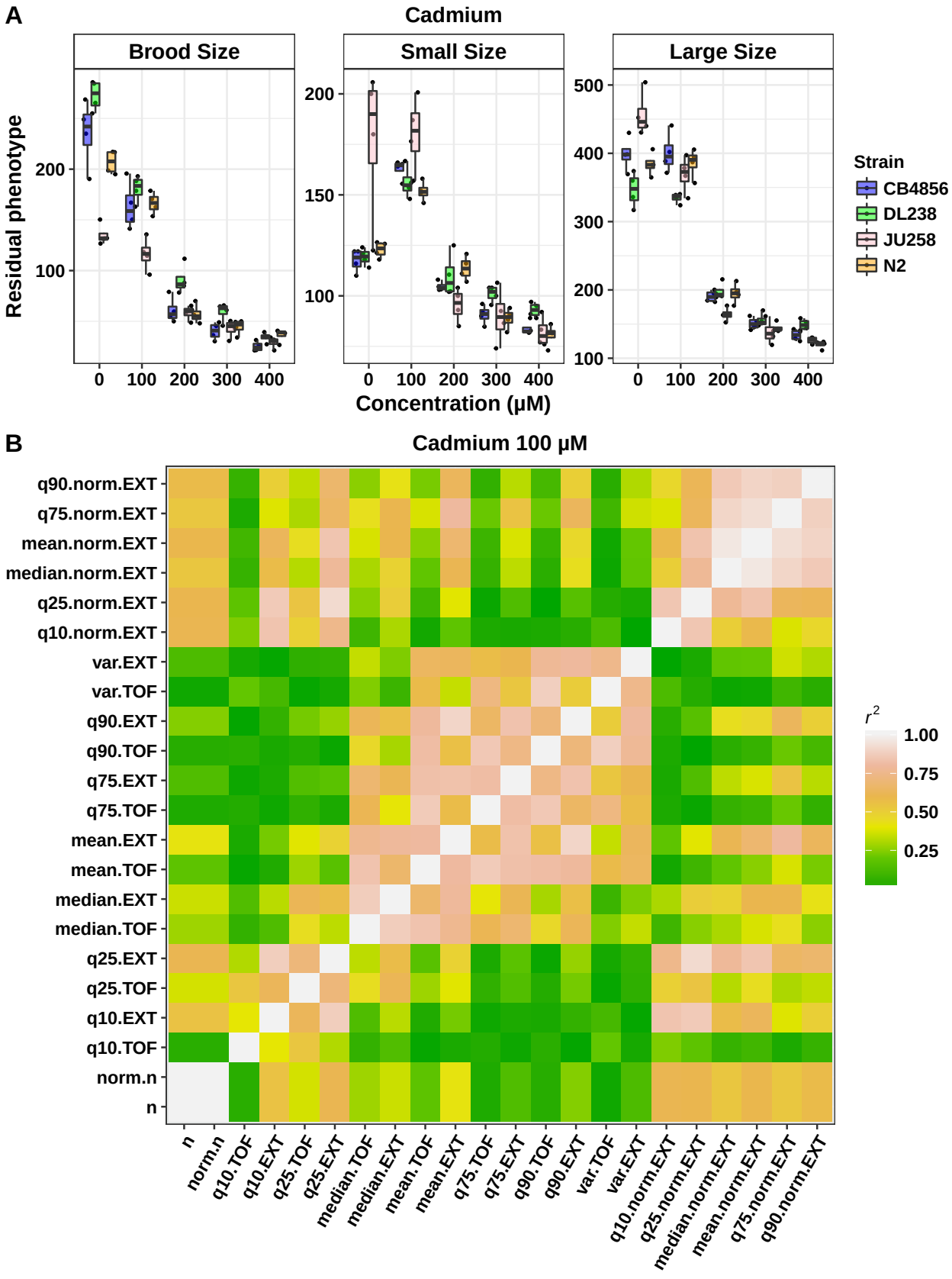
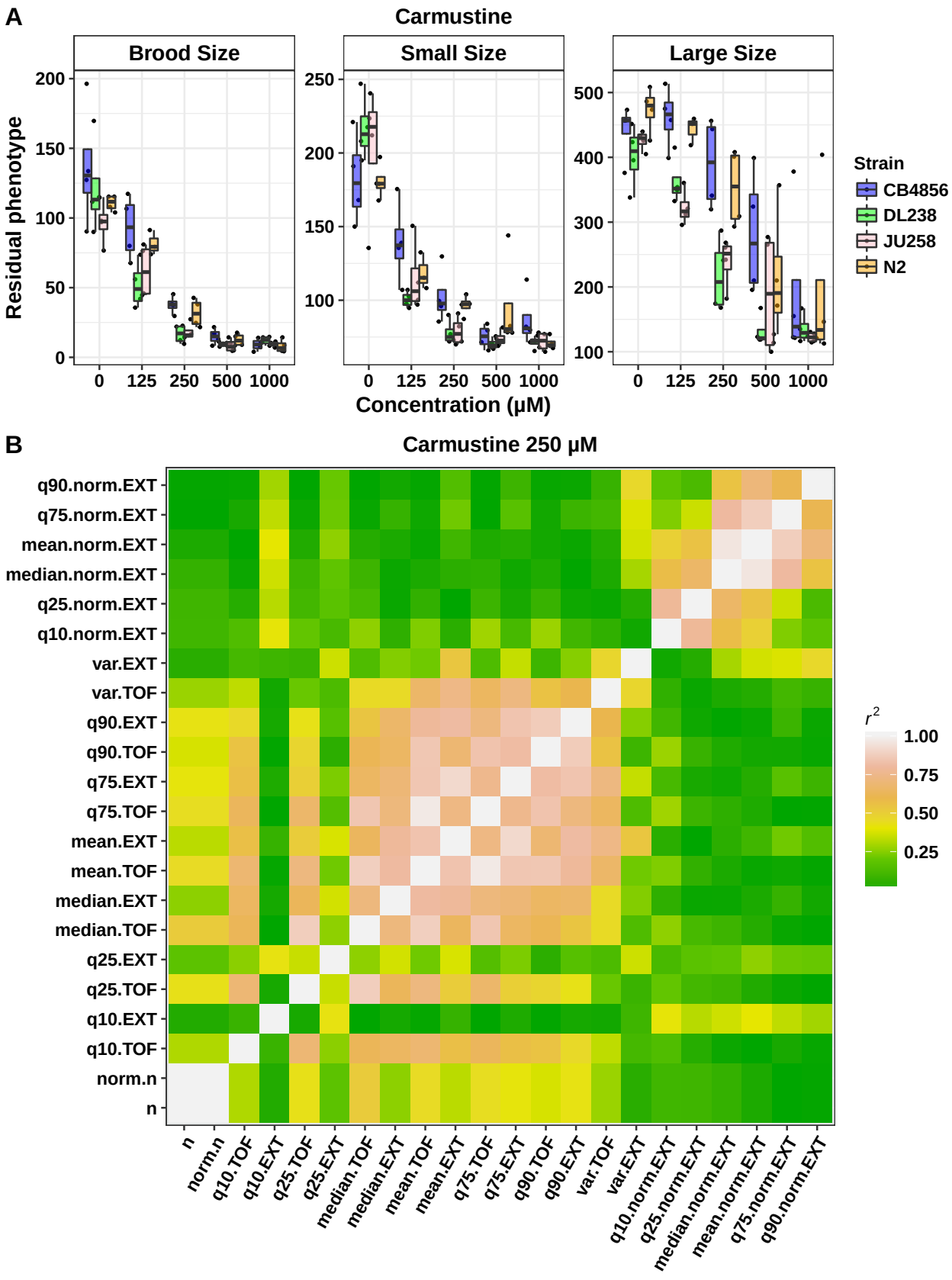
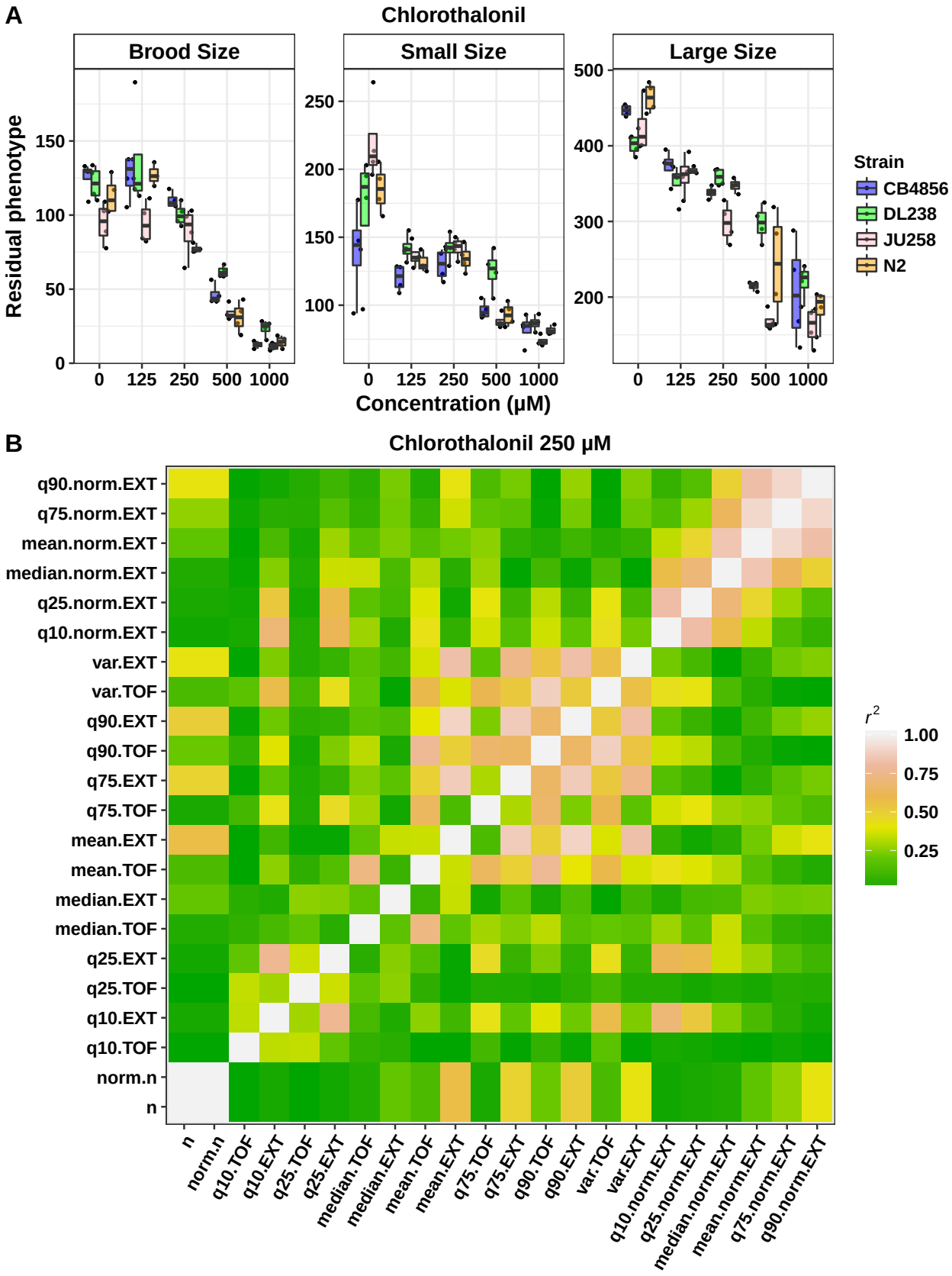
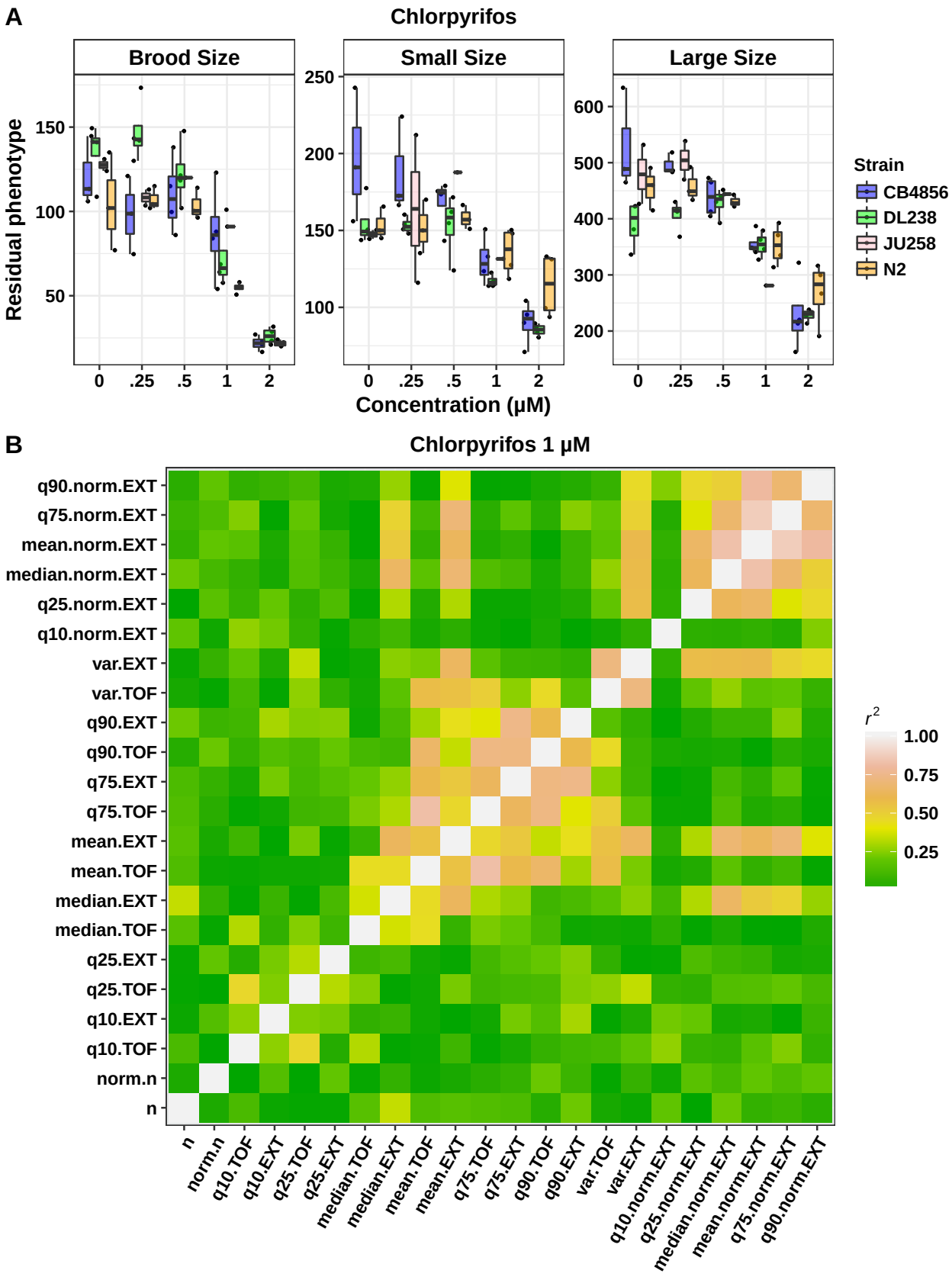
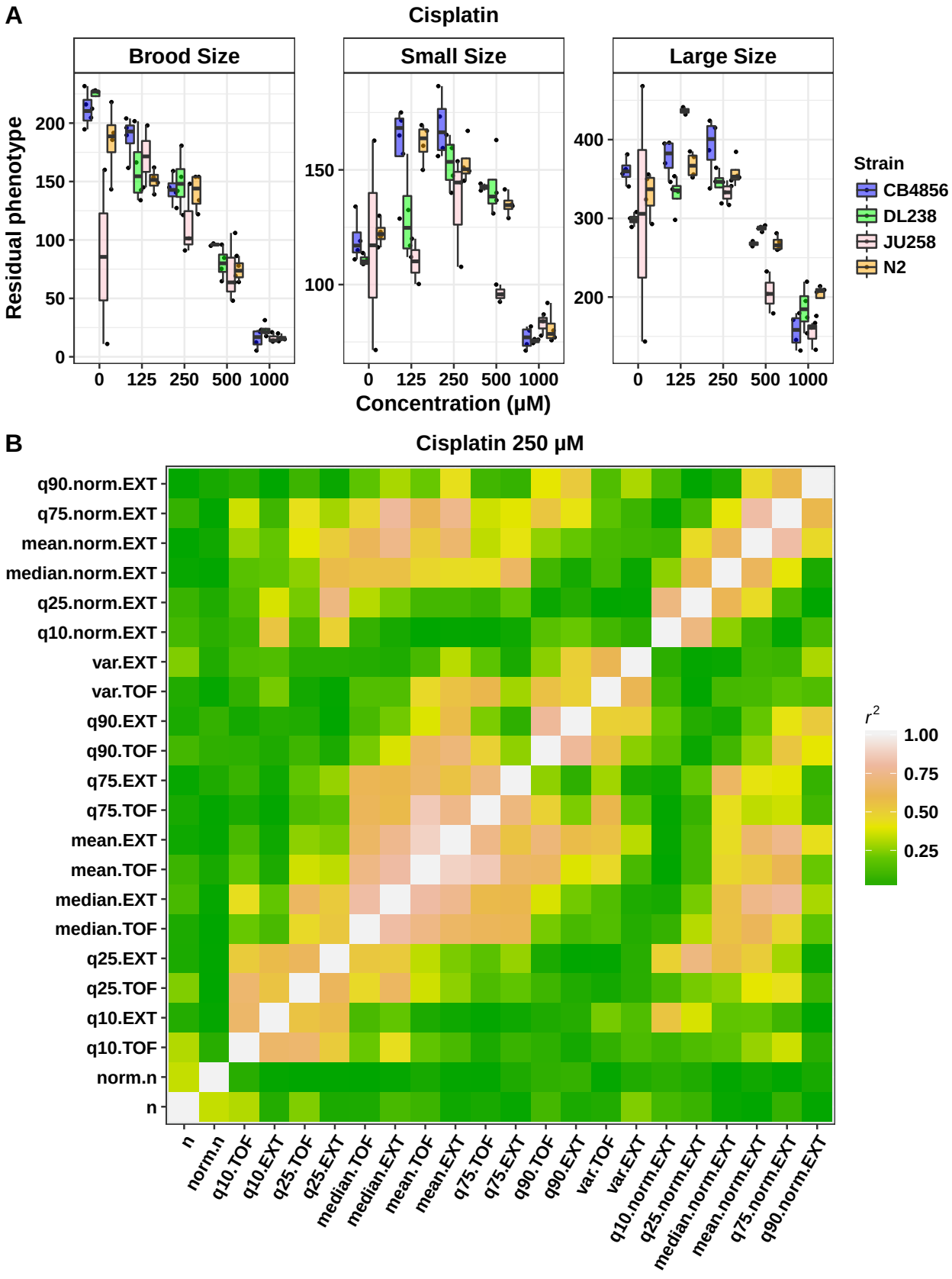
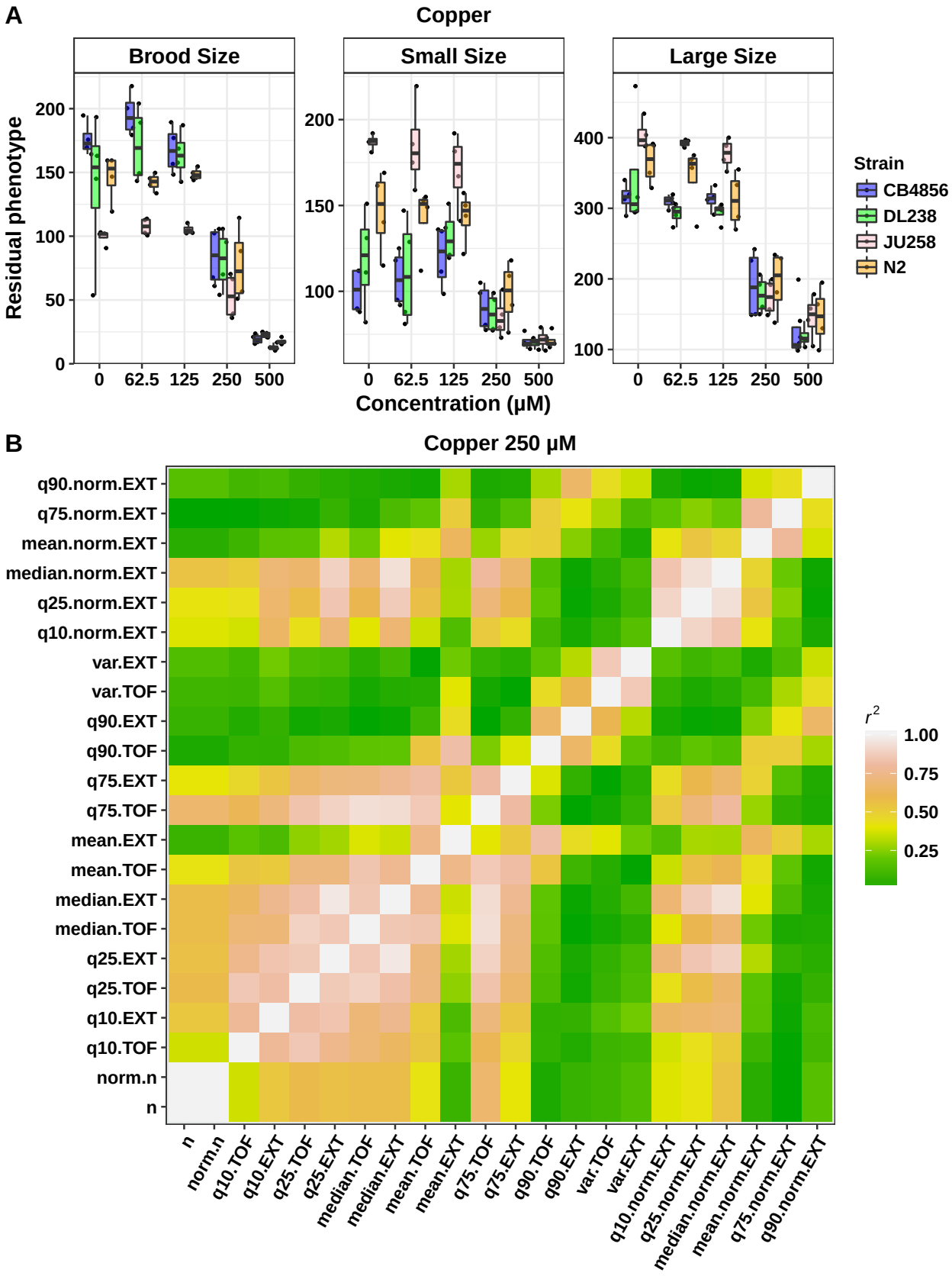

A
Cadmium
Brood Size
Small Size
Large Size
Residual phenotype
Concentration (µM)
Strain
CB4856
DL238
JU258
N2
B
Cadmium 100 µM
q90.norm.EXT
q75.norm.EXT
mean.norm.EXT
median.norm.EXT
q25.norm.EXT
q10.norm.EXT
var.EXT
var.TOF
q90.EXT
q90.TOF
q75.EXT
q75.TOF
mean.EXT
mean.TOF
median.EXT
median.TOF
q25.EXT
q25.TOF
q10.EXT
q10.TOF
norm.n
n
r2
1.00
0.75
0.50
0.25

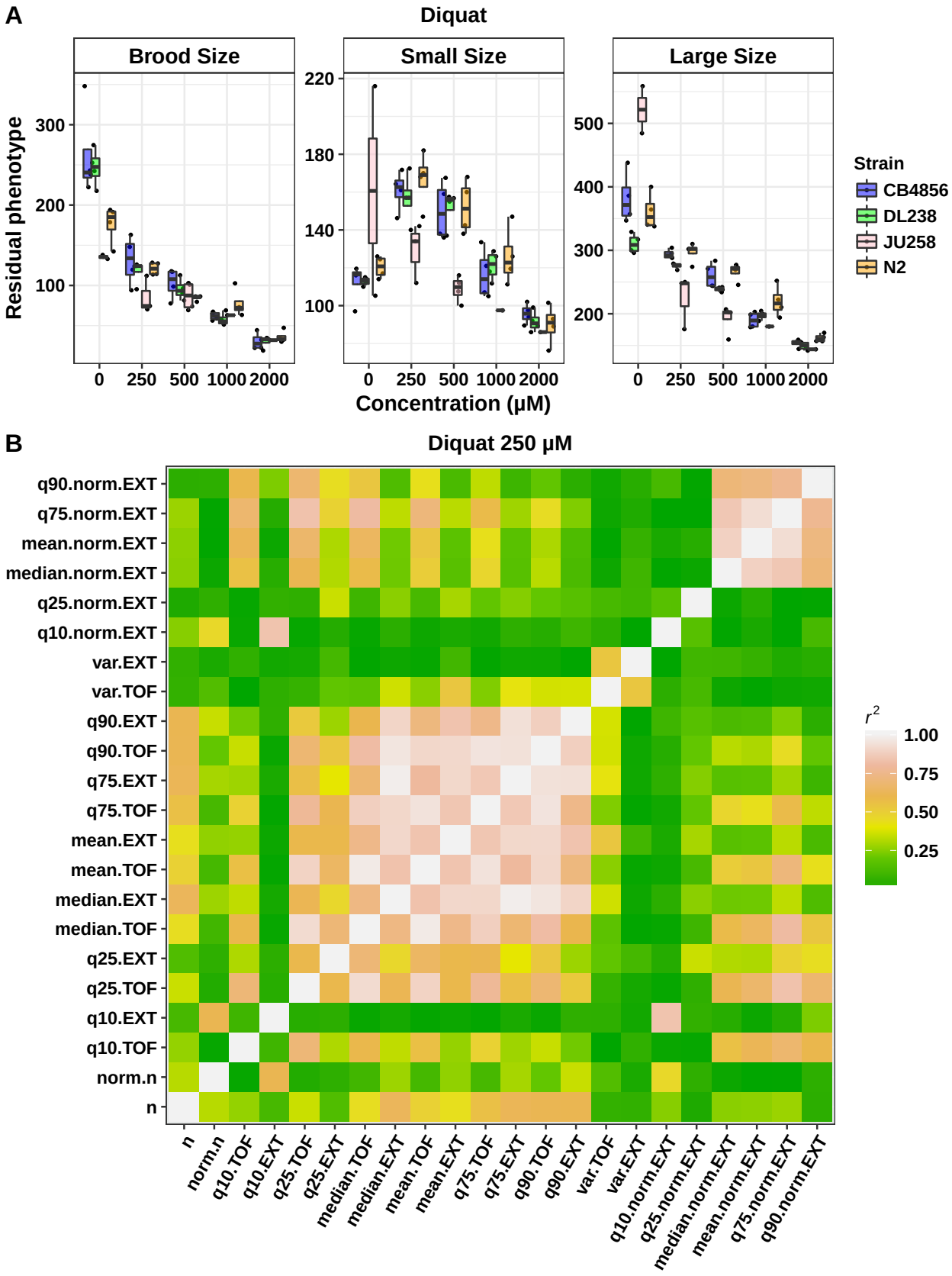

A
Carmustine
Brood Size
Small Size
Large Size
Residual phenotype
Concentration (μM)
Strain
CB4856
DL238
JU258
N2
B
Carmustine 250 μM
q90.norm.EXT
q75.norm.EXT
mean.norm.EXT
median.norm.EXT
q25.norm.EXT
q10.norm.EXT
var.EXT
var.TOF
q90.EXT
q90.TOF
q75.EXT
q75.TOF
mean.EXT
mean.TOF
median.EXT
median.TOF
q25.EXT
q25.TOF
q10.EXT
q10.TOF
norm.n
n
r2
1.00
0.75
0.50
0.25

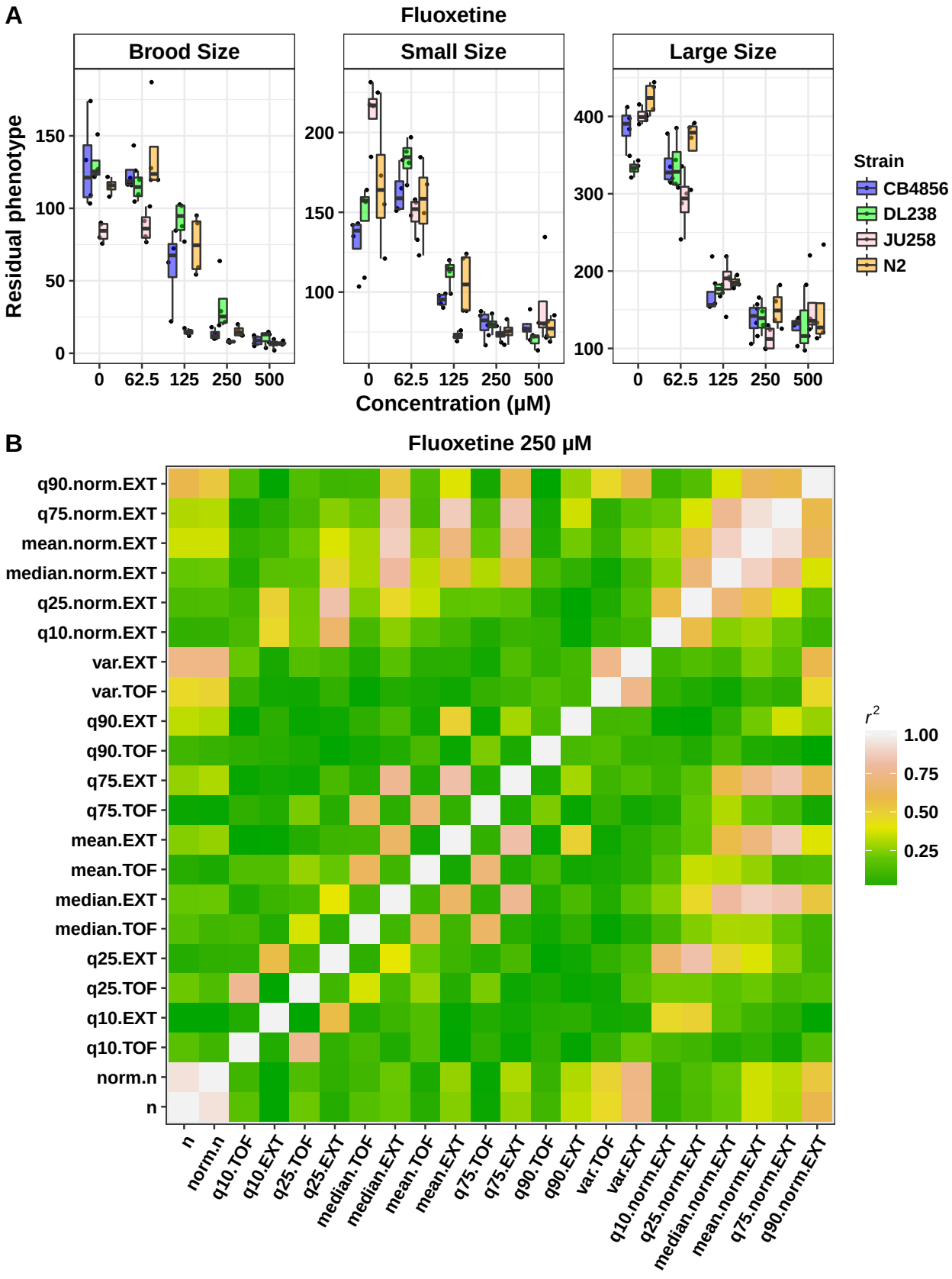

A
Chlorothalonil
Brood Size
Small Size
Large Size
Residual phenotype
Concentration (μM)
Strain
CB4856
DL238
JU258
N2
B
Chlorothalonil 250 μM
q90.norm.EXT
q75.norm.EXT
mean.norm.EXT
median.norm.EXT
q25.norm.EXT
q10.norm.EXT
var.EXT
var.TOF
q90.EXT
q90.TOF
q75.EXT
q75.TOF
mean.EXT
mean.TOF
median.EXT
median.TOF
q25.EXT
q25.TOF
q10.EXT
q10.TOF
norm.n
n
r2
1.00
0.75
0.50
0.25

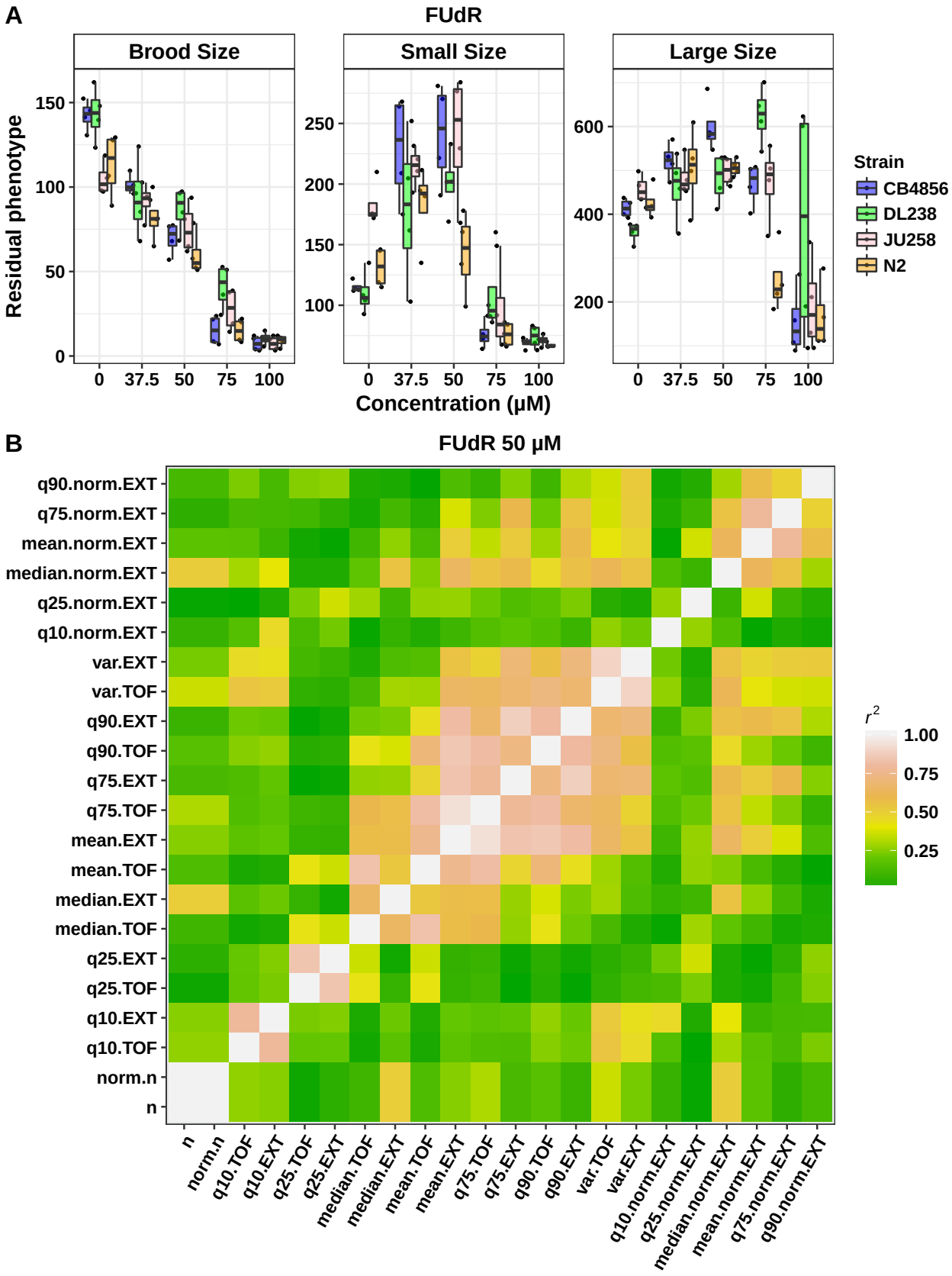

A
Chlorpyrifos
Brood Size
Small Size
Large Size
Residual phenotype
Concentration (µM)
Strain
CB4856
DL238
JU258
N2
B
Chlorpyrifos 1 µM
q90.norm.EXT
q75.norm.EXT
mean.norm.EXT
median.norm.EXT
q25.norm.EXT
q10.norm.EXT
var.EXT
var.TOF
q90.EXT
q90.TOF
q75.EXT
q75.TOF
mean.EXT
mean.TOF
median.EXT
median.TOF
q25.EXT
q25.TOF
q10.EXT
q10.TOF
norm.n
n
r^2
1.00
0.75
0.50
0.25

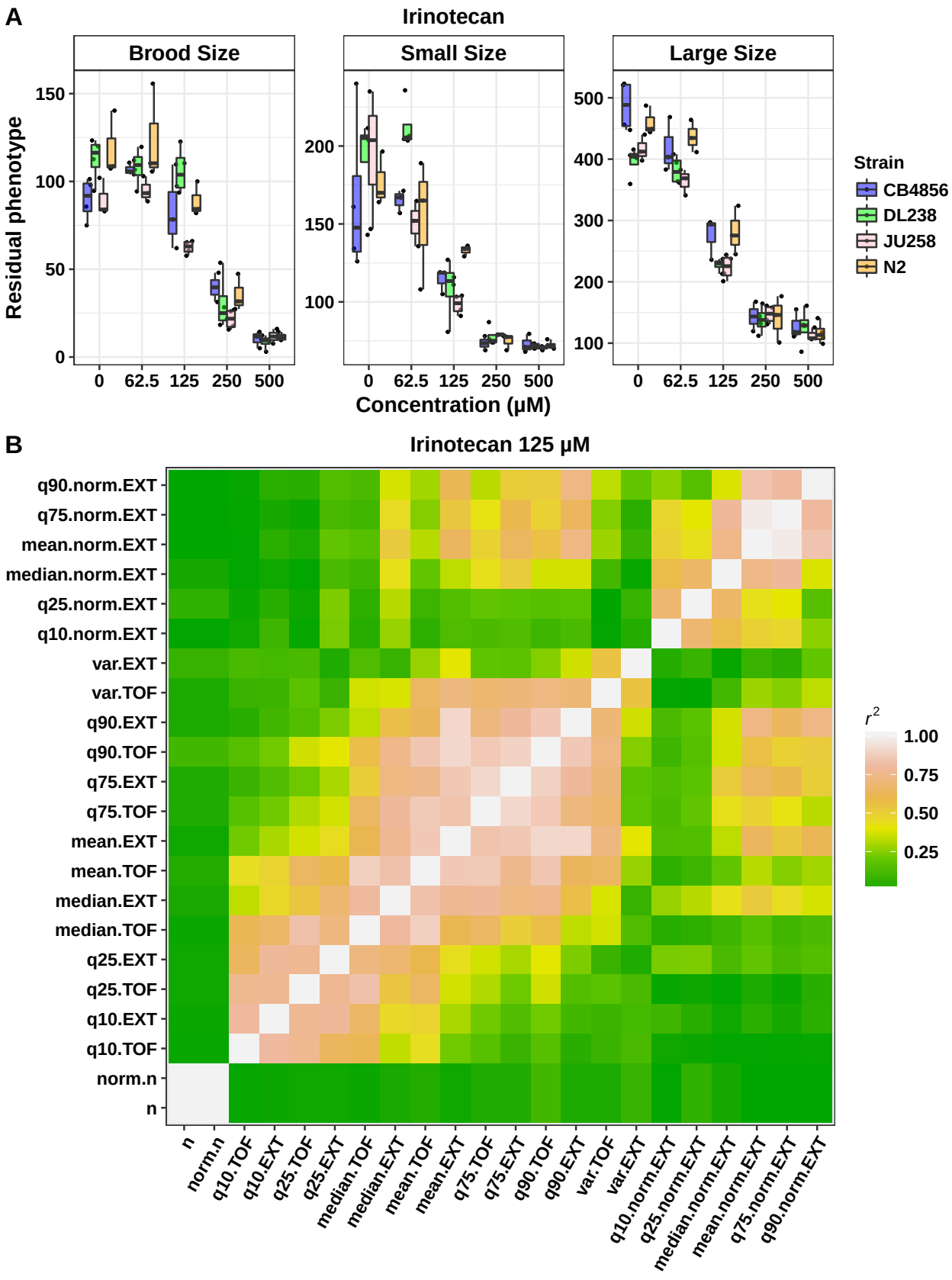

A
Cisplatin
Brood Size
Small Size
Large Size
Residual phenotype
Concentration (μM)
Strain
CB4856
DL238
JU258
N2
B
Cisplatin 250 μM
q90.norm.EXT
q75.norm.EXT
mean.norm.EXT
median.norm.EXT
q25.norm.EXT
q10.norm.EXT
var.EXT
var.TOF
q90.EXT
q90.TOF
q75.EXT
q75.TOF
mean.EXT
mean.TOF
median.EXT
median.TOF
q25.EXT
q25.TOF
q10.EXT
q10.TOF
norm.n
n
r^2
1.00
0.75
0.50
0.25

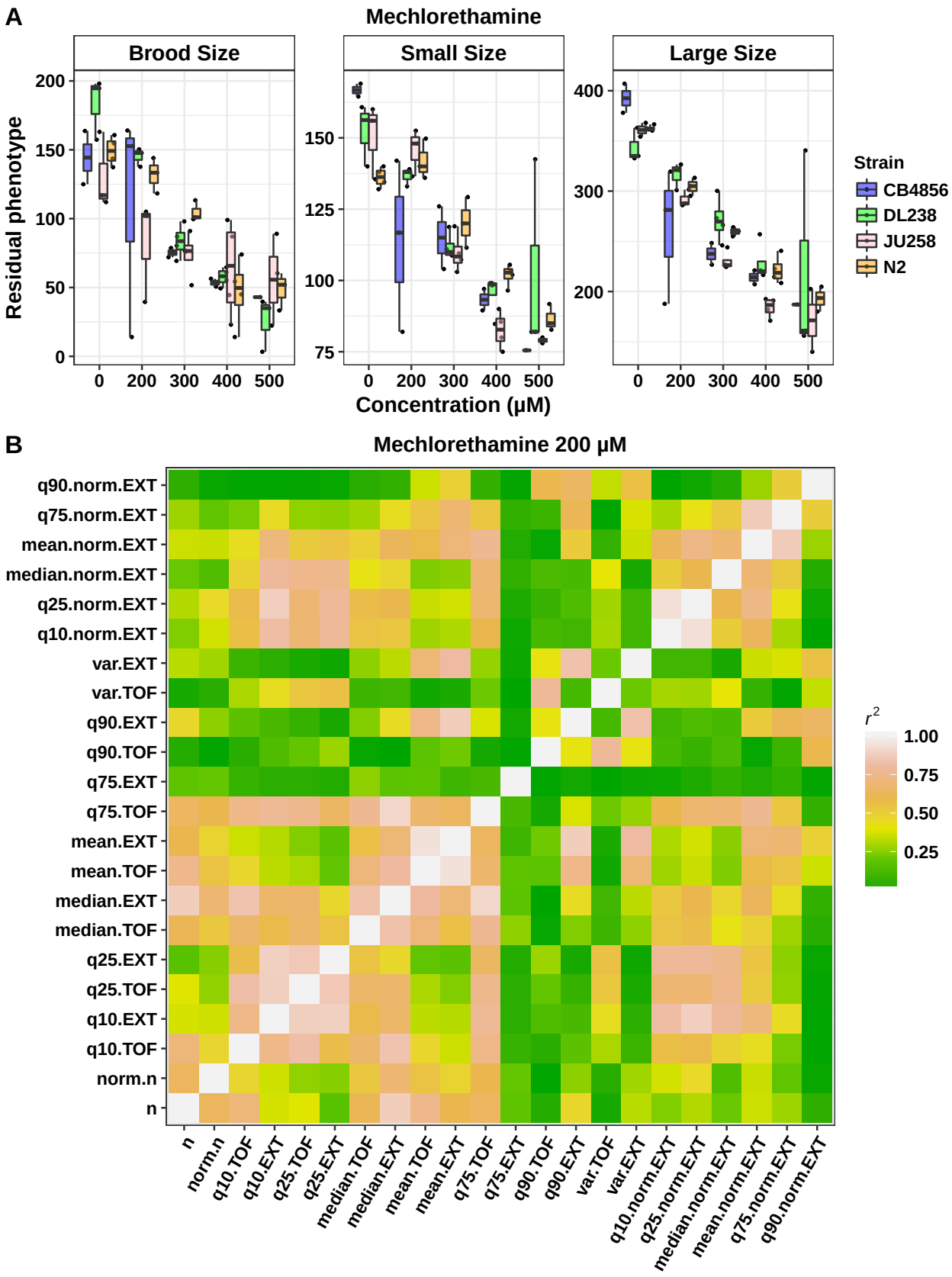

A
Copper
Brood Size
Small Size
Large Size
Residual phenotype
Concentration (μM)
0
62.5
125
250
500
Strain
CB4856
DL238
JU258
N2
B
Copper 250 μM
q90.norm.EXT
q75.norm.EXT
mean.norm.EXT
median.norm.EXT
q25.norm.EXT
q10.norm.EXT
var.EXT
var.TOF
q90.EXT
q90.TOF
q75.EXT
q75.TOF
mean.EXT
mean.TOF
median.EXT
median.TOF
q25.EXT
q25.TOF
q10.EXT
q10.TOF
norm.n
n
r^2
1.00
0.75
0.50
0.25

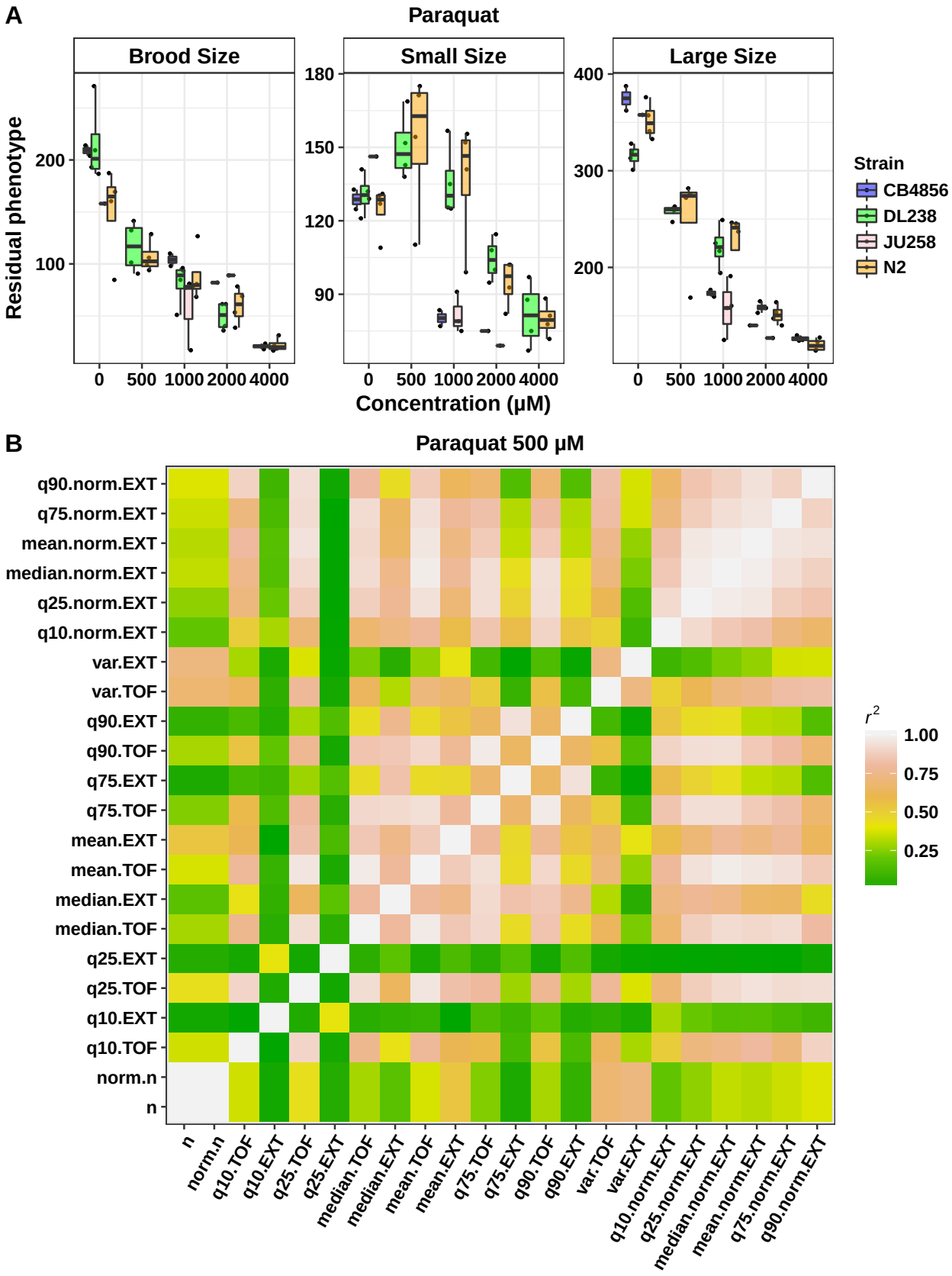

A
Diquat
Brood Size
Small Size
Large Size
Residual phenotype
Concentration (μM)
Strain
CB4856
DL238
JU258
N2
B
Diquat 250 μM
q90.norm.EXT
q75.norm.EXT
mean.norm.EXT
median.norm.EXT
q25.norm.EXT
q10.norm.EXT
var.EXT
var.TOF
q90.EXT
q90.TOF
q75.EXT
q75.TOF
mean.EXT
mean.TOF
median.EXT
median.TOF
q25.EXT
q25.TOF
q10.EXT
q10.TOF
norm.n
n
r2
1.00
0.75
0.50
0.25

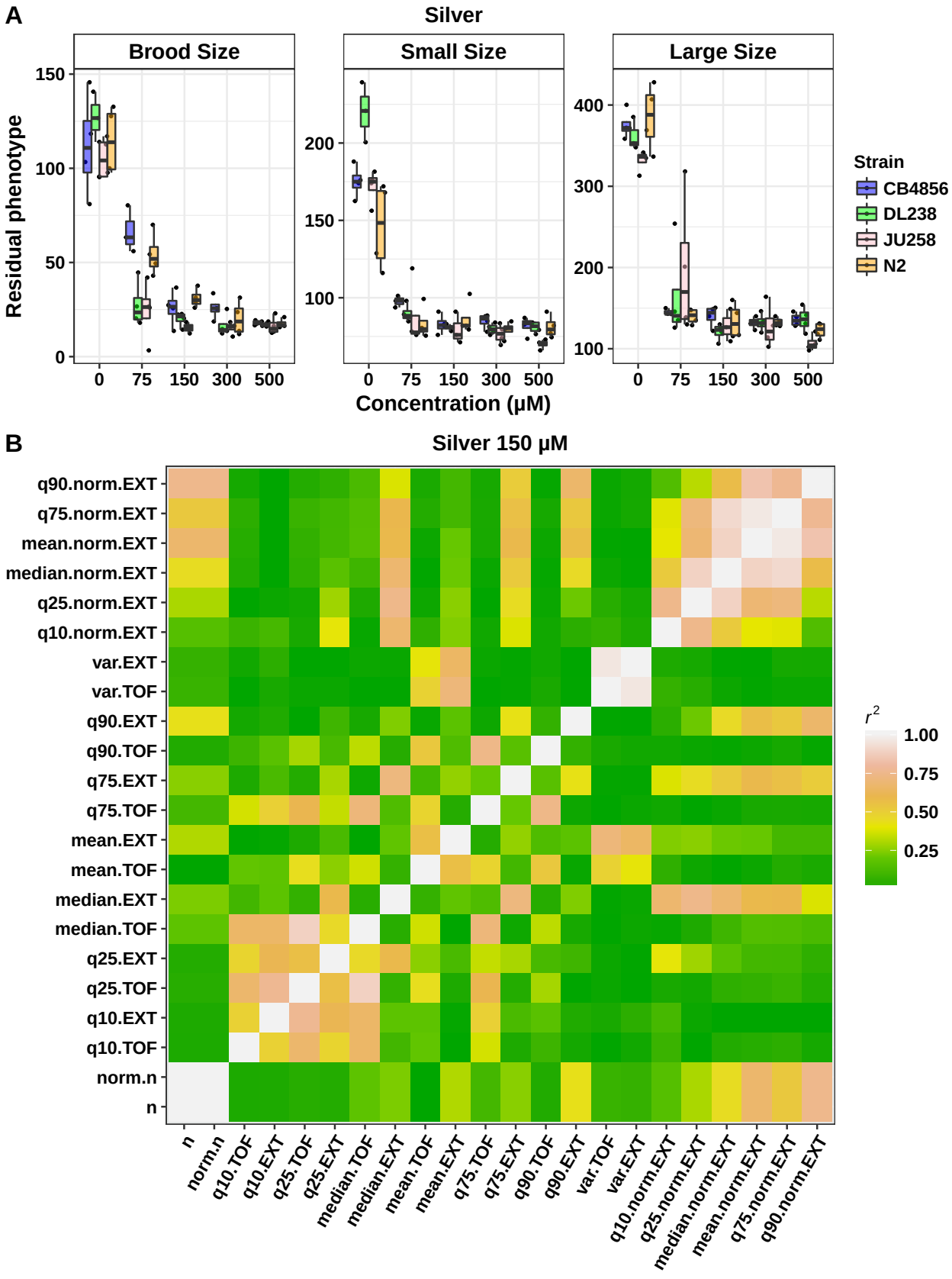

A
Fluoxetine
Brood Size
Small Size
Large Size
Residual phenotype
Concentration (μM)
0
62.5
125
250
500
Strain
CB4856
DL238
JU258
N2
B
Fluoxetine 250 μM
q90.norm.EXT
q75.norm.EXT
mean.norm.EXT
median.norm.EXT
q25.norm.EXT
q10.norm.EXT
var.EXT
var.TOF
q90.EXT
q90.TOF
q75.EXT
q75.TOF
mean.EXT
mean.TOF
median.EXT
median.TOF
q25.EXT
q25.TOF
q10.EXT
q10.TOF
norm.n
n
r^2
1.00
0.75
0.50
0.25

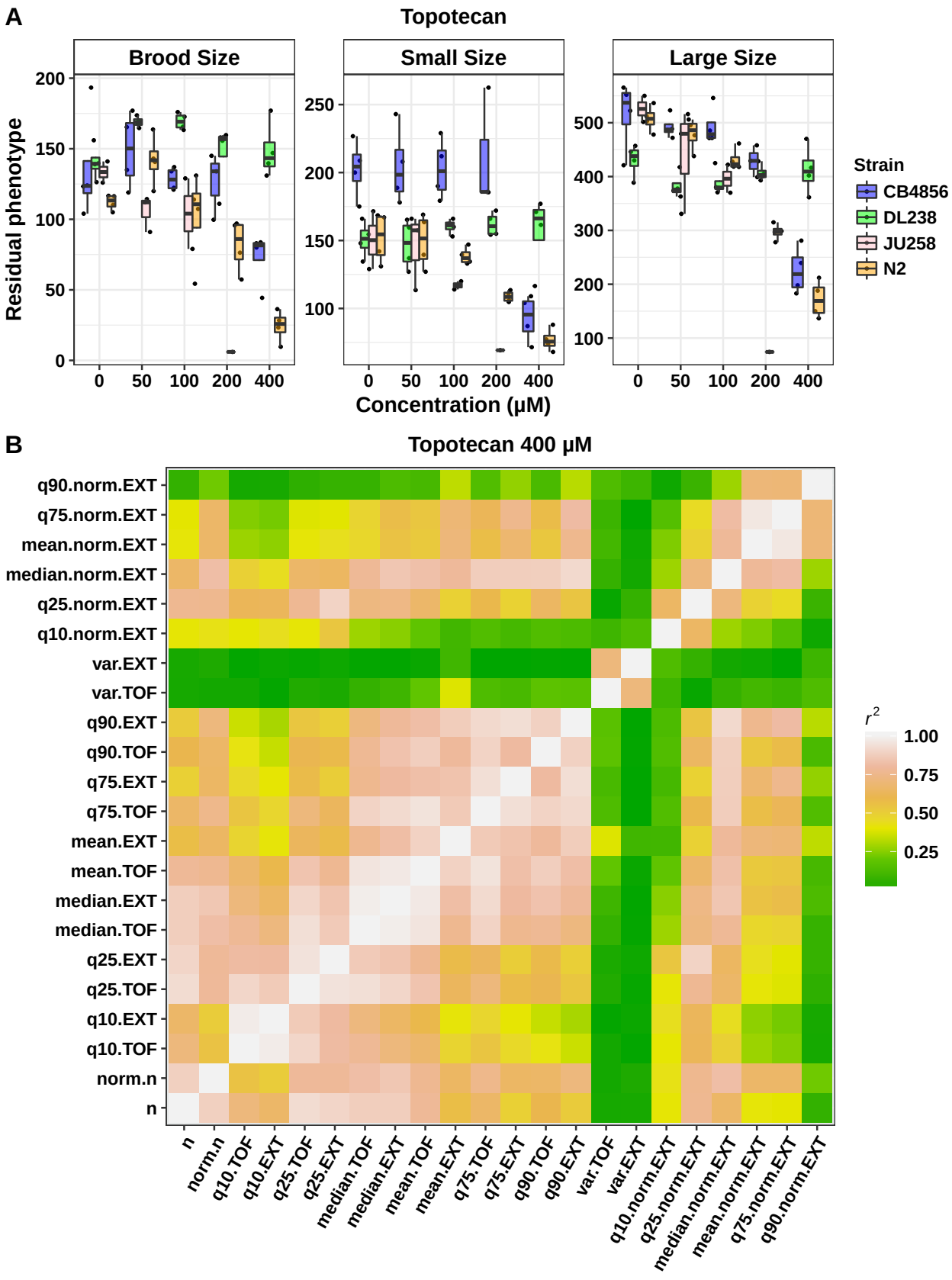

A
FUdR
Brood Size
Small Size
Large Size
Residual phenotype
Concentration (μM)
Strain
CB4856
DL238
JU258
N2
B
FUdR 50 μM
q90.norm.EXT
q75.norm.EXT
mean.norm.EXT
median.norm.EXT
q25.norm.EXT
q10.norm.EXT
var.EXT
var.TOF
q90.EXT
q90.TOF
q75.EXT
q75.TOF
mean.EXT
mean.TOF
median.EXT
median.TOF
q25.EXT
q25.TOF
q10.EXT
q10.TOF
norm.n
n
r2
1.00
0.75
0.50
0.25

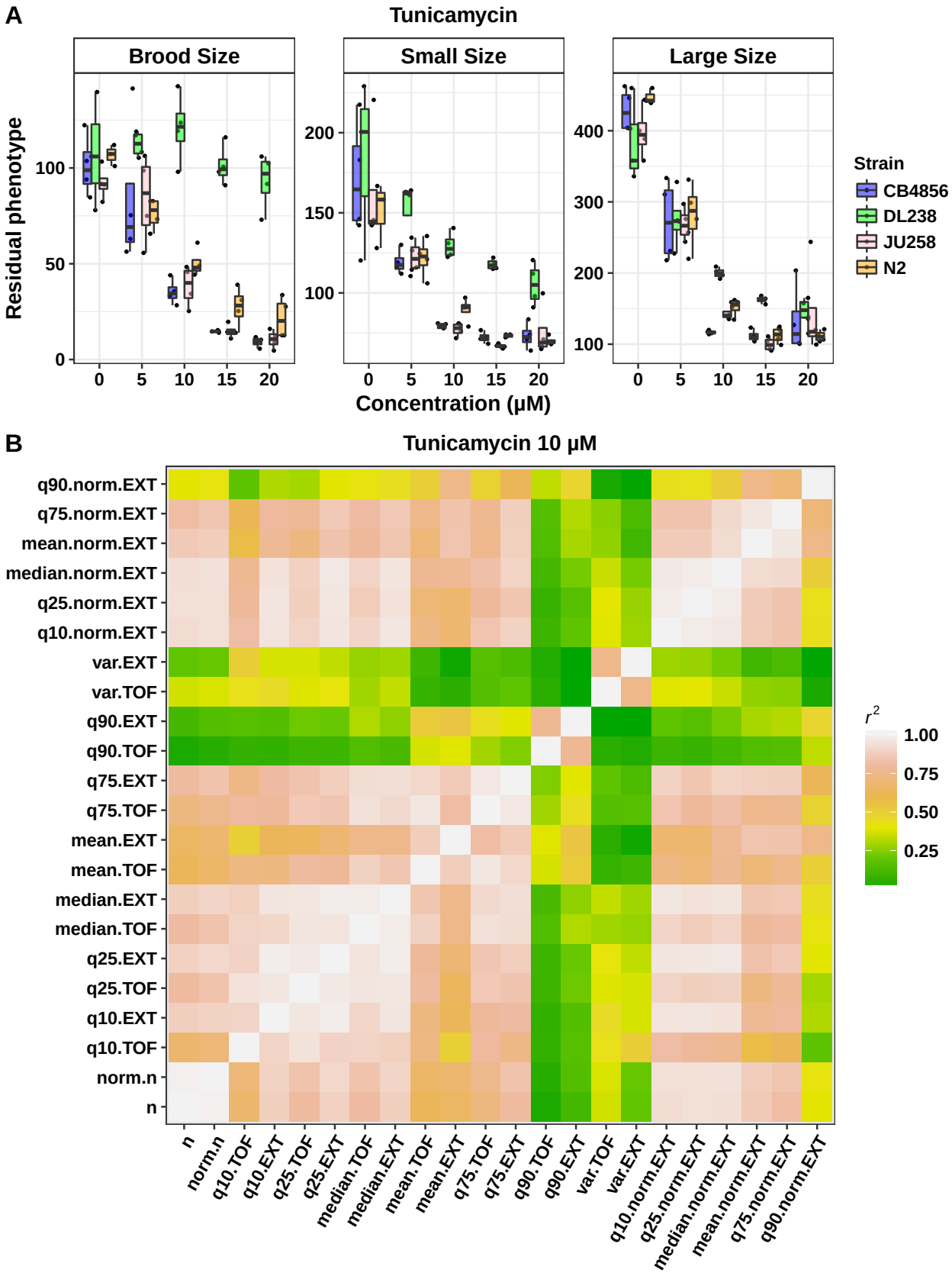

A
Irinotecan
Brood Size
Small Size
Large Size
Residual phenotype
Concentration (μM)
Strain
CB4856
DL238
JU258
N2
B
Irinotecan 125 μM
q90.norm.EXT
q75.norm.EXT
mean.norm.EXT
median.norm.EXT
q25.norm.EXT
q10.norm.EXT
var.EXT
var.TOF
q90.EXT
q90.TOF
q75.EXT
q75.TOF
mean.EXT
mean.TOF
median.EXT
median.TOF
q25.EXT
q25.TOF
q10.EXT
q10.TOF
norm.n
n
r^2
1.00
0.75
0.50
0.25


A
Mechlorethamine
Brood Size
Small Size
Large Size
Residual phenotype
Concentration (μM)
Strain
CB4856
DL238
JU258
N2
B
Mechlorethamine 200 μM
q90.norm.EXT
q75.norm.EXT
mean.norm.EXT
median.norm.EXT
q25.norm.EXT
q10.norm.EXT
var.EXT
var.TOF
q90.EXT
q90.TOF
q75.EXT
q75.TOF
mean.EXT
mean.TOF
median.EXT
median.TOF
q25.EXT
q25.TOF
q10.EXT
q10.TOF
norm.n
n
r2
1.00
0.75
0.50
0.25


A
Paraquat
Brood Size
Small Size
Large Size
Residual phenotype
Concentration (μM)
Strain
CB4856
DL238
JU258
N2
B
Paraquat 500 μM
q90.norm.EXT
q75.norm.EXT
mean.norm.EXT
median.norm.EXT
q25.norm.EXT
q10.norm.EXT
var.EXT
var.TOF
q90.EXT
q90.TOF
q75.EXT
q75.TOF
mean.EXT
mean.TOF
median.EXT
median.TOF
q25.EXT
q25.TOF
q10.EXT
q10.TOF
norm.n
n
r^2
1.00
0.75
0.50
0.25


A
Silver
Brood Size
Small Size
Large Size
Residual phenotype
Concentration (μM)
Strain
CB4856
DL238
JU258
N2
B
Silver 150 μM
q90.norm.EXT
q75.norm.EXT
mean.norm.EXT
median.norm.EXT
q25.norm.EXT
q10.norm.EXT
var.EXT
var.TOF
q90.EXT
q90.TOF
q75.EXT
q75.TOF
mean.EXT
mean.TOF
median.EXT
median.TOF
q25.EXT
q25.TOF
q10.EXT
q10.TOF
norm.n
n
r2
1.00
0.75
0.50
0.25


A
Topotecan
Brood Size
Small Size
Large Size
Residual phenotype
Concentration (μM)
Strain
CB4856
DL238
JU258
N2
B
Topotecan 400 μM
q90.norm.EXT
q75.norm.EXT
mean.norm.EXT
median.norm.EXT
q25.norm.EXT
q10.norm.EXT
var.EXT
var.TOF
q90.EXT
q90.TOF
q75.EXT
q75.TOF
mean.EXT
mean.TOF
median.EXT
median.TOF
q25.EXT
q25.TOF
q10.EXT
q10.TOF
norm.n
n
r^2
1.00
0.75
0.50
0.25


A
Tunicamycin
Brood Size
Small Size
Large Size
Residual phenotype
Concentration (μM)
Strain
CB4856
DL238
JU258
N2
B
Tunicamycin 10 μM
q90.norm.EXT
q75.norm.EXT
mean.norm.EXT
median.norm.EXT
q25.norm.EXT
q10.norm.EXT
var.EXT
var.TOF
q90.EXT
q90.TOF
q75.EXT
q75.TOF
mean.EXT
mean.TOF
median.EXT
median.TOF
q25.EXT
q25.TOF
q10.EXT
q10.TOF
norm.n
n
r^2
1.00
0.75
0.50
0.25

