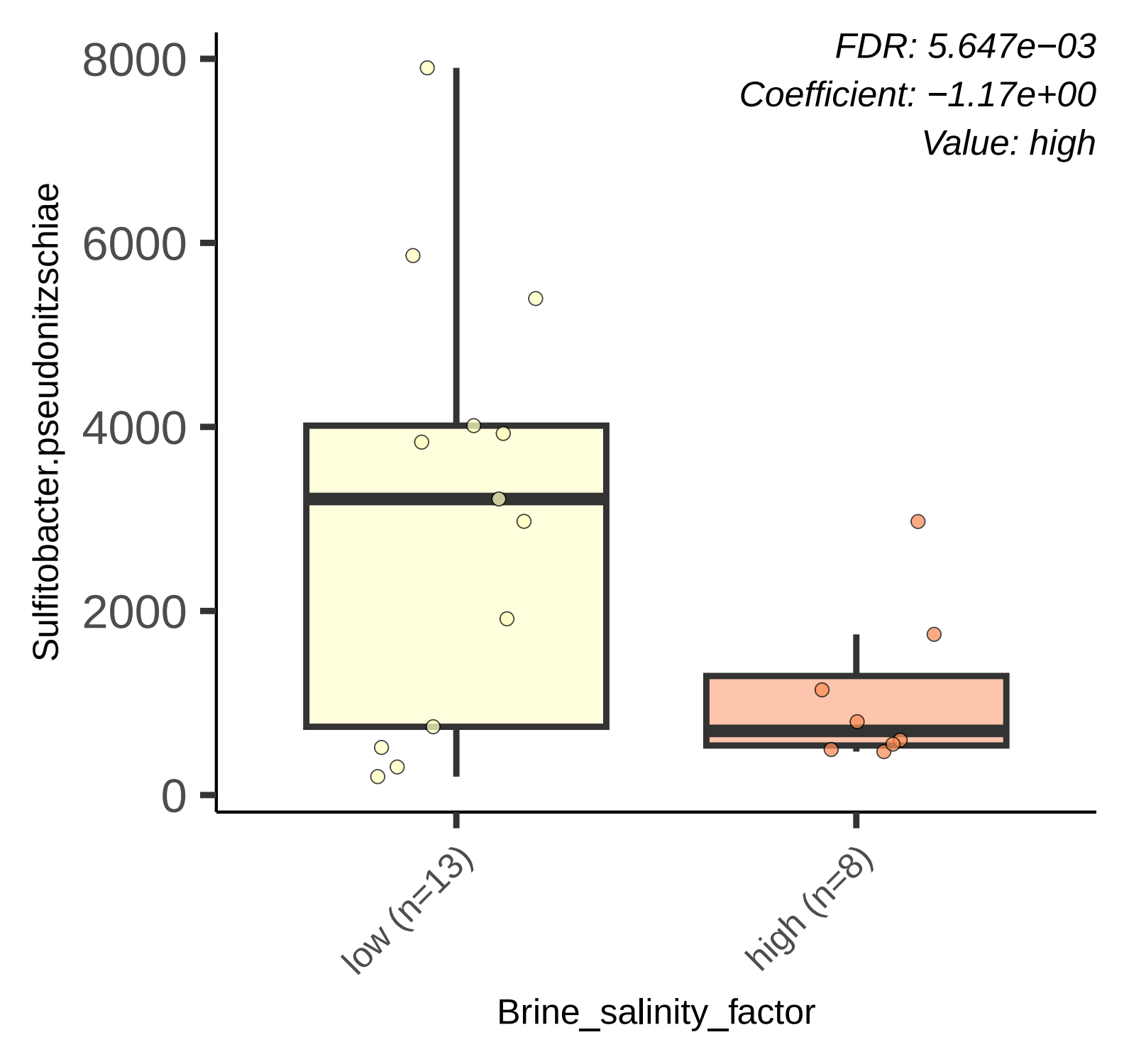

FDR: 4.809e−03
Coefficient: −1.03e+00
Value: high
Roseobacter.litoralis
2000
1500
1000
500
0
low (n=13)
high (n=8)
Brine_salinity_factor

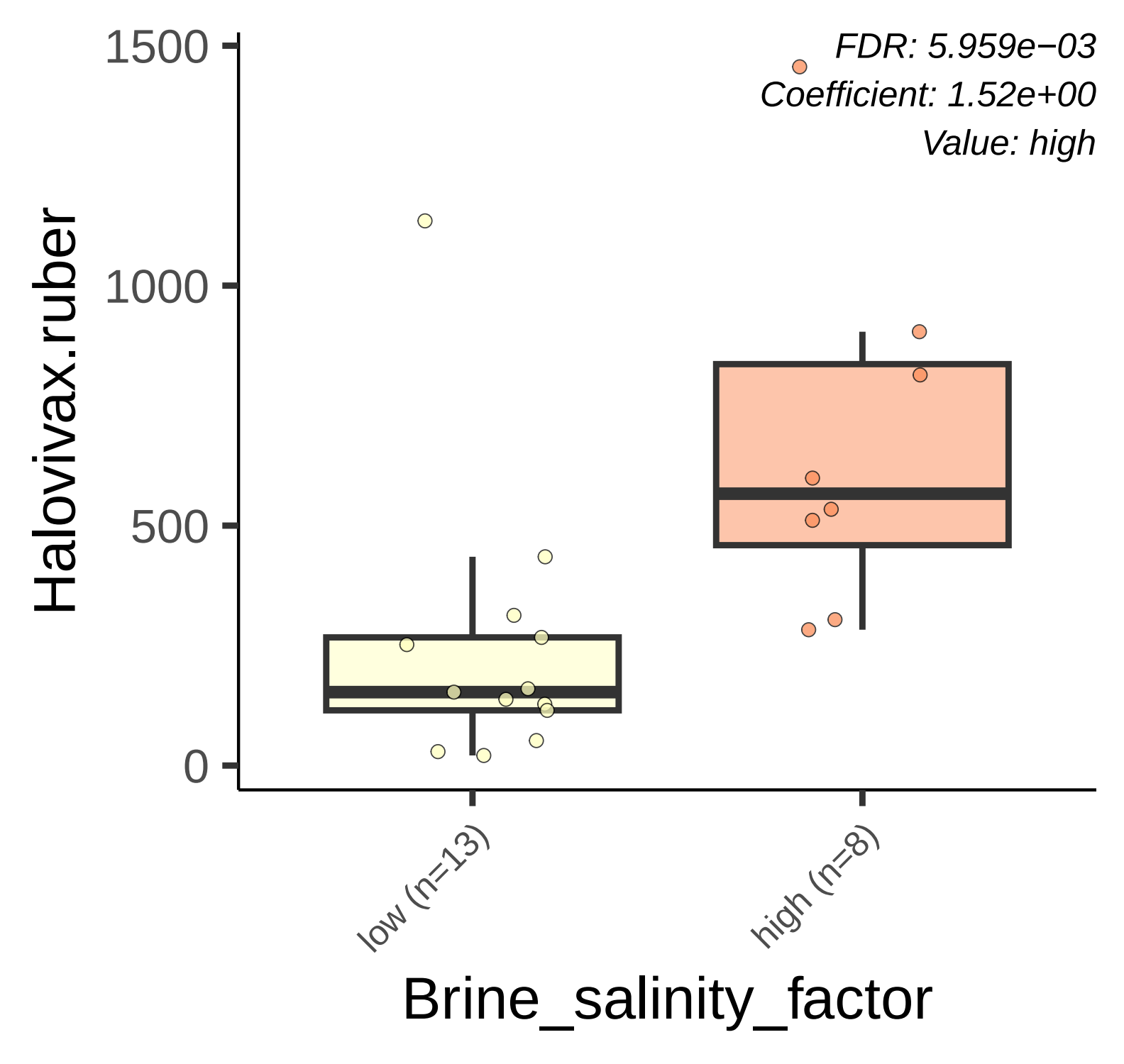

FDR: 5.042e−03
Coefficient: 1.46e+00
Value: high
Marinobacter.salinus
9000
6000
3000
0
low (n=13)
high (n=8)
Brine_salinity_factor

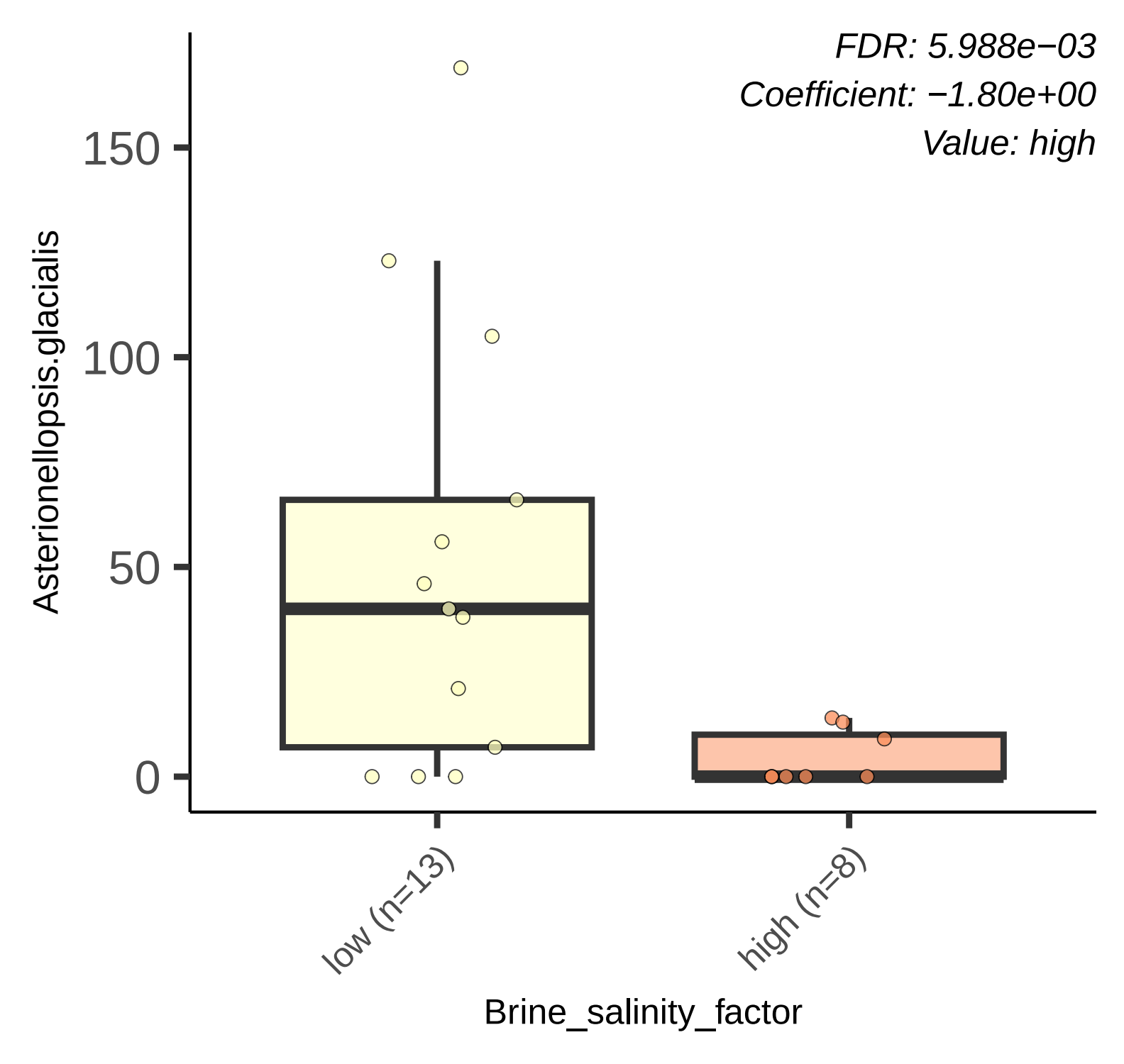

FDR: 5.148e−03
Coefficient: −1.81e+00
Value: high
Tamlana.sp..UJ94
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

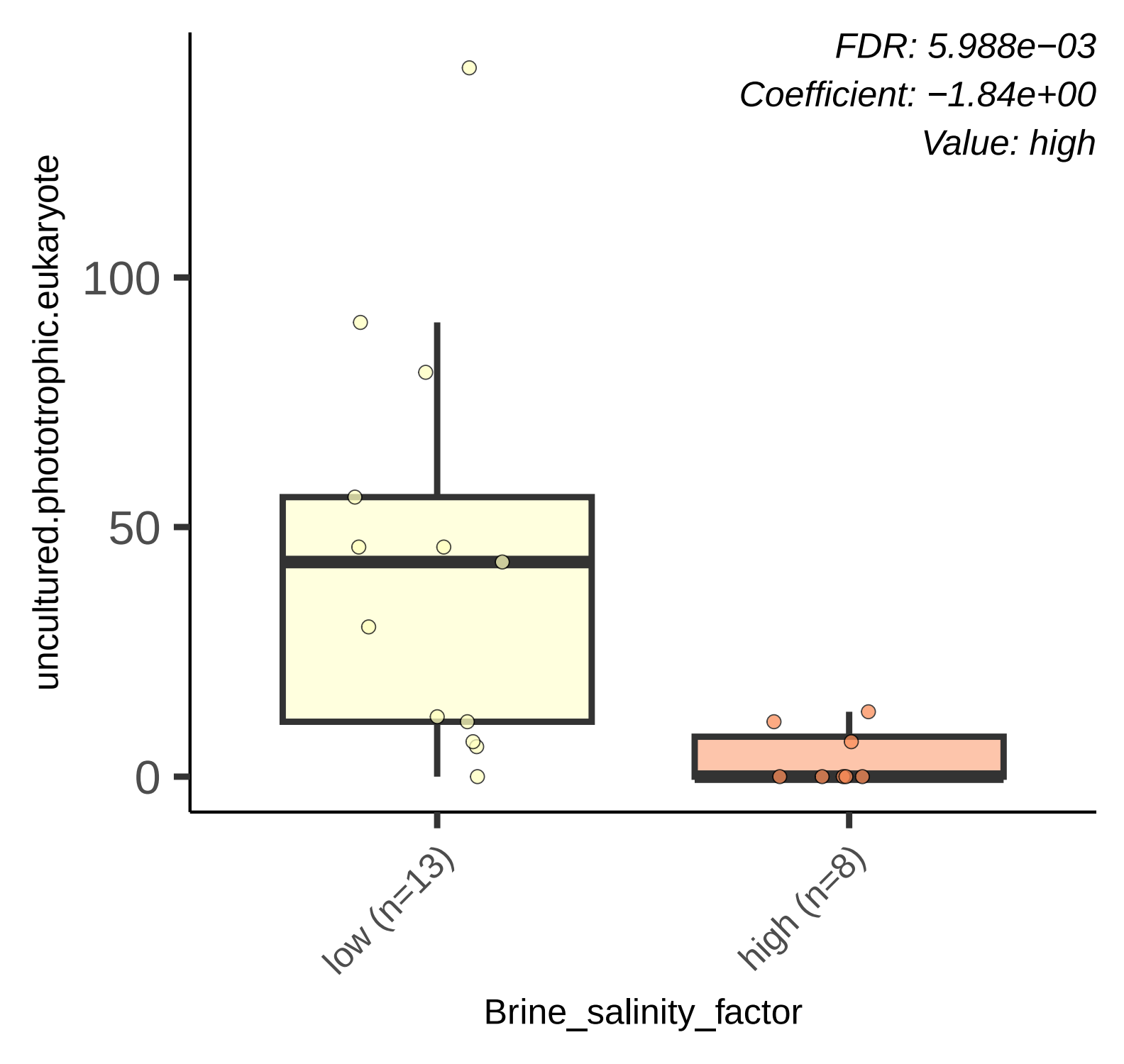

FDR: 5.452e−03
Coefficient: −4.50e−01
Value: high
Paracoccus.zhejiangensis
600
400
200
low (n=13)
high (n=8)
Brine_salinity_factor

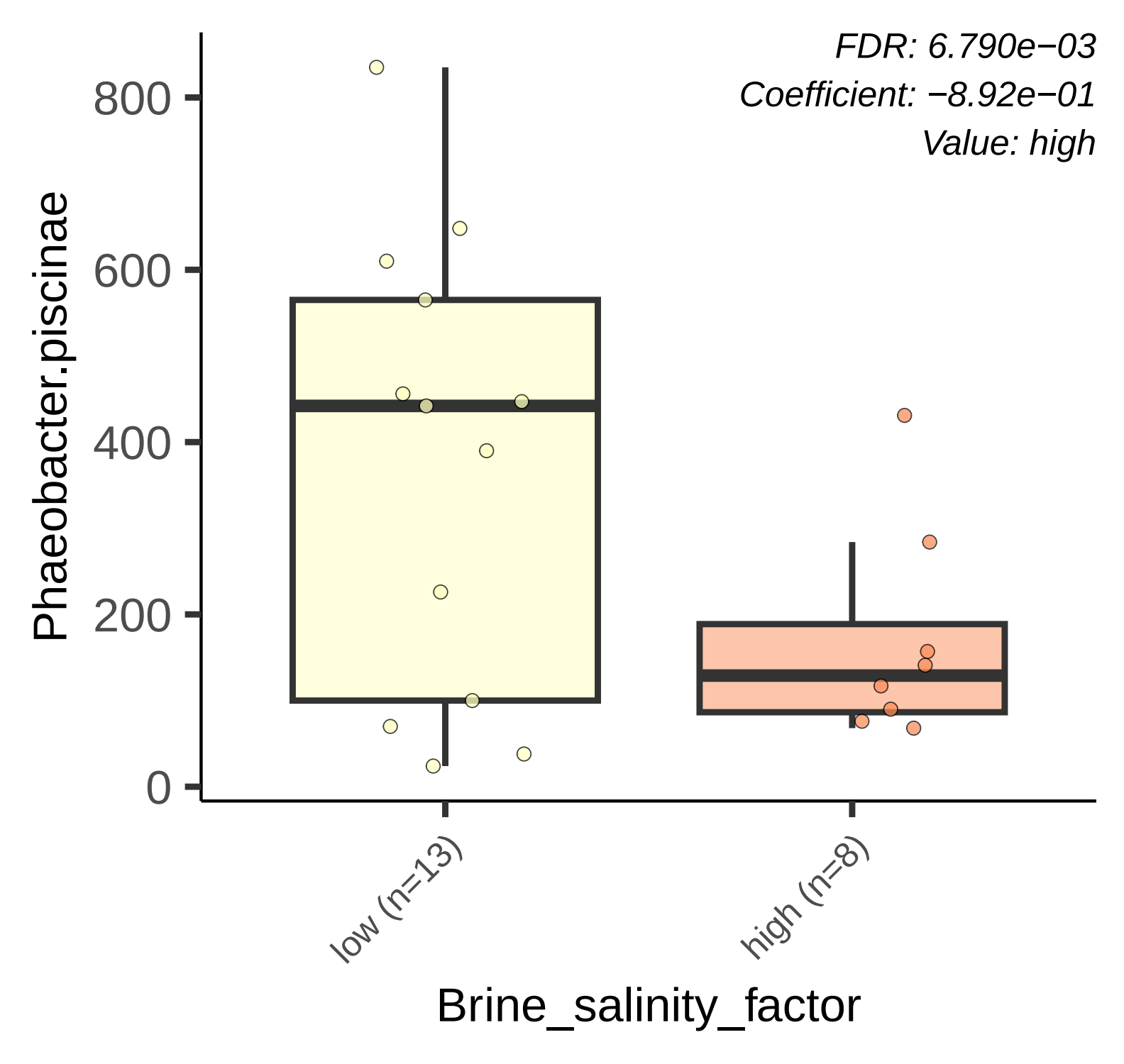

FDR: 5.459e−03
Coefficient: −1.30e+00
Value: high
Eunotia.naegelii
400
300
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

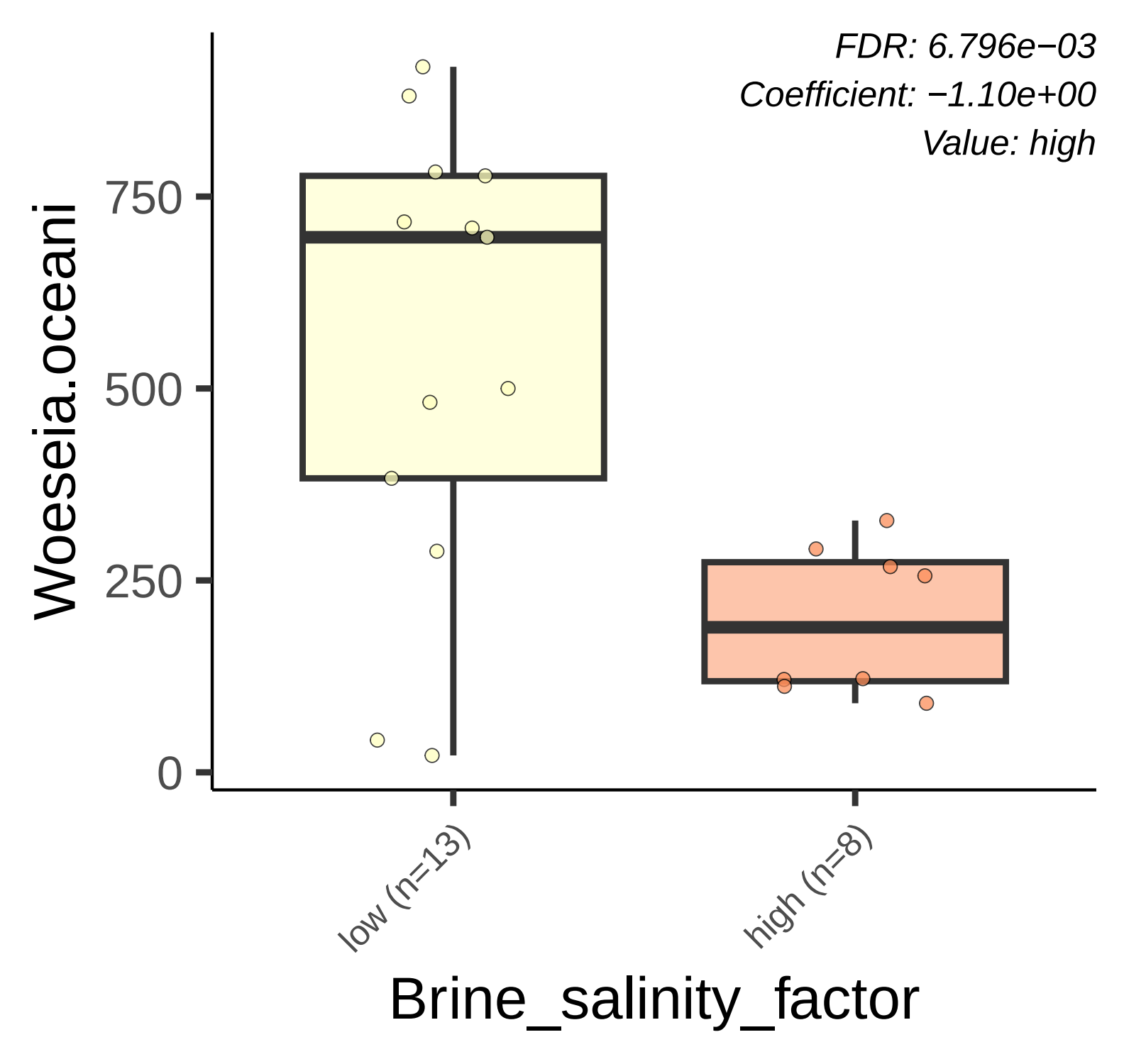

FDR: 5.647e−03
Coefficient: −1.17e+00
Value: high
8000
6000
4000
2000
0
Sulfitobacter.pseudonitzschiae
low (n=13)
high (n=8)
Brine_salinity_factor

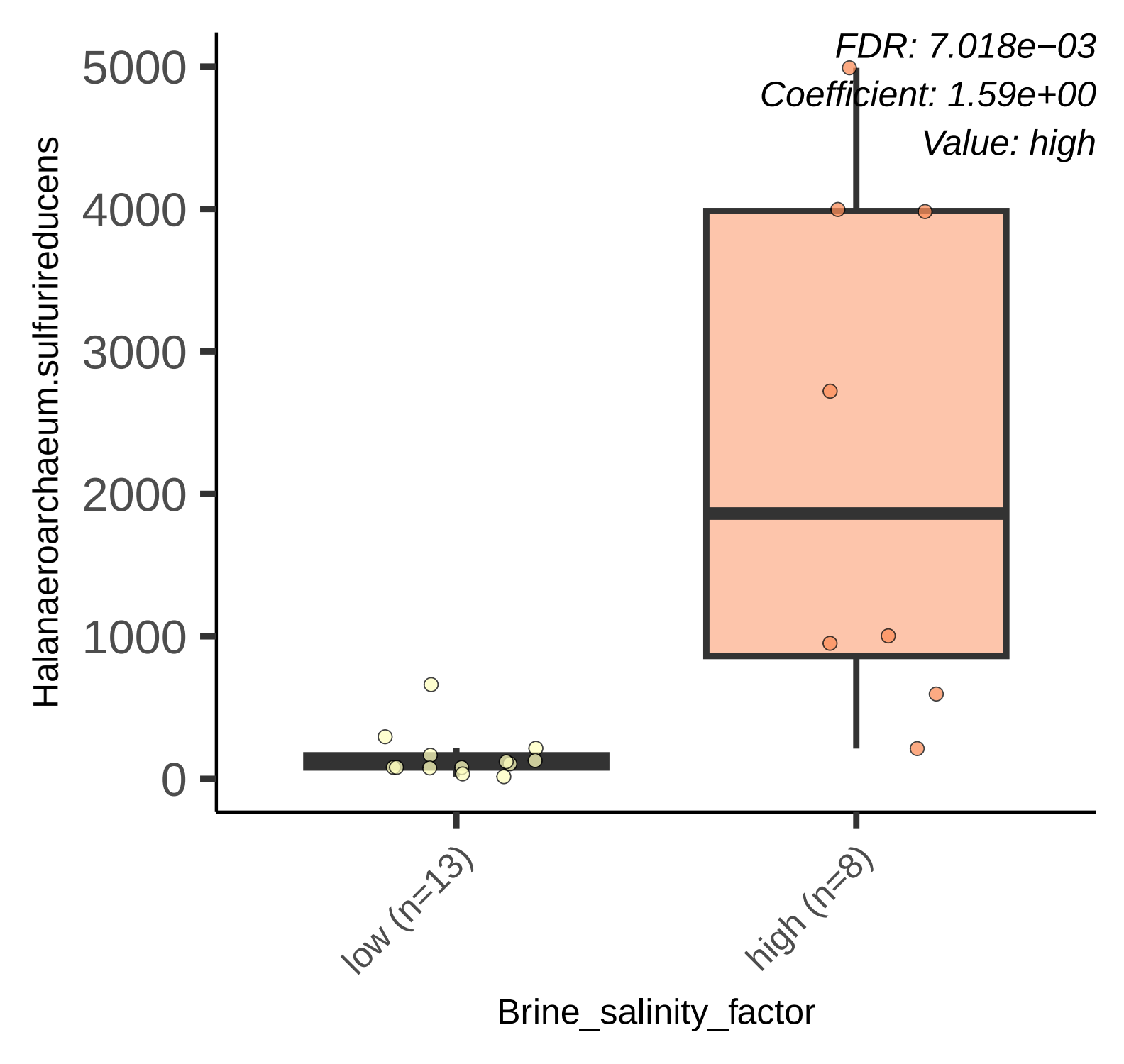

FDR: 5.959e−03
Coefficient: 1.52e+00
Value: high
1500
1000
500
0
Halovivax.ruber
low (n=13)
high (n=8)
Brine_salinity_factor

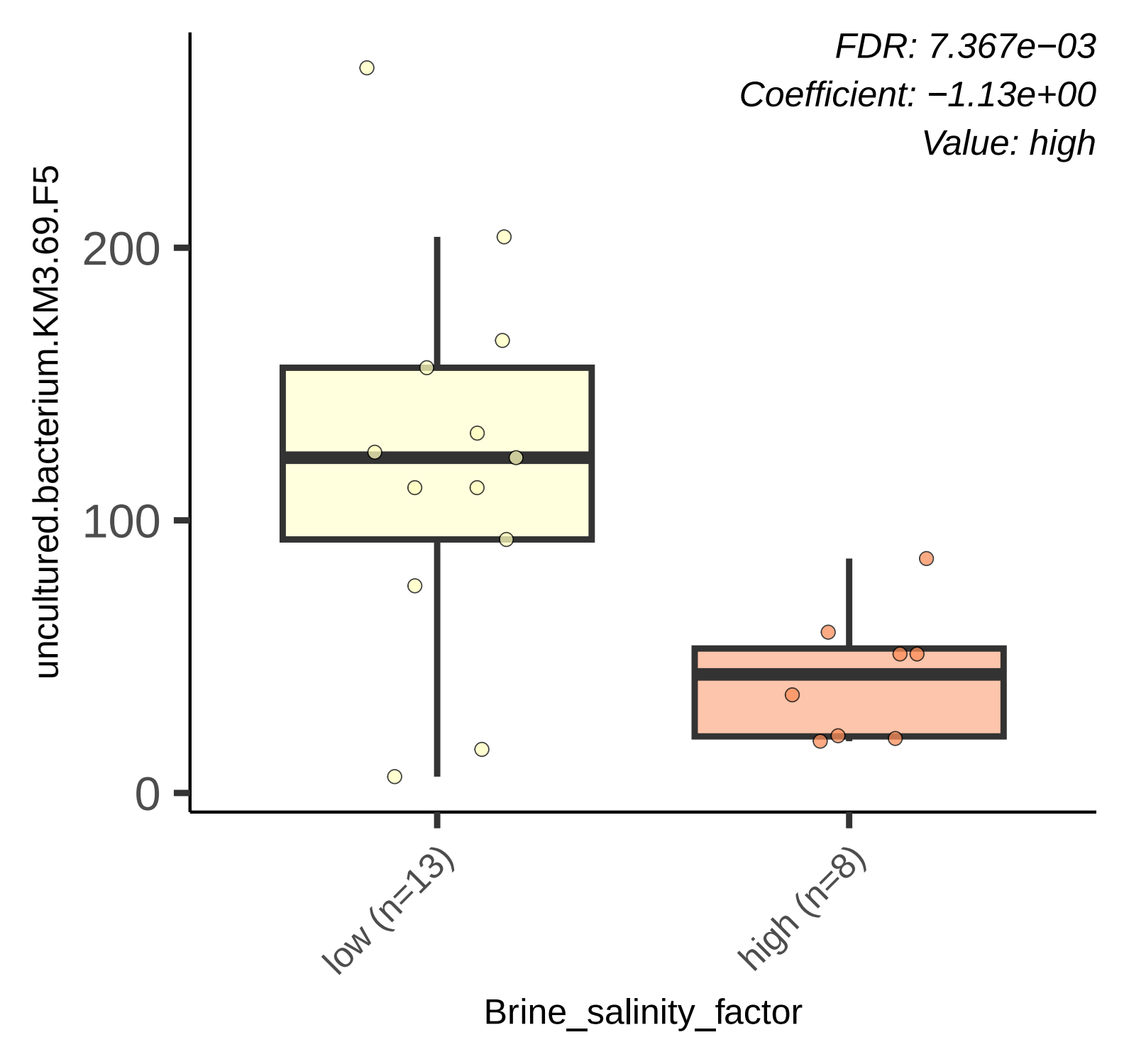

FDR: 5.988e−03
Coefficient: −1.80e+00
Value: high
Asterionellopsis.glacialis
150
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

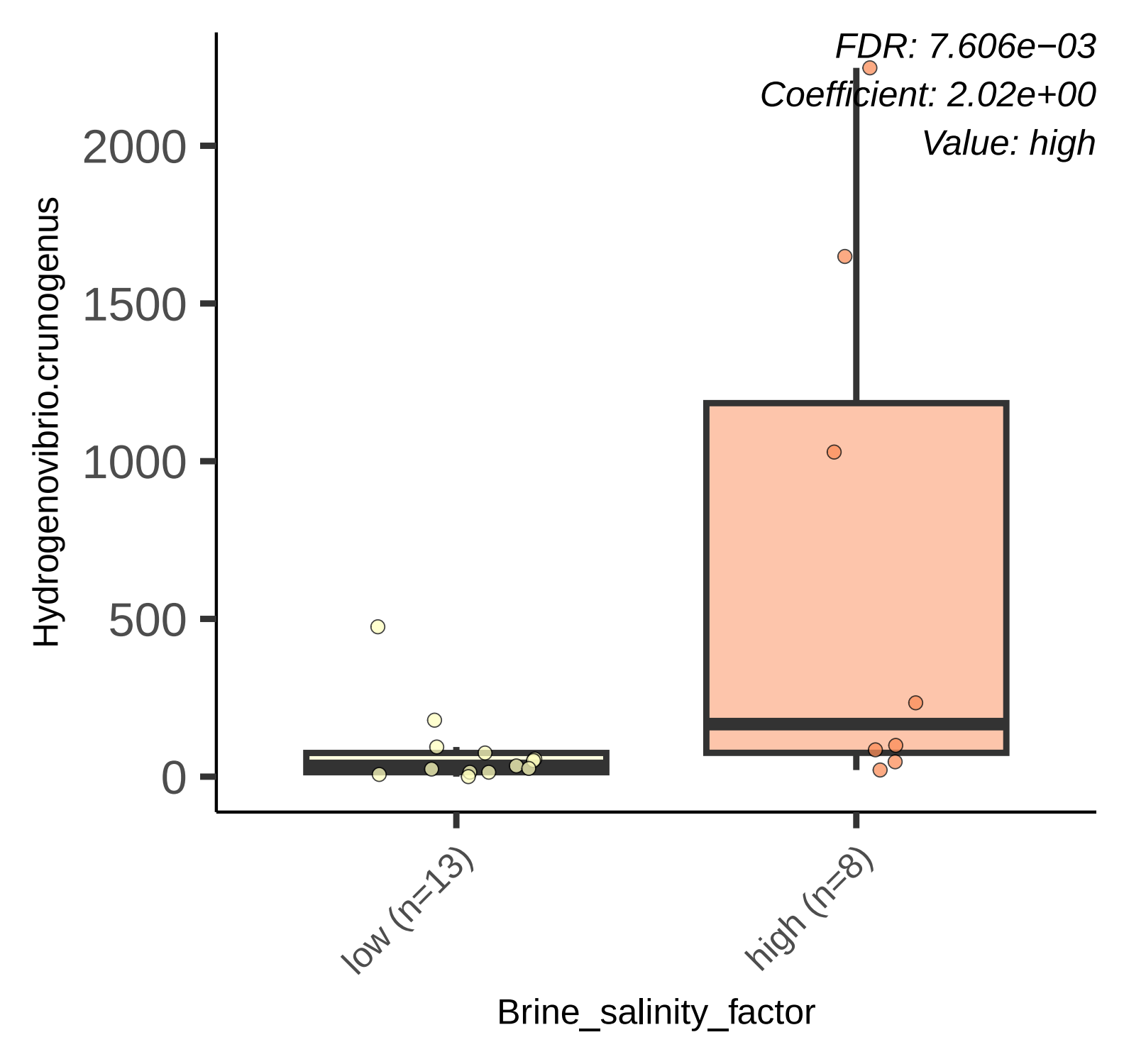

FDR: 5.988e−03
Coefficient: −1.84e+00
Value: high
uncultured.phototrophic.eukaryote
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