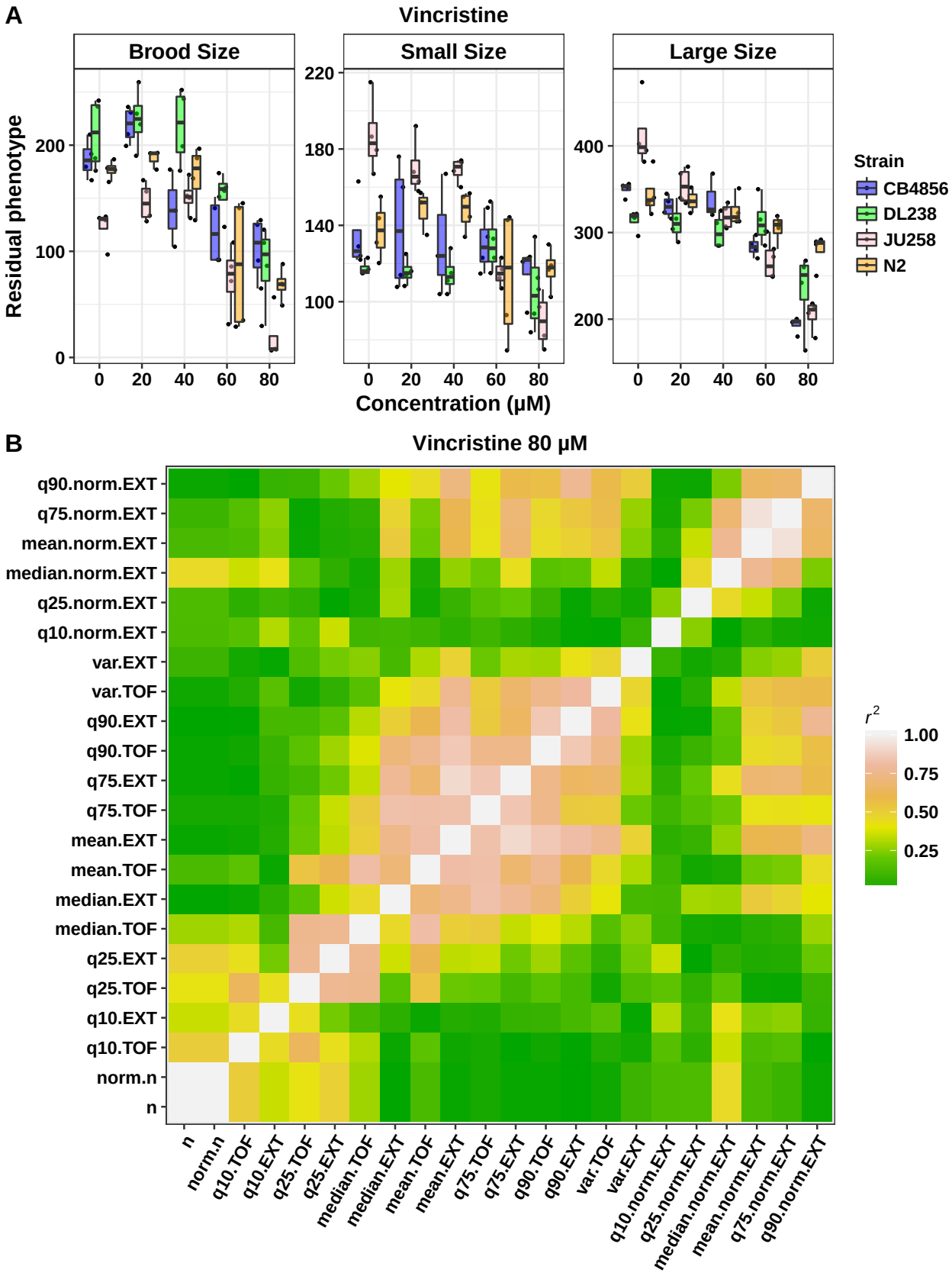
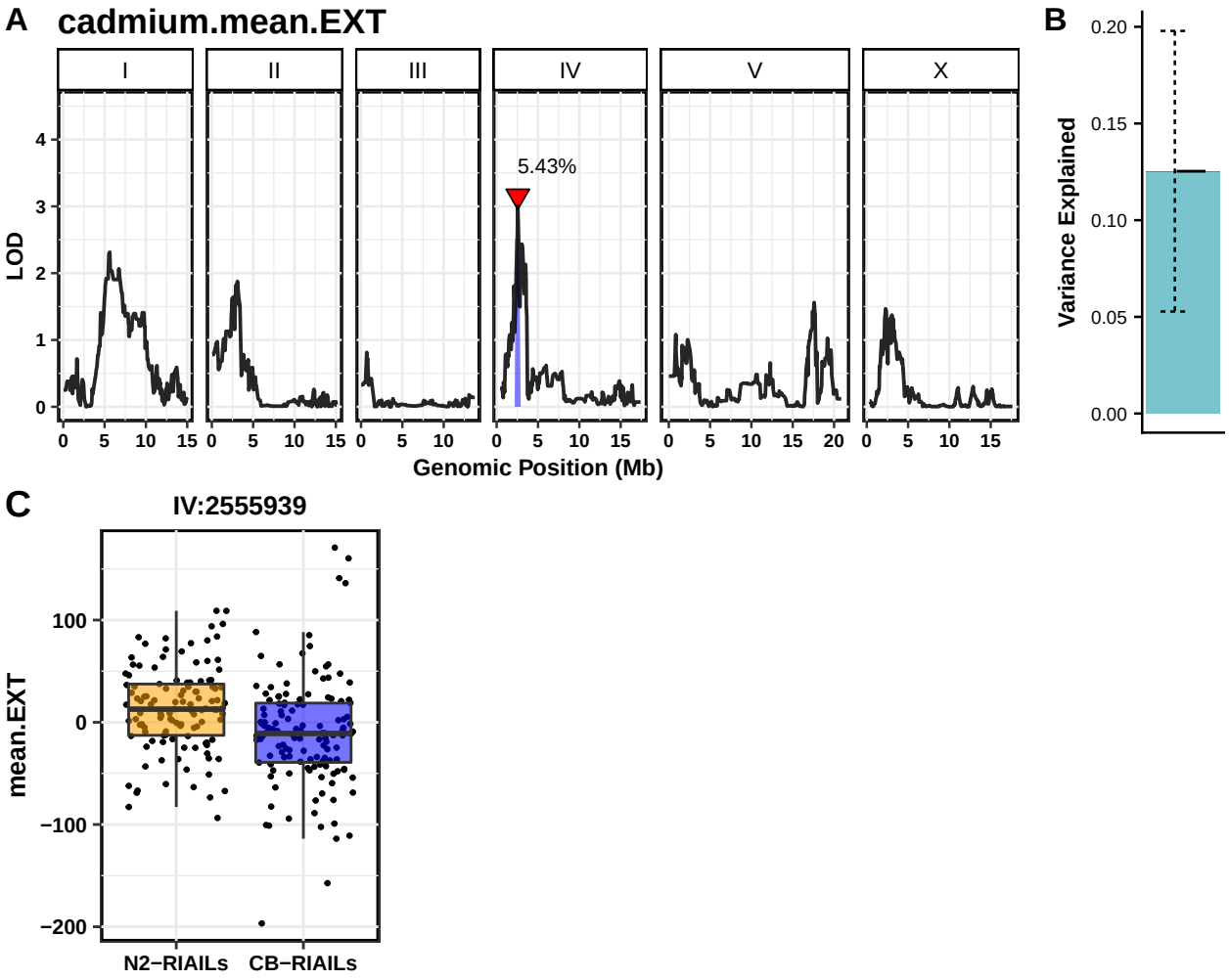
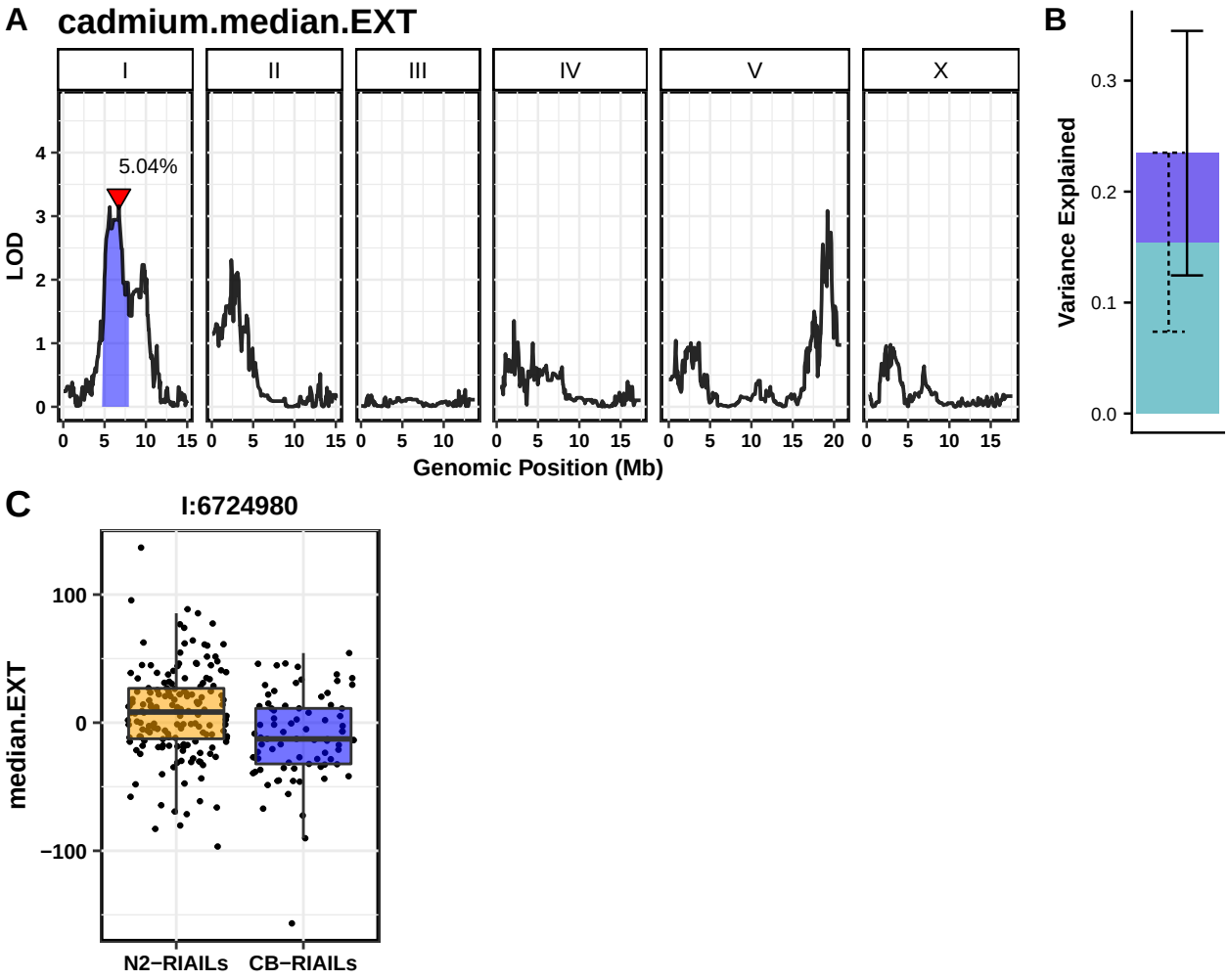
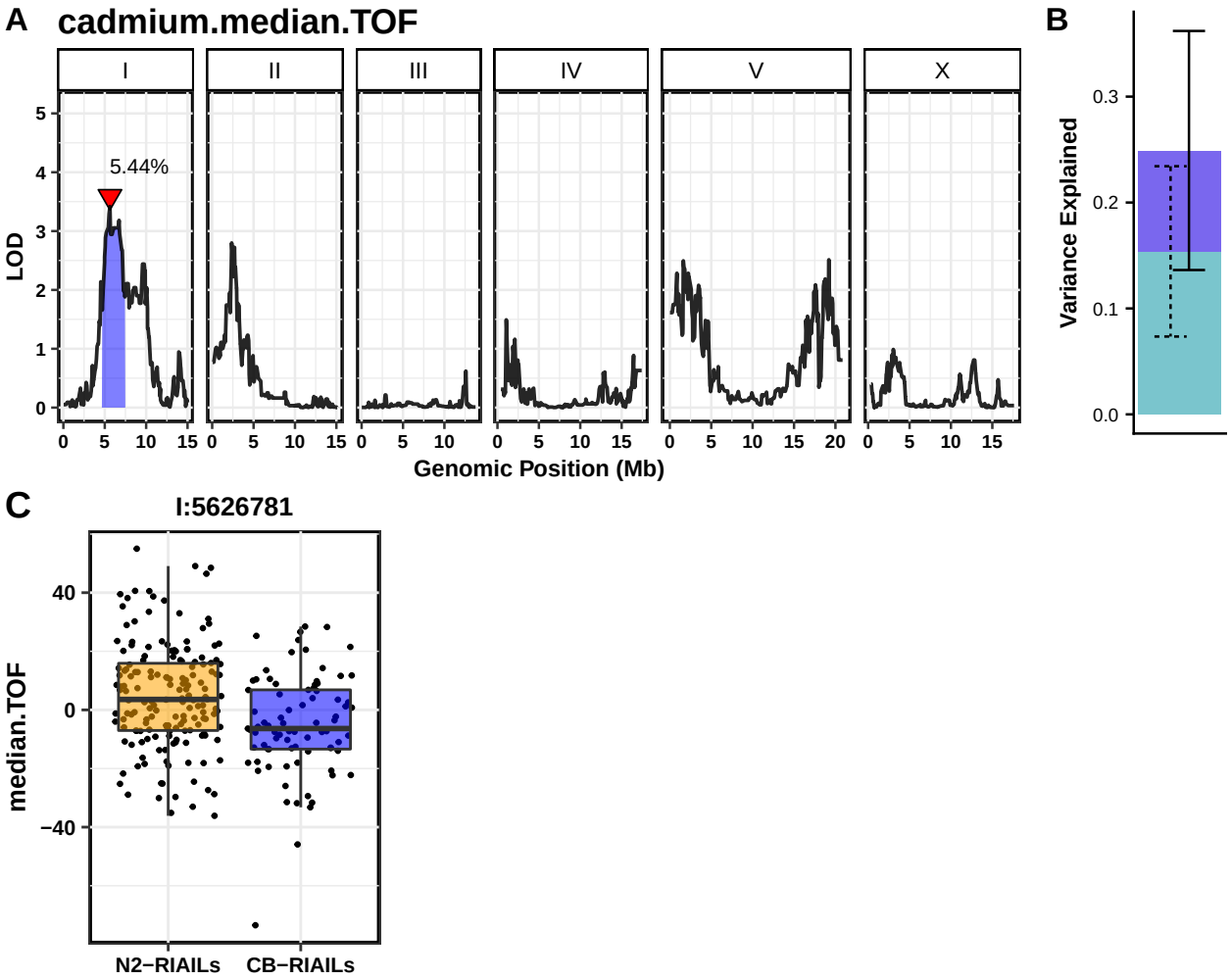
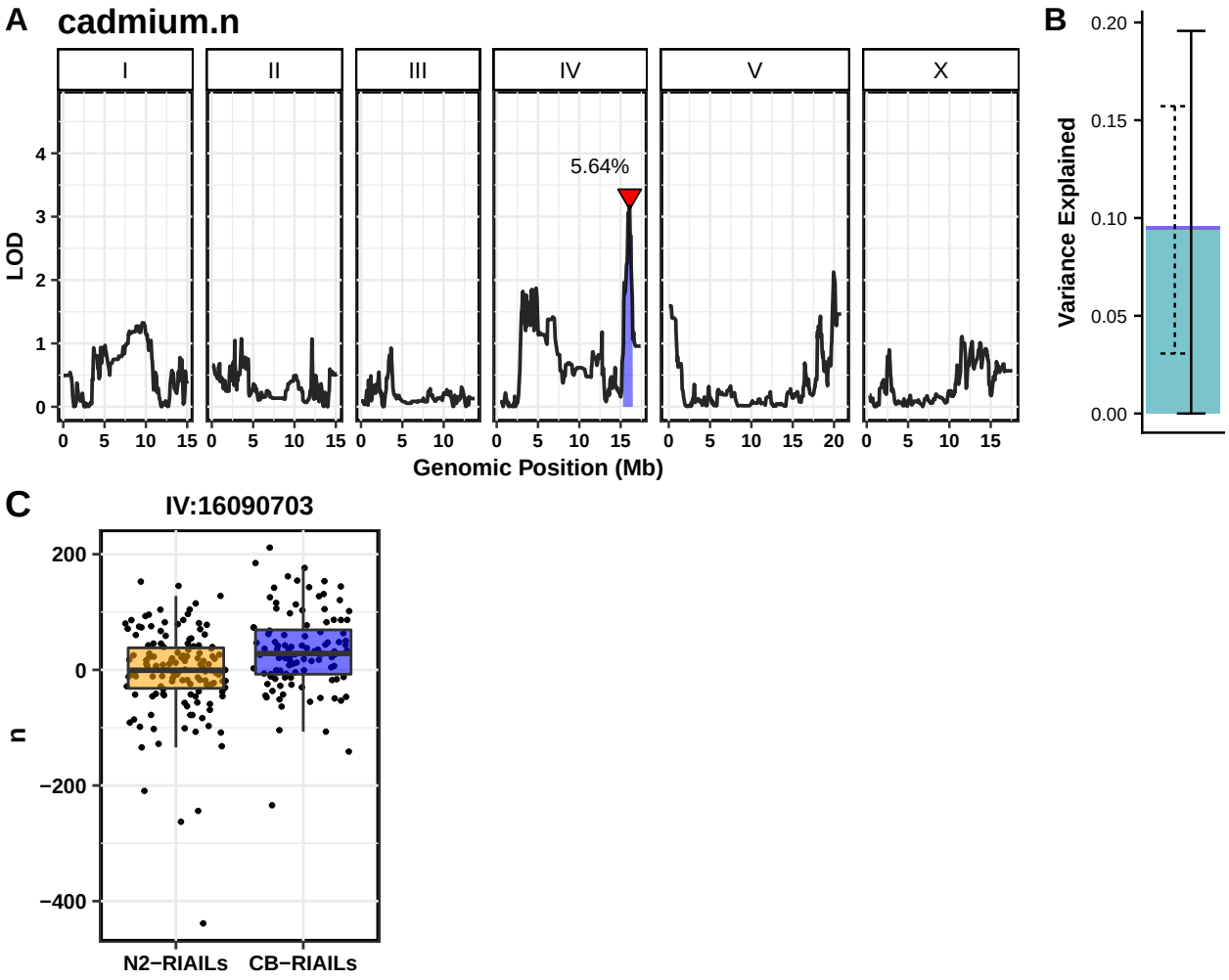

A
Vincristine
Brood Size
Small Size
Large Size
Residual phenotype
Concentration (μM)
Strain
CB4856
DL238
JU258
N2
B
Vincristine 80 μM
q90.norm.EXT
q75.norm.EXT
mean.norm.EXT
median.norm.EXT
q25.norm.EXT
q10.norm.EXT
var.EXT
var.TOF
q90.EXT
q90.TOF
q75.EXT
q75.TOF
mean.EXT
mean.TOF
median.EXT
median.TOF
q25.EXT
q25.TOF
q10.EXT
q10.TOF
norm.n
n
r2
1.00
0.75
0.50
0.25

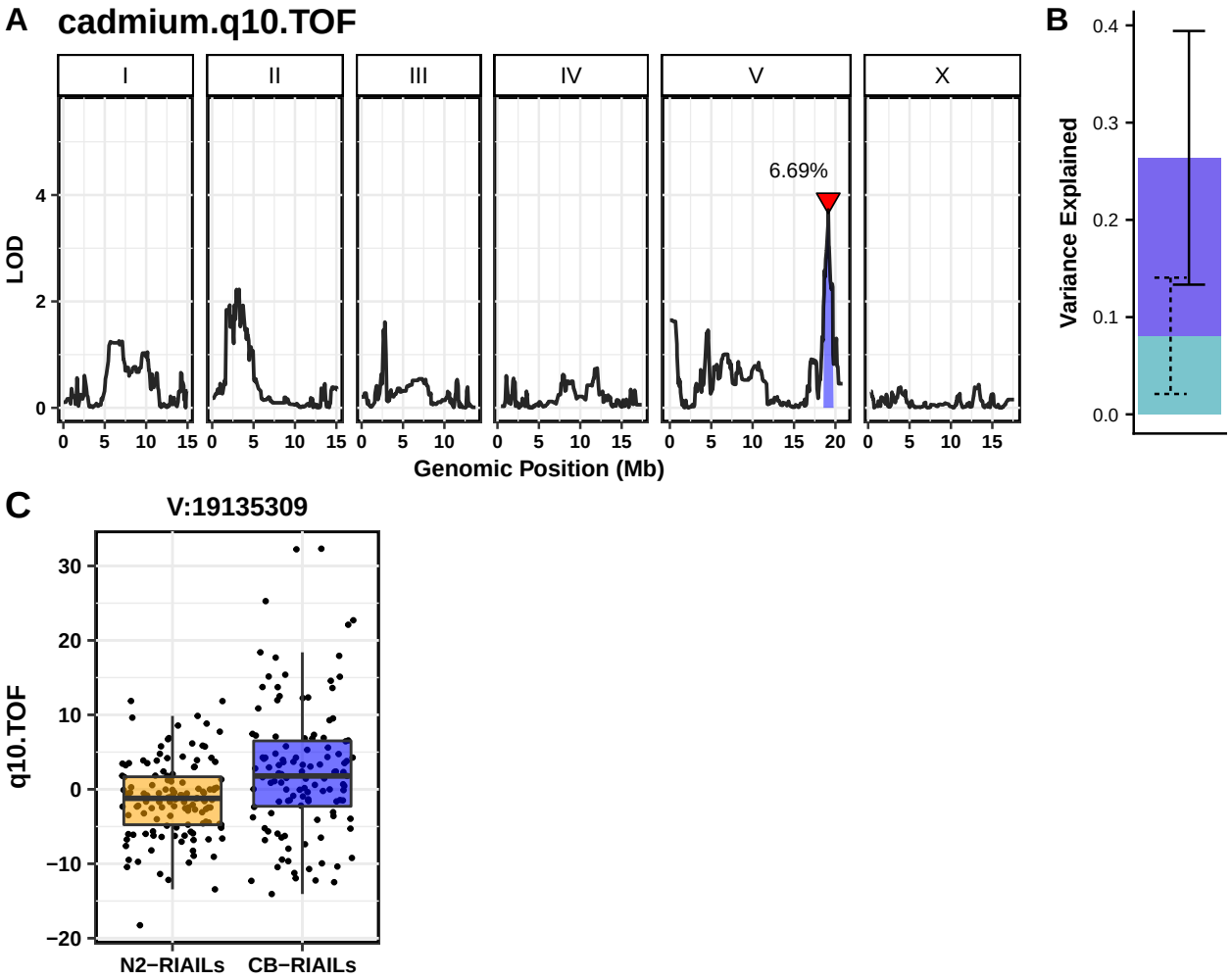
Figure S1 Dose-response and trait correlation estimates. (**A**) Phenotypic values for four divergent strains, CB4856 (blue), DL238 (green), JU258 (pink), and N2 (orange), in response to various concentrations of each toxin are plotted as Tukey box plots. Toxin responses for traits representing three distinct population parameters (q25.TOF, q75.TOF, and norm.n) are shown. The x-axis indicates either the control (water or DMSO) or the concentration (µM) of the toxin, and the y-axis shows the raw phenotypic value for each trait. (**B**) Correlation coefficients (r^2) between all pairwise combinations of traits for the indicated concentration of the toxin are plotted as a heat map. Traits are labeled on the x- and y-axes and colors represent correlation coefficients increasing from green to yellow to pink to white.

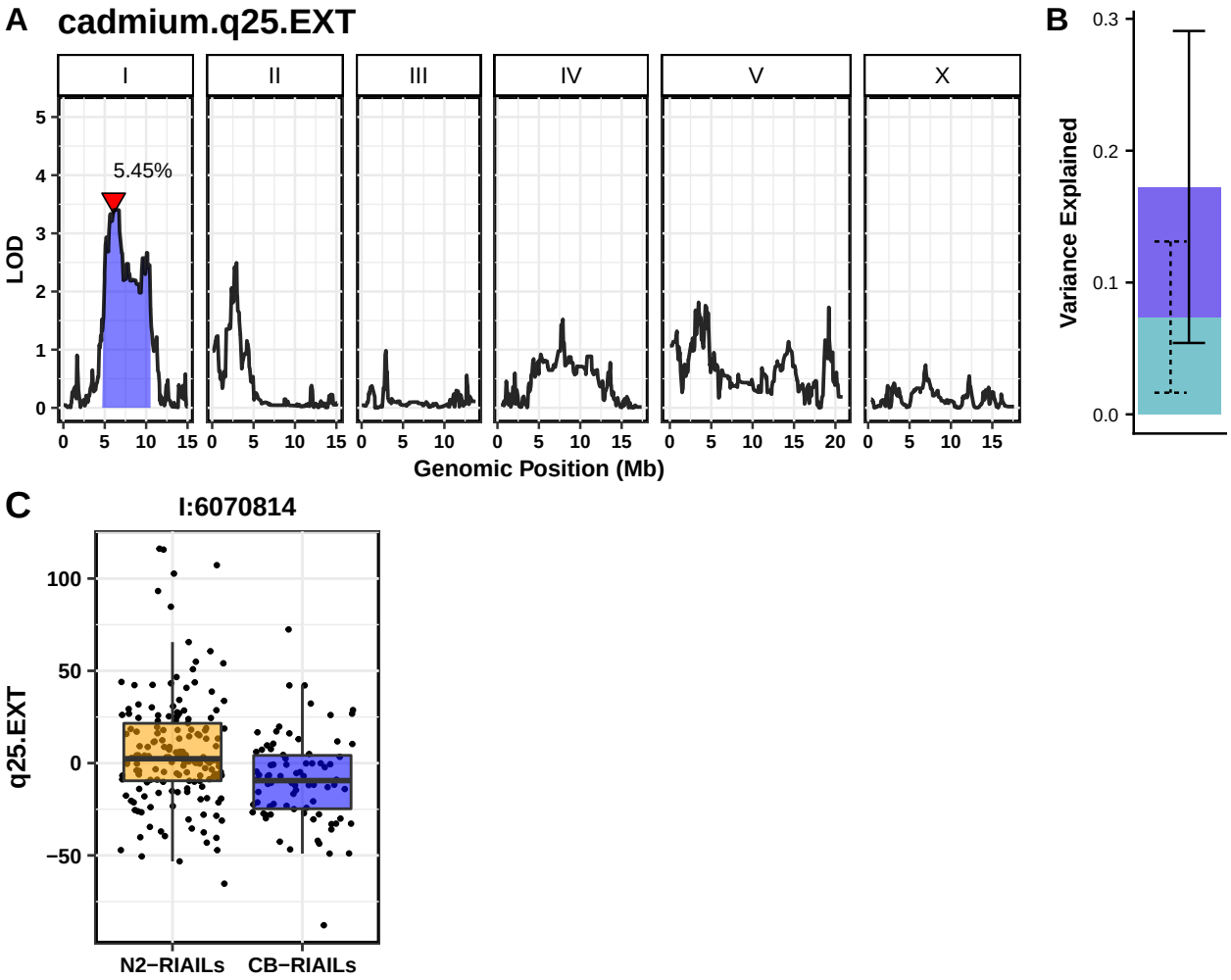

A
cadmium.mean.EXT
I
II
III
IV
V
X
5.43%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:2555939
mean.EXT
N2−RIAILs
CB−RIAILs

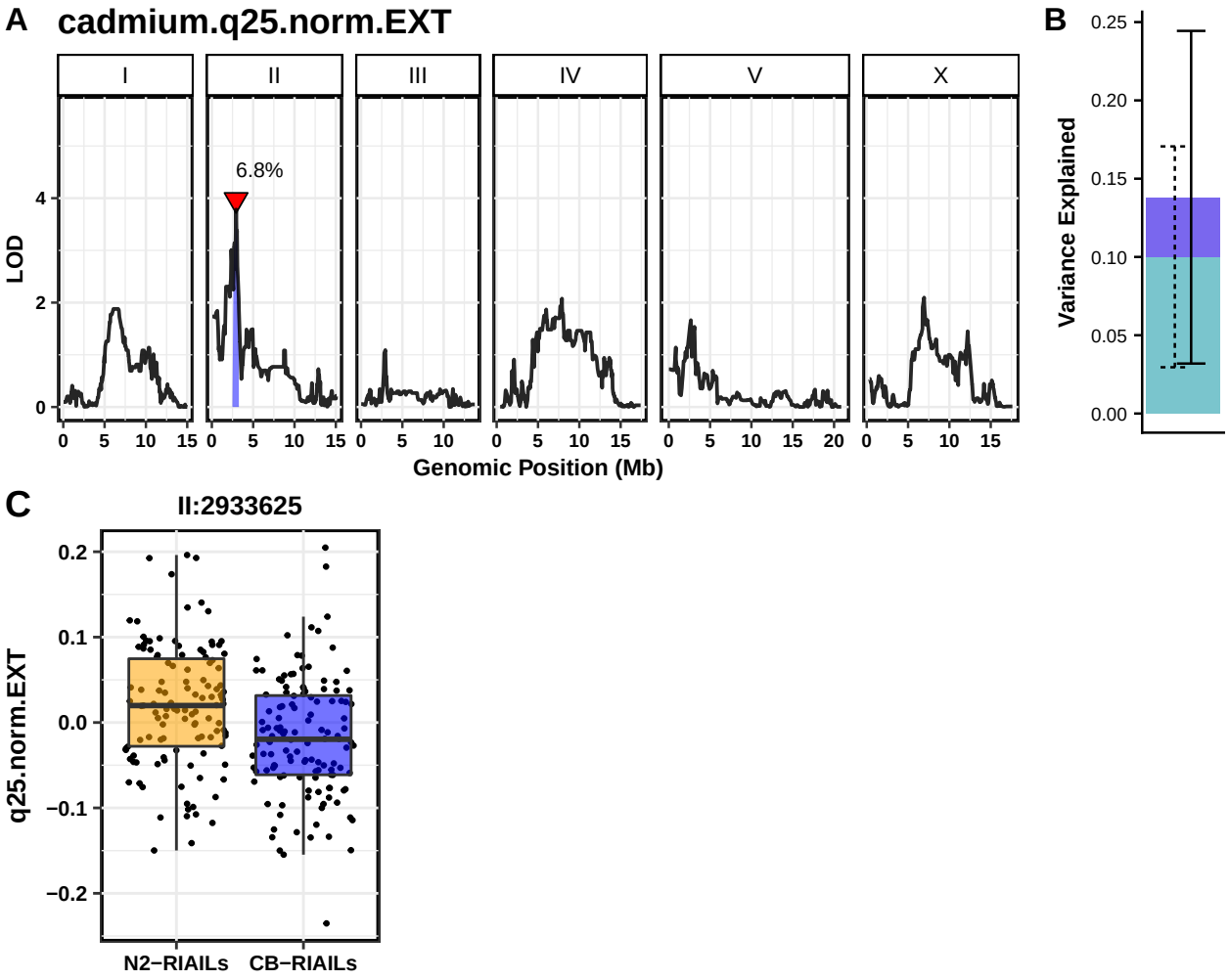

A
cadmium.median.EXT
I
II
III
IV
V
X
5.04%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:6724980
median.EXT
N2−RIAILs
CB−RIAILs

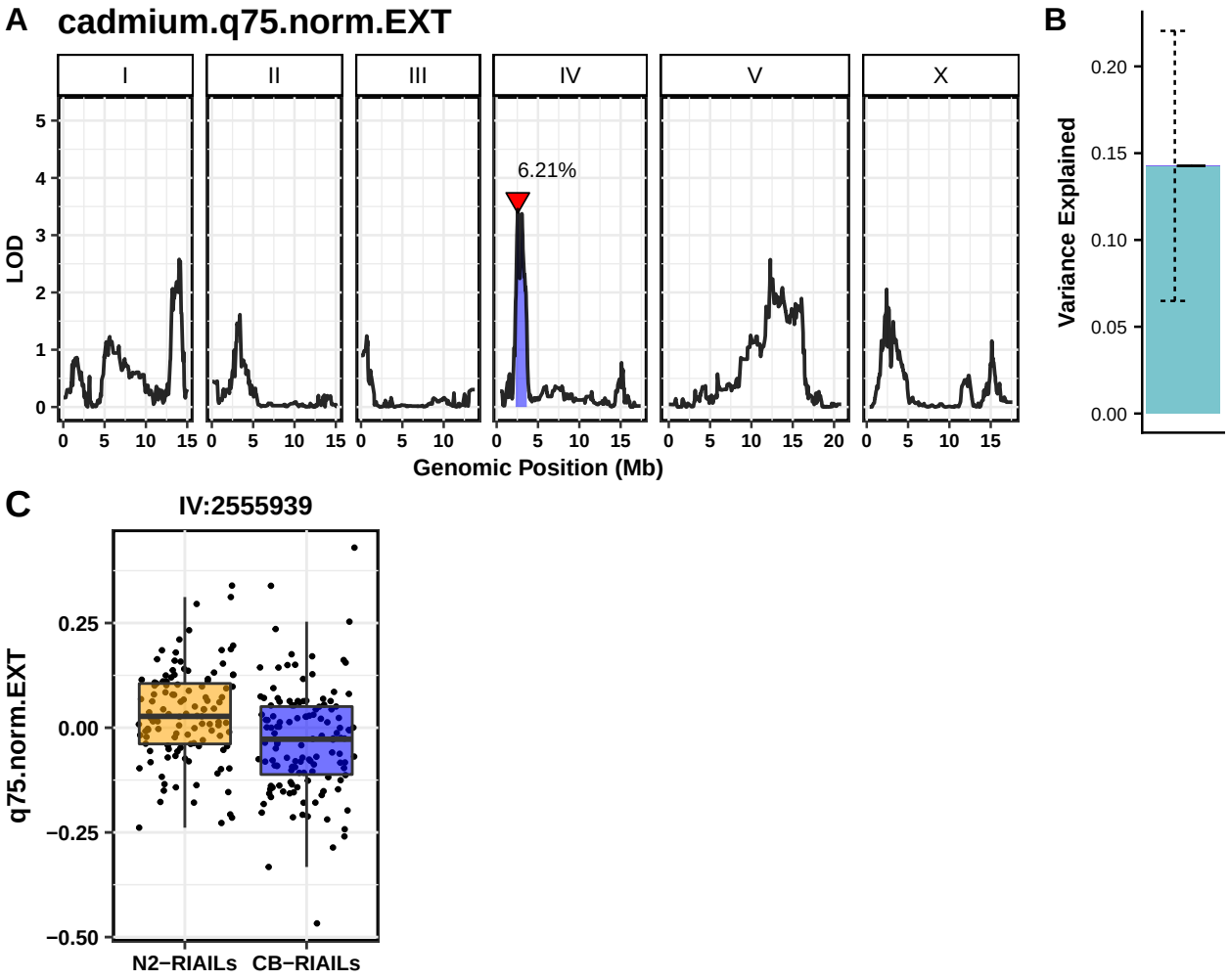

A
cadmium.median.TOF
I
II
III
IV
V
X
5.44%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:5626781
median.TOF
N2−RIAILs
CB−RIAILs

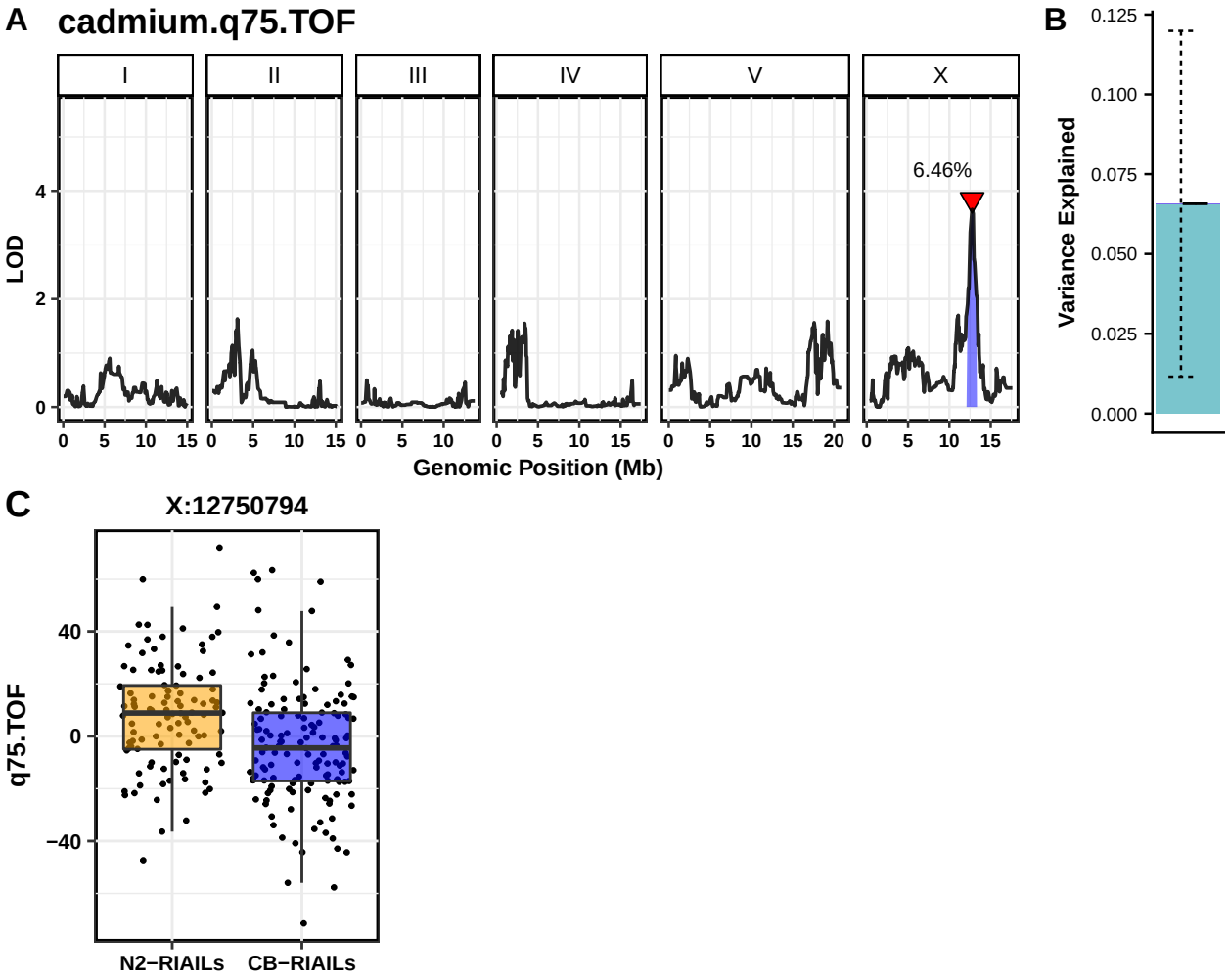

A
cadmium.n
I
II
III
IV
V
X
5.64%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:16090703
n
N2−RIAILs
CB−RIAILs

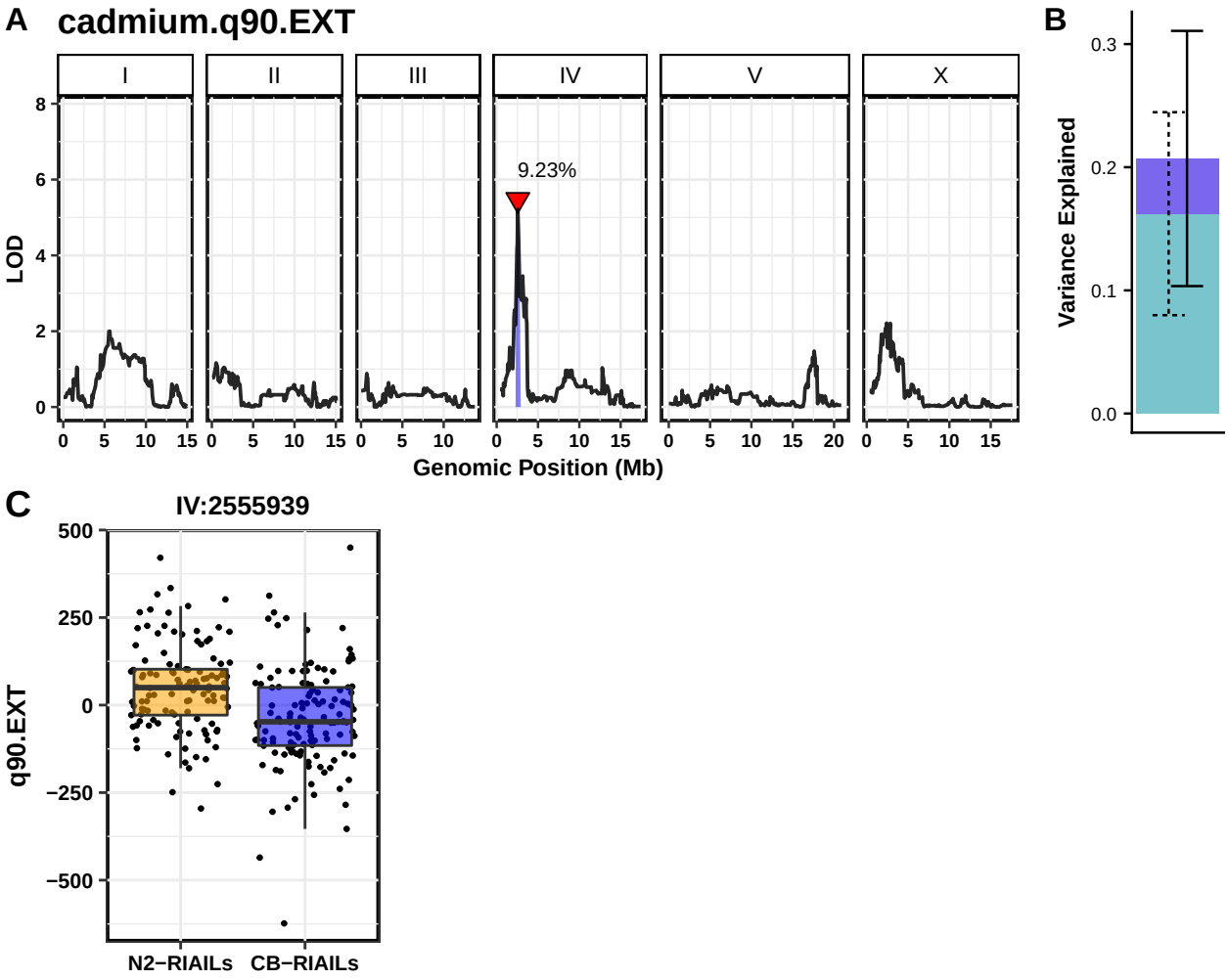

A
cadmium.q10.TOF
I
II
III
IV
V
X
6.69%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:19135309
q10.TOF
N2−RIAILs
CB−RIAILs

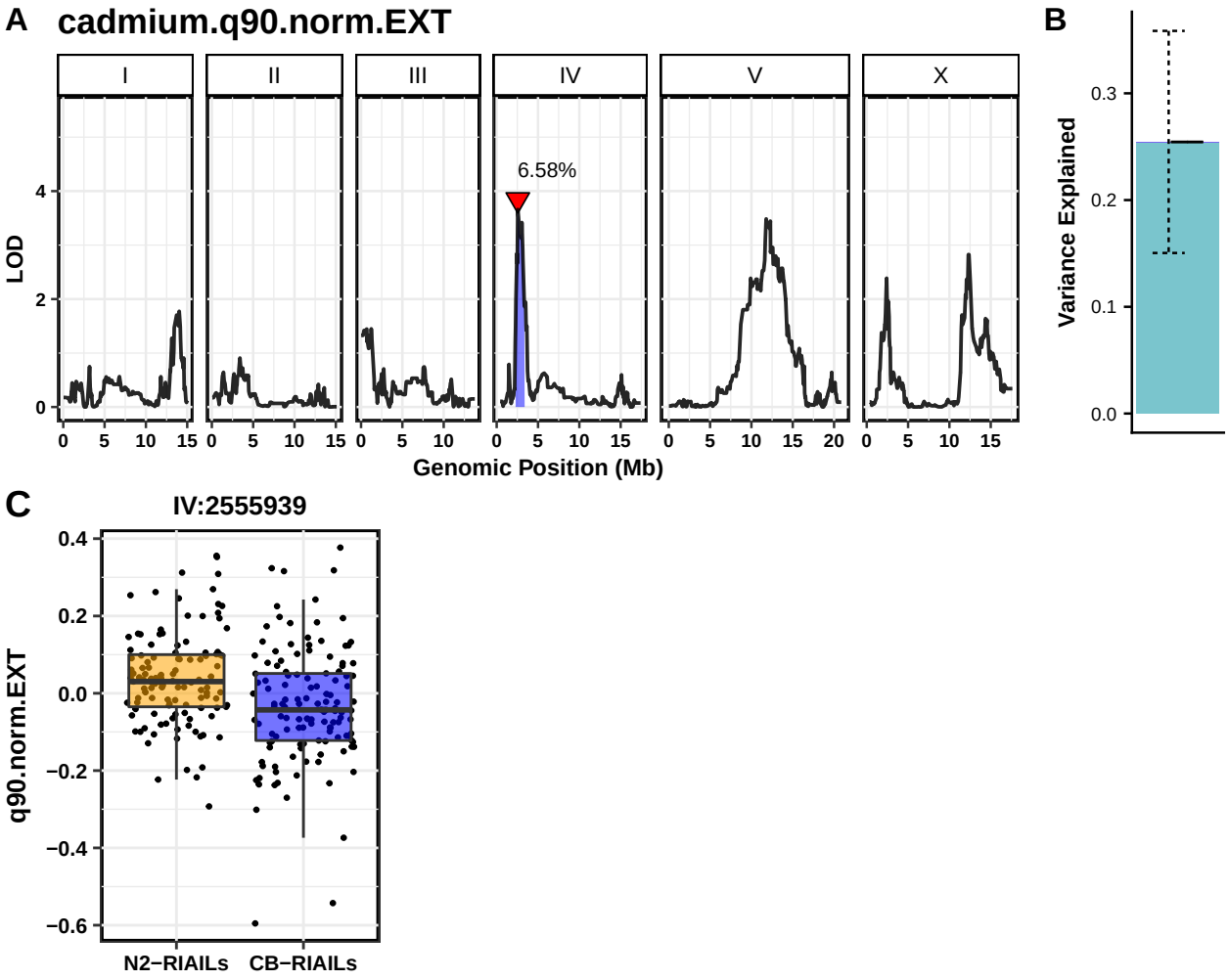

A
cadmium.q25.EXT
I
II
III
IV
V
X
5.45%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:6070814
q25.EXT
N2−RIAILs
CB−RIAILs

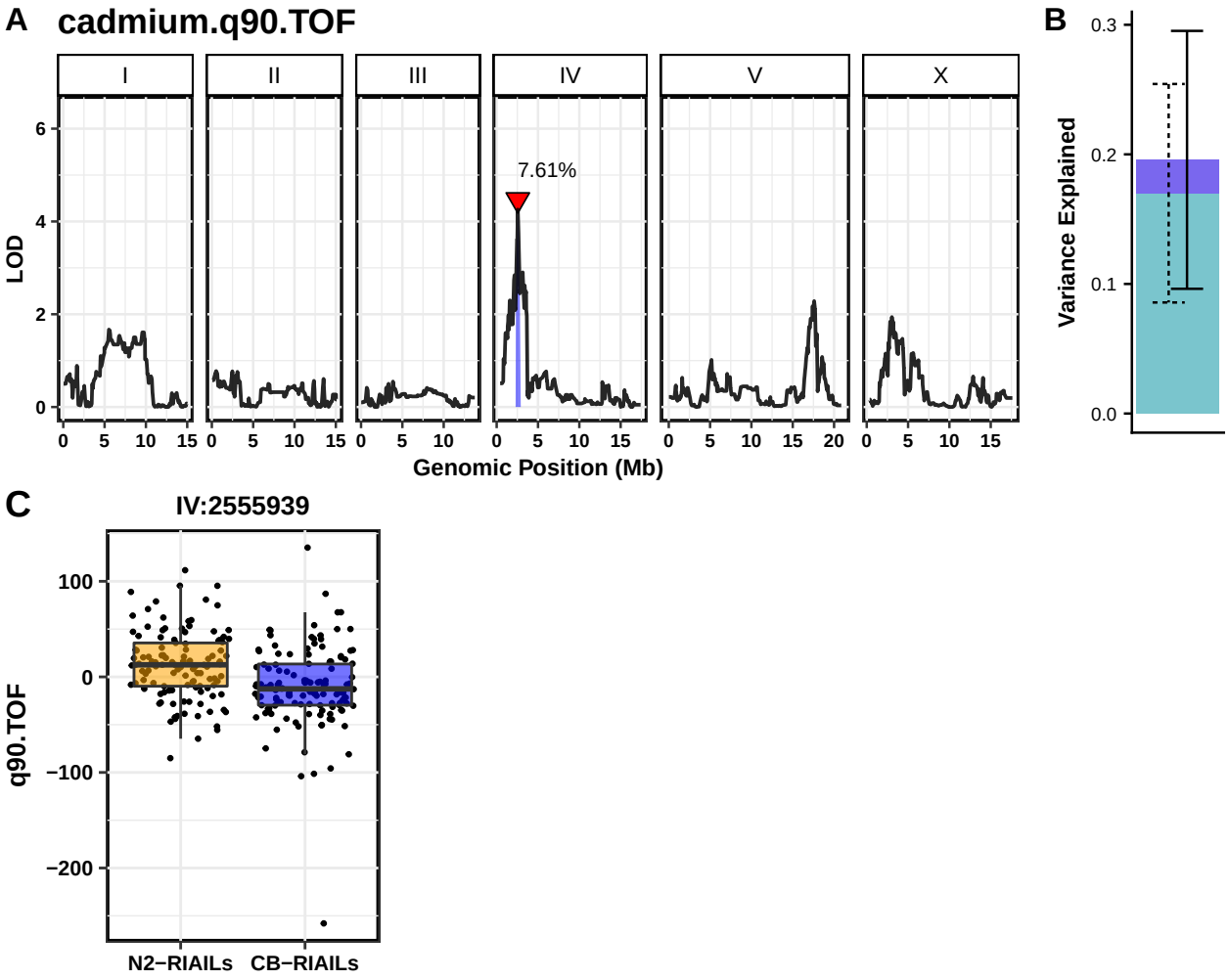

A
cadmium.q25.norm.EXT
I
II
III
IV
V
X
6.8%
LOD
Genomic Position (Mb)
B
Variance Explained
C
II:2933625
q25.norm.EXT
N2−RIAILs
CB−RIAILs

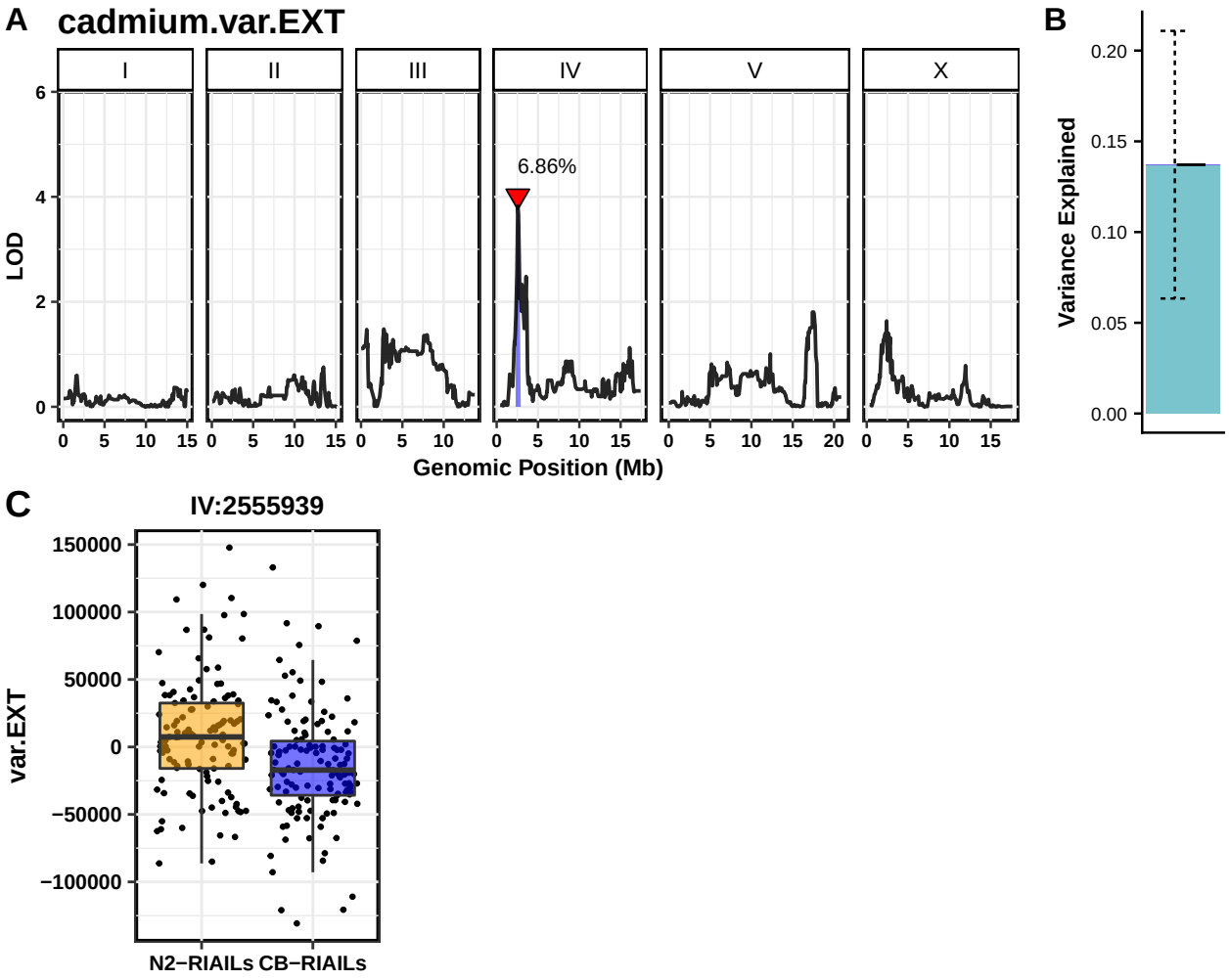

A
cadmium.q75.norm.EXT
I
II
III
IV
V
X
6.21%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:2555939
q75.norm.EXT
N2−RIAILs
CB−RIAILs

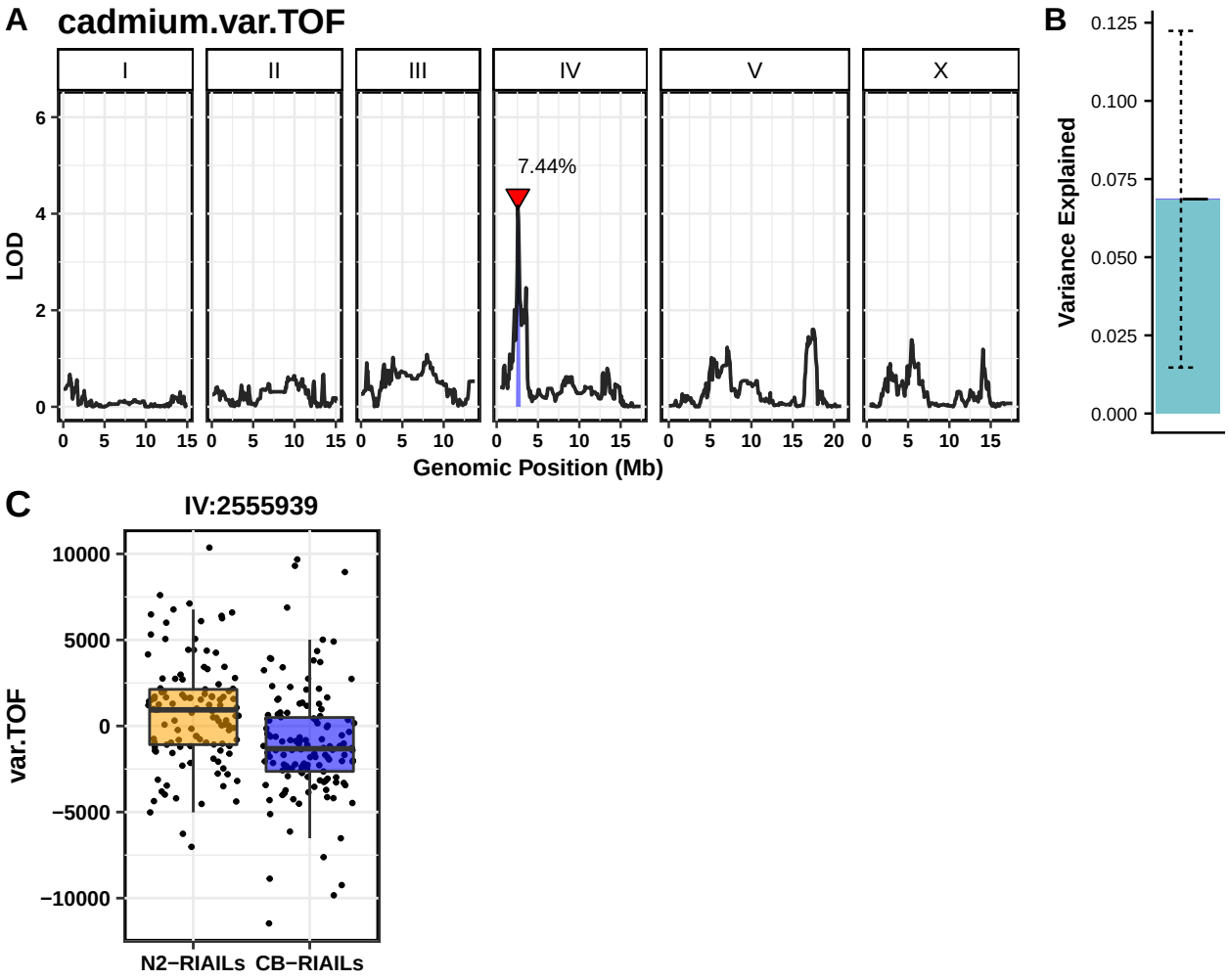

A
cadmium.q75.TOF
I
II
III
IV
V
X
6.46%
LOD
Genomic Position (Mb)
B
Variance Explained
C
X:12750794
q75.TOF
N2−RIAILs
CB−RIAILs

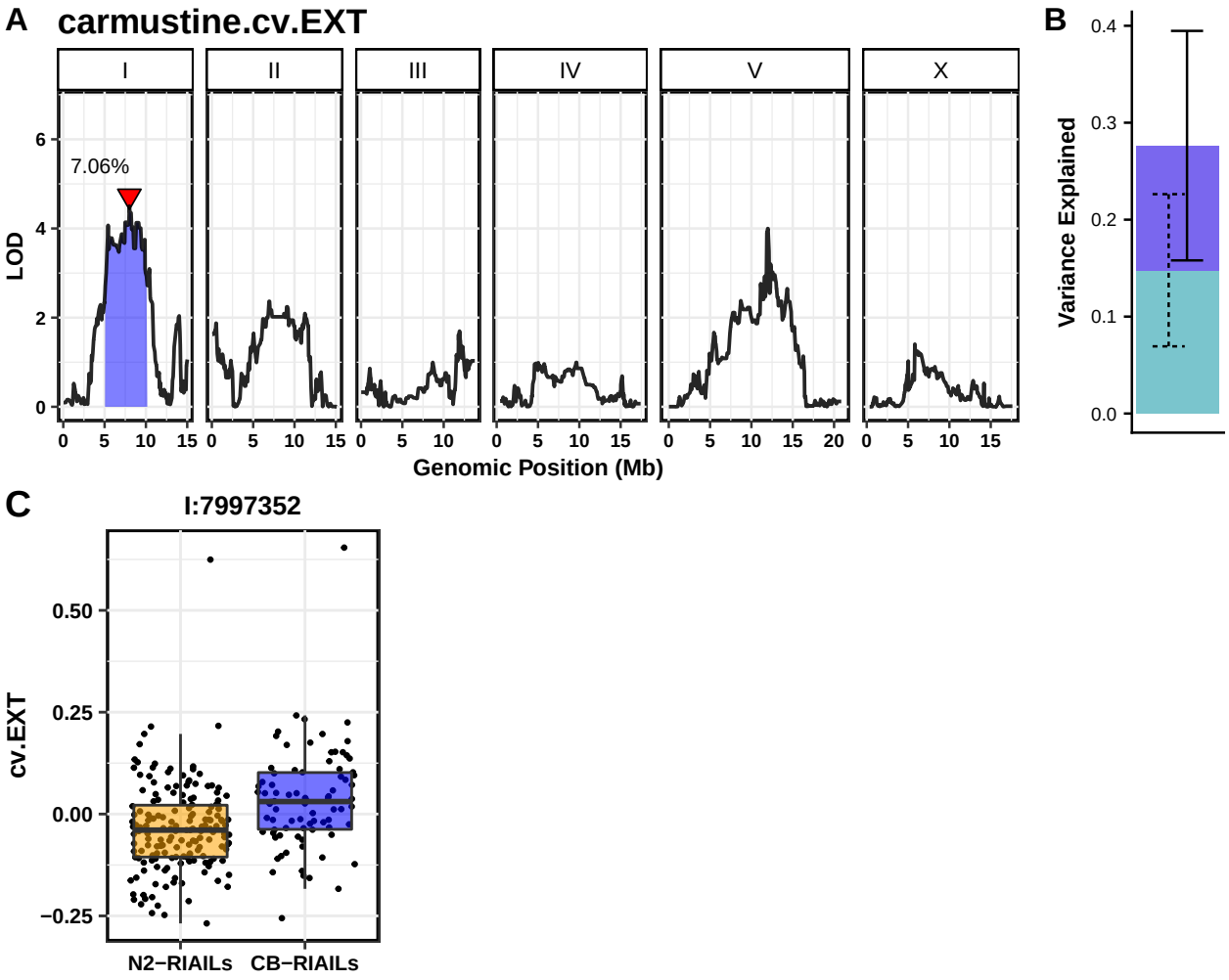

A
cadmium.q90.EXT
I
II
III
IV
V
X
9.23%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:2555939
q90.EXT
N2−RIAILs
CB−RIAILs

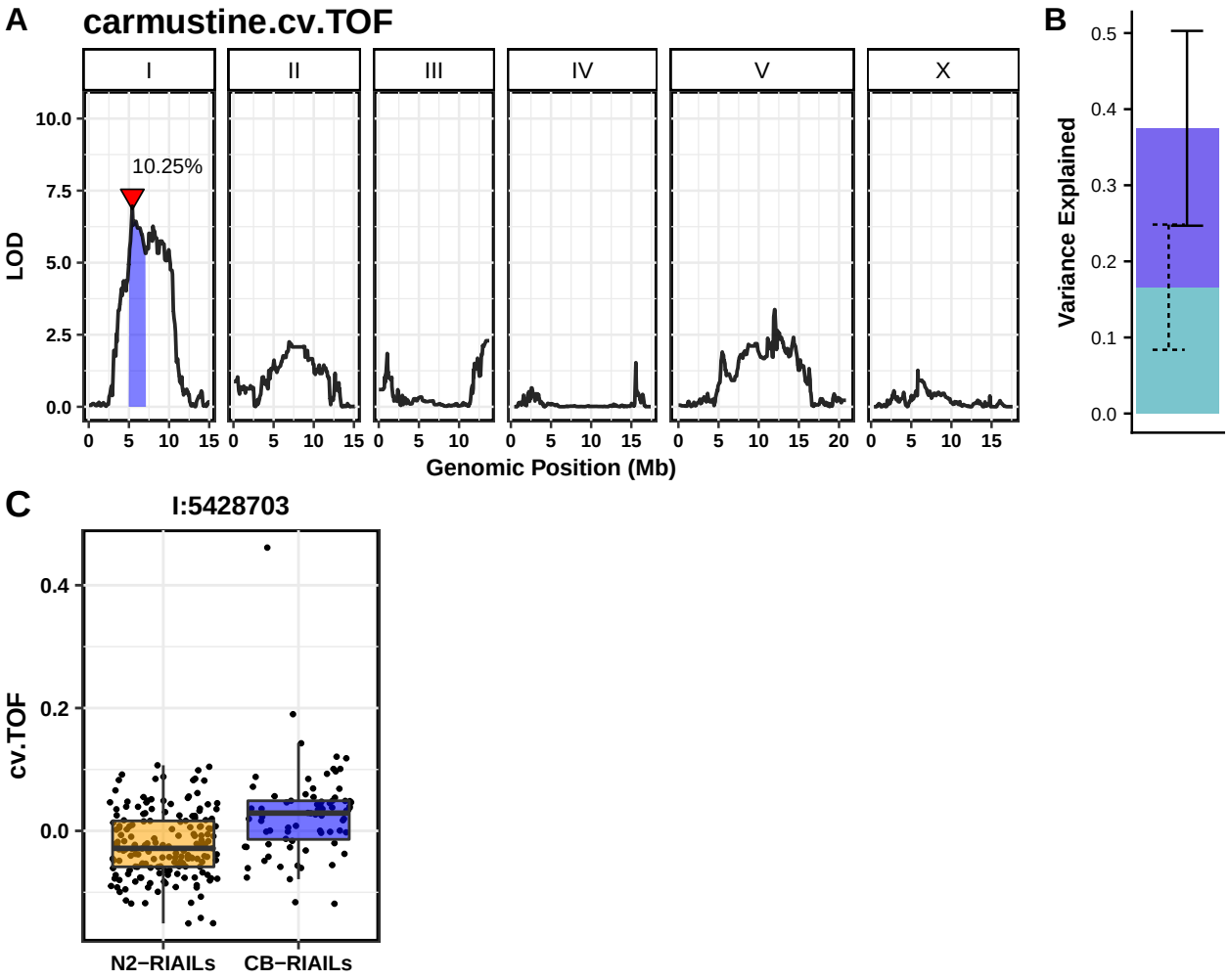

A
cadmium.q90.norm.EXT
I
II
III
IV
V
X
6.58%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:2555939
q90.norm.EXT
N2−RIAILs
CB−RIAILs

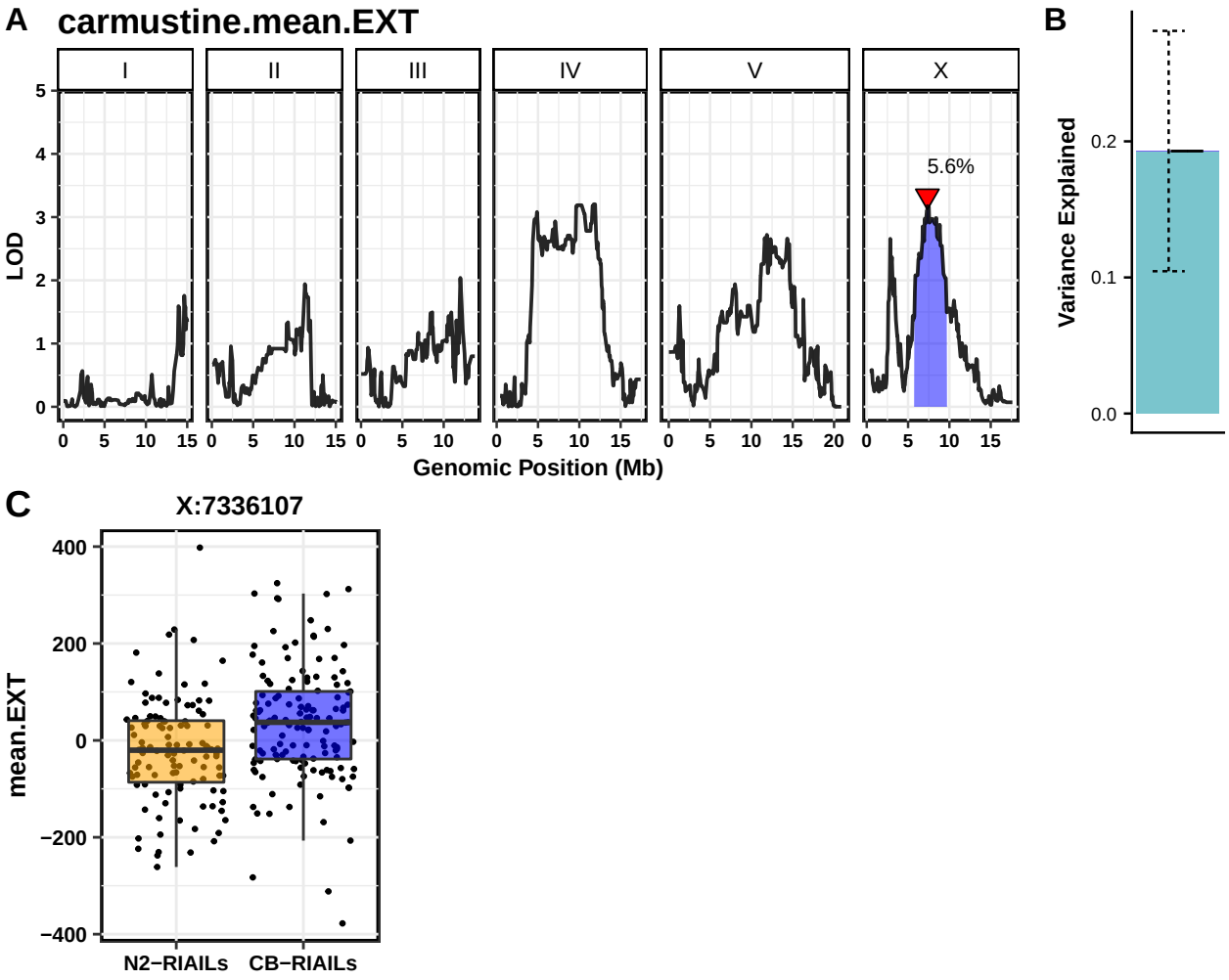

A
cadmium.q90.TOF
I
II
III
IV
V
X
7.61%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:2555939
q90.TOF
N2−RIAILs
CB−RIAILs

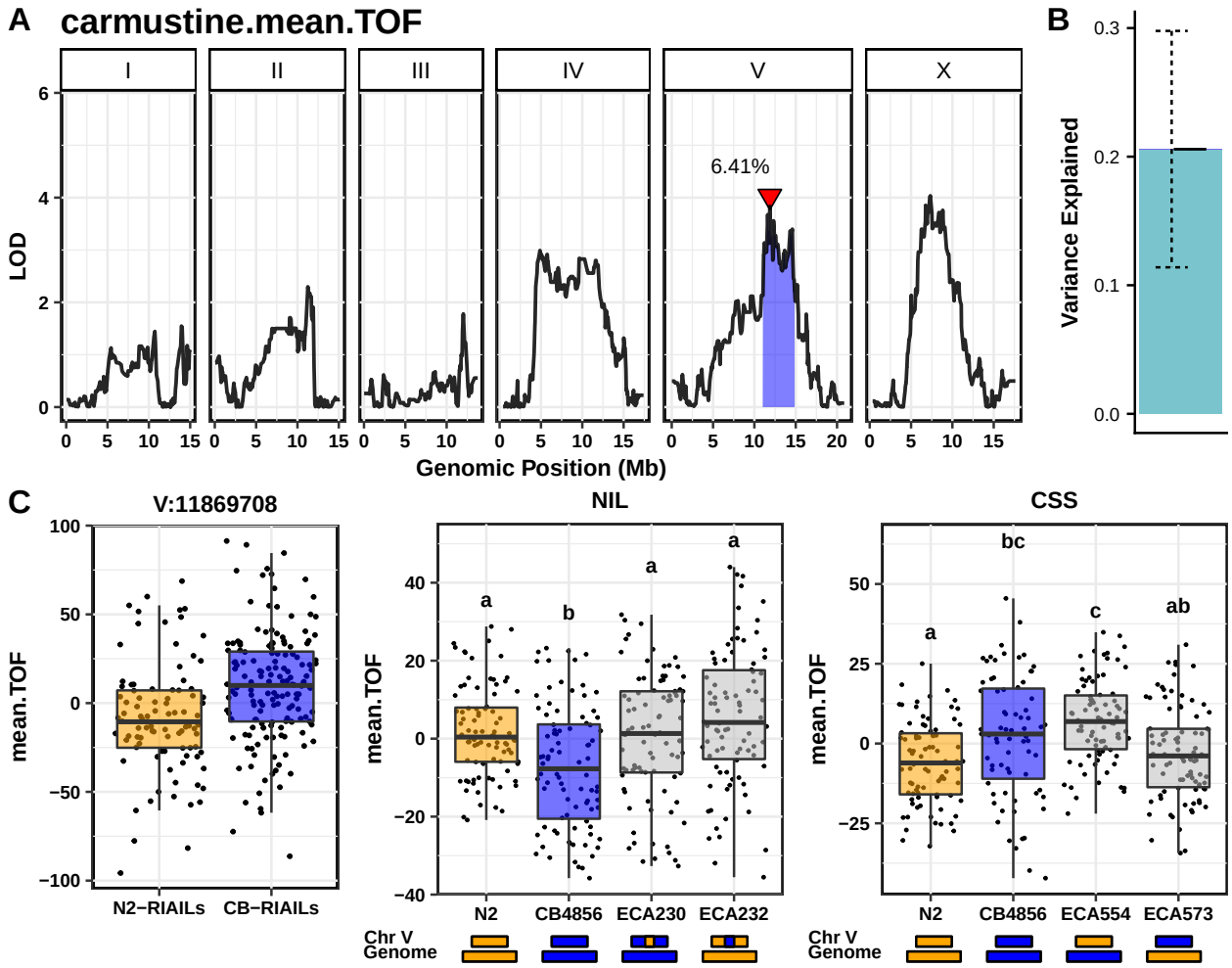

A
cadmium.var.EXT
I
II
III
IV
V
X
6.86%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:2555939
var.EXT
N2−RIAILs
CB−RIAILs

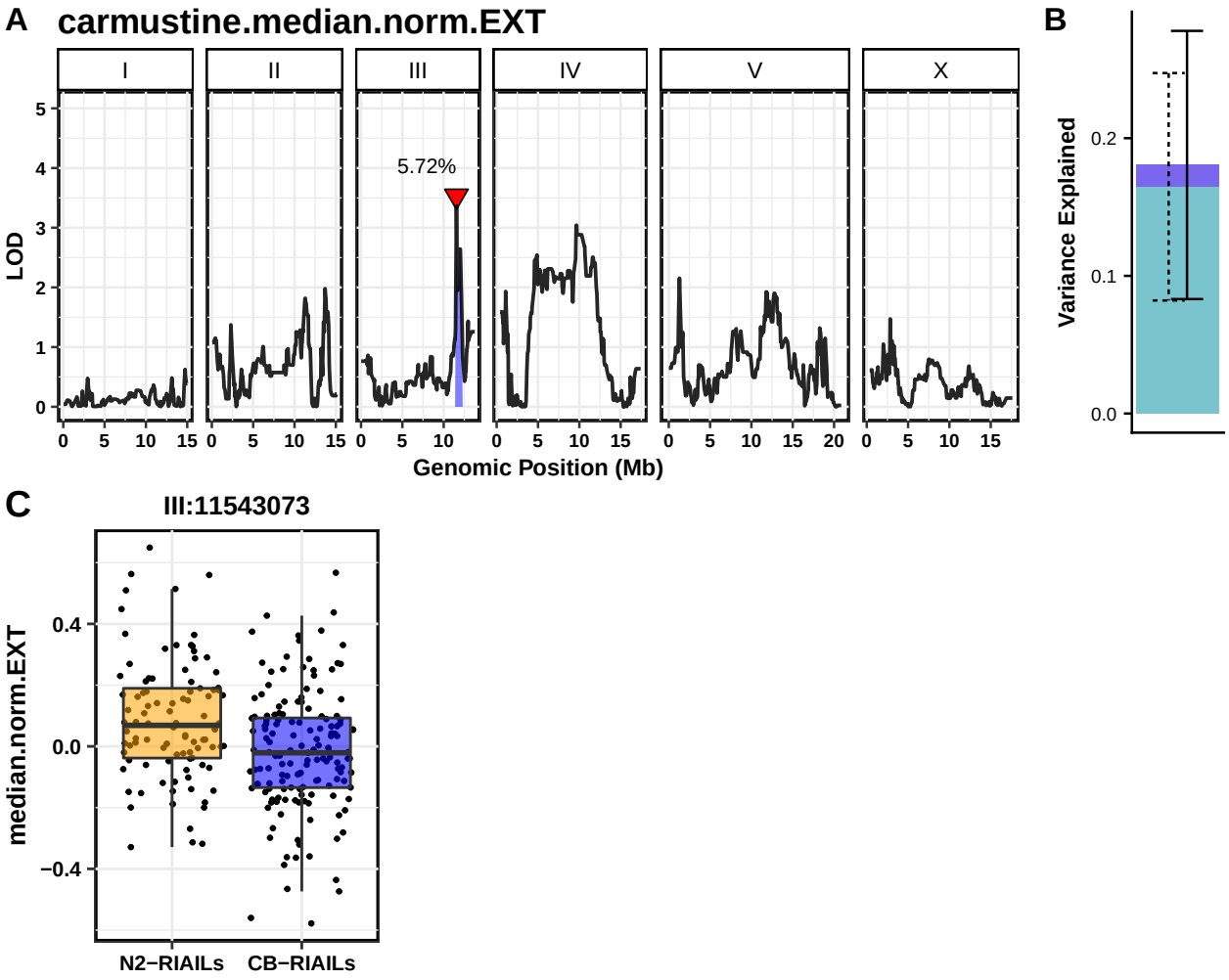

A
cadmium.var.TOF
I
II
III
IV
V
X
7.44%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:2555939
var.TOF
N2−RIAILs
CB−RIAILs

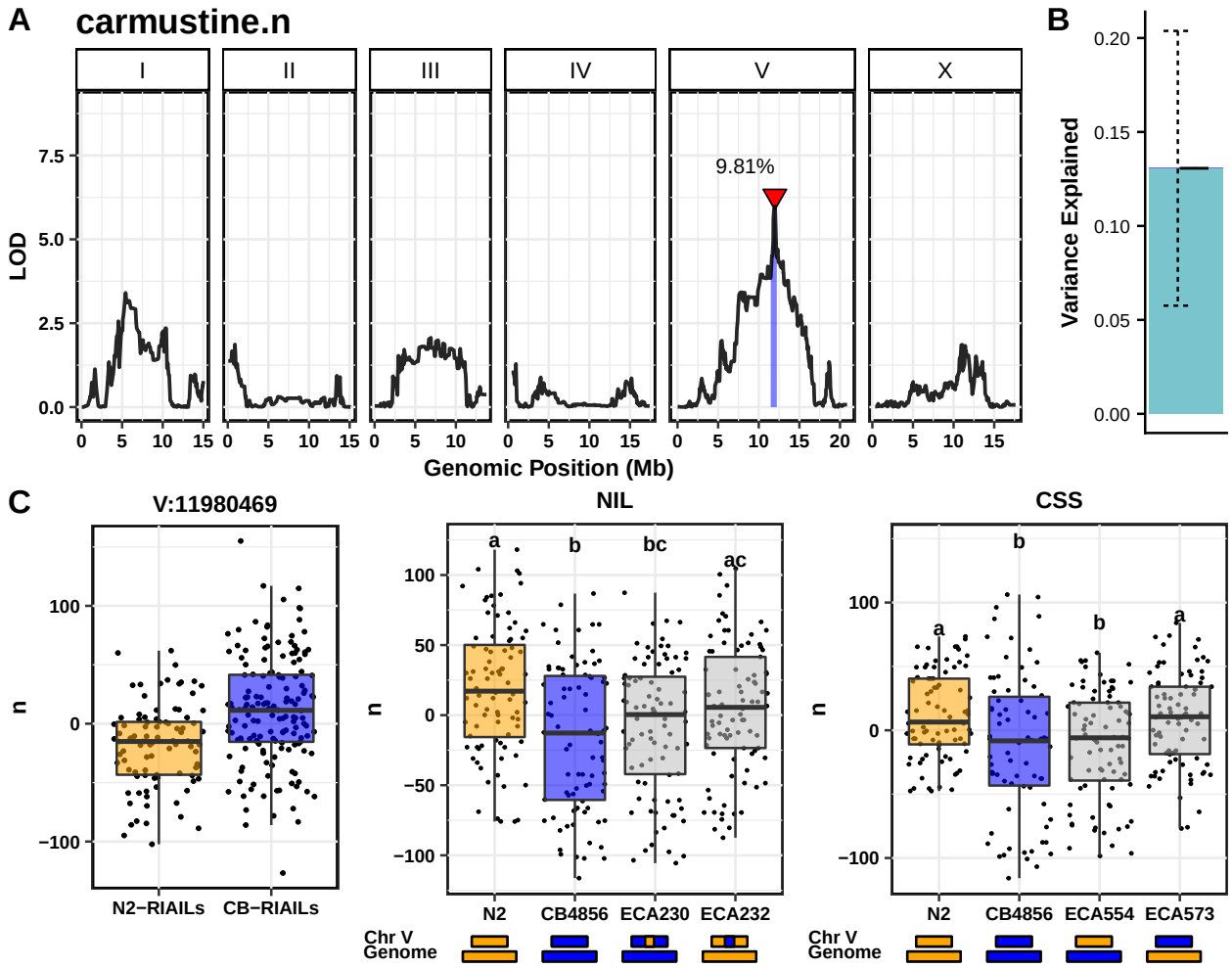

A
carmustine.cv.EXT
I
II
III
IV
V
X
7.06%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:7997352
cv.EXT
N2−RIAILs
CB−RIAILs

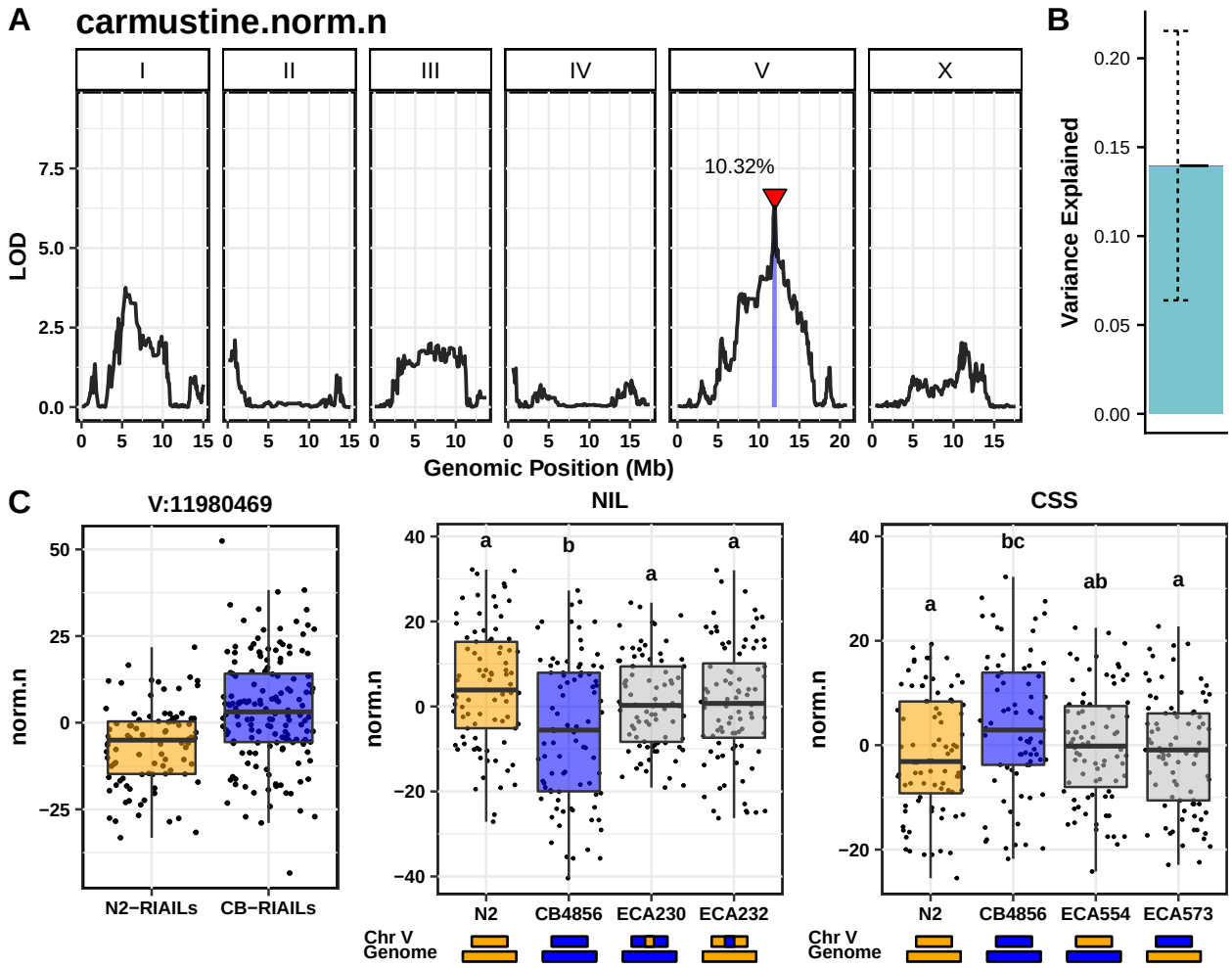

A
carmustine.cv.TOF
I
II
III
IV
V
X
10.25%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:5428703
cv.TOF
N2−RIAILs
CB−RIAILs

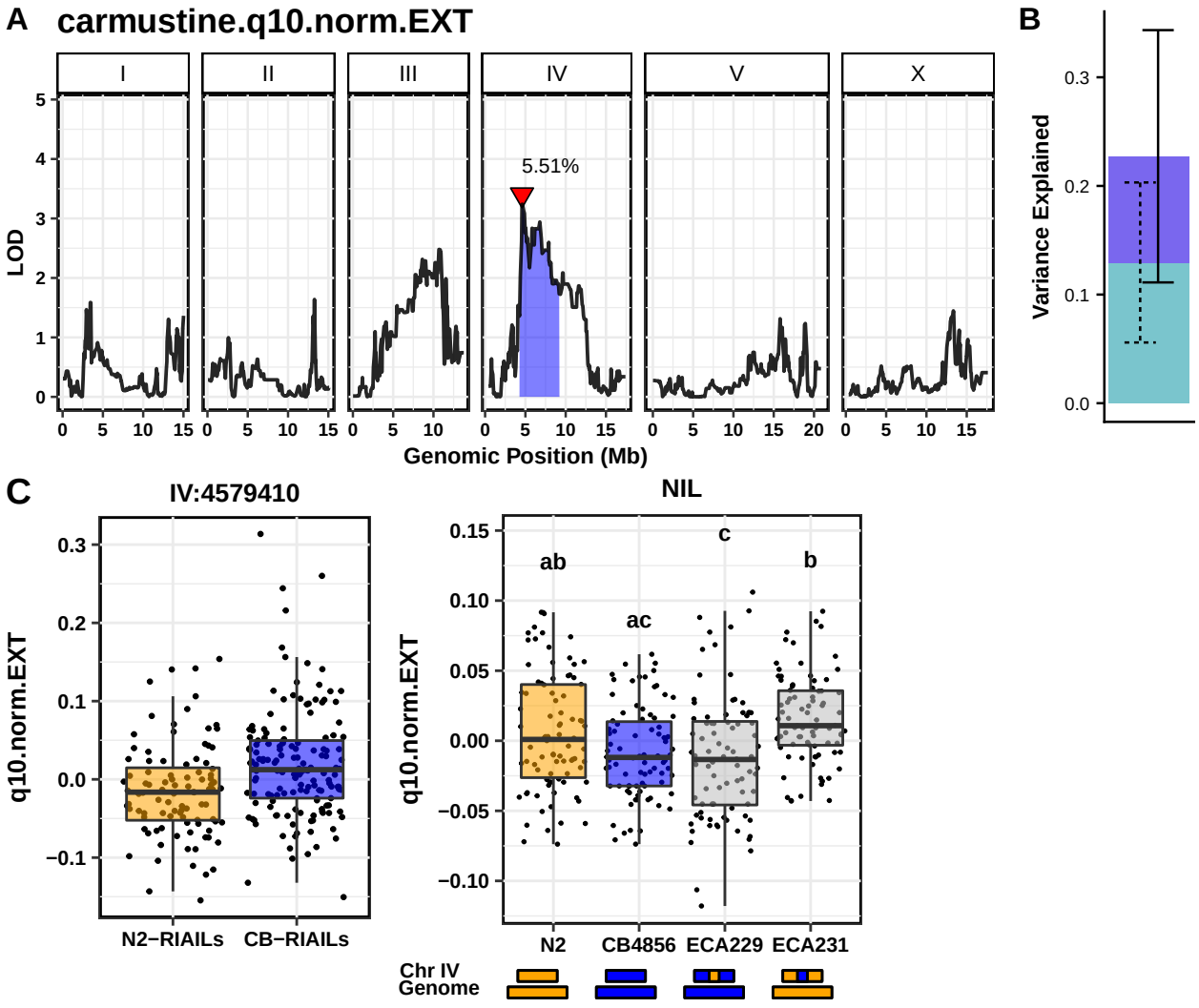

A
carmustine.mean.EXT
I
II
III
IV
V
X
LOD
5.6%
Genomic Position (Mb)
B
Variance Explained
C
X:7336107
mean.EXT
N2−RIAILs
CB−RIAILs

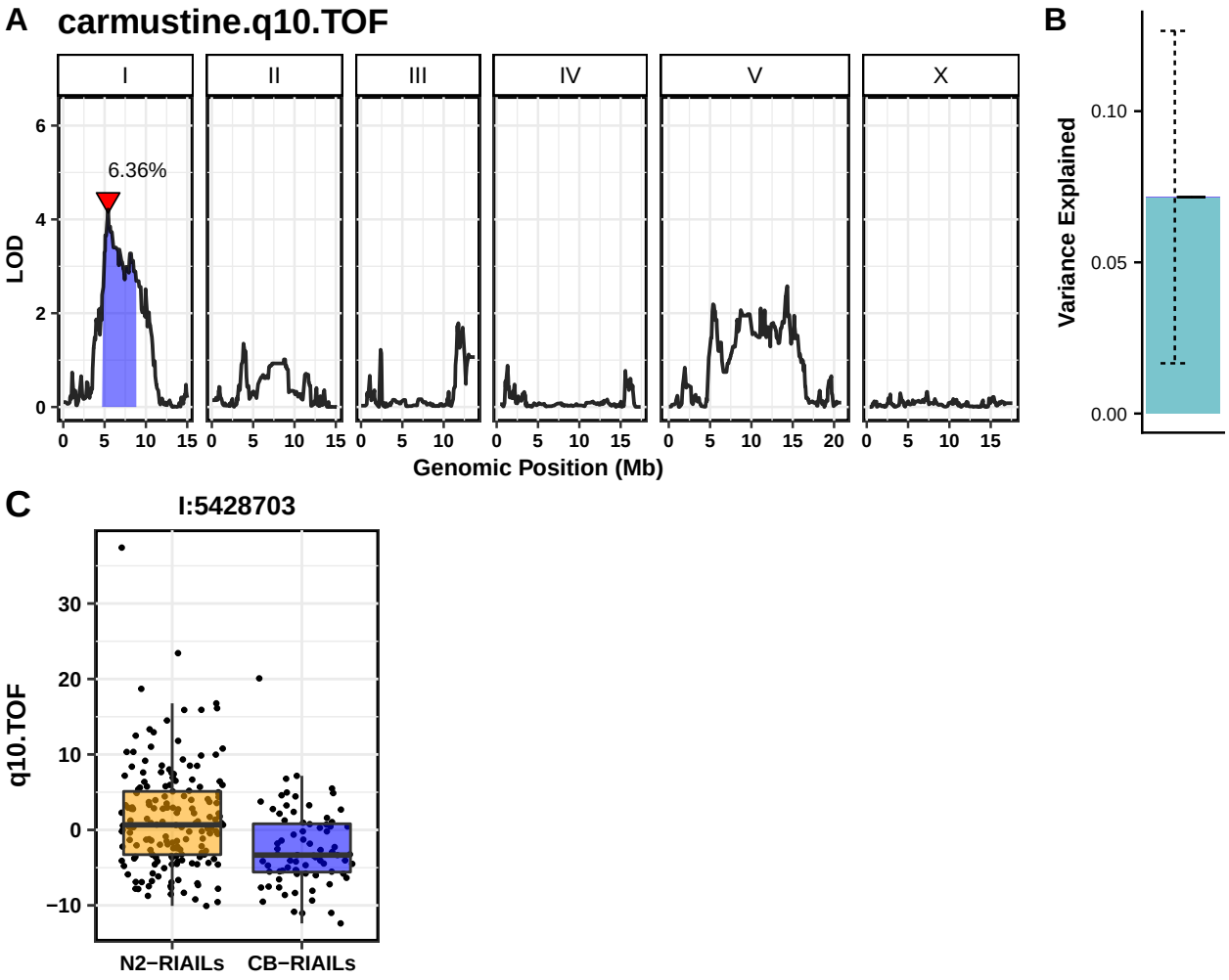

A
carmustine.mean.TOF
I
II
III
IV
V
X
LOD
6.41%
Genomic Position (Mb)
B
Variance Explained
C
V:11869708
mean.TOF
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

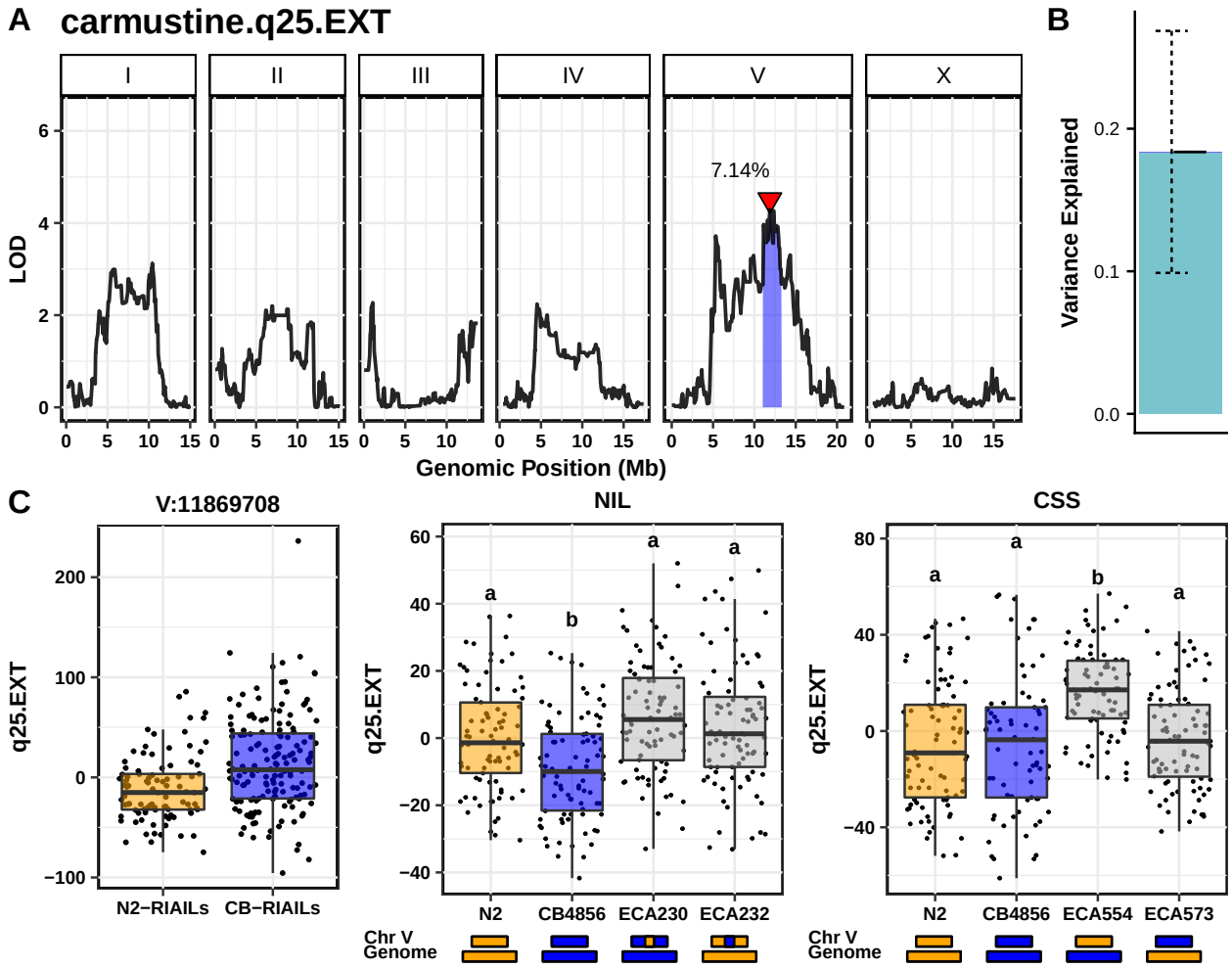

A
carmustine.median.norm.EXT
I
II
III
IV
V
X
5.72%
LOD
Genomic Position (Mb)
B
Variance Explained
C
III:11543073
median.norm.EXT
N2−RIAILs
CB−RIAILs

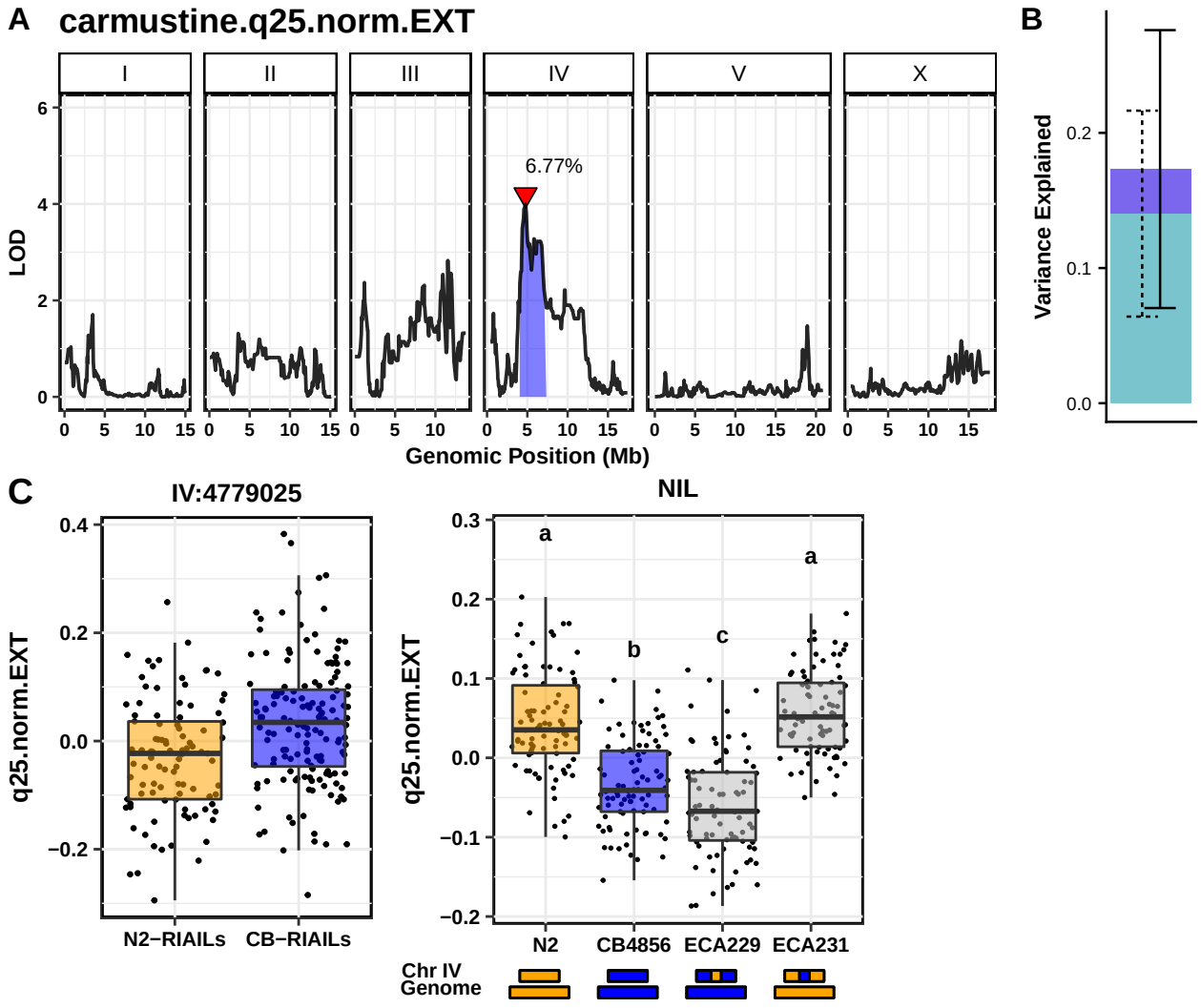

A
carmustine.n
I
II
III
IV
V
X
LOD
9.81%
Genomic Position (Mb)
B
Variance Explained
C
V:11980469
N2−RIAILs
CB−RIAILs
n
NIL
a
b
bc
ac
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
a
b
b
a
N2
CB4856
ECA554
ECA573
Chr V Genome

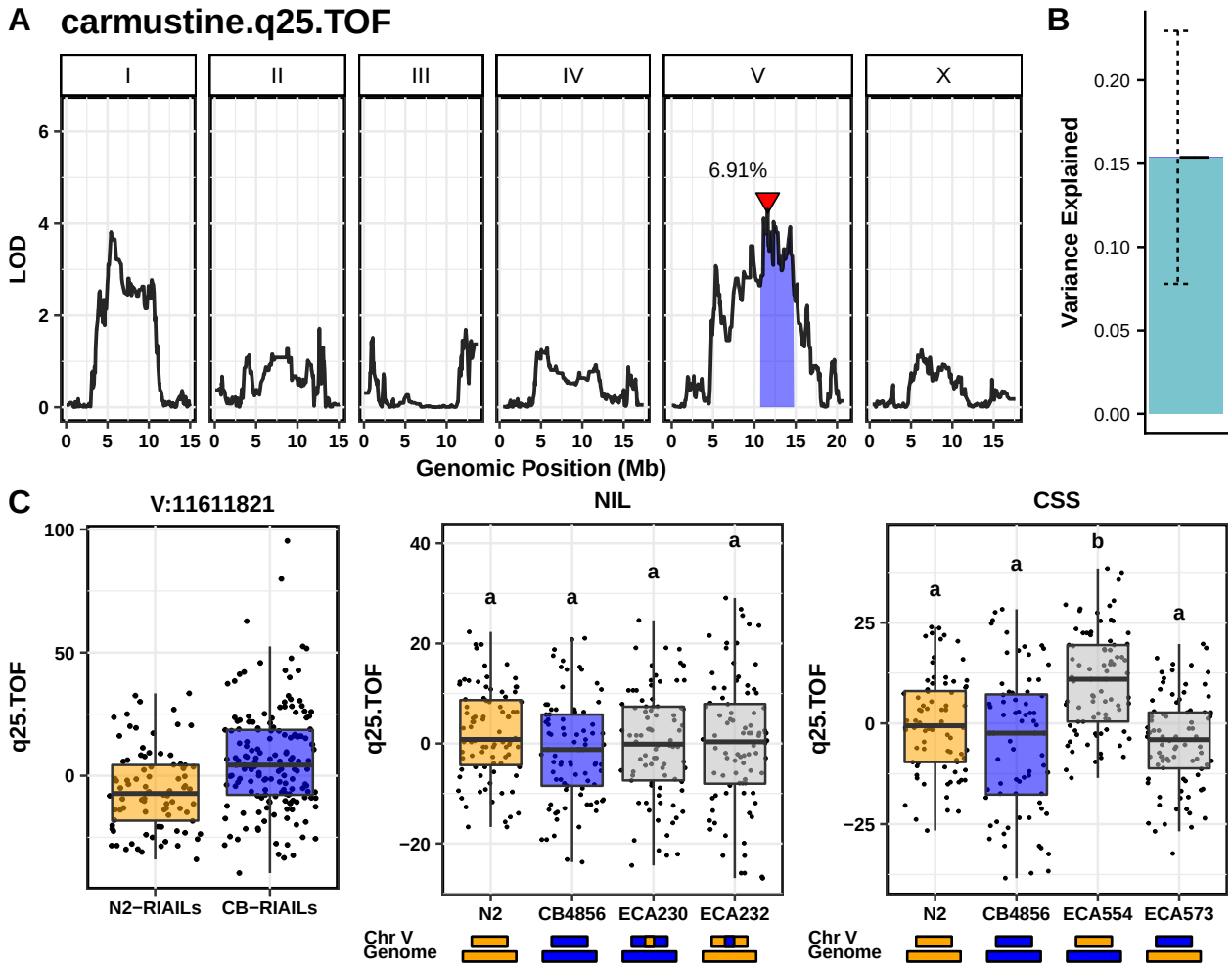

A
carmustine.norm.n
I
II
III
IV
V
X
10.32%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:11980469
norm.n
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

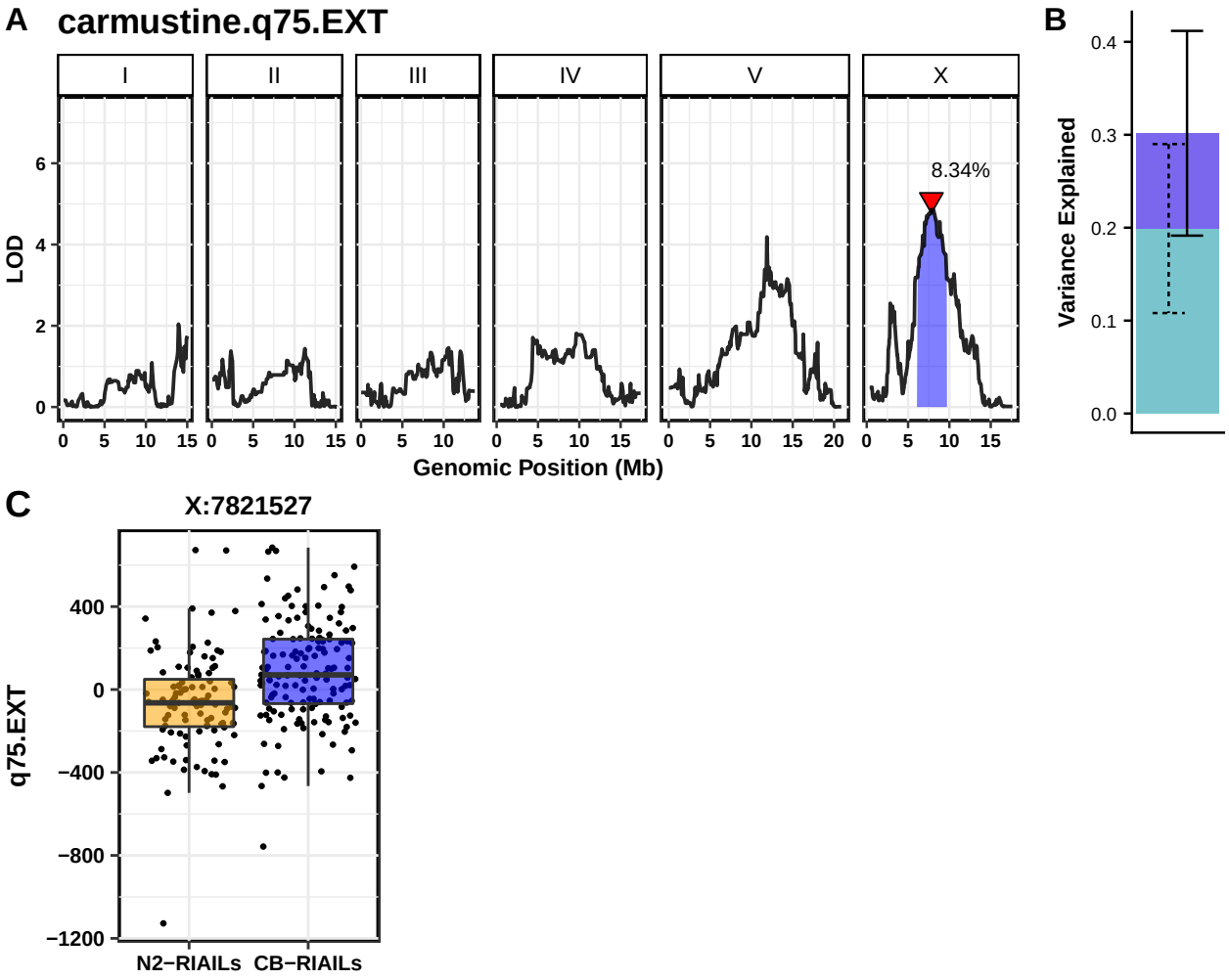

A
carmustine.q10.norm.EXT
I
II
III
IV
V
X
5.51%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:4579410
q10.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
ab
ac
c
b
N2
CB4856
ECA229
ECA231
Chr IV
Genome

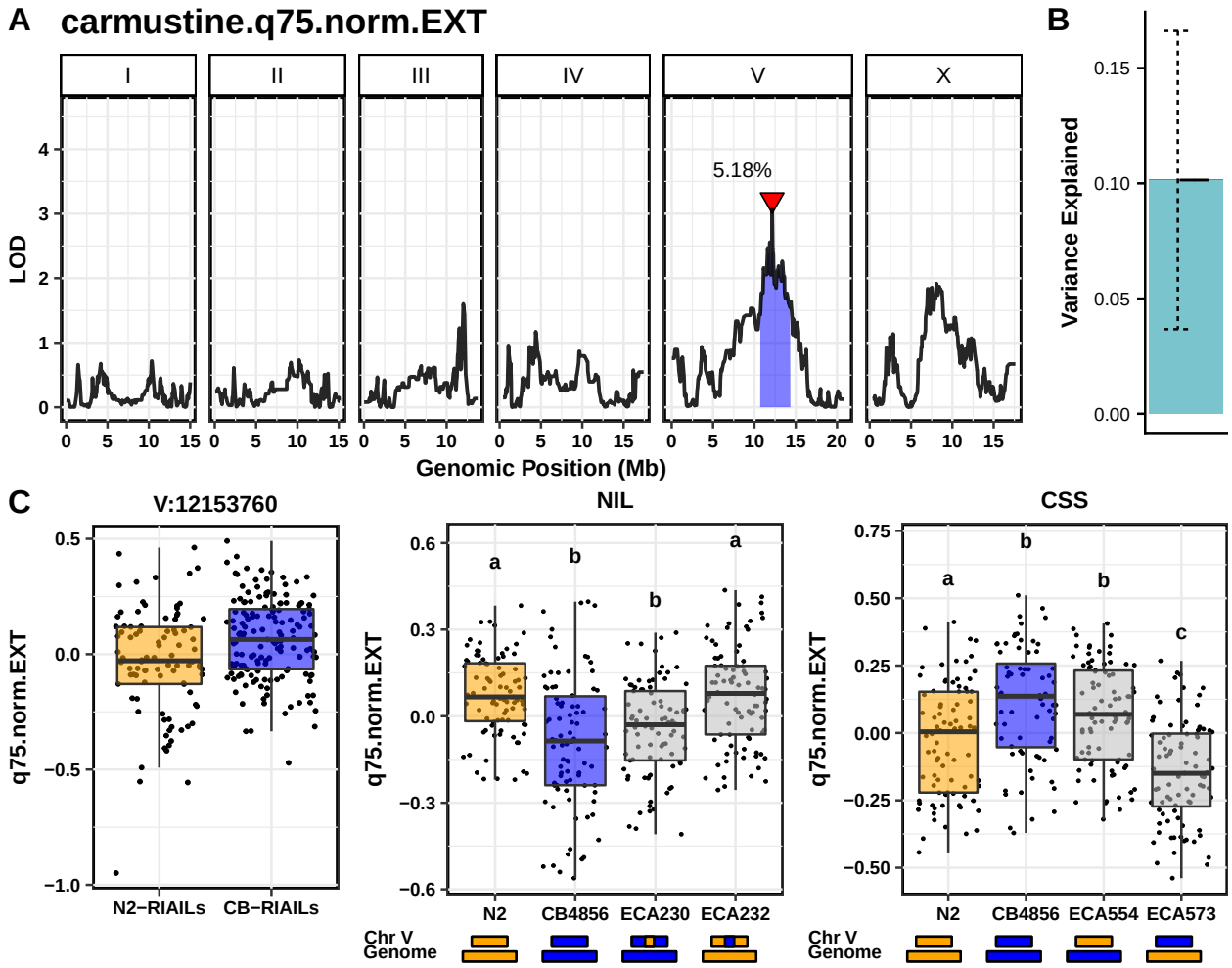

A
carmustine.q10.TOF
I
II
III
IV
V
X
6.36%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:5428703
q10.TOF
N2−RIAILs
CB−RIAILs

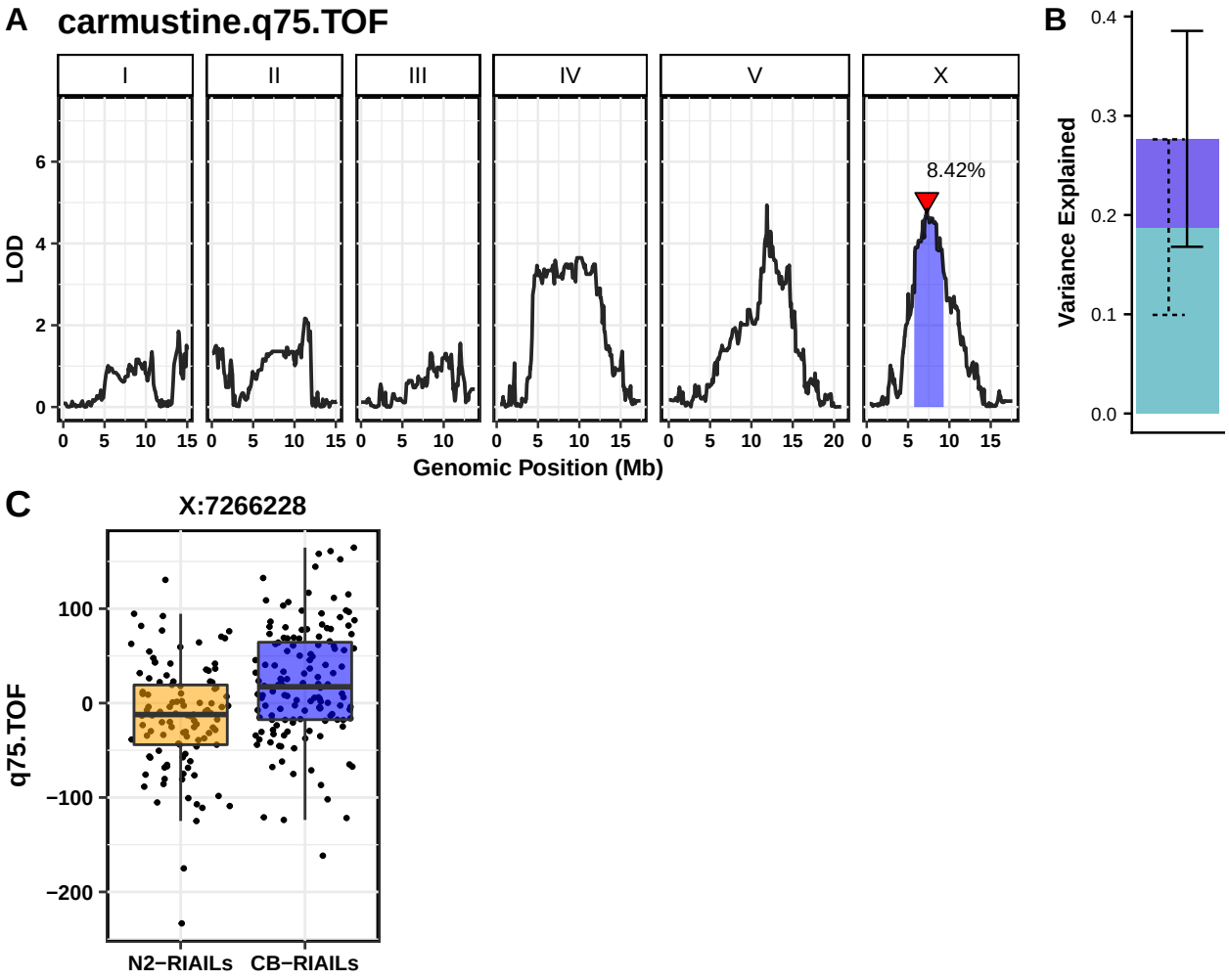

A
carmustine.q25.EXT
I
II
III
IV
V
X
LOD
7.14%
Genomic Position (Mb)
B
Variance Explained
C
V:11869708
q25.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
ECA554
ECA573

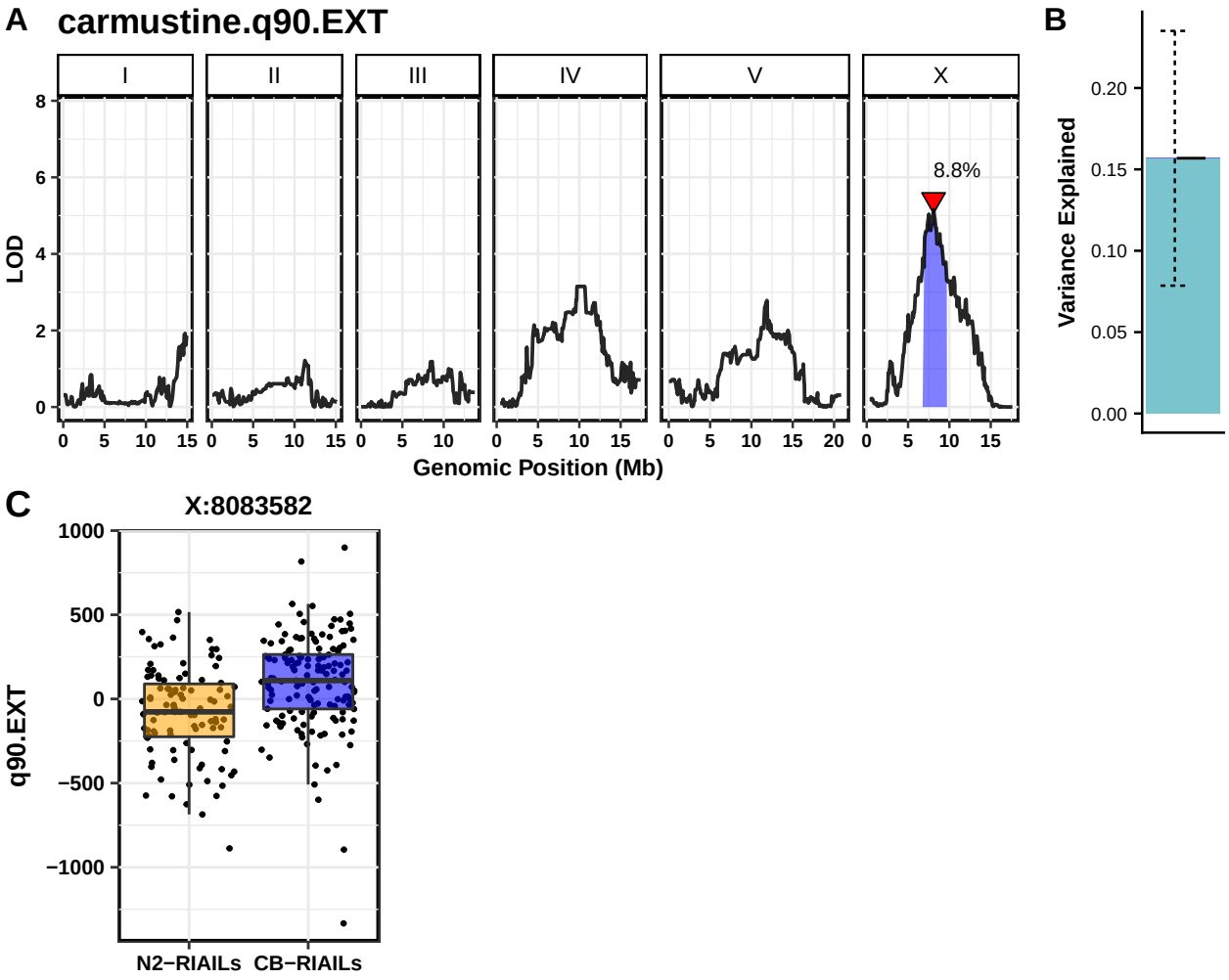

A
carmustine.q25.norm.EXT
I
II
III
IV
V
X
6.77%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:4779025
q25.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
a
b
c
a
N2
CB4856
ECA229
ECA231
Chr IV
Genome

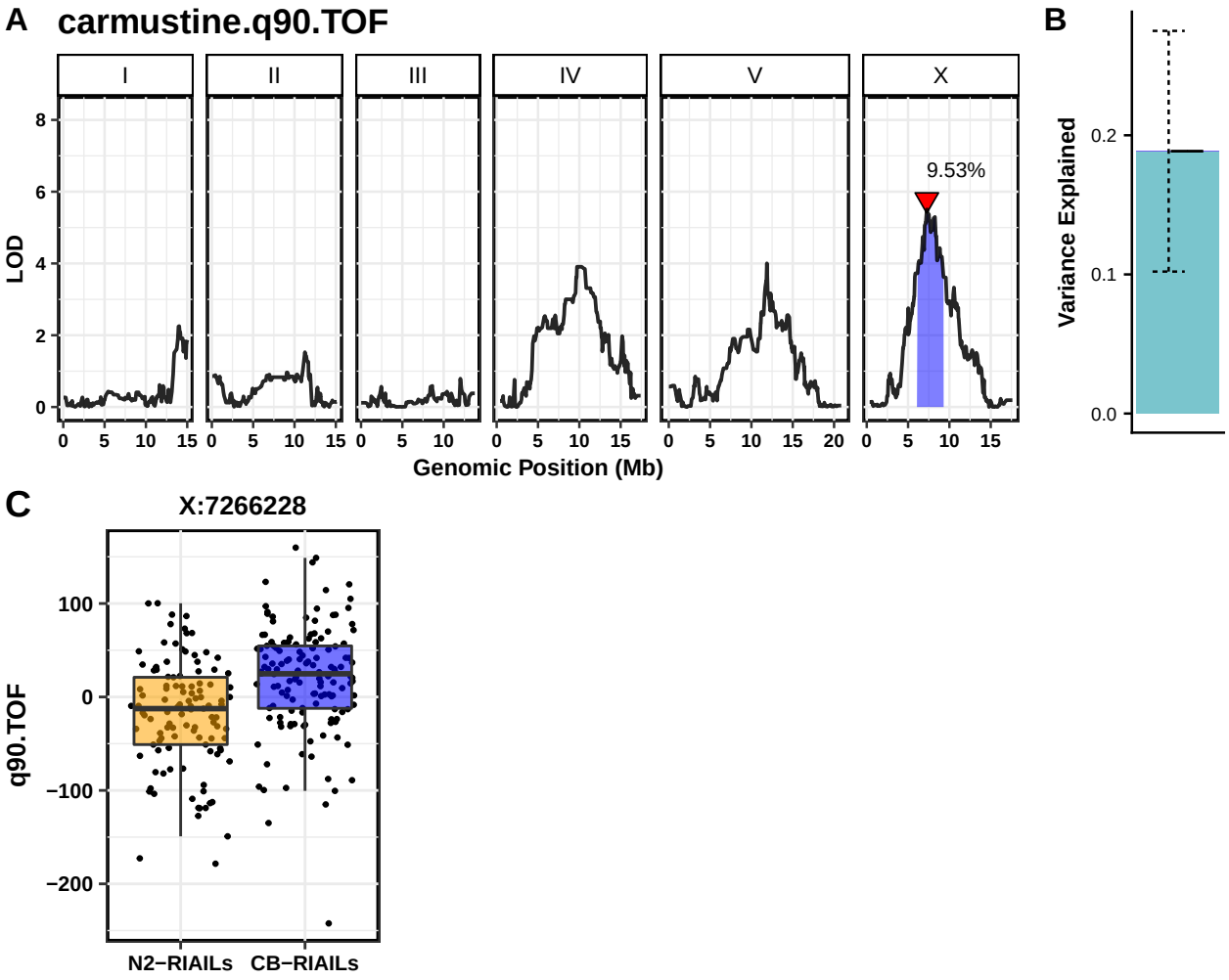

A
carmustine.q25.TOF
I
II
III
IV
V
X
6.91%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:11611821
q25.TOF
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

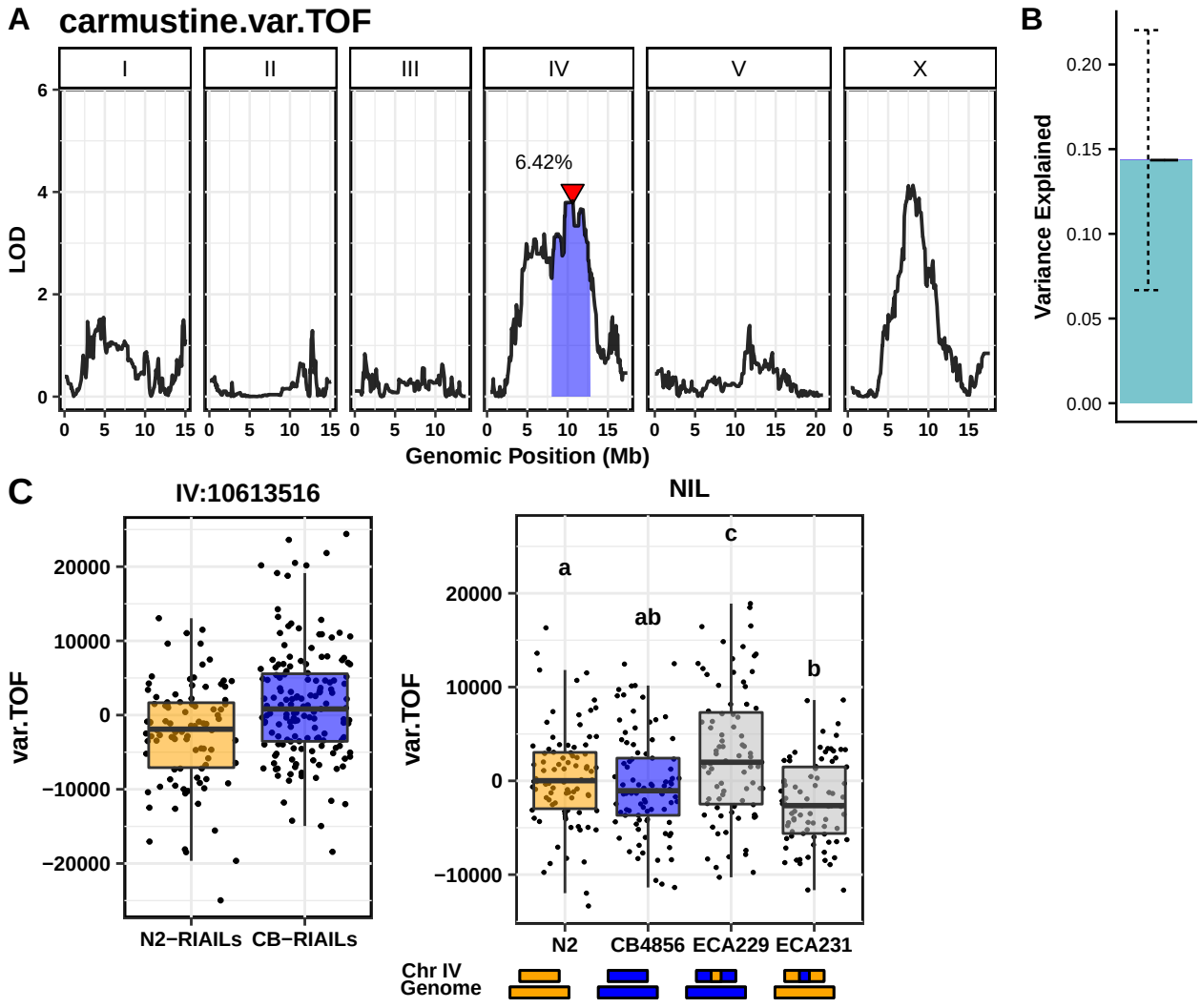

A
carmustine.q75.EXT
I
II
III
IV
V
X
8.34%
LOD
Genomic Position (Mb)
B
Variance Explained
C
X:7821527
q75.EXT
N2−RIAILs
CB−RIAILs

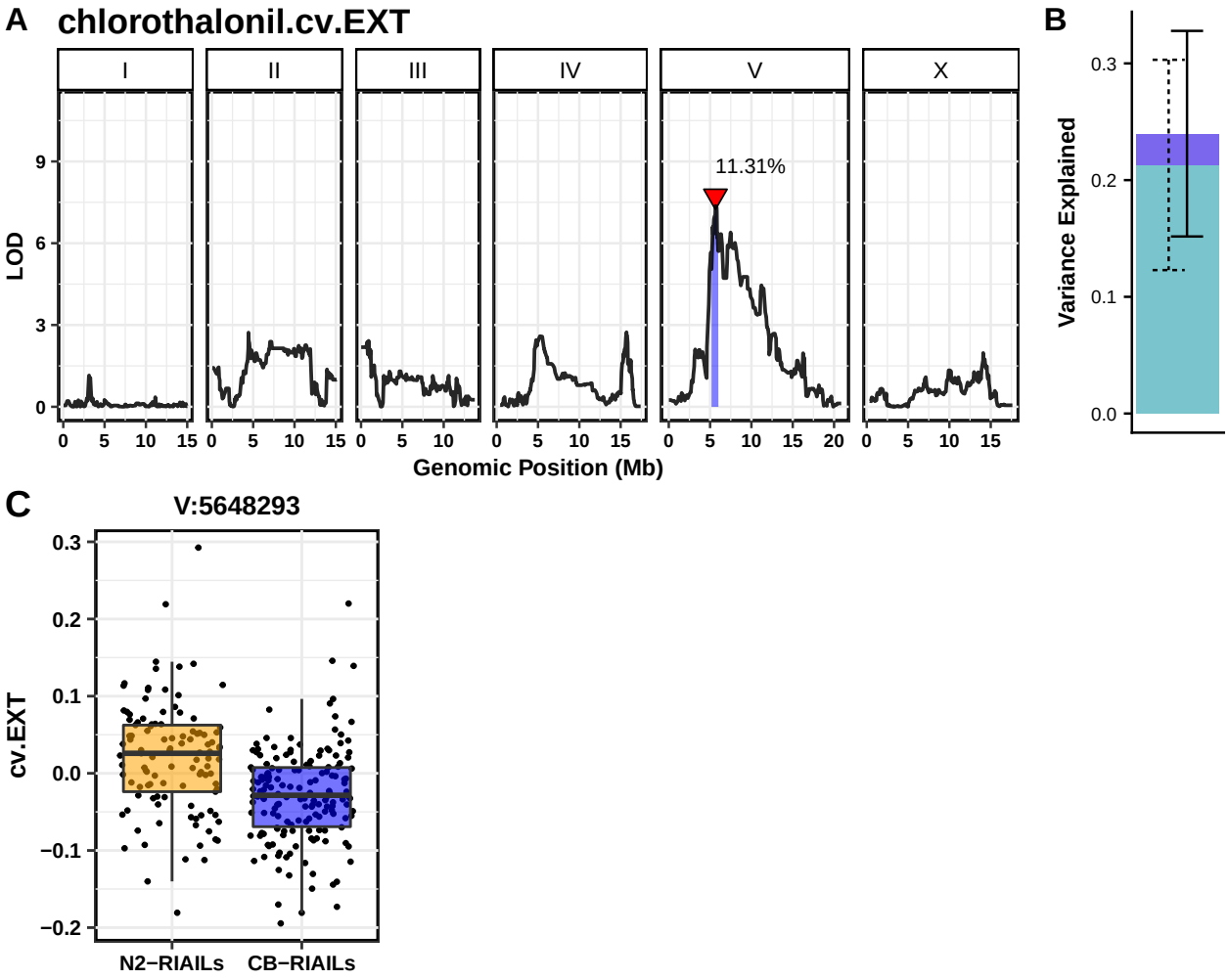

A
carmustine.q75.norm.EXT
I
II
III
IV
V
X
LOD
5.18%
Genomic Position (Mb)
B
Variance Explained
C
V:12153760
q75.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

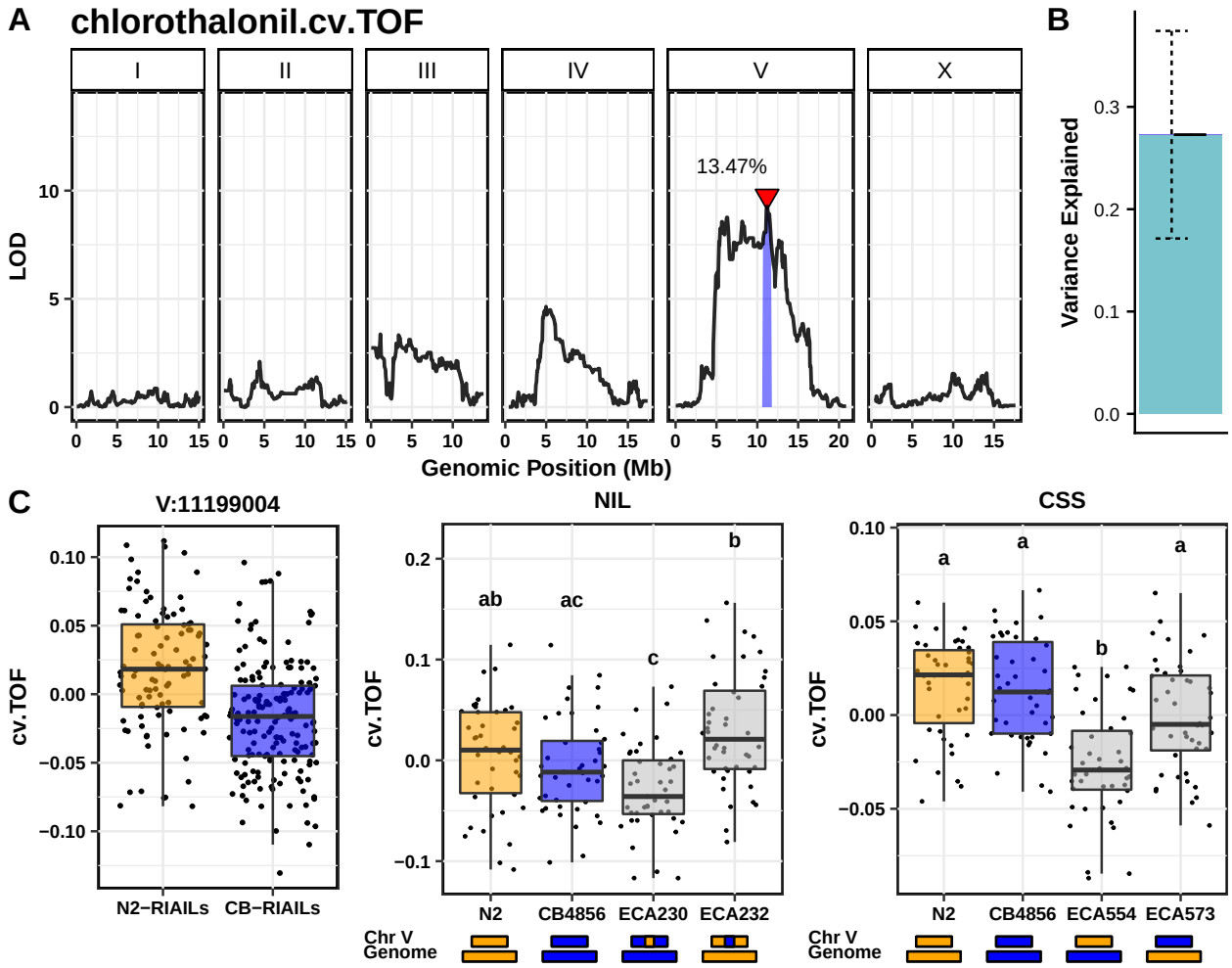

A
carmustine.q75.TOF
I
II
III
IV
V
X
8.42%
LOD
Genomic Position (Mb)
B
Variance Explained
C
X:7266228
q75.TOF
N2−RIAILs
CB−RIAILs