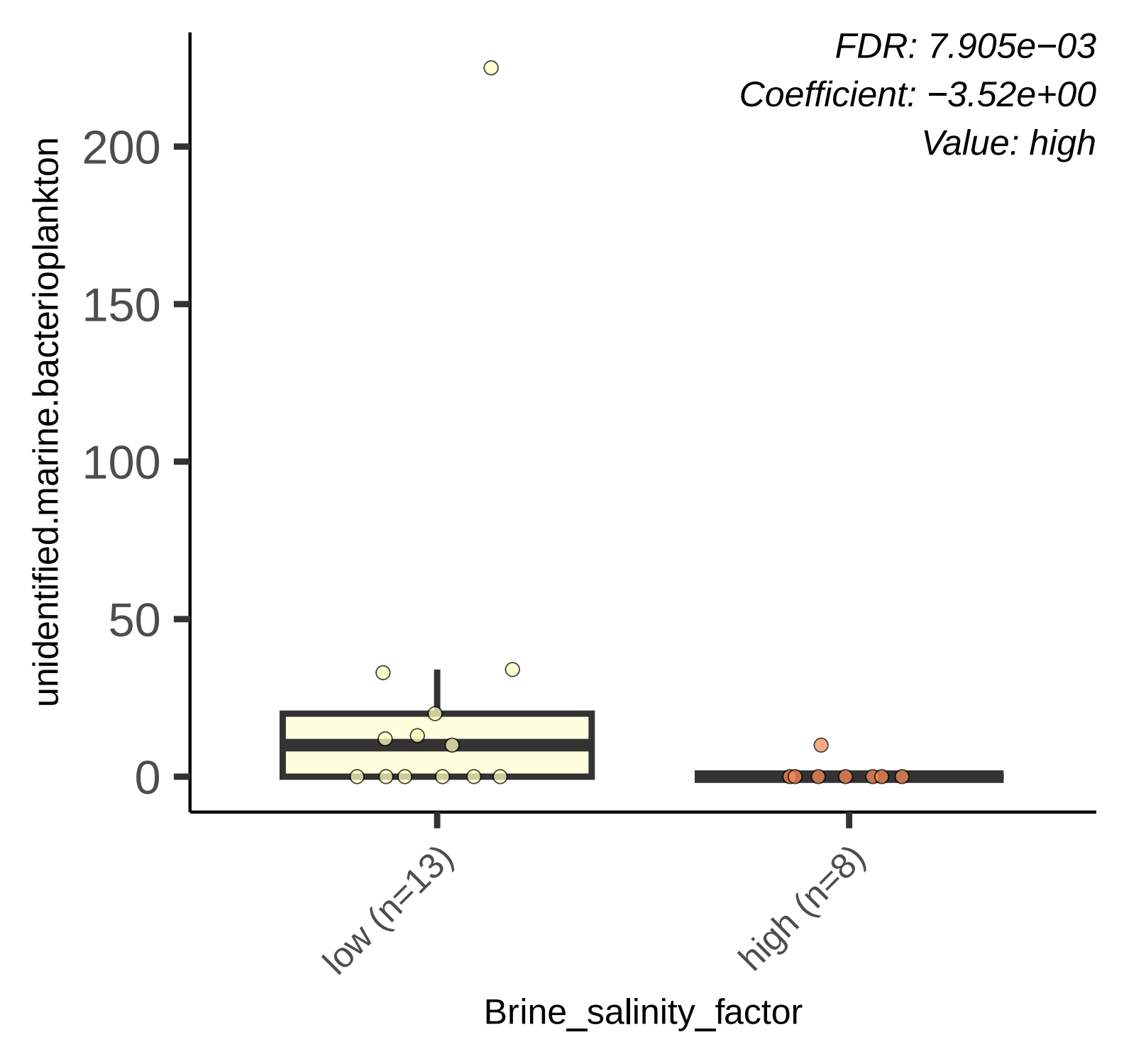

FDR: 6.790e−03
Coefficient: −8.92e−01
Value: high
Phaeobacter.piscinae
800
600
400
200
0
low (n=13)
high (n=8)
Brine_salinity_factor

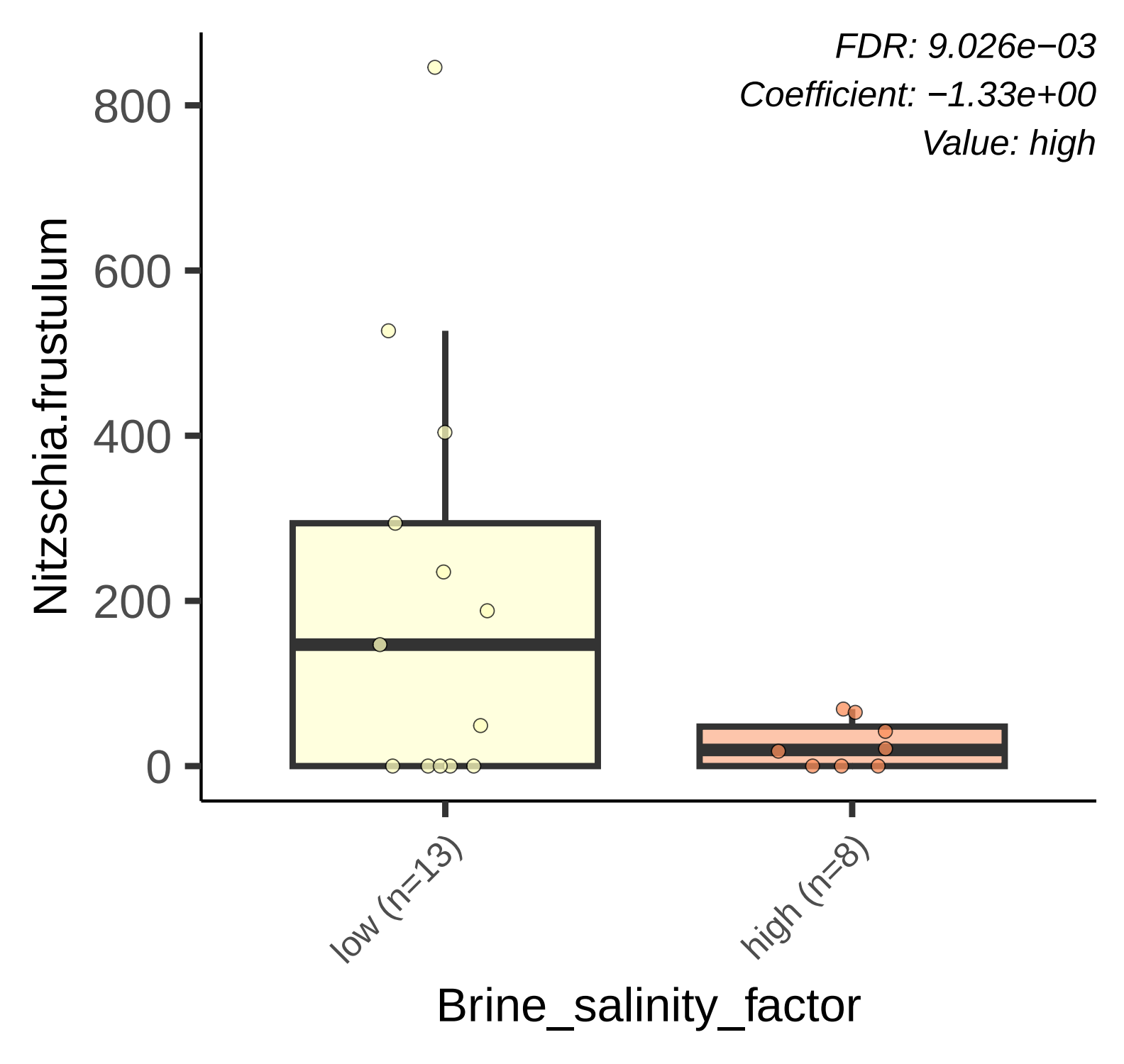

FDR: 6.796e−03
Coefficient: −1.10e+00
Value: high
Woeseia.oceani
750
500
250
0
low (n=13)
high (n=8)
Brine_salinity_factor

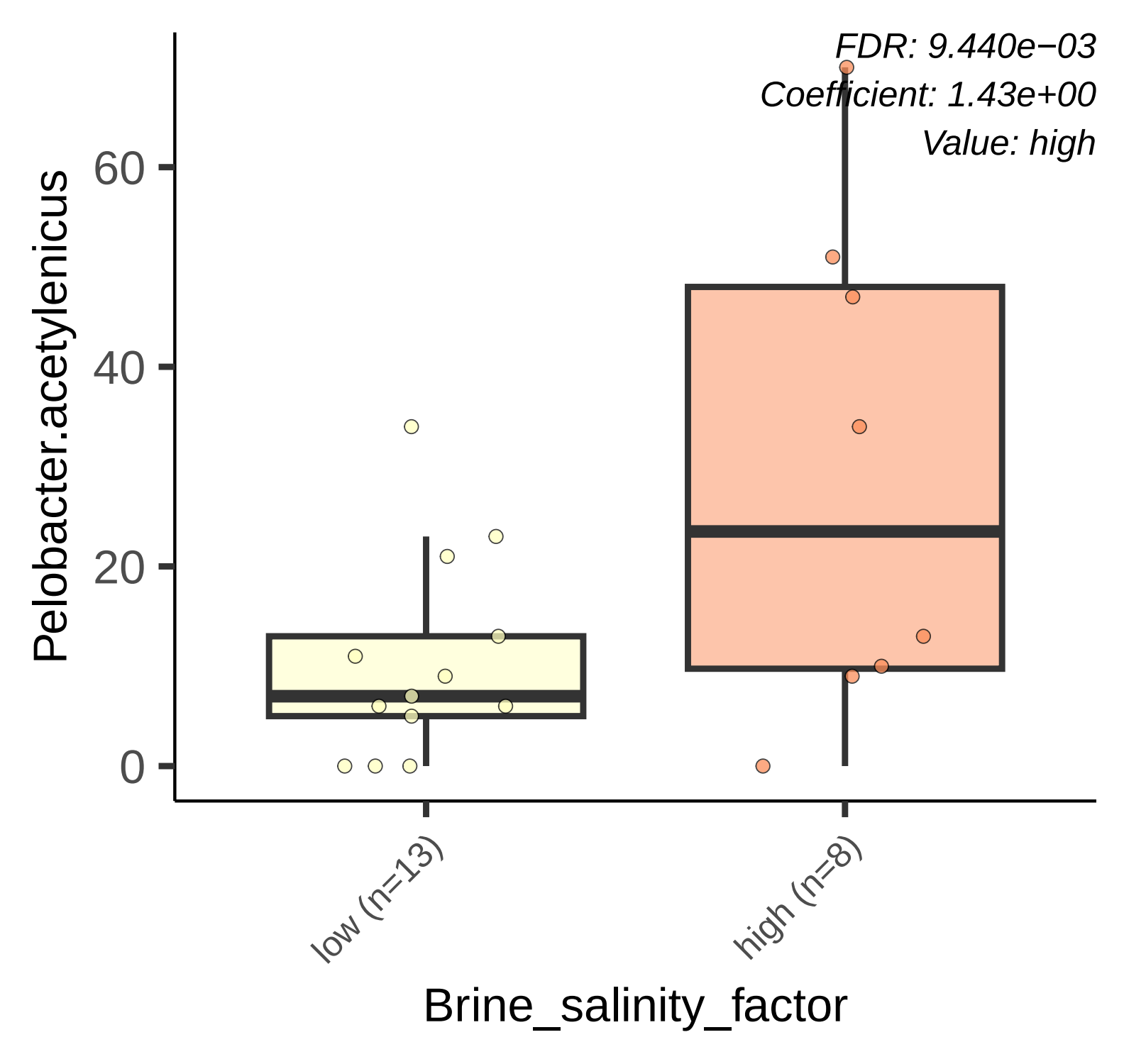

FDR: 7.018e−03
Coefficient: 1.59e+00
Value: high
5000
4000
3000
2000
1000
0
Halanaeroarchaeum.sulfurireducens
low (n=13)
high (n=8)
Brine_salinity_factor

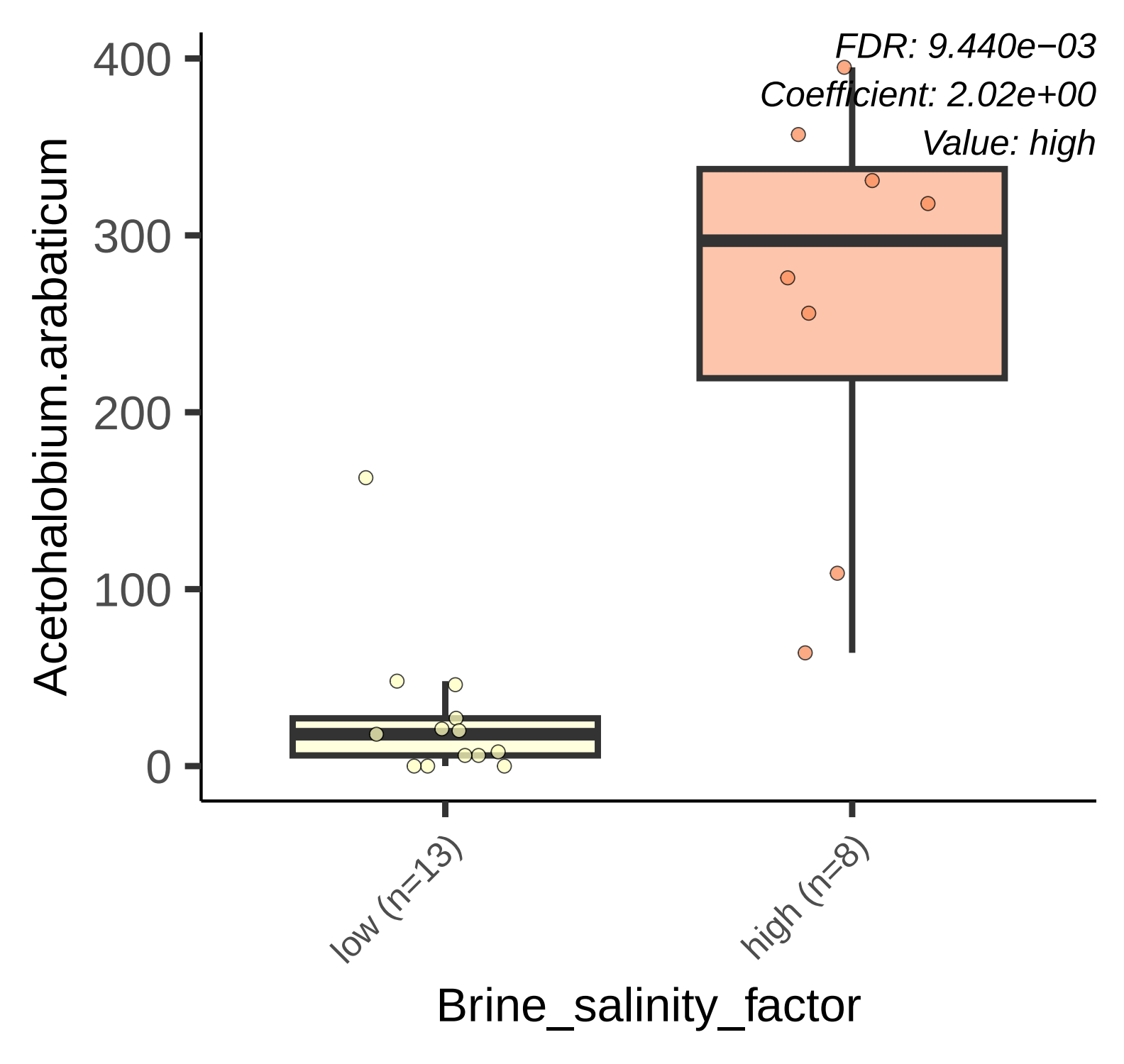

FDR: 7.367e−03
Coefficient: −1.13e+00
Value: high
uncultured.bacterium.KM3.69.F5
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

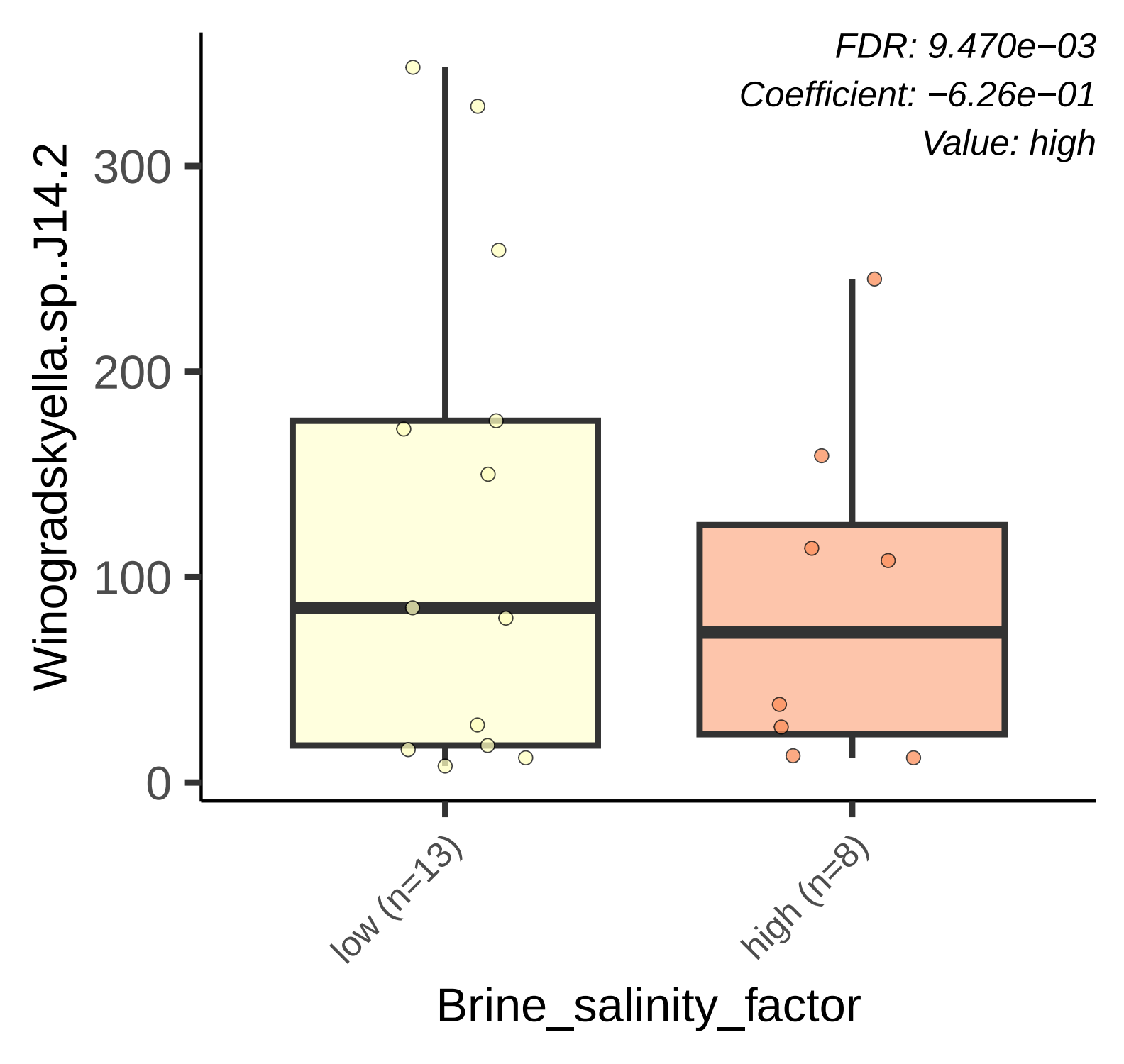

FDR: 7.606e−03
Coefficient: 2.02e+00
Value: high
Hydrogenovibrio.crunogenus
2000
1500
1000
500
0
low (n=13)
high (n=8)
Brine_salinity_factor

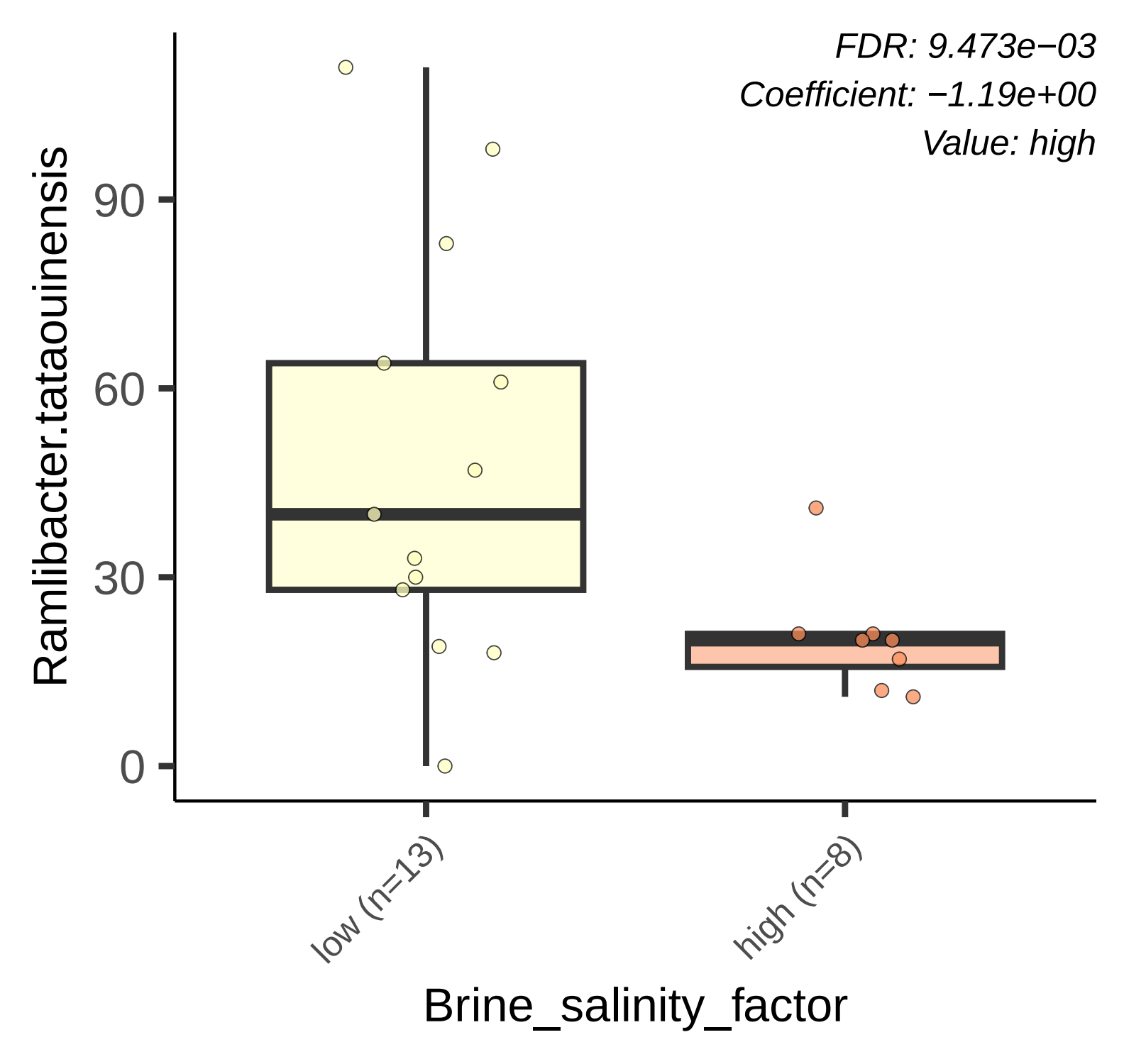

FDR: 7.905e−03
Coefficient: −3.52e+00
Value: high
unidentified.marine.bacterioplankton
200
150
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

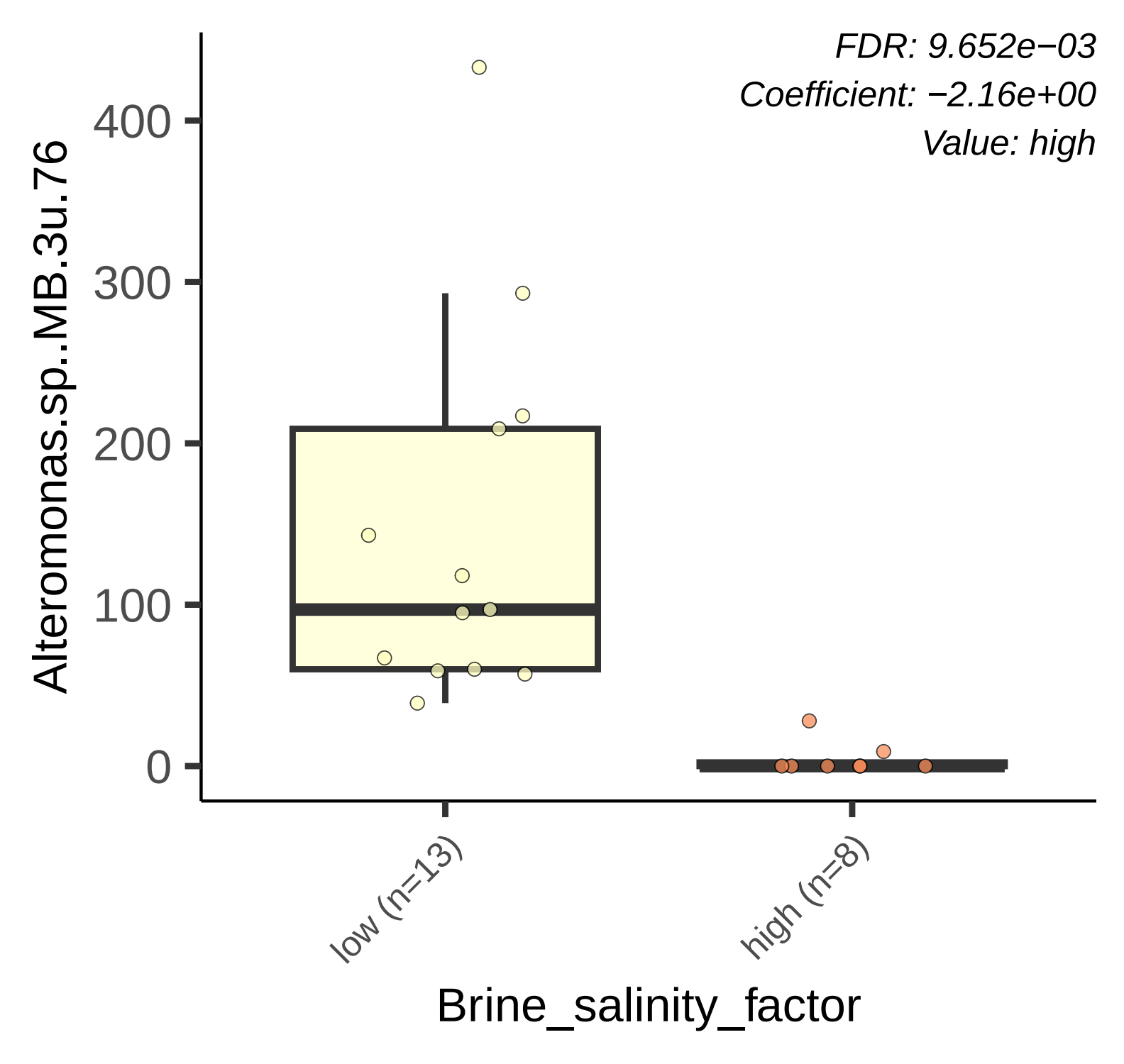

FDR: 9.026e−03
Coefficient: −1.33e+00
Value: high
800
600
400
200
0
Nitzschia.frustulum
low (n=13)
high (n=8)
Brine_salinity_factor

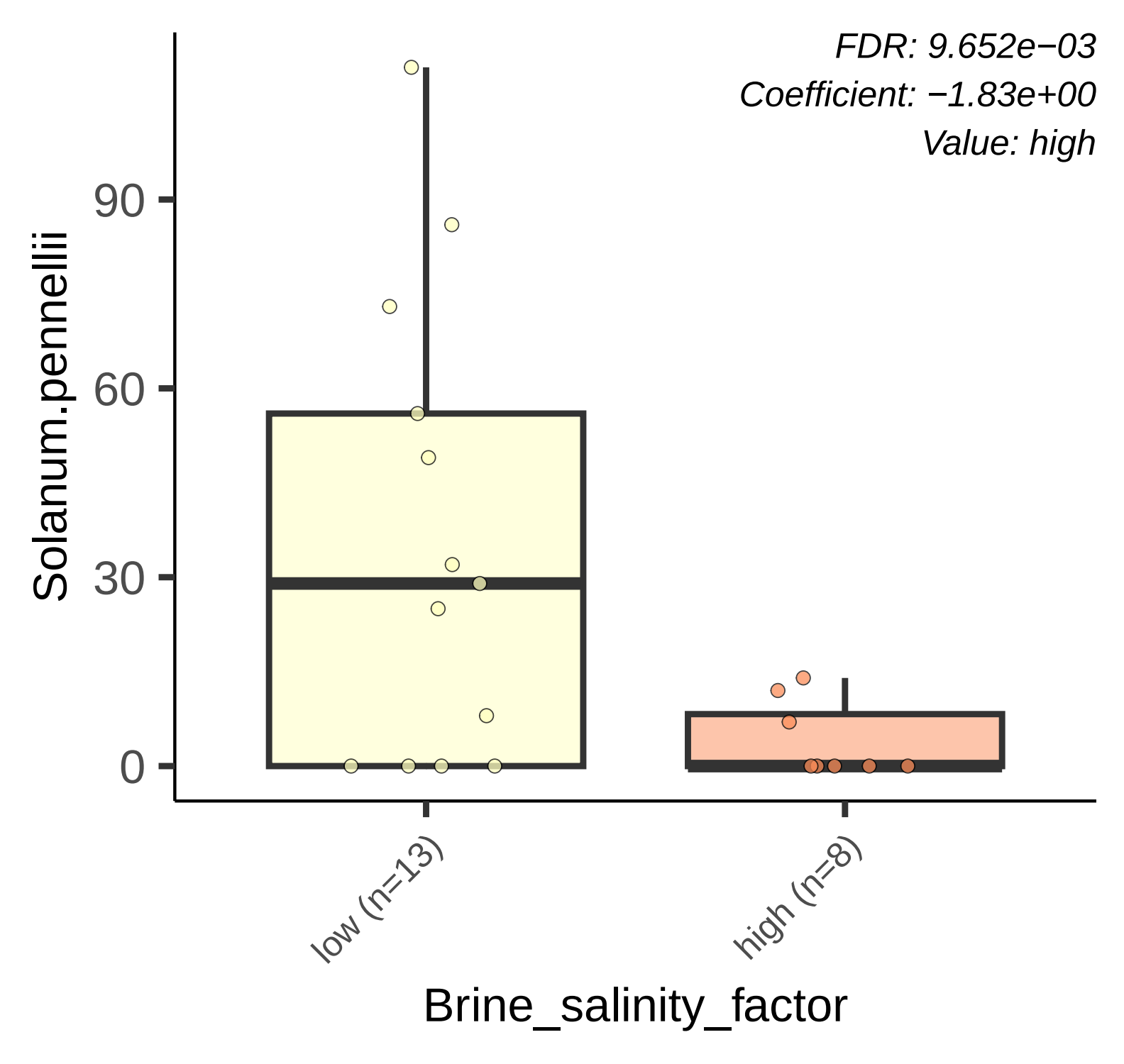

FDR: 9.440e−03
Coefficient: 1.43e+00
Value: high
Pelobacter.acetylenicus
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

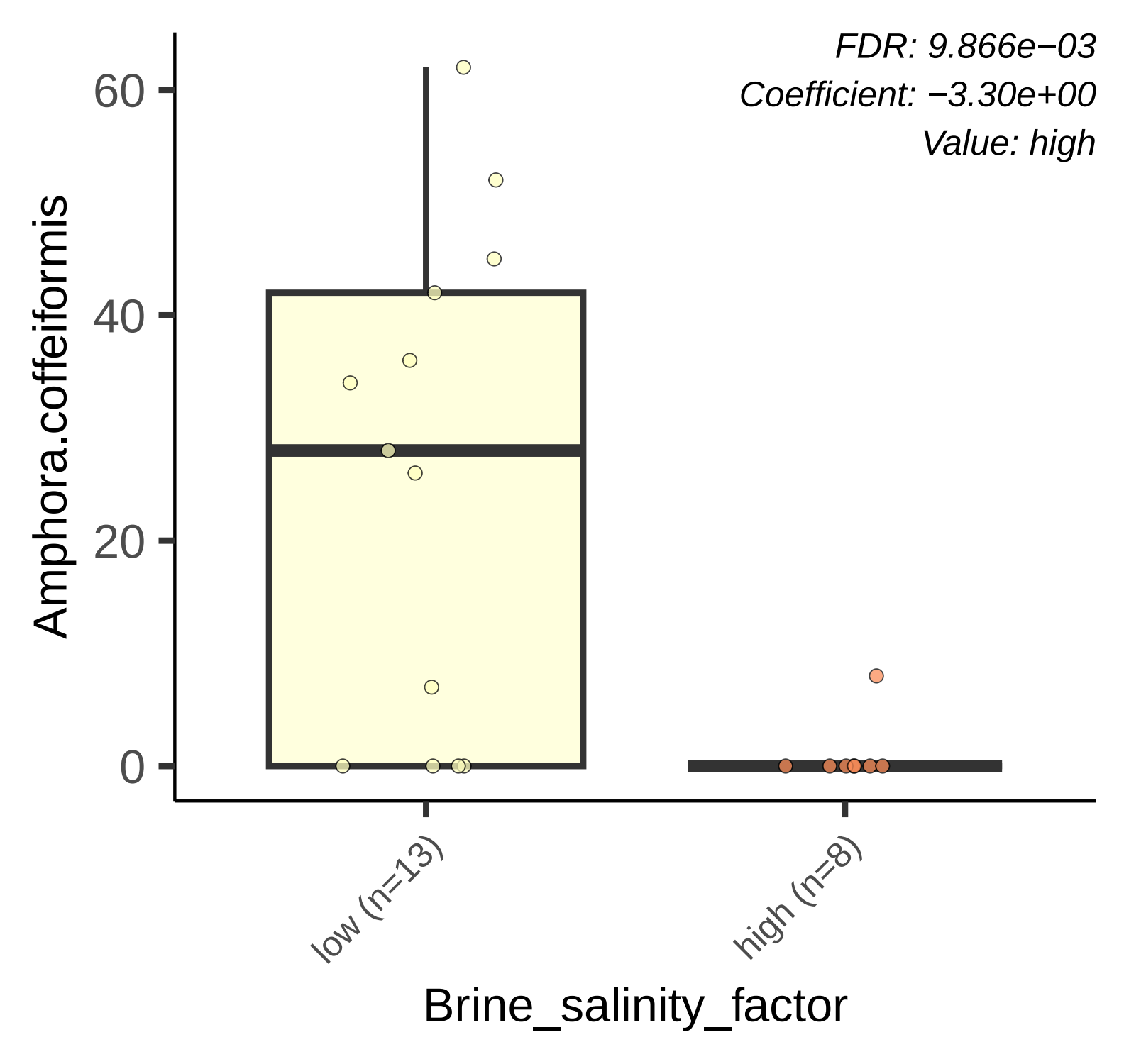

FDR: 9.440e−03
Coefficient: 2.02e+00
Value: high
Acetohalobium.arabaticum
400
300
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

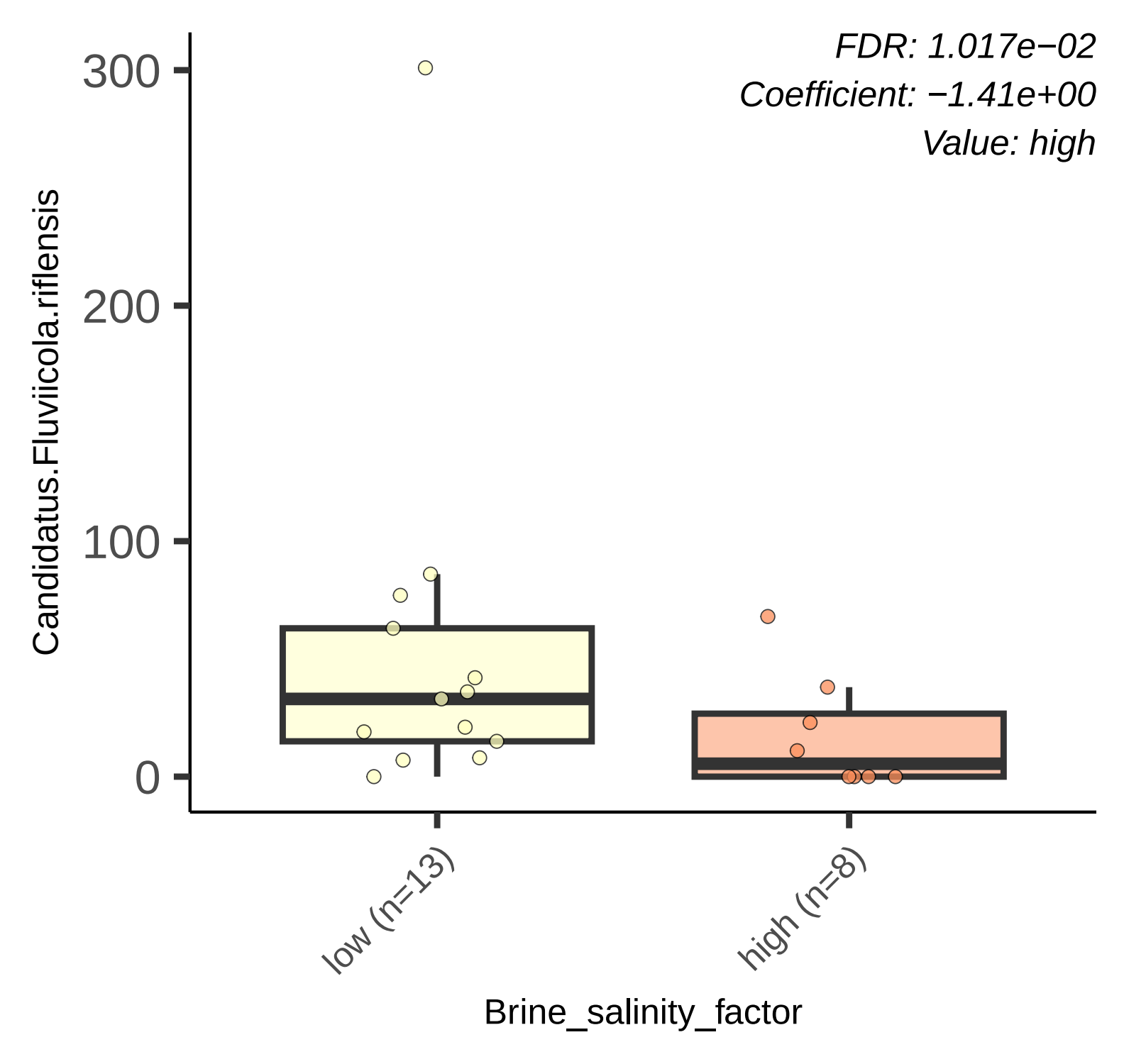

FDR: 9.470e−03
Coefficient: −6.26e−01
Value: high
Winogradskyella.sp..J14.2
300
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