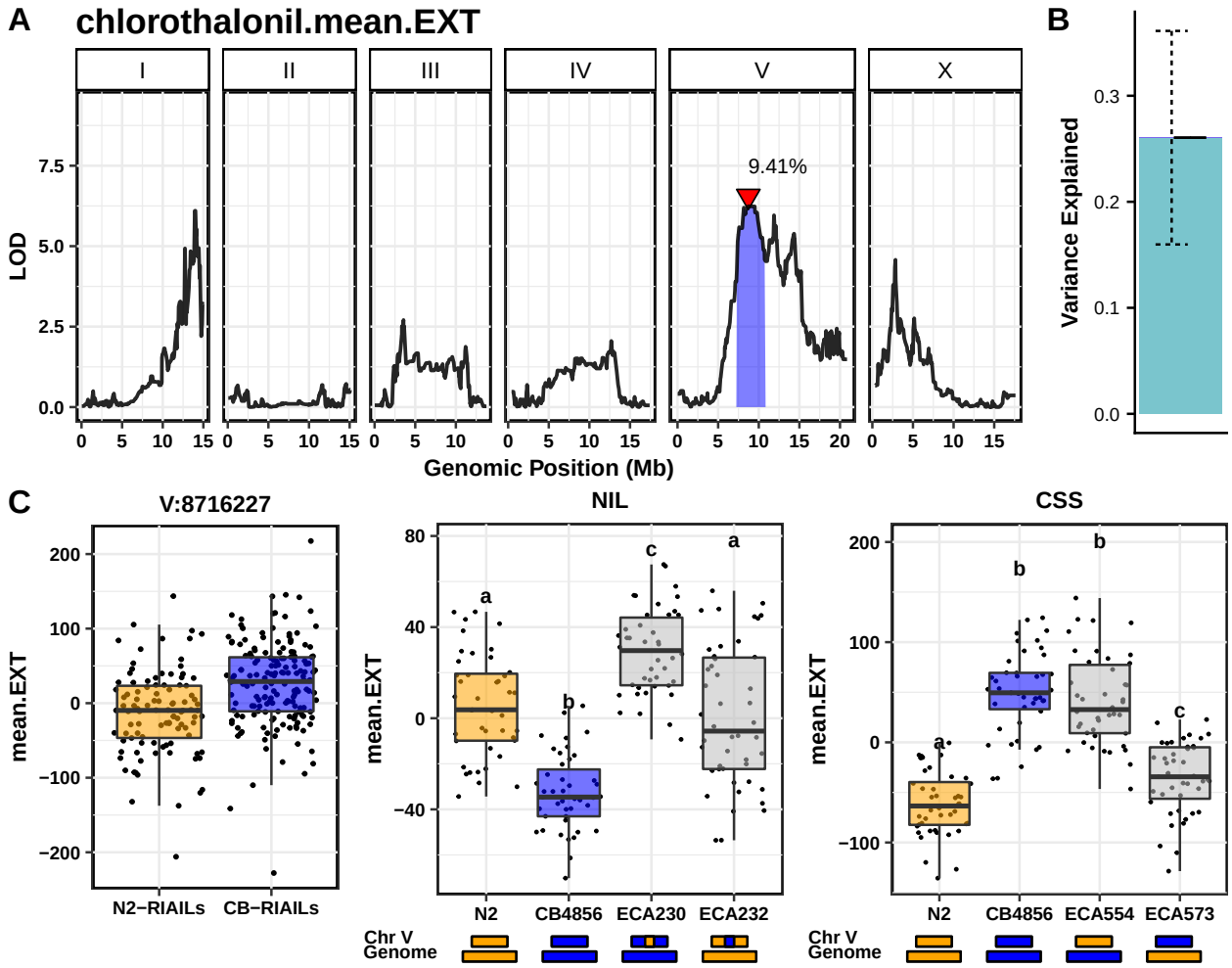

A
carmustine.q90.EXT
I
II
III
IV
V
X
LOD
8.8%
Genomic Position (Mb)
B
Variance Explained
C
X:8083582
q90.EXT
N2−RIAILs
CB−RIAILs

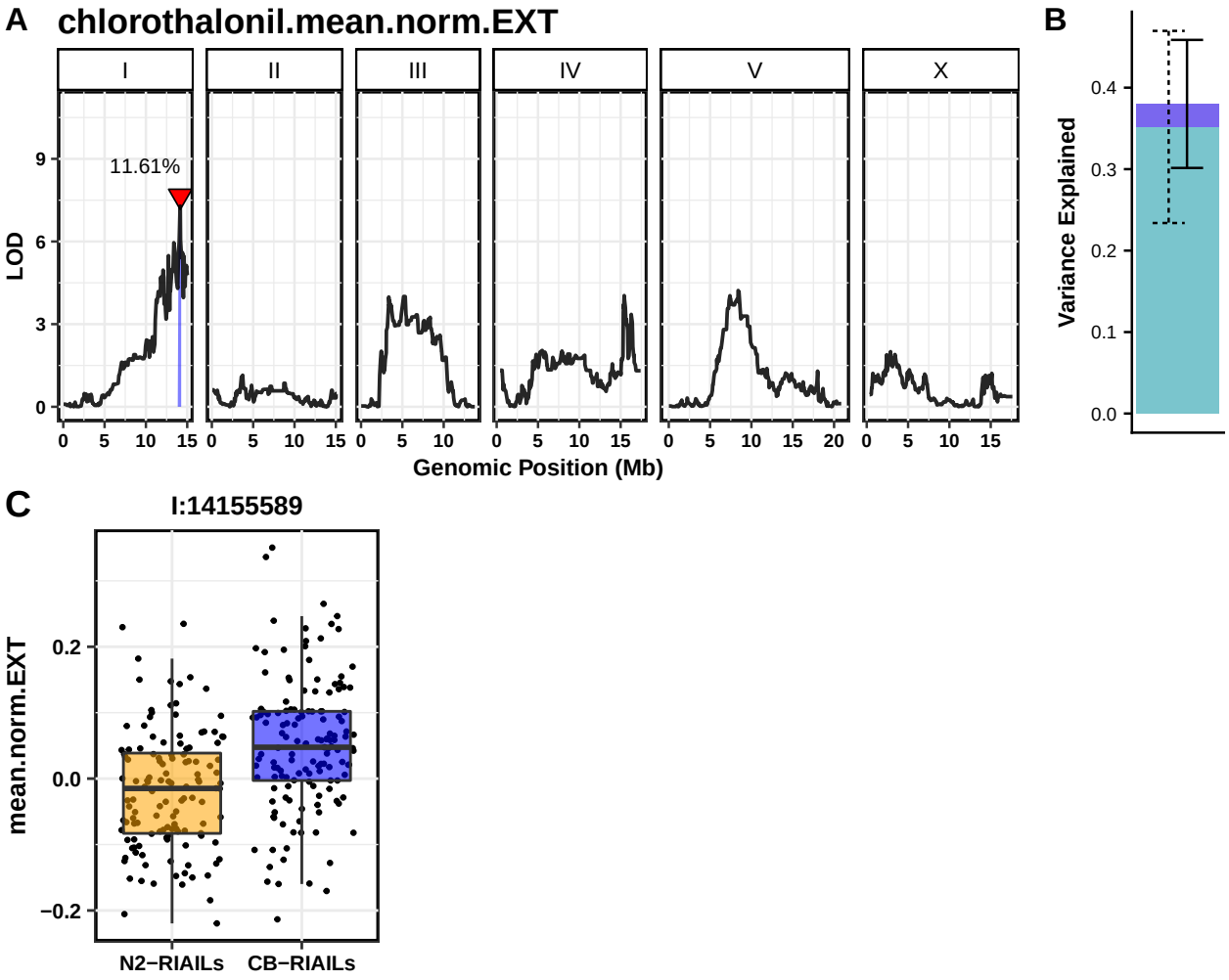

A
carmustine.q90.TOF
I
II
III
IV
V
X
LOD
9.53%
Genomic Position (Mb)
B
Variance Explained
C
X:7266228
q90.TOF
N2−RIAILs
CB−RIAILs

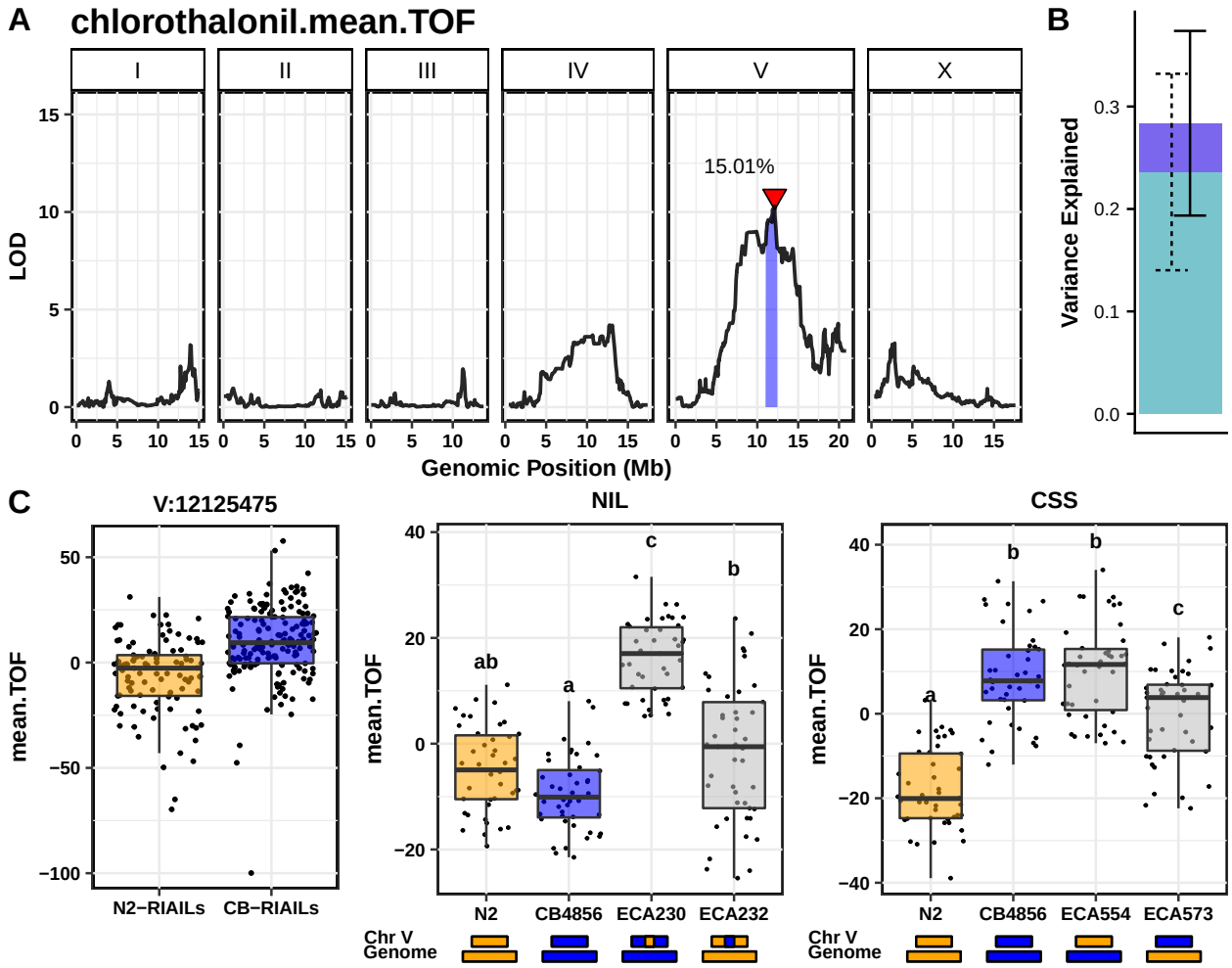

A
carmustine.var.TOF
I
II
III
IV
V
X
6.42%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:10613516
var.TOF
N2−RIAILs
CB−RIAILs
NIL
a
ab
c
b
N2
CB4856
ECA229
ECA231
Chr IV
Genome

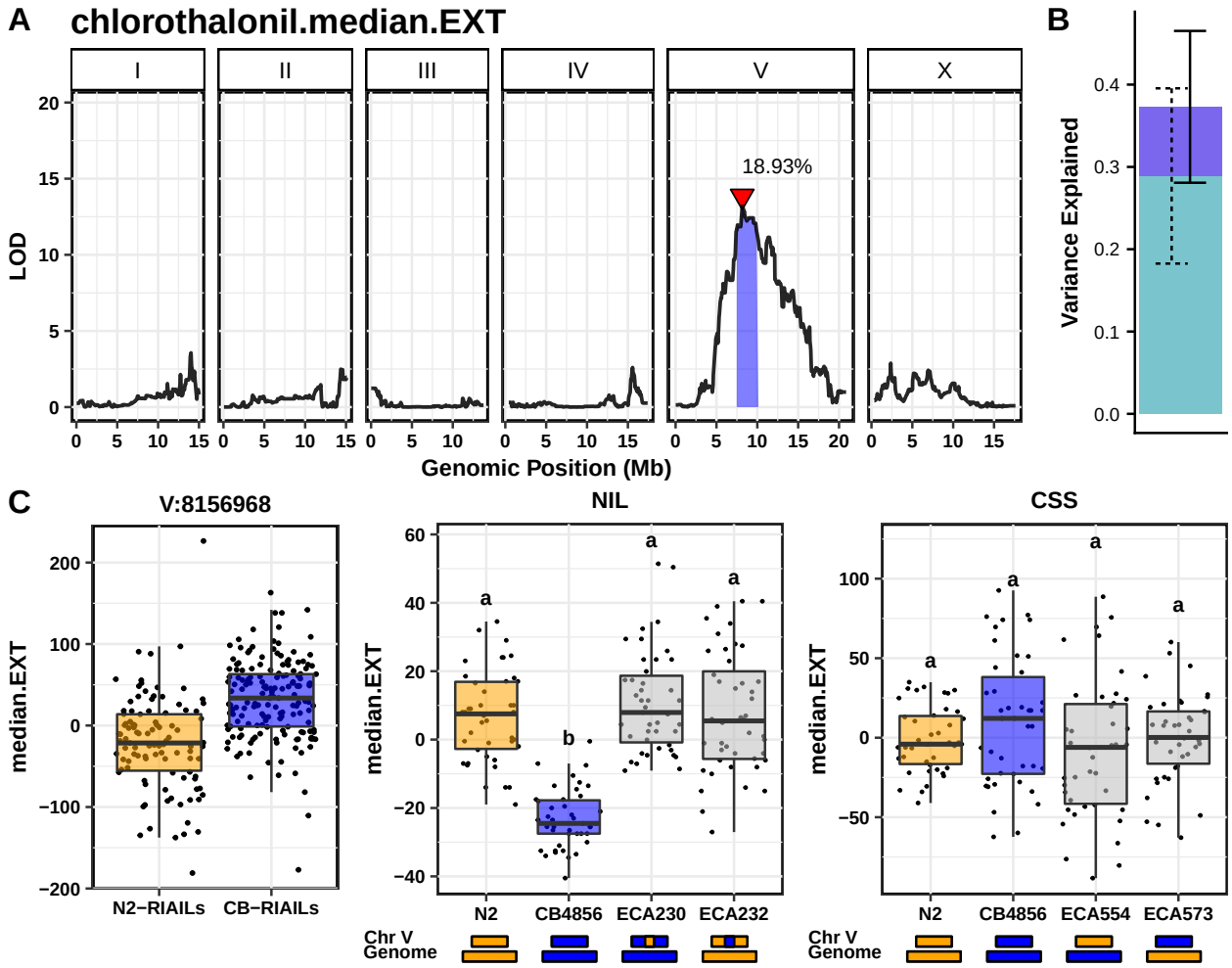

A
chlorothalonil.cv.EXT
I
II
III
IV
V
X
LOD
11.31%
Genomic Position (Mb)
B
Variance Explained
C
V:5648293
cv.EXT
N2−RIAILs
CB−RIAILs

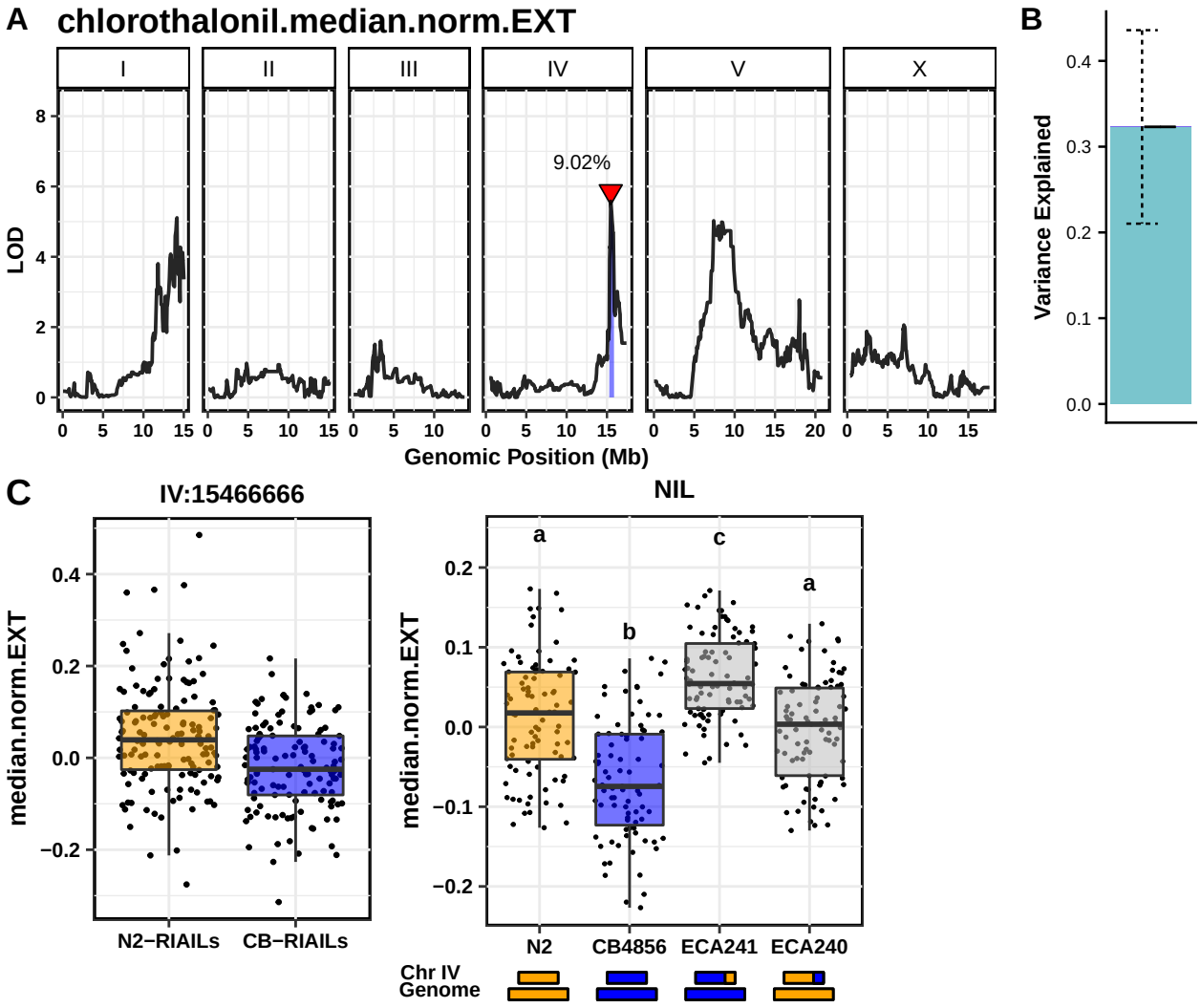

A
chlorothalonil.cv.TOF
I
II
III
IV
V
X
13.47%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:11199004
cv.TOF
N2−RIAILs
CB−RIAILs
NIL
ab
ac
c
b
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
a
a
b
a
N2
CB4856
ECA554
ECA573
Chr V Genome

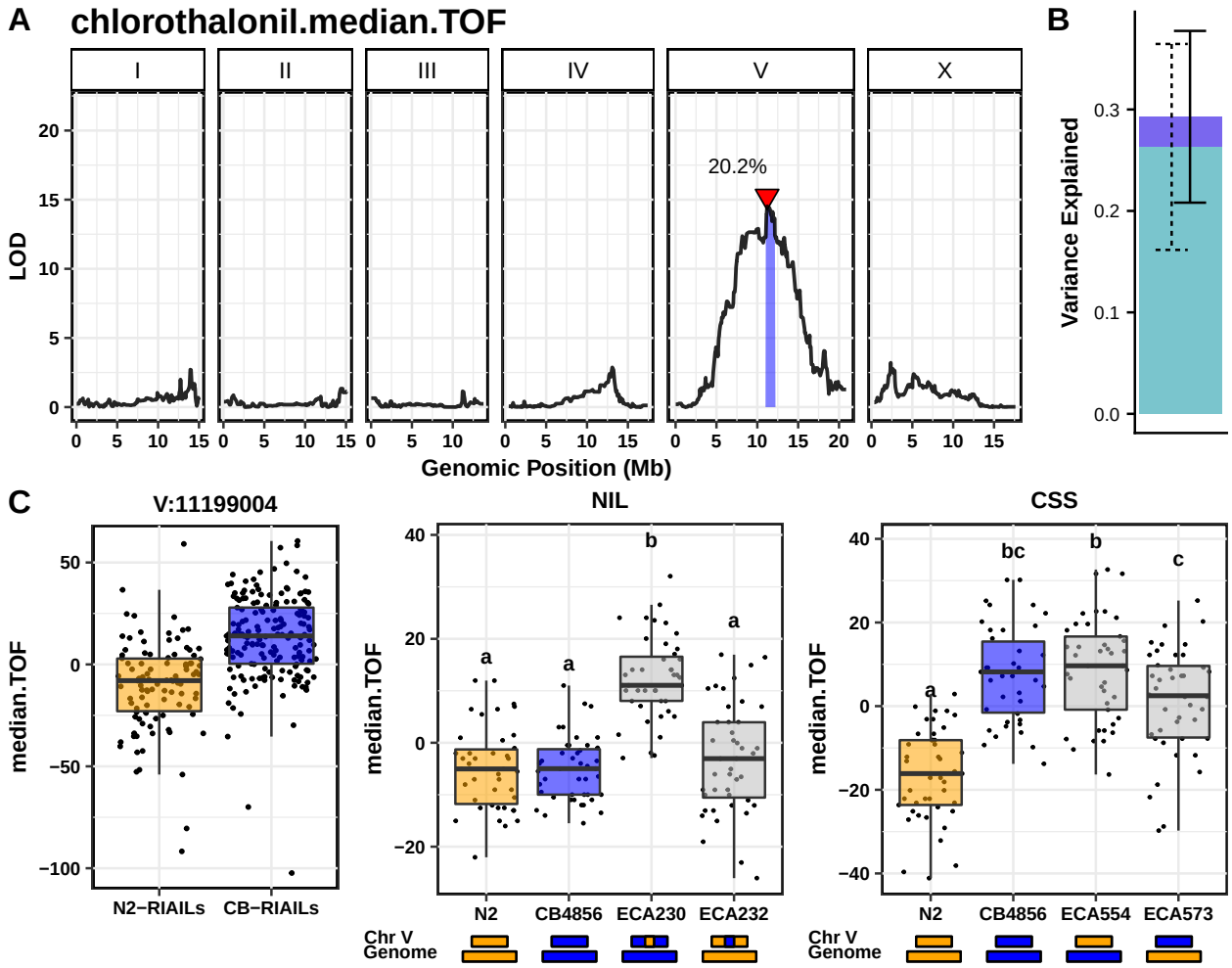

A
chlorothalonil.mean.EXT
I
II
III
IV
V
X
LOD
9.41%
Genomic Position (Mb)
B
Variance Explained
C
V:8716227
mean.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573

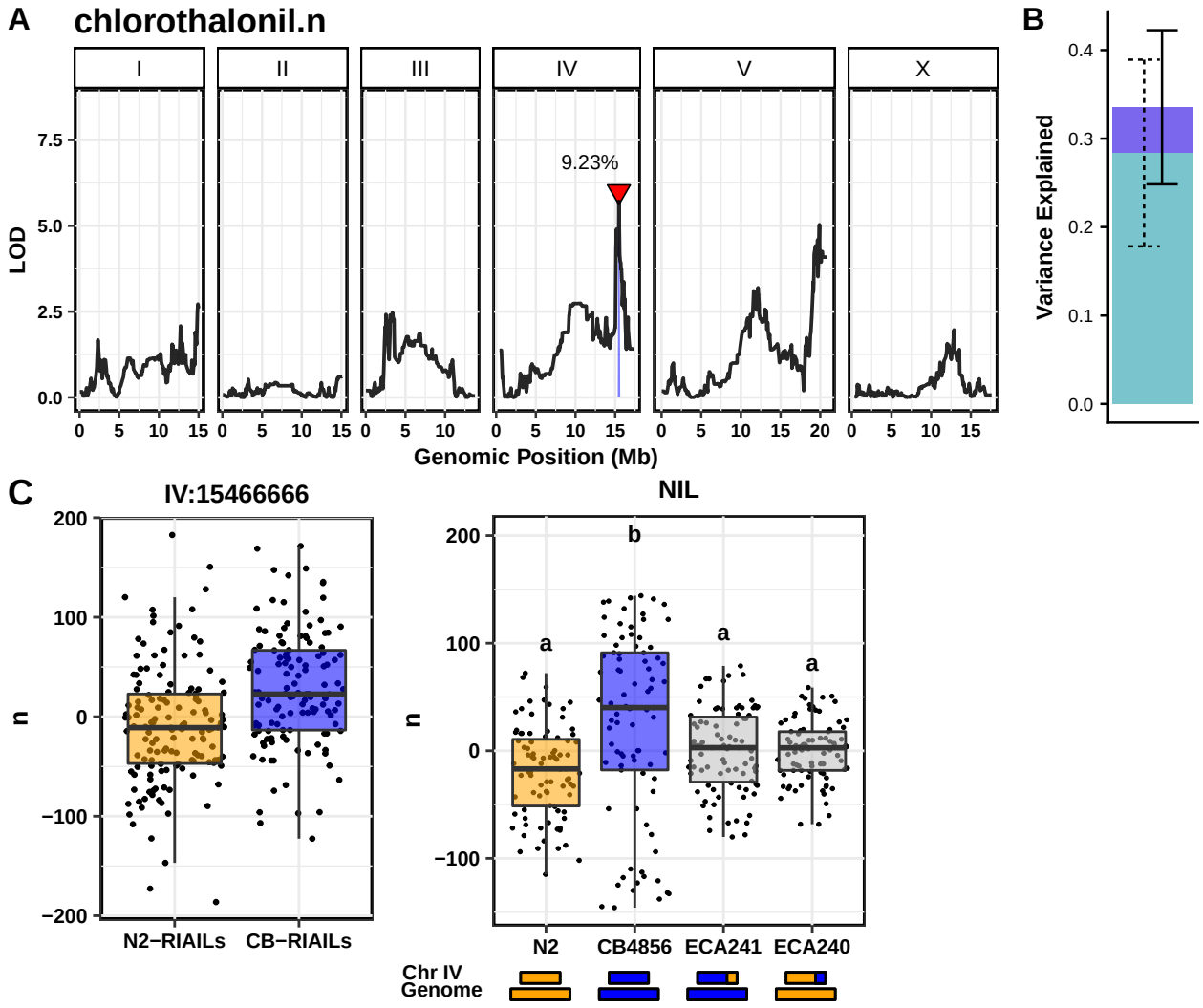

A
chlorothalonil.mean.norm.EXT
I
II
III
IV
V
X
11.61%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:14155589
mean.norm.EXT
N2−RIAILs
CB−RIAILs

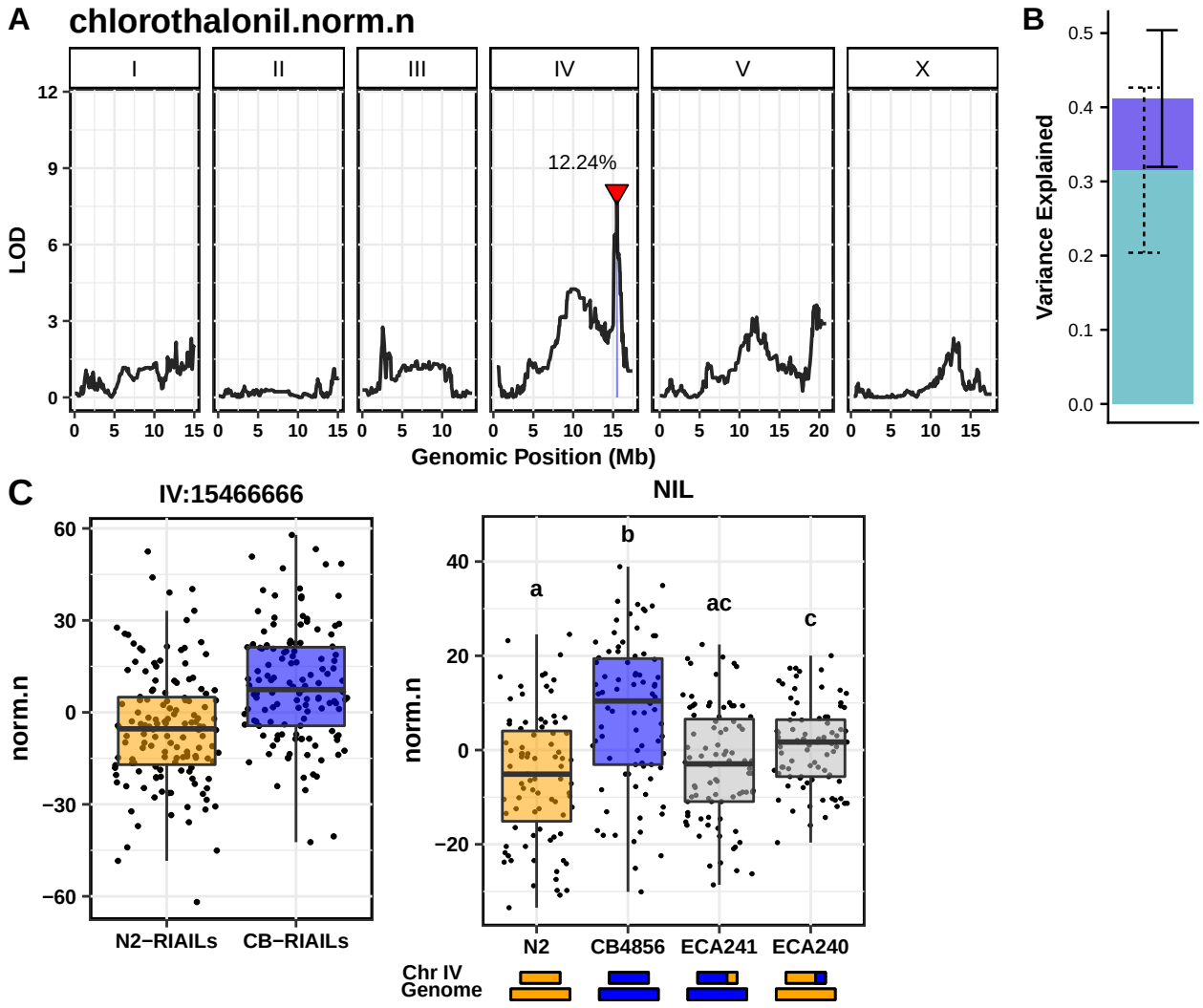

A
chlorothalonil.mean.TOF
I
II
III
IV
V
X
15.01%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:12125475
mean.TOF
N2−RIAILs
CB−RIAILs
NIL
ab
a
c
b
N2
CB4856
ECA230
ECA232
Chr V
Genome
CSS
a
b
b
c
N2
CB4856
ECA554
ECA573
Chr V
Genome

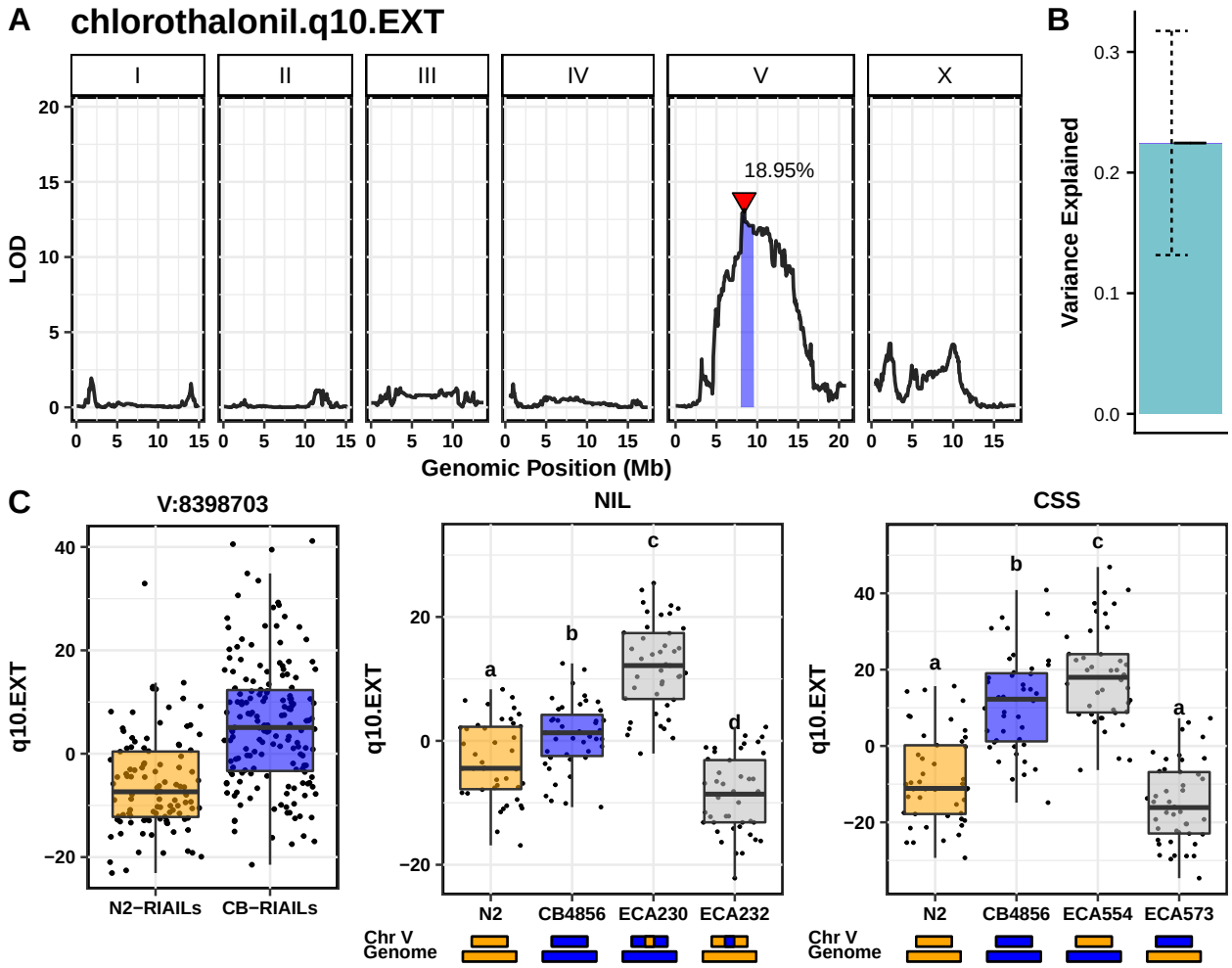

A
chlorothalonil.median.EXT
I
II
III
IV
V
X
LOD
18.93%
Genomic Position (Mb)
B
Variance Explained
C
V:8156968
median.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
ECA554
ECA573

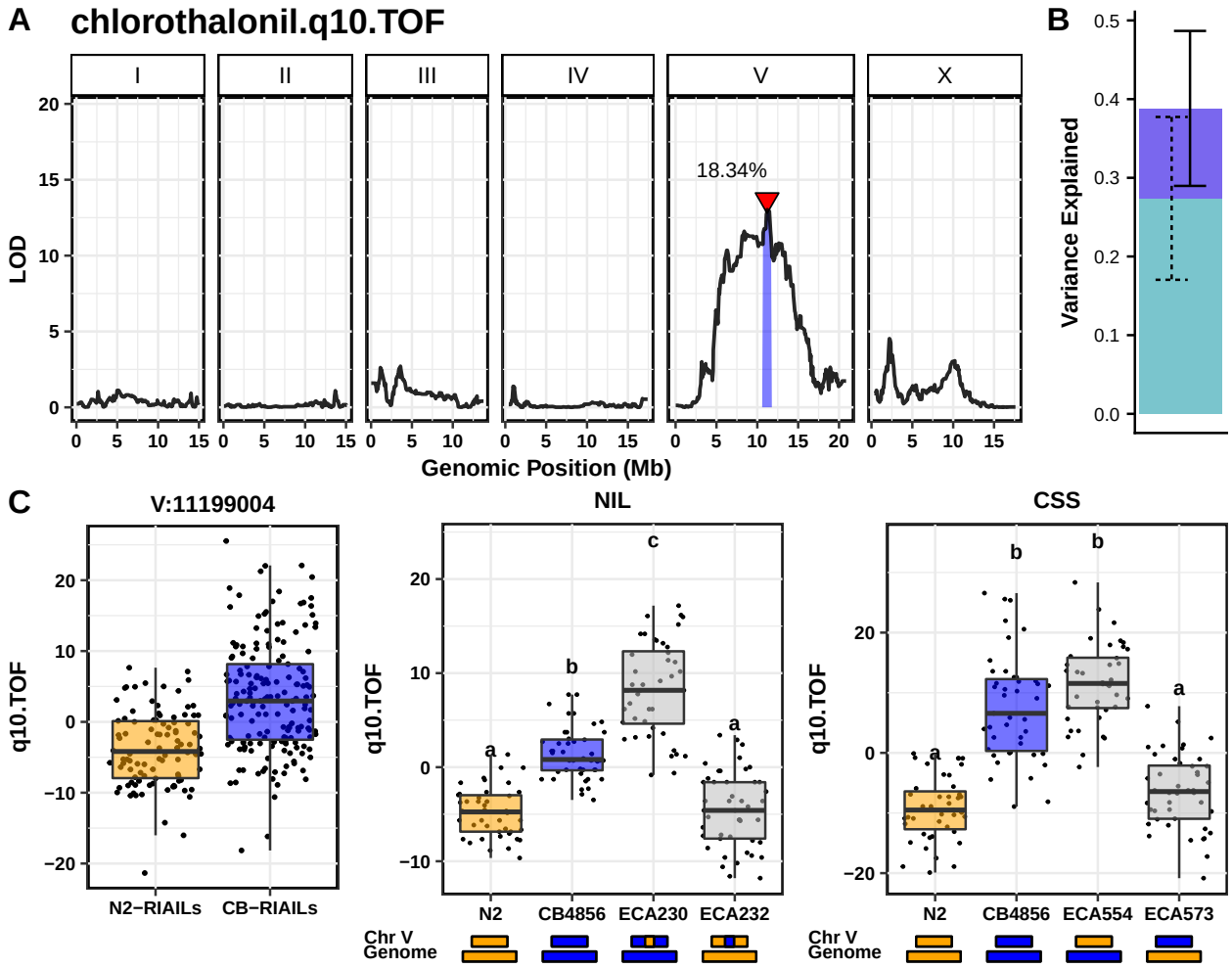

A
chlorothalonil.median.norm.EXT
I
II
III
IV
V
X
9.02%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:15466666
median.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
a
b
c
a
N2
CB4856
ECA241
ECA240
Chr IV
Genome

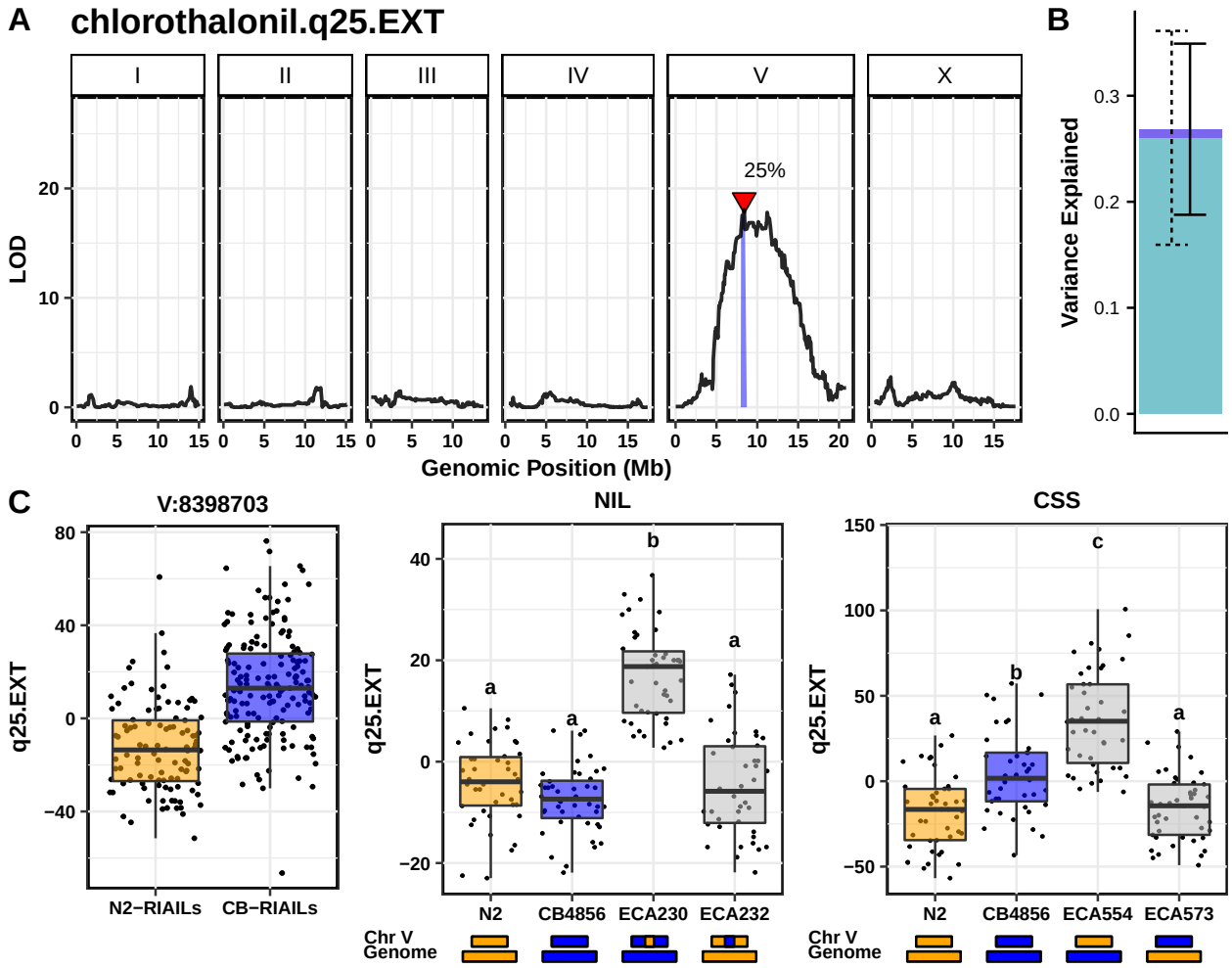

A
chlorothalonil.median.TOF
I
II
III
IV
V
X
LOD
20.2%
Genomic Position (Mb)
B
Variance Explained
C
V:11199004
median.TOF
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

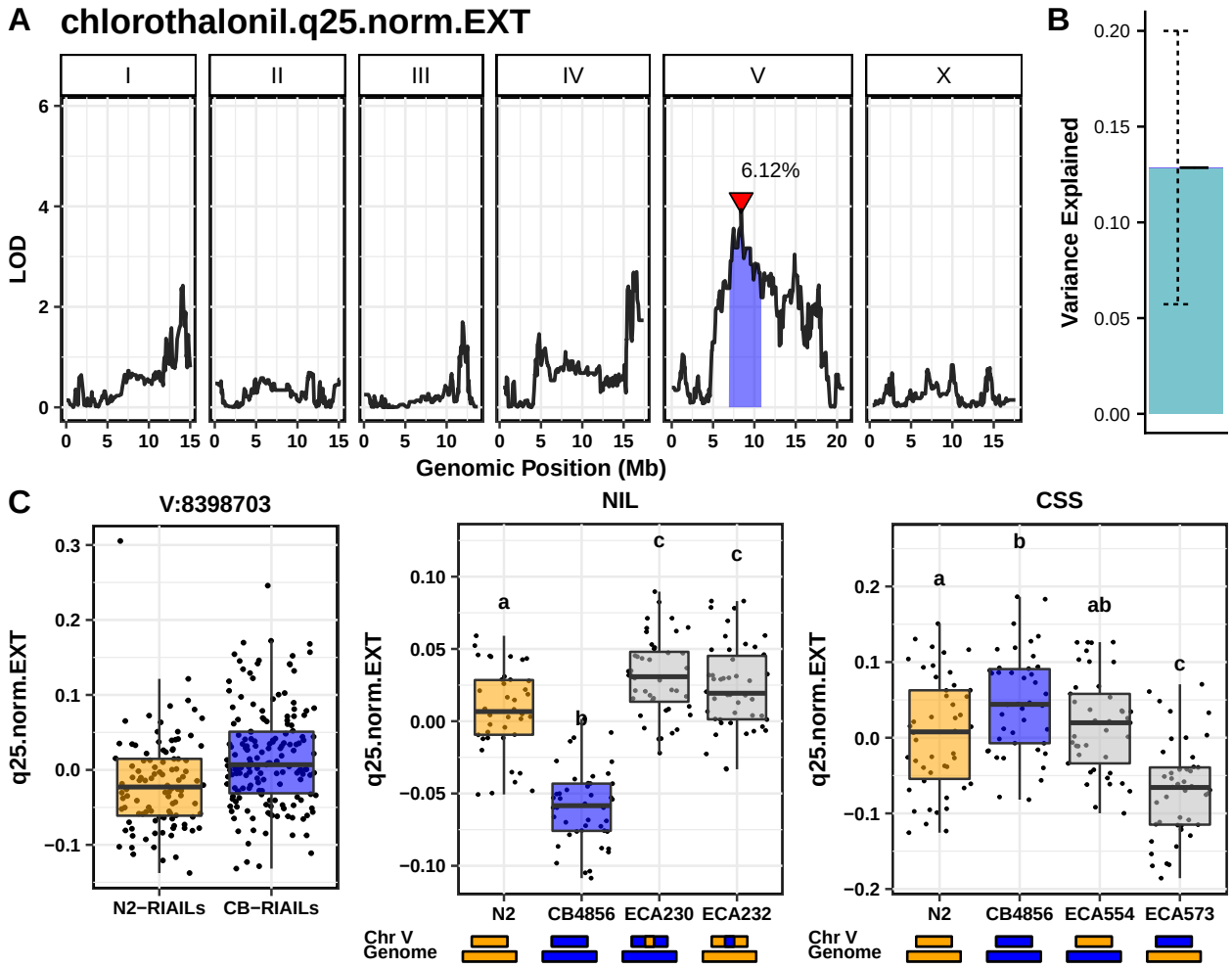

A
chlorothalonil.n
I
II
III
IV
V
X
9.23%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:15466666
n
N2−RIAILs
CB−RIAILs
NIL
a
b
a
a
N2
CB4856
ECA241
ECA240
Chr IV
Genome

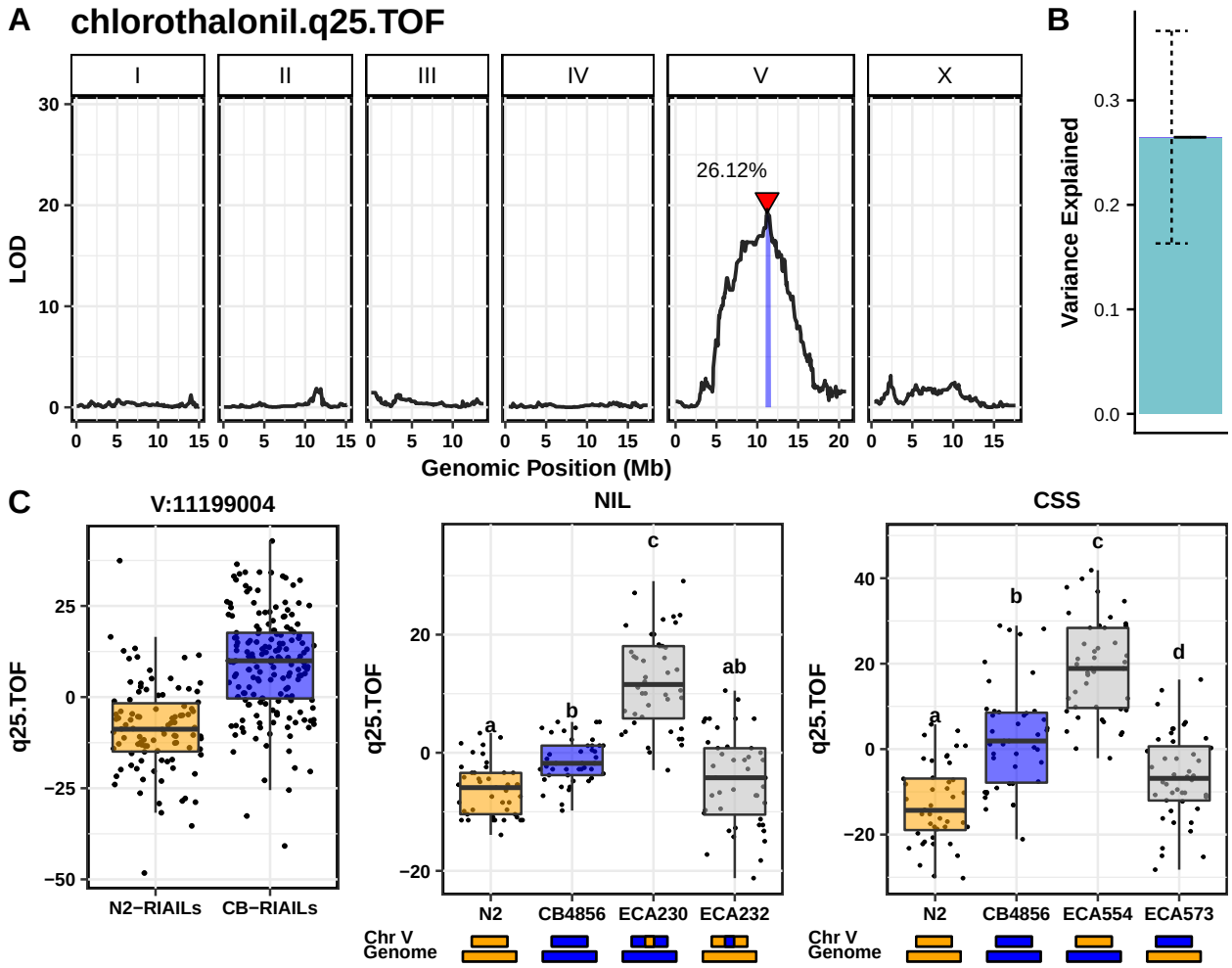

A
chlorothalonil.norm.n
I
II
III
IV
V
X
LOD
12.24%
Genomic Position (Mb)
B
Variance Explained
C
IV:15466666
norm.n
N2−RIAILs
CB−RIAILs
NIL
a
b
ac
c
N2
CB4856
ECA241
ECA240
Chr IV
Genome

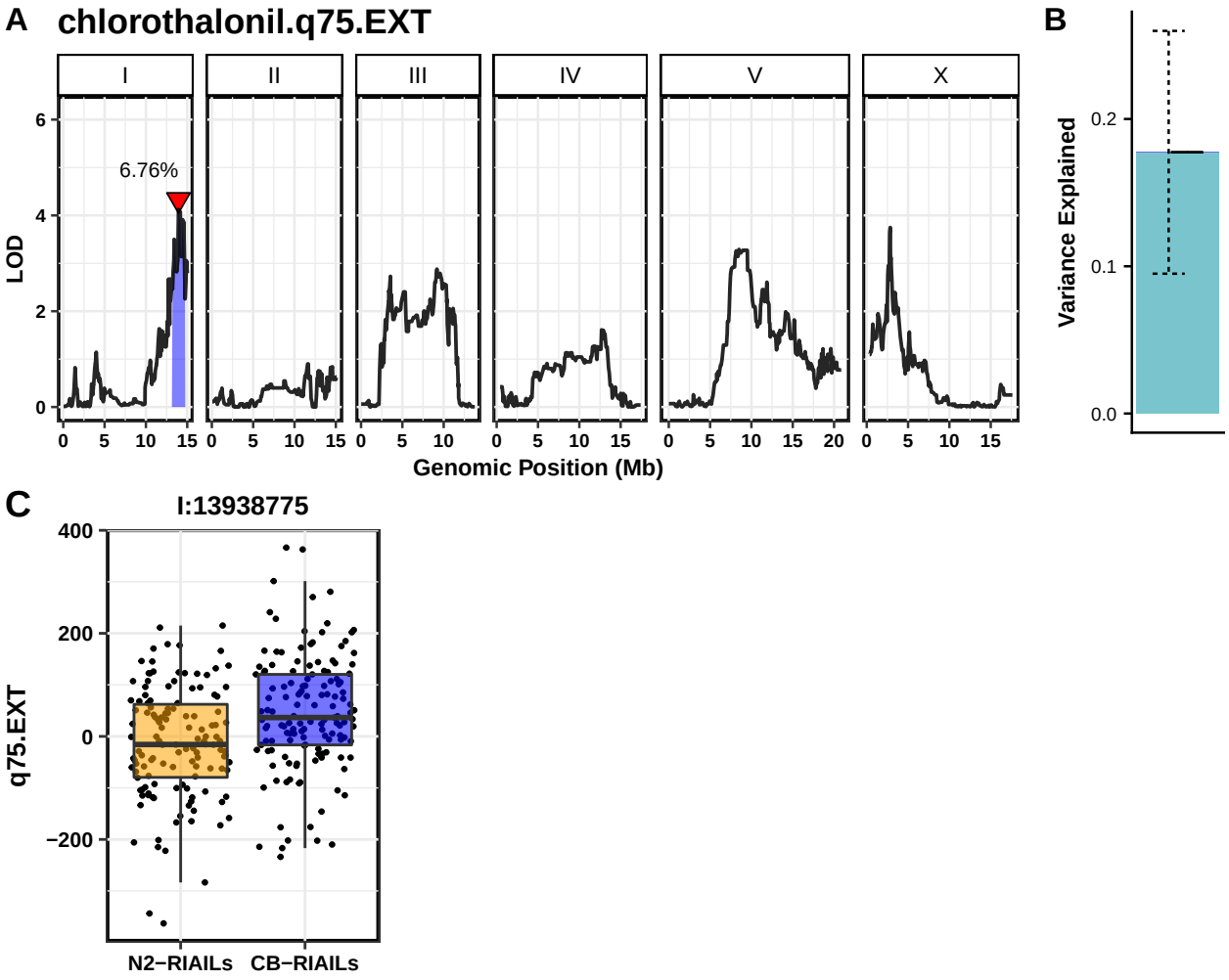

A
chlorothalonil.q10.EXT
I
II
III
IV
V
X
LOD
18.95%
Genomic Position (Mb)
B
Variance Explained
C
V:8398703
q10.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

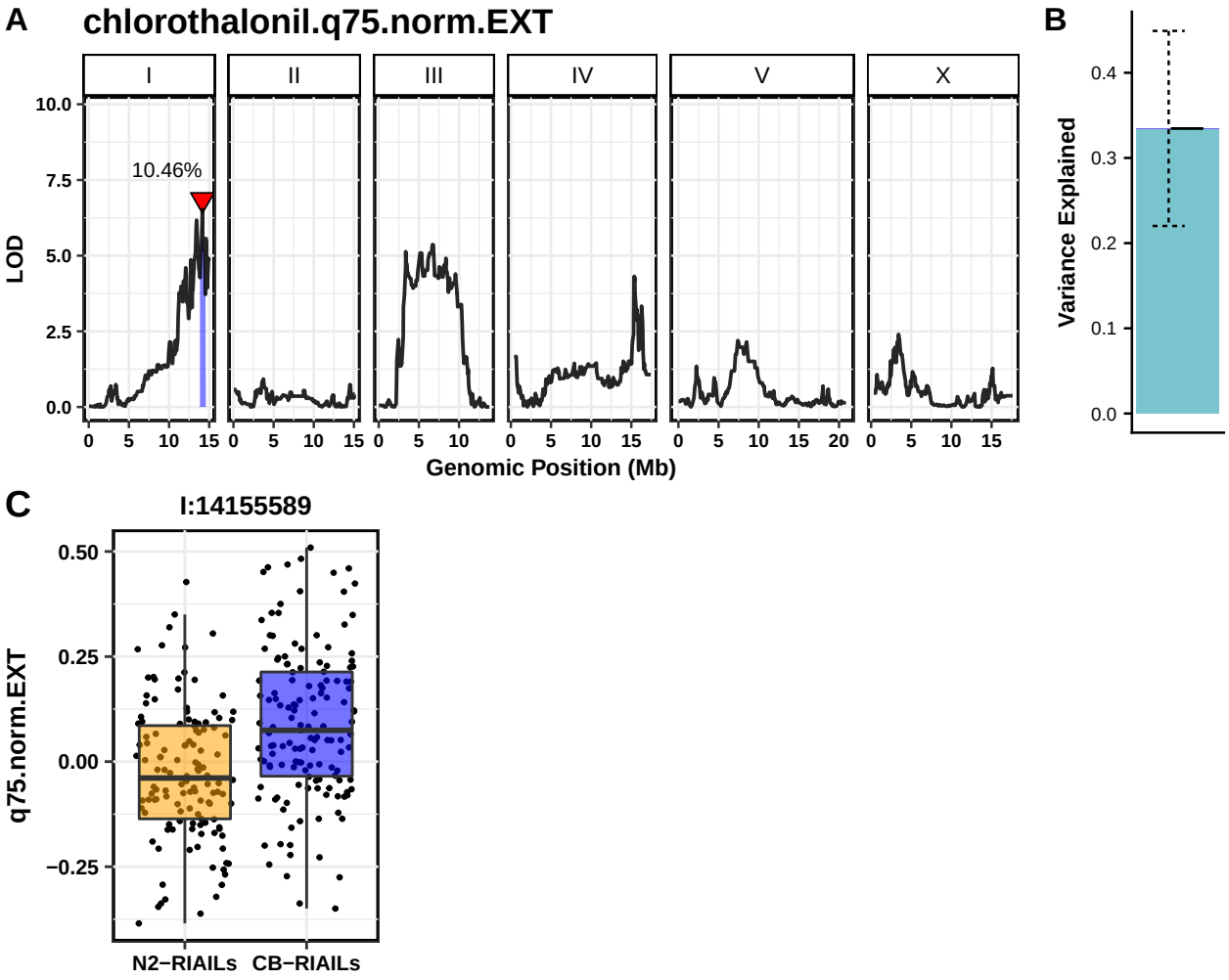

A
chlorothalonil.q10.TOF
I
II
III
IV
V
X
18.34%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:11199004
q10.TOF
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

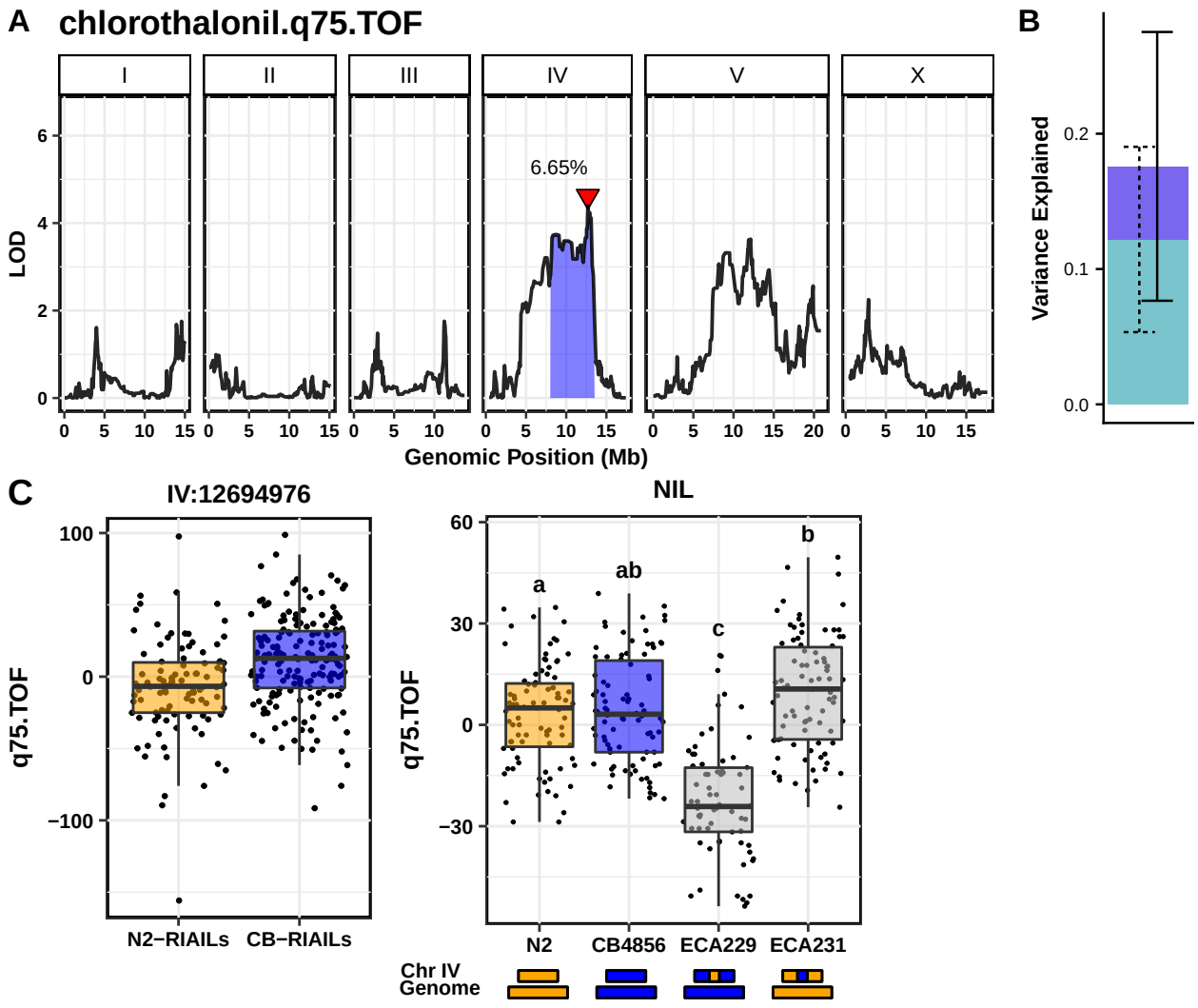

A
chlorothalonil.q25.EXT
I
II
III
IV
V
X
25%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:8398703
q25.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

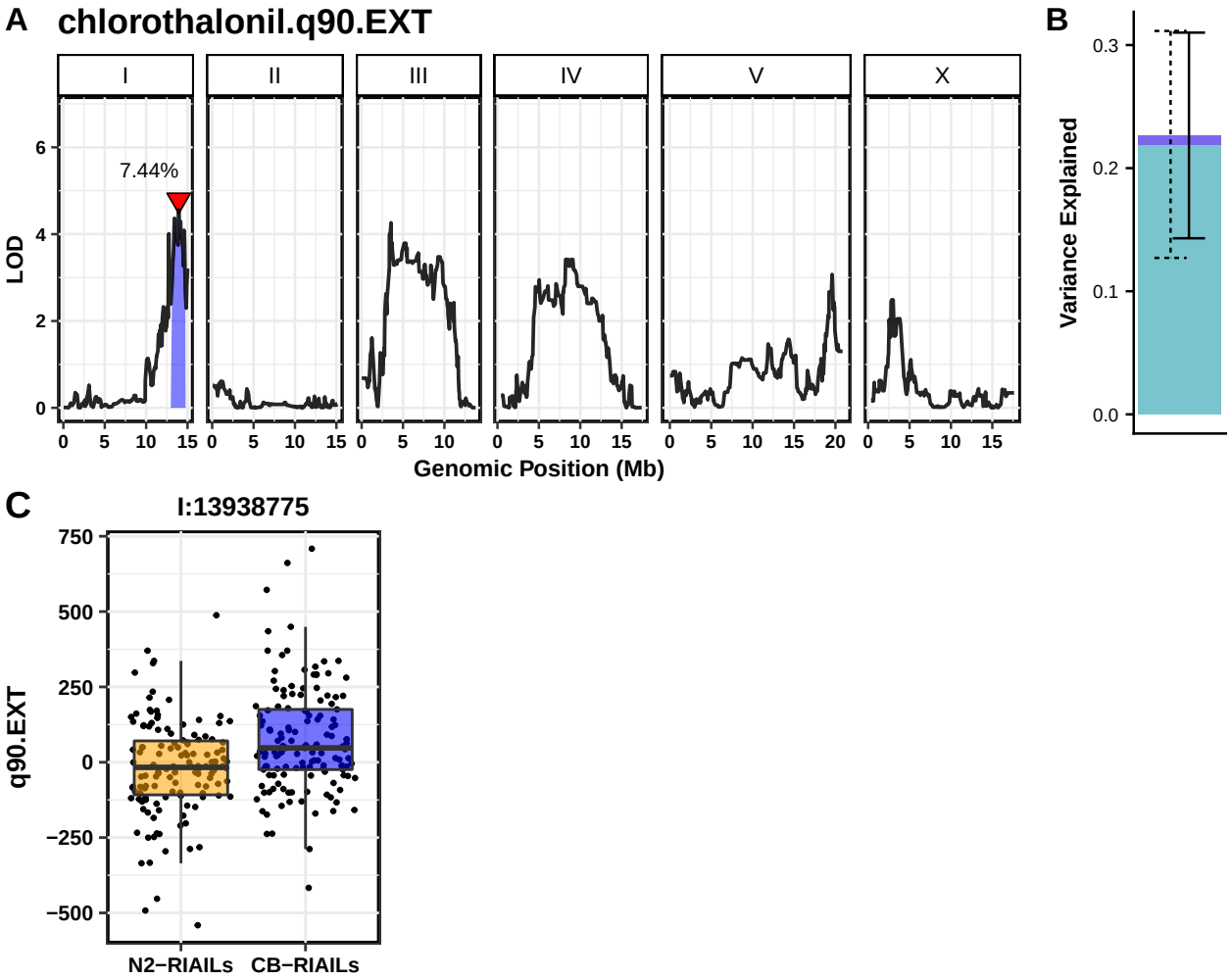

A
chlorothalonil.q25.norm.EXT
I
II
III
IV
V
X
6.12%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:8398703
q25.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

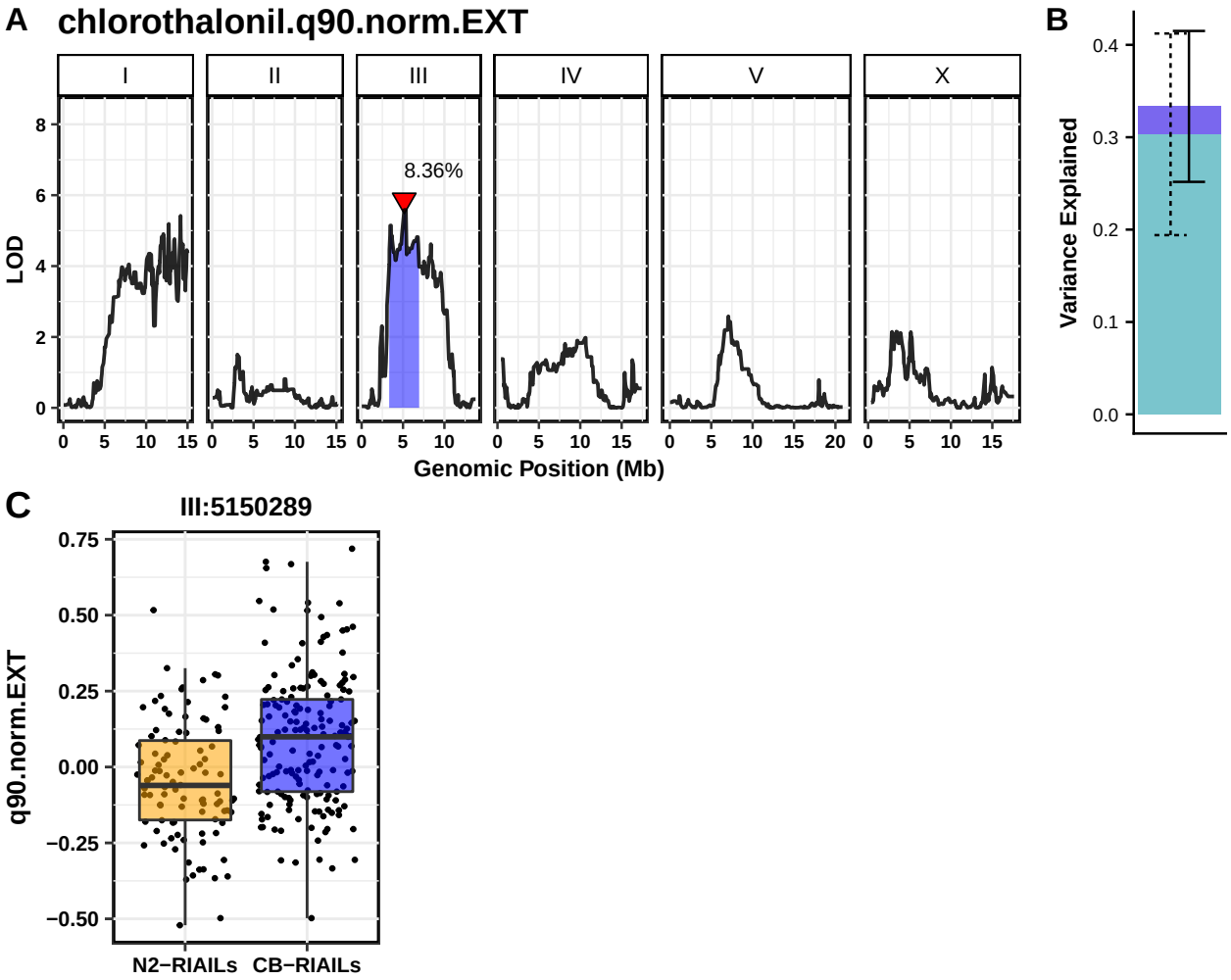

A
chlorothalonil.q25.TOF
I
II
III
IV
V
X
26.12%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:11199004
q25.TOF
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

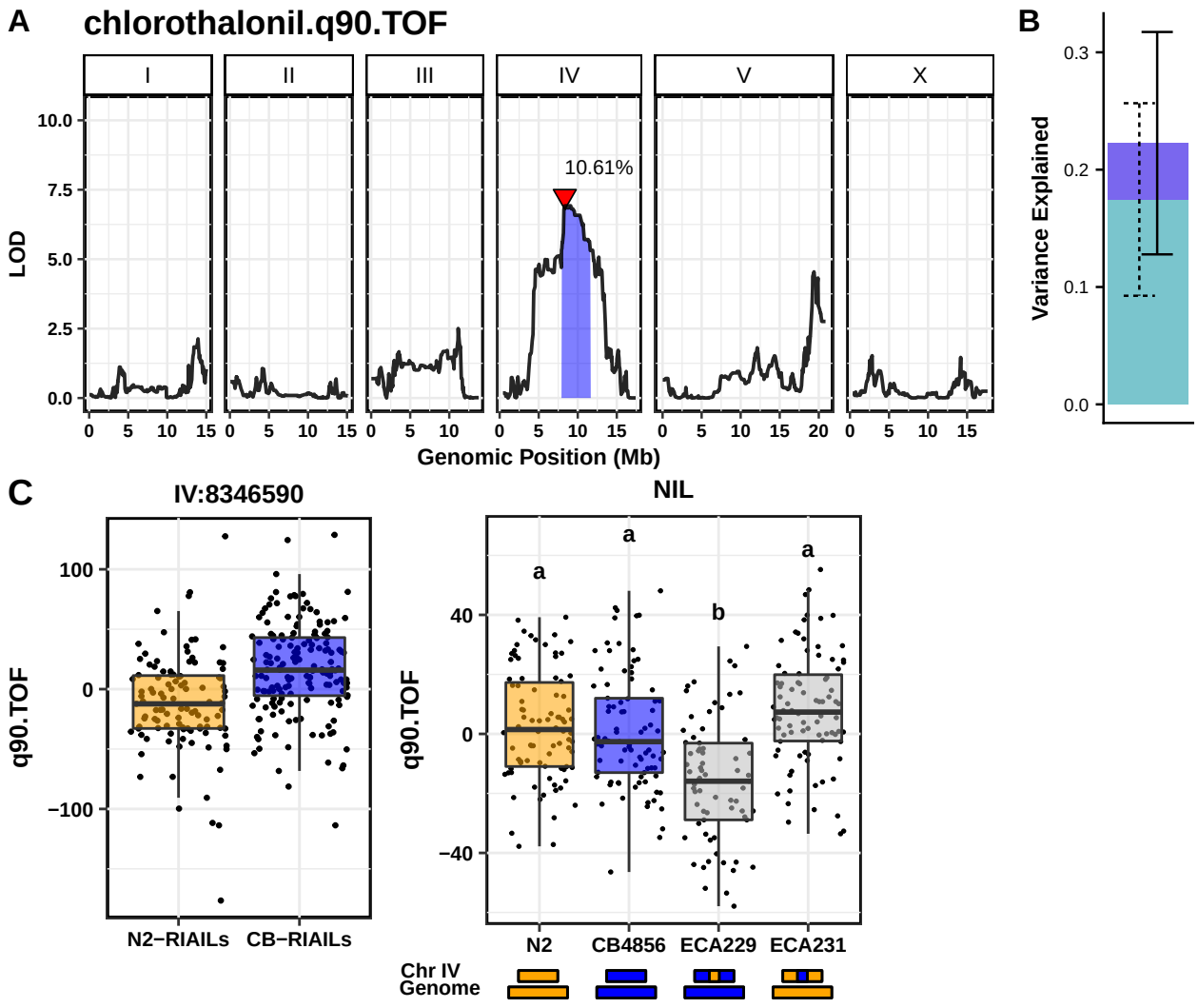

A
chlorothalonil.q75.EXT
I
II
III
IV
V
X
6.76%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:13938775
q75.EXT
N2−RIAILs
CB−RIAILs

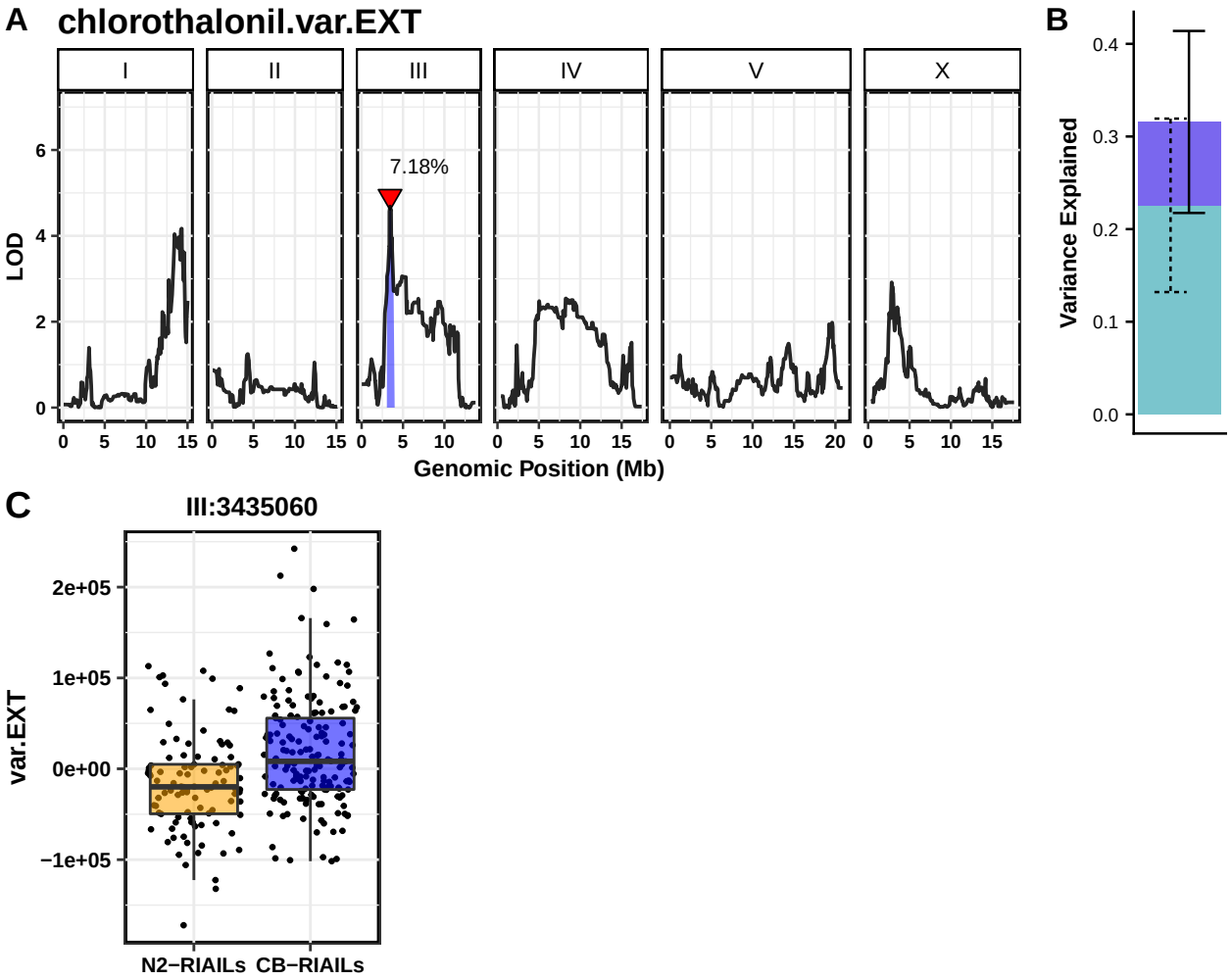

A
chlorothalonil.q75.norm.EXT
I
II
III
IV
V
X
10.46%
LOD
10.0
7.5
5.0
2.5
0.0
0 5 10 15
0 5 10 15
0 5 10
0 5 10 15
0 5 10 15 20
0 5 10 15
Genomic Position (Mb)
B
Variance Explained
0.4
0.3
0.2
0.1
0.0
C
I:14155589
q75.norm.EXT
0.50
0.25
0.00
−0.25
N2−RIAILs
CB−RIAILs

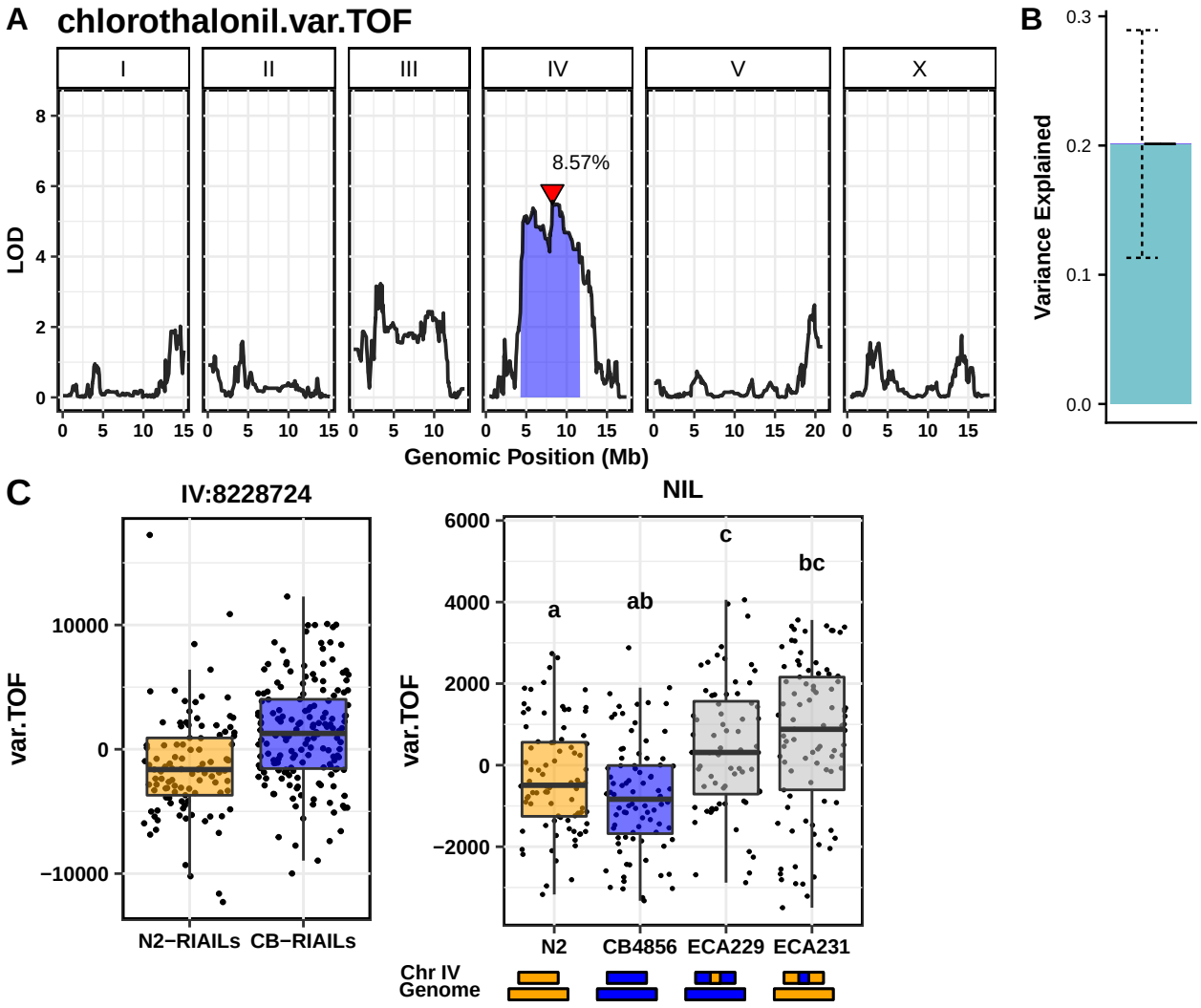

A
chlorothalonil.q75.TOF
I
II
III
IV
V
X
6.65%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:12694976
q75.TOF
N2−RIAILs
CB−RIAILs
NIL
a
ab
c
b
N2
CB4856
ECA229
ECA231
Chr IV
Genome

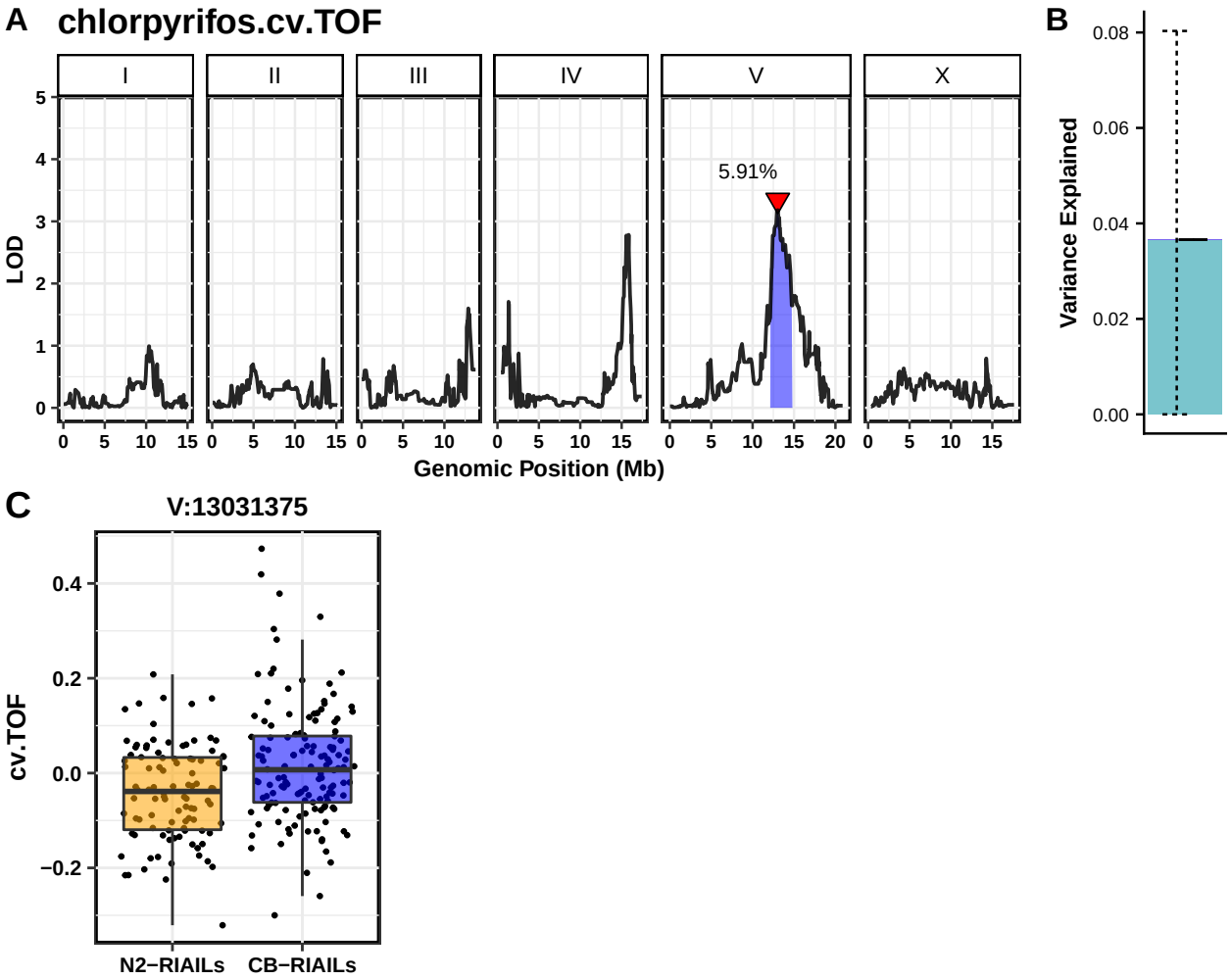

A
chlorothalonil.q90.EXT
I
II
III
IV
V
X
7.44%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:13938775
q90.EXT
N2−RIAILs
CB−RIAILs

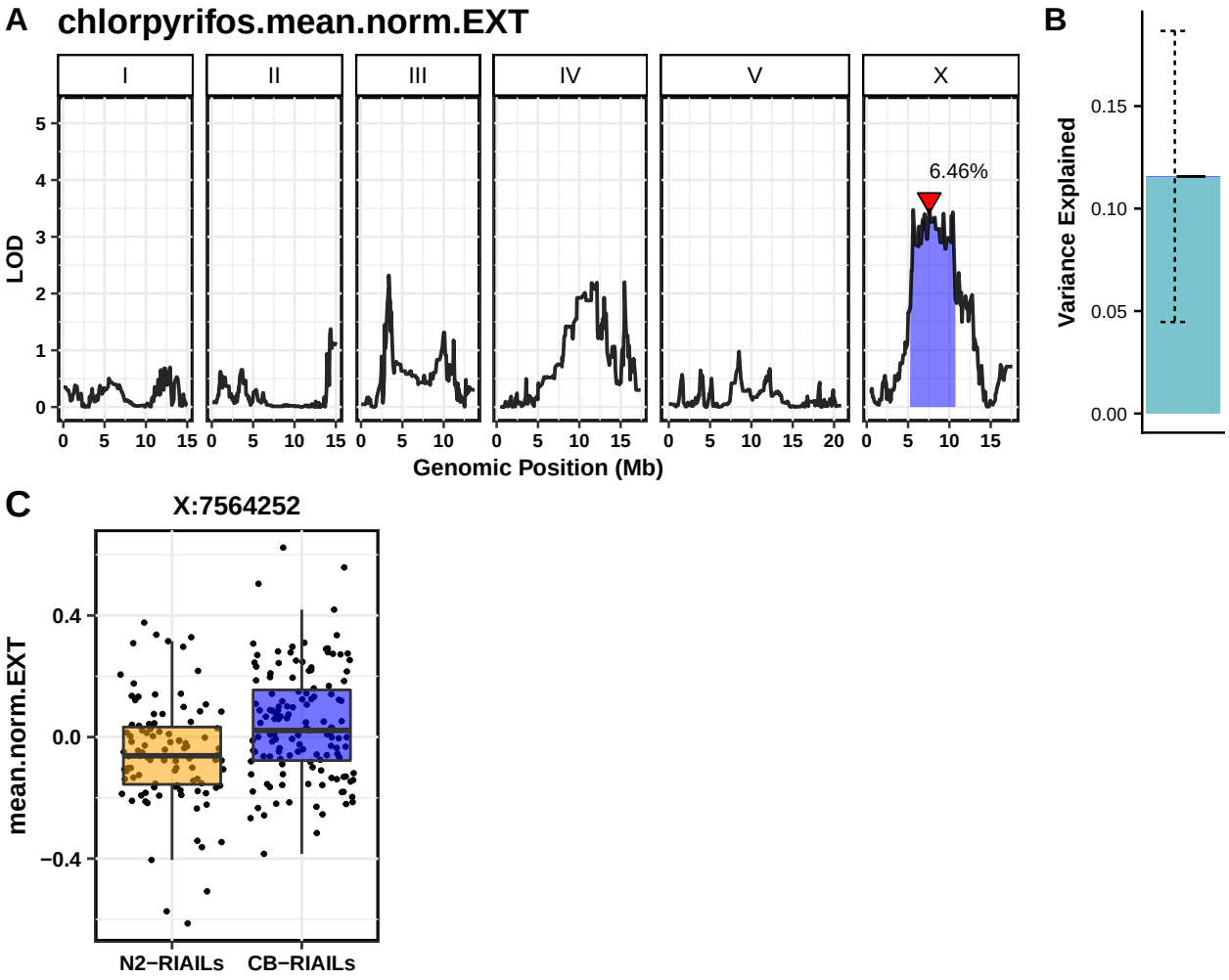

A
chlorothalonil.q90.norm.EXT
I
II
III
IV
V
X
8.36%
LOD
Genomic Position (Mb)
B
Variance Explained
C
III:5150289
q90.norm.EXT
N2−RIAILs
CB−RIAILs

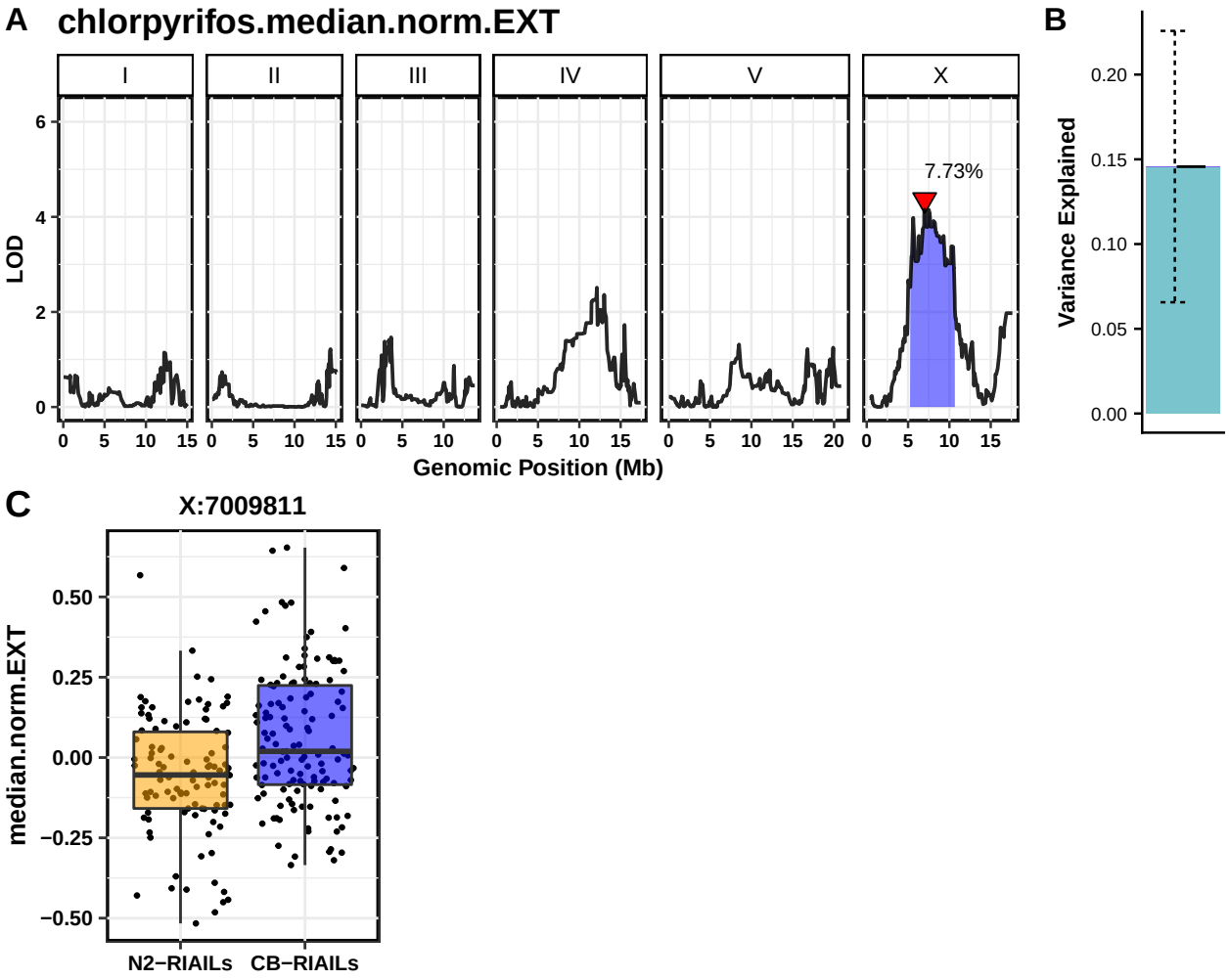

A
chlorothalonil.q90.TOF
I
II
III
IV
V
X
10.61%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:8346590
q90.TOF
N2−RIAILs
CB−RIAILs
NIL
a
a
b
a
N2
CB4856
ECA229
ECA231
Chr IV
Genome

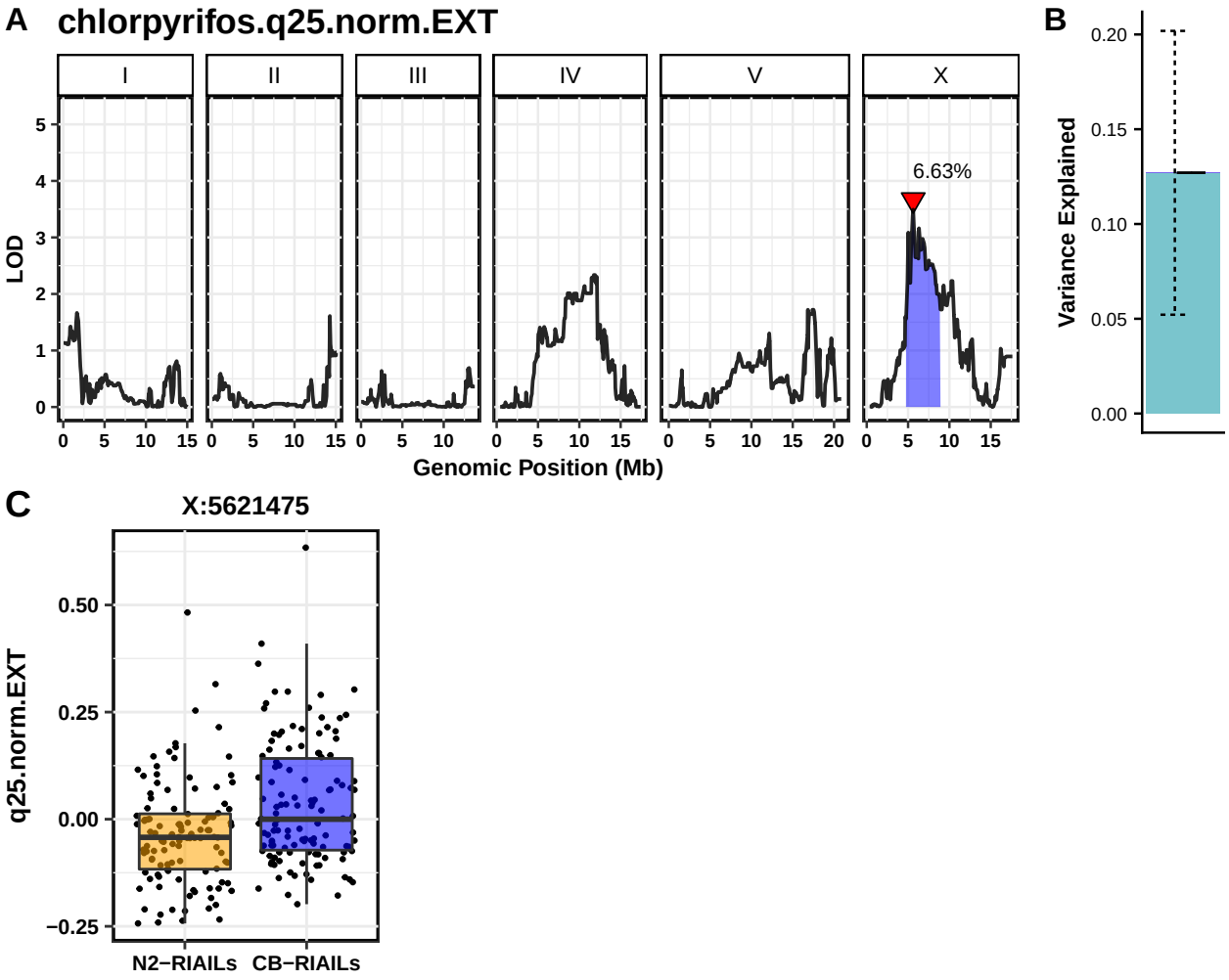

A
chlorothalonil.var.EXT
I
II
III
IV
V
X
7.18%
LOD
Genomic Position (Mb)
B
Variance Explained
C
III:3435060
var.EXT
N2−RIAILs
CB−RIAILs

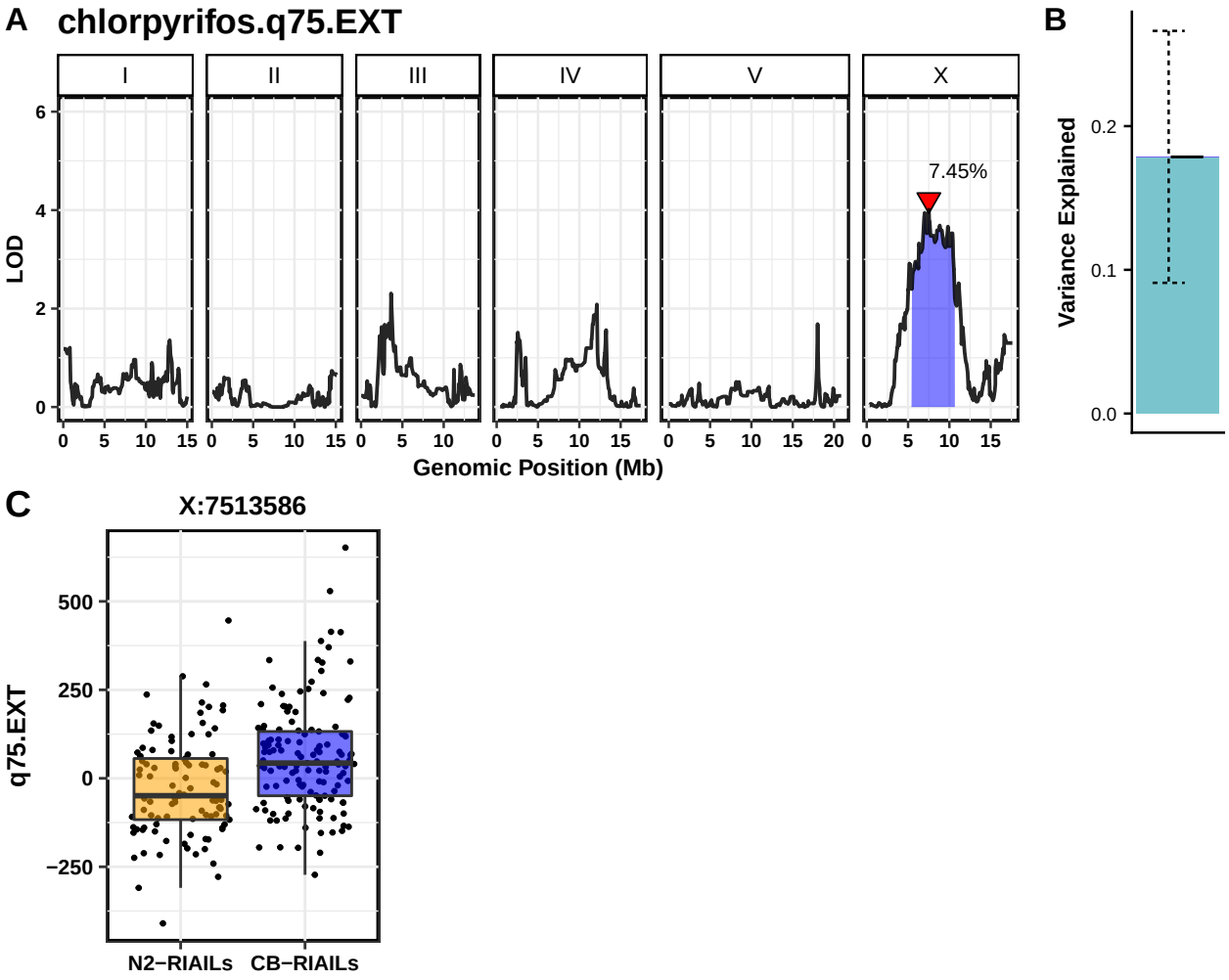

A
chlorothalonil.var.TOF
I
II
III
IV
V
X
LOD
8.57%
Genomic Position (Mb)
B
Variance Explained
C
IV:8228724
var.TOF
N2−RIAILs
CB−RIAILs
NIL
a
ab
c
bc
N2
CB4856
ECA229
ECA231
Chr IV
Genome

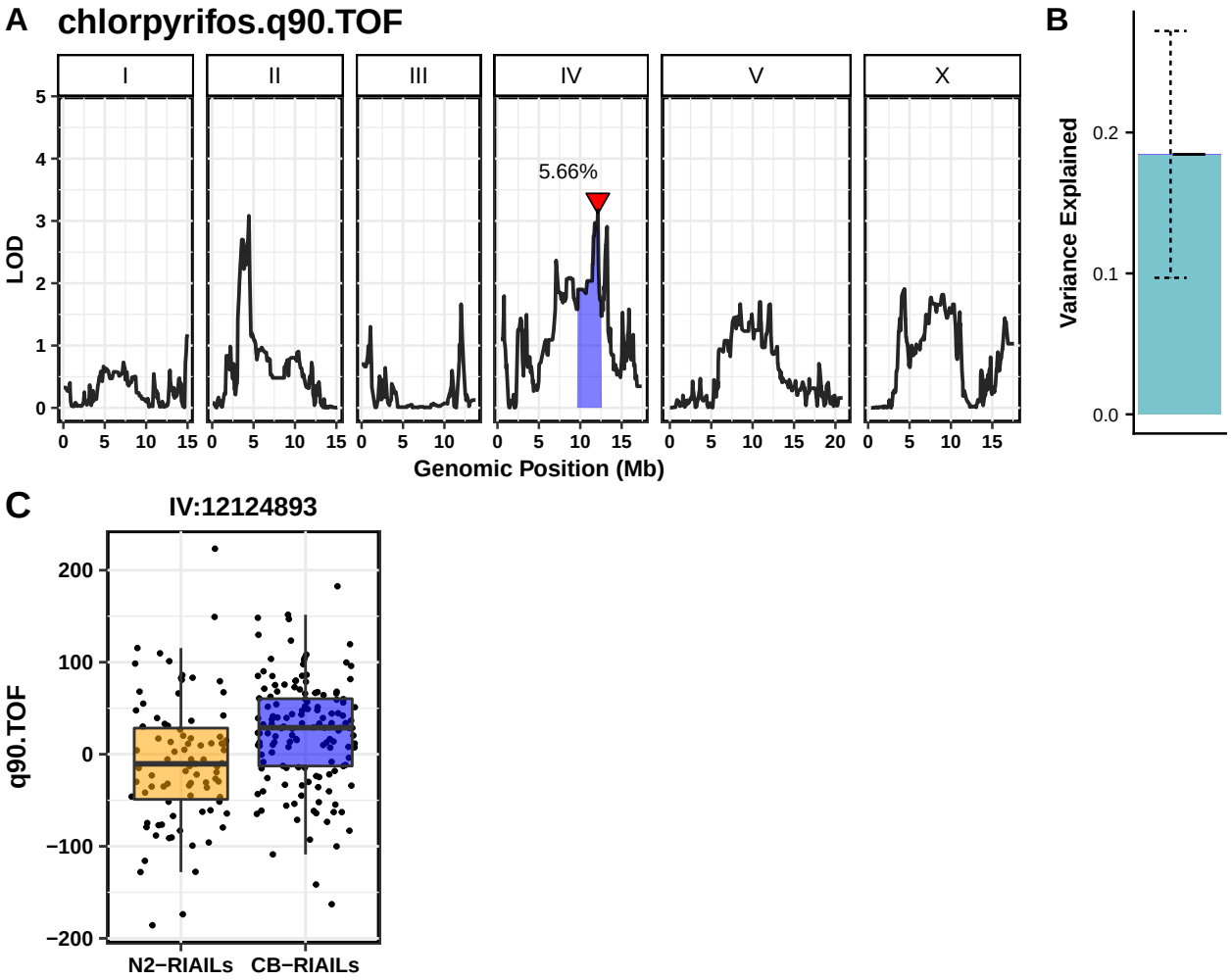

A
chlorpyrifos.cv.TOF
I
II
III
IV
V
X
5.91%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:13031375
cv.TOF
N2−RIAILs
CB−RIAILs

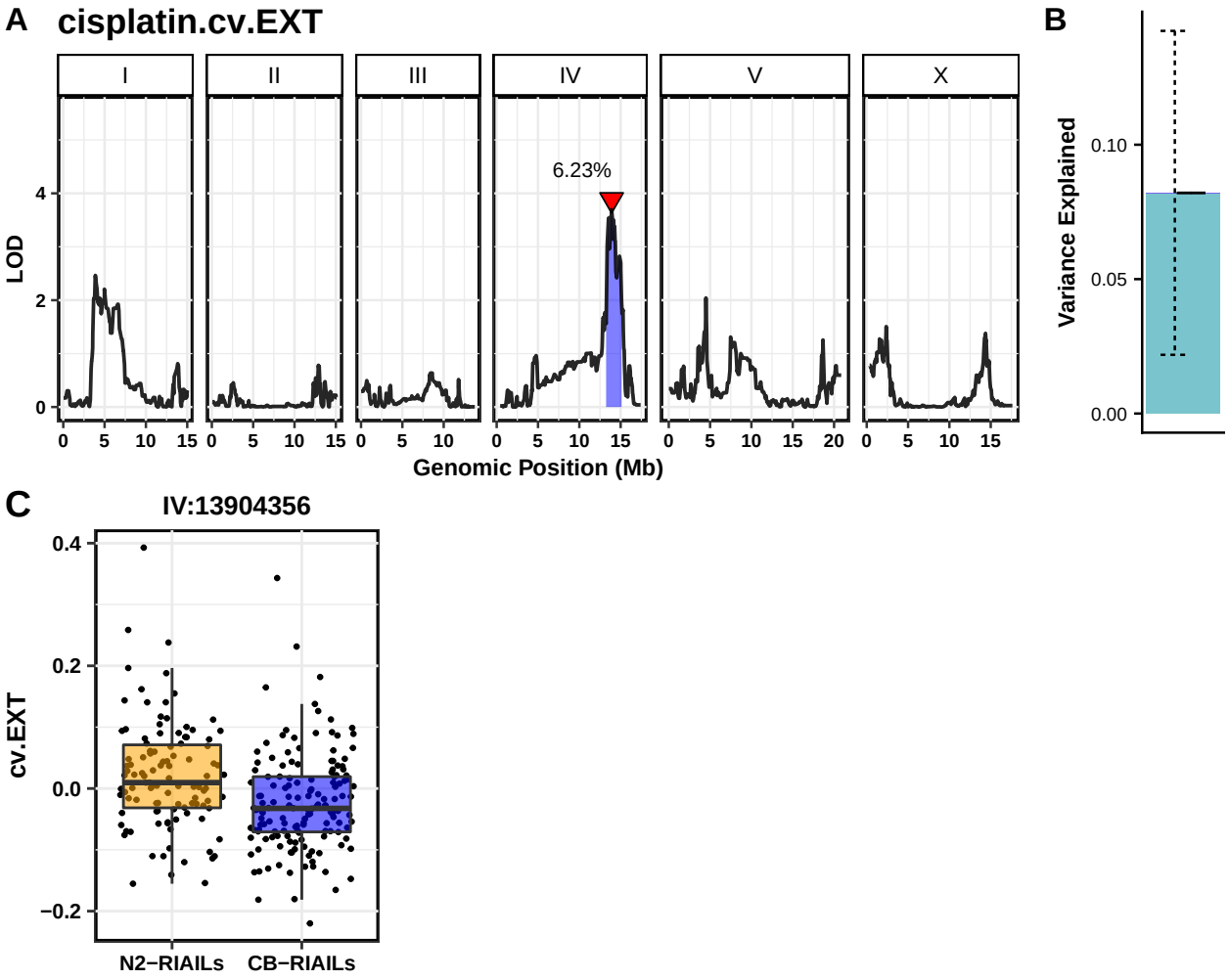

A
chlorpyrifos.mean.norm.EXT
I
II
III
IV
V
X
6.46%
LOD
Genomic Position (Mb)
B
Variance Explained
C
X:7564252
mean.norm.EXT
N2−RIAILs
CB−RIAILs

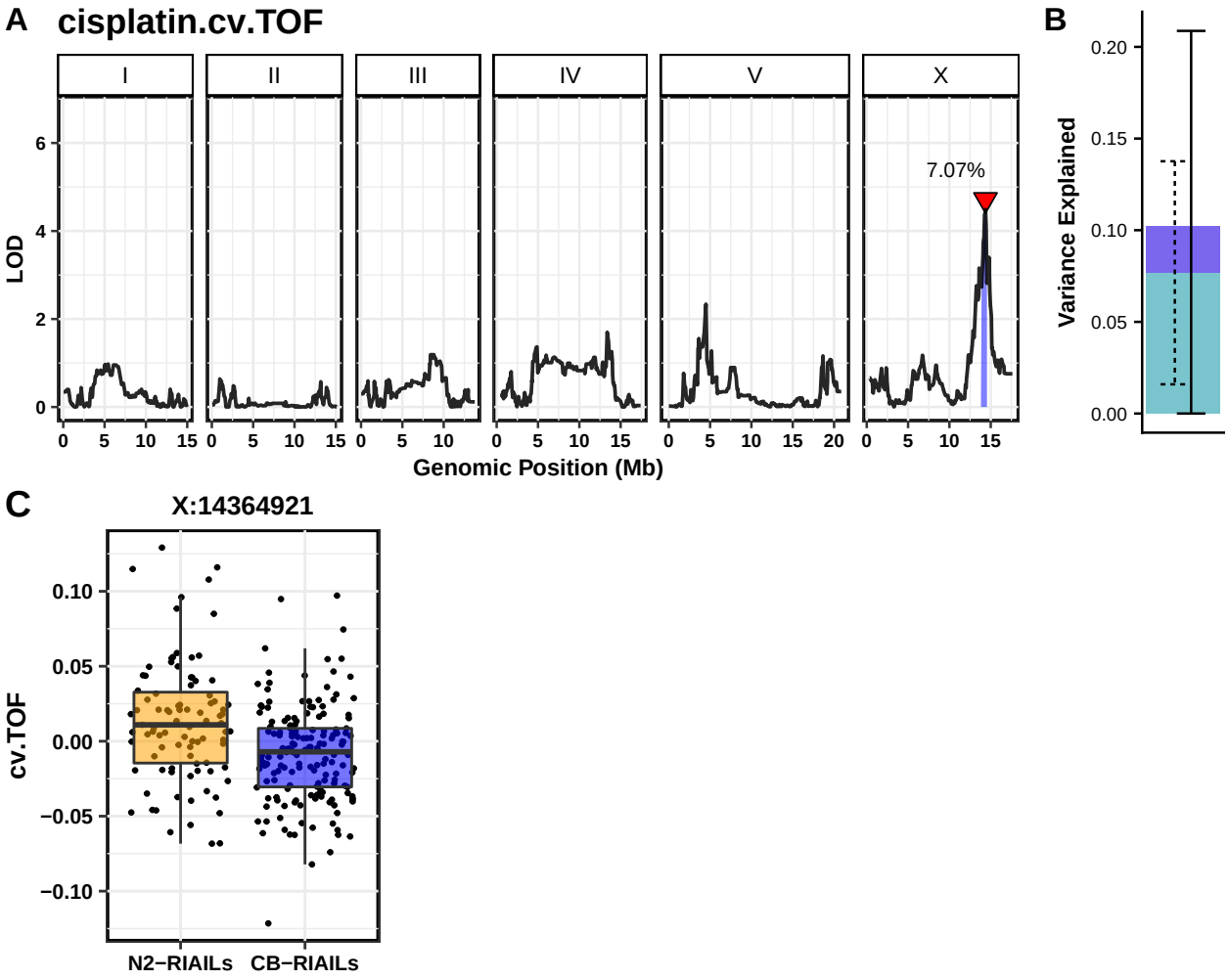

A
chlorpyrifos.median.norm.EXT
I
II
III
IV
V
X
7.73%
LOD
Genomic Position (Mb)
B
Variance Explained
C
X:7009811
median.norm.EXT
N2−RIAILs
CB−RIAILs

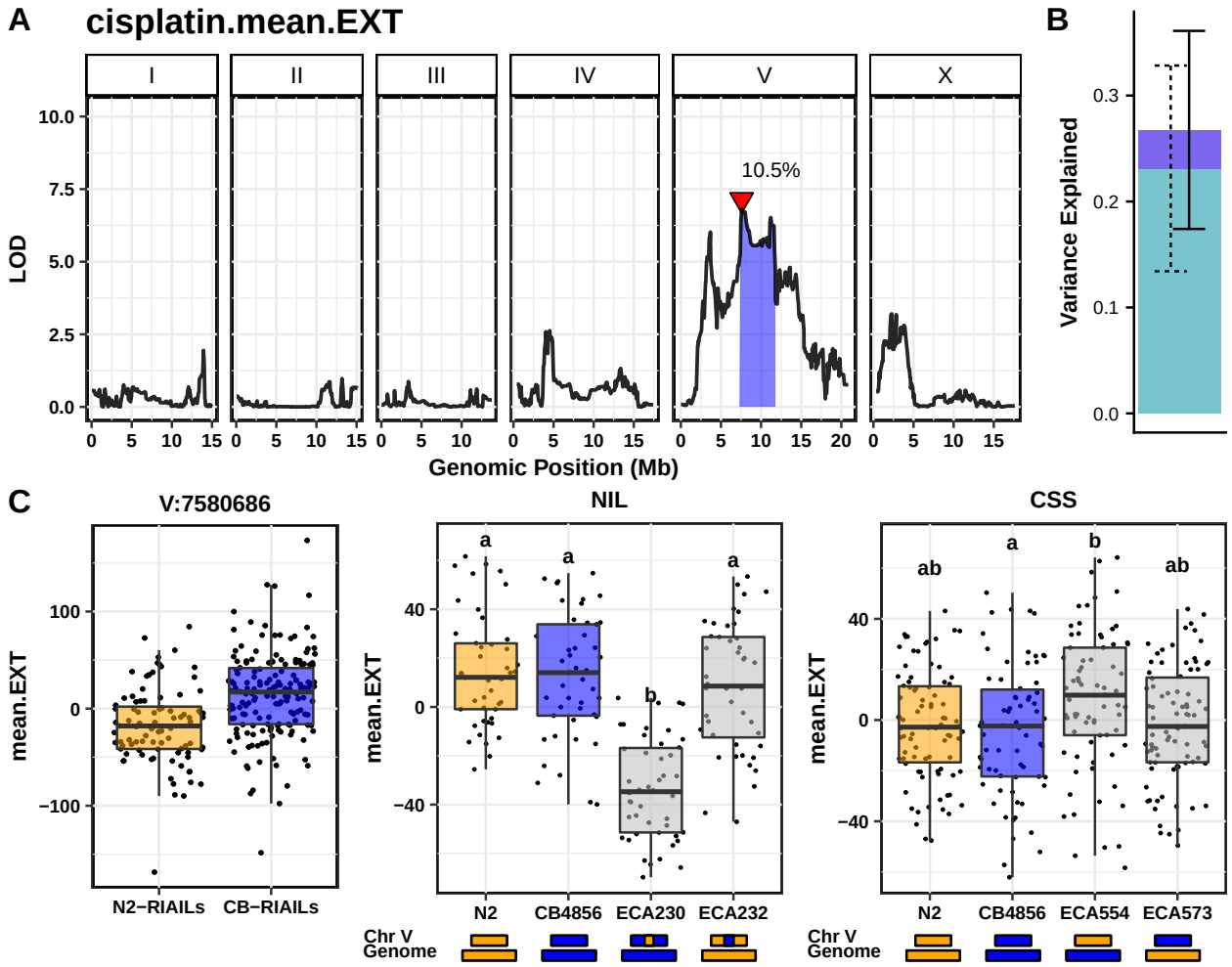

A
chlorpyrifos.q25.norm.EXT
I
II
III
IV
V
X
LOD
6.63%
Genomic Position (Mb)
B
Variance Explained
C
X:5621475
q25.norm.EXT
N2−RIAILs
CB−RIAILs

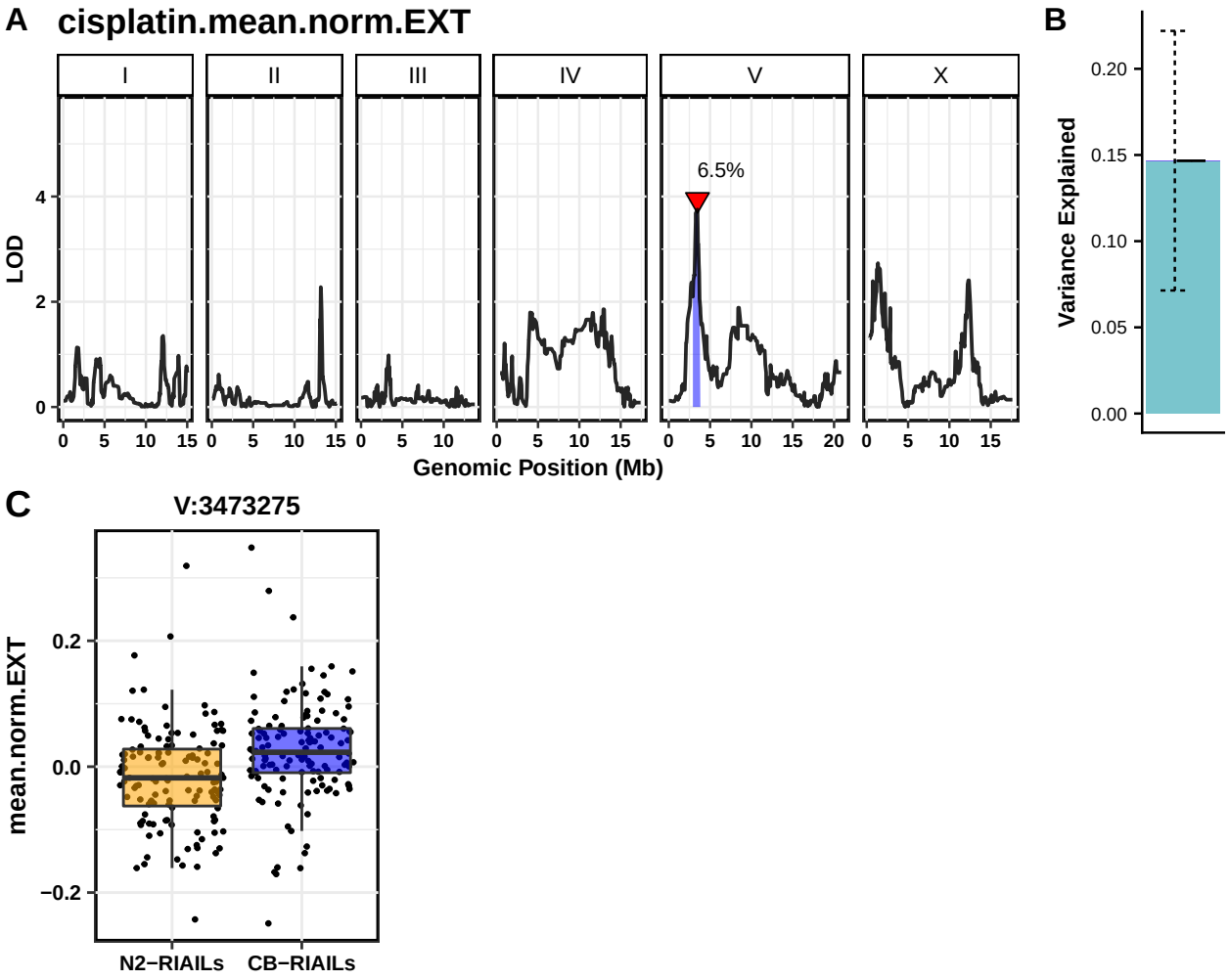

A
chlorpyrifos.q75.EXT
I
II
III
IV
V
X
LOD
7.45%
Genomic Position (Mb)
B
Variance Explained
C
X:7513586
q75.EXT
N2−RIAILs
CB−RIAILs

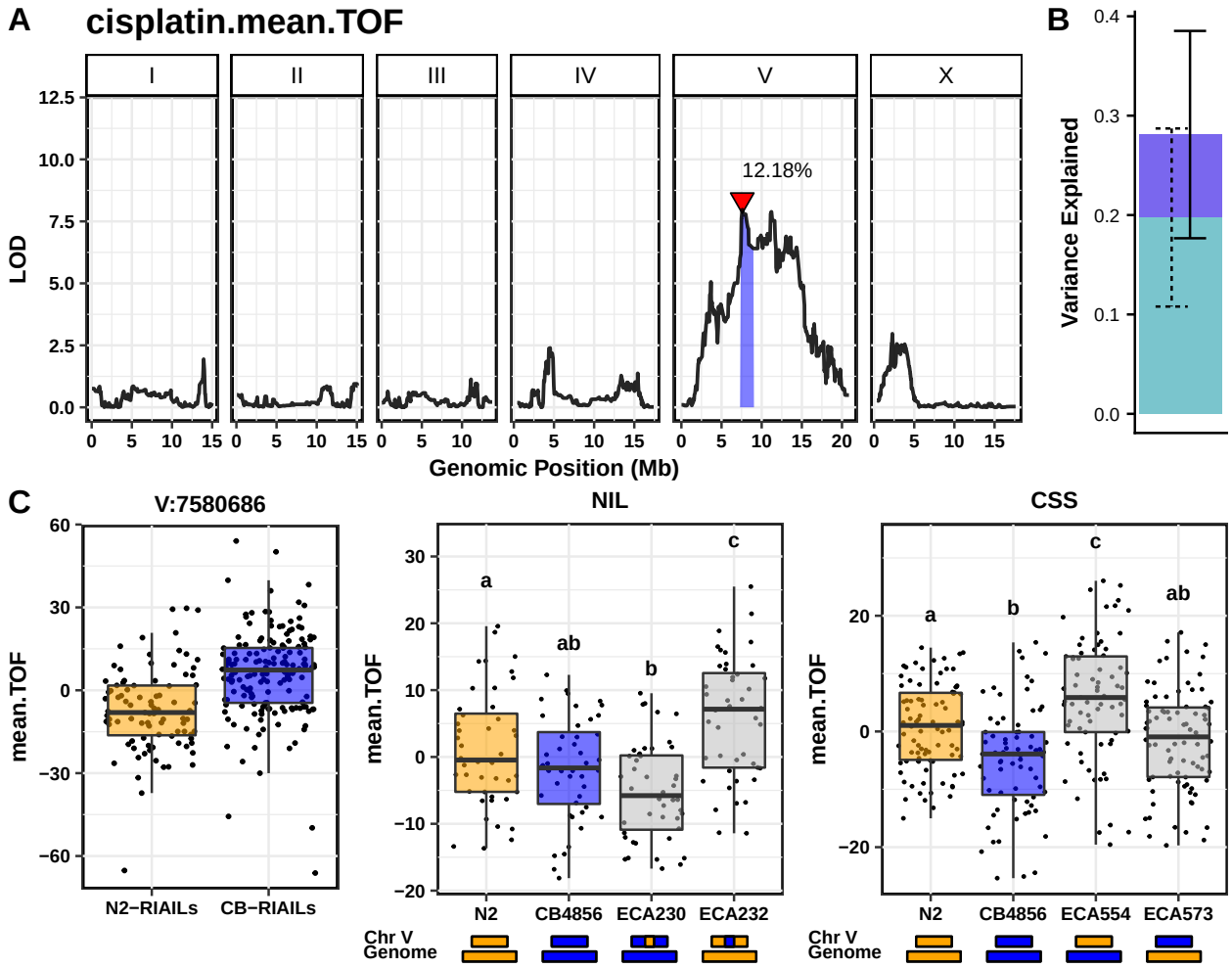

A
chlorpyrifos.q90.TOF
I
II
III
IV
V
X
5.66%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:12124893
q90.TOF
N2−RIAILs
CB−RIAILs

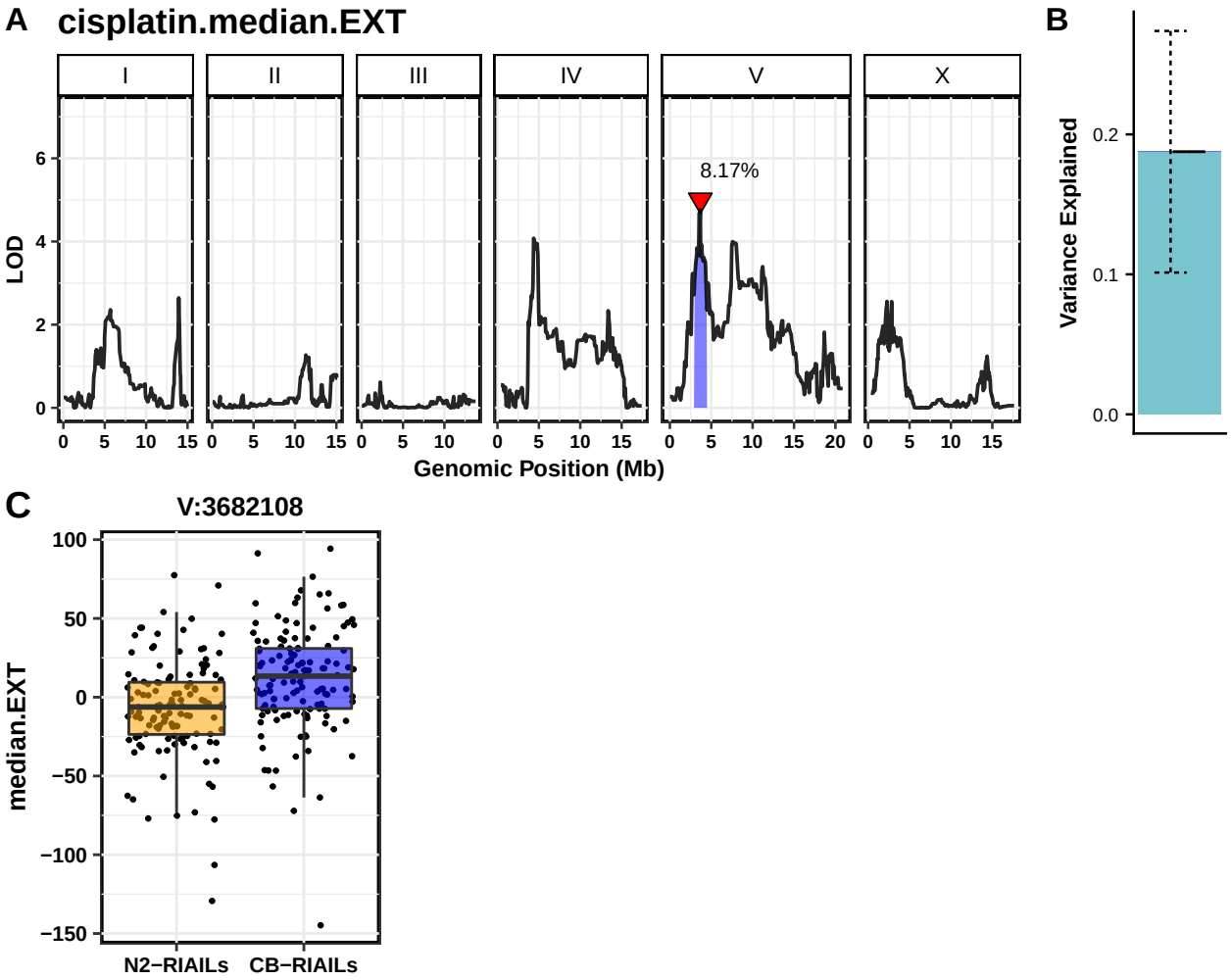

A
cisplatin.cv.EXT
I
II
III
IV
V
X
6.23%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:13904356
cv.EXT
N2−RIAILs
CB−RIAILs

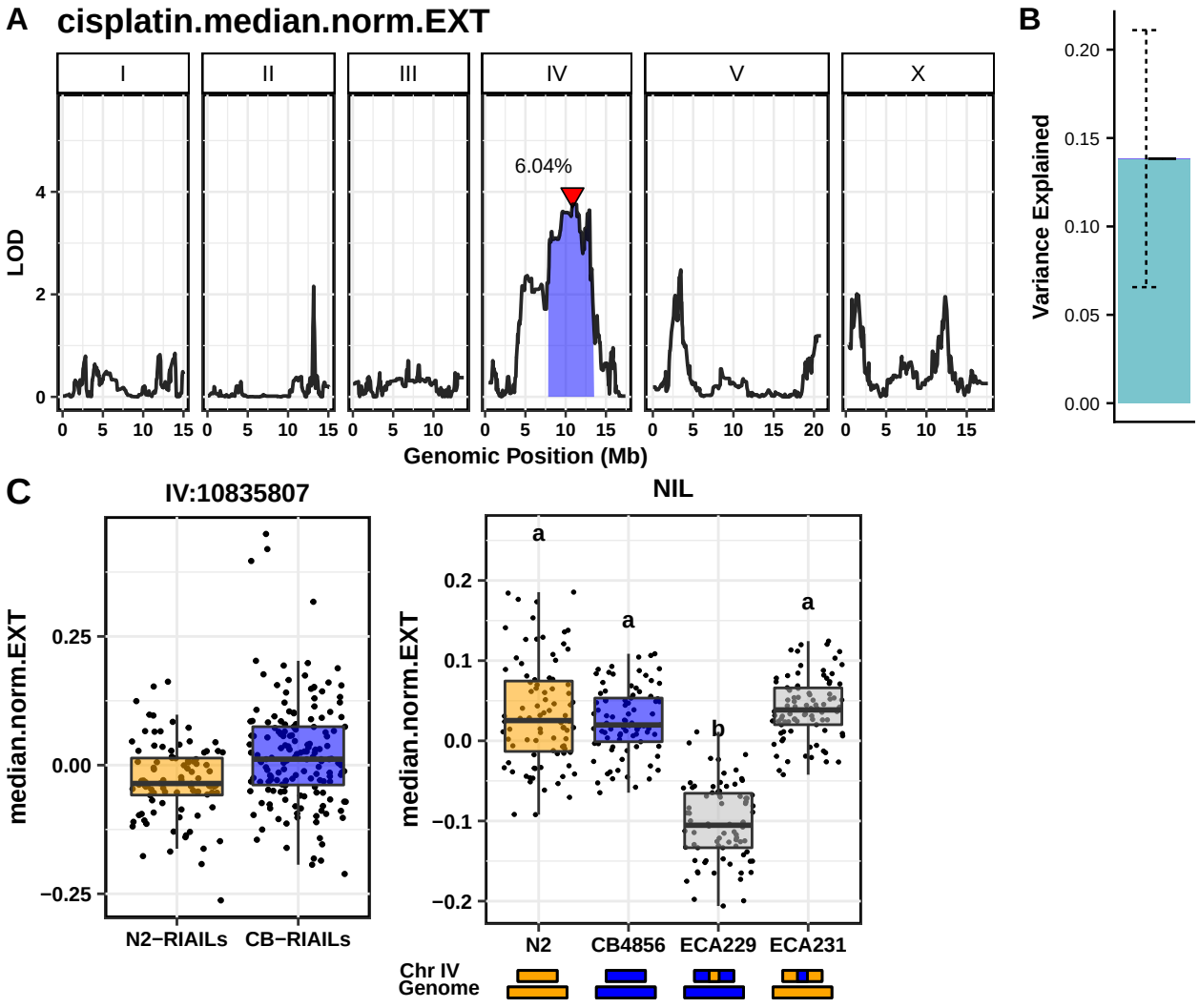

A
cisplatin.cv.TOF
I
II
III
IV
V
X
LOD
7.07%
Genomic Position (Mb)
B
Variance Explained
C
X:14364921
cv.TOF
N2−RIAILs
CB−RIAILs