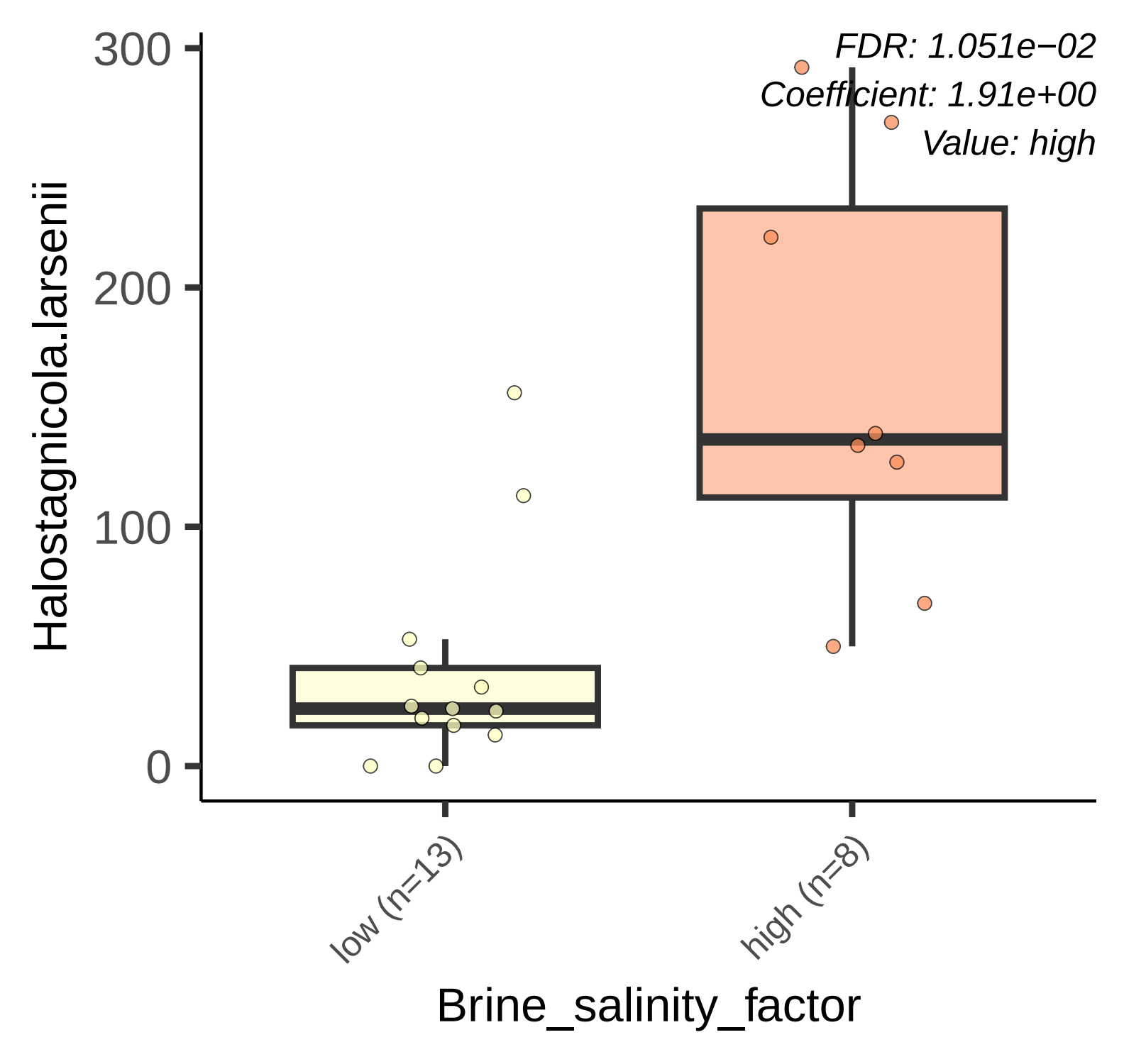

FDR: 9.473e−03
Coefficient: −1.19e+00
Value: high
Ramlibacter.tataouinensis
90
60
30
0
low (n=13)
high (n=8)
Brine_salinity_factor

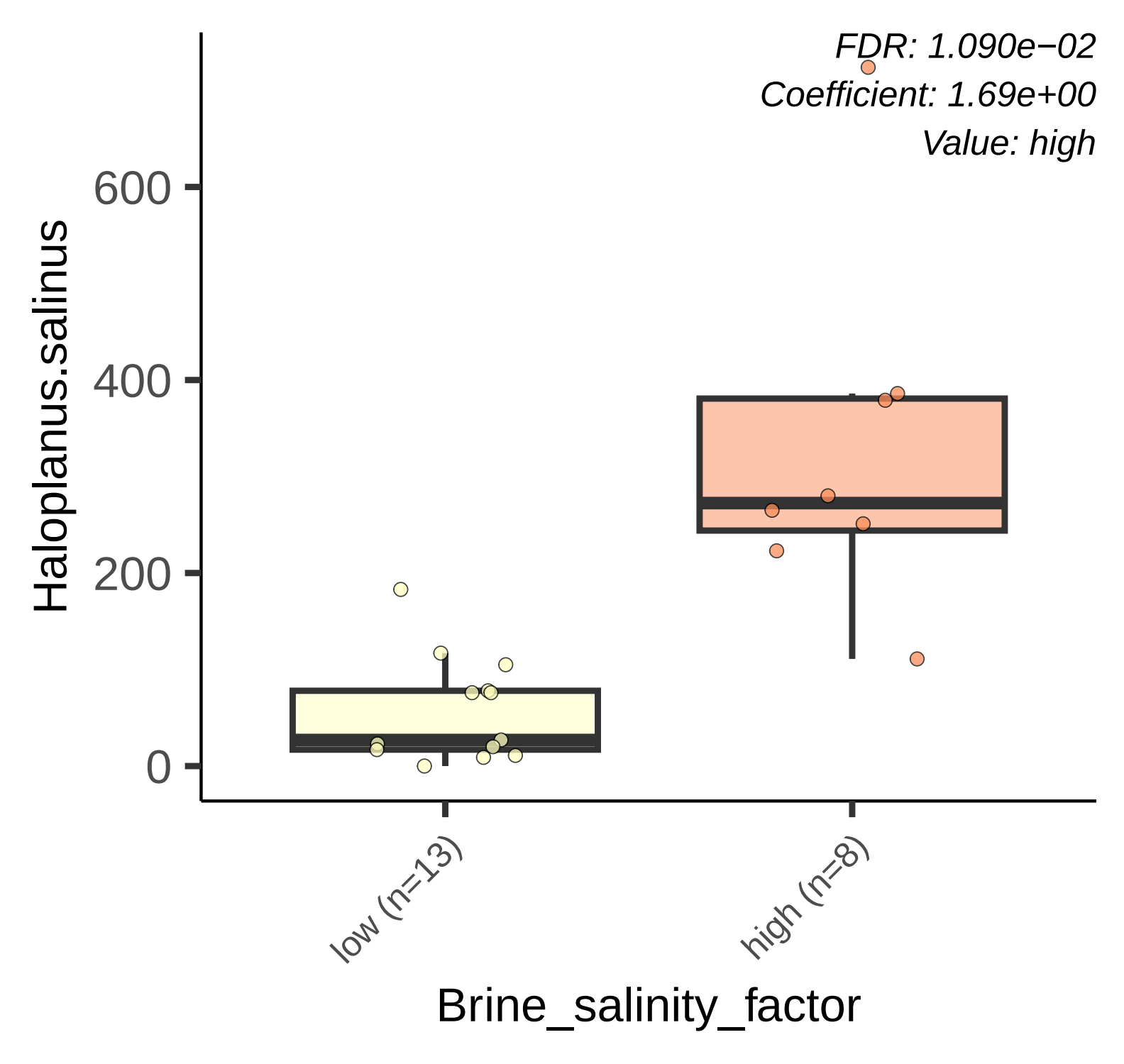

FDR: 9.652e−03
Coefficient: −2.16e+00
Value: high
Alteromonas.sp..MB.3u.76
400
300
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

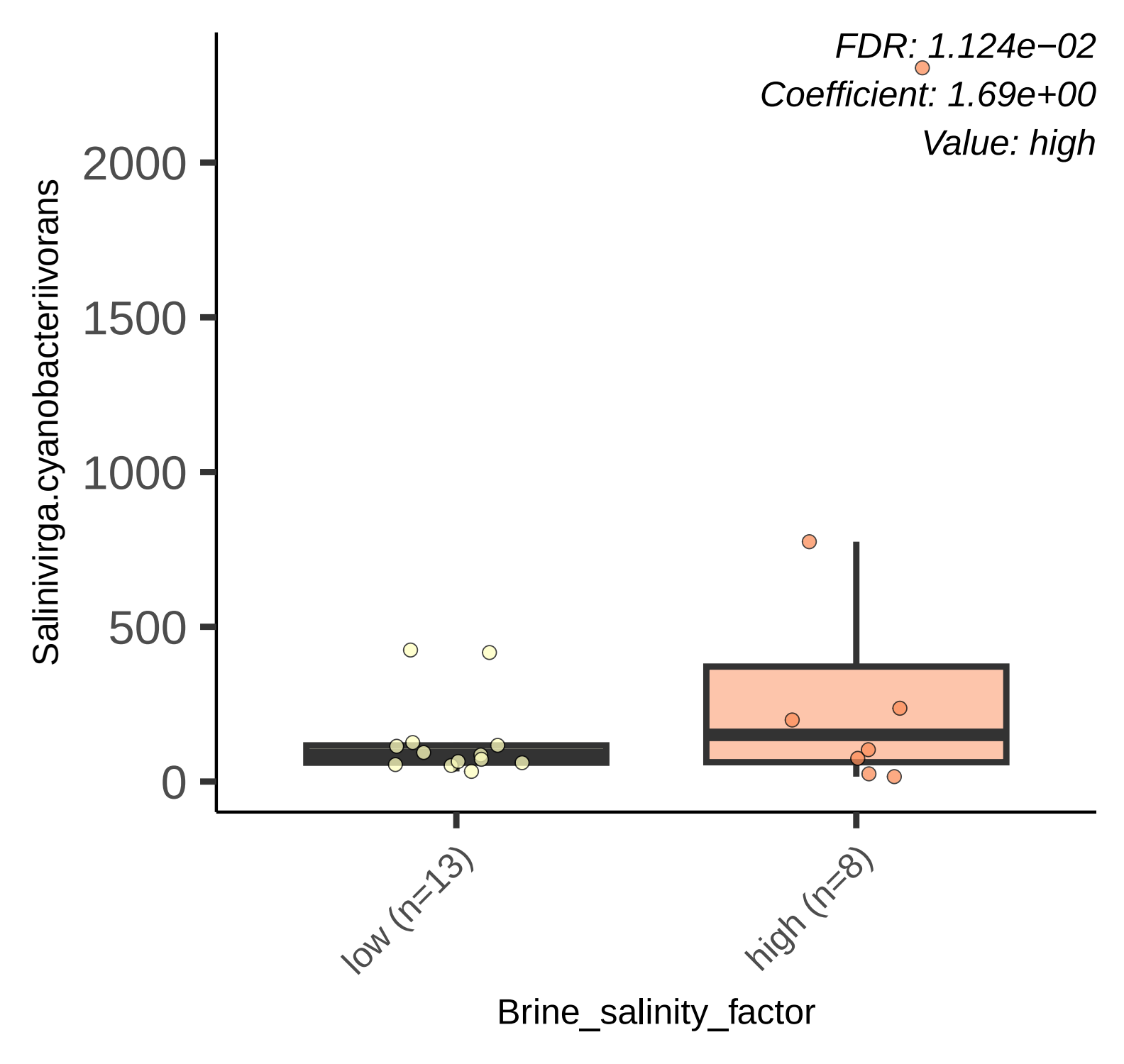

FDR: 9.652e−03
Coefficient: −1.83e+00
Value: high
Solanum.pennellii
90
60
30
0
low (n=13)
high (n=8)
Brine_salinity_factor

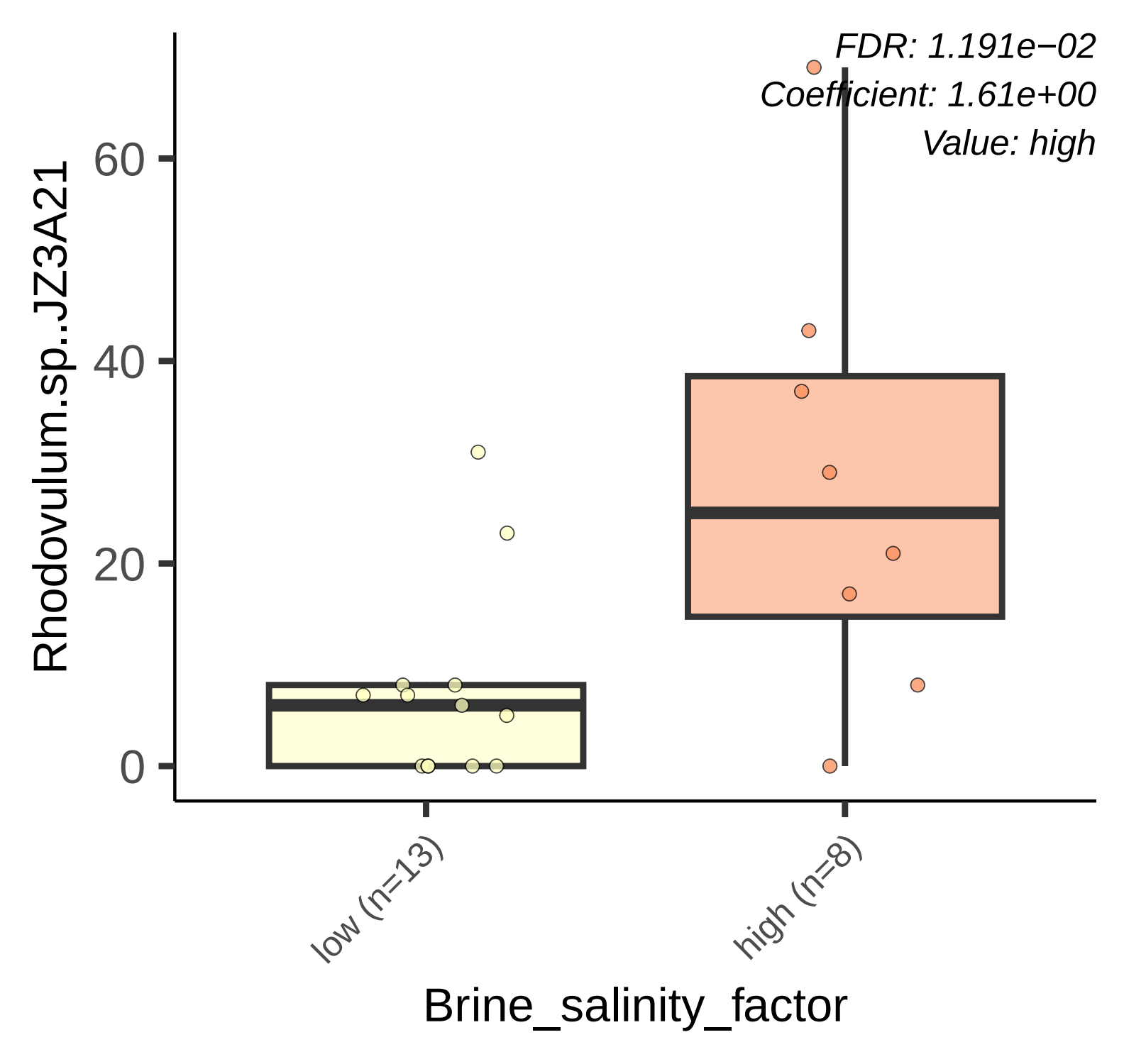

FDR: 9.866e−03
Coefficient: −3.30e+00
Value: high
Amphora.coffeiformis
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

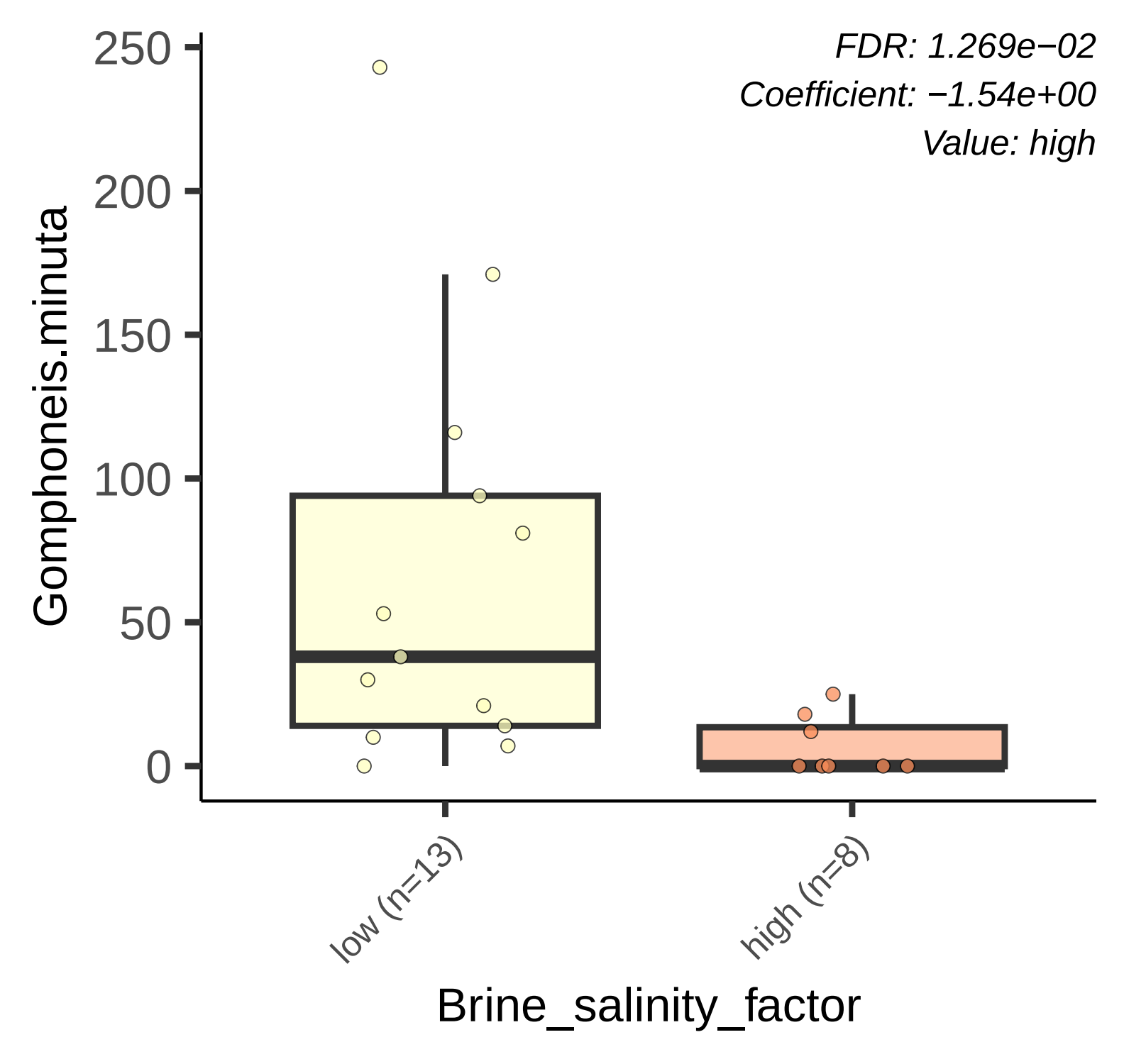

FDR: 1.017e−02
Coefficient: −1.41e+00
Value: high
300
200
100
0
Candidatus.Fluviicola.riflensis
low (n=13)
high (n=8)
Brine_salinity_factor

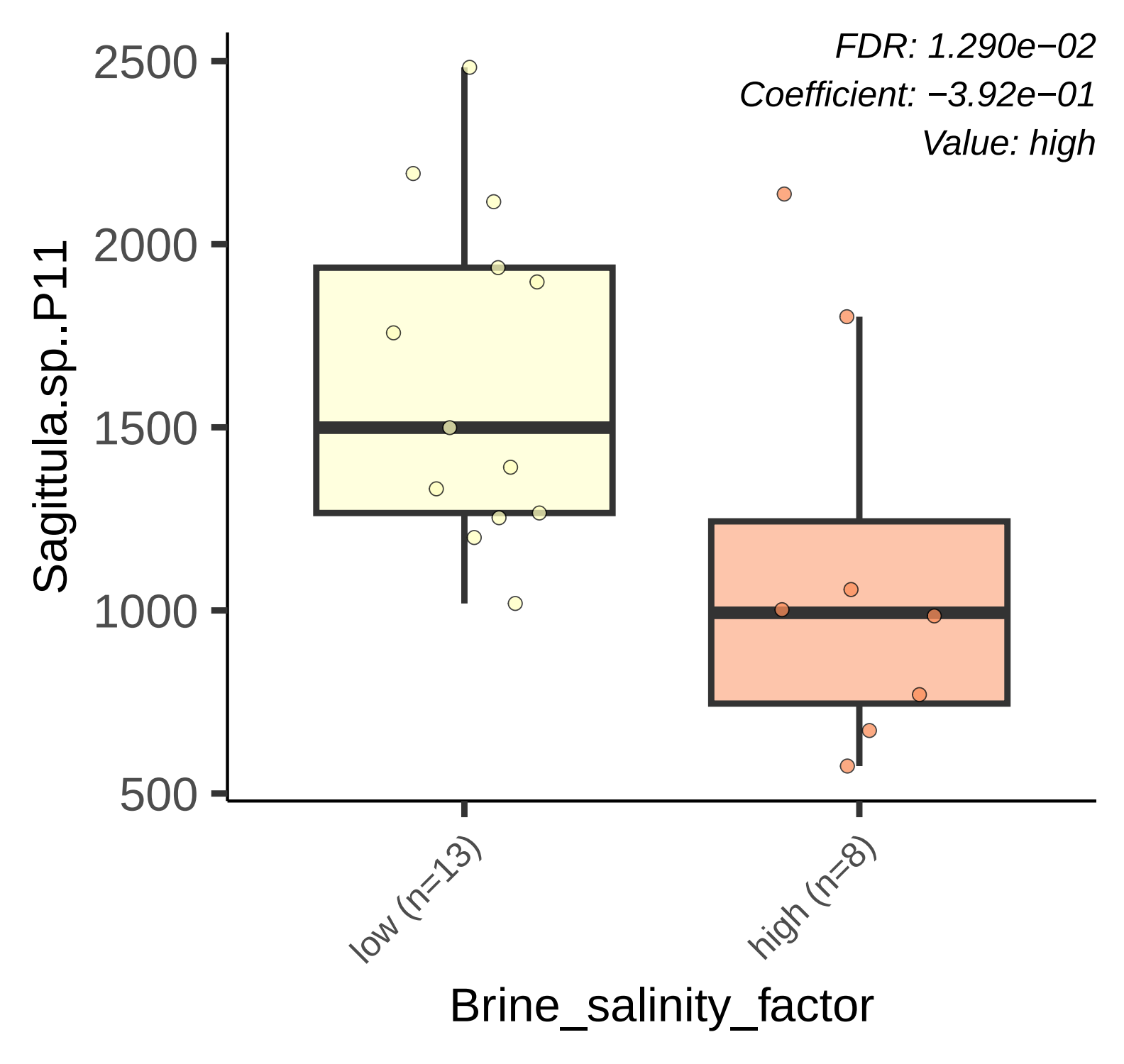

FDR: 1.051e−02
Coefficient: 1.91e+00
Value: high
Halostagnicola.larsenii
300
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

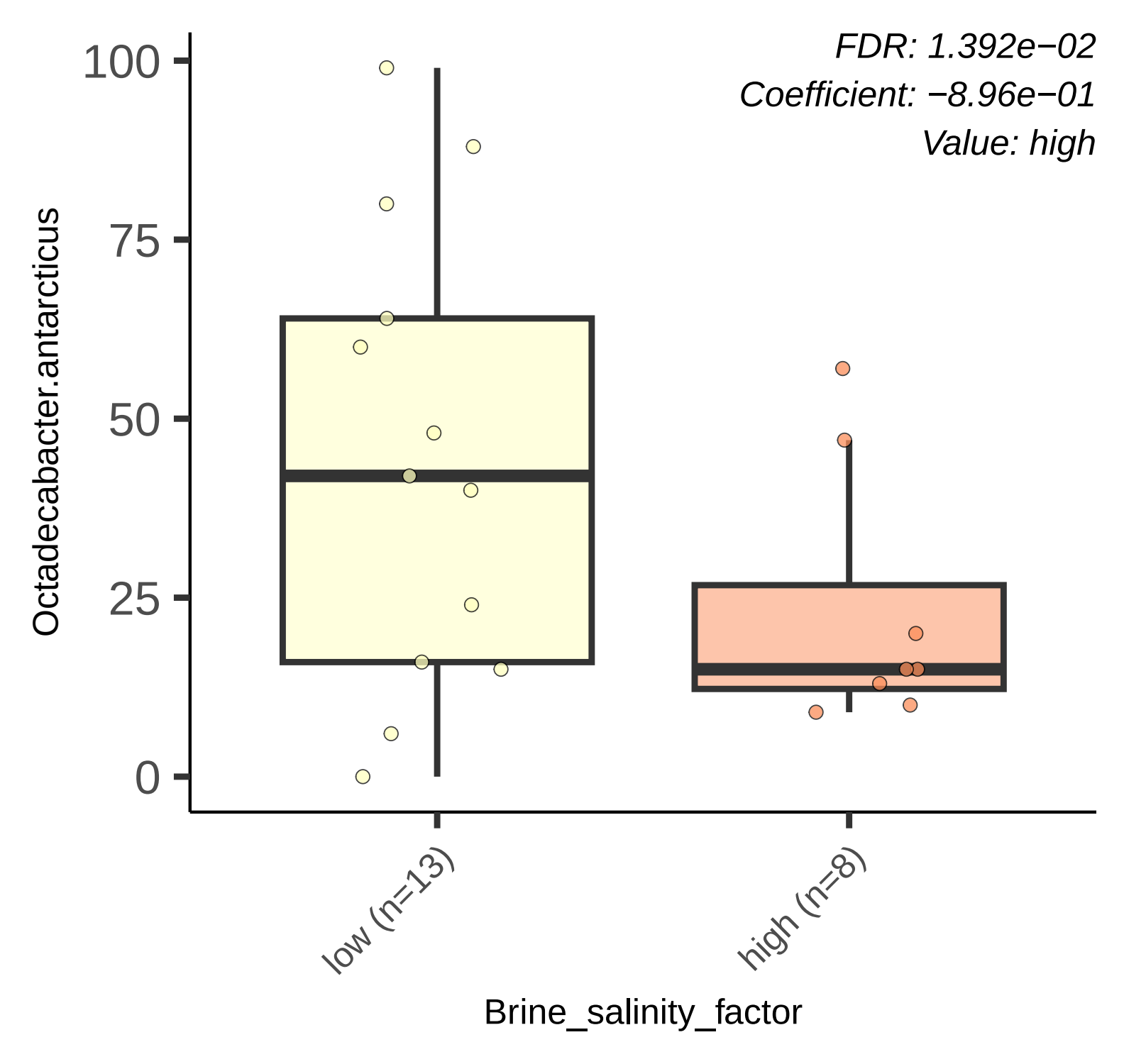

FDR: 1.090e−02
Coefficient: 1.69e+00
Value: high
Haloplanus.salinus
600
400
200
0
low (n=13)
high (n=8)
Brine_salinity_factor

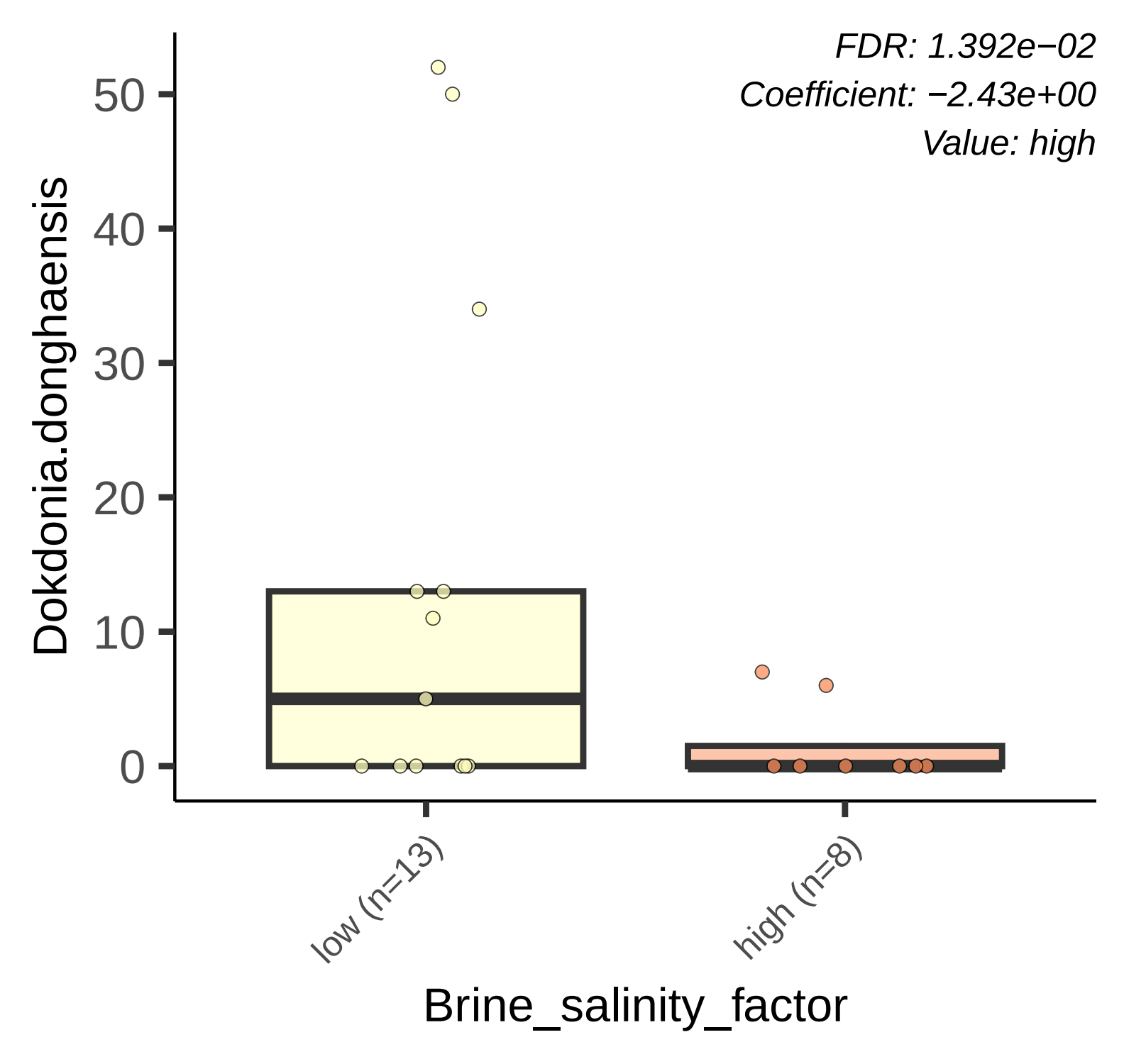

FDR: 1.124e−02
Coefficient: 1.69e+00
Value: high
Salinivirga.cyanobacteriivorans
2000
1500
1000
500
0
low (n=13)
high (n=8)
Brine_salinity_factor

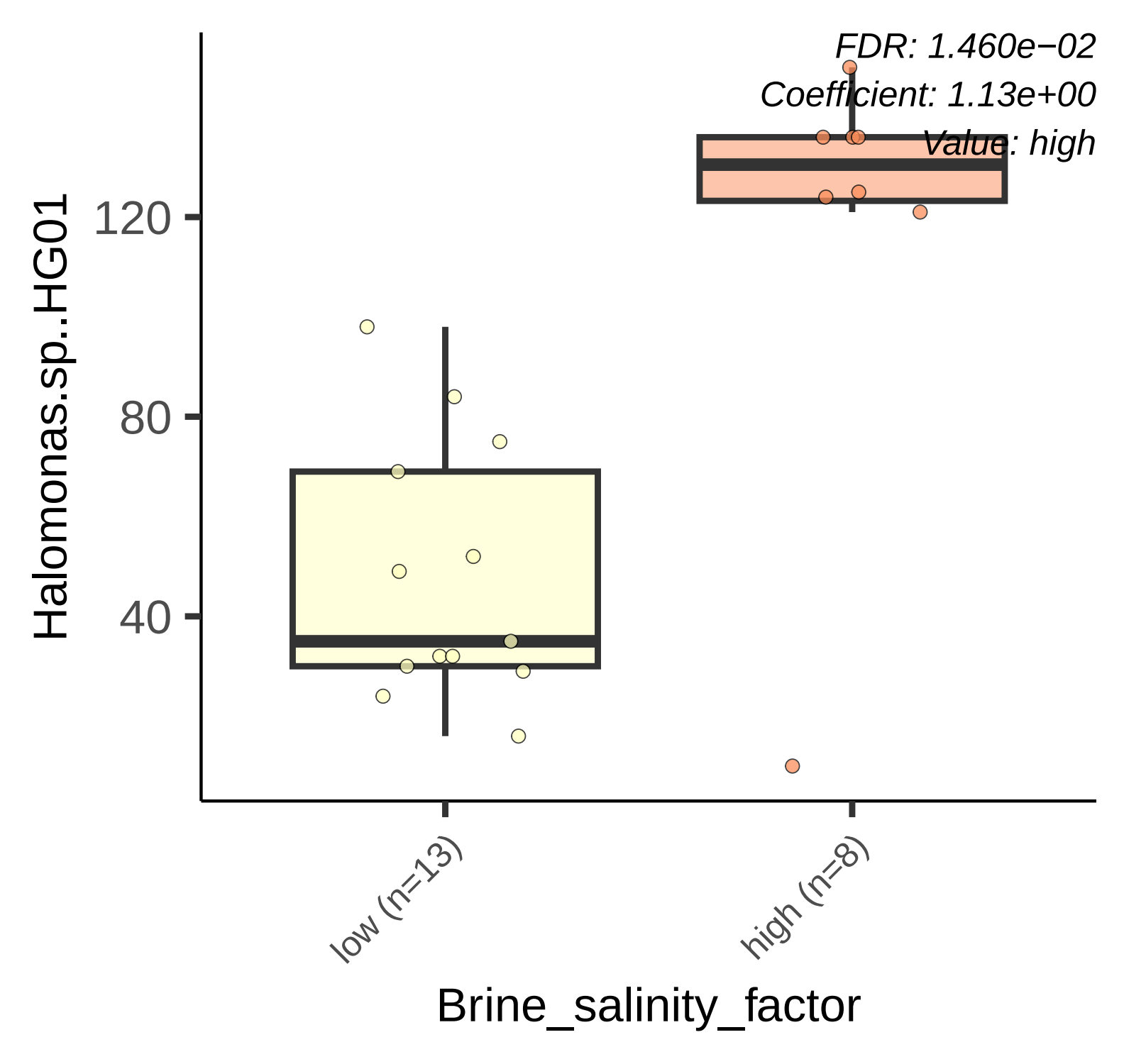

FDR: 1.191e−02
Coefficient: 1.61e+00
Value: high
Rhodovulum.sp..JZ3A21
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