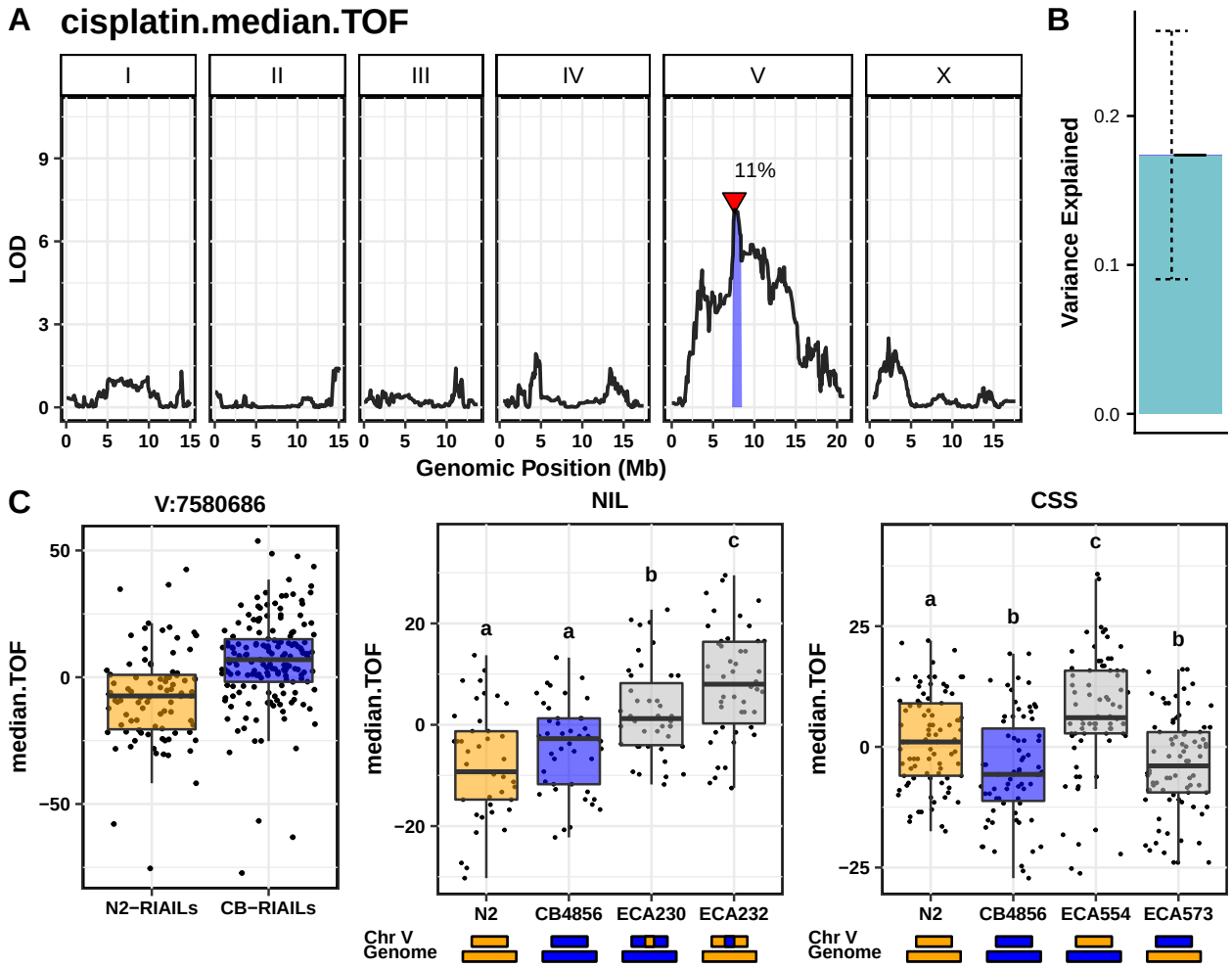

A
cisplatin.mean.EXT
I
II
III
IV
V
X
10.5%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:7580686
mean.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
ECA554
ECA573

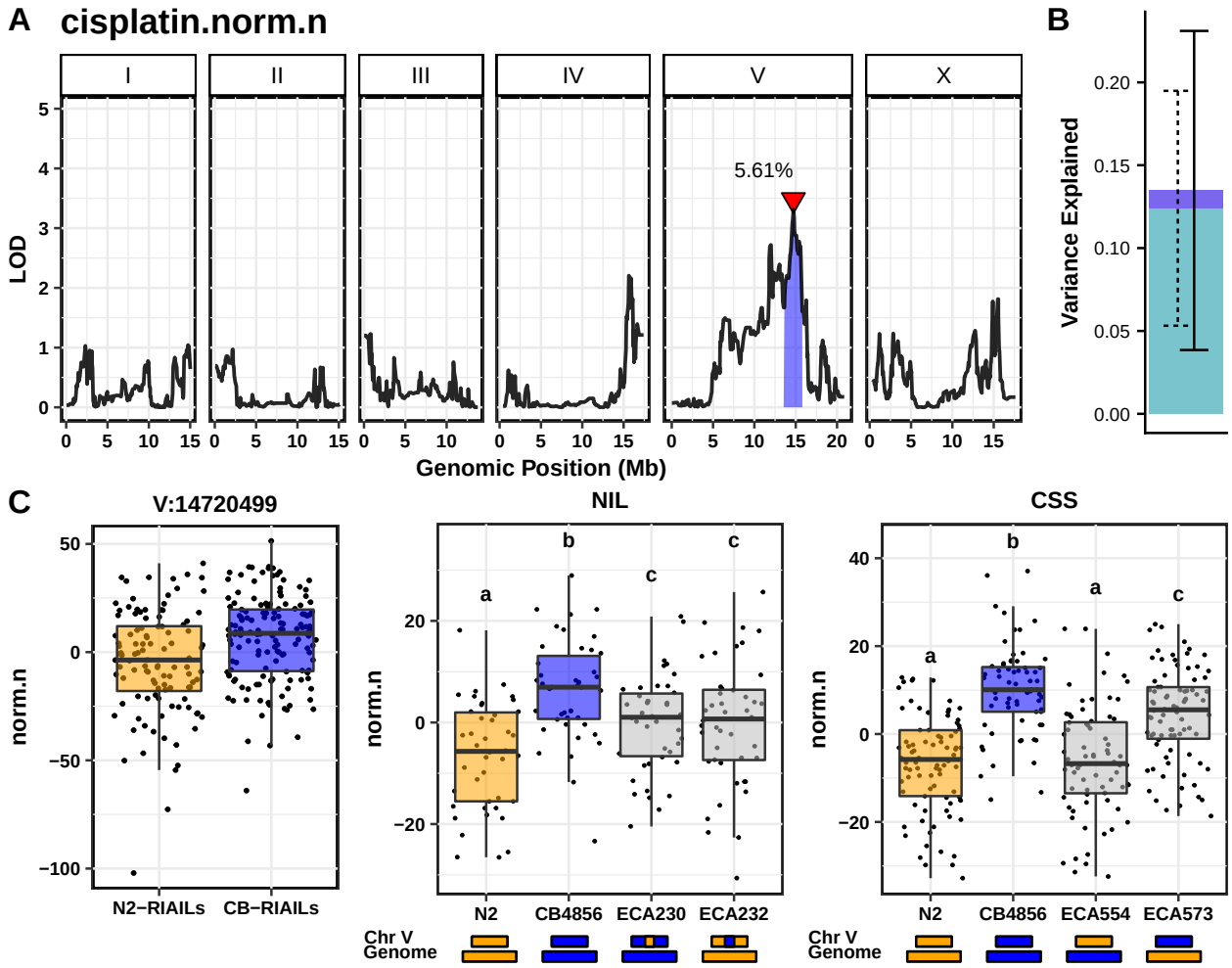

A
cisplatin.mean.norm.EXT
I
II
III
IV
V
X
6.5%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:3473275
mean.norm.EXT
N2−RIAILs
CB−RIAILs

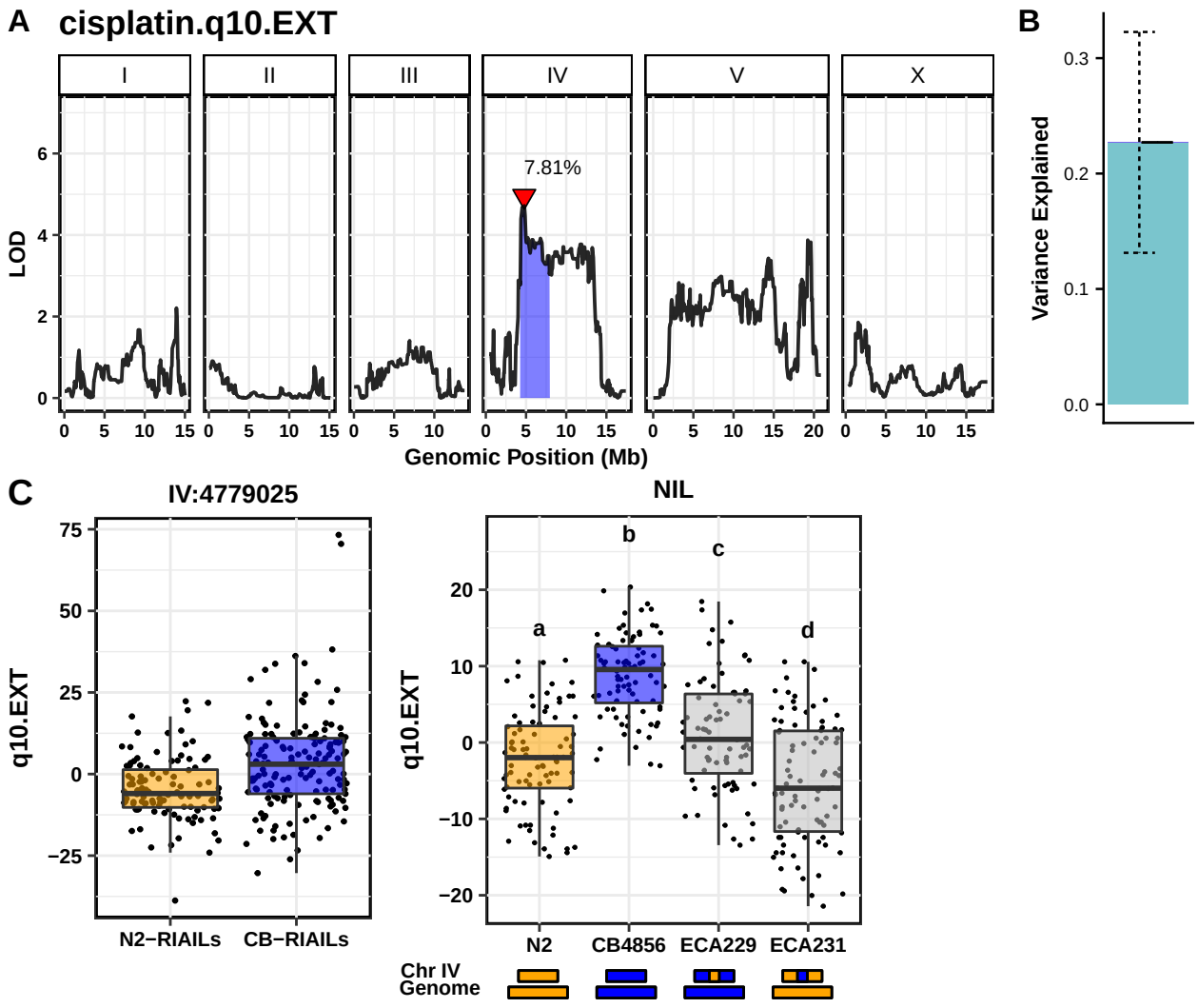

A
cisplatin.mean.TOF
I
II
III
IV
V
X
LOD
12.5
10.0
7.5
5.0
2.5
0.0
12.18%
Genomic Position (Mb)
B
Variance Explained
0.4
0.3
0.2
0.1
0.0
C
V:7580686
mean.TOF
N2−RIAILs
CB−RIAILs
NIL
a
ab
b
c
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
a
b
c
ab
N2
CB4856
ECA554
ECA573
Chr V Genome

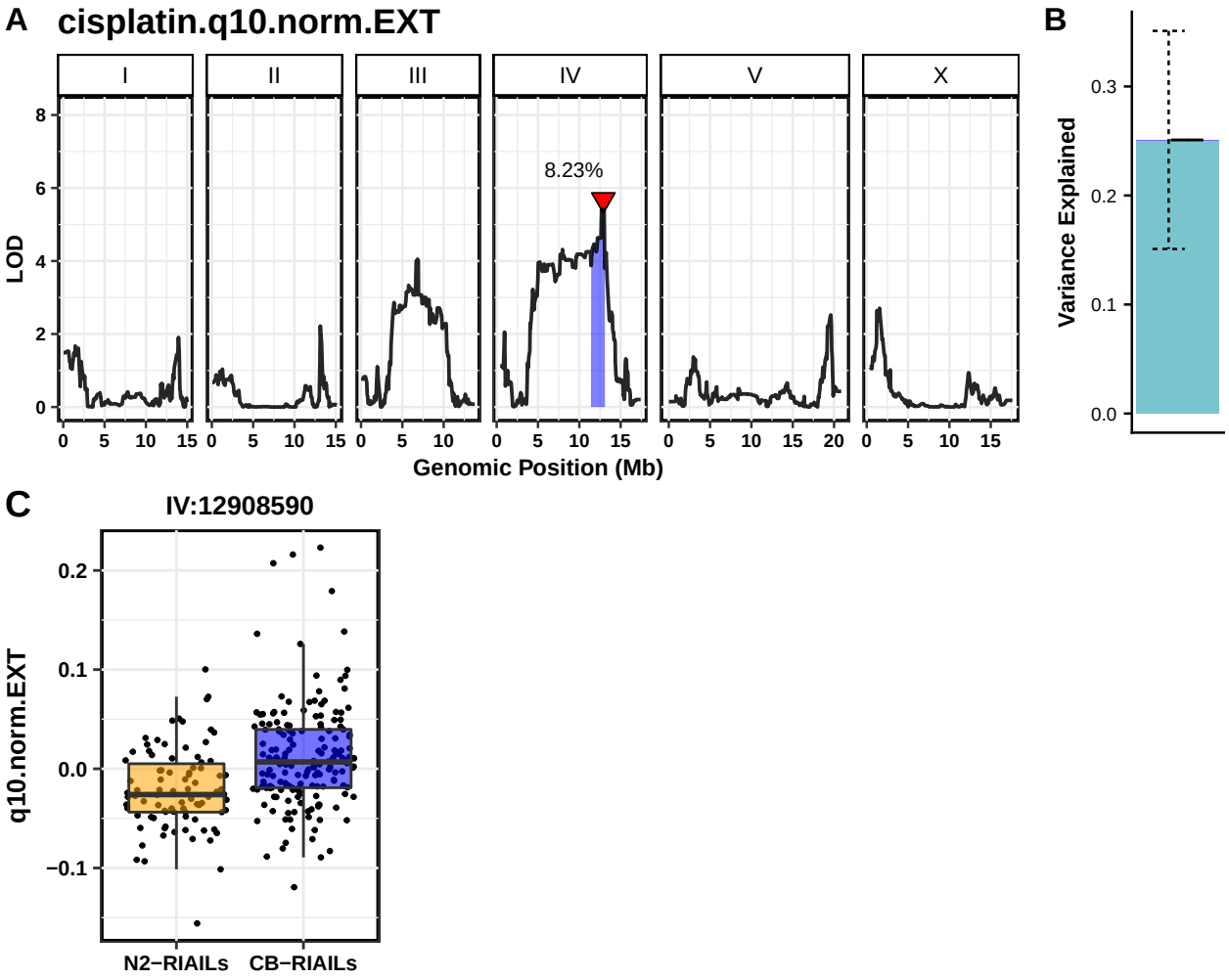

A
cisplatin.median.EXT
I
II
III
IV
V
X
LOD
8.17%
Genomic Position (Mb)
B
Variance Explained
C
V:3682108
median.EXT
N2−RIAILs
CB−RIAILs

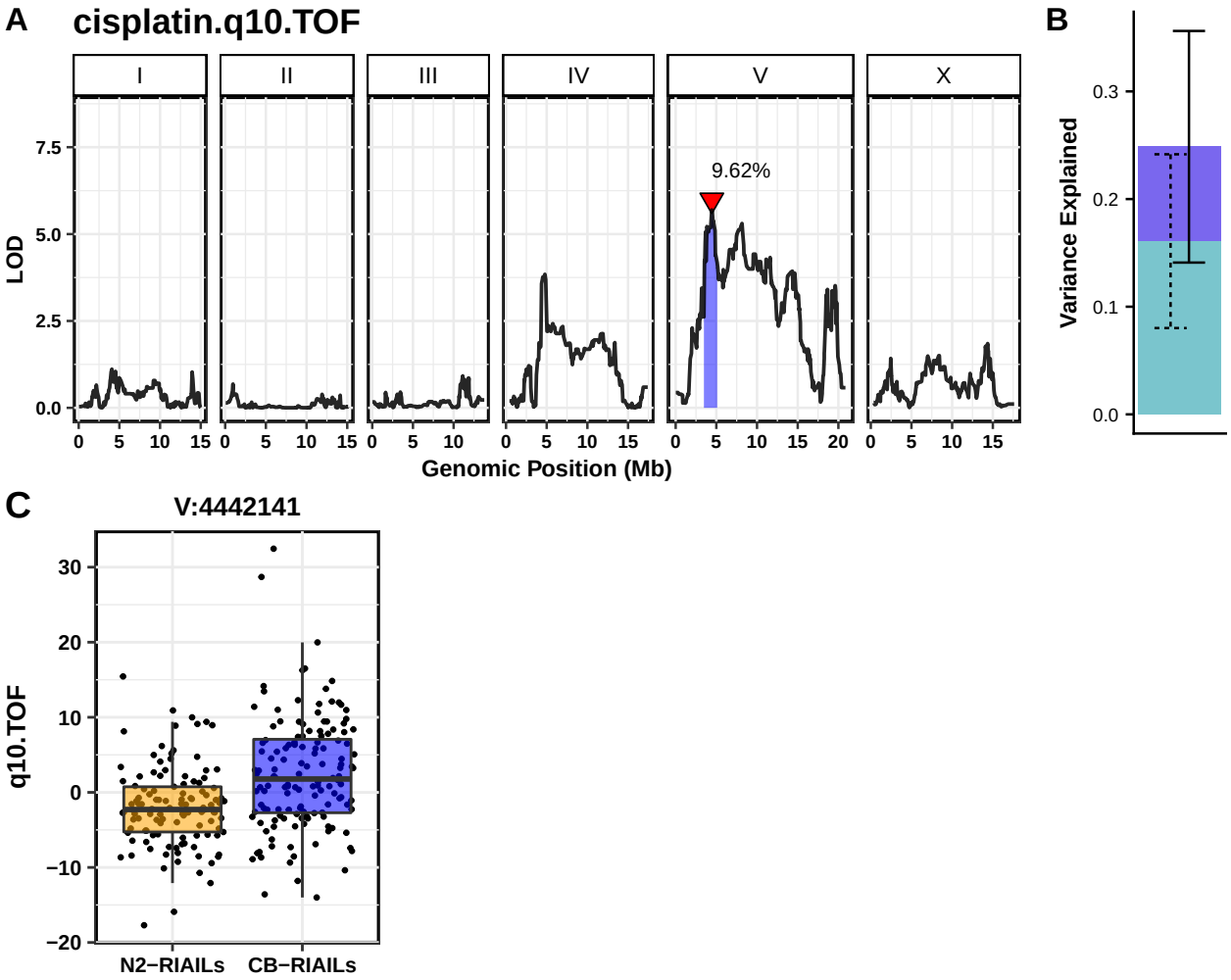

A
cisplatin.median.norm.EXT
I
II
III
IV
V
X
6.04%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:10835807
median.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
a
a
b
a
N2
CB4856
ECA229
ECA231
Chr IV
Genome

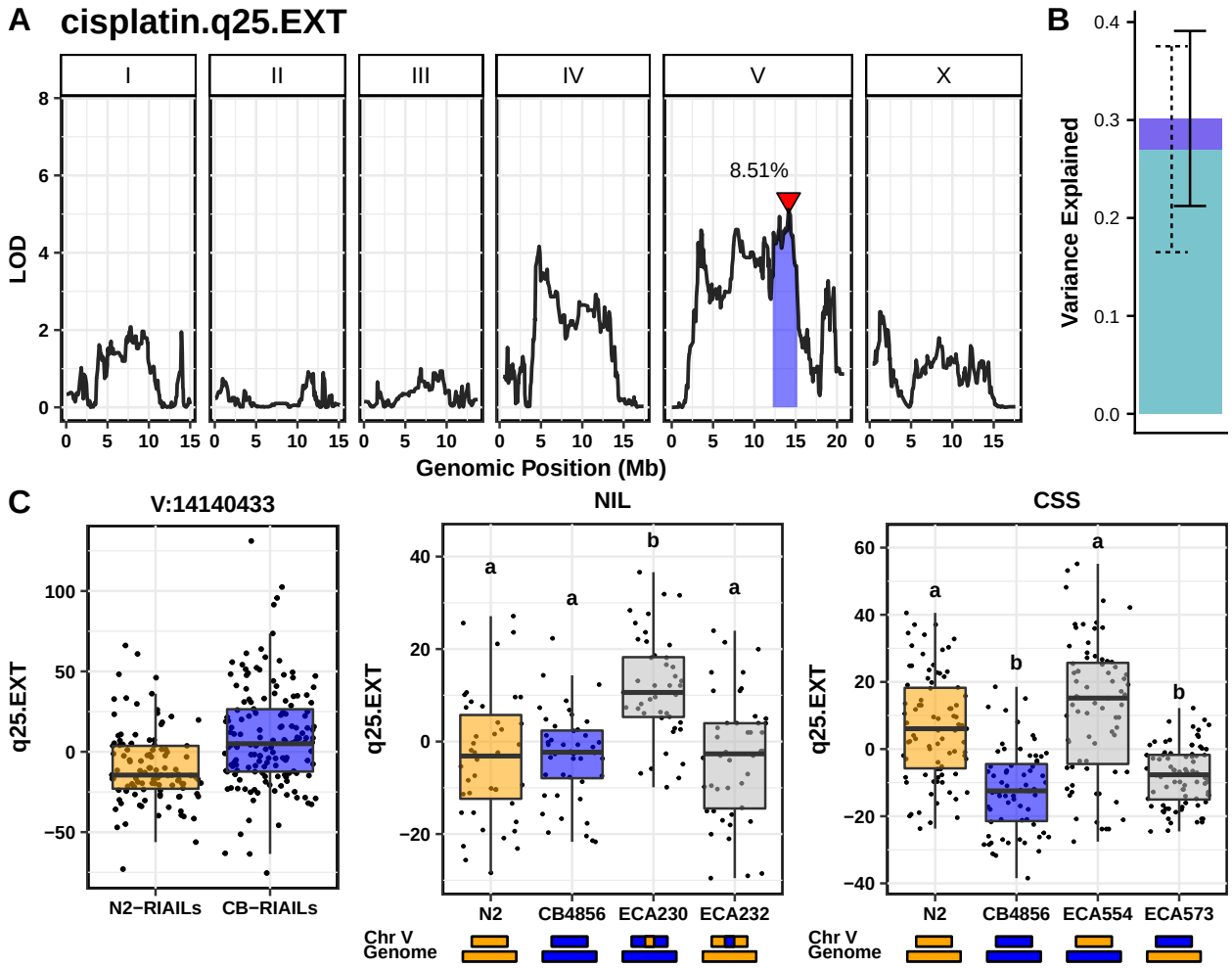

A
cisplatin.median.TOF
I
II
III
IV
V
X
LOD
11%
Genomic Position (Mb)
B
Variance Explained
C
V:7580686
median.TOF
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

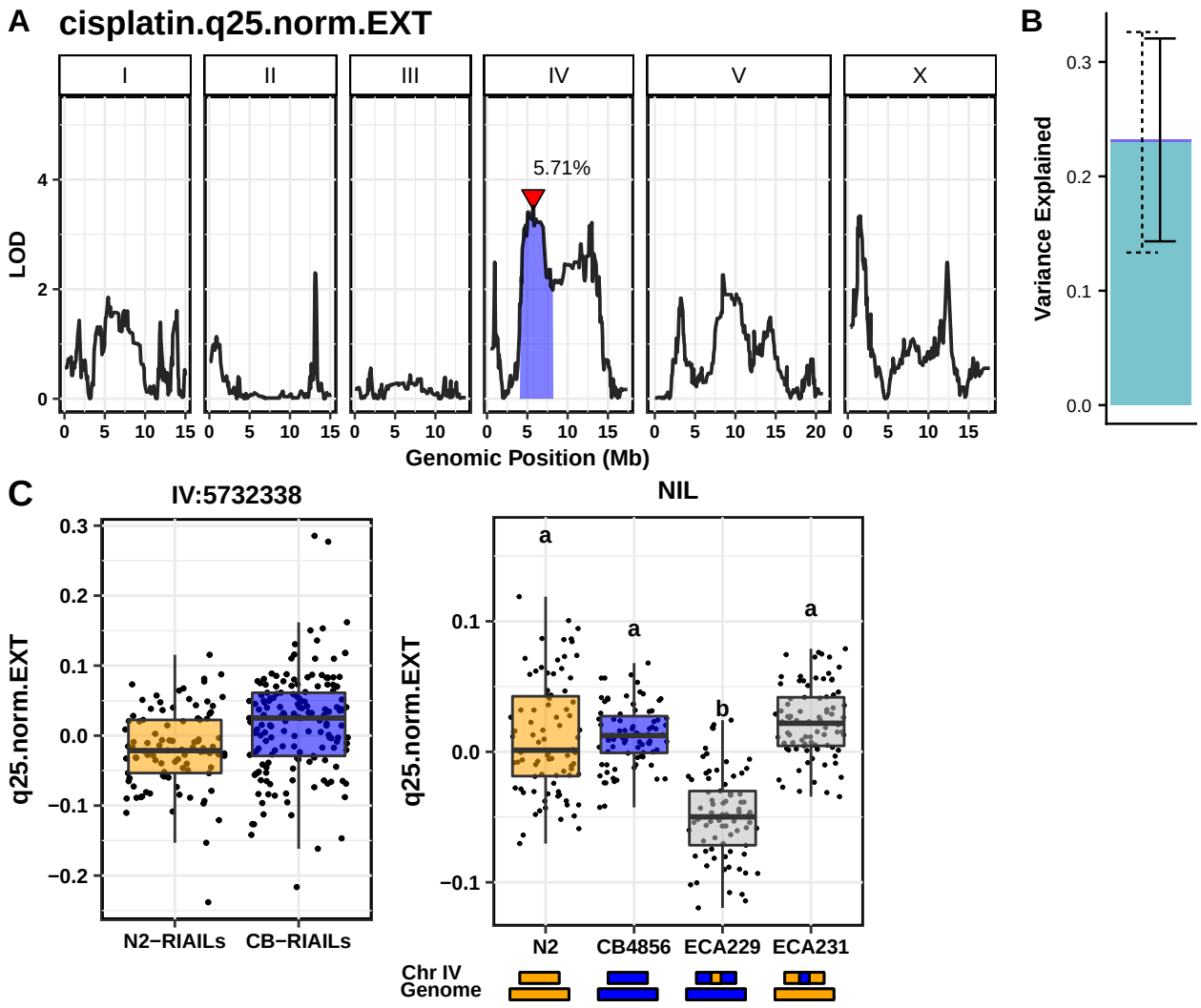

A
cisplatin.norm.n
I
II
III
IV
V
X
LOD
5.61%
Genomic Position (Mb)
B
Variance Explained
C
V:14720499
norm.n
N2−RIAILs
CB−RIAILs
NIL
a
b
c
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
ECA554
ECA573

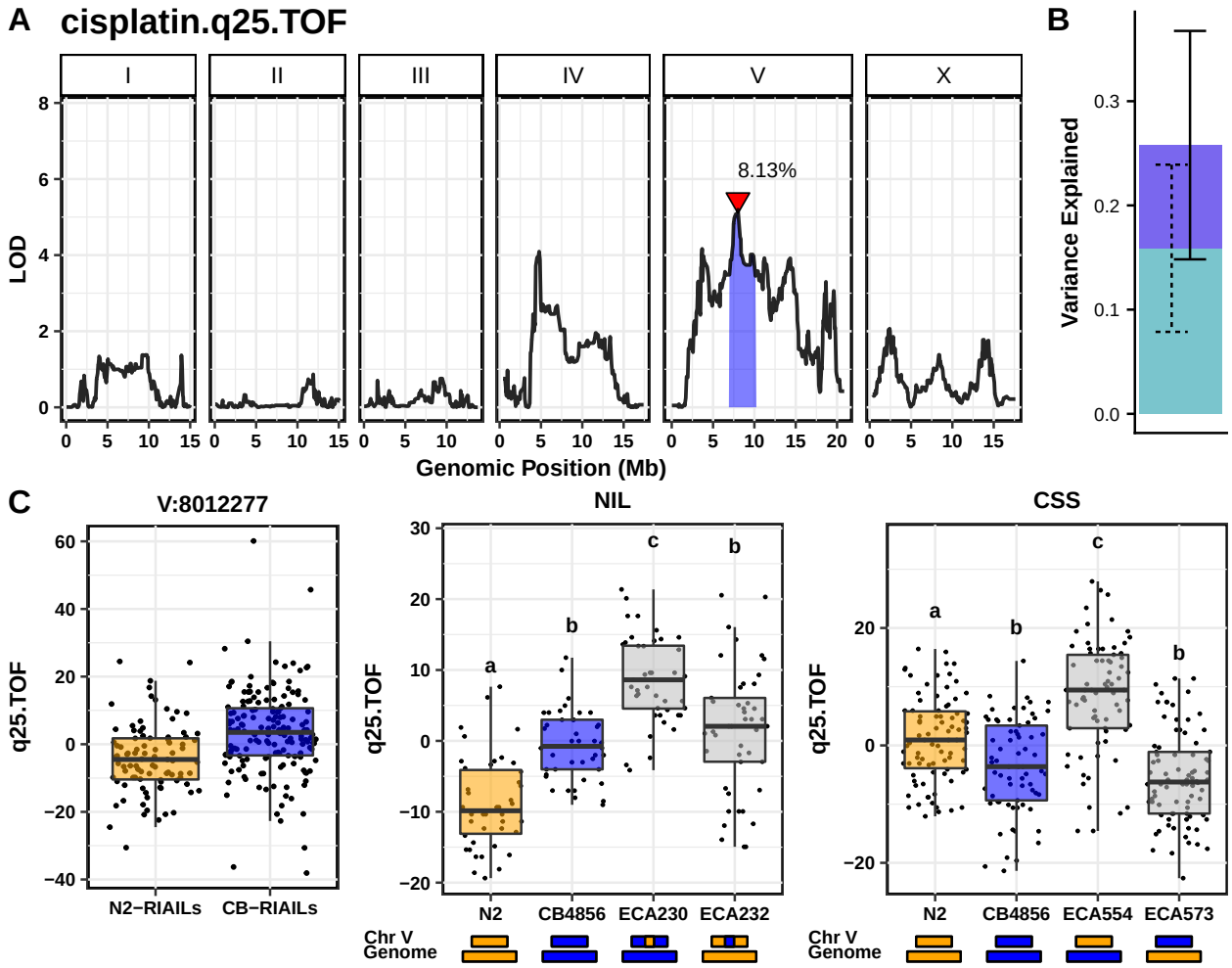

A
cisplatin.q10.EXT
I
II
III
IV
V
X
LOD
7.81%
Genomic Position (Mb)
B
Variance Explained
C
IV:4779025
q10.EXT
N2−RIAILs
CB−RIAILs
NIL
a
b
c
d
N2
CB4856
ECA229
ECA231
Chr IV
Genome

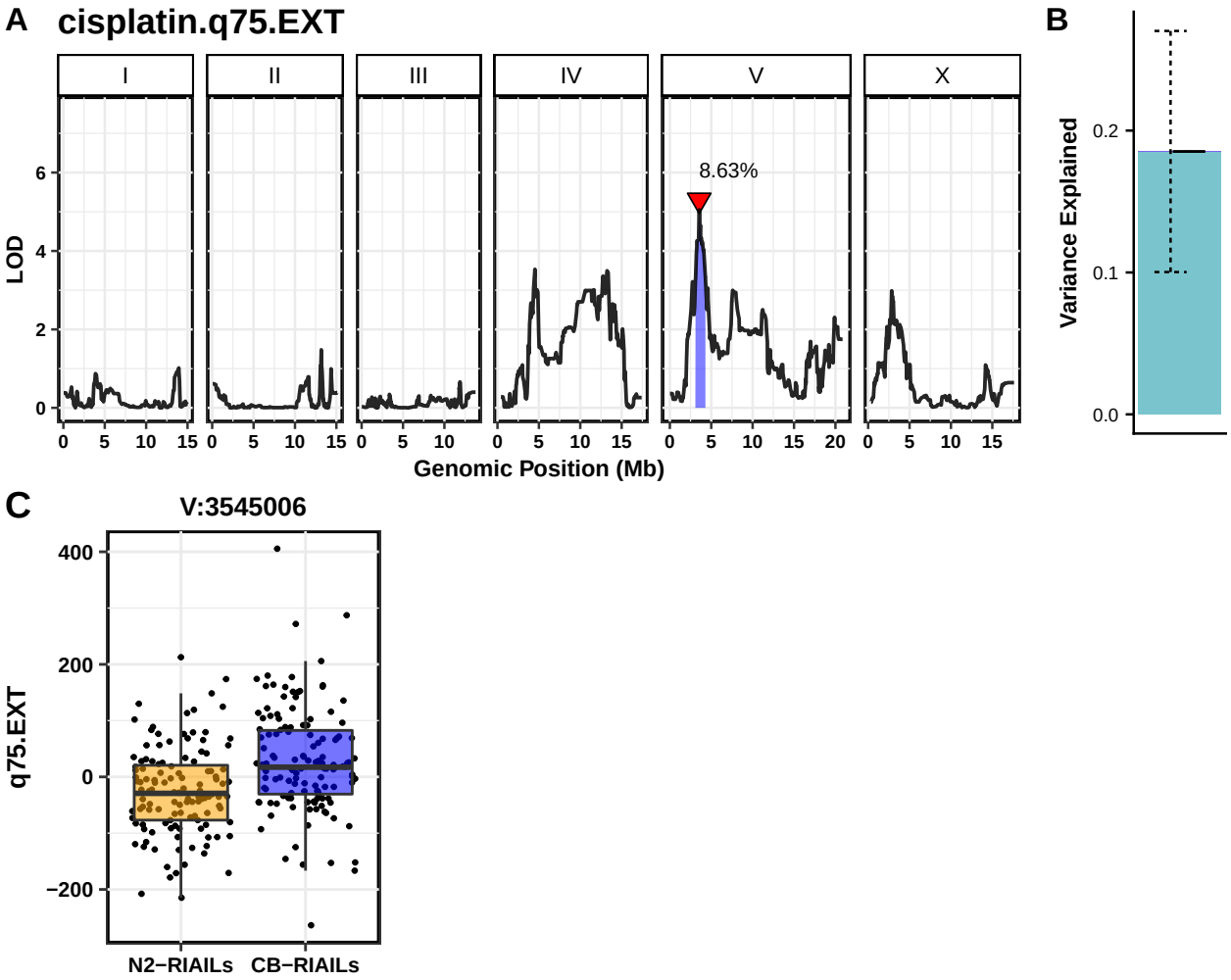

A
cisplatin.q10.norm.EXT
I
II
III
IV
V
X
8.23%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:12908590
q10.norm.EXT
N2−RIAILs
CB−RIAILs

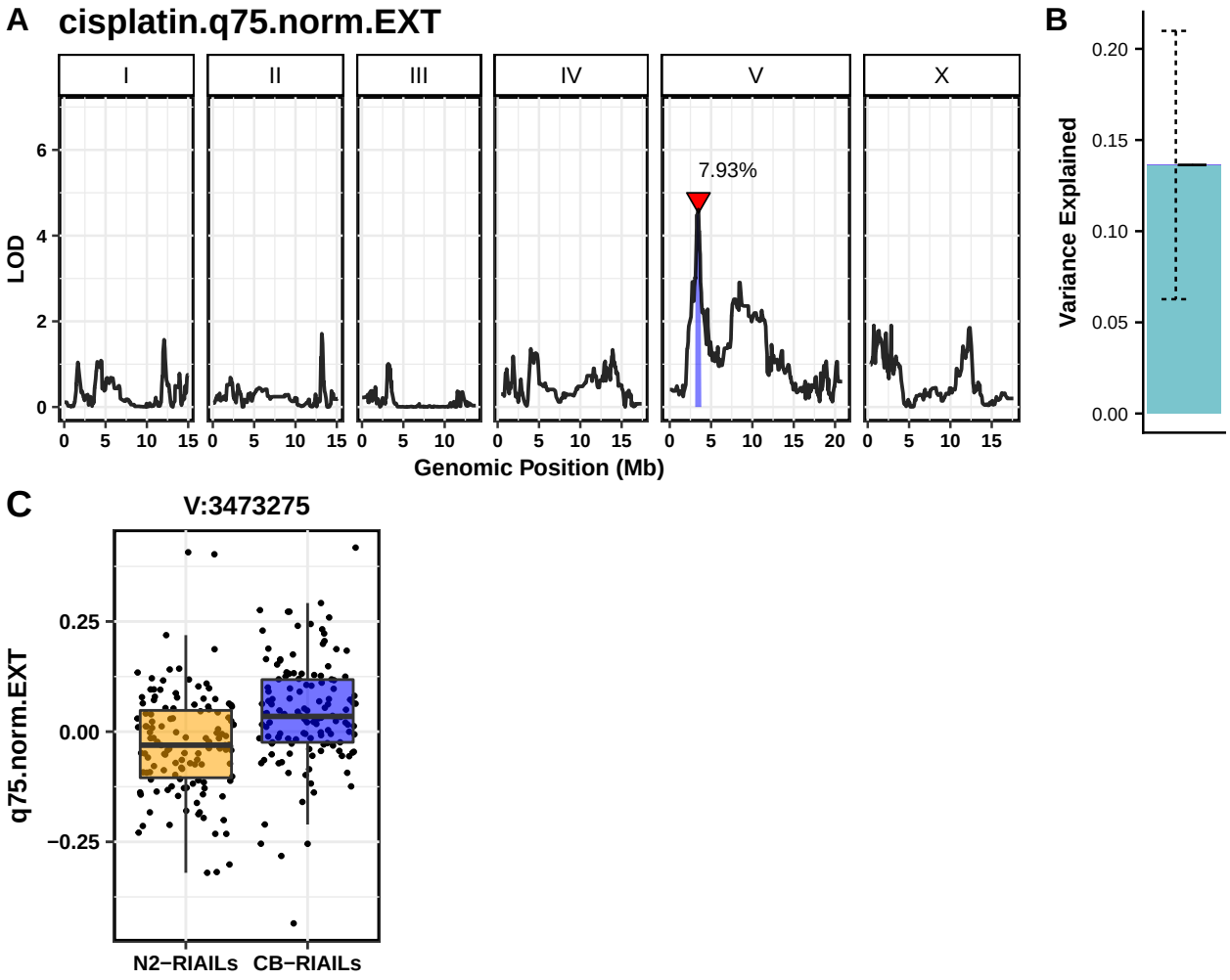

A
cisplatin.q10.TOF
I
II
III
IV
V
X
LOD
7.5
5.0
2.5
0.0
9.62%
0 5 10 15
0 5 10 15
0 5 10
0 5 10 15
0 5 10 15 20
0 5 10 15
Genomic Position (Mb)
B
Variance Explained
0.3
0.2
0.1
0.0
C
V:4442141
q10.TOF
30
20
10
0
−10
−20
N2−RIAILs
CB−RIAILs

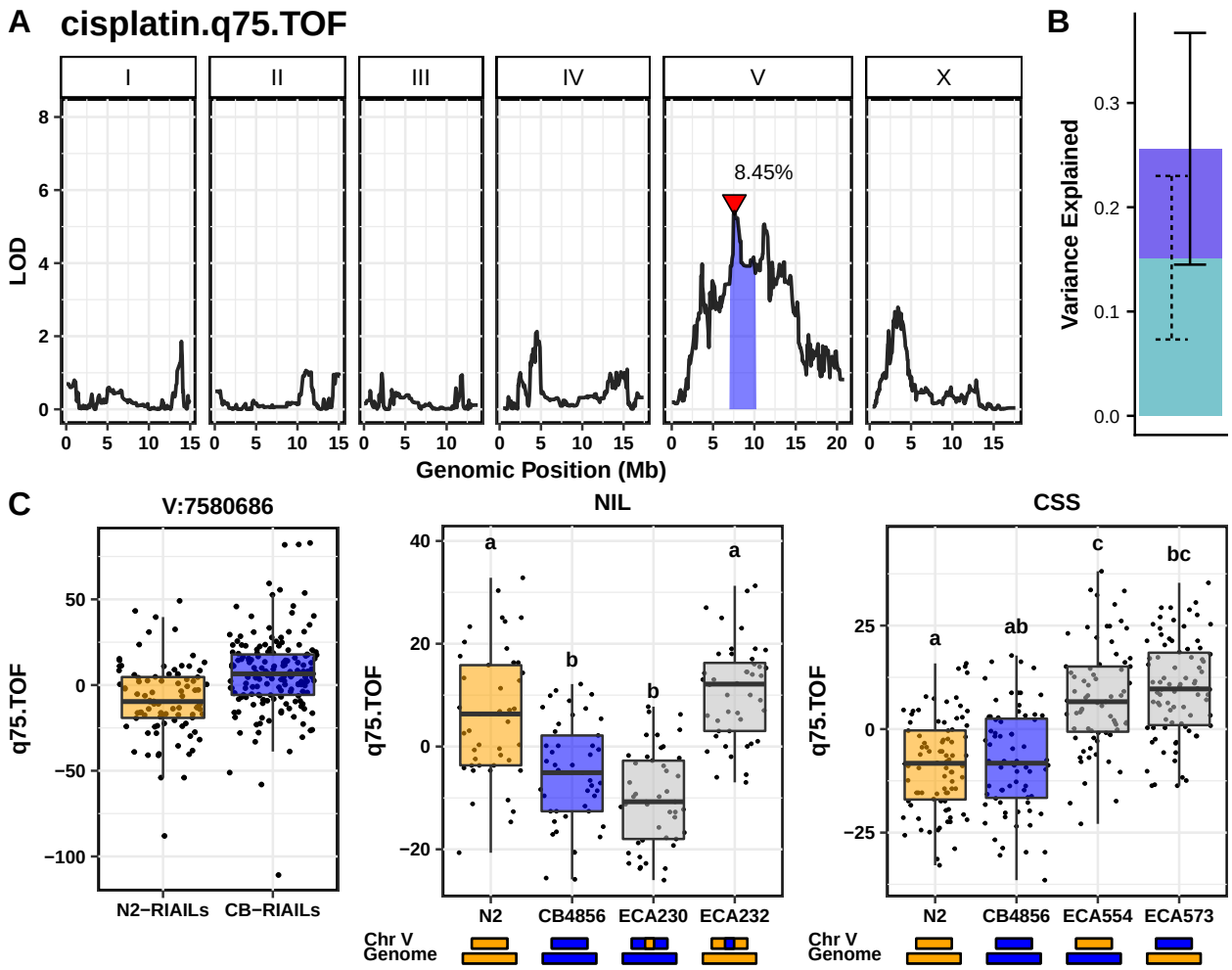

A
cisplatin.q25.EXT
I
II
III
IV
V
X
8.51%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:14140433
q25.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

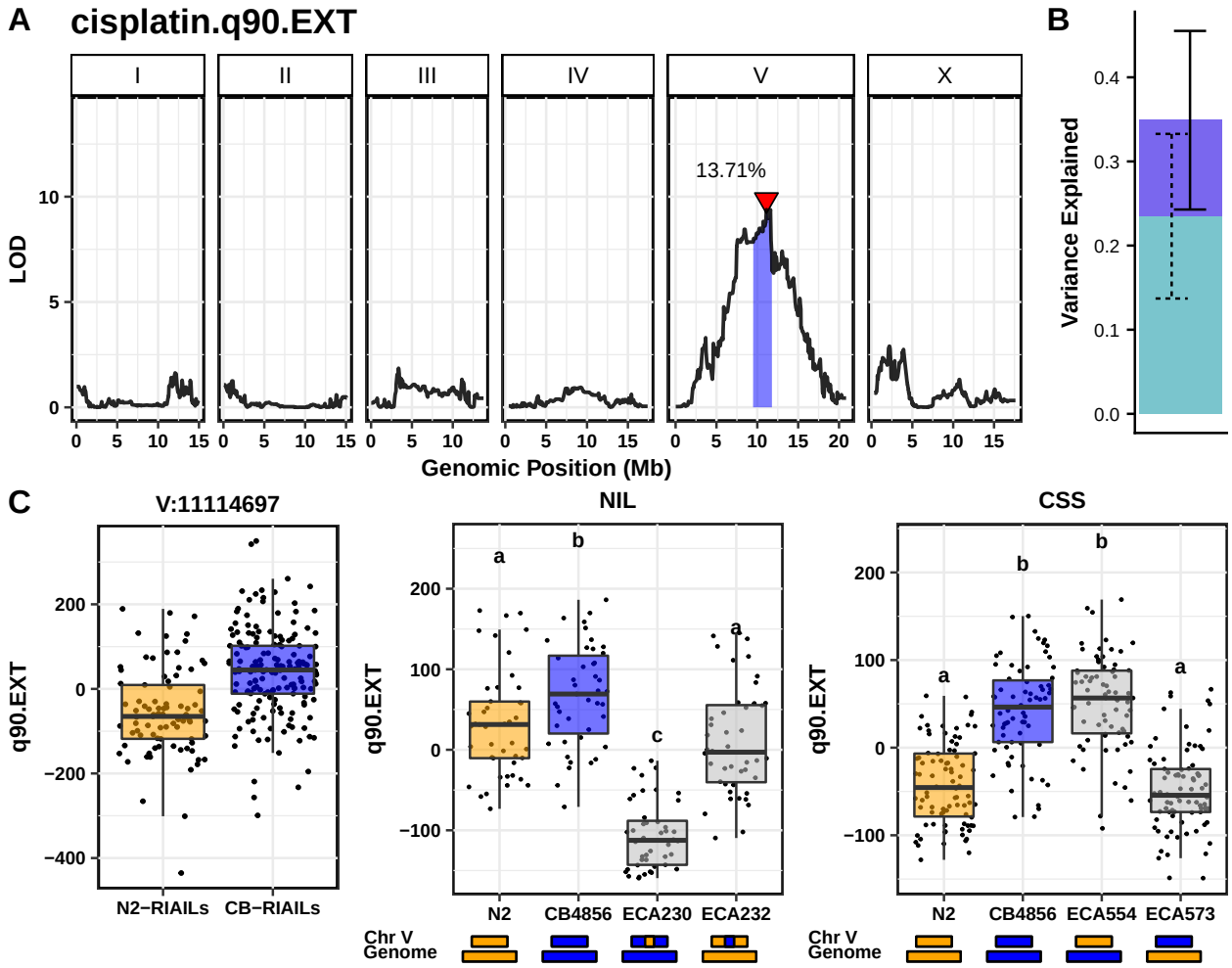

A
cisplatin.q25.norm.EXT
I
II
III
IV
V
X
5.71%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:5732338
q25.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
a
a
b
a
N2
CB4856
ECA229
ECA231
Chr IV
Genome

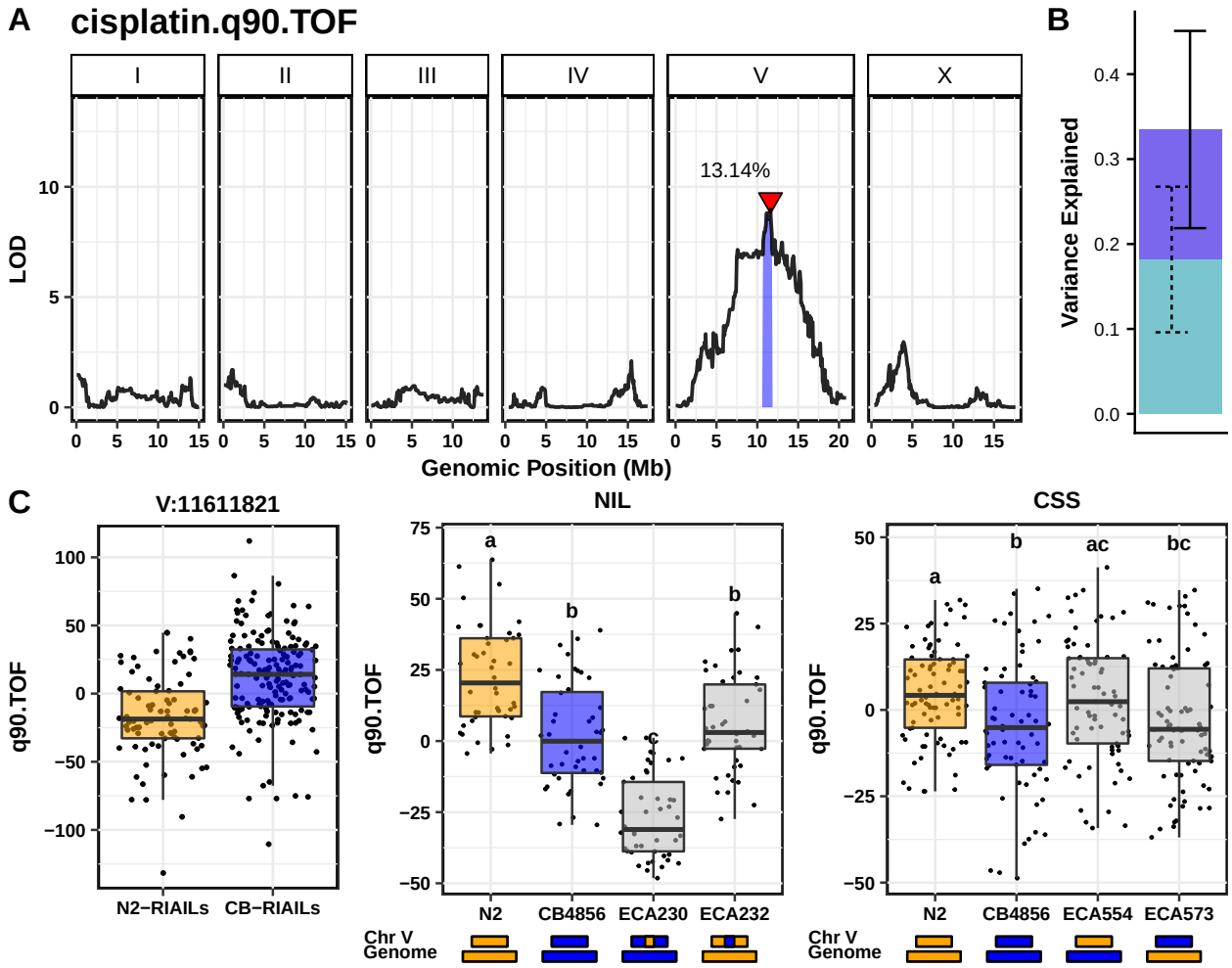

A
cisplatin.q25.TOF
I
II
III
IV
V
X
8.13%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:8012277
q25.TOF
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

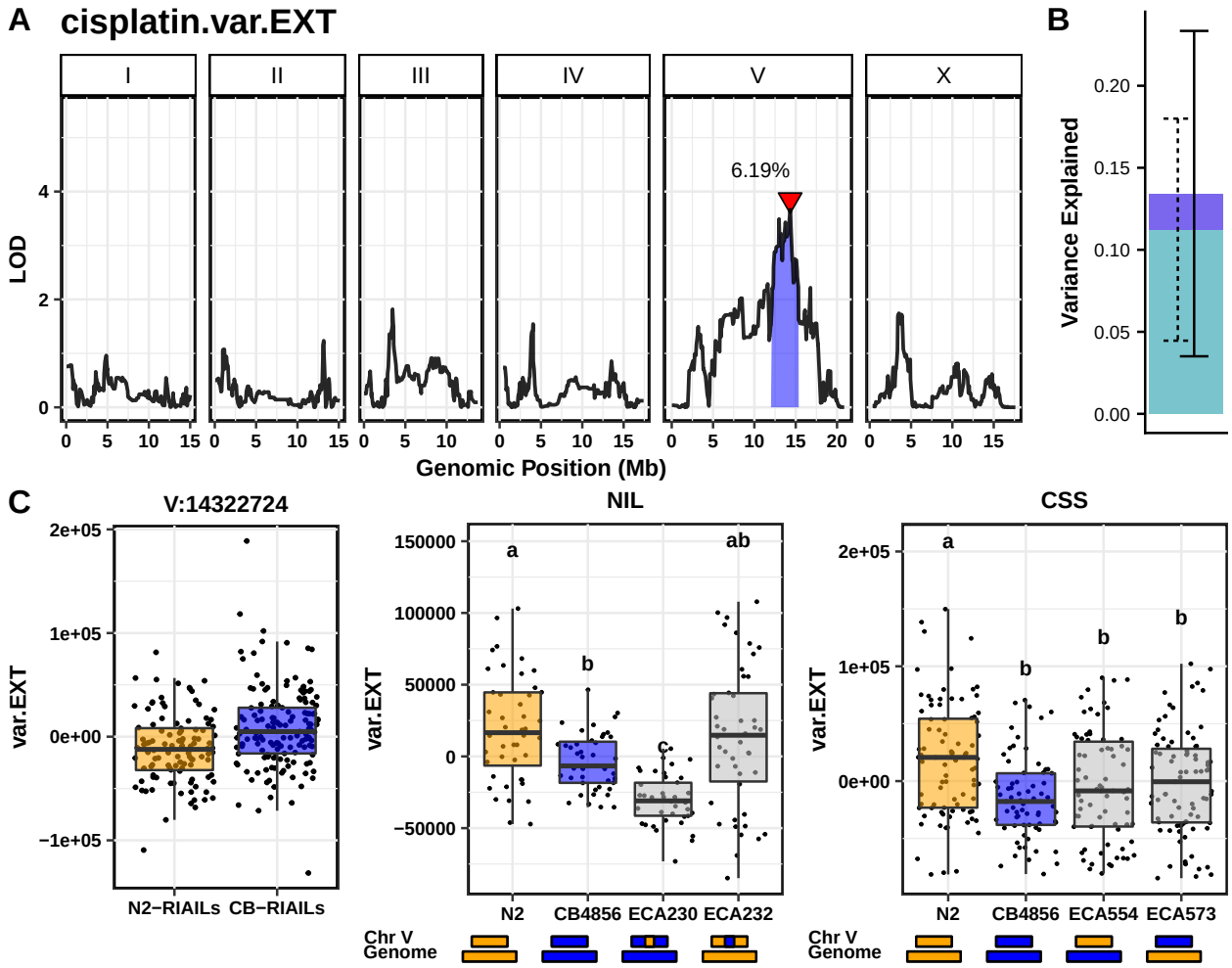

A
cisplatin.q75.EXT
I
II
III
IV
V
X
8.63%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:3545006
q75.EXT
N2−RIAILs
CB−RIAILs

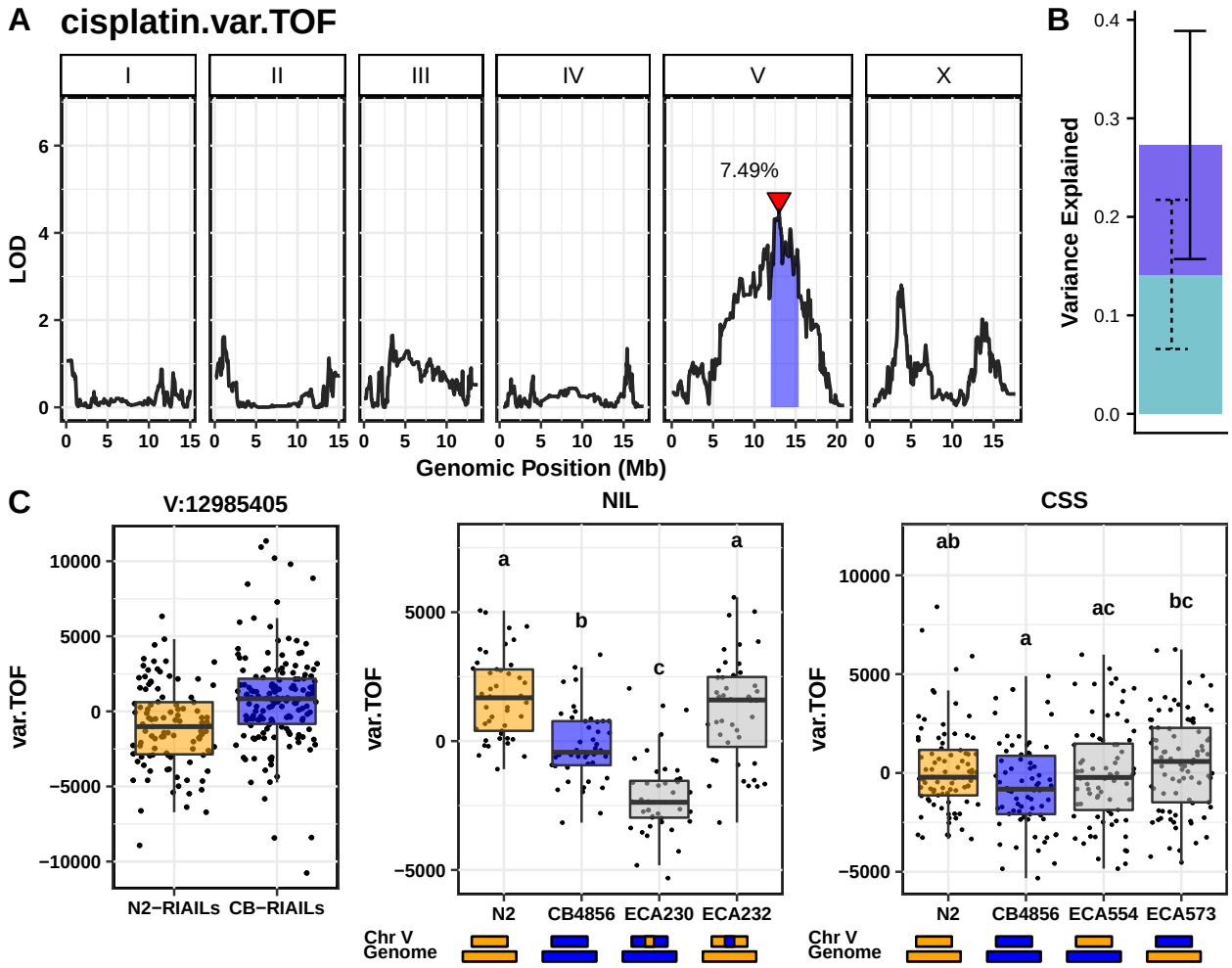

A
cisplatin.q75.norm.EXT
I
II
III
IV
V
X
7.93%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:3473275
q75.norm.EXT
N2−RIAILs
CB−RIAILs

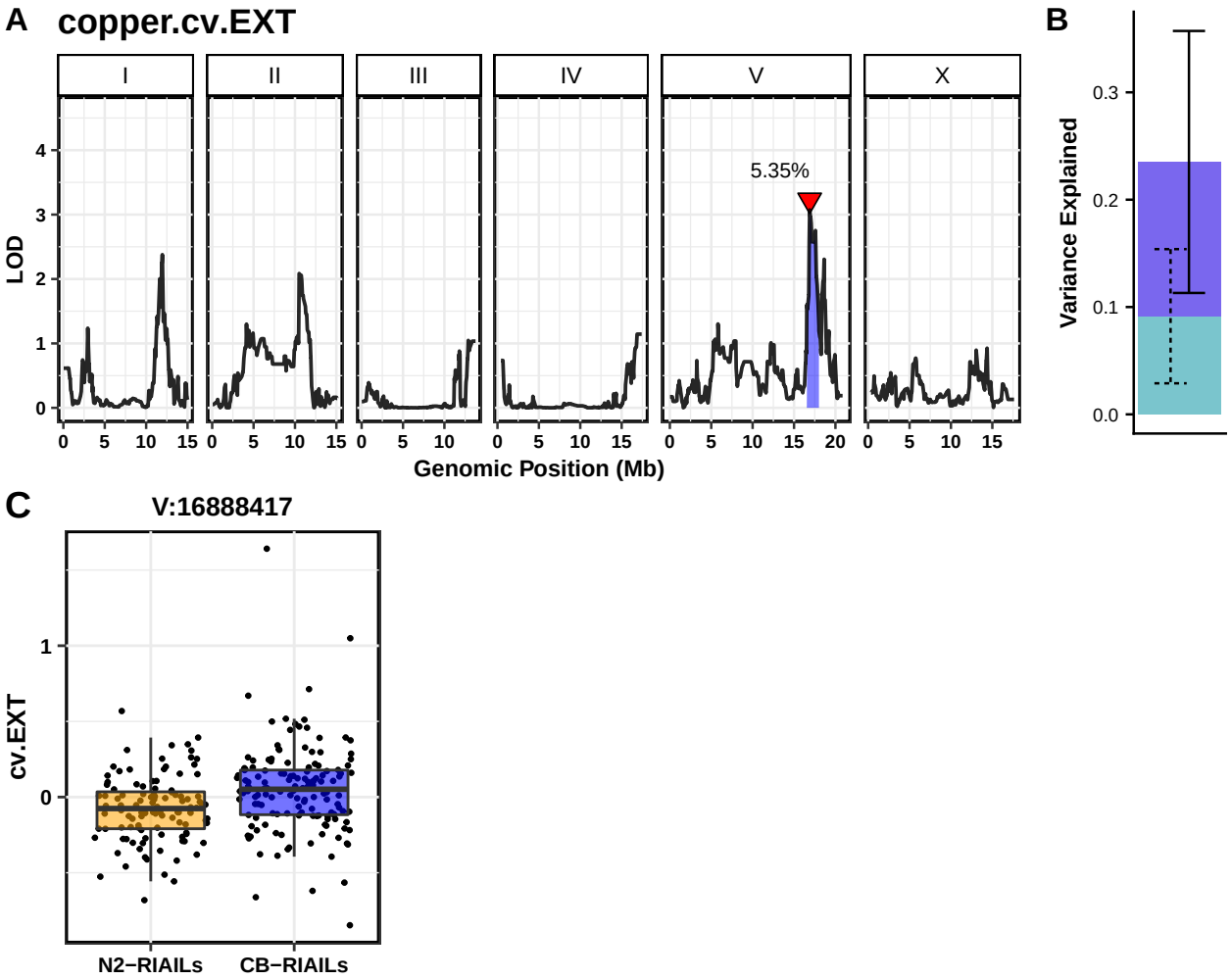

A
cisplatin.q75.TOF
I
II
III
IV
V
X
8.45%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:7580686
q75.TOF
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

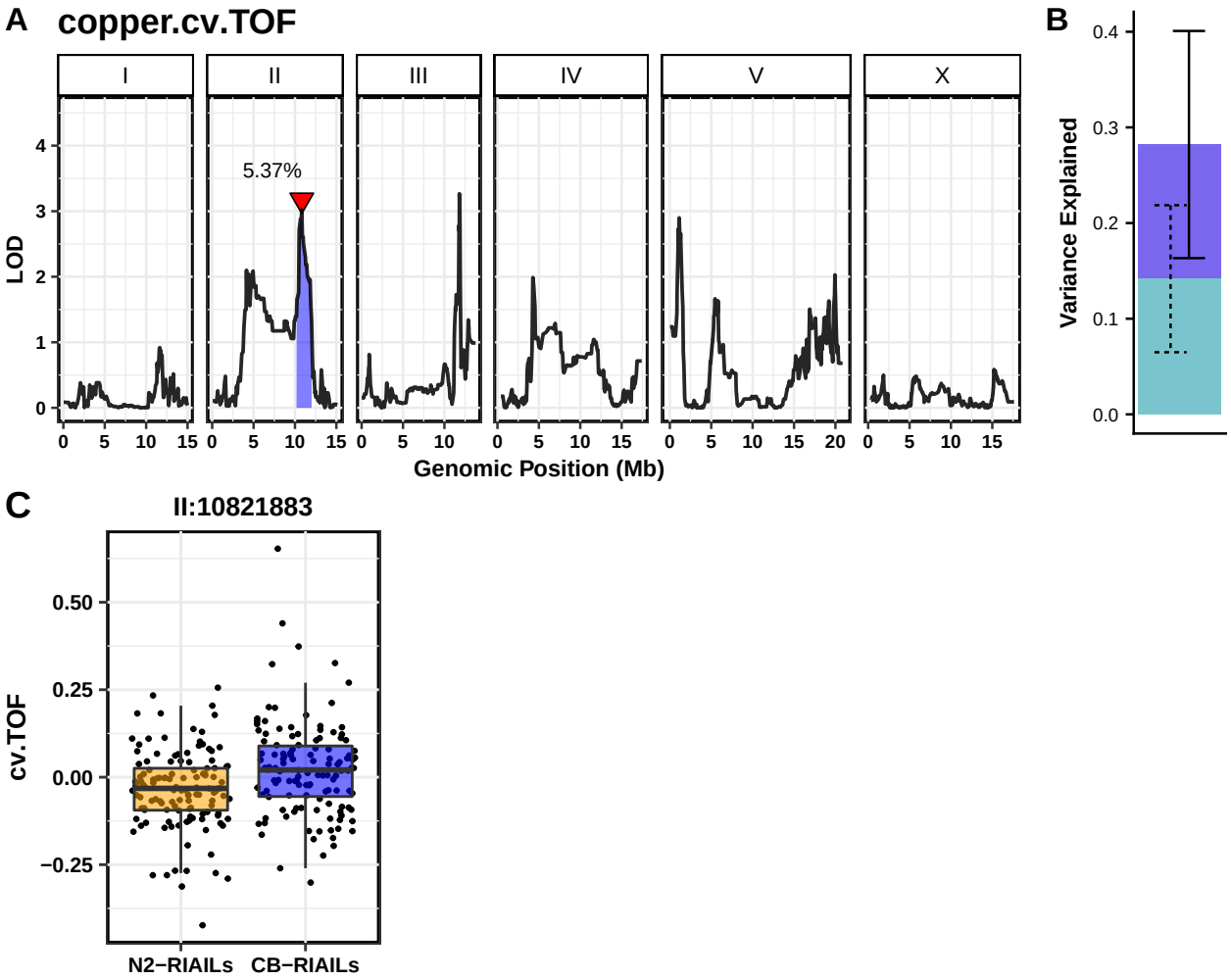

A
cisplatin.q90.EXT
I
II
III
IV
V
X
13.71%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:11114697
q90.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

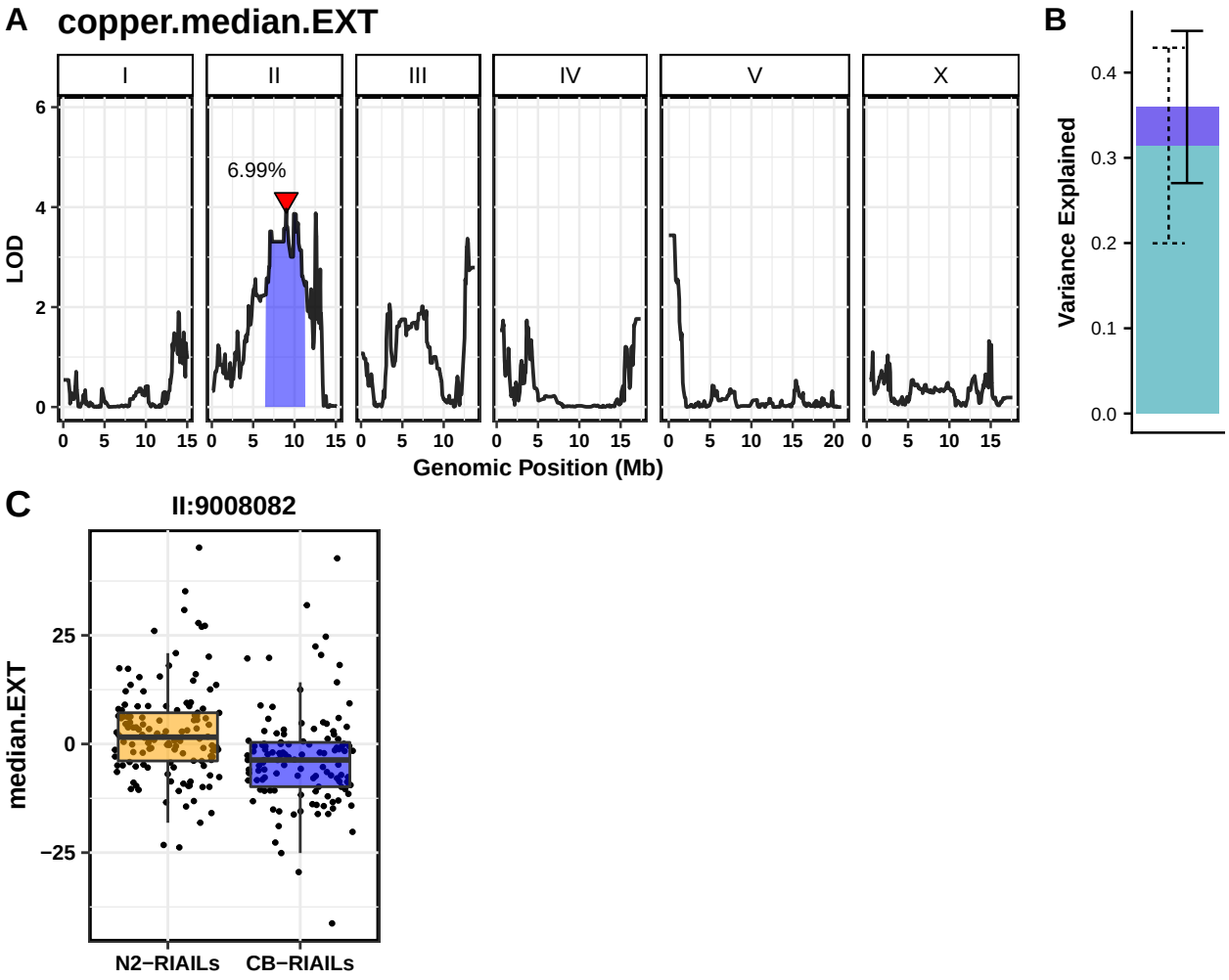

A
cisplatin.q90.TOF
I
II
III
IV
V
X
13.14%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:11611821
q90.TOF
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573