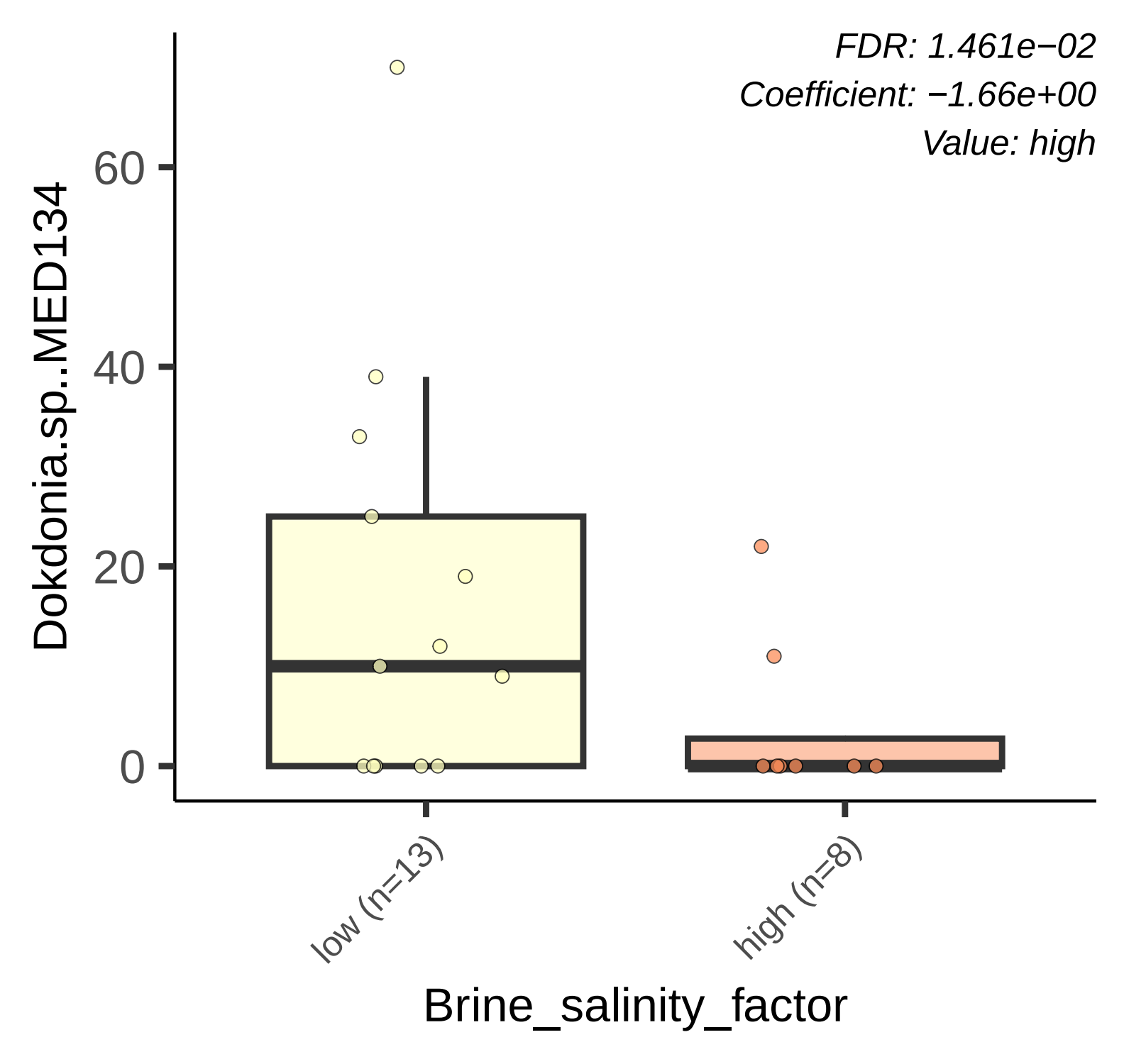

FDR: 1.269e−02
Coefficient: −1.54e+00
Value: high
Gomphoneis.minuta
250
200
150
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

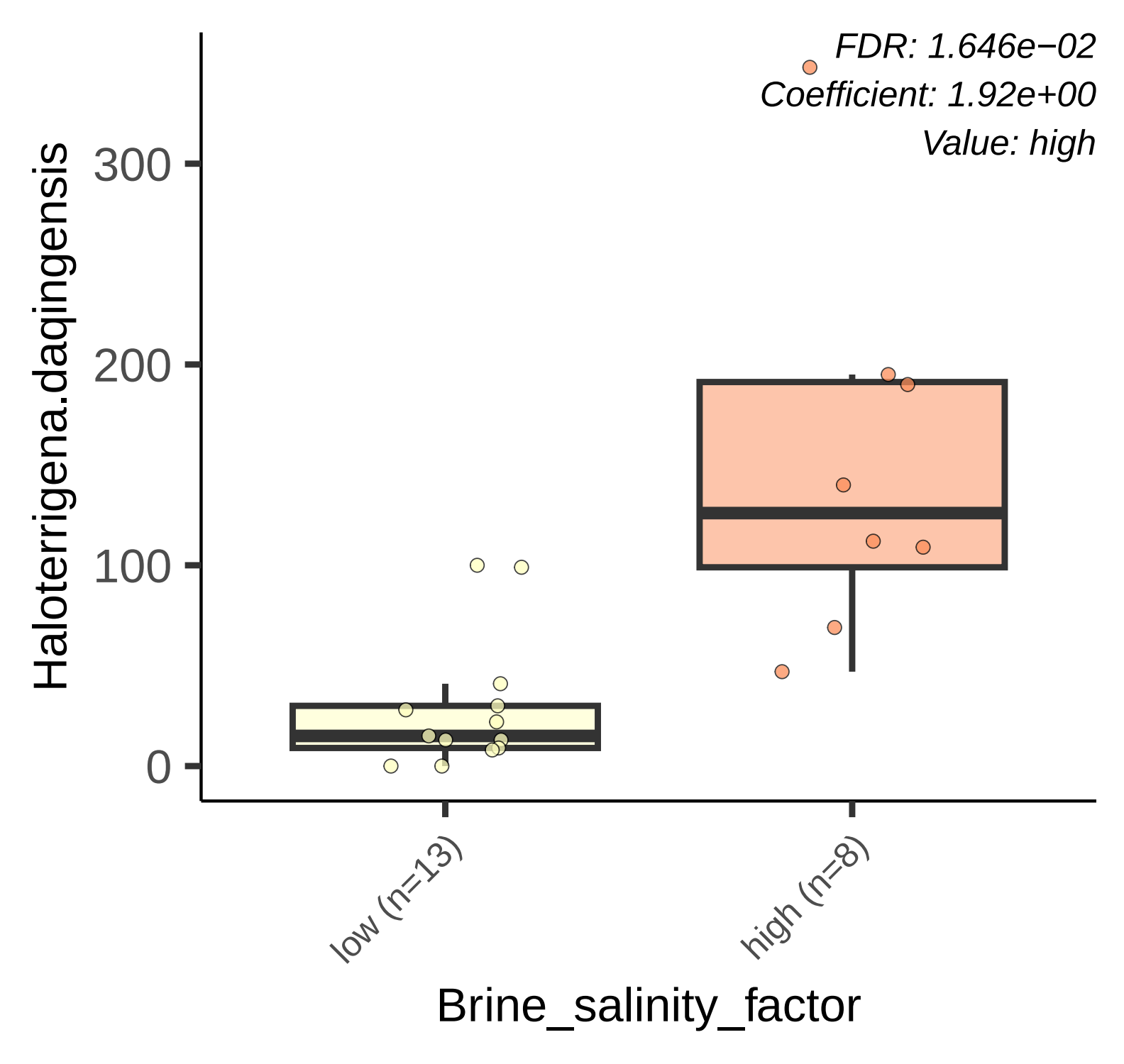

FDR: 1.290e−02
Coefficient: −3.92e−01
Value: high
2500
2000
1500
1000
500
Sagittula.sp..P11
low (n=13)
high (n=8)
Brine_salinity_factor

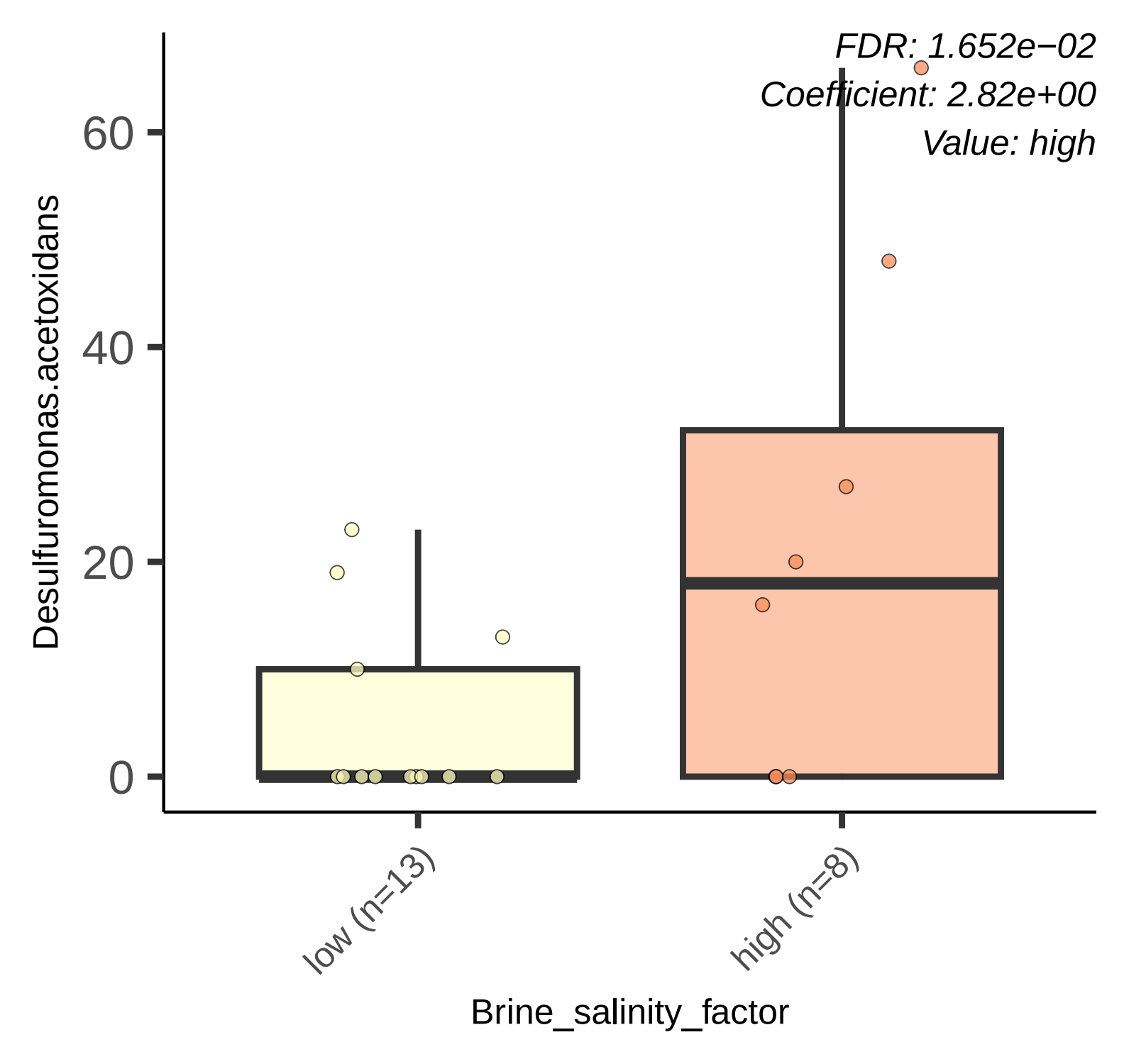

FDR: 1.392e−02
Coefficient: −8.96e−01
Value: high
Octadecabacter.antarcticus
100
75
50
25
0
low (n=13)
high (n=8)
Brine_salinity_factor

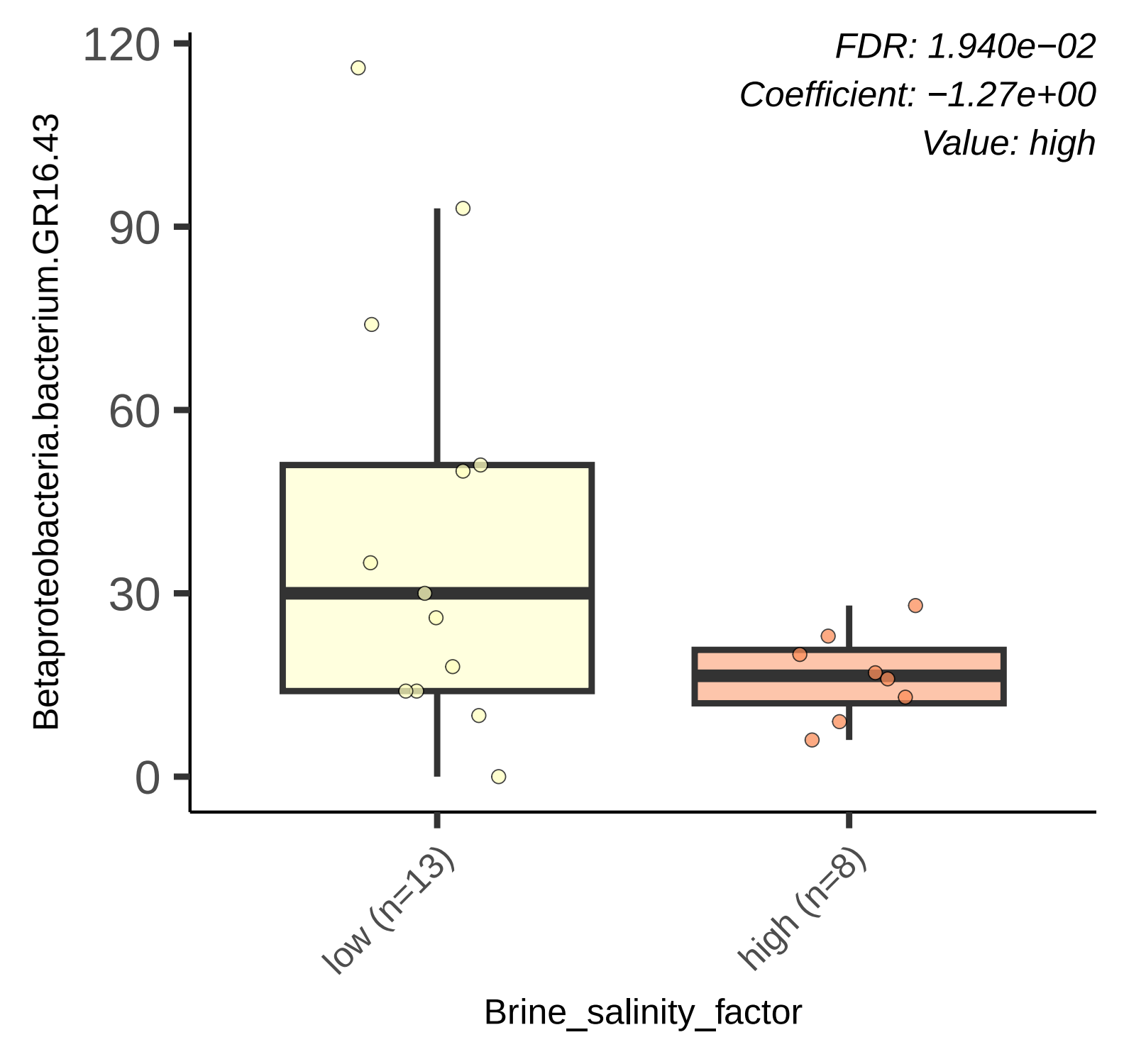

FDR: 1.392e−02
Coefficient: −2.43e+00
Value: high
Dokdonia.donghaensis
50
40
30
20
10
0
low (n=13)
high (n=8)
Brine_salinity_factor

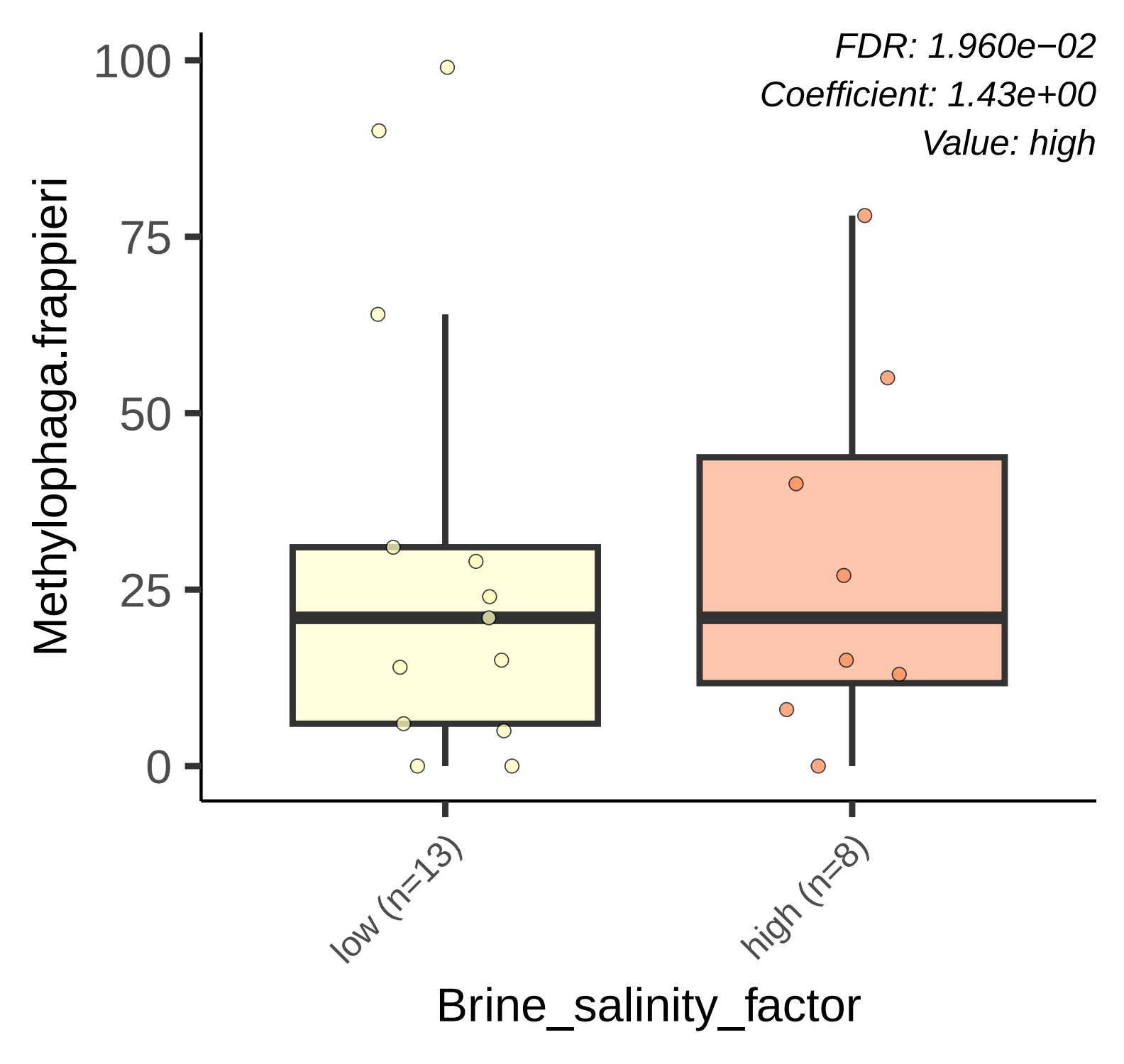

FDR: 1.460e−02
Coefficient: 1.13e+00
Value: high
Halomonas.sp..HG01
120
80
40
low (n=13)
high (n=8)
Brine_salinity_factor

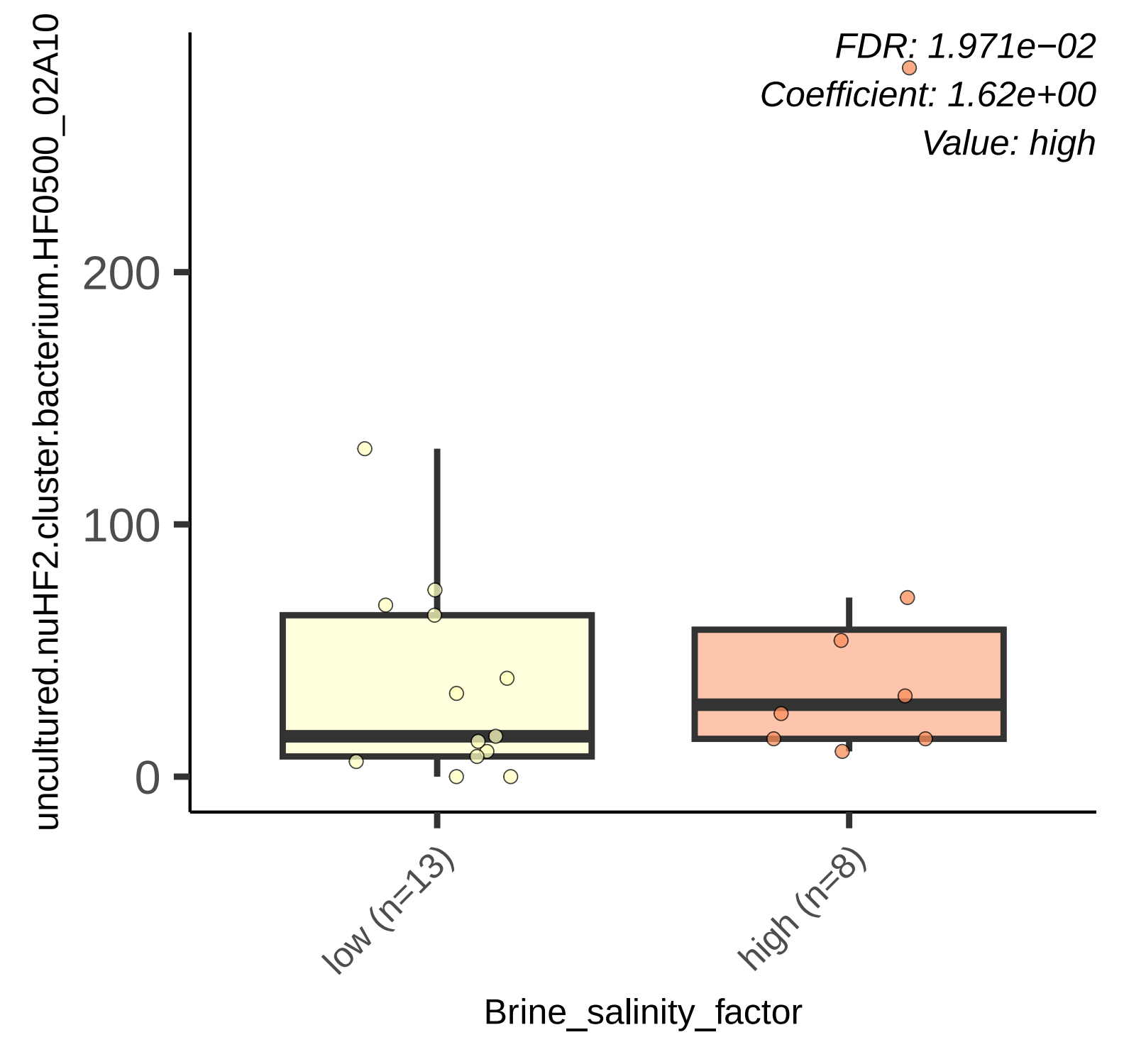

FDR: 1.461e−02
Coefficient: −1.66e+00
Value: high
Dokdonia.sp..MED134
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

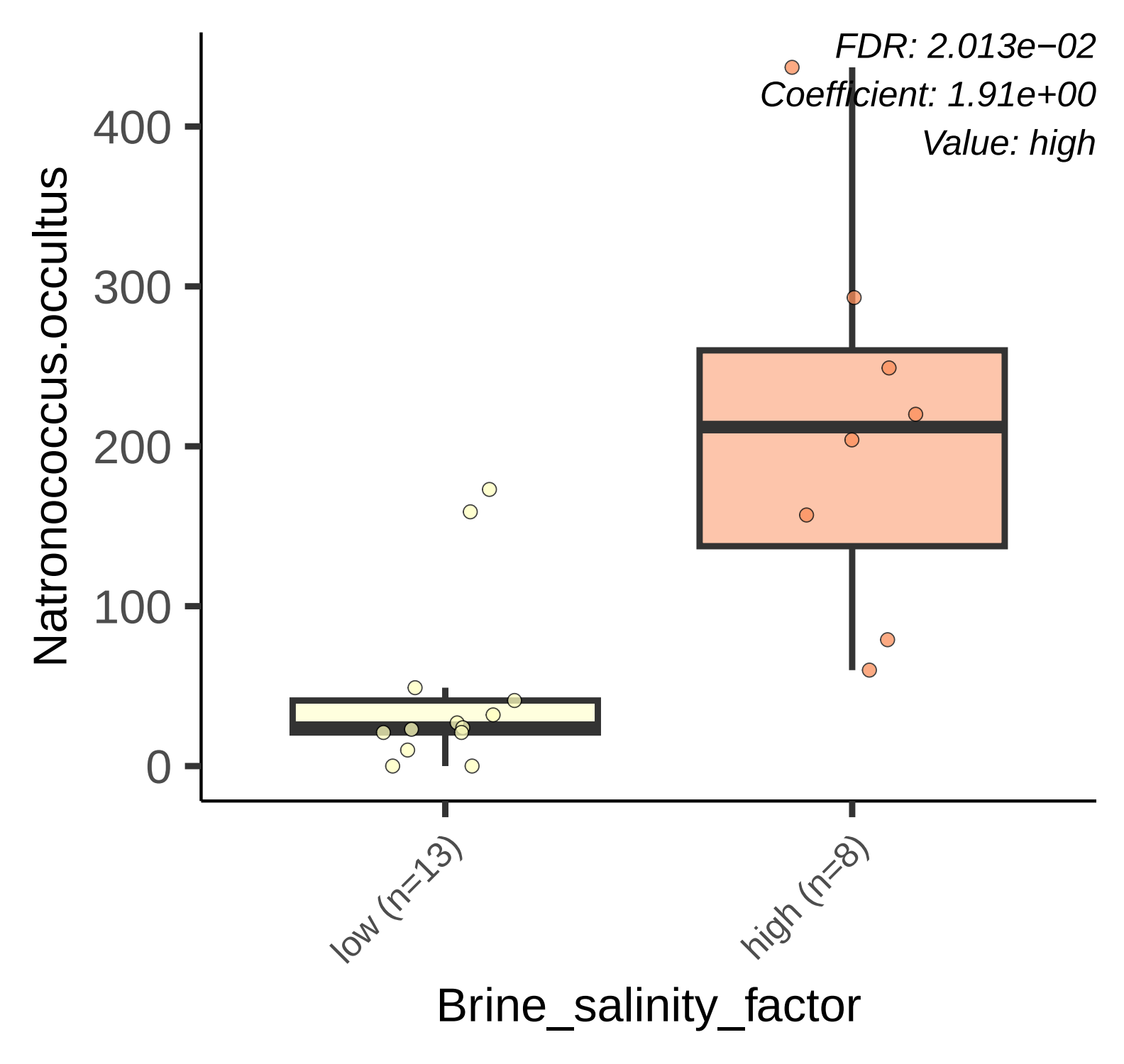

FDR: 1.646e−02
Coefficient: 1.92e+00
Value: high
Haloterrigena.daqingensis
300
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

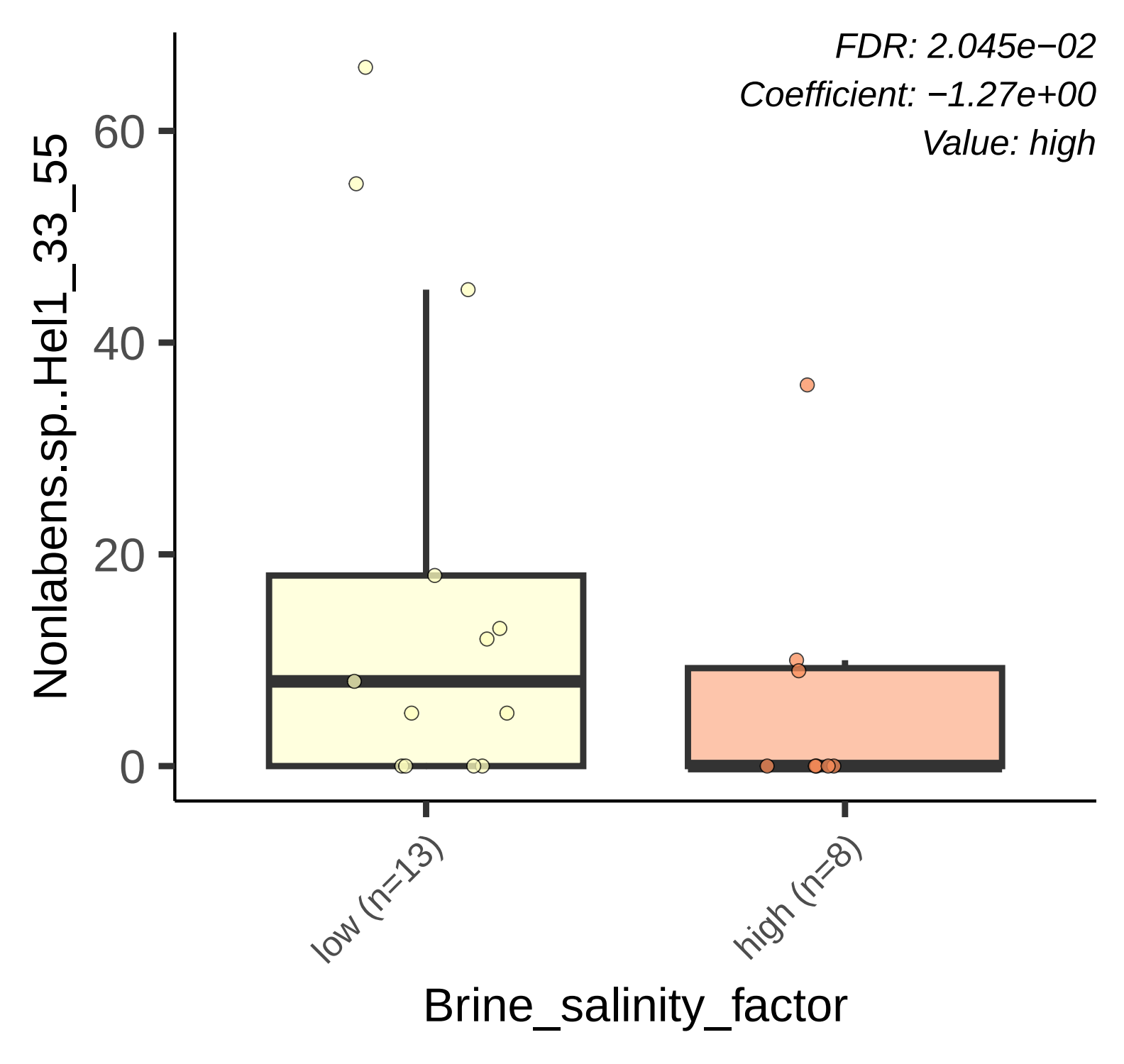

FDR: 1.652e−02
Coefficient: 2.82e+00
Value: high
Desulfuromonas.acetoxidans
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

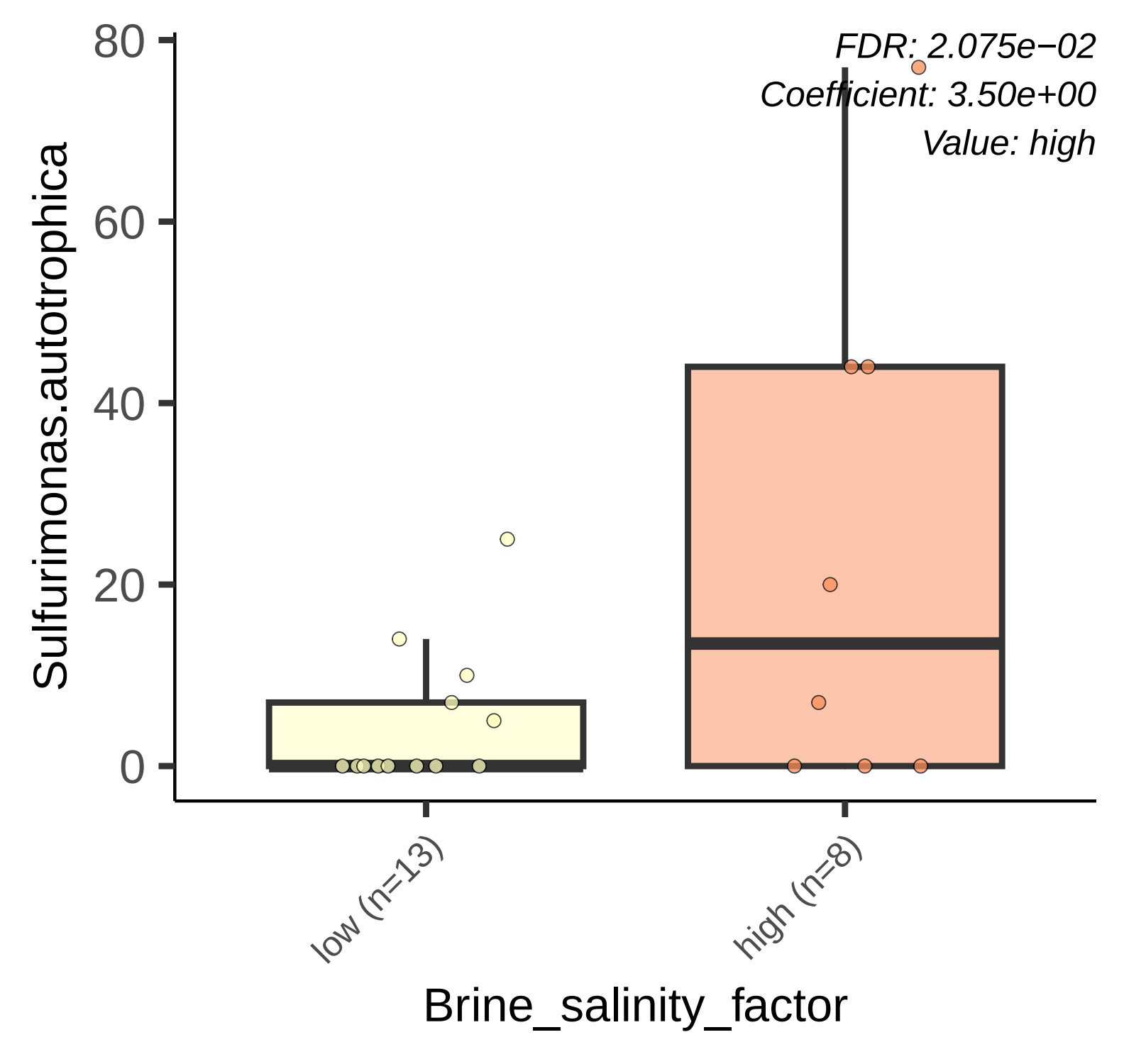

FDR: 1.940e−02
Coefficient: −1.27e+00
Value: high
Betaproteobacteria.bacterium.GR16.43
120
90
60
30
0
low (n=13)
high (n=8)
Brine_salinity_factor

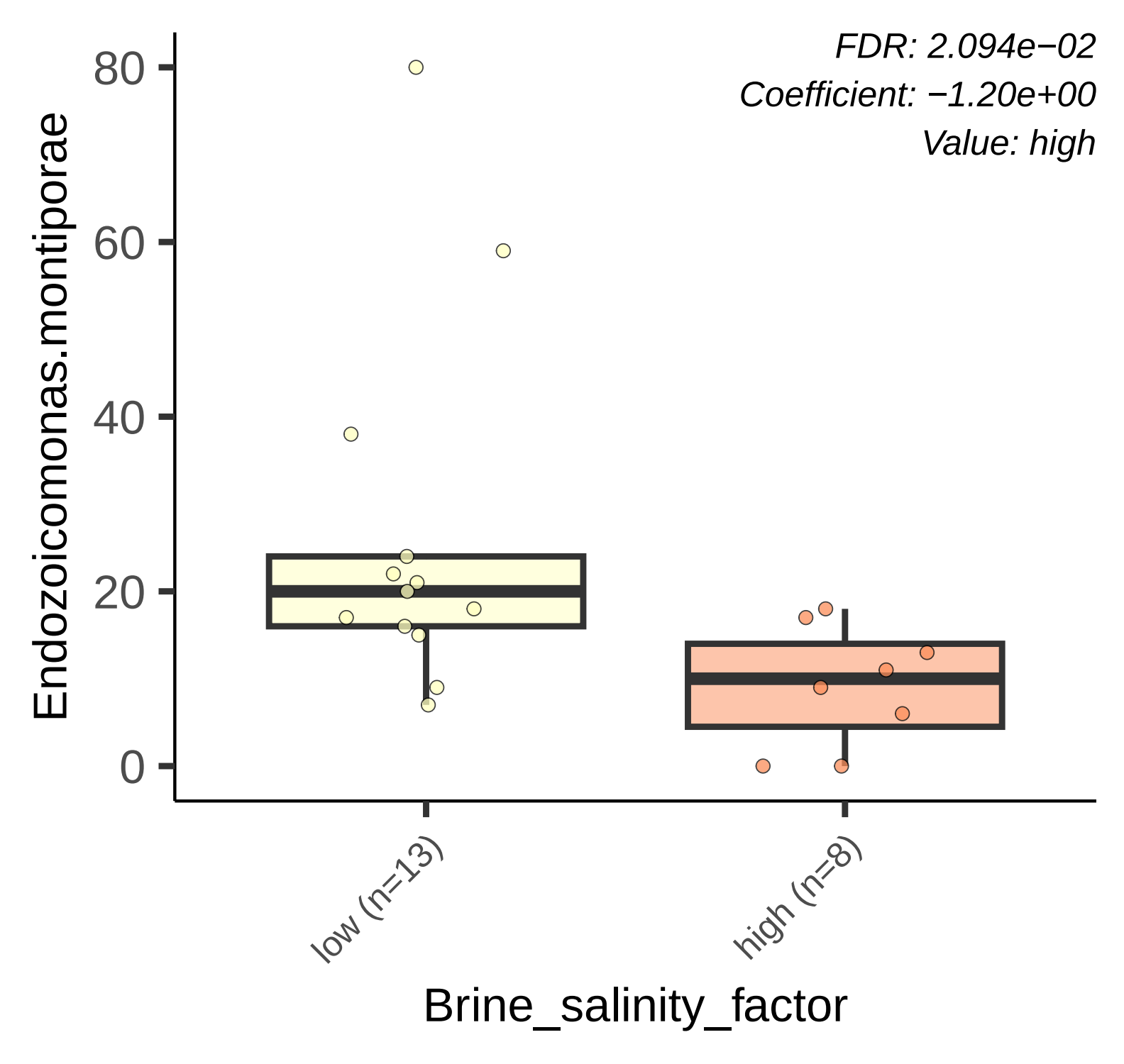

FDR: 1.960e−02
Coefficient: 1.43e+00
Value: high
Methylophaga.frappieri
100
75
50
25
0
low (n=13)
high (n=8)
Brine_salinity_factor