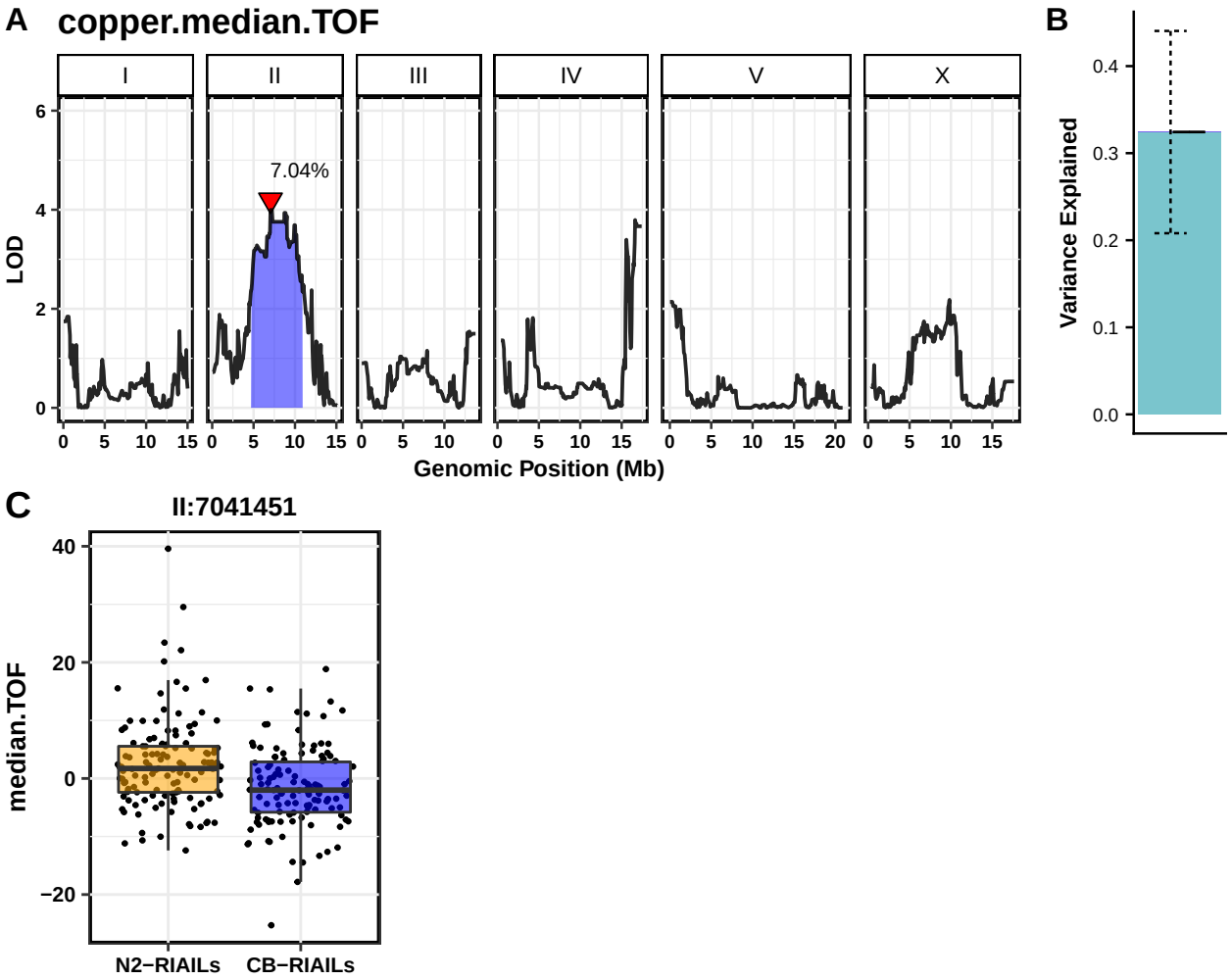

A
cisplatin.var.EXT
I
II
III
IV
V
X
6.19%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:14322724
var.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

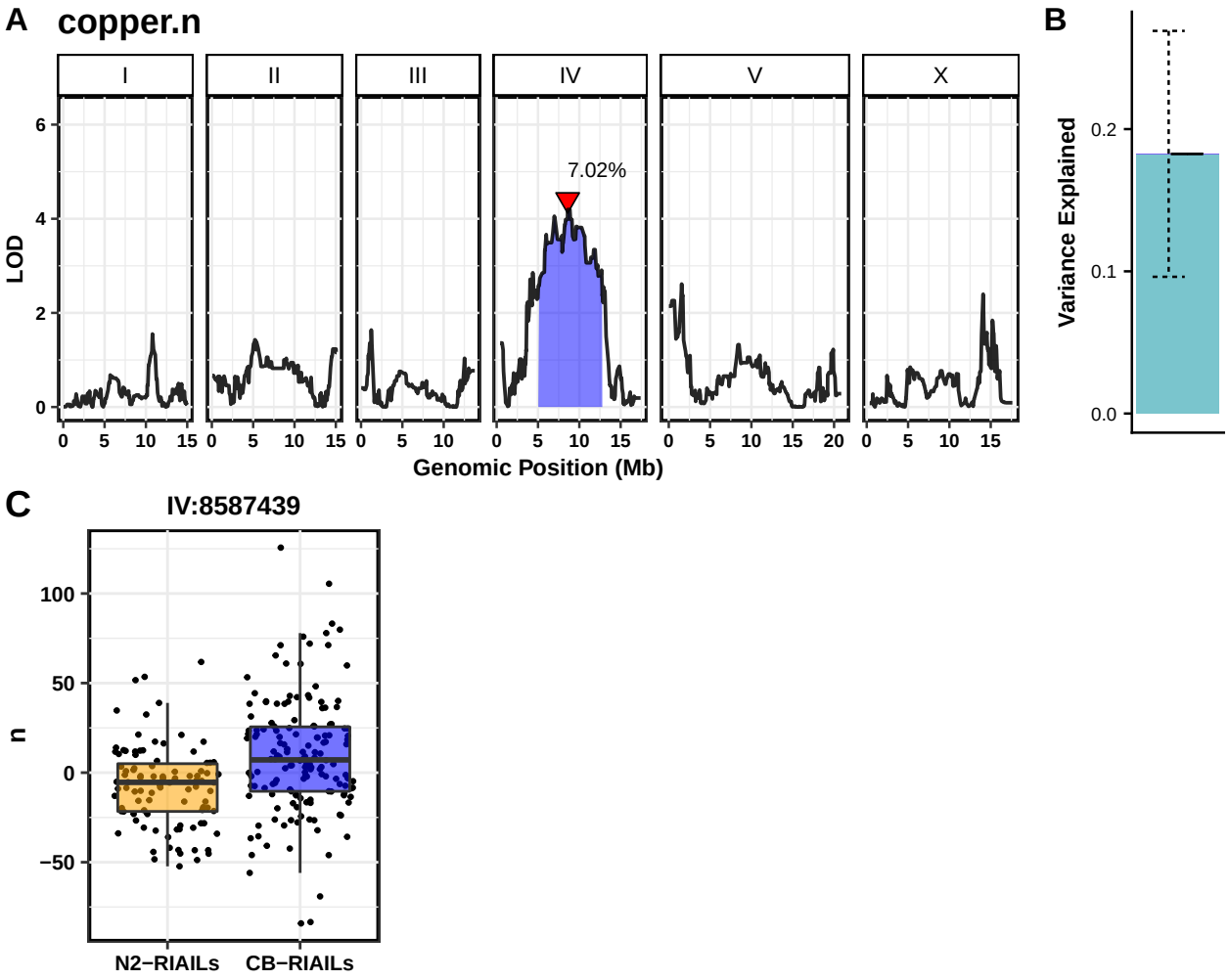

A
cisplatin.var.TOF
I
II
III
IV
V
X
7.49%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:12985405
var.TOF
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
ECA554
ECA573

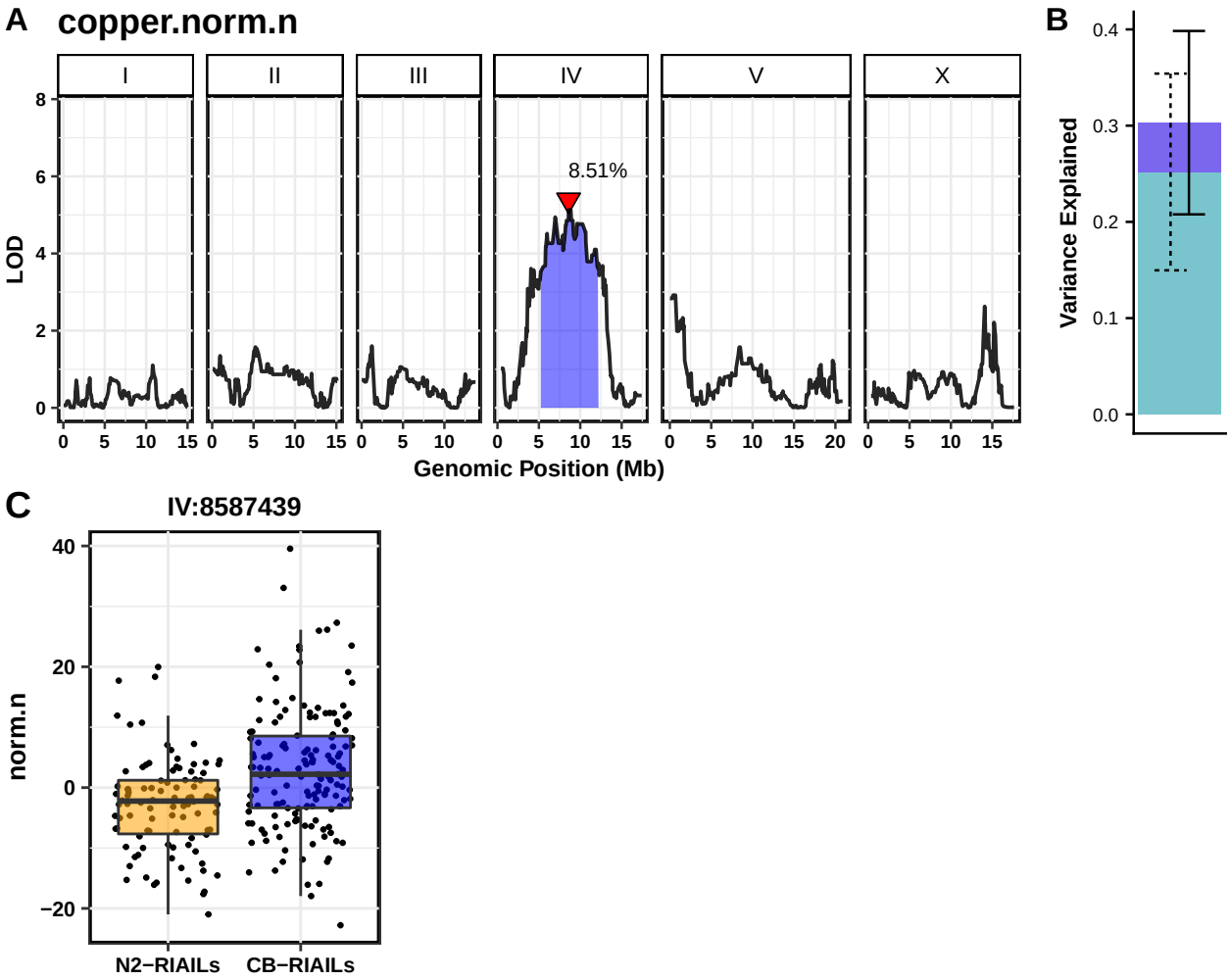

A
copper.cv.EXT
I
II
III
IV
V
X
5.35%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:16888417
cv.EXT
N2−RIAILs
CB−RIAILs

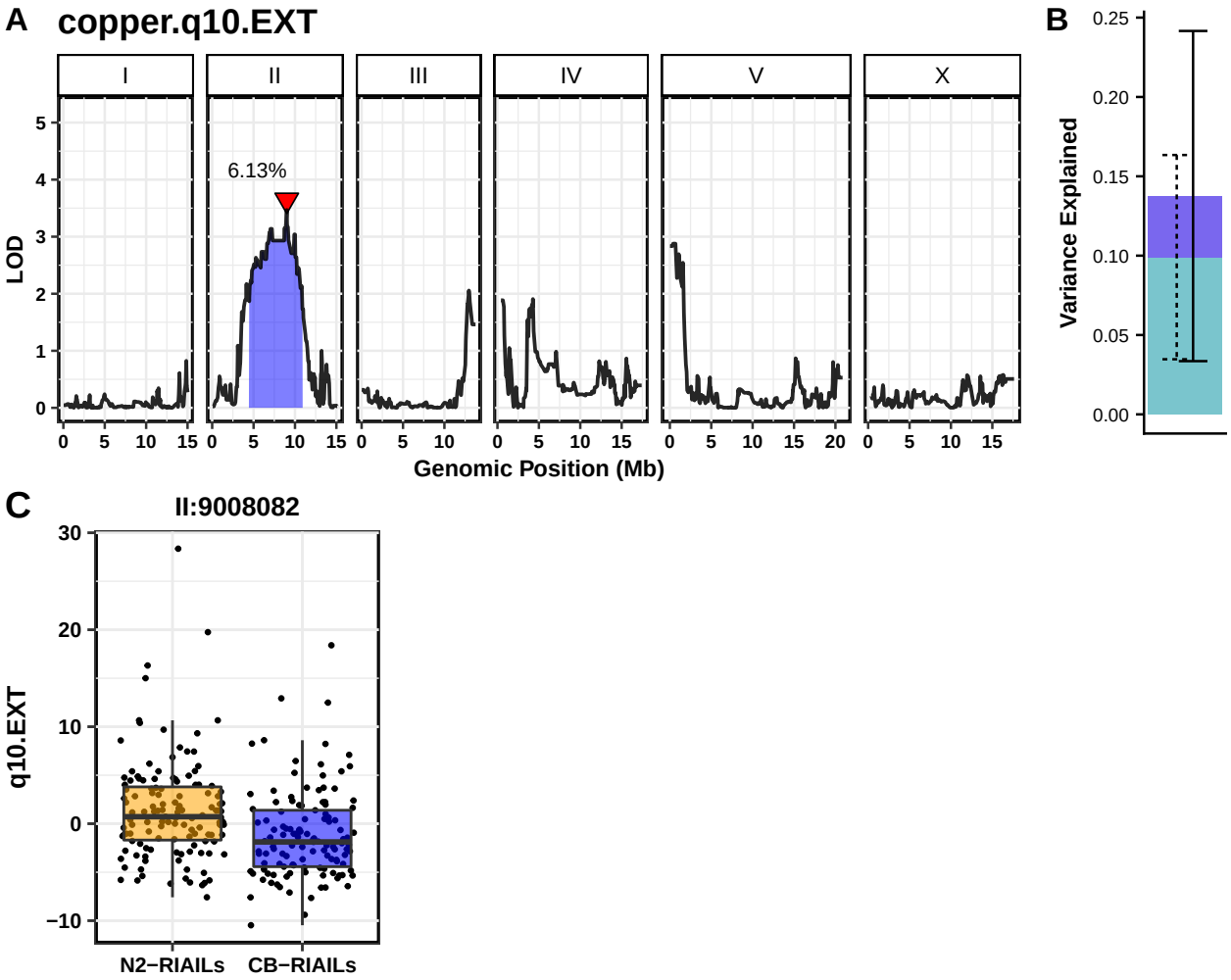

A
copper.cv.TOF
I
II
III
IV
V
X
5.37%
LOD
Genomic Position (Mb)
B
Variance Explained
C
II:10821883
cv.TOF
N2−RIAILs
CB−RIAILs

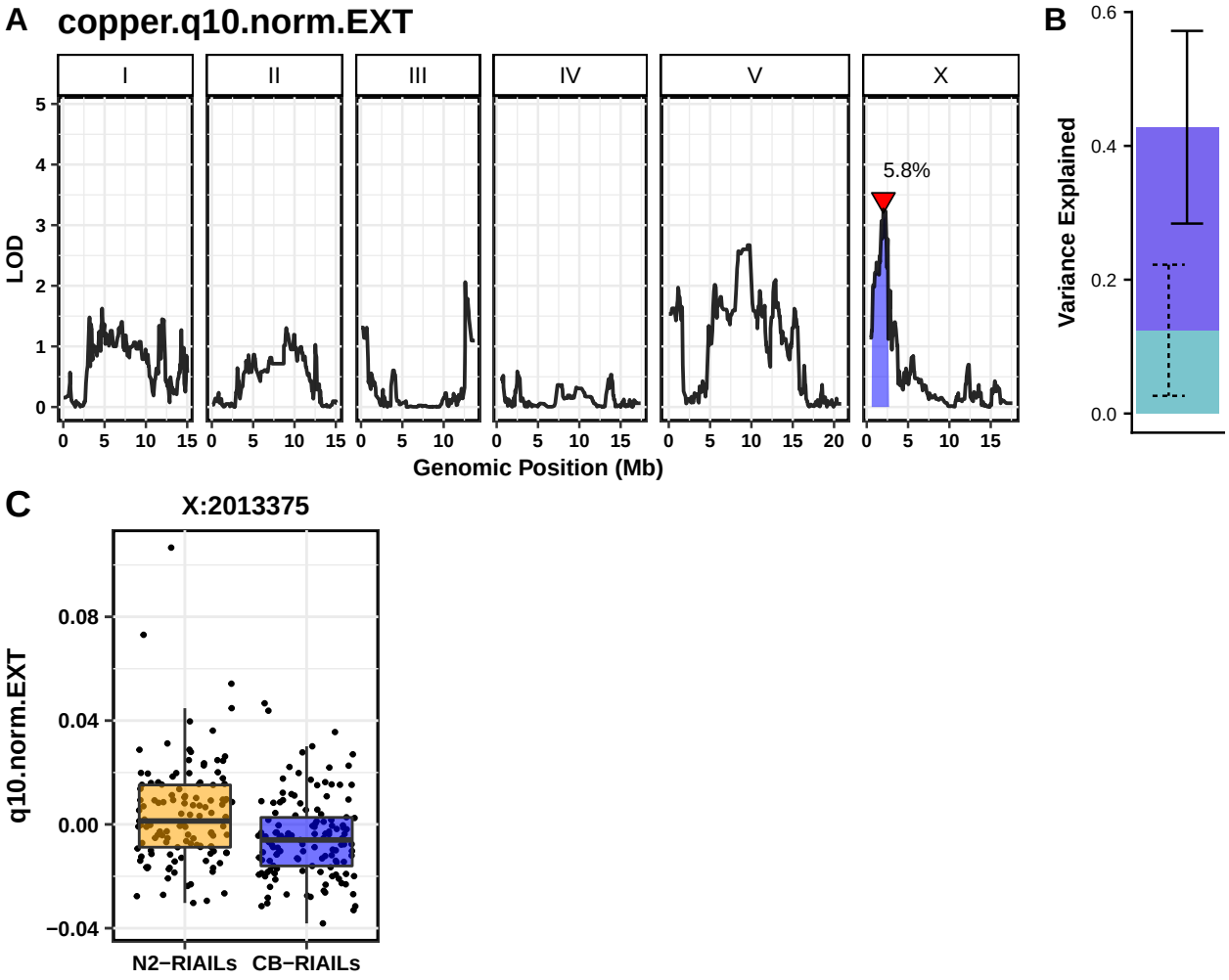

A
copper.median.EXT
I
II
III
IV
V
X
6.99%
LOD
Genomic Position (Mb)
B
Variance Explained
C
II:9008082
median.EXT
N2−RIAILs
CB−RIAILs

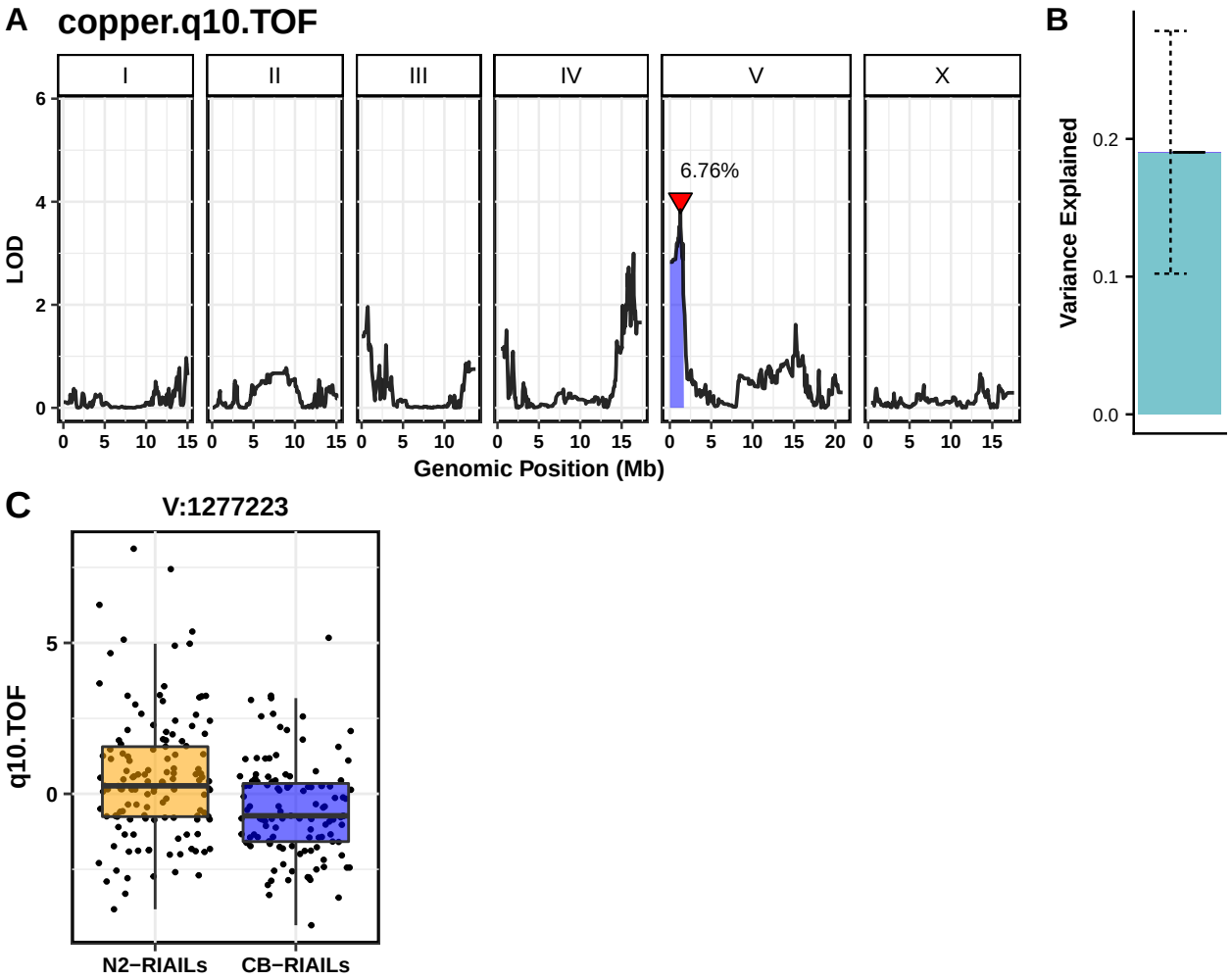

A
copper.median.TOF
I
II
III
IV
V
X
7.04%
LOD
Genomic Position (Mb)
B
Variance Explained
C
II:7041451
median.TOF
N2−RIAILs
CB−RIAILs

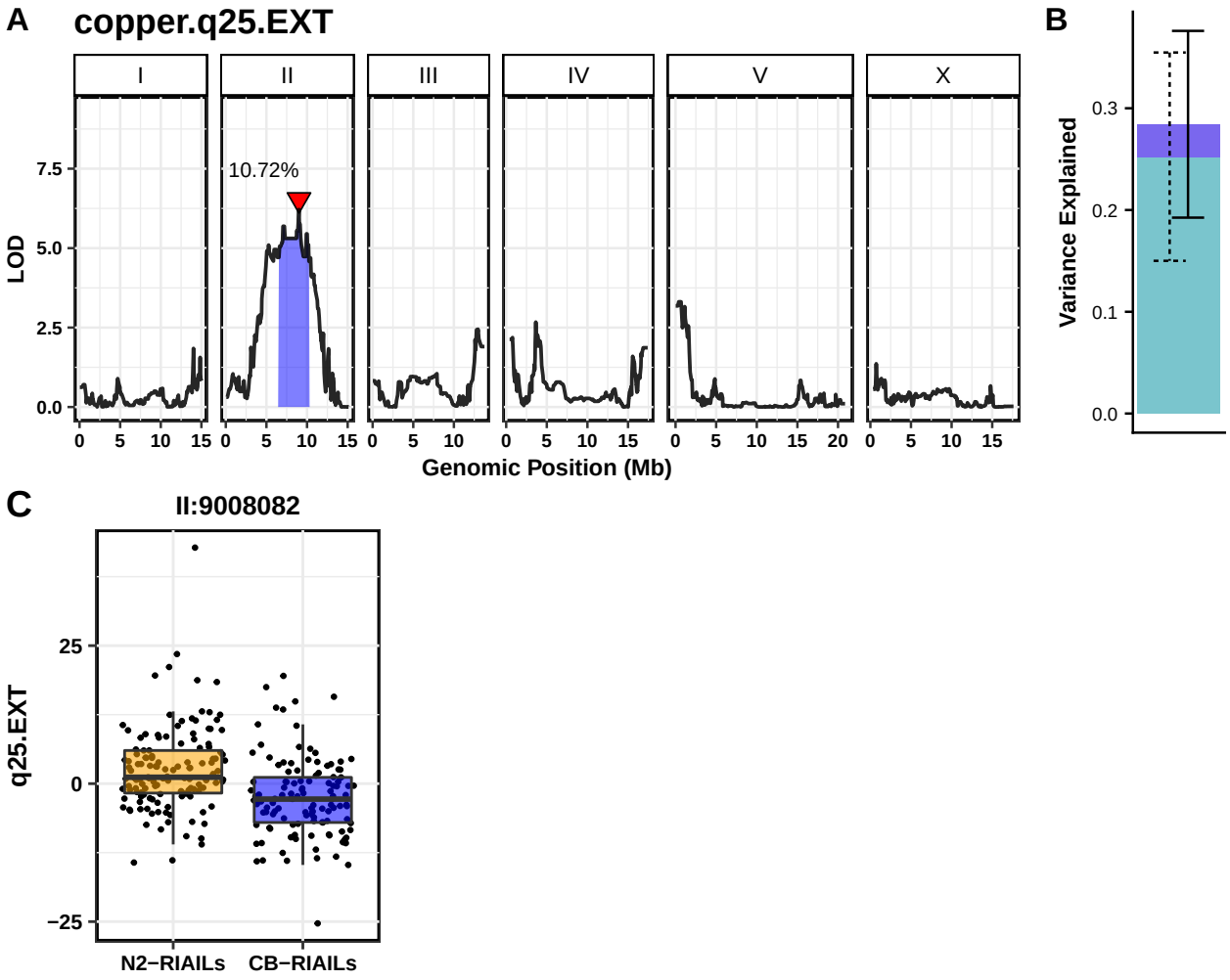

A
copper.n
I
II
III
IV
V
X
7.02%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:8587439
n
N2−RIAILs
CB−RIAILs

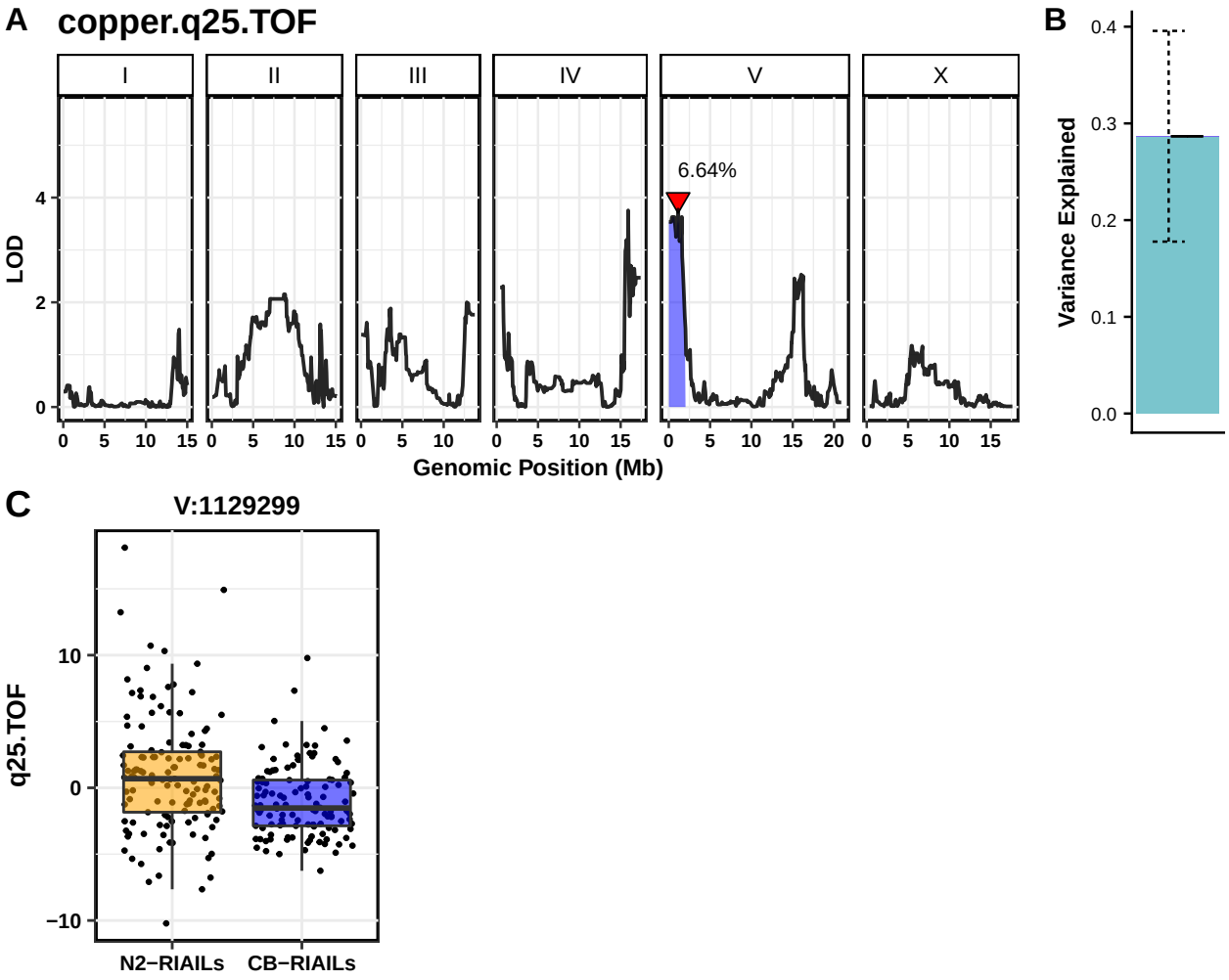

A
copper.norm.n
I
II
III
IV
V
X
8.51%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:8587439
norm.n
N2−RIAILs
CB−RIAILs

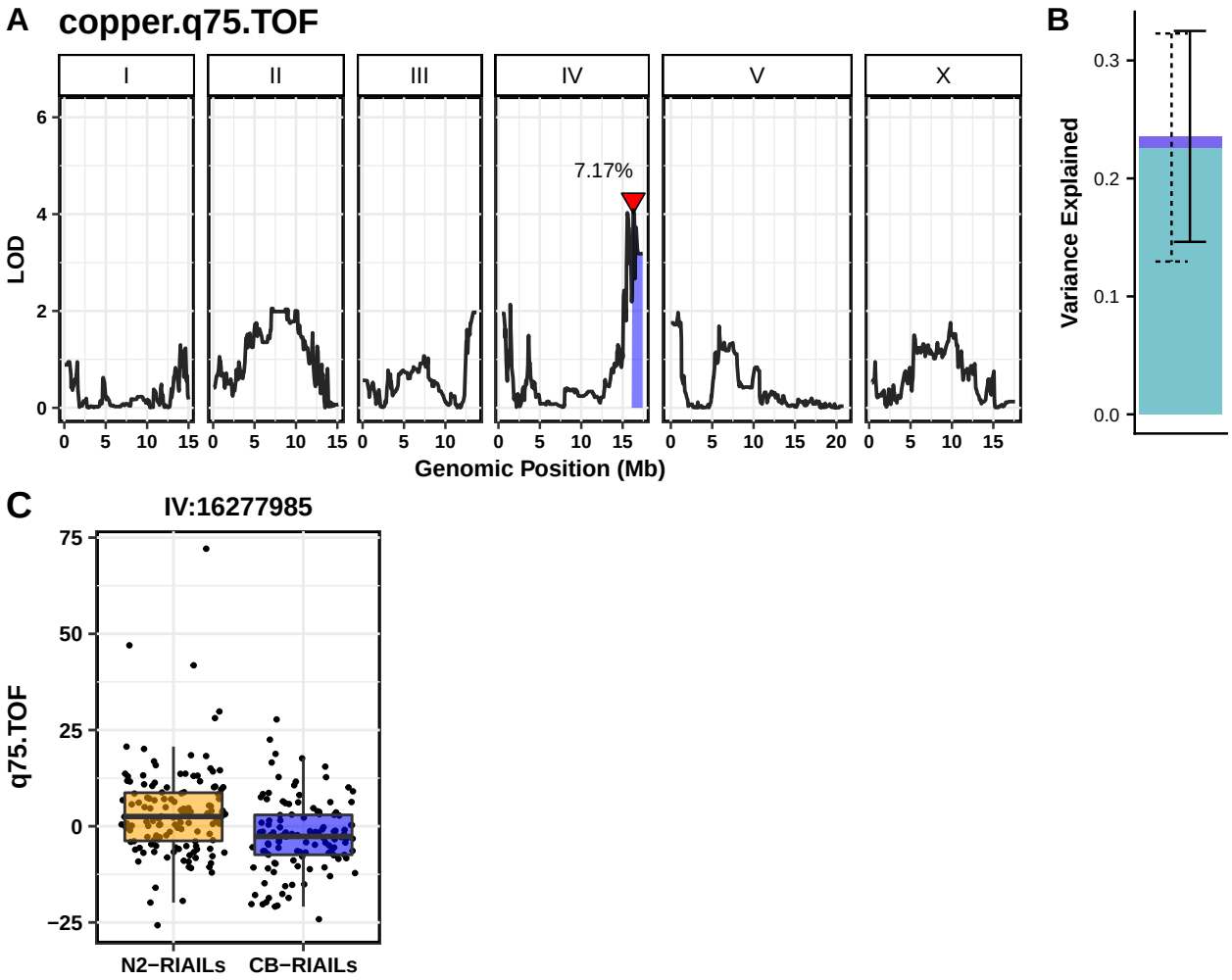

A
copper.q10.EXT
I
II
III
IV
V
X
6.13%
LOD
Genomic Position (Mb)
B
Variance Explained
C
II:9008082
q10.EXT
N2−RIAILs
CB−RIAILs

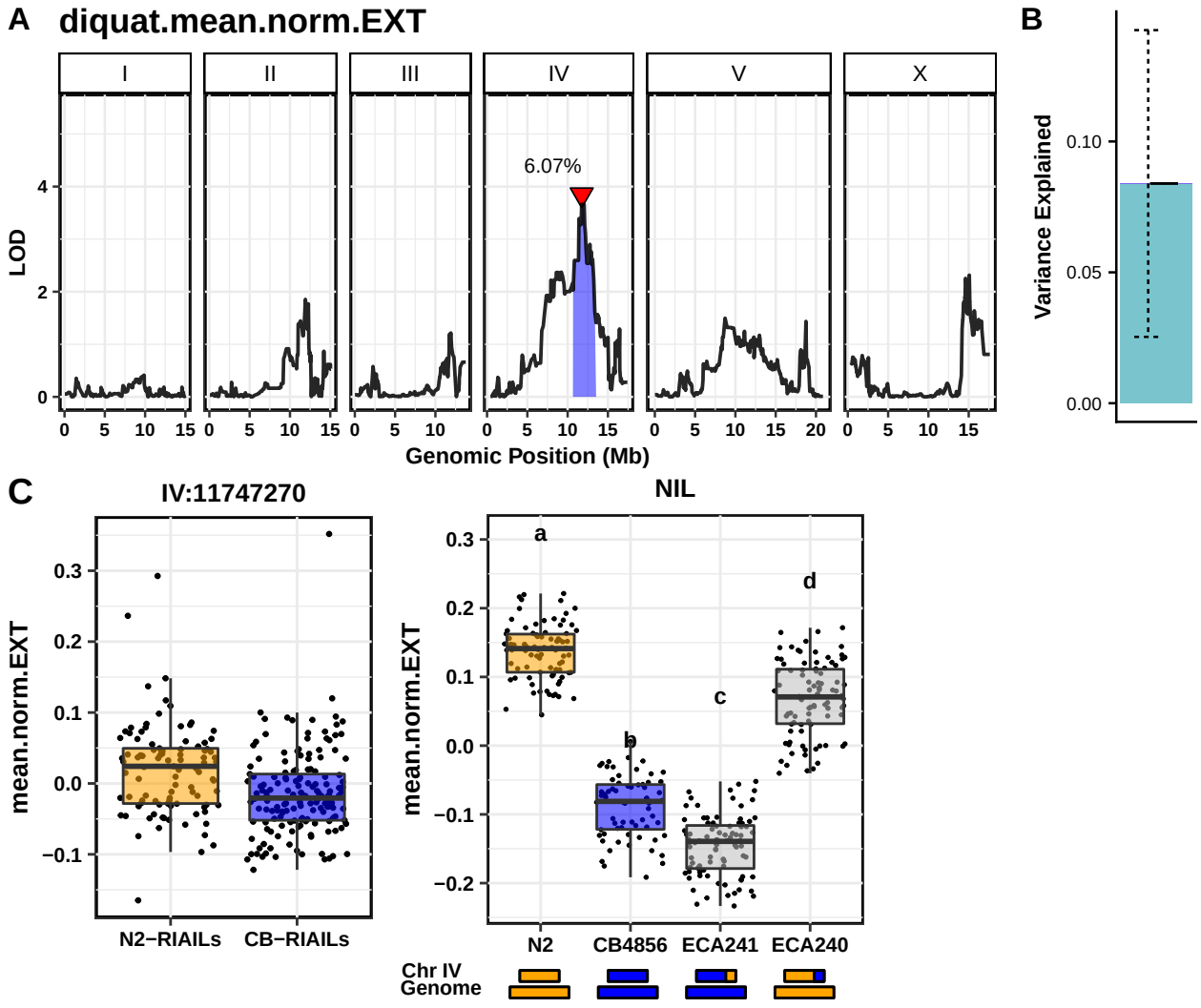

A
copper.q10.norm.EXT
I
II
III
IV
V
X
LOD
5.8%
Genomic Position (Mb)
B
Variance Explained
C
X:2013375
q10.norm.EXT
N2−RIAILs
CB−RIAILs

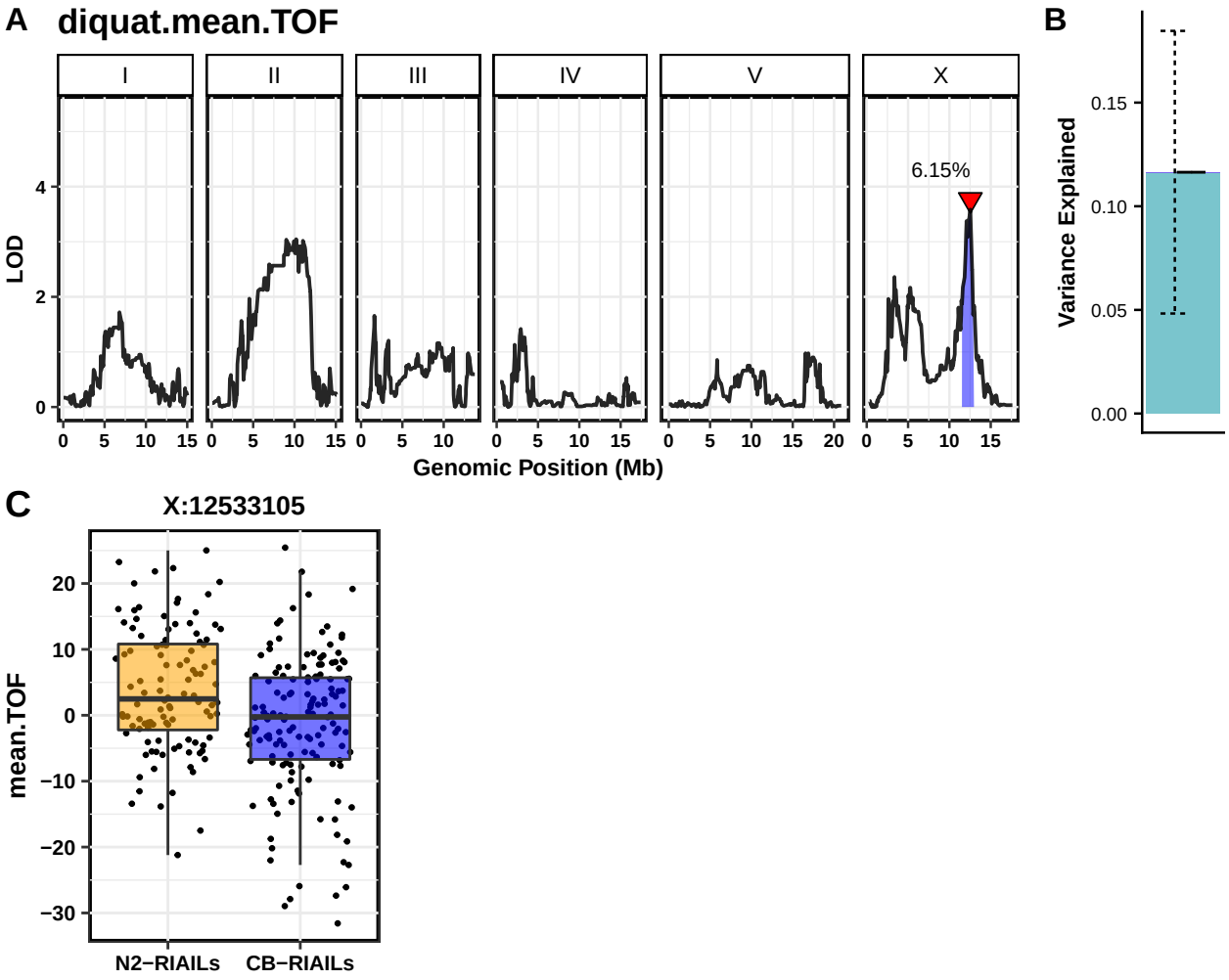

A
copper.q10.TOF
I
II
III
IV
V
X
6.76%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:1277223
q10.TOF
N2−RIAILs
CB−RIAILs

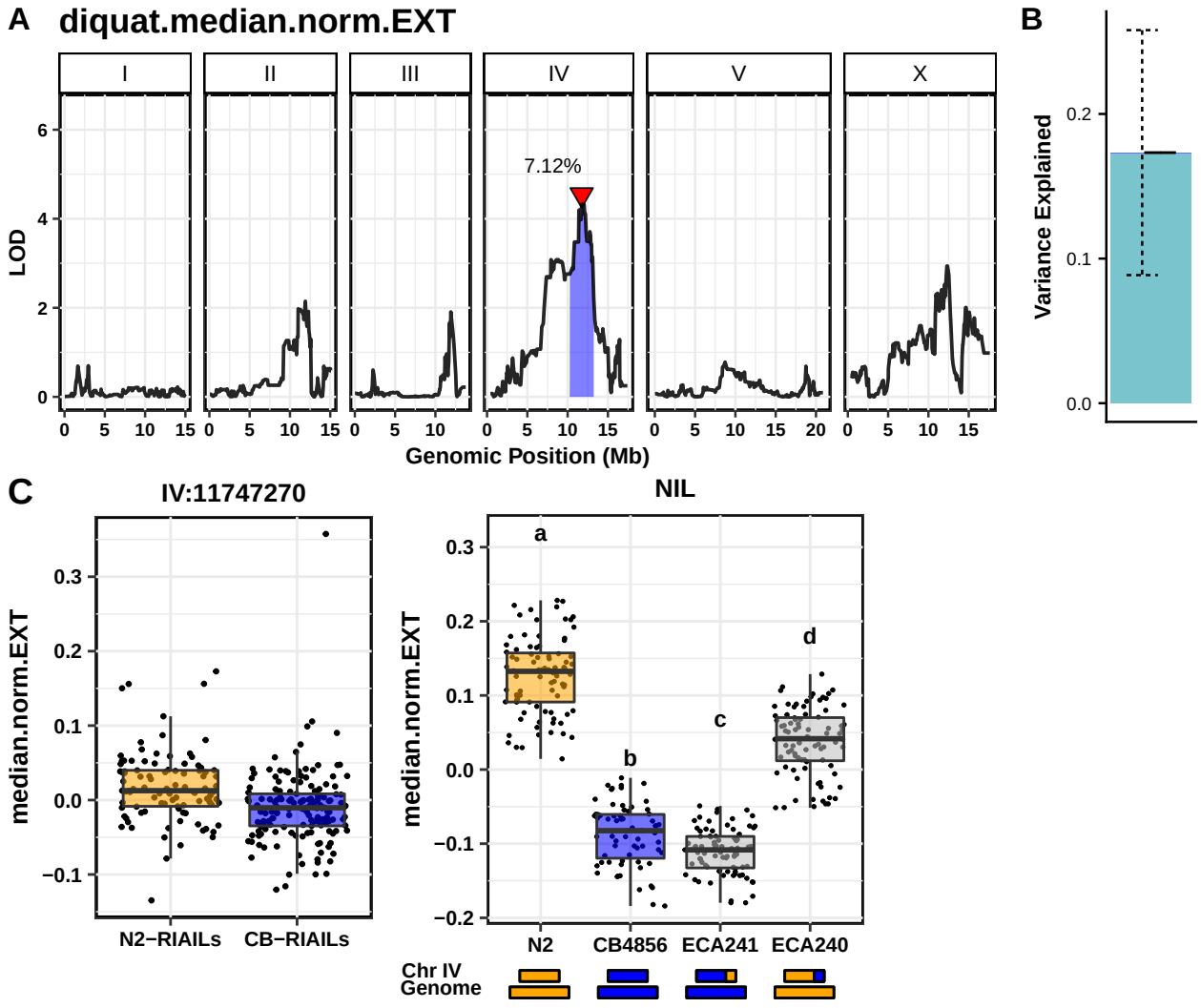

A
copper.q25.EXT
I
II
III
IV
V
X
10.72%
LOD
7.5
5.0
2.5
0.0
0 5 10 15
0 5 10 15
0 5 10
0 5 10 15
0 5 10 15 20
0 5 10 15
Genomic Position (Mb)
B
Variance Explained
0.3
0.2
0.1
0.0
C
II:9008082
q25.EXT
25
0
−25
N2−RIAILs
CB−RIAILs

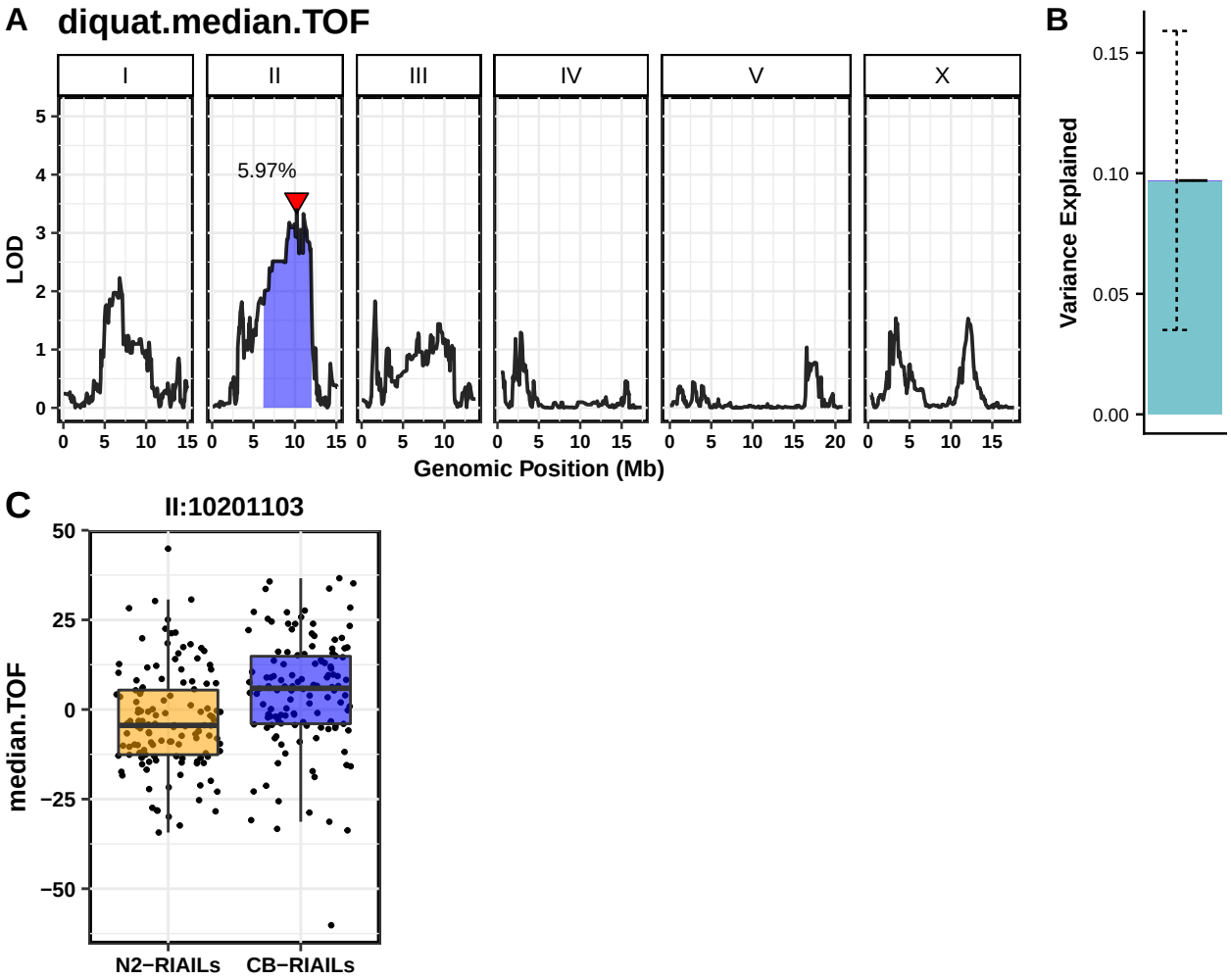

A
copper.q25.TOF
I
II
III
IV
V
X
6.64%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:1129299
q25.TOF
N2−RIAILs
CB−RIAILs

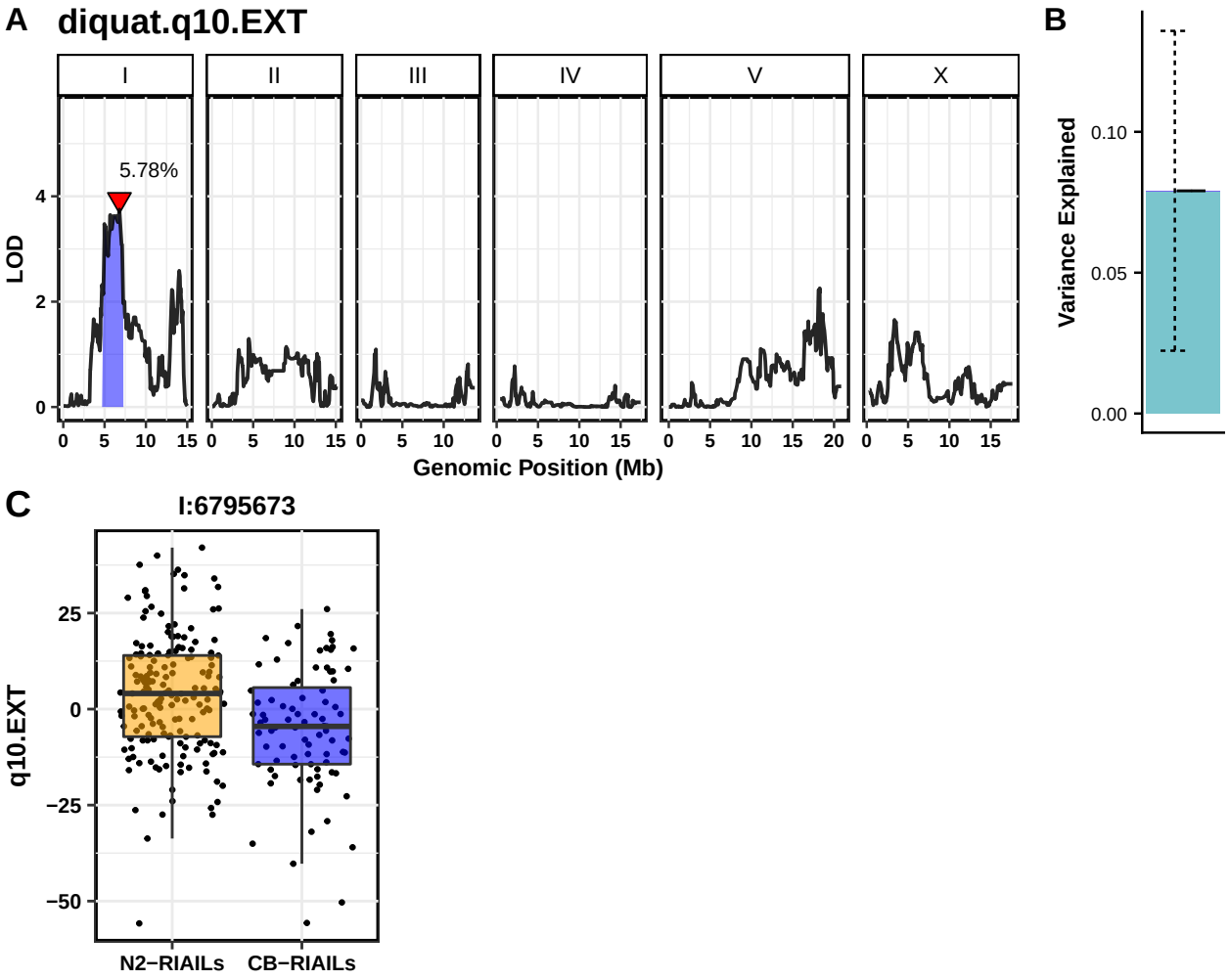

A
copper.q75.TOF
I
II
III
IV
V
X
7.17%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:16277985
q75.TOF
N2−RIAILs
CB−RIAILs

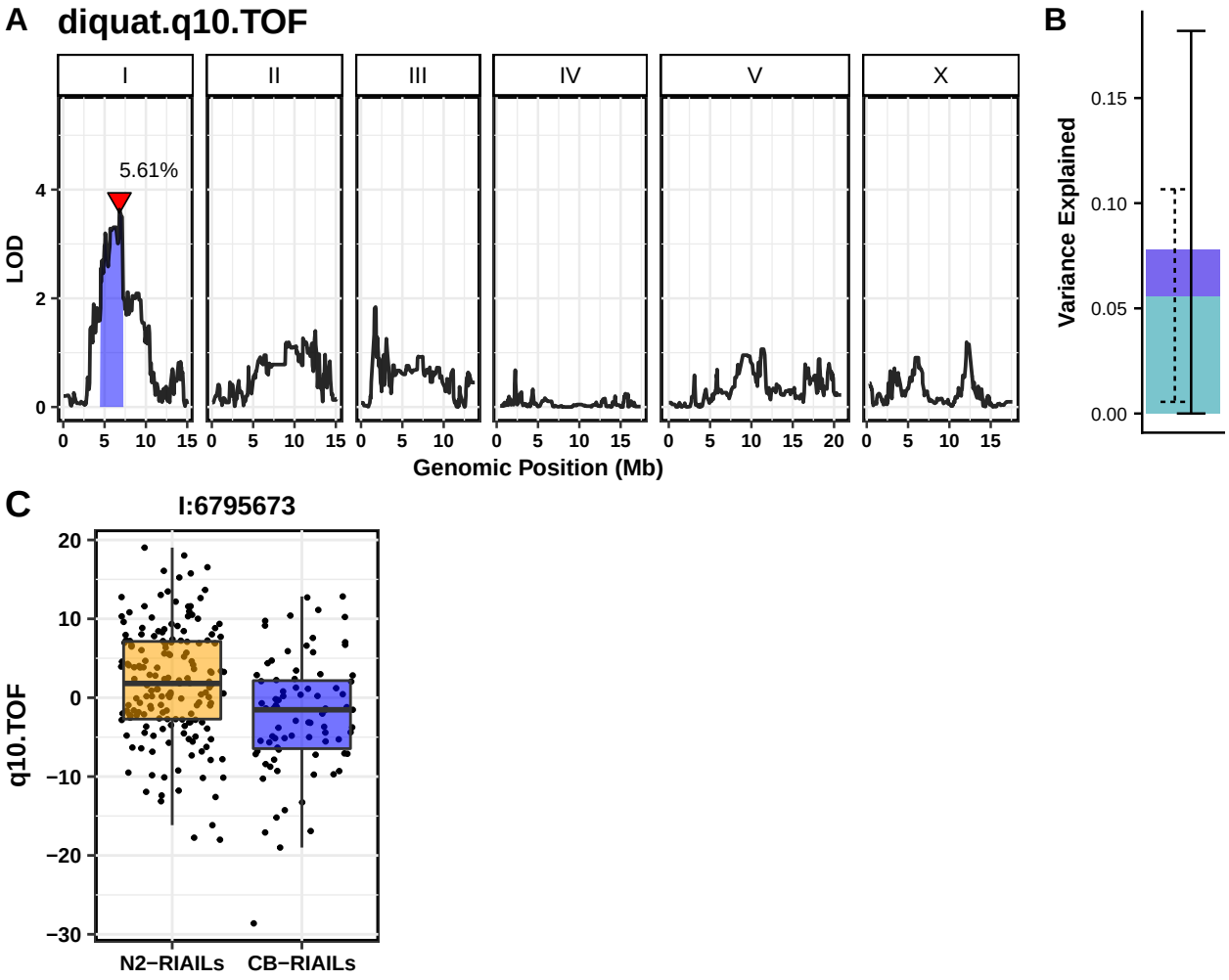

A
diquat.mean.norm.EXT
I
II
III
IV
V
X
6.07%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:11747270
mean.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
a
b
c
d
N2
CB4856
ECA241
ECA240
Chr IV
Genome

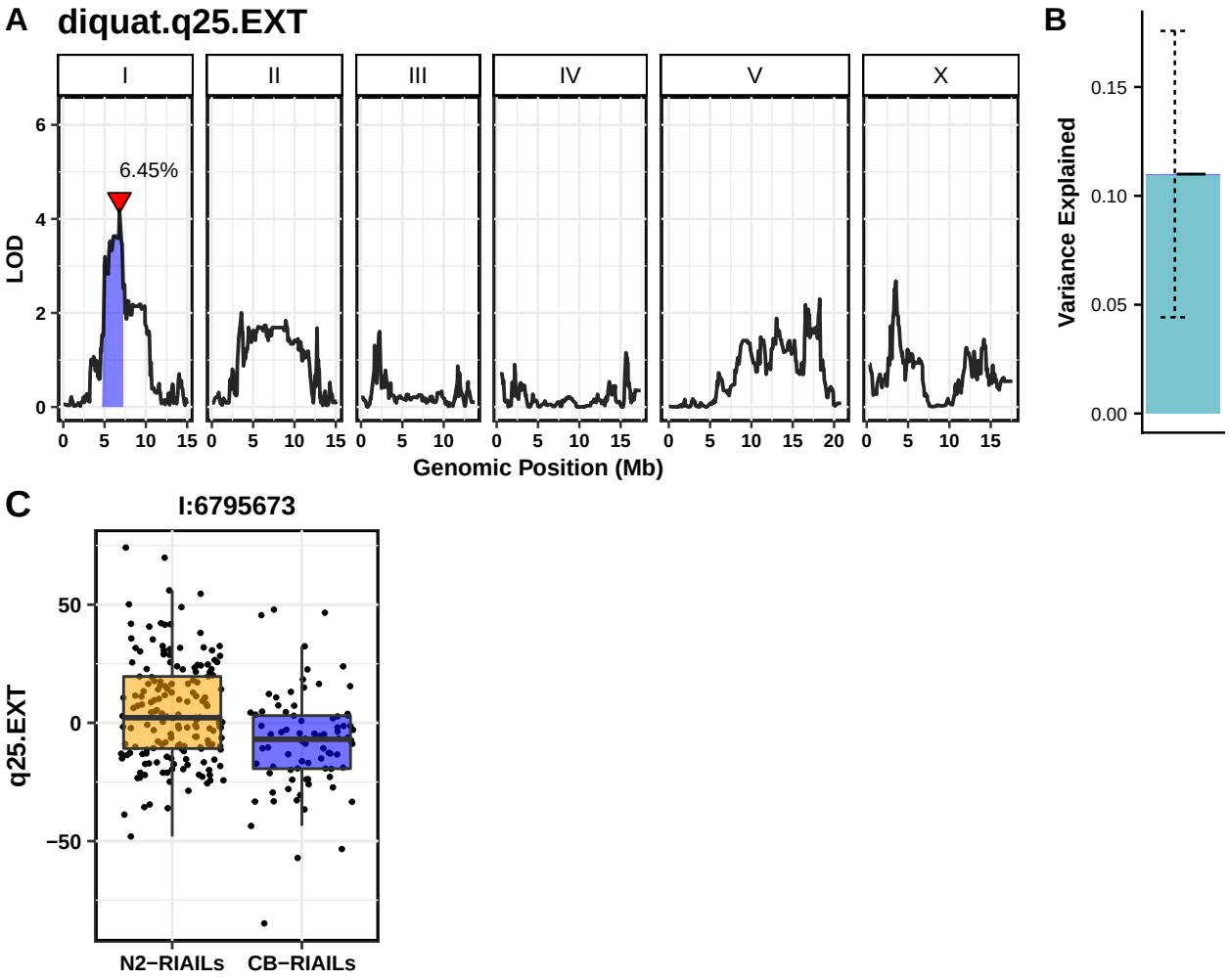

A
diquat.mean.TOF
I
II
III
IV
V
X
6.15%
LOD
Genomic Position (Mb)
B
Variance Explained
C
X:12533105
mean.TOF
N2−RIAILs
CB−RIAILs

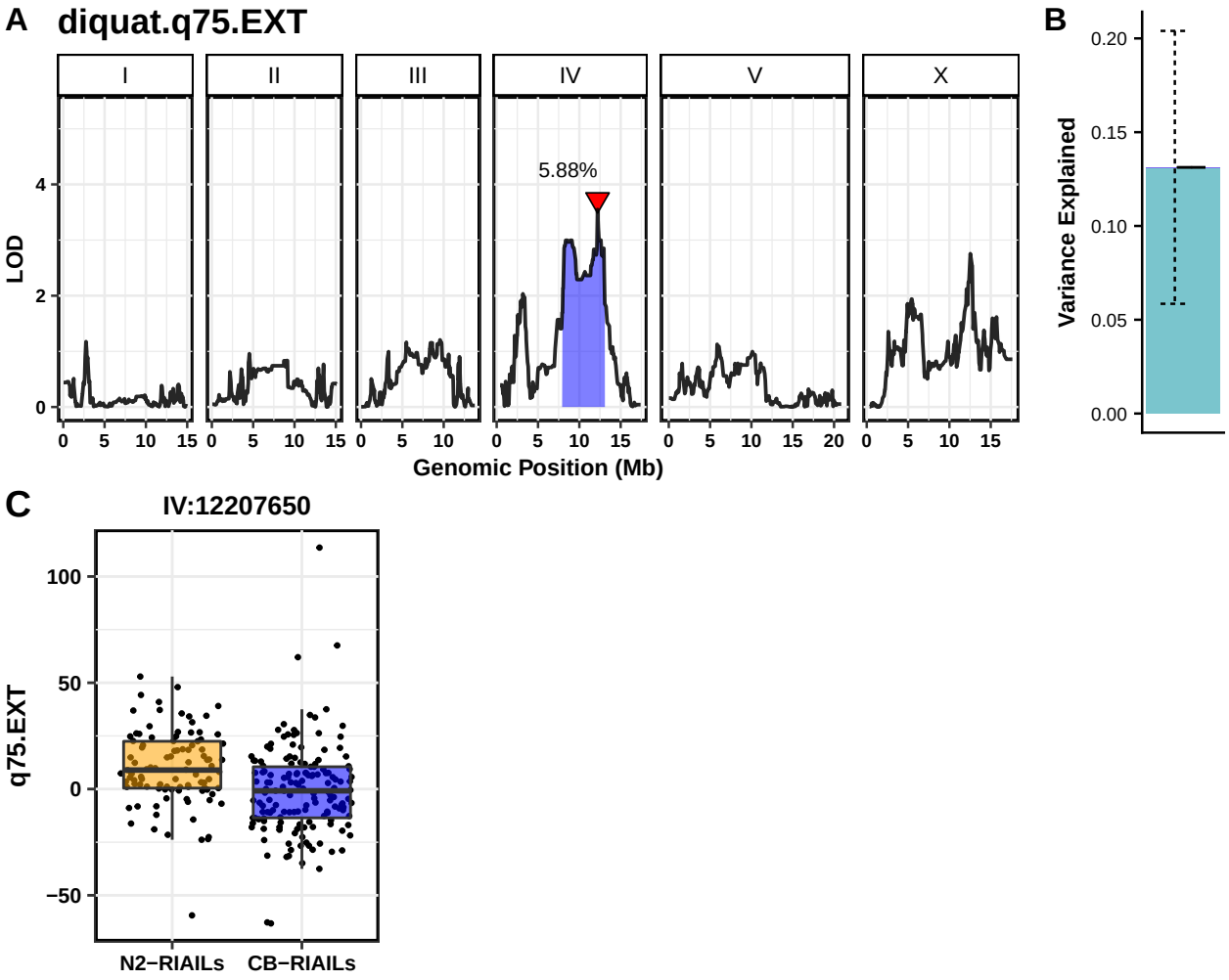

A
diquat.median.norm.EXT
I
II
III
IV
V
X
7.12%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:11747270
median.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
a
b
c
d
N2
CB4856
ECA241
ECA240
Chr IV
Genome