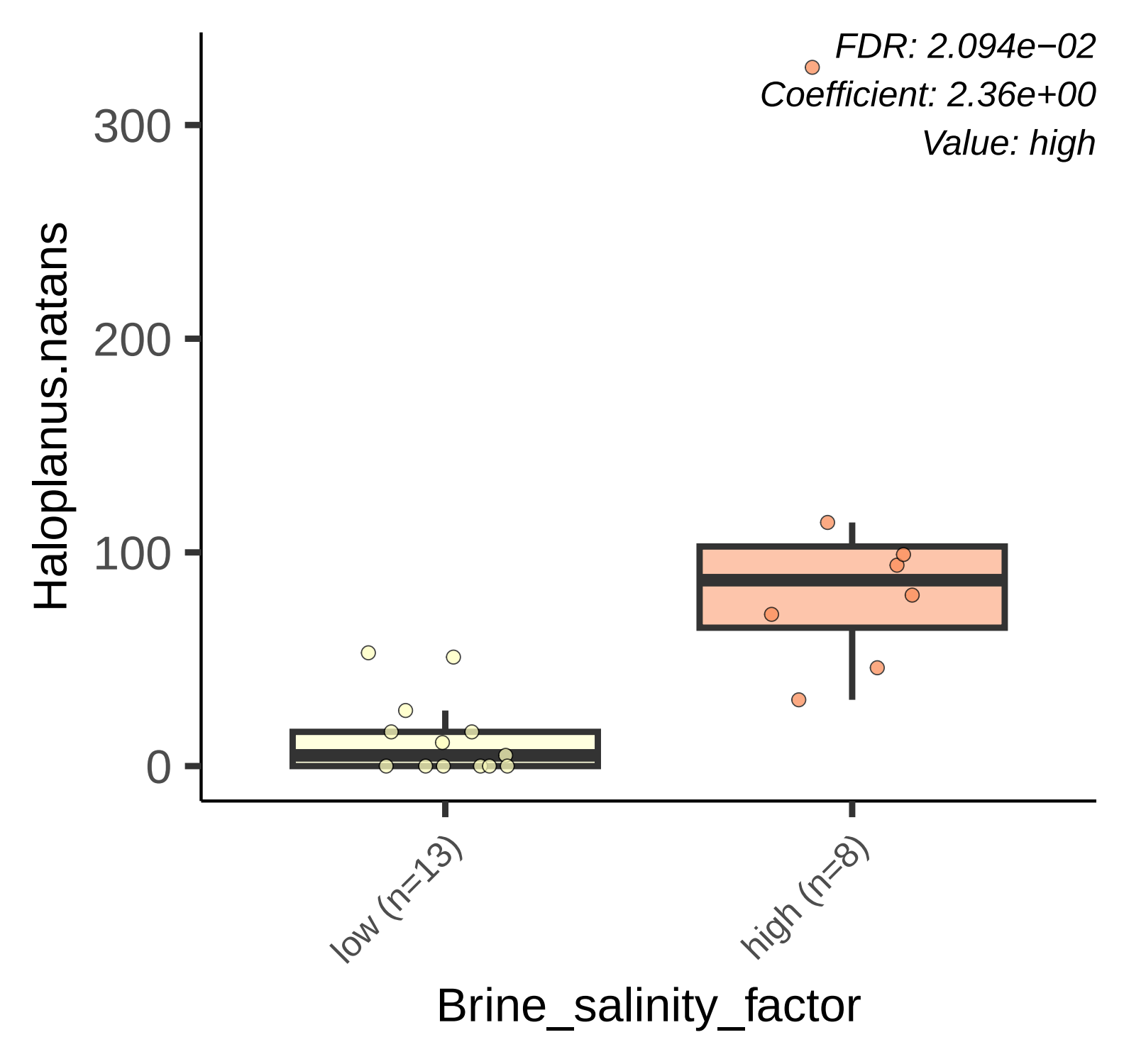

FDR: 1.971e−02
Coefficient: 1.62e+00
Value: high
uncultured.nuHF2.cluster.bacterium.HF0500_02A10
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

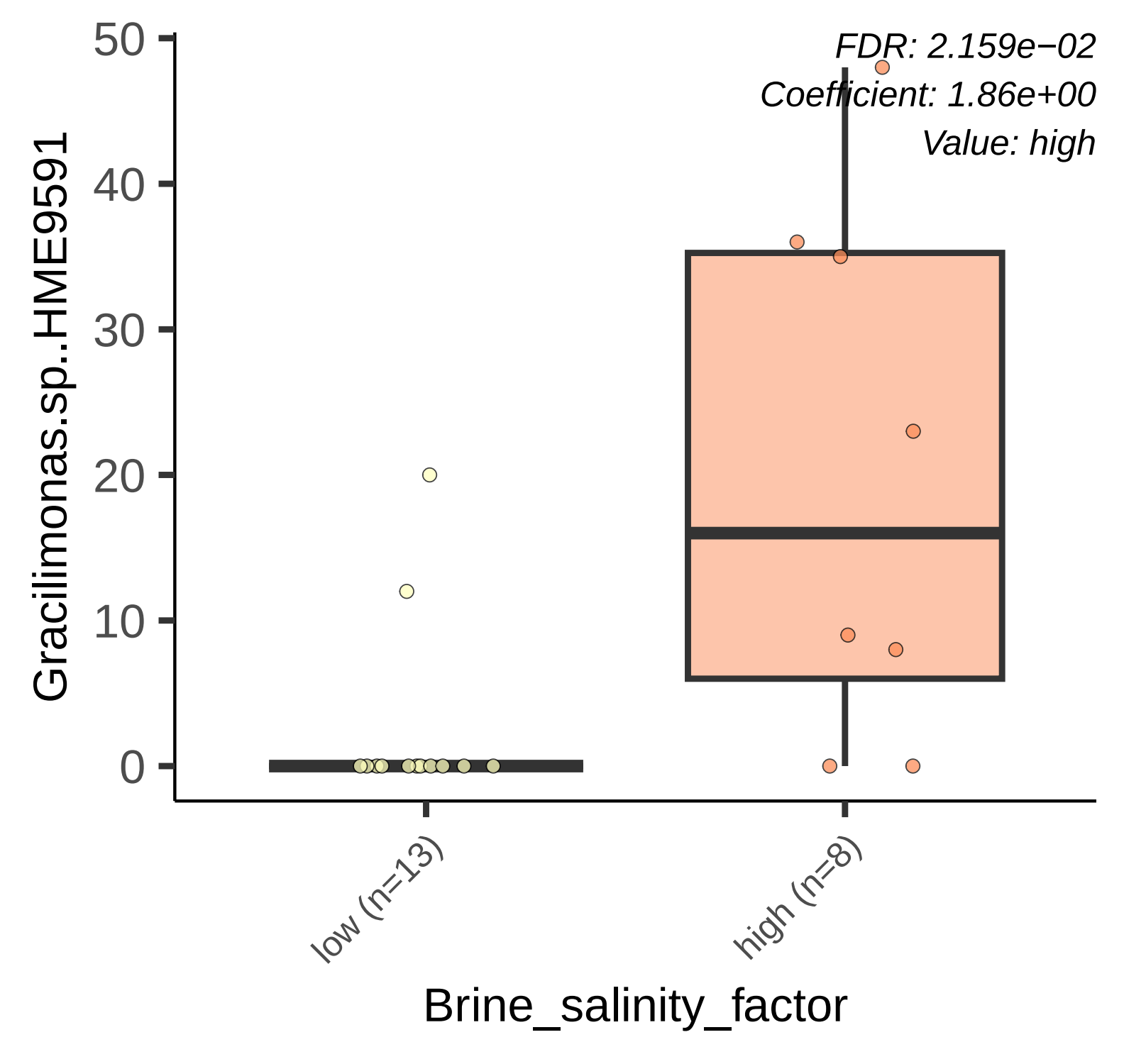

FDR: 2.013e−02
Coefficient: 1.91e+00
Value: high
Natronococcus.occultus
400
300
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

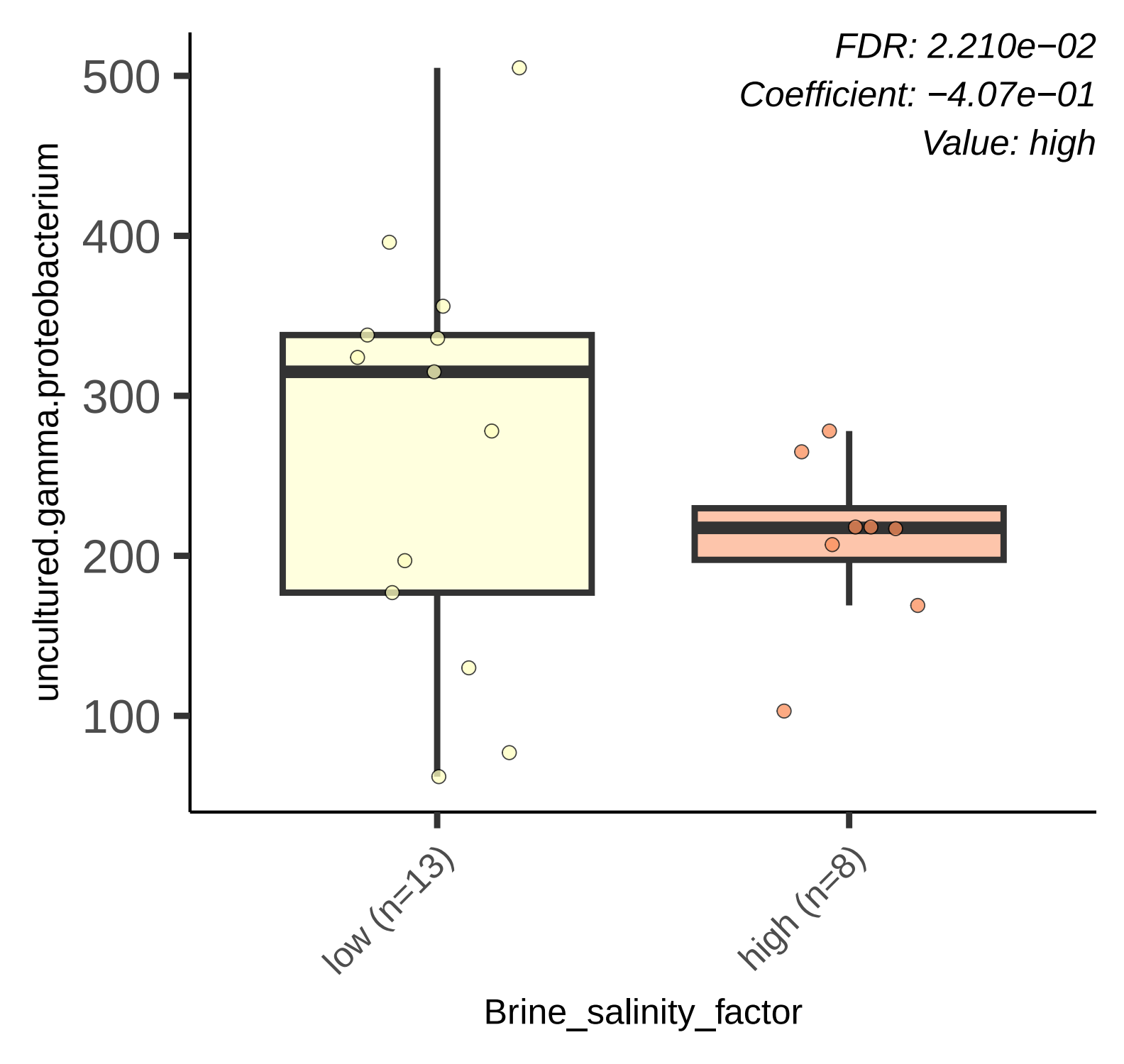

FDR: 2.045e−02
Coefficient: −1.27e+00
Value: high
Nonlabens.sp..Hel1_33_55
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

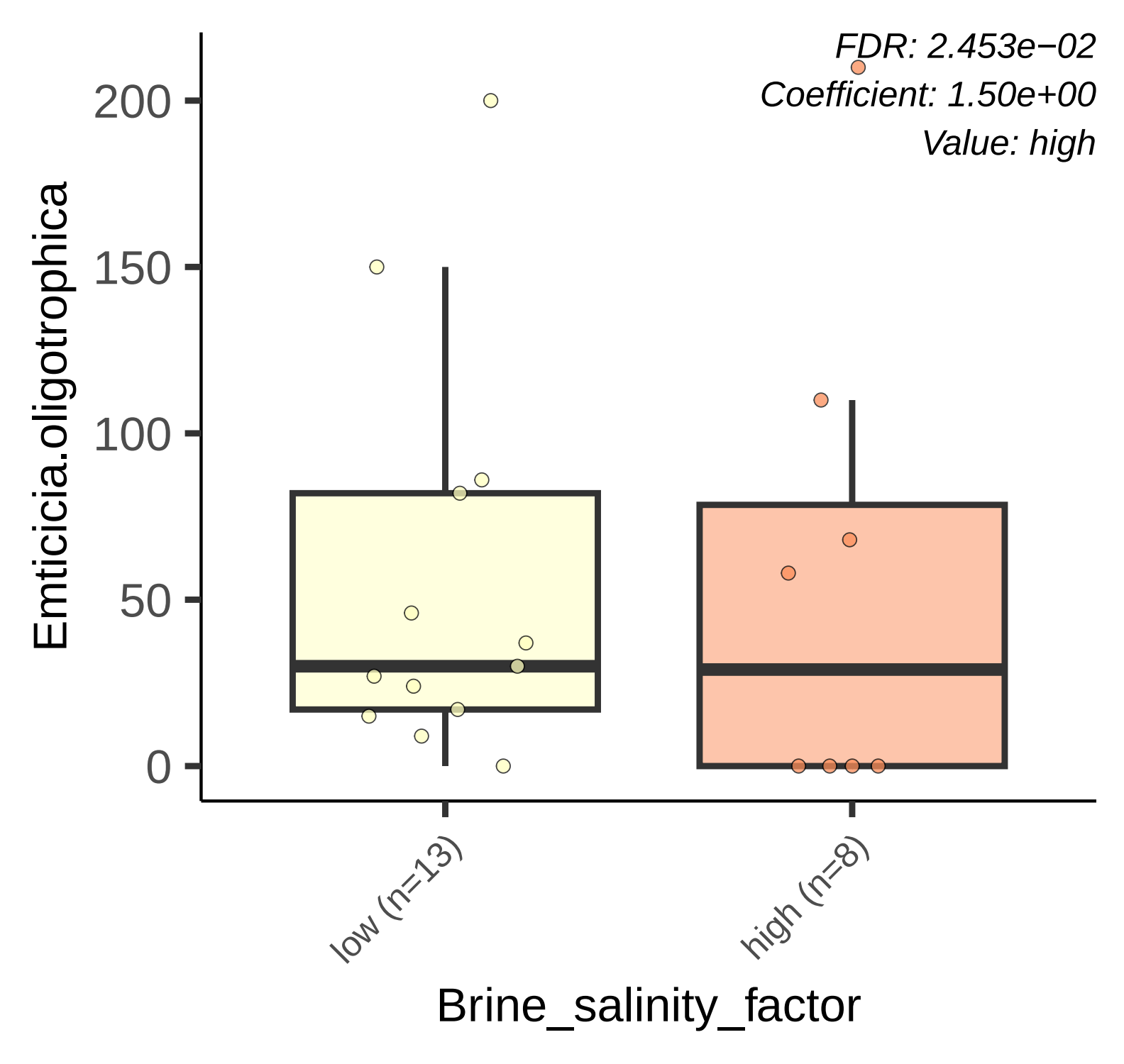

FDR: 2.075e−02
Coefficient: 3.50e+00
Value: high
Sulfurimonas.autotrophica
80
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

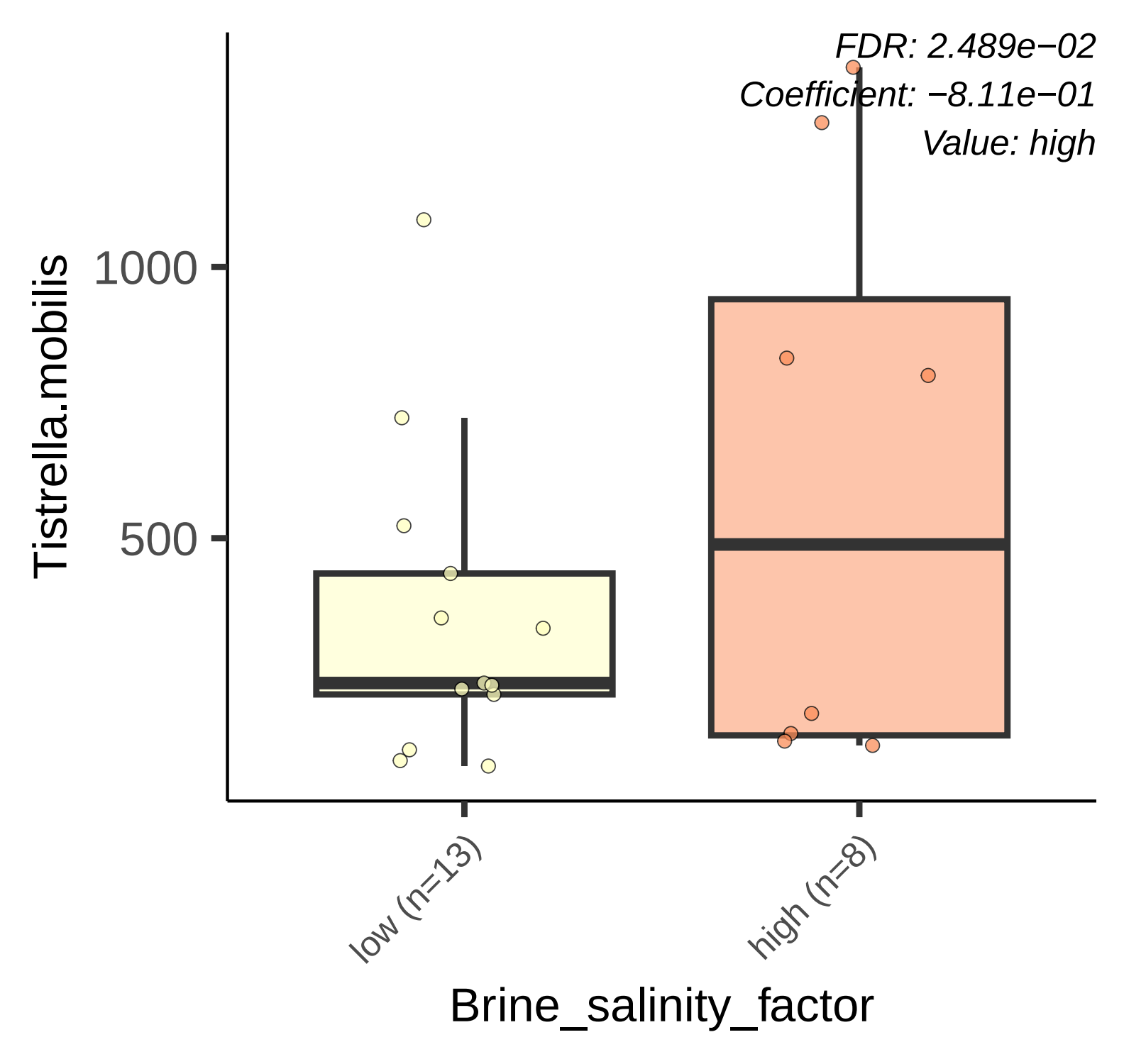

FDR: 2.094e−02
Coefficient: −1.20e+00
Value: high
Endozoicomonas.montiporae
80
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

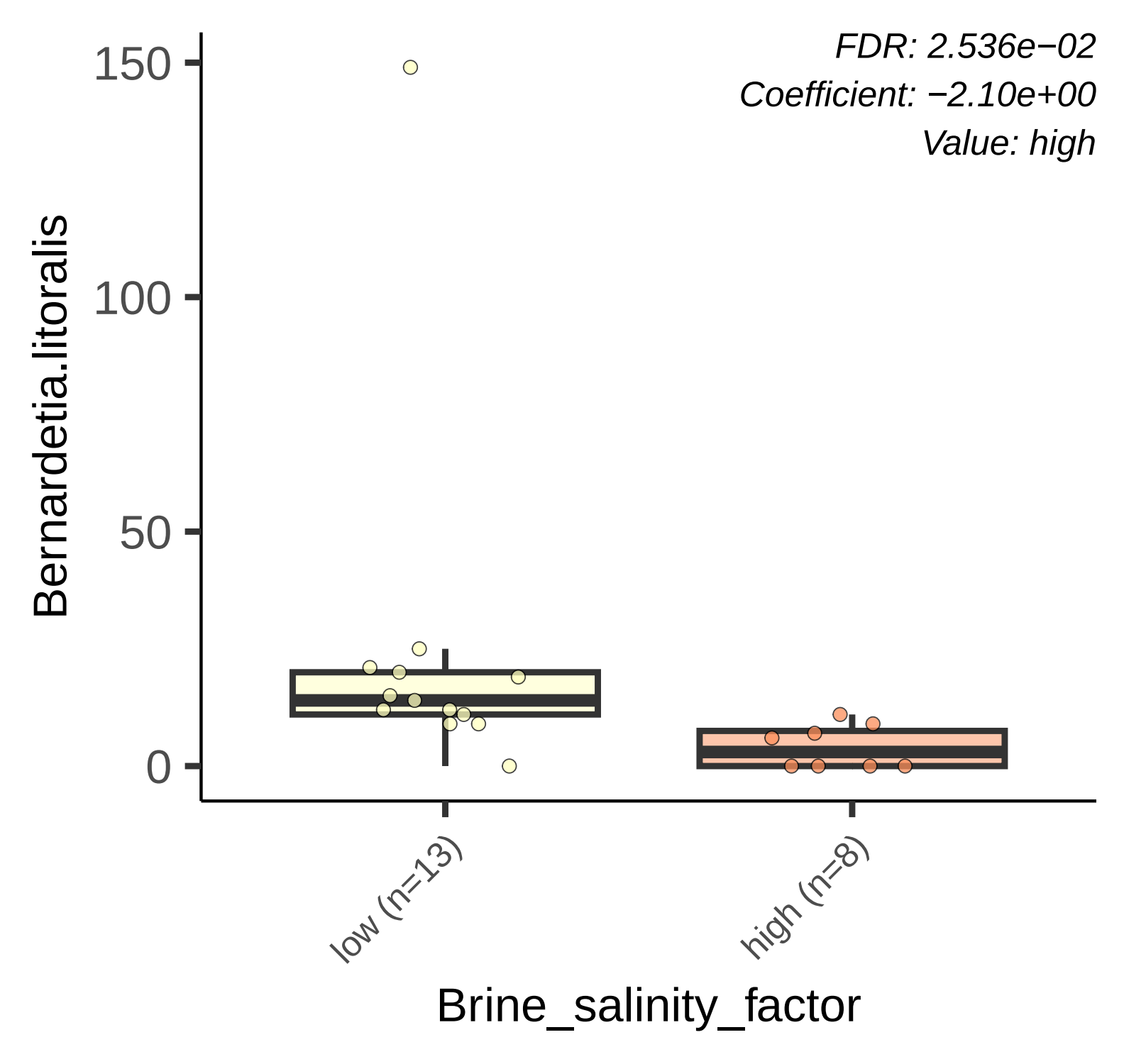

FDR: 2.094e−02
Coefficient: 2.36e+00
Value: high
Haloplanus.natans
300
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

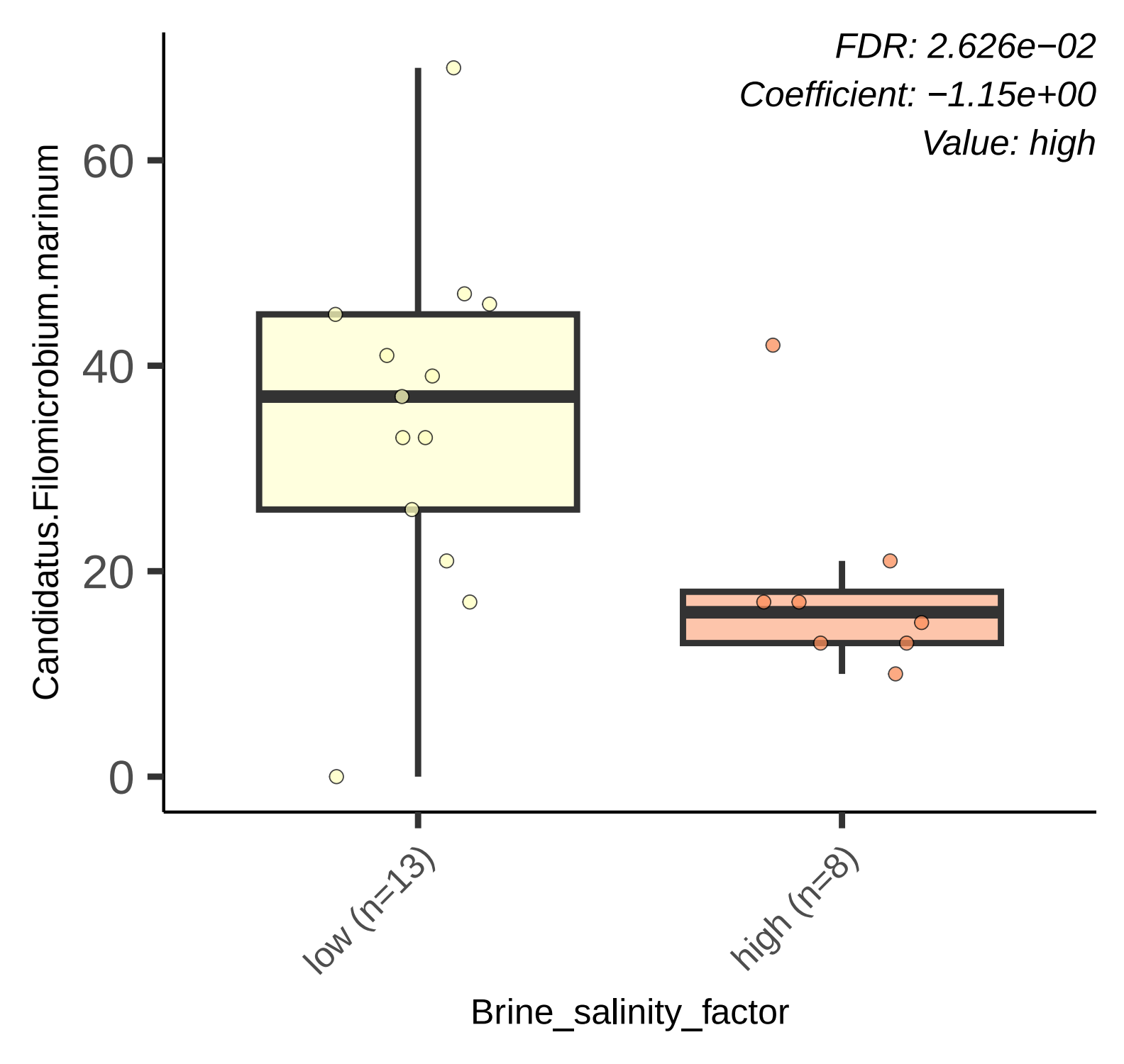

FDR: 2.159e−02
Coefficient: 1.86e+00
Value: high
Gracilimonas.sp..HME9591
50
40
30
20
10
0
low (n=13)
high (n=8)
Brine_salinity_factor

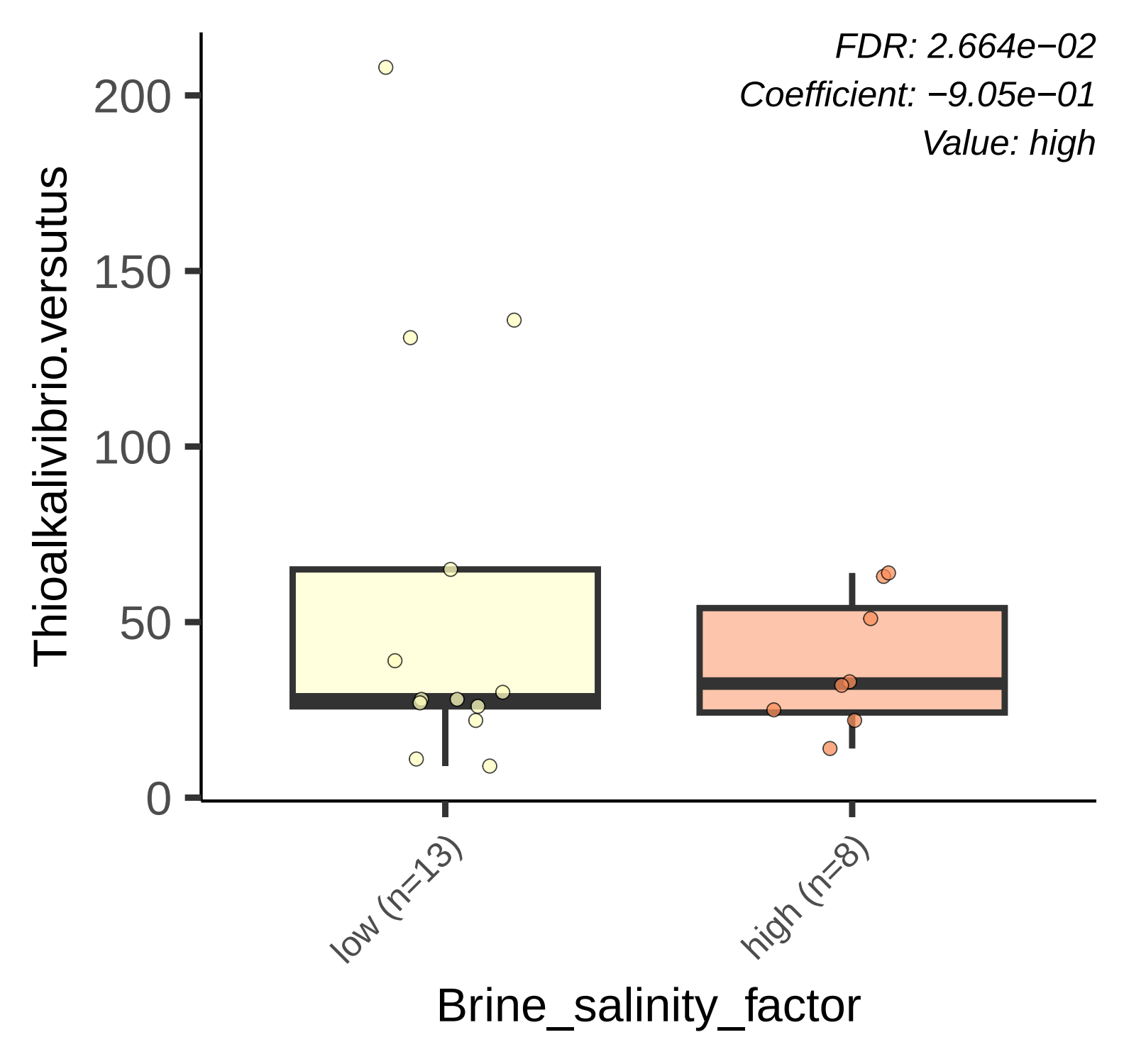

FDR: 2.210e−02
Coefficient: −4.07e−01
Value: high
uncultured.gamma.proteobacterium
500
400
300
200
100
low (n=13)
high (n=8)
Brine_salinity_factor

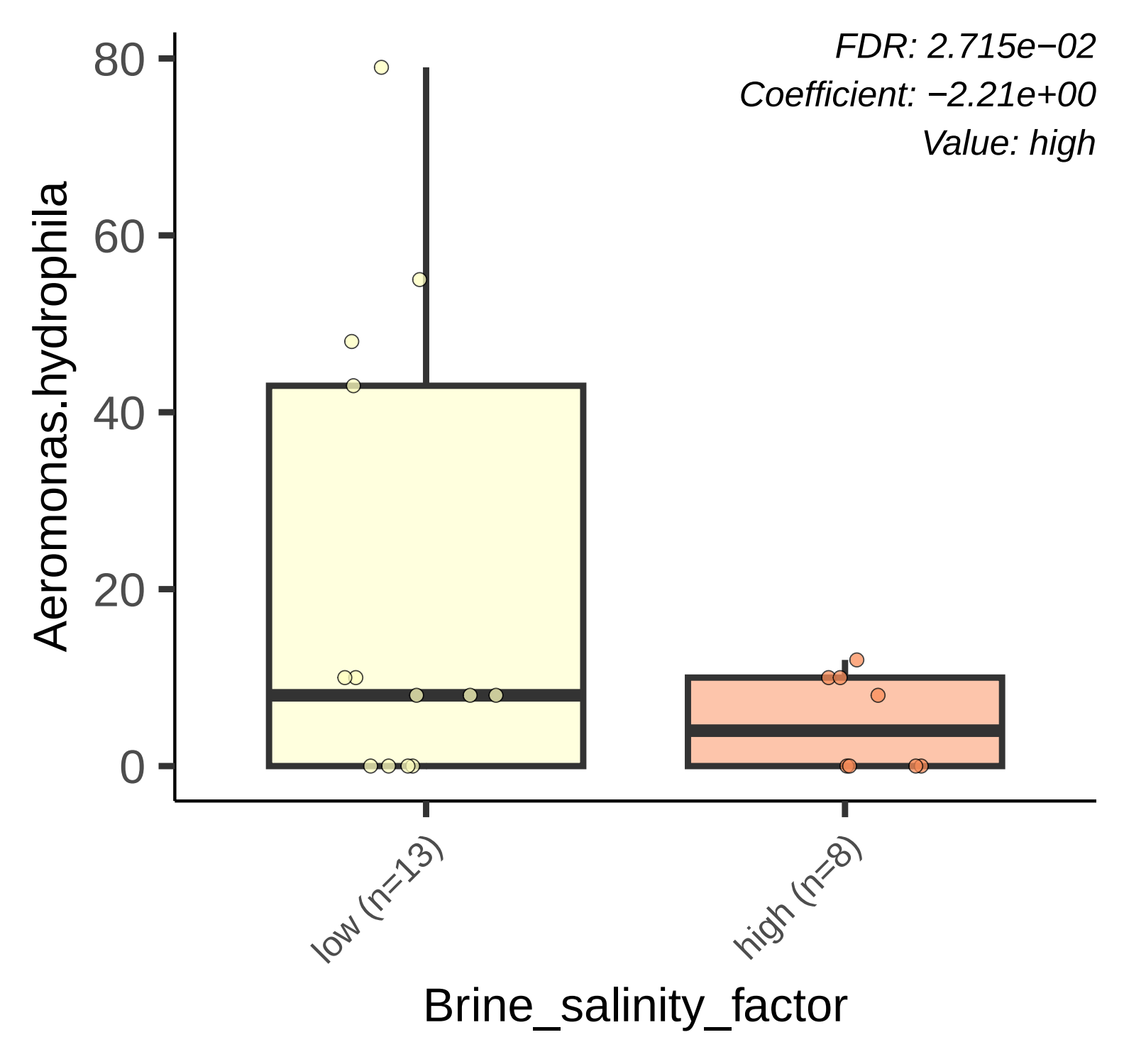

FDR: 2.453e−02
Coefficient: 1.50e+00
Value: high
Emticicia.oligotrophica
200
150
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

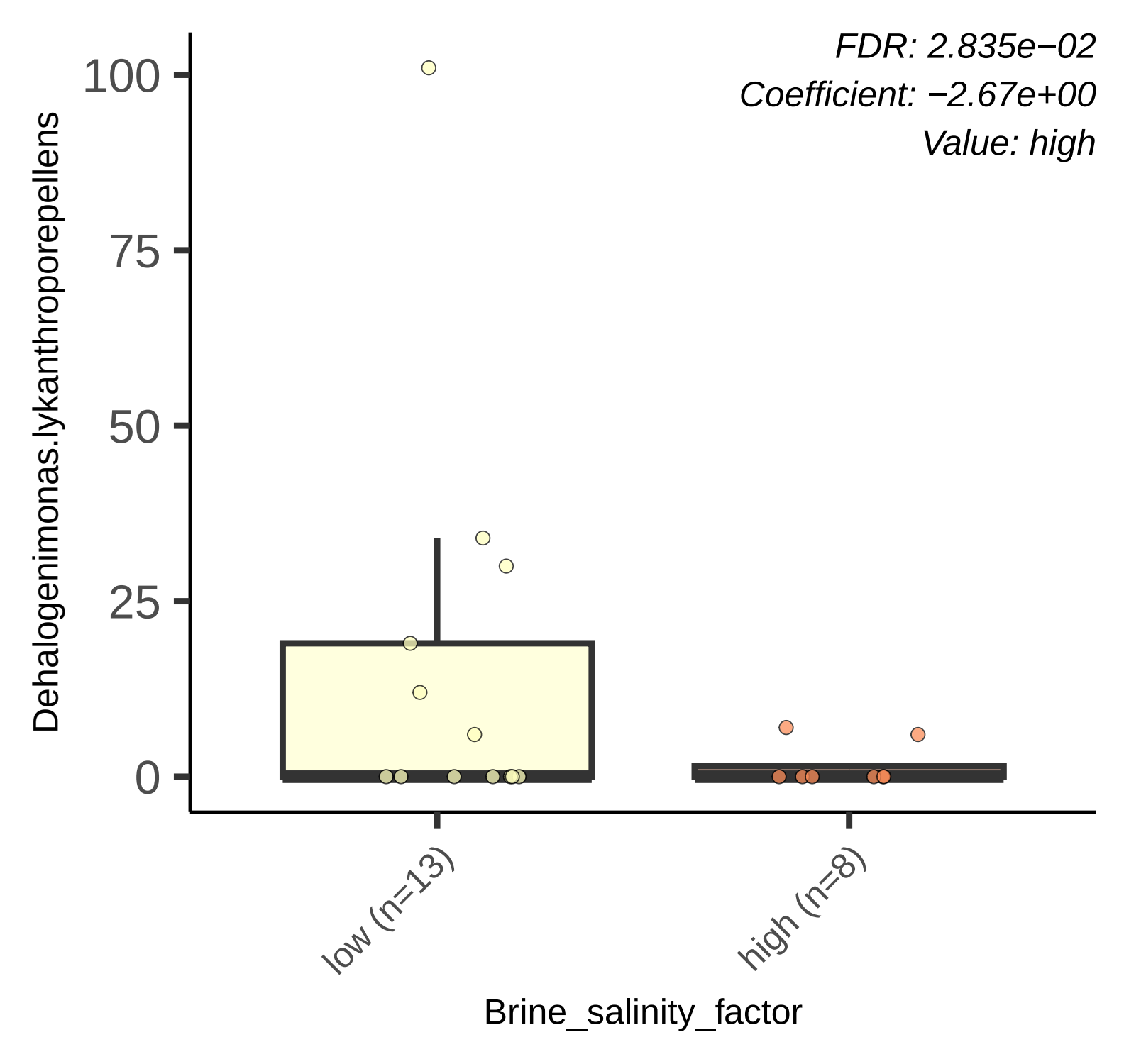

FDR: 2.489e−02
Coefficient: −8.11e−01
Value: high
Tistrella.mobilis
1000
500
low (n=13)
high (n=8)
Brine_salinity_factor

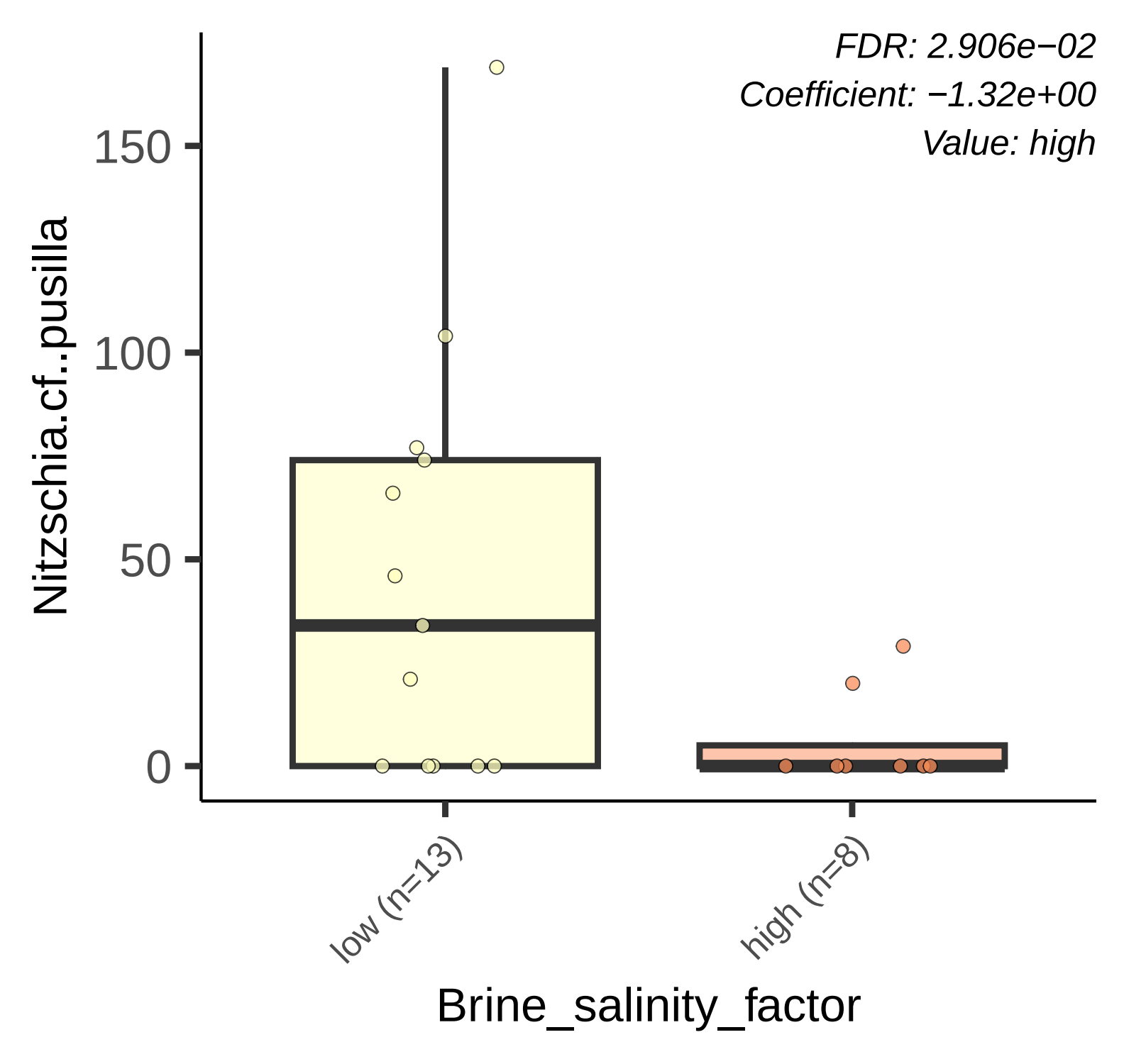

FDR: 2.536e−02
Coefficient: −2.10e+00
Value: high
Bernardetia.litoralis
150
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

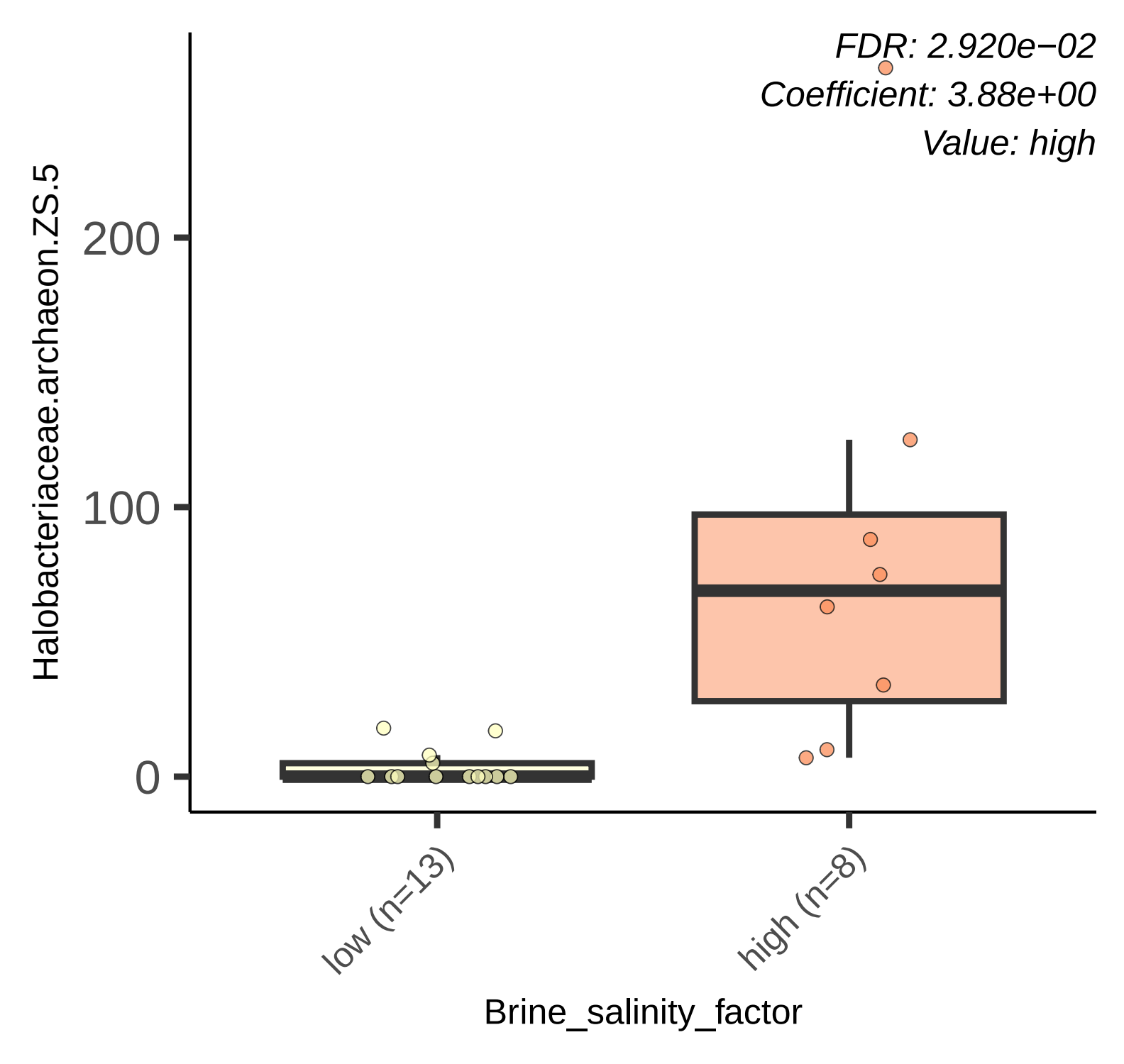

FDR: 2.626e−02
Coefficient: −1.15e+00
Value: high
Candidatus.Filomicrobium.marinum
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

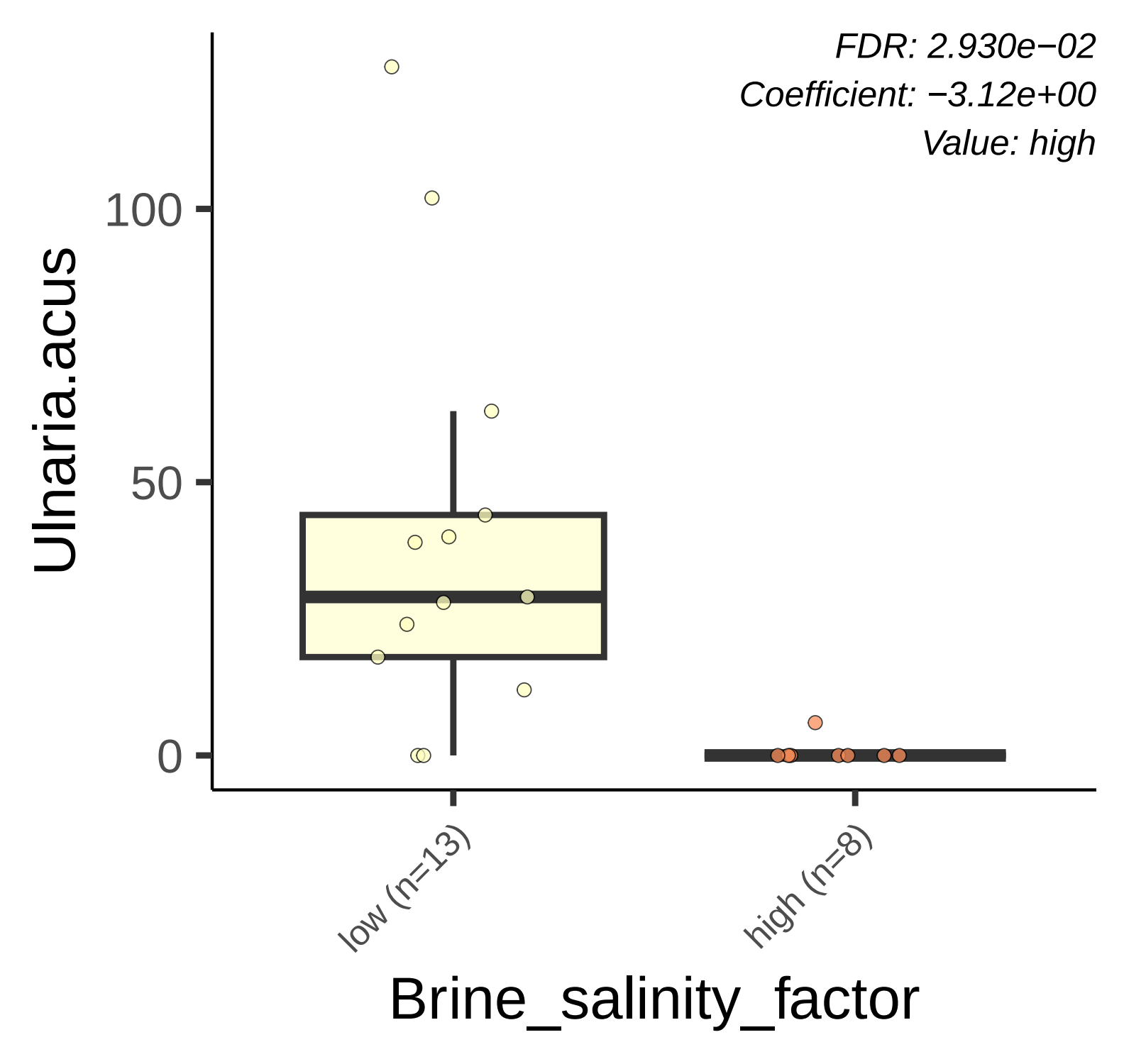

FDR: 2.664e−02
Coefficient: −9.05e−01
Value: high
Thioalkalivibrio.versutus
200
150
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

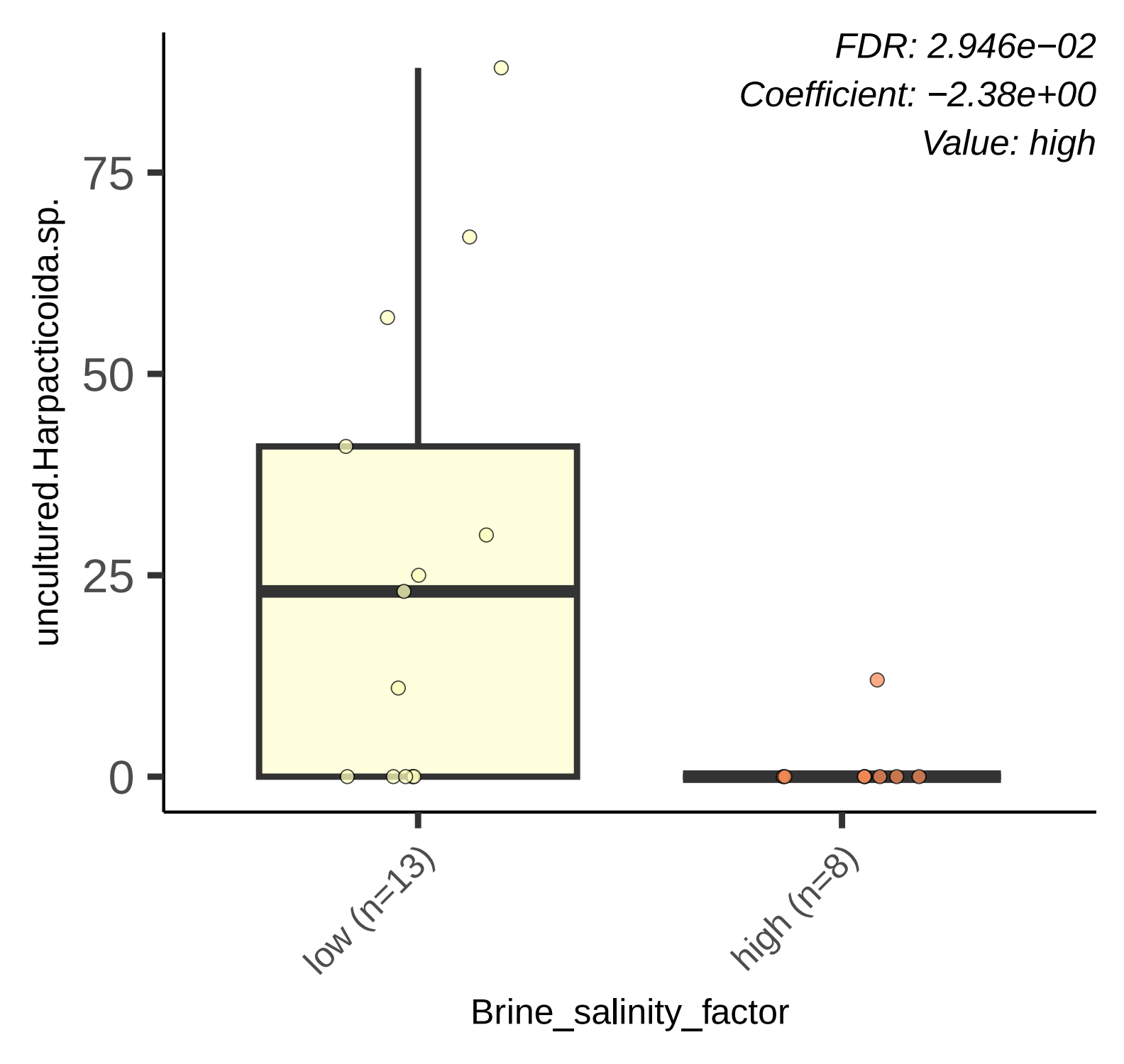

FDR: 2.715e−02
Coefficient: −2.21e+00
Value: high
Aeromonas.hydrophila
80
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

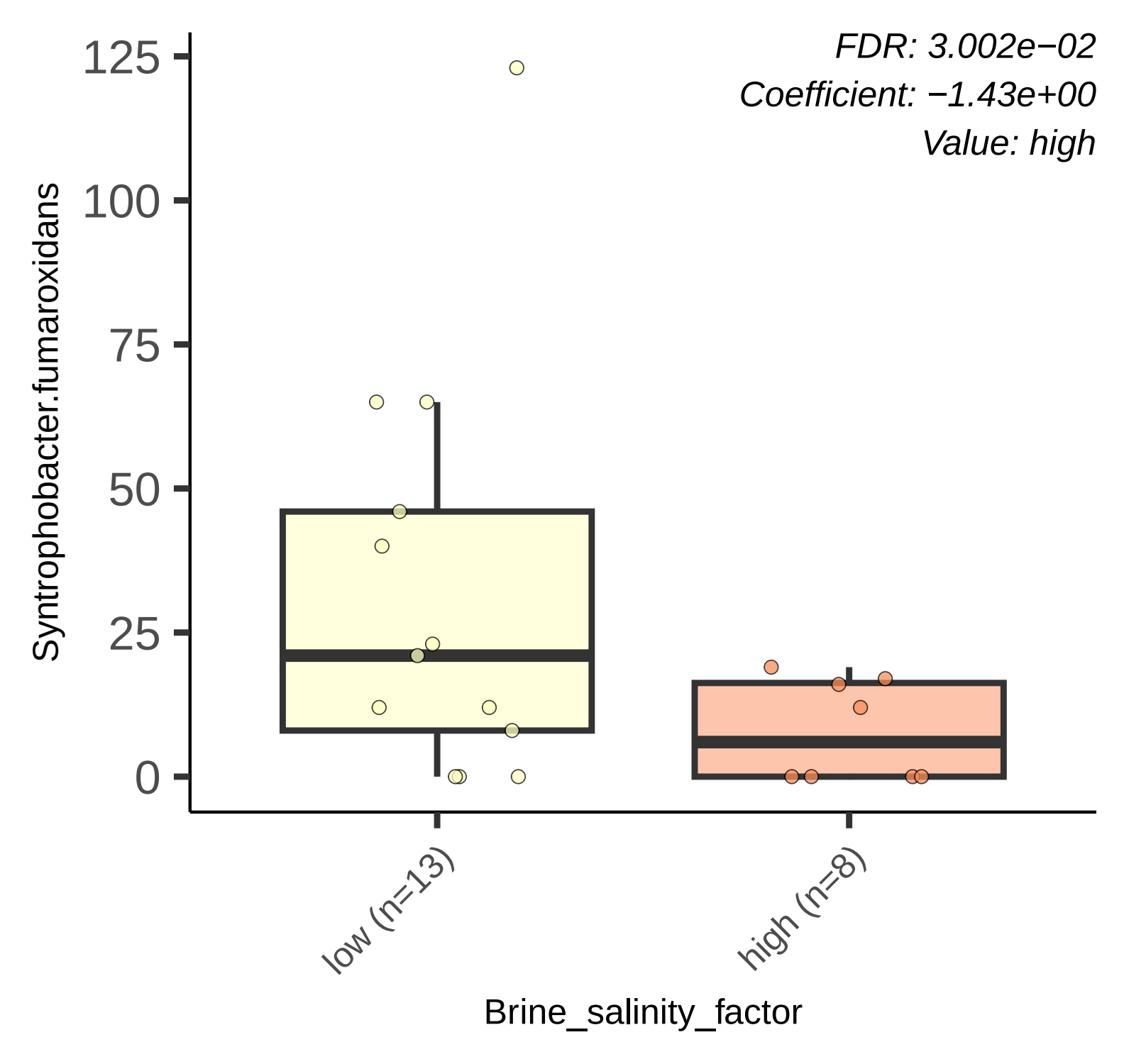

FDR: 2.835e−02
Coefficient: −2.67e+00
Value: high
Dehalogenimonas.lykanthroporepellens
100
75
50
25
0
low (n=13)
high (n=8)
Brine_salinity_factor

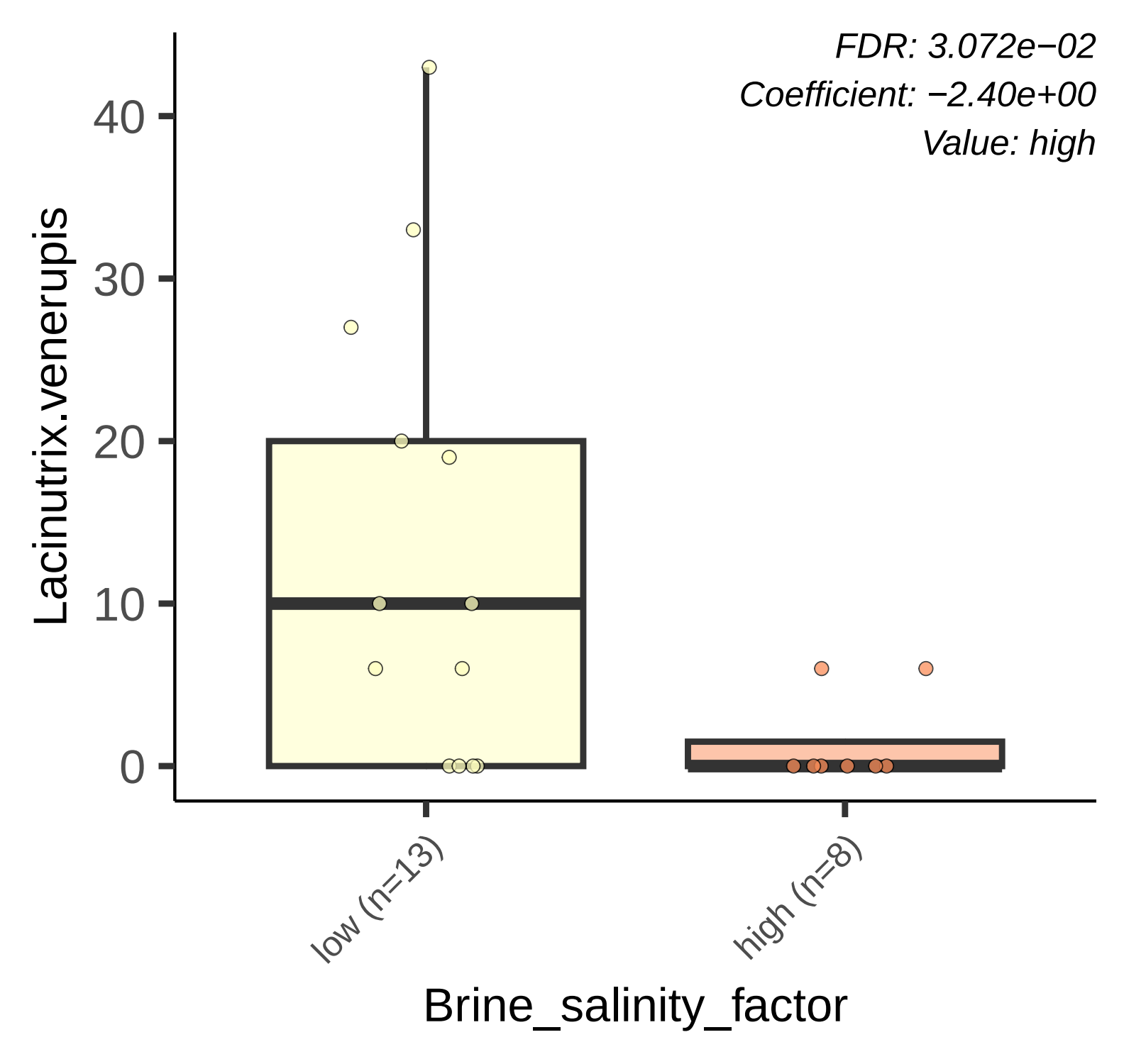

FDR: 2.906e−02
Coefficient: −1.32e+00
Value: high
Nitzschia.cf..pusilla
150
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

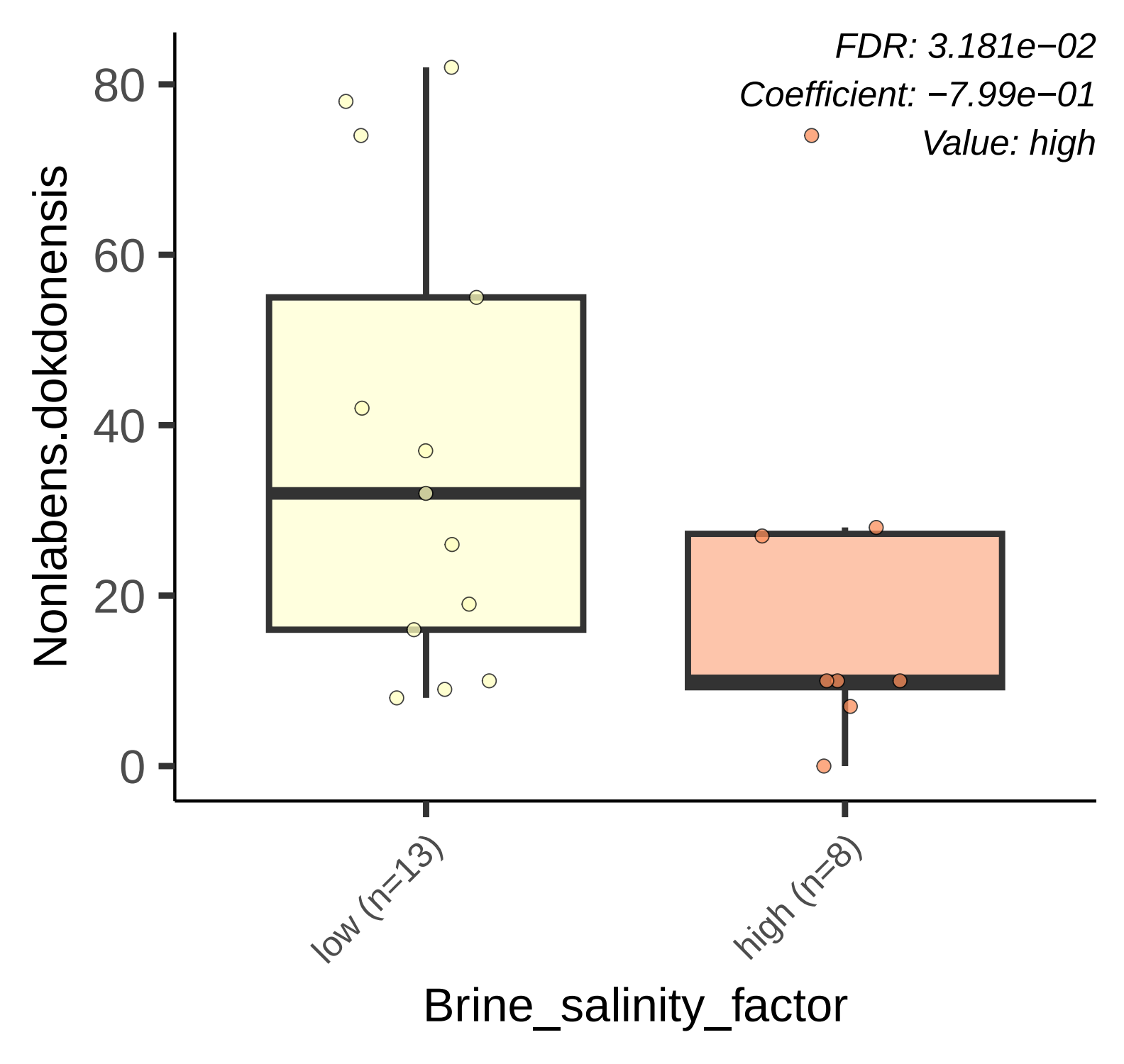

FDR: 2.920e−02
Coefficient: 3.88e+00
Value: high
Halobacteriaceae.archaeon.ZS.5
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

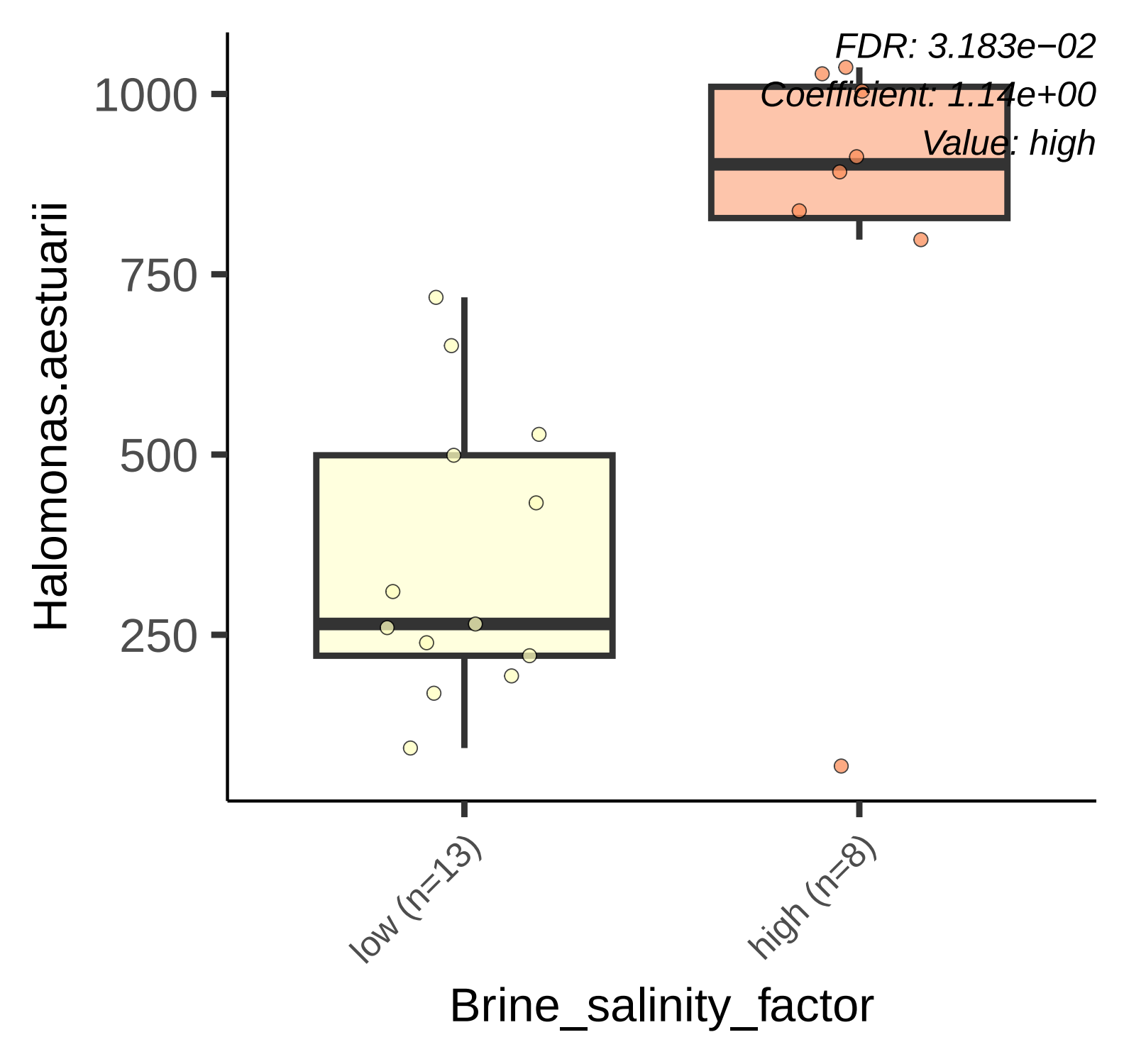

FDR: 2.930e−02
Coefficient: −3.12e+00
Value: high
Ulnaria.acus
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

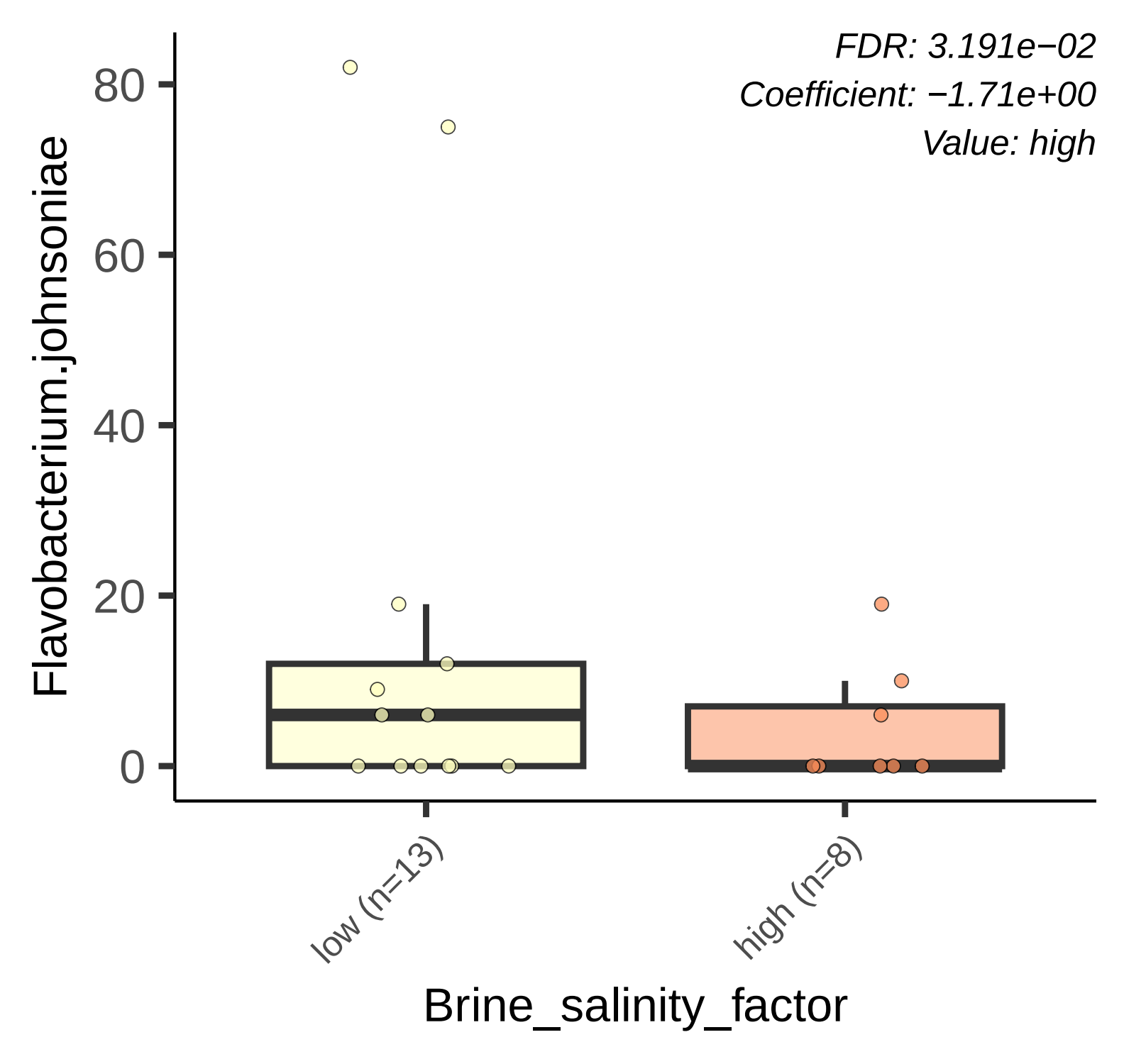

FDR: 2.946e−02
Coefficient: −2.38e+00
Value: high
uncultured.Harpacticoida.sp.
75
50
25
0
low (n=13)
high (n=8)
Brine_salinity_factor

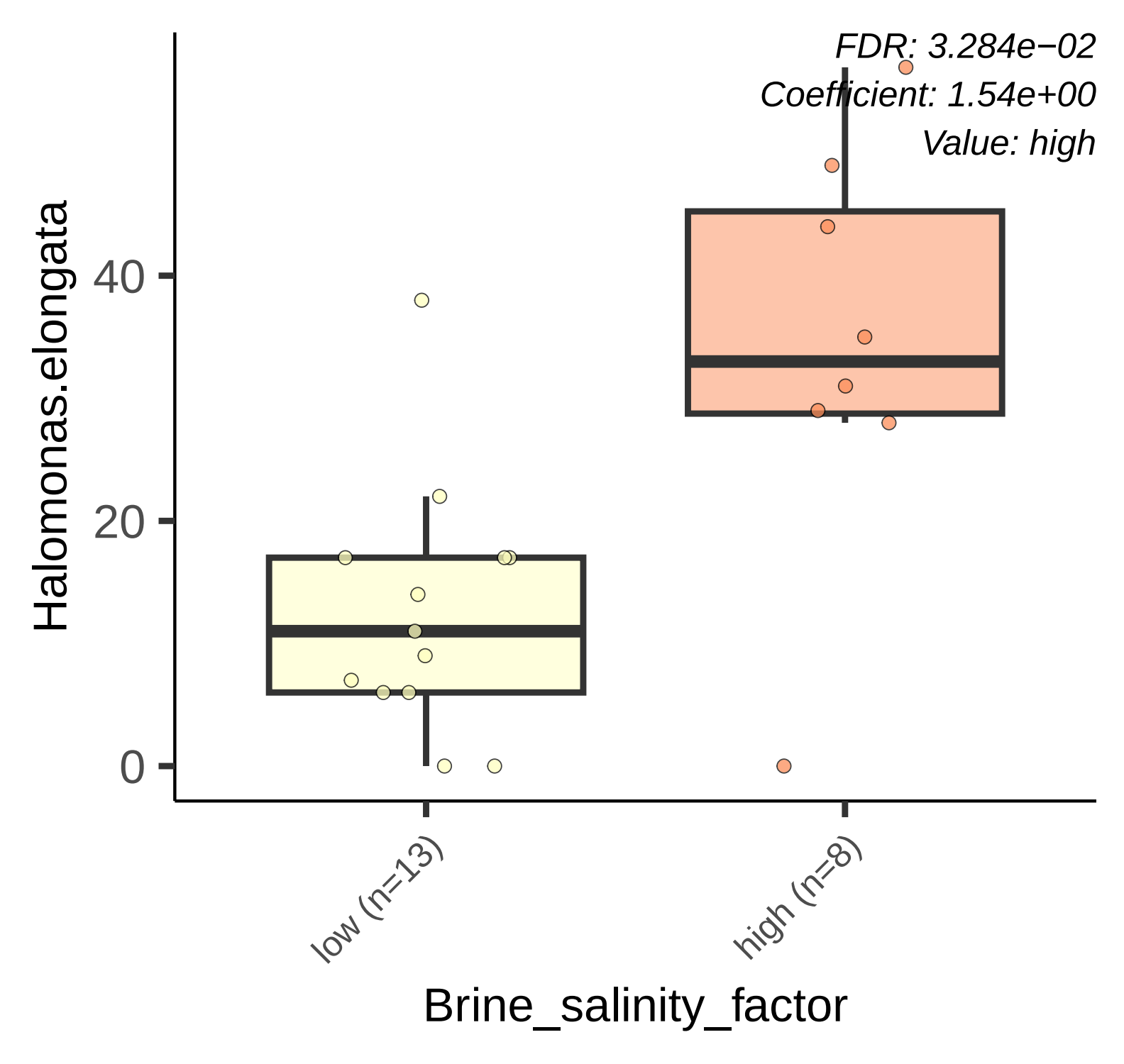

FDR: 3.002e−02
Coefficient: −1.43e+00
Value: high
125
100
75
50
25
0
Syntrophobacter.fumaroxidans
low (n=13)
high (n=8)
Brine_salinity_factor

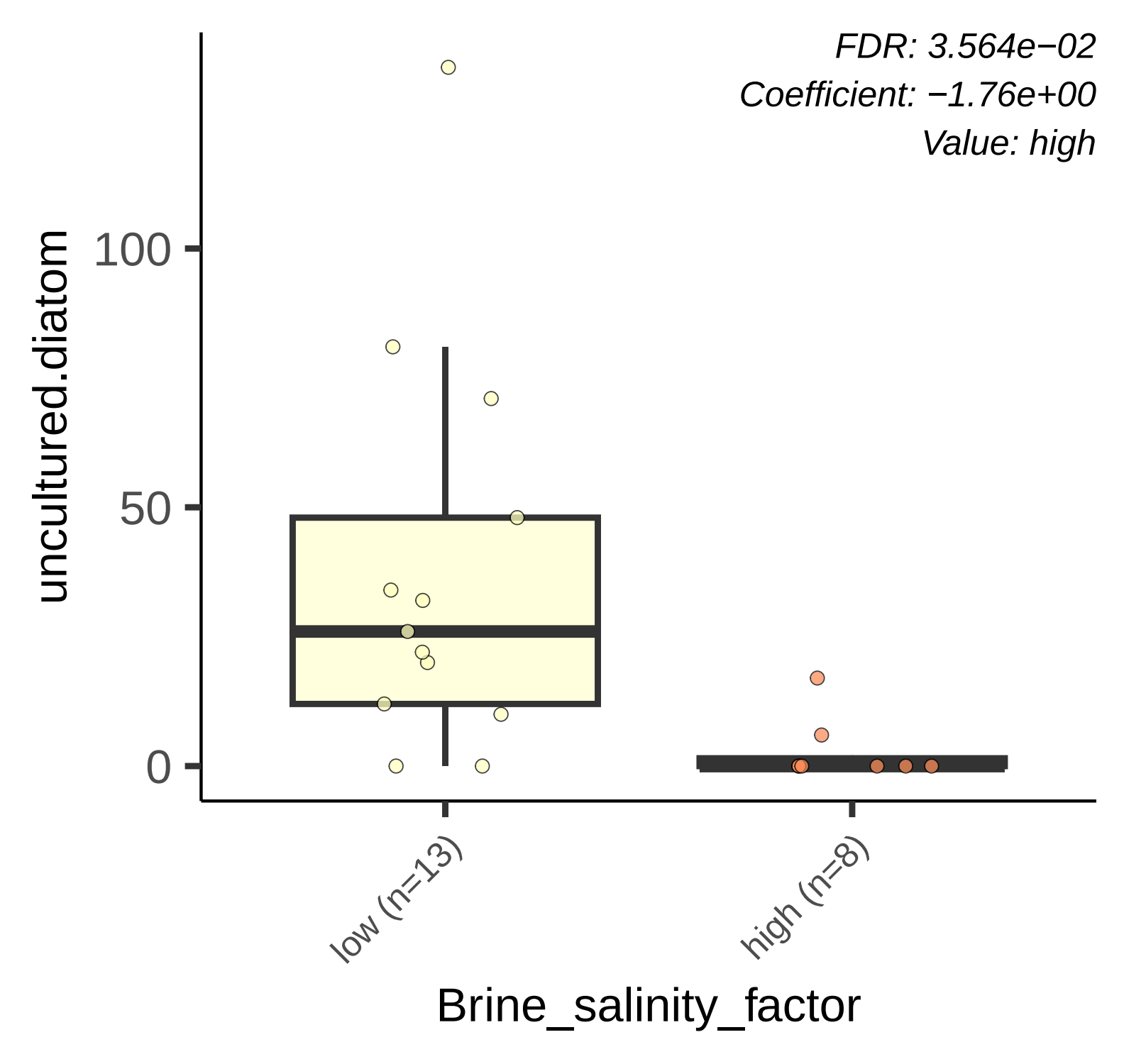

FDR: 3.072e−02
Coefficient: −2.40e+00
Value: high
Lacinutrix.venerupis
40
30
20
10
0
low (n=13)
high (n=8)
Brine_salinity_factor

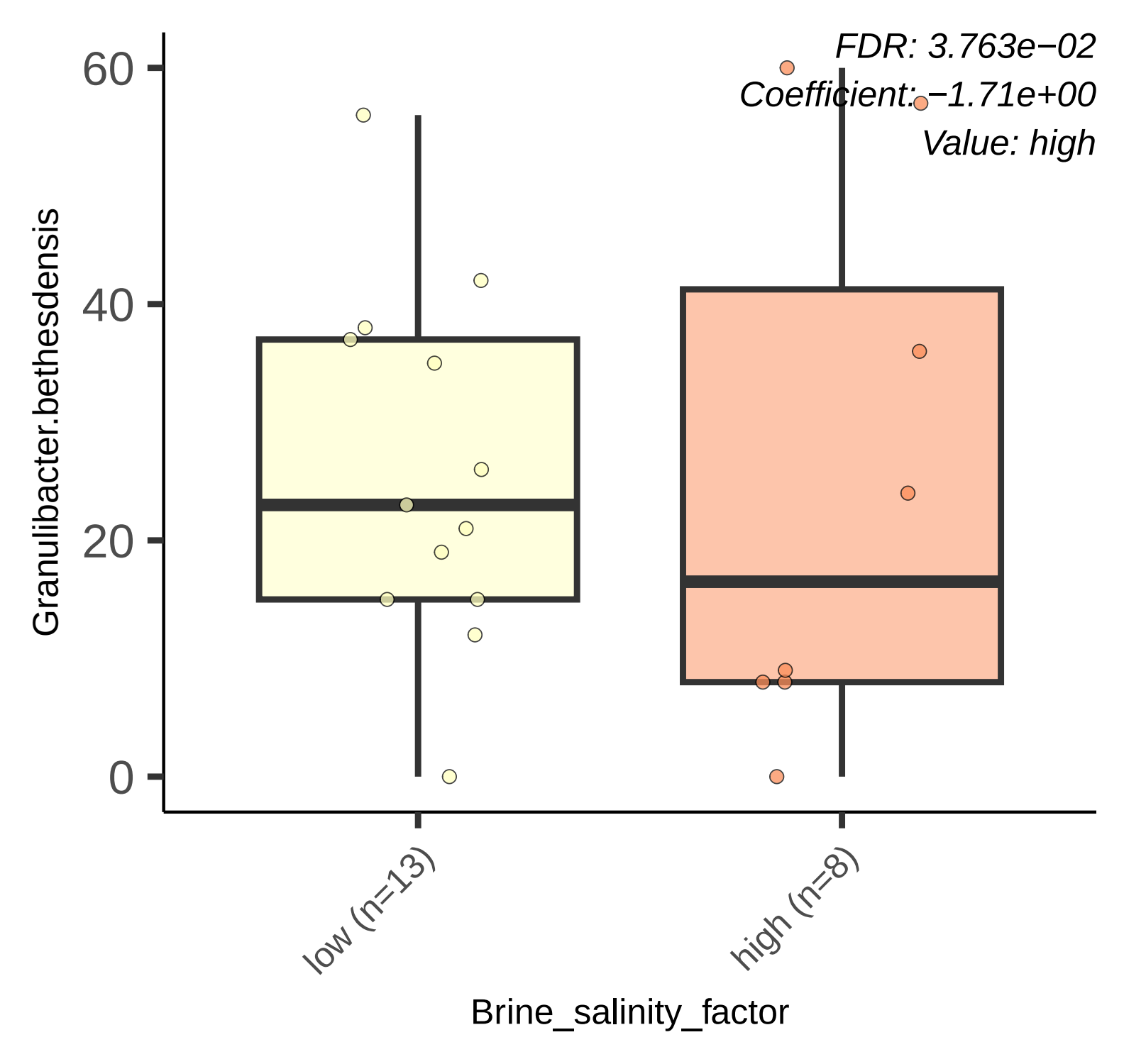

FDR: 3.181e−02
Coefficient: −7.99e−01
Value: high
Nonlabens.dokdonensis
80
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

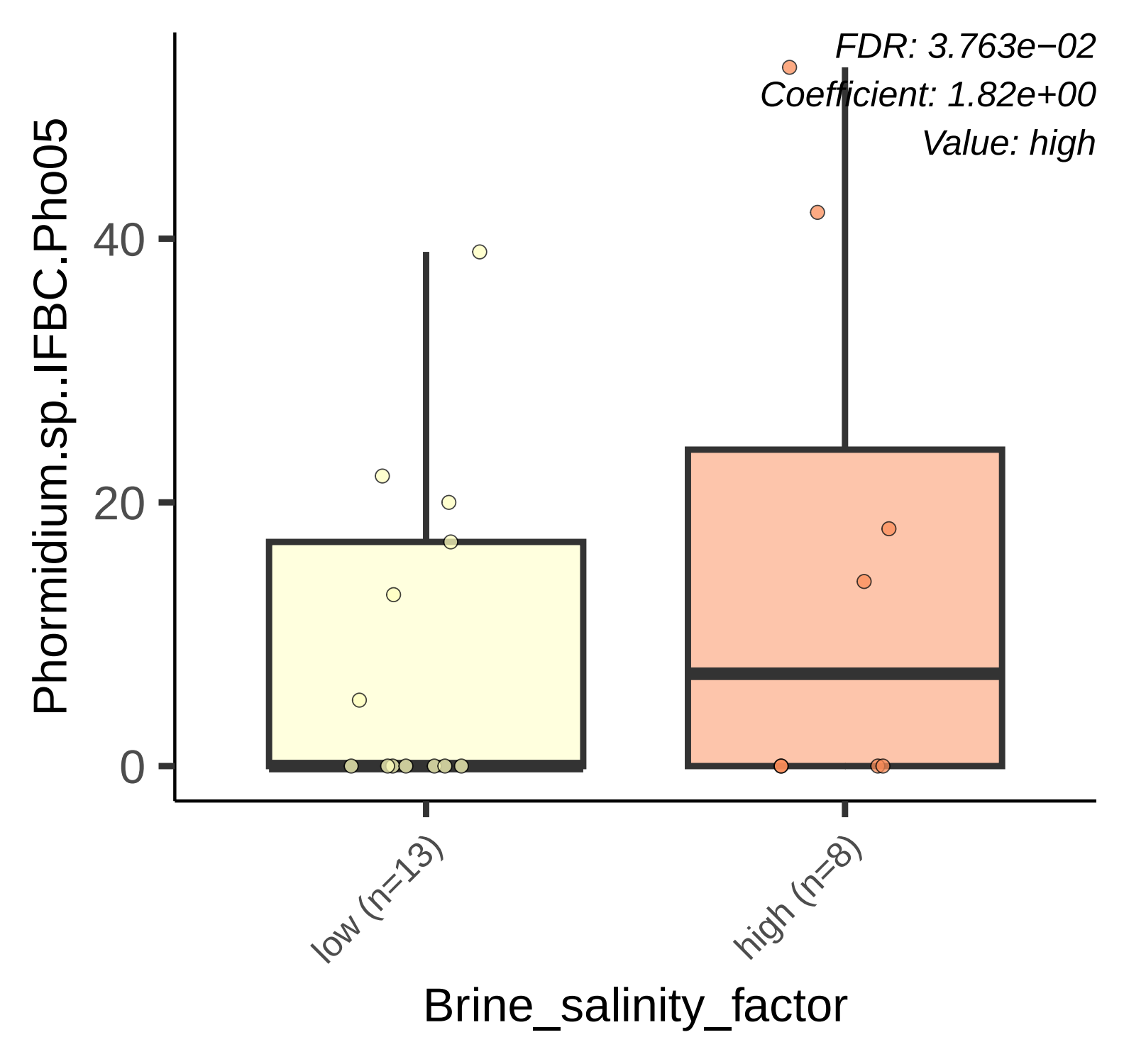

FDR: 3.183e−02
Coefficient: 1.14e+00
Value: high
1000
750
500
250
Halomonas.aestuarii
low (n=13)
high (n=8)
Brine_salinity_factor

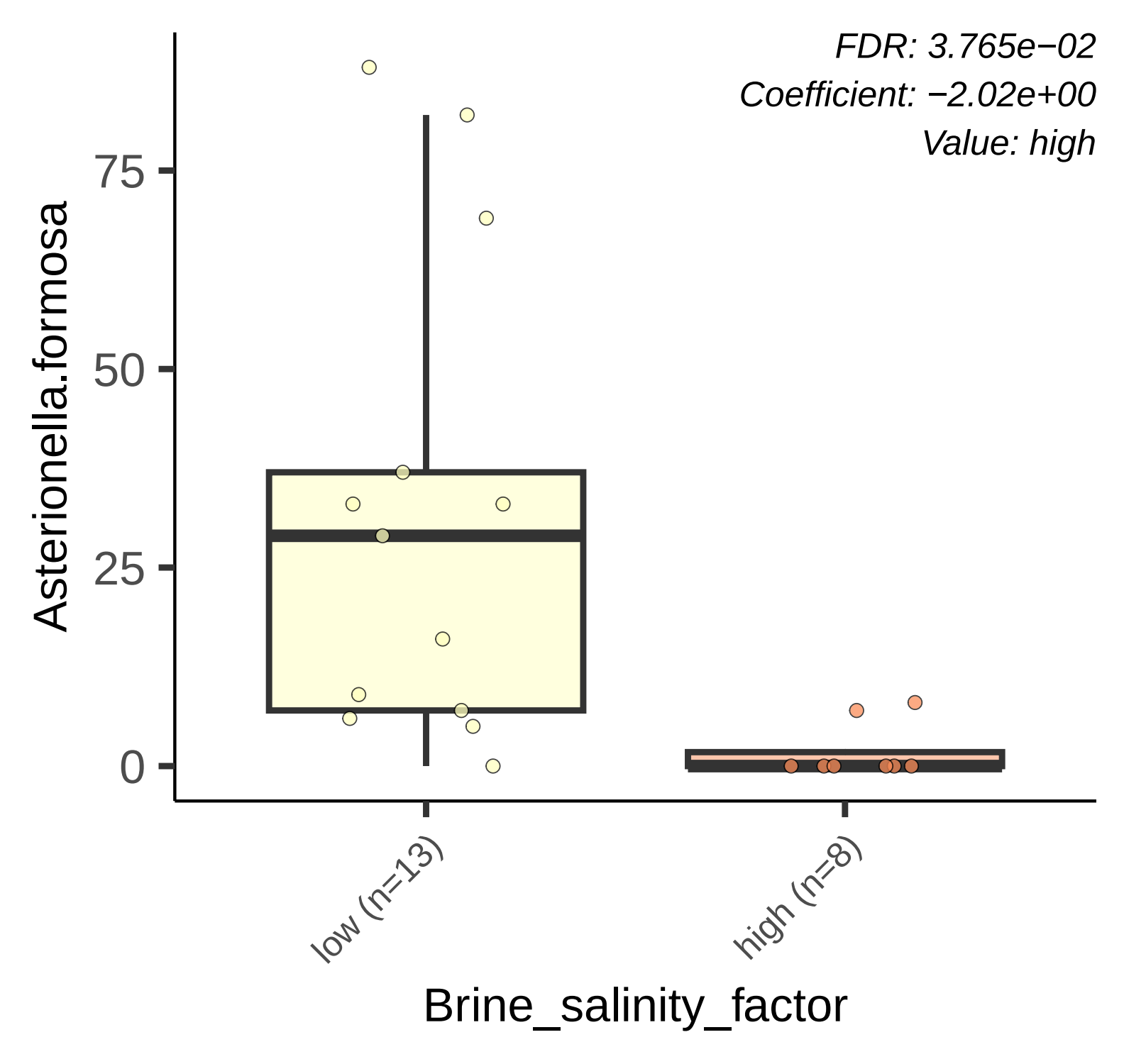

FDR: 3.191e−02
Coefficient: −1.71e+00
Value: high
Flavobacterium.johnsoniae
80
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

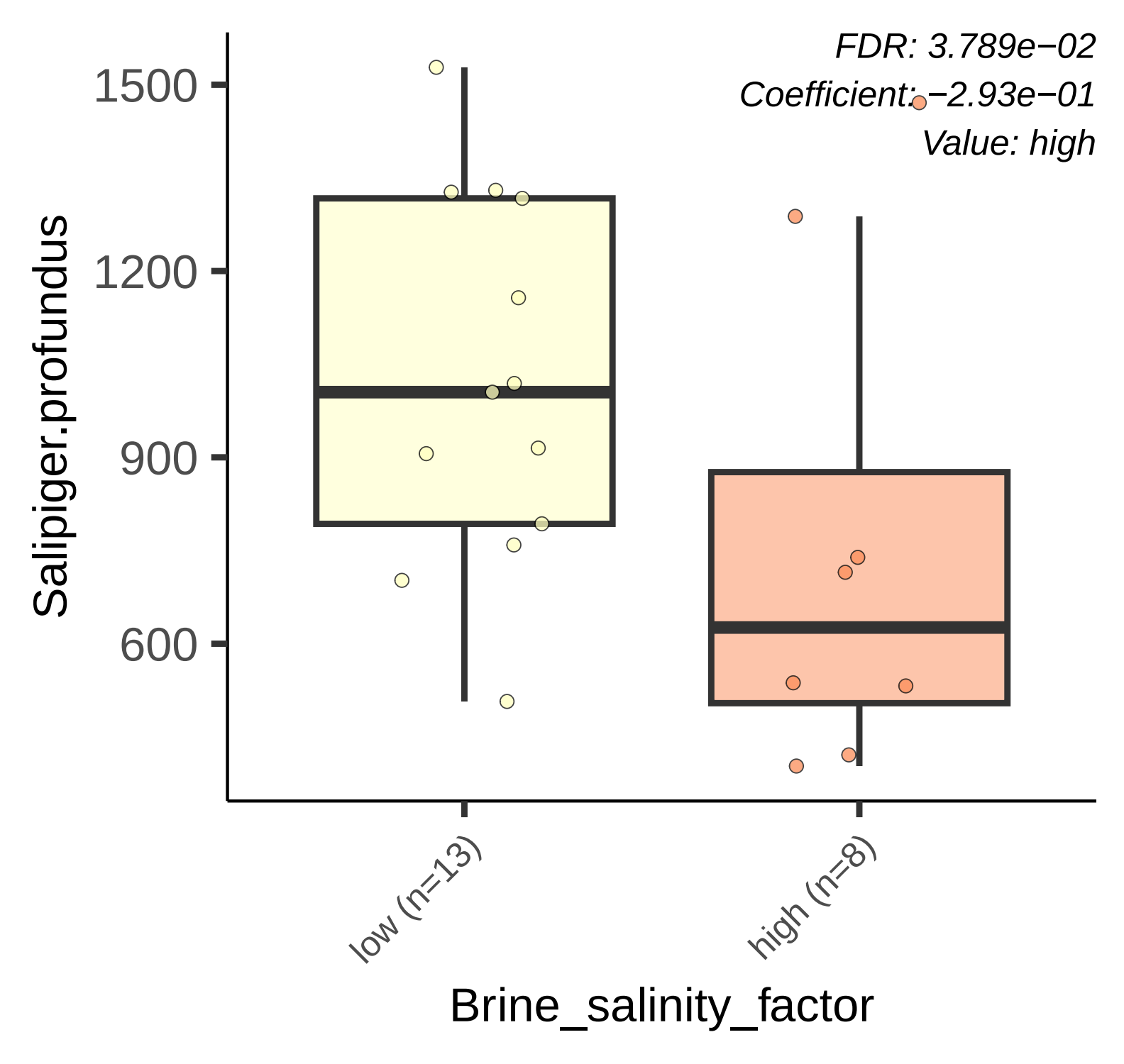

FDR: 3.284e−02
Coefficient: 1.54e+00
Value: high
Halomonas.elongata
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

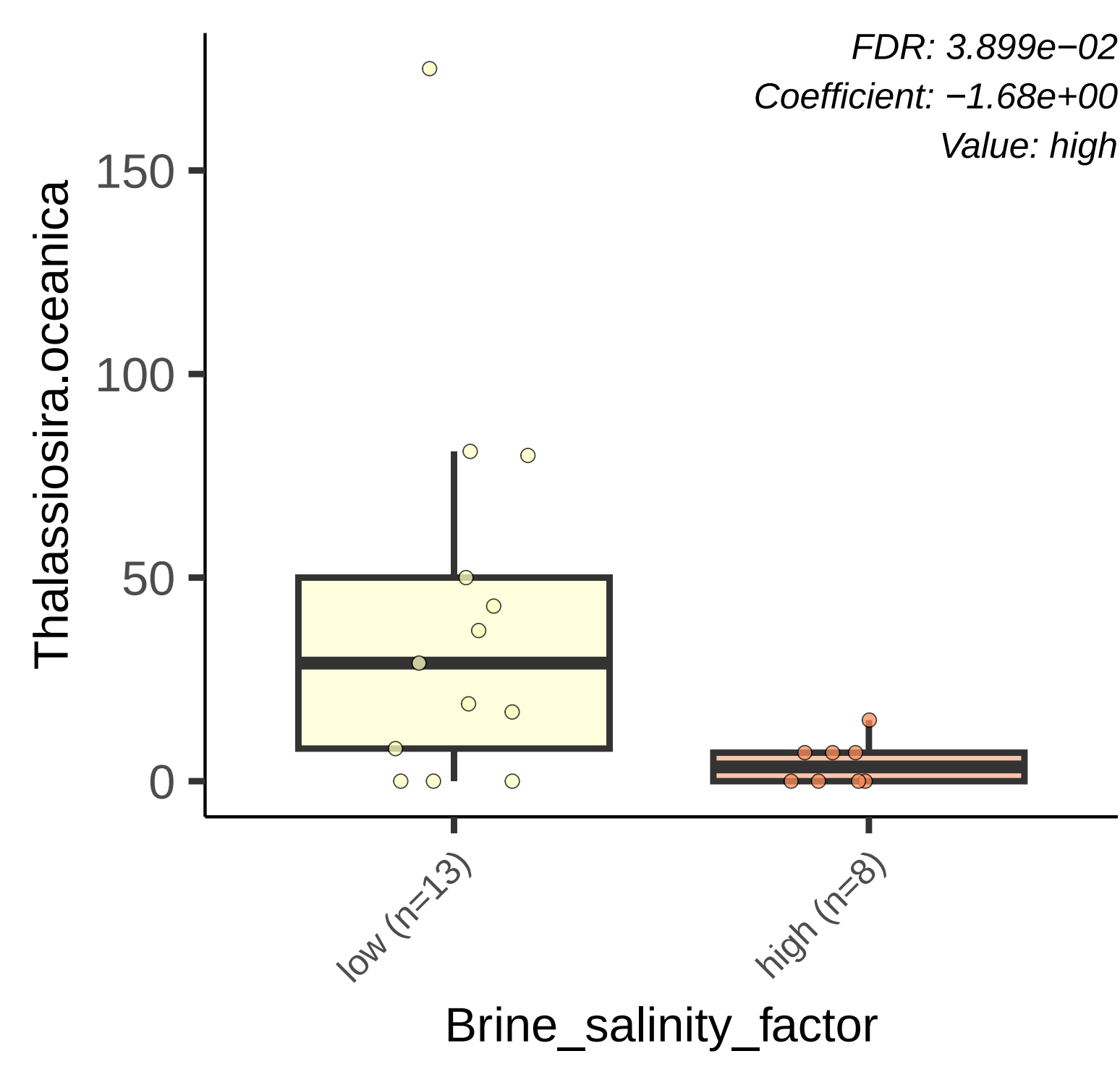

FDR: 3.564e−02
Coefficient: −1.76e+00
Value: high
uncultured.diatom
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

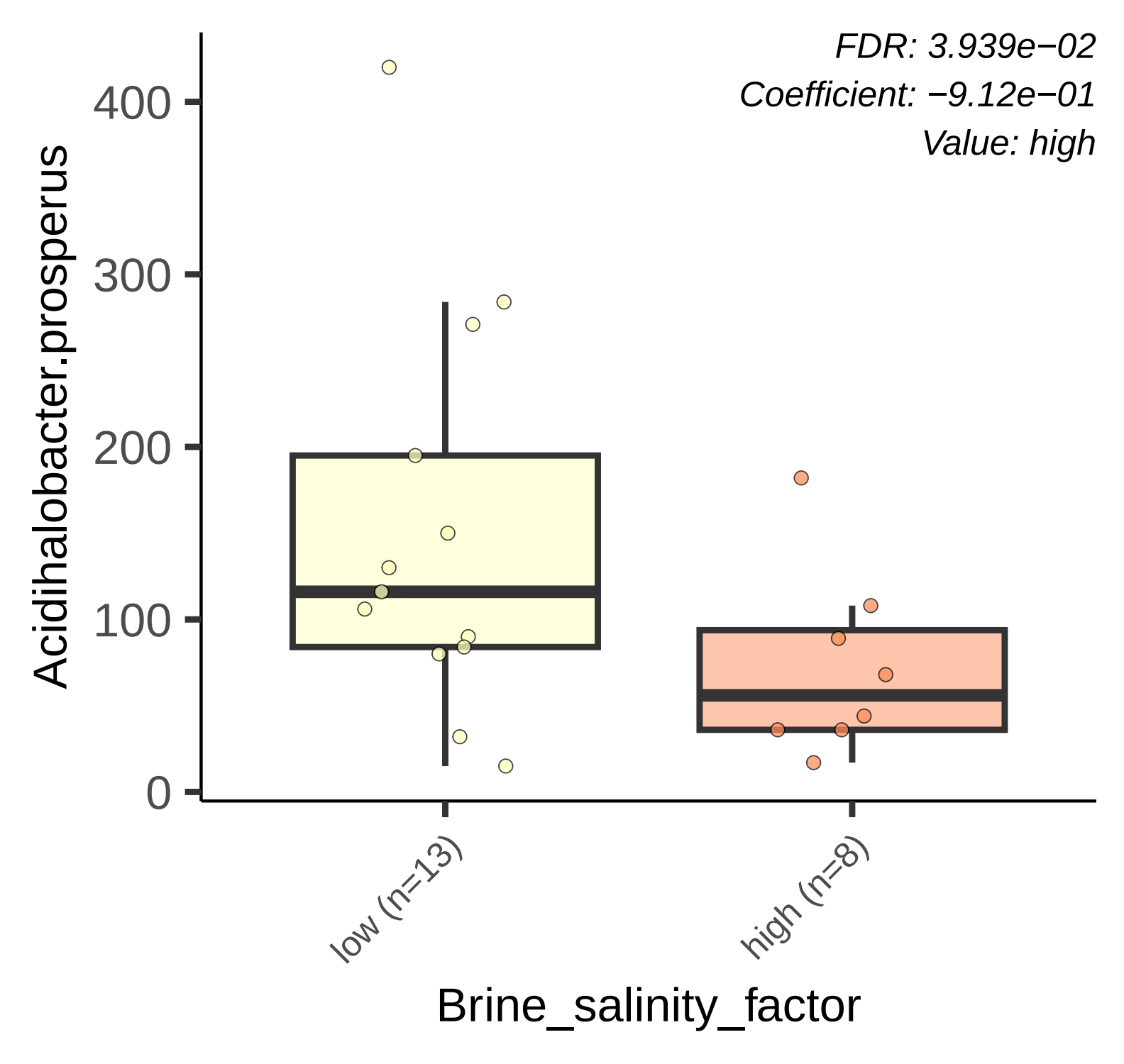

FDR: 3.763e−02
Coefficient: −1.71e+00
Value: high
Granulibacter.bethesdensis
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

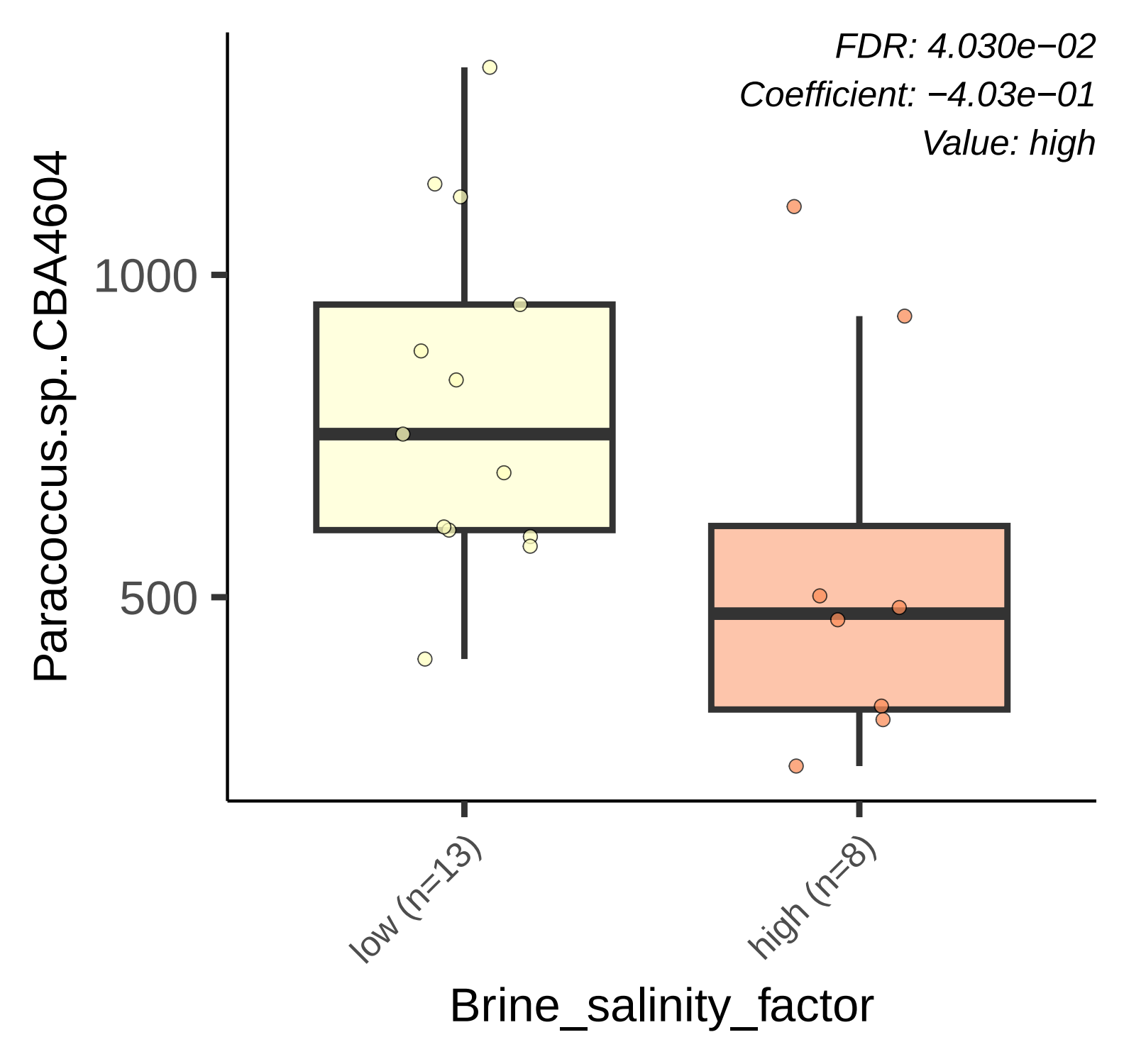

FDR: 3.763e−02
Coefficient: 1.82e+00
Value: high
Phormidium.sp..IFBC.Pho05
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor

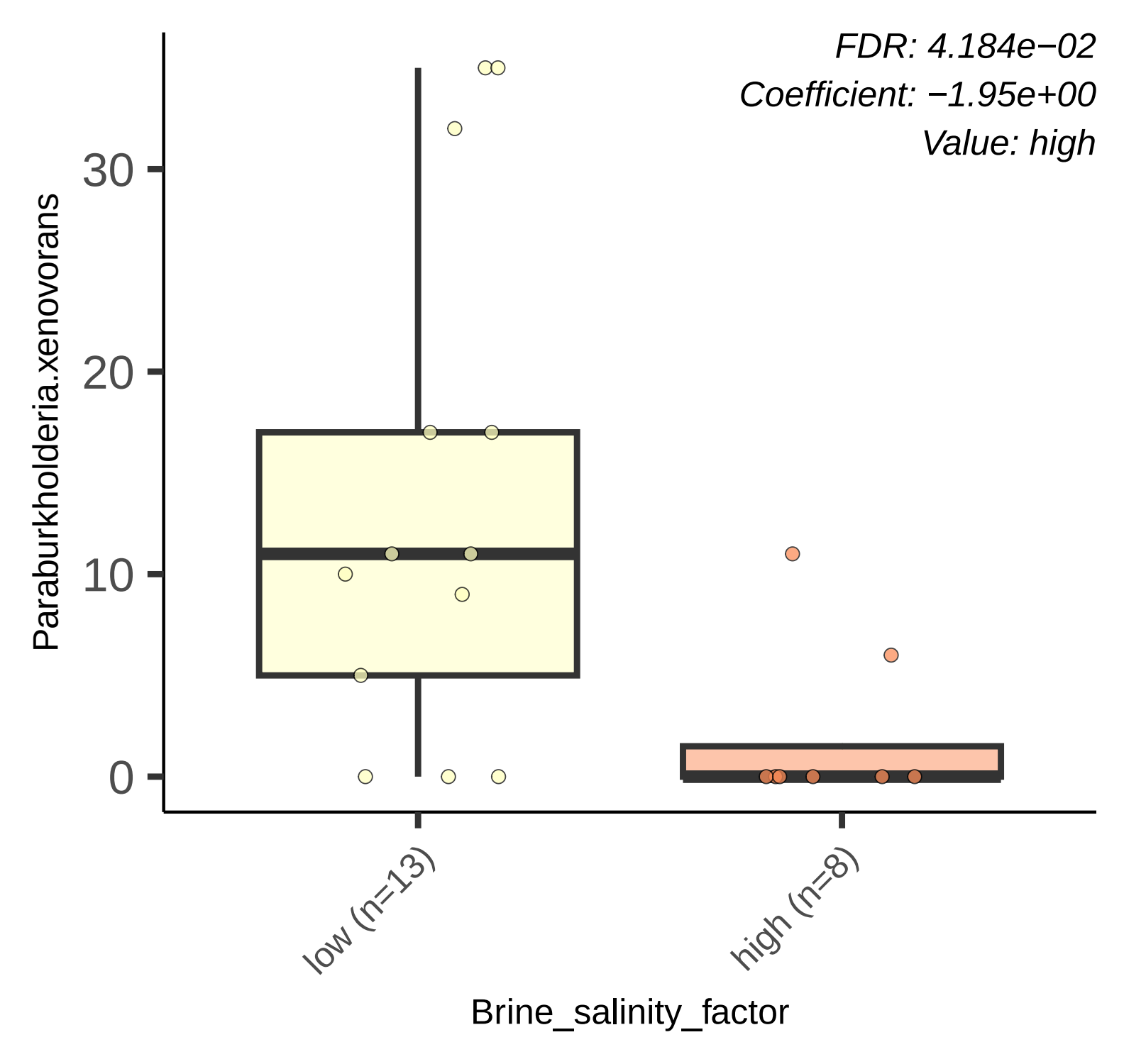

FDR: 3.765e−02
Coefficient: −2.02e+00
Value: high
Asterionella.formosa
75
50
25
0
low (n=13)
high (n=8)
Brine_salinity_factor

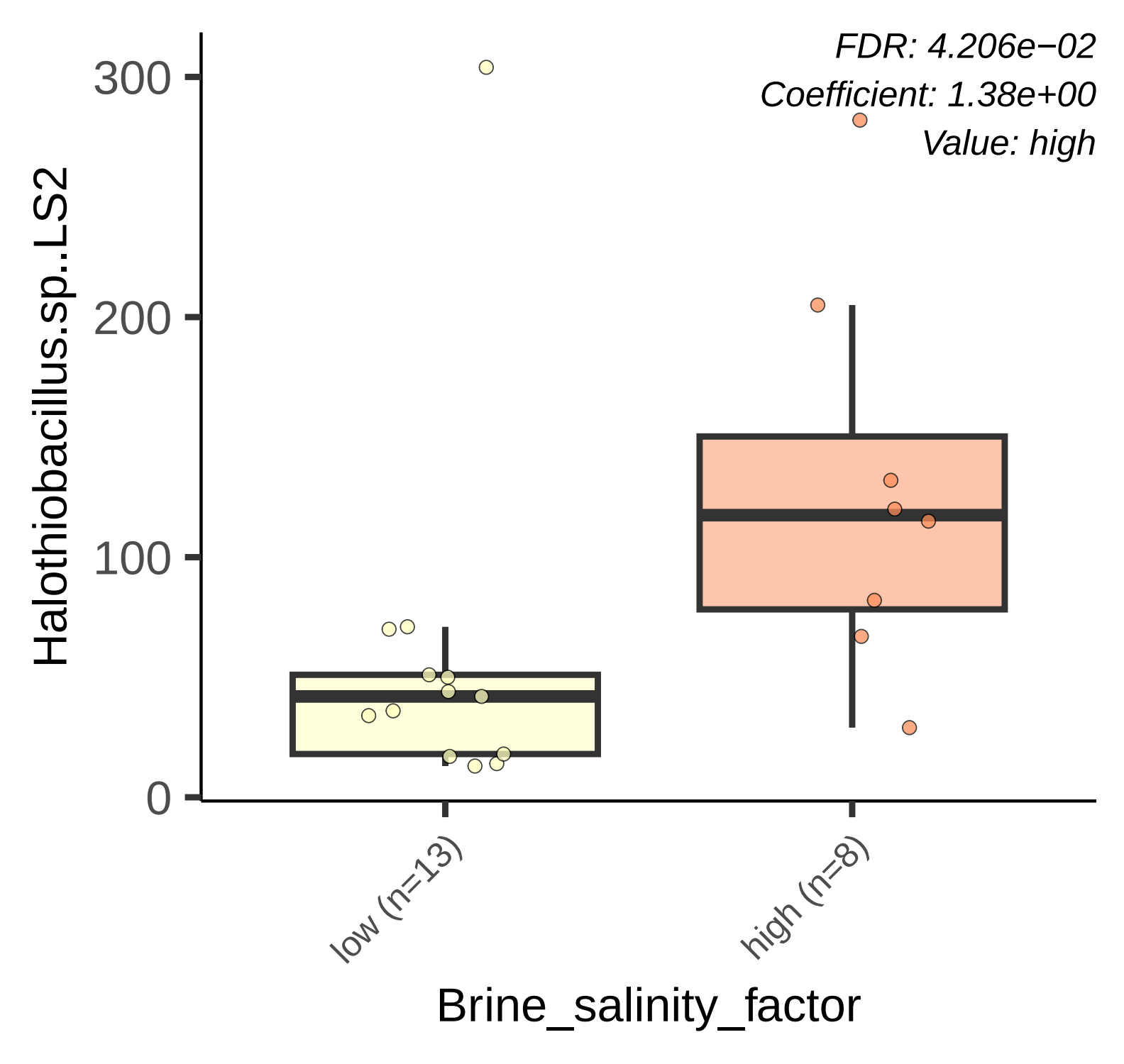

FDR: 3.789e−02
Coefficient: −2.93e−01
Value: high
1500
1200
900
600
Salipiger.profundus
low (n=13)
high (n=8)
Brine_salinity_factor

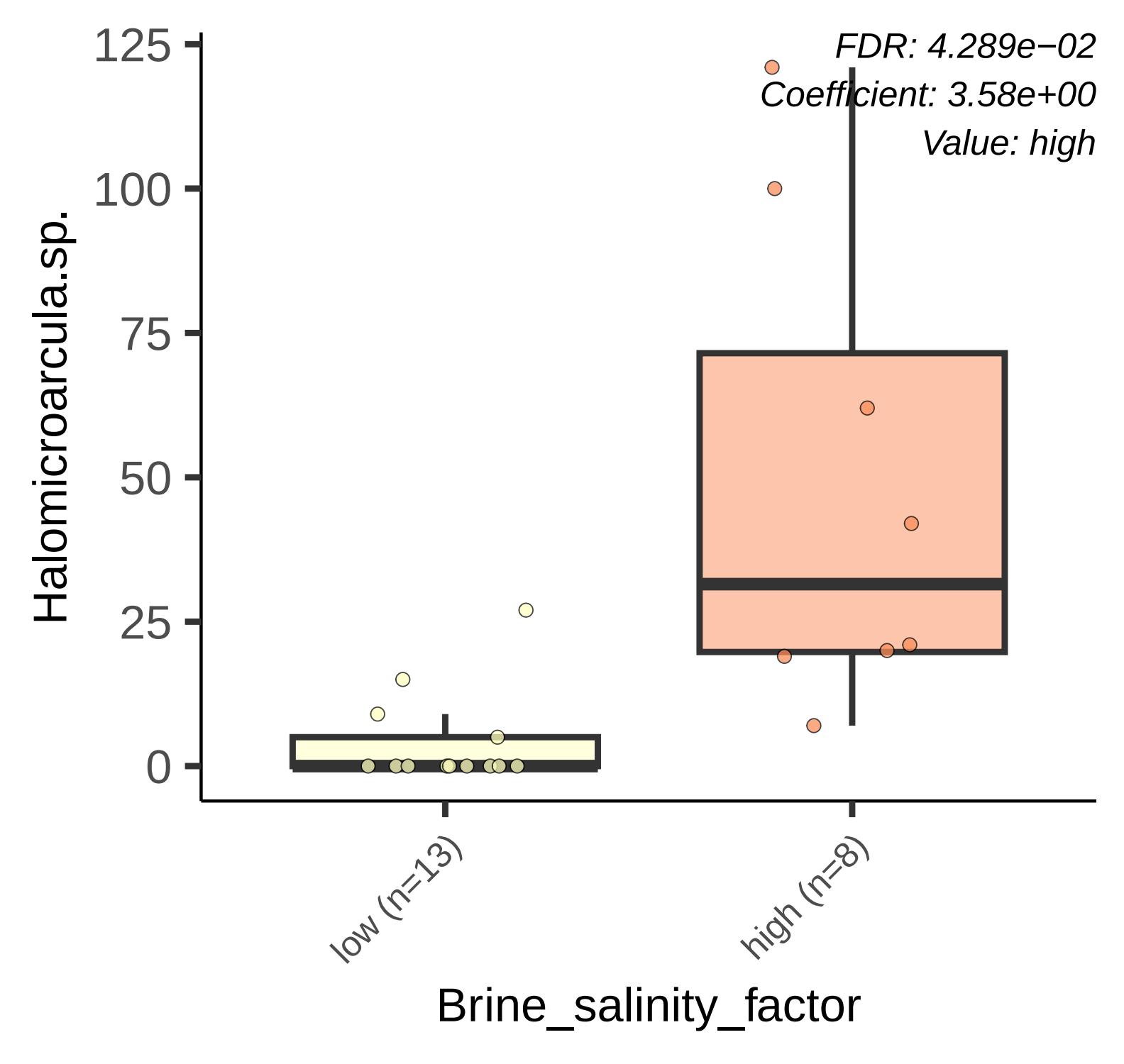

FDR: 3.899e−02
Coefficient: −1.68e+00
Value: high
Thalassiosira.oceanica
150
100
50
0
low (n=13)
high (n=8)
Brine_salinity_factor

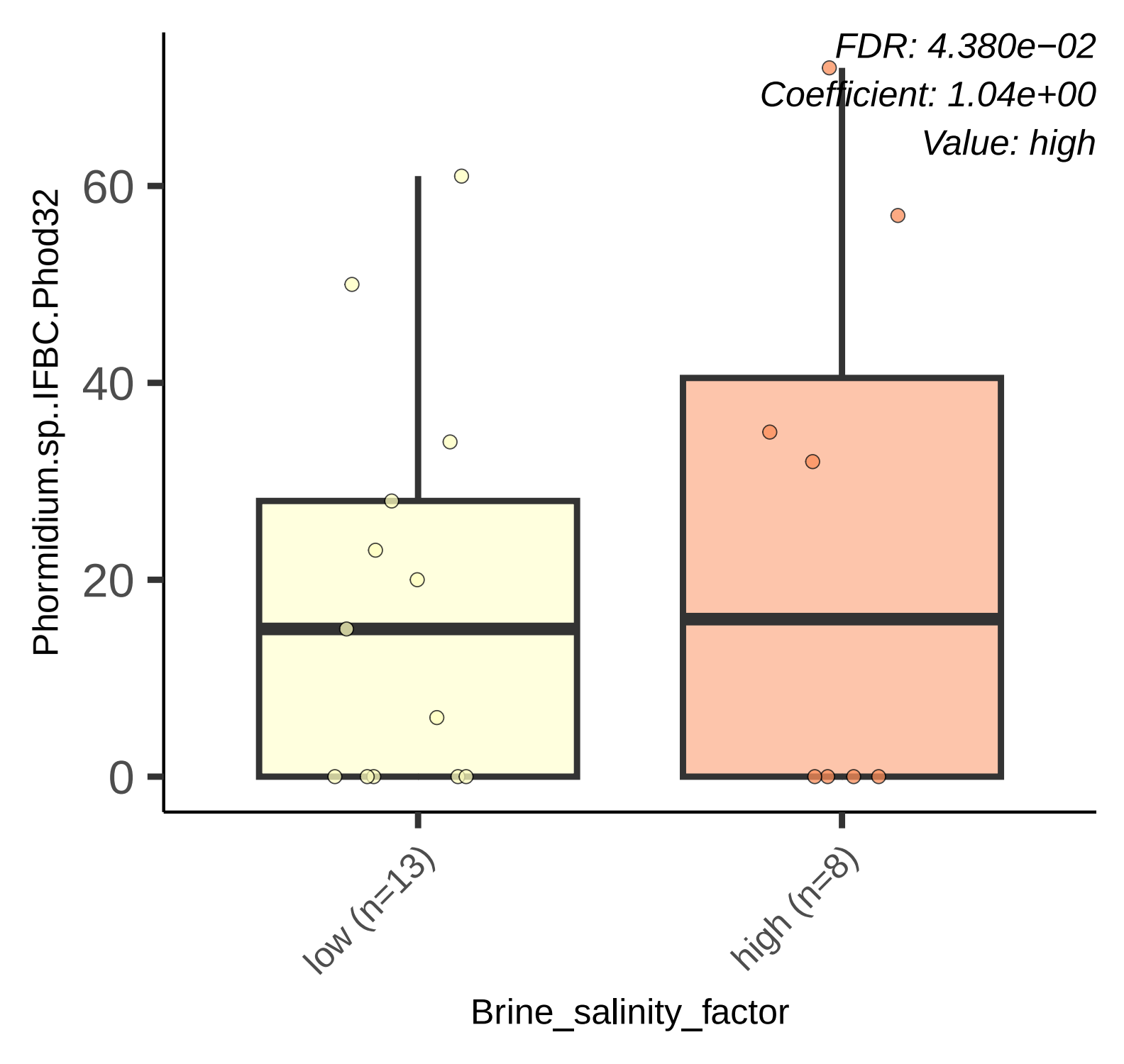

FDR: 3.939e−02
Coefficient: −9.12e−01
Value: high
Acidihalobacter.prosperus
400
300
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

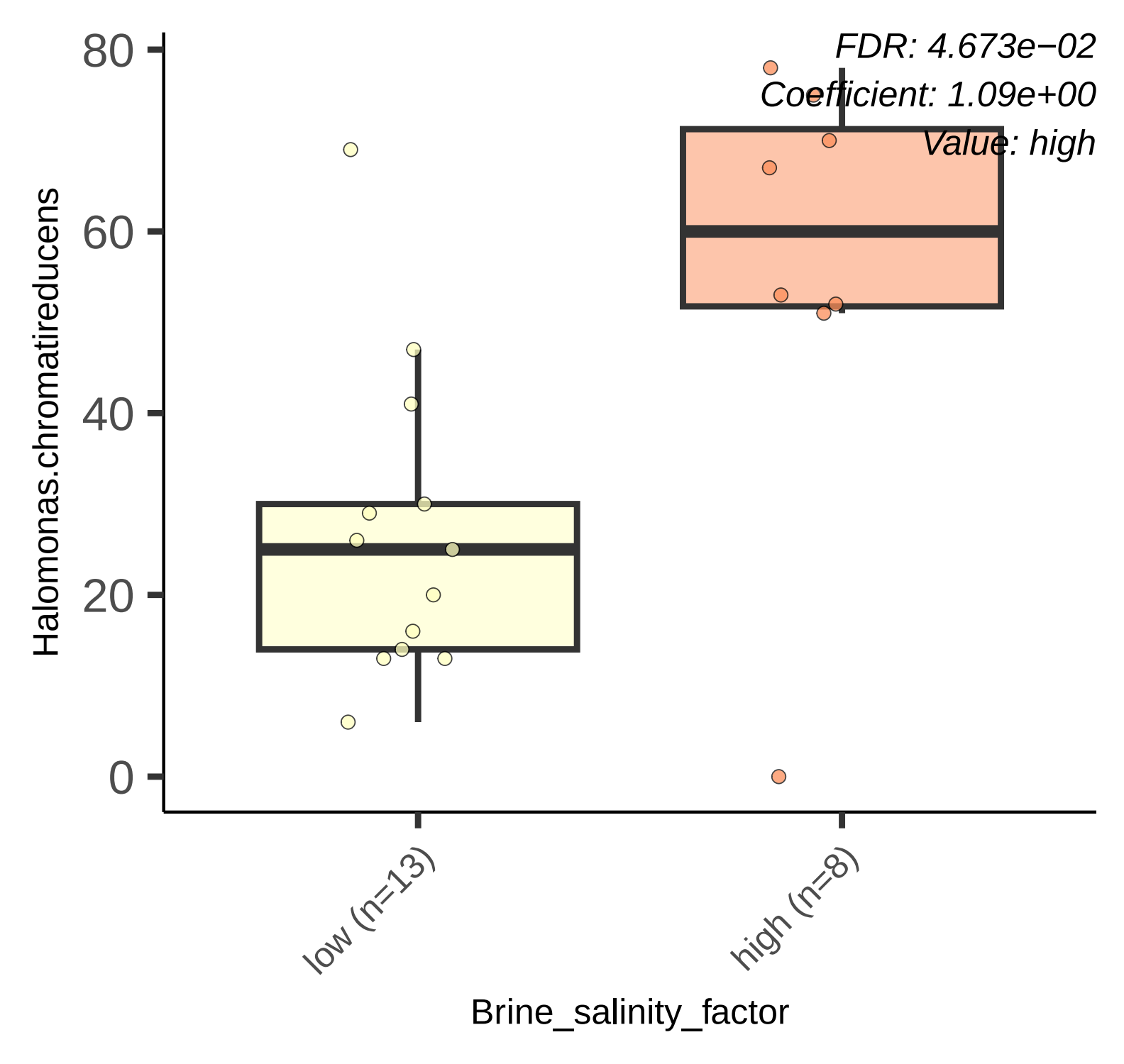

FDR: 4.030e−02
Coefficient: −4.03e−01
Value: high
Paracoccus.sp..CBA4604
1000
500
low (n=13)
high (n=8)
Brine_salinity_factor

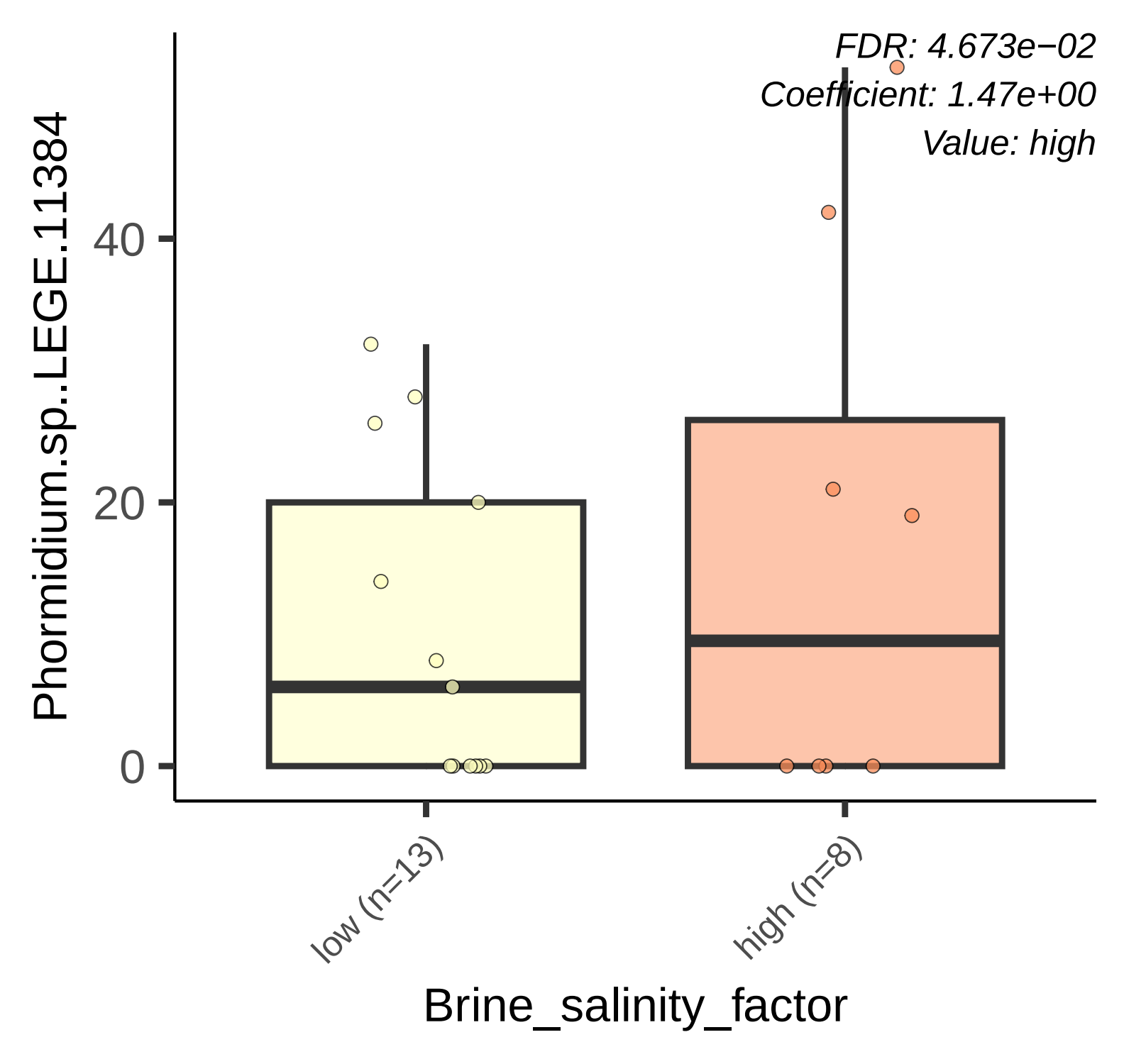

FDR: 4.184e−02
Coefficient: −1.95e+00
Value: high
Paraburkholderia.xenovorans
30
20
10
0
low (n=13)
high (n=8)
Brine_salinity_factor

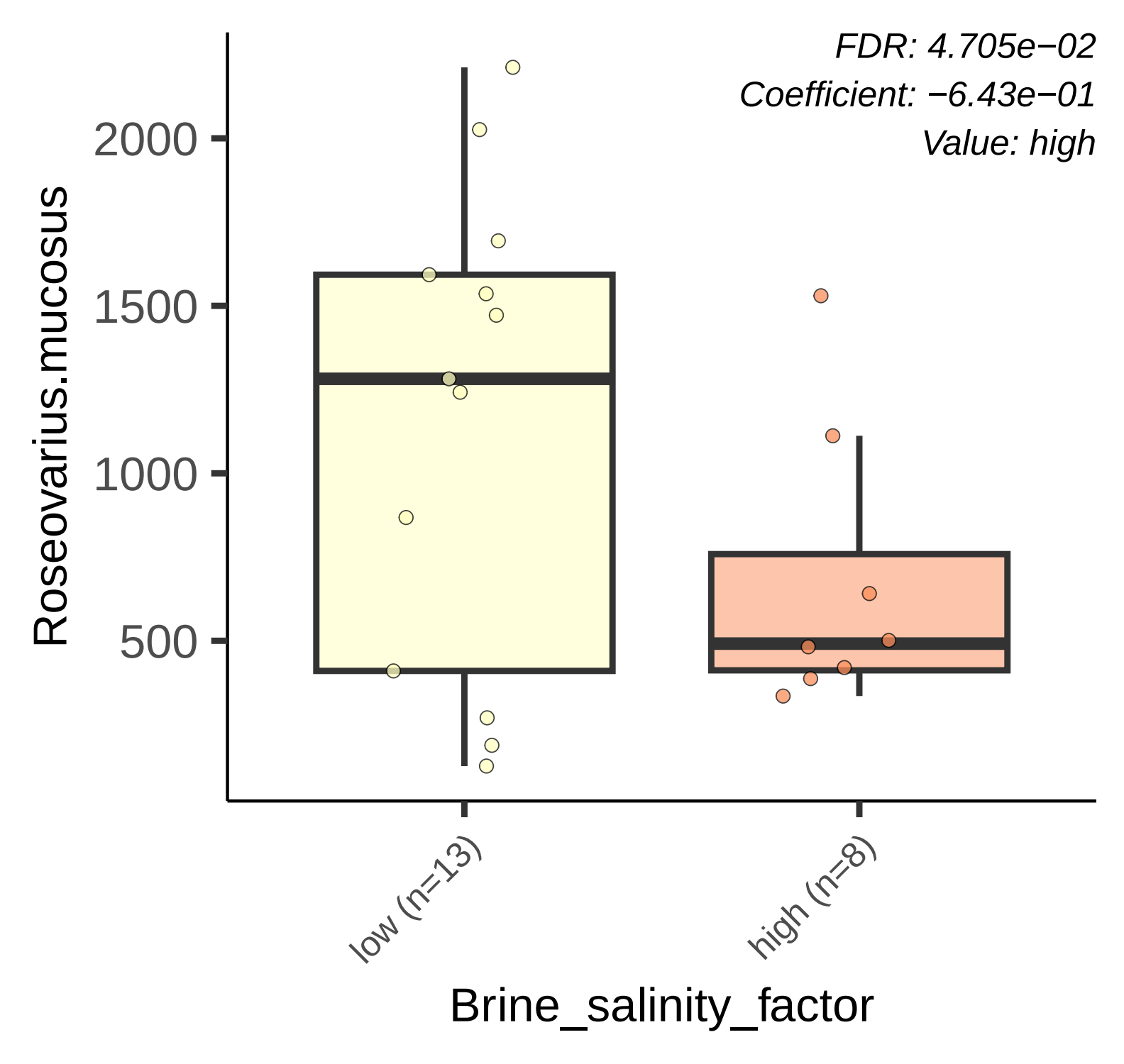

FDR: 4.206e−02
Coefficient: 1.38e+00
Value: high
Halothiobacillus.sp..LS2
300
200
100
0
low (n=13)
high (n=8)
Brine_salinity_factor

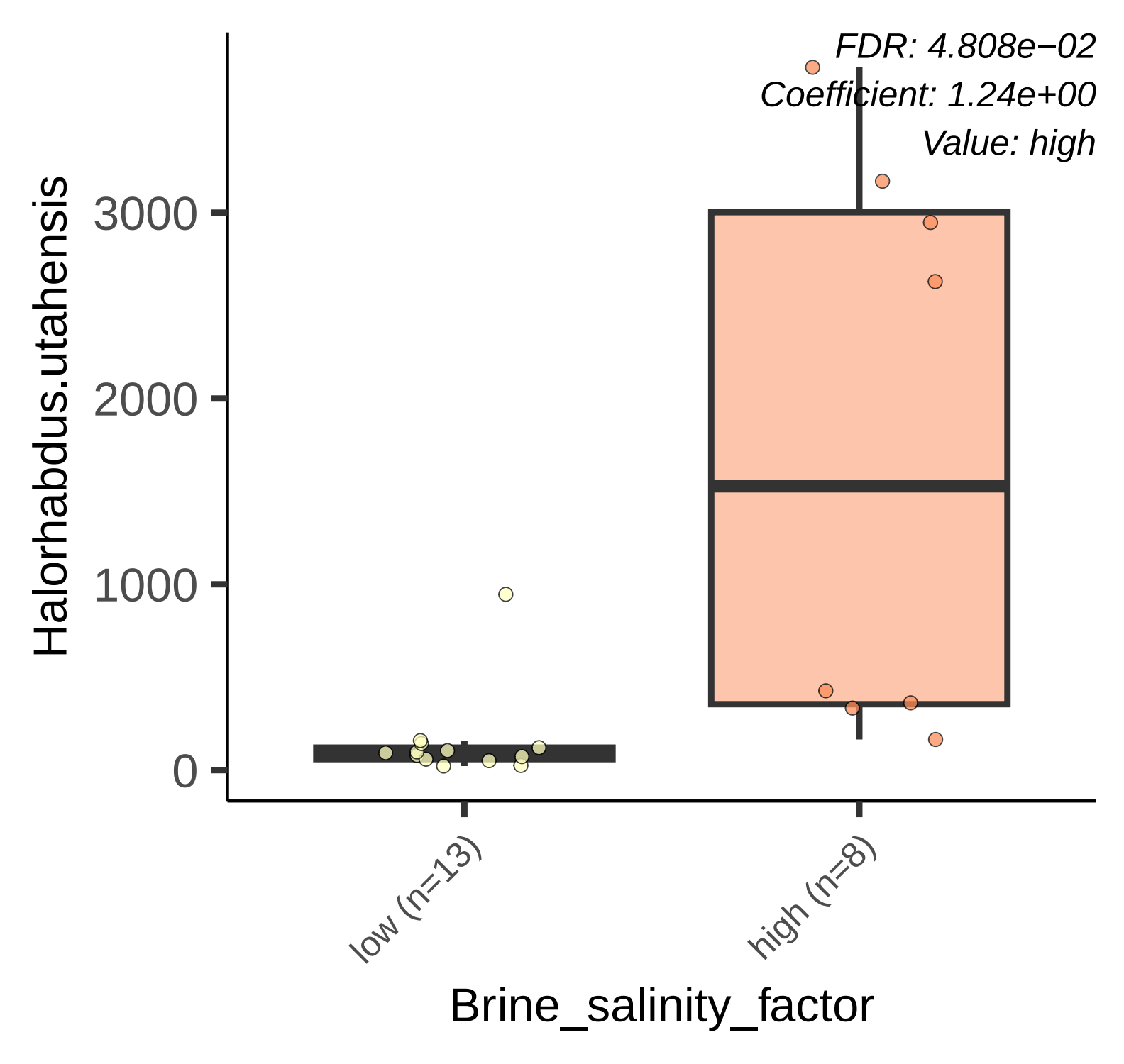

FDR: 4.289e−02
Coefficient: 3.58e+00
Value: high
125
100
75
50
25
0
Halomicroarcula.sp.
low (n=13)
high (n=8)
Brine_salinity_factor

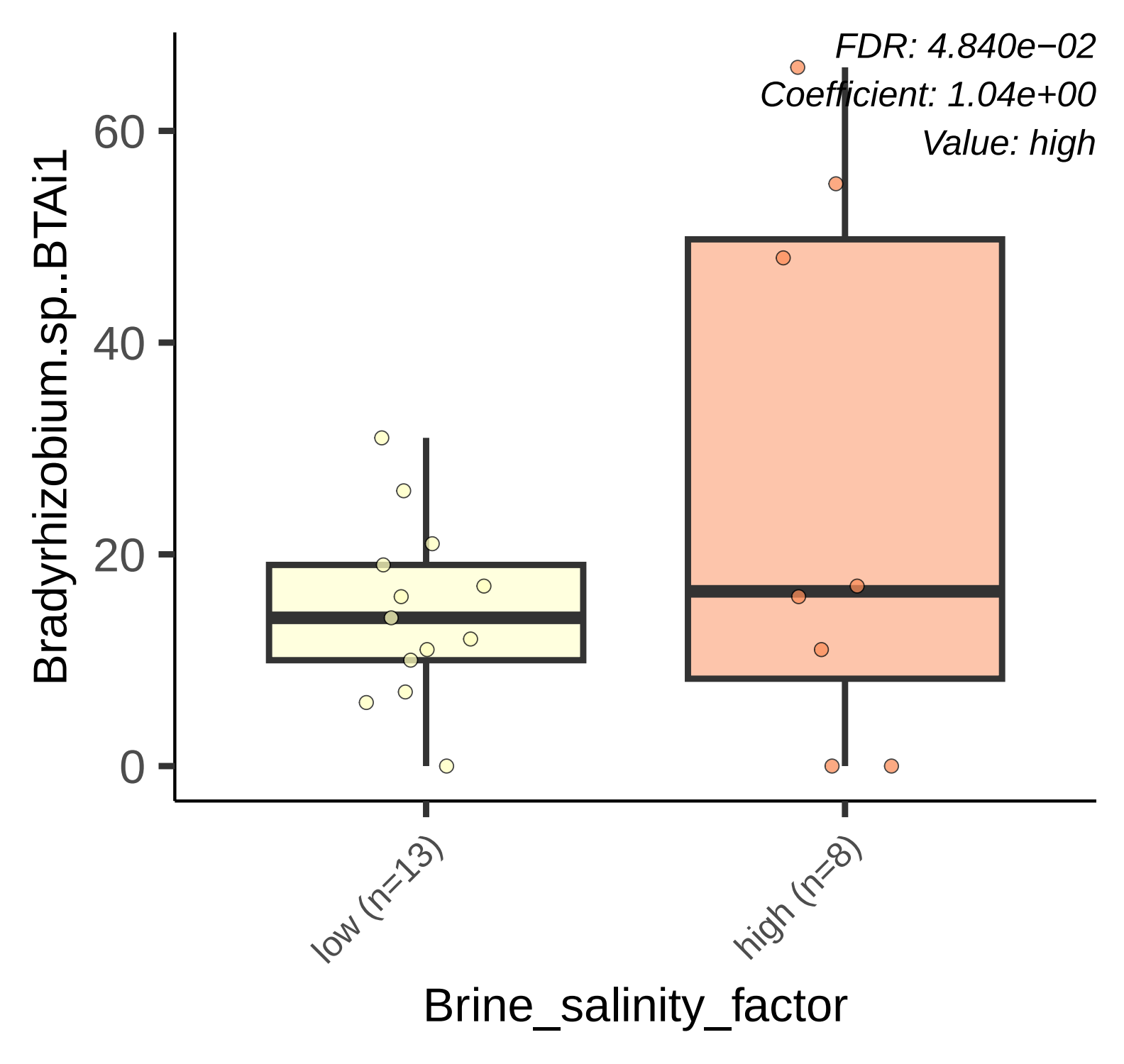

FDR: 4.380e−02
Coefficient: 1.04e+00
Value: high
Phormidium.sp..IFBC.Phod32
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor


FDR: 4.673e−02
Coefficient: 1.09e+00
Value: high
Halomonas.chromatireducens
80
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor


FDR: 4.673e−02
Coefficient: 1.47e+00
Value: high
Phormidium.sp..LEGE.11384
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor


FDR: 4.705e−02
Coefficient: −6.43e−01
Value: high
2000
1500
1000
500
Roseovarius.mucosus
low (n=13)
high (n=8)
Brine_salinity_factor


FDR: 4.808e−02
Coefficient: 1.24e+00
Value: high
Halorhabdus.utahensis
3000
2000
1000
0
low (n=13)
high (n=8)
Brine_salinity_factor


FDR: 4.840e−02
Coefficient: 1.04e+00
Value: high
Bradyrhizobium.sp..BTAi1
60
40
20
0
low (n=13)
high (n=8)
Brine_salinity_factor