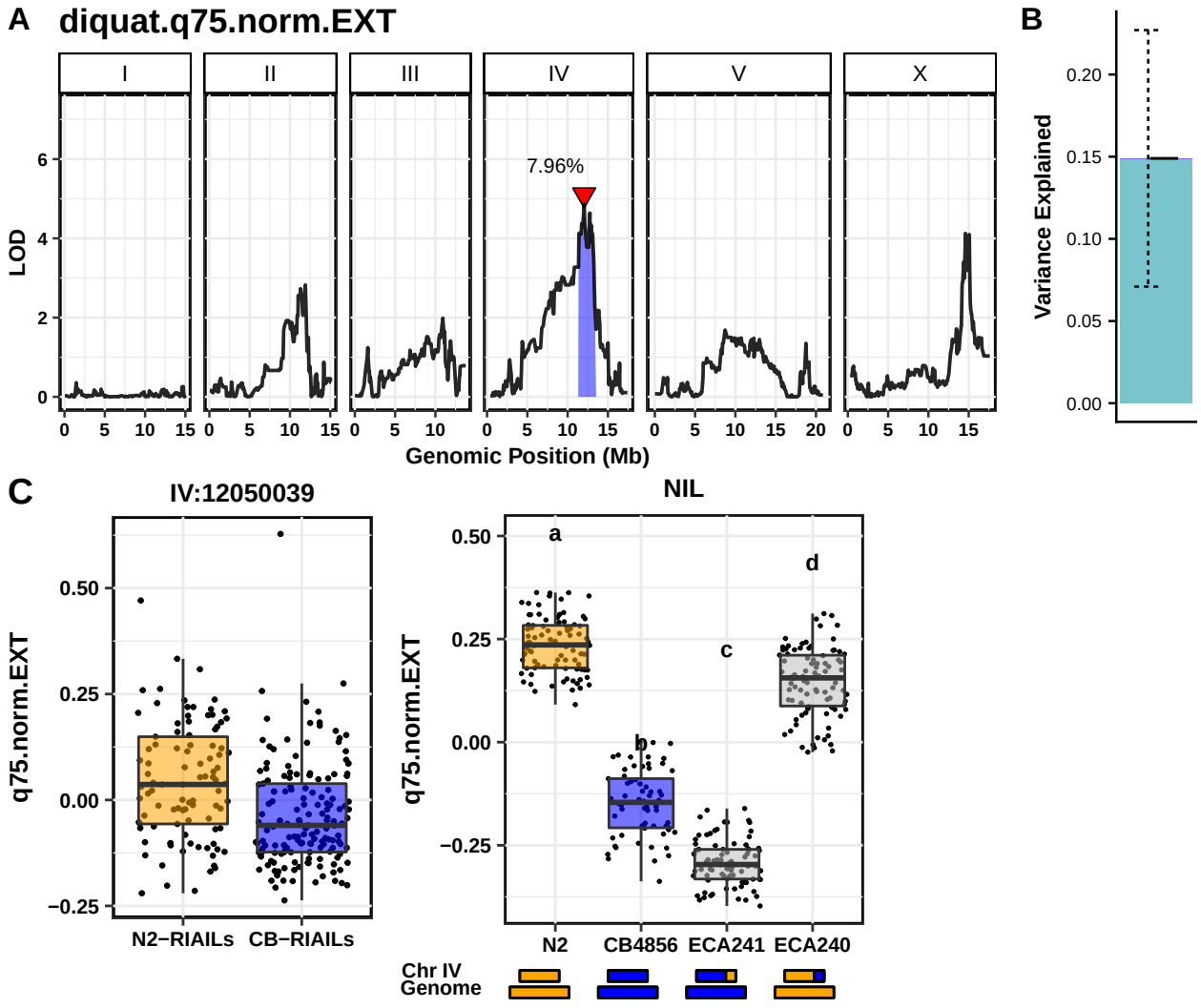

A
diquat.median.TOF
I
II
III
IV
V
X
5.97%
LOD
Genomic Position (Mb)
B
Variance Explained
C
II:10201103
median.TOF
N2−RIAILs
CB−RIAILs

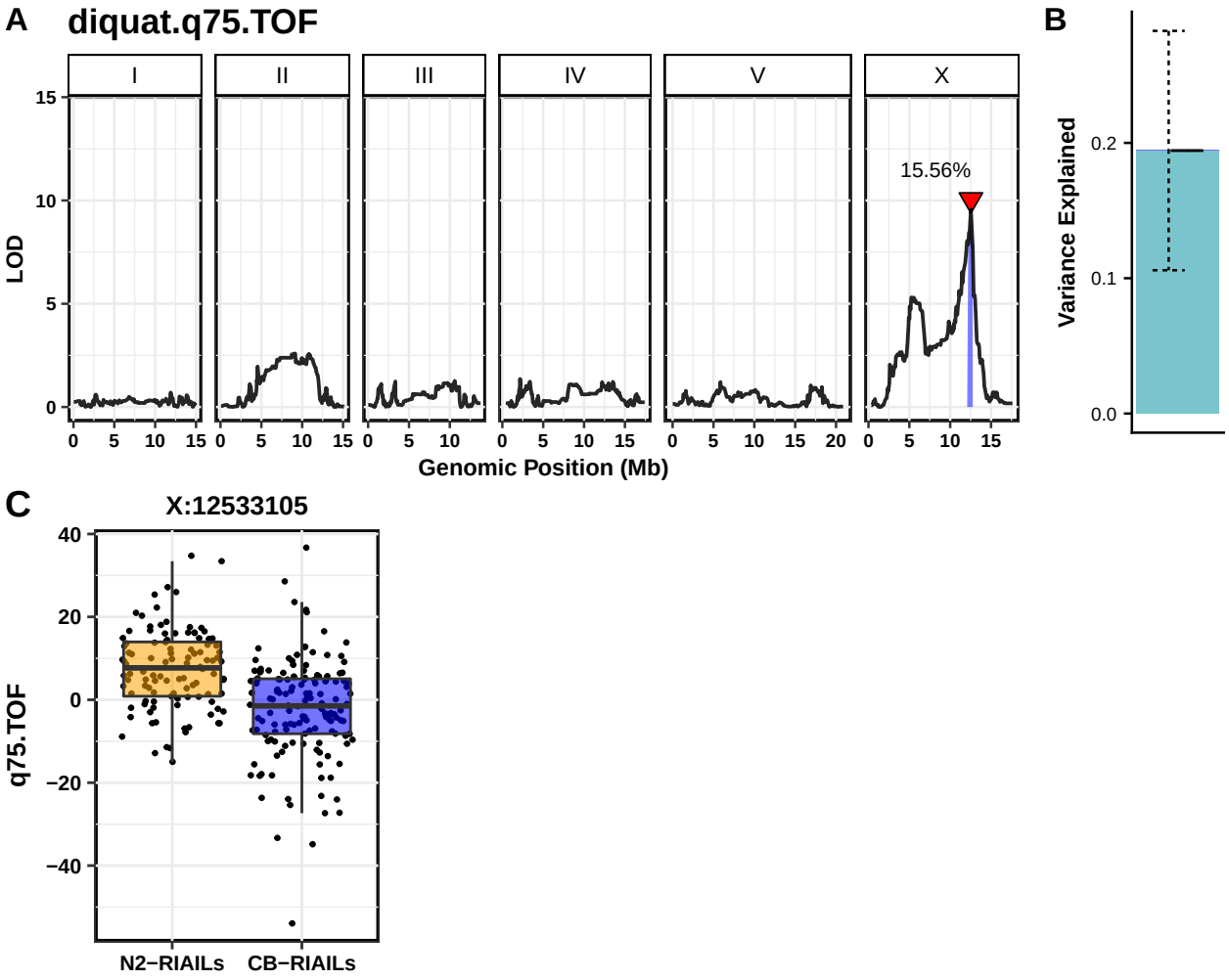

A
diquat.q10.EXT
I
II
III
IV
V
X
5.78%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:6795673
q10.EXT
N2−RIAILs
CB−RIAILs

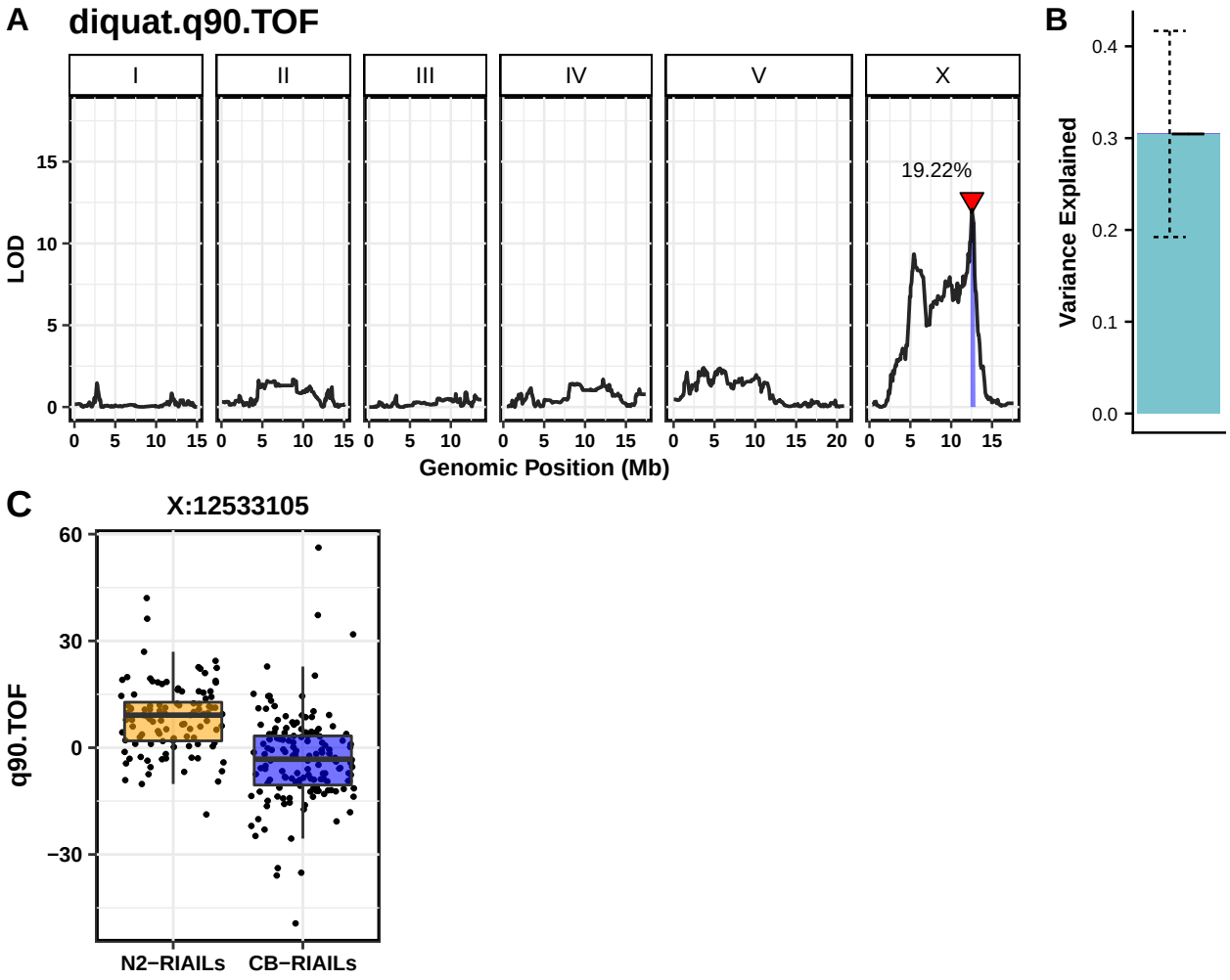

A
diquat.q10.TOF
I
II
III
IV
V
X
5.61%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:6795673
q10.TOF
N2−RIAILs
CB−RIAILs

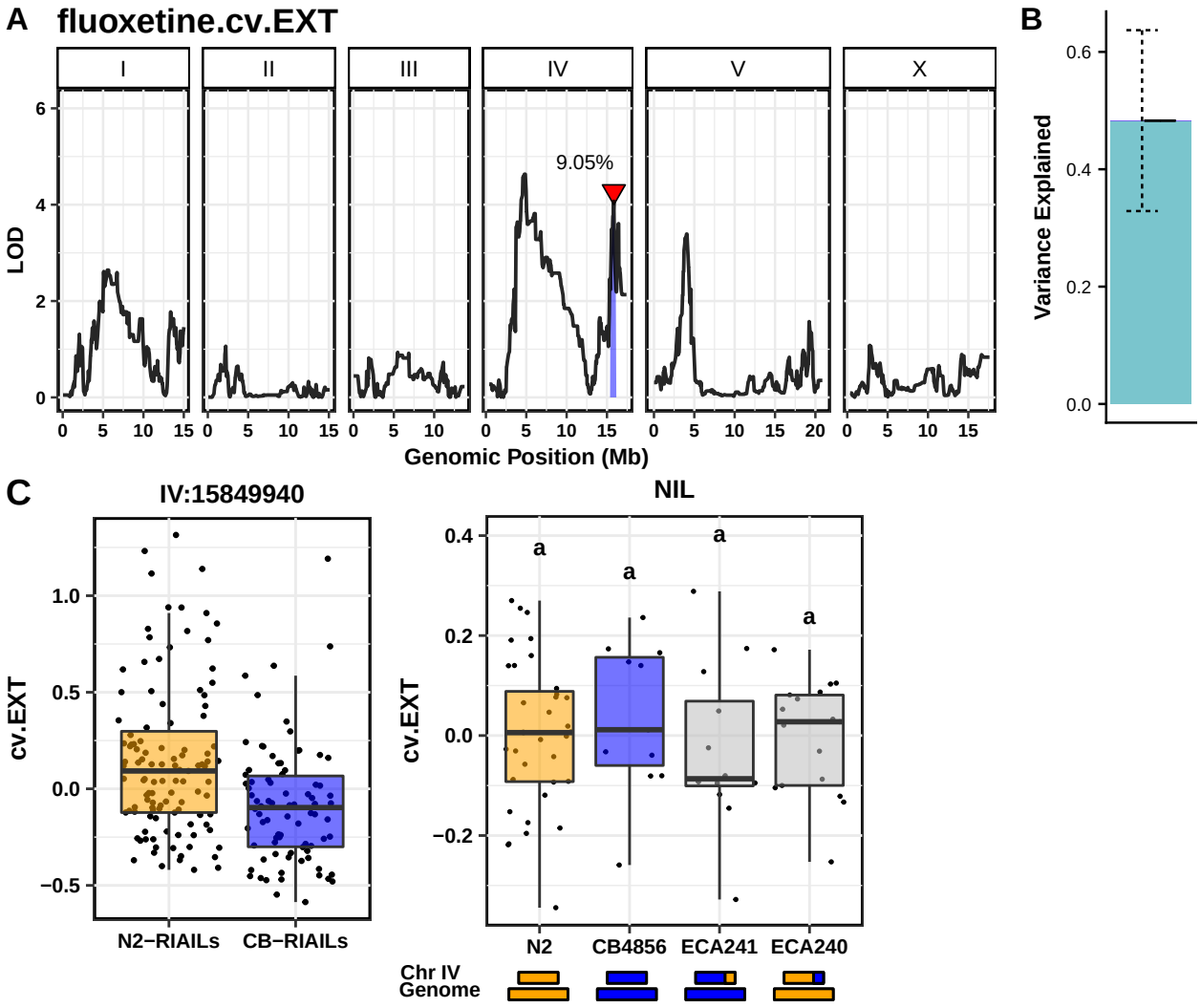

A
diquat.q25.EXT
I
II
III
IV
V
X
6.45%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:6795673
q25.EXT
N2−RIAILs
CB−RIAILs

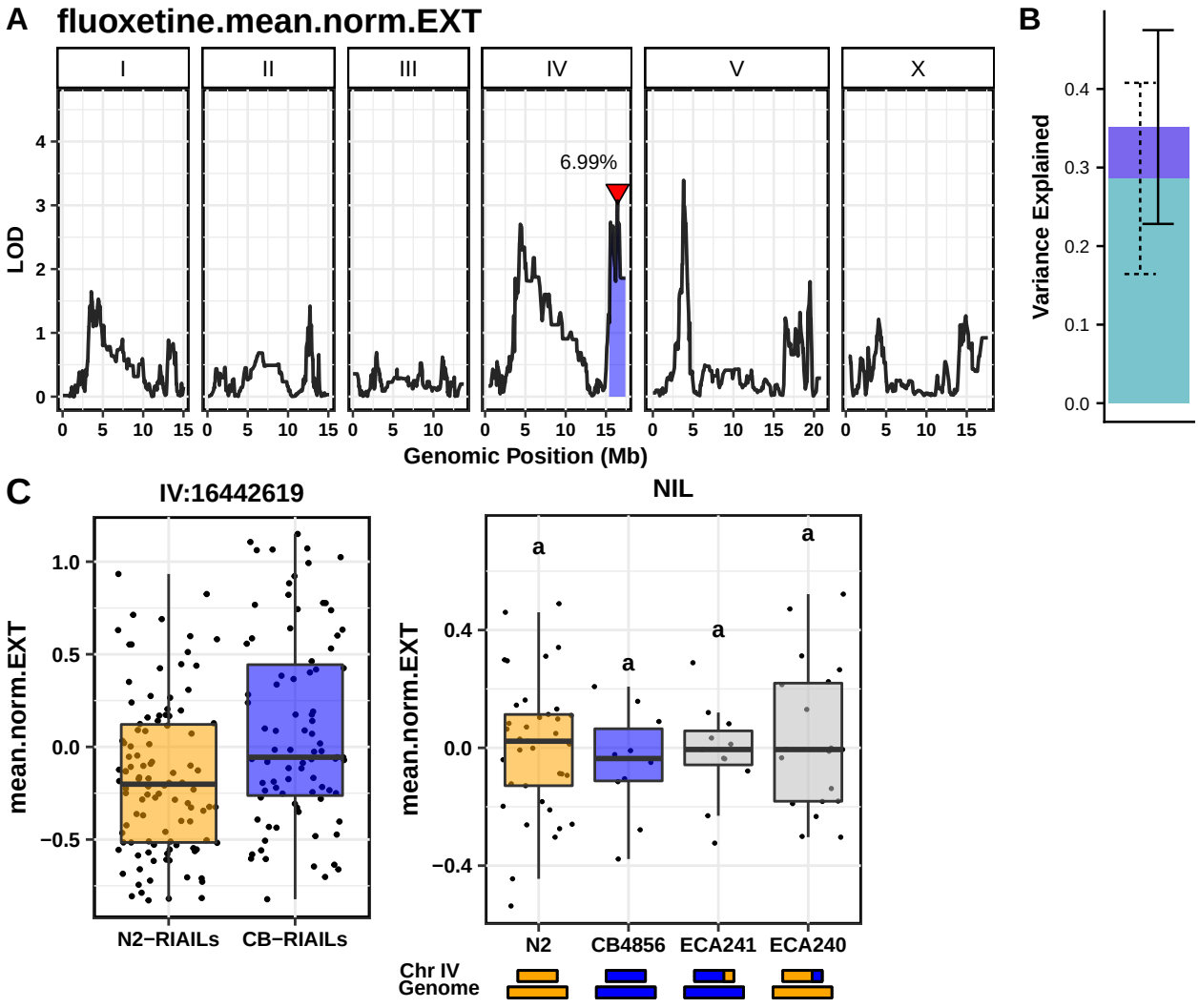

A
diquat.q75.EXT
I
II
III
IV
V
X
5.88%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:12207650
q75.EXT
N2−RIAILs
CB−RIAILs

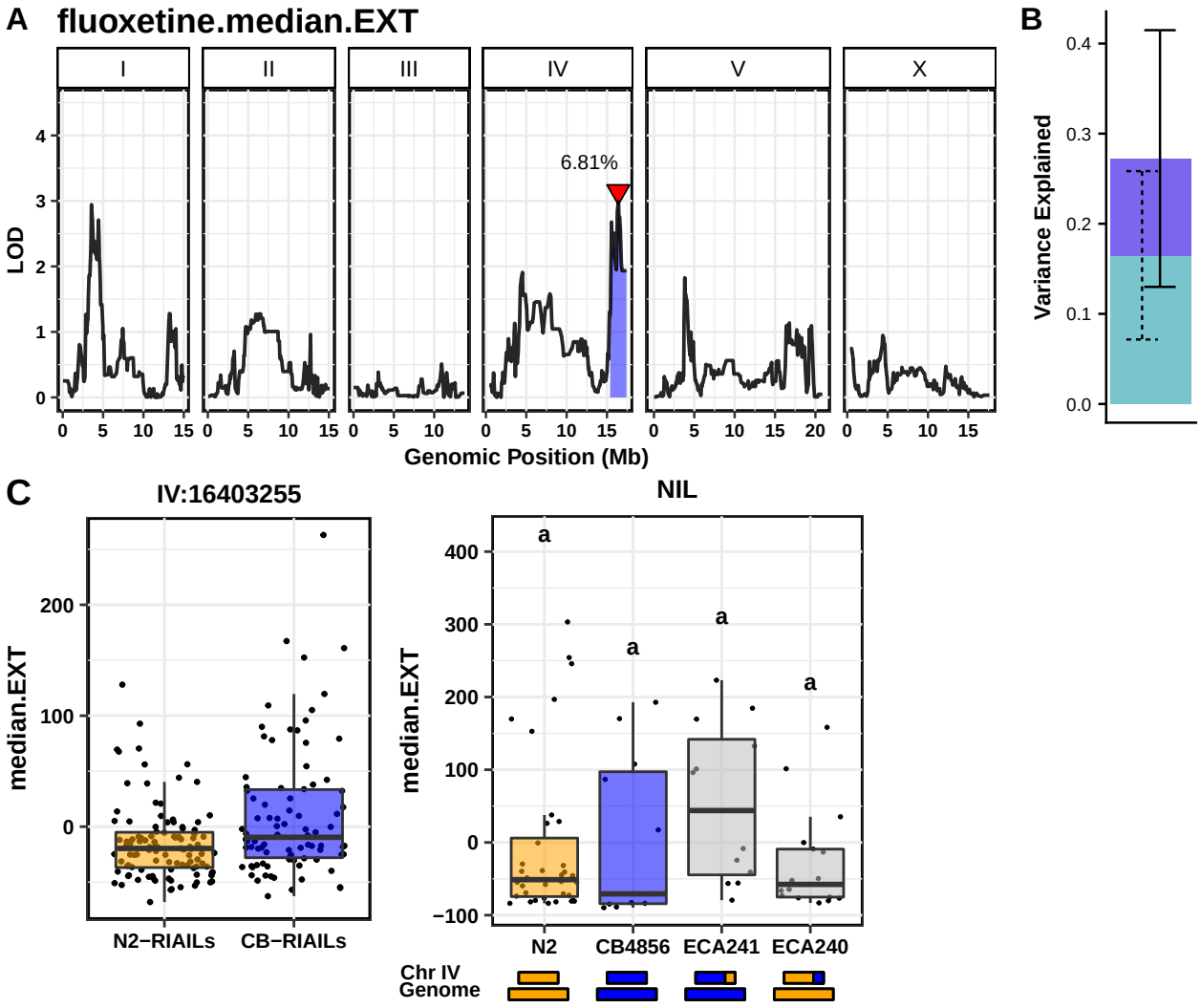

A
diquat.q75.norm.EXT
I
II
III
IV
V
X
7.96%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:12050039
q75.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
a
b
c
d
N2
CB4856
ECA241
ECA240
Chr IV
Genome

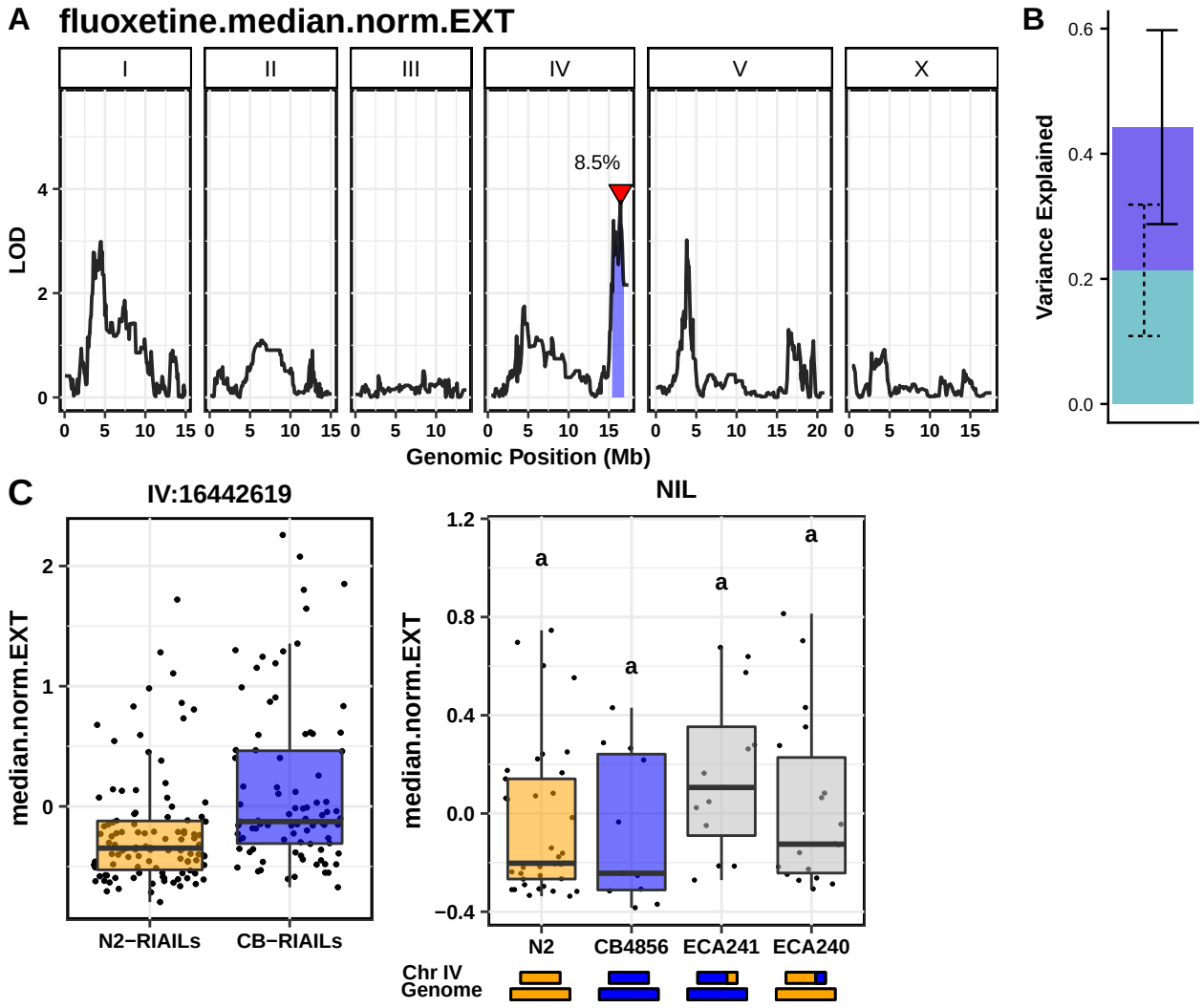

A
diquat.q75.TOF
I
II
III
IV
V
X
LOD
15
10
5
0
15.56%
0 5 10 15
0 5 10 15
0 5 10
0 5 10 15
0 5 10 15 20
0 5 10 15
Genomic Position (Mb)
B
Variance Explained
0.2
0.1
0.0
C
X:12533105
q75.TOF
40
20
0
−20
−40
N2−RIAILs
CB−RIAILs

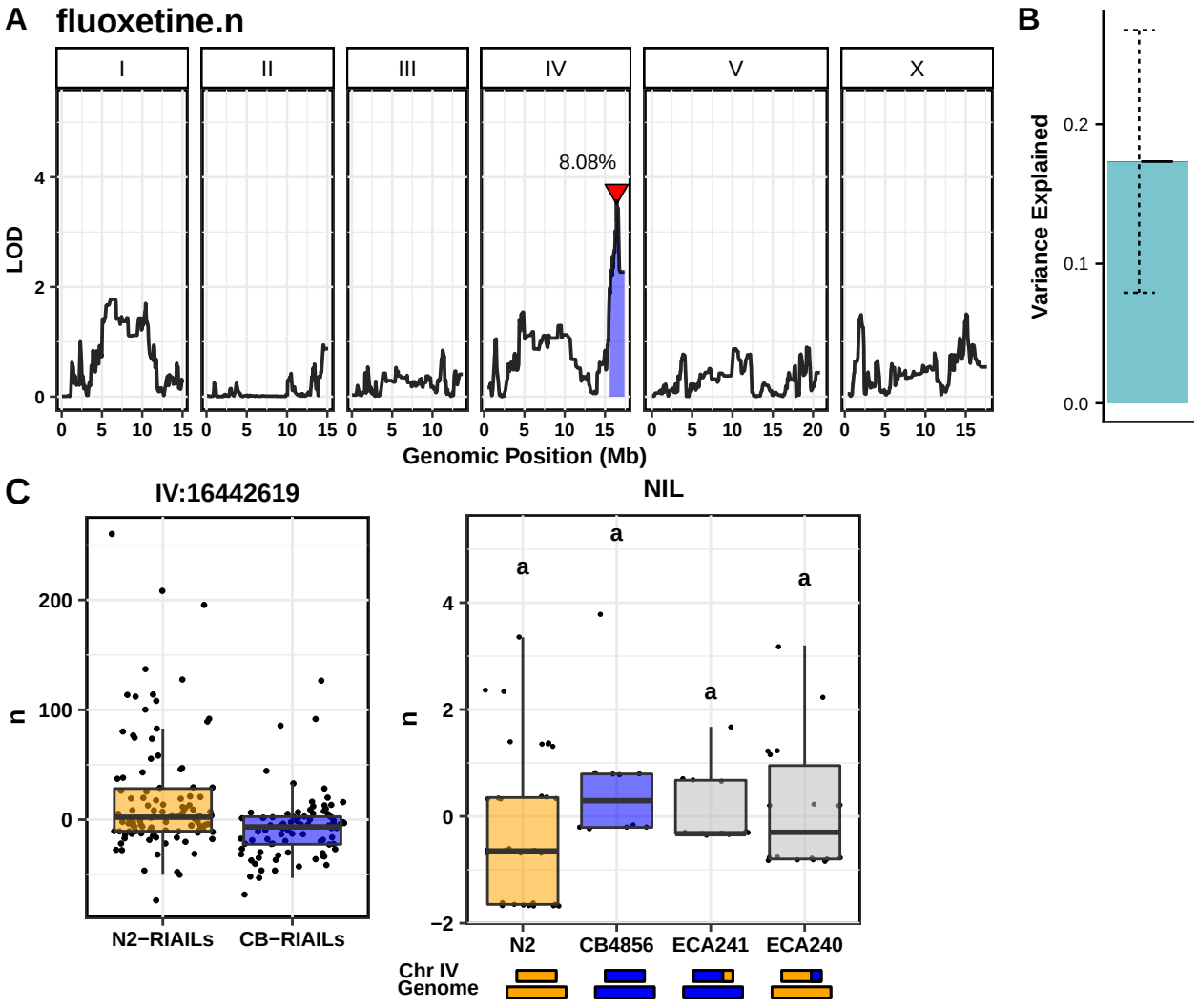

A
diquat.q90.TOF
I
II
III
IV
V
X
LOD
19.22%
Genomic Position (Mb)
B
Variance Explained
C
X:12533105
q90.TOF
N2−RIAILs
CB−RIAILs

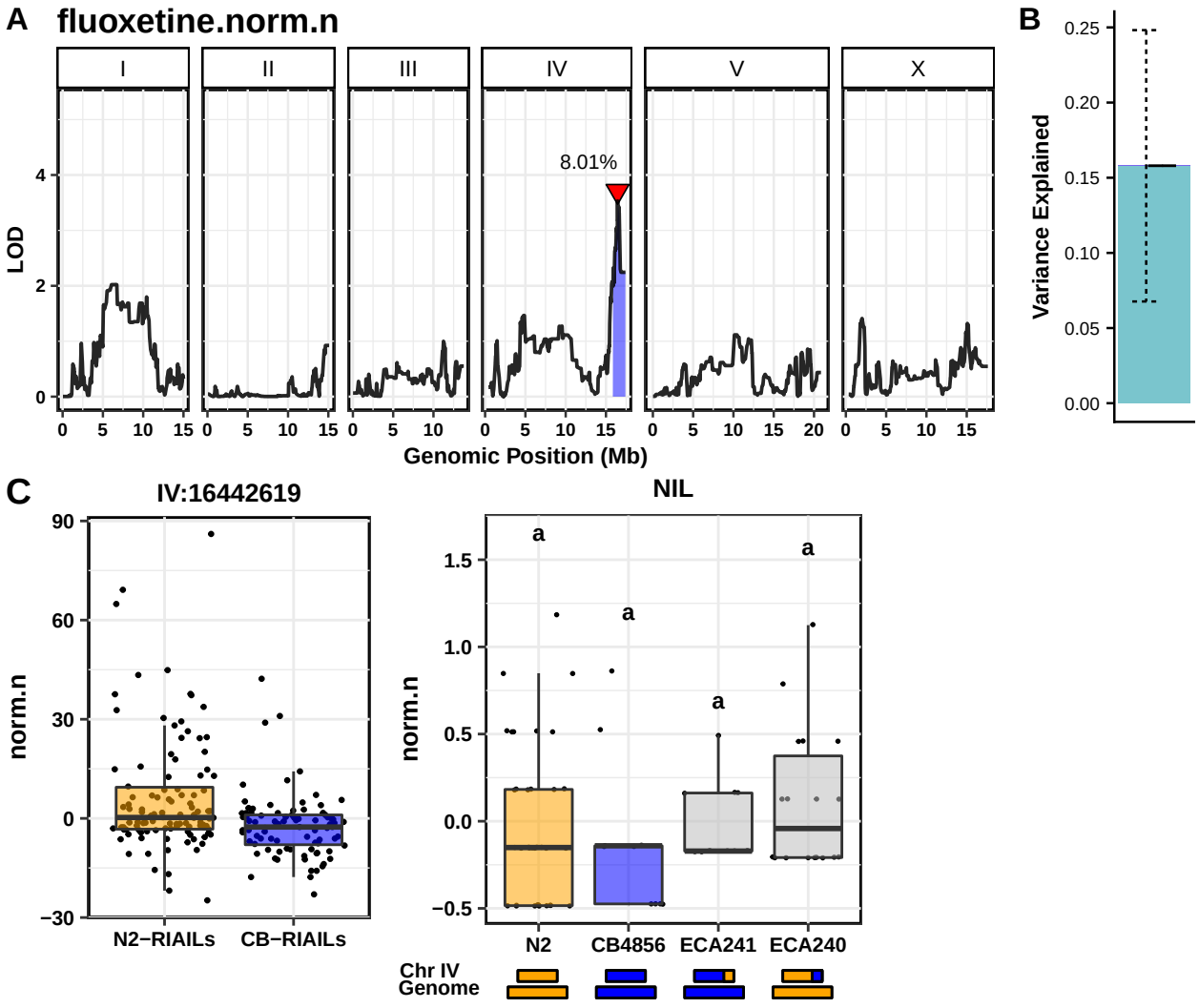

A
fluoxetine.cv.EXT
I
II
III
IV
V
X
9.05%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:15849940
cv.EXT
N2−RIAILs
CB−RIAILs
NIL
a
N2
CB4856
ECA241
ECA240
Chr IV
Genome

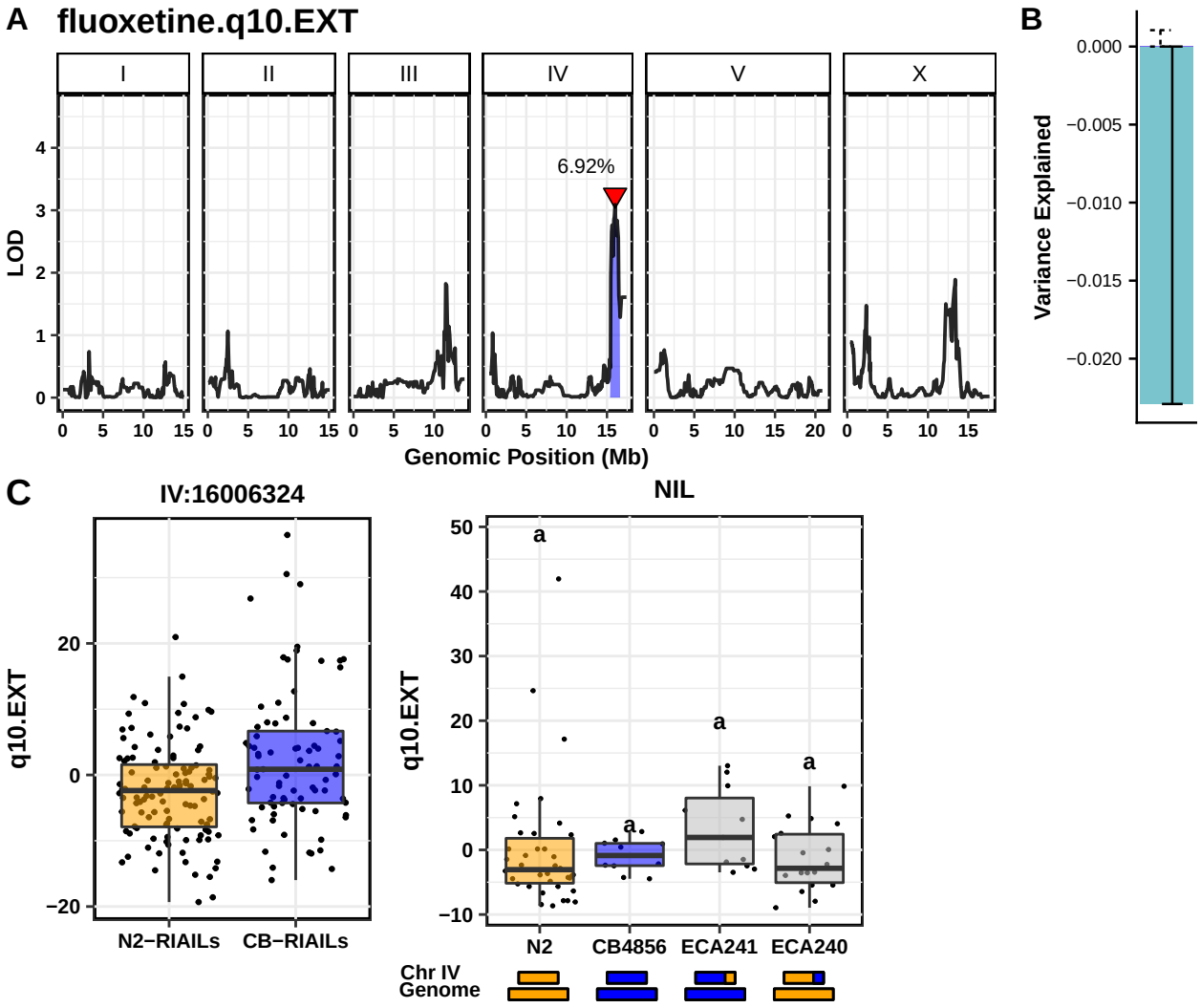

A
fluoxetine.mean.norm.EXT
I
II
III
IV
V
X
6.99%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:16442619
mean.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
a
N2
CB4856
ECA241
ECA240
Chr IV
Genome

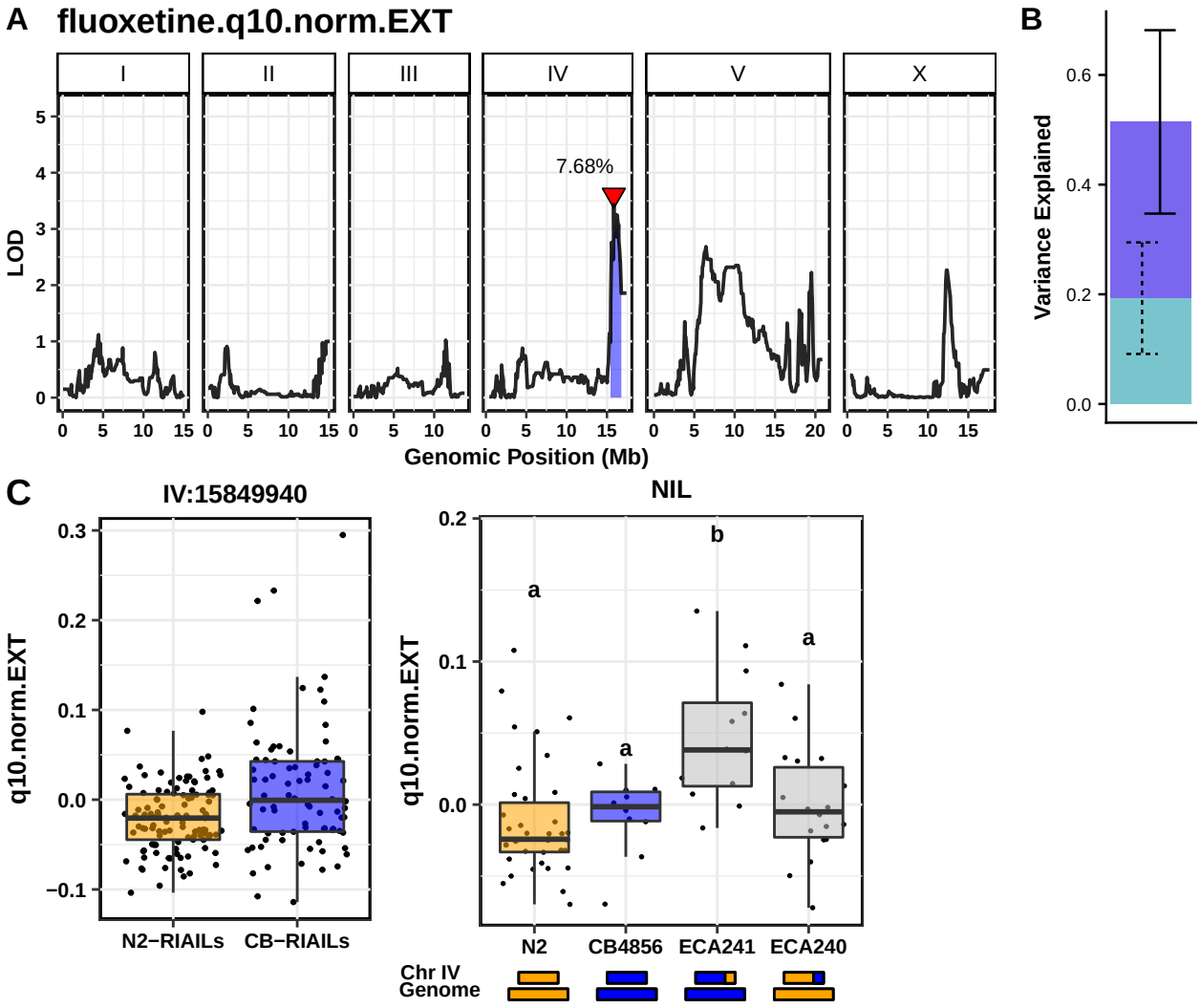

A
fluoxetine.median.EXT
I
II
III
IV
V
X
6.81%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:16403255
median.EXT
N2−RIAILs
CB−RIAILs
NIL
a
N2
CB4856
ECA241
ECA240
Chr IV
Genome

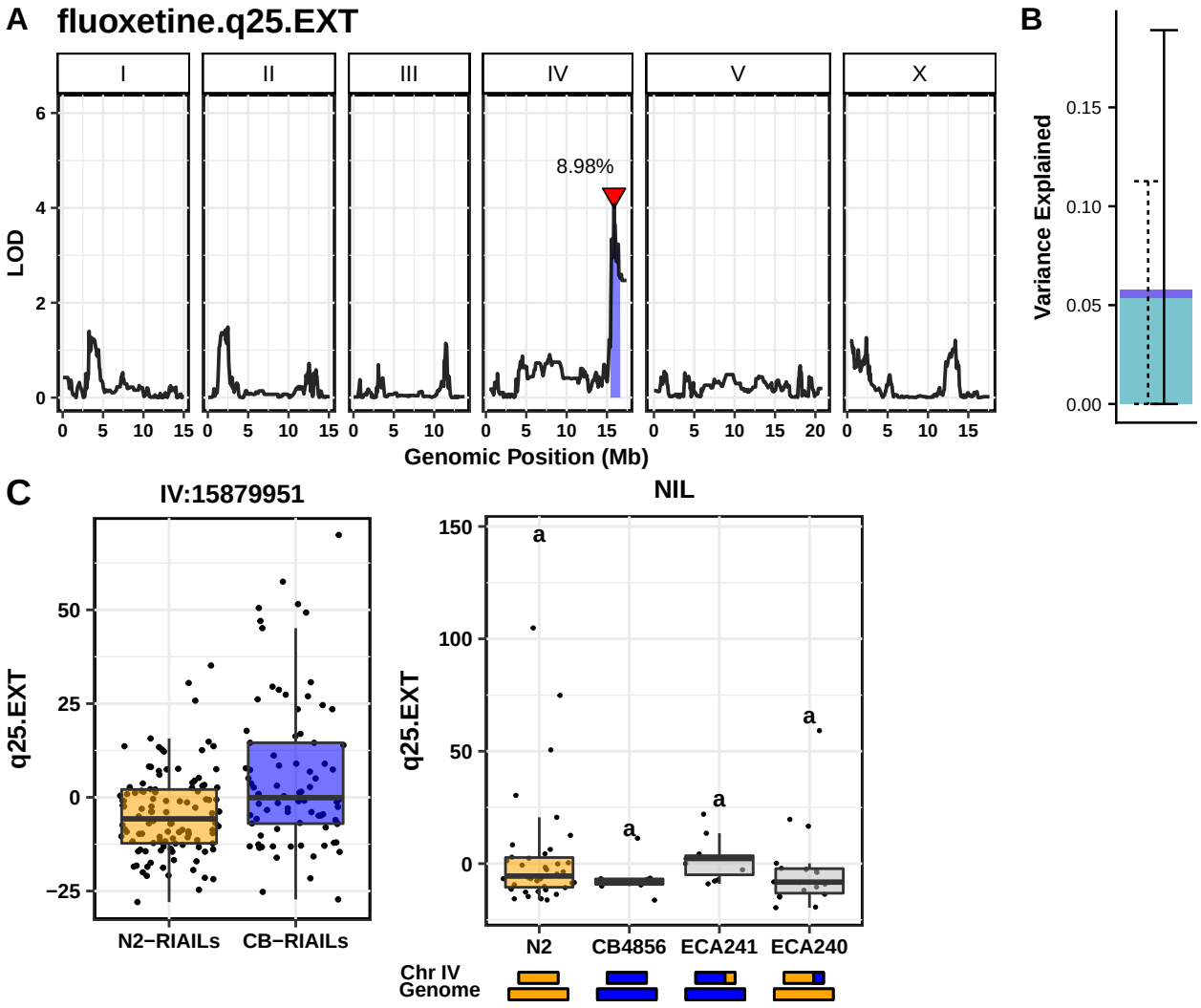

A
fluoxetine.median.norm.EXT
I
II
III
IV
V
X
8.5%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:16442619
median.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
a
N2
CB4856
ECA241
ECA240
Chr IV
Genome

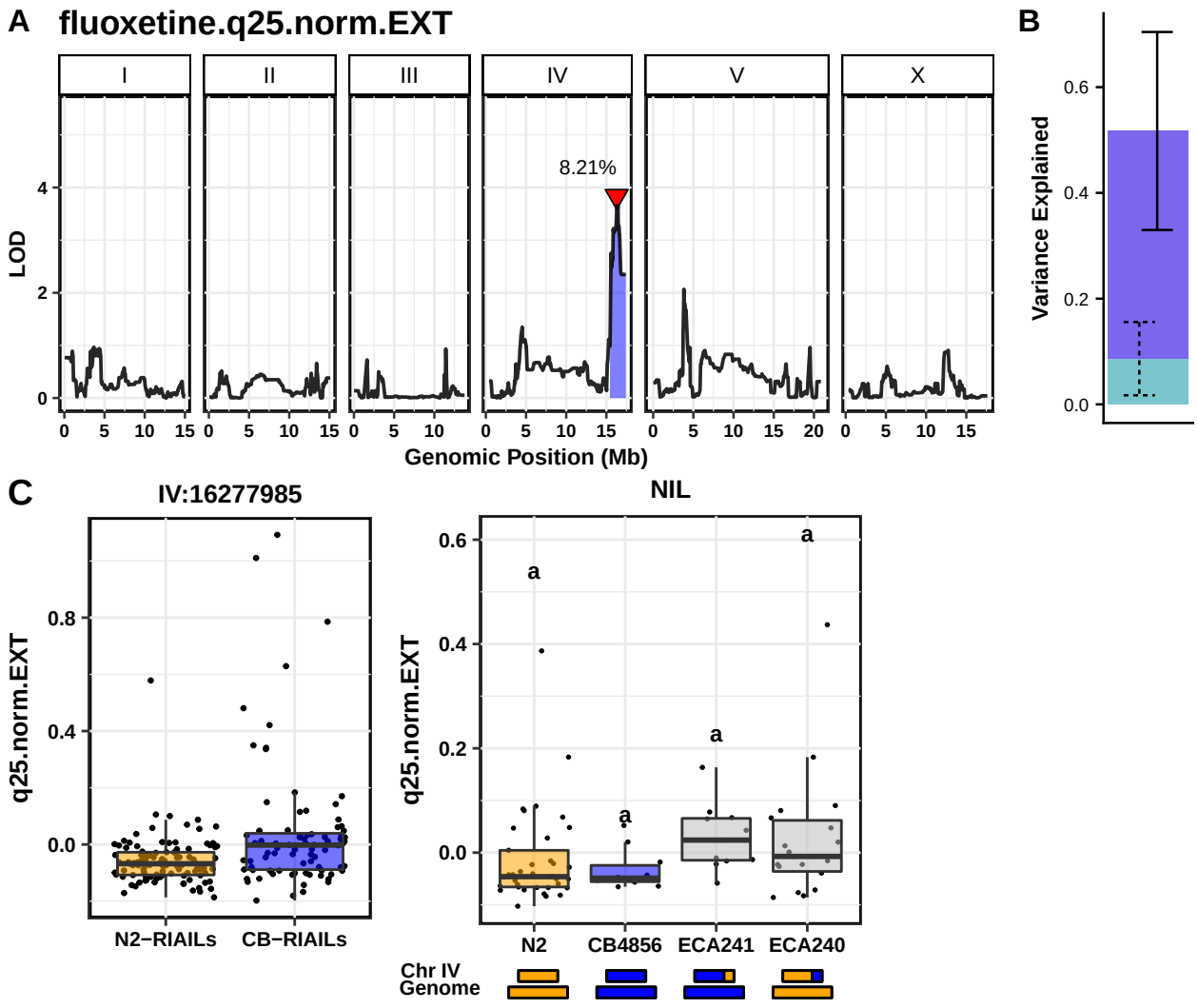

A
fluoxetine.n
I
II
III
IV
V
X
8.08%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:16442619
n
N2−RIAILs
CB−RIAILs
NIL
a
N2
CB4856
ECA241
ECA240
Chr IV
Genome

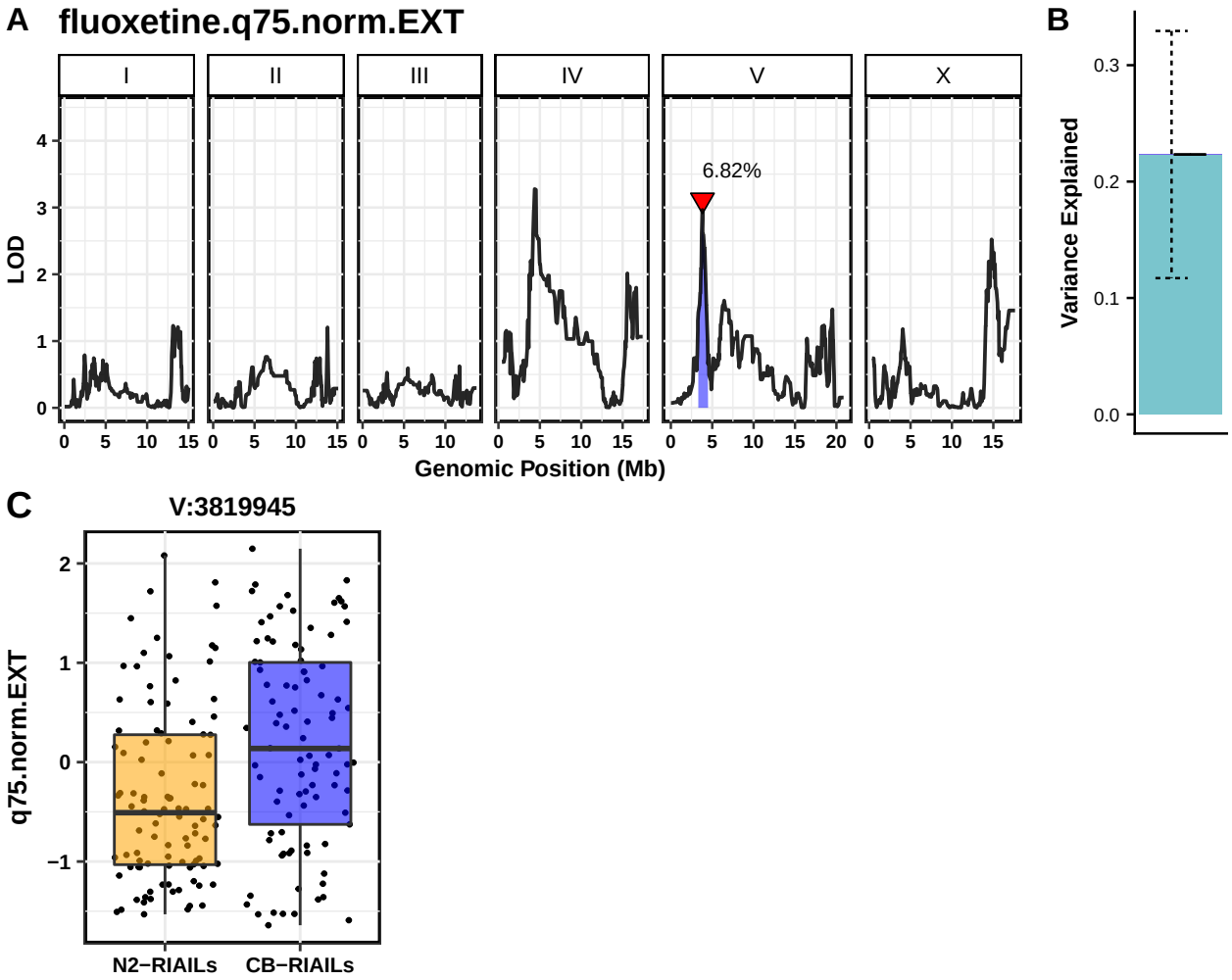

A
fluoxetine.norm.n
I
II
III
IV
V
X
8.01%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:16442619
norm.n
N2−RIAILs
CB−RIAILs
NIL
a
N2
CB4856
ECA241
ECA240
Chr IV
Genome

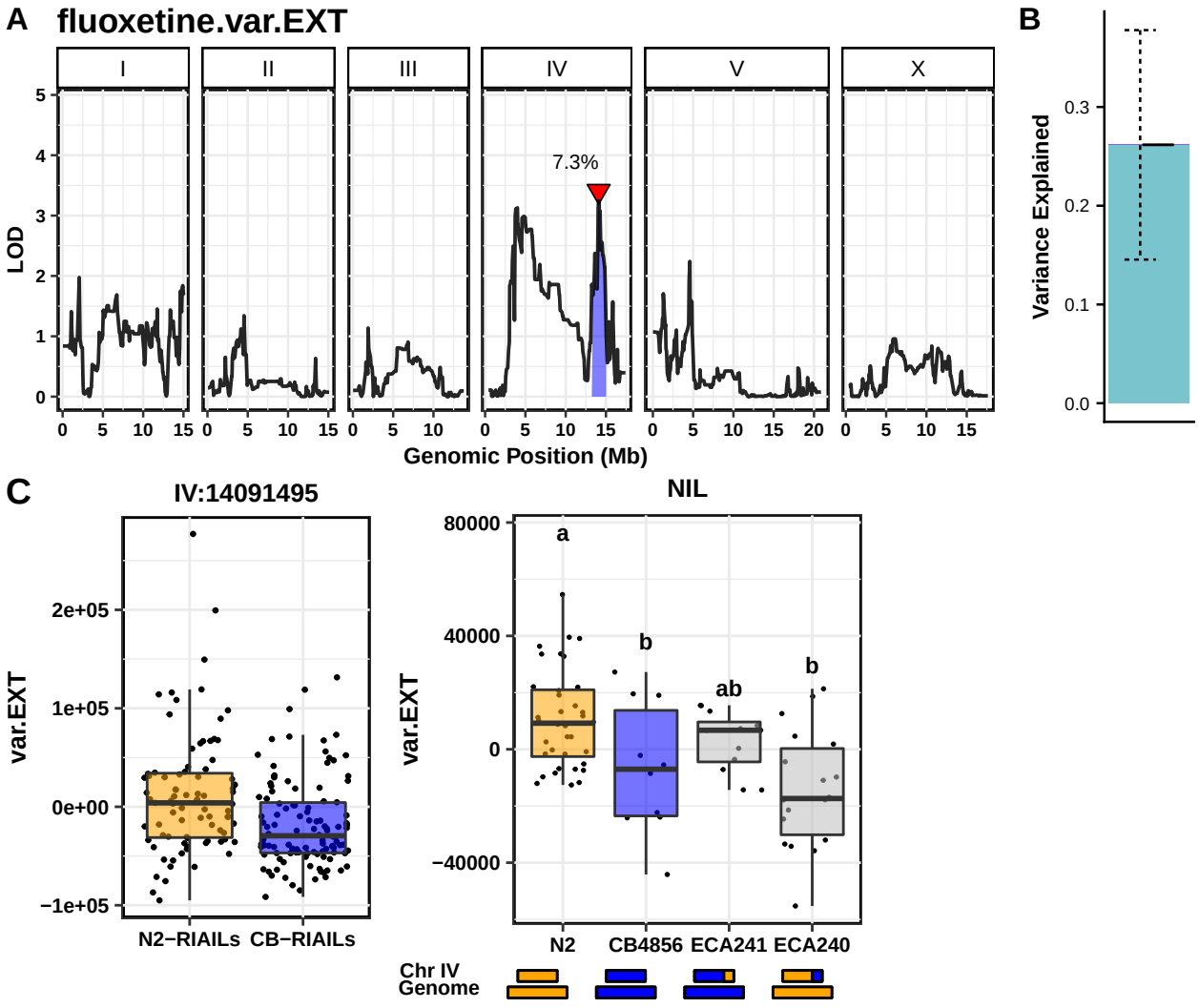

A
fluoxetine.q10.EXT
I
II
III
IV
V
X
6.92%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:16006324
q10.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA241
ECA240
Chr IV
Genome

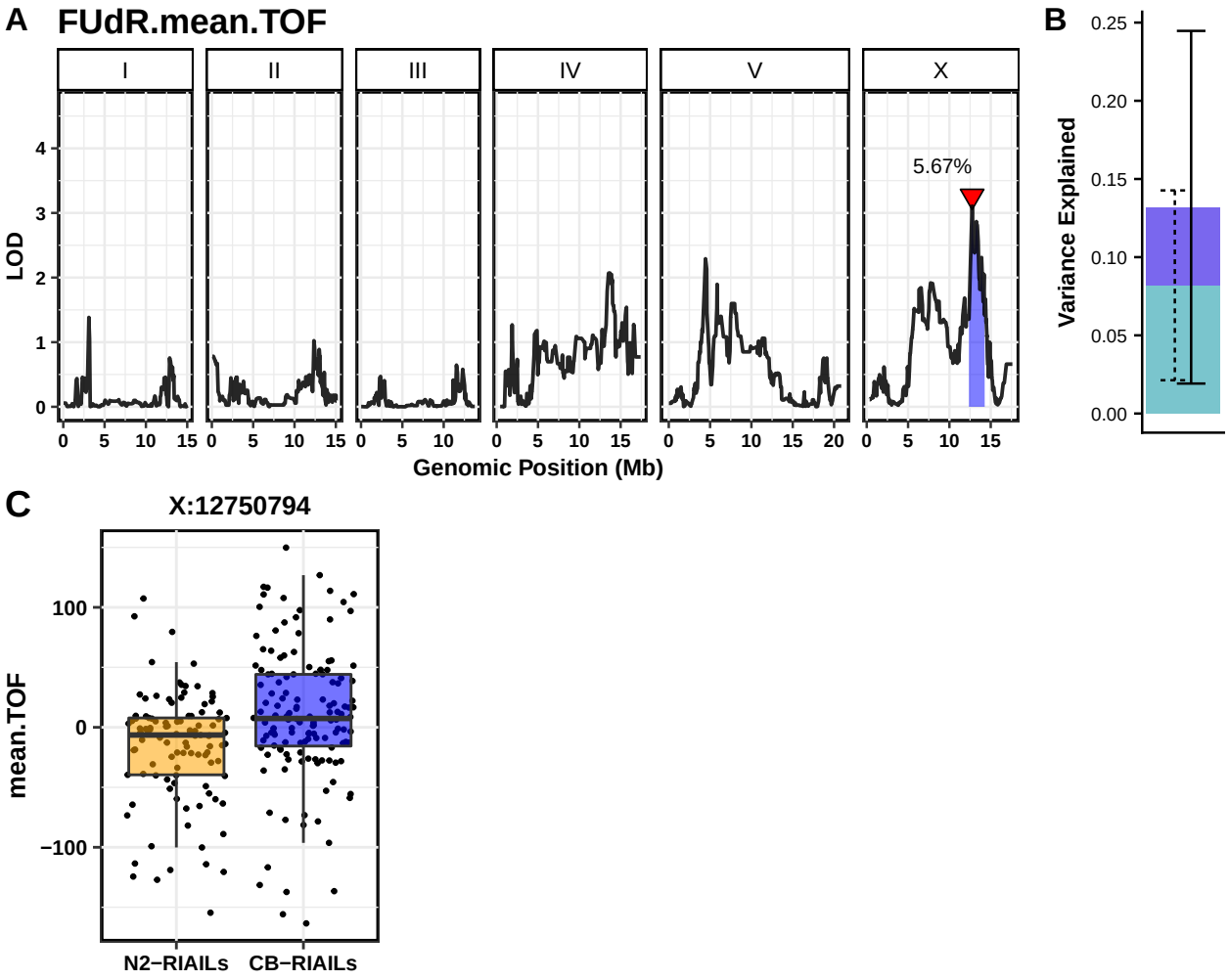

A
fluoxetine.q10.norm.EXT
I
II
III
IV
V
X
7.68%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:15849940
q10.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
a
a
b
a
N2
CB4856
ECA241
ECA240
Chr IV
Genome

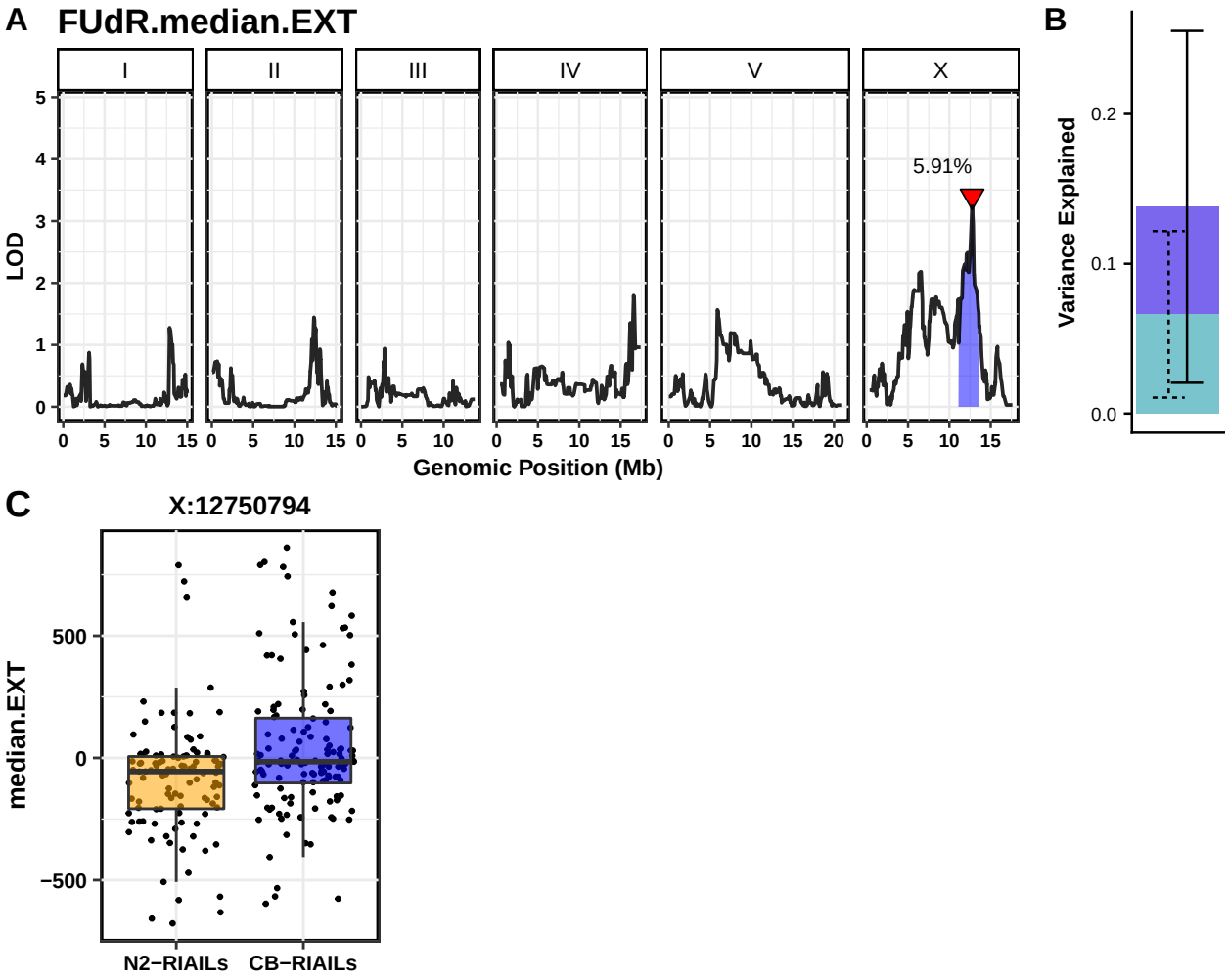

A
fluoxetine.q25.EXT
I
II
III
IV
V
X
8.98%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:15879951
q25.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA241
ECA240
Chr IV
Genome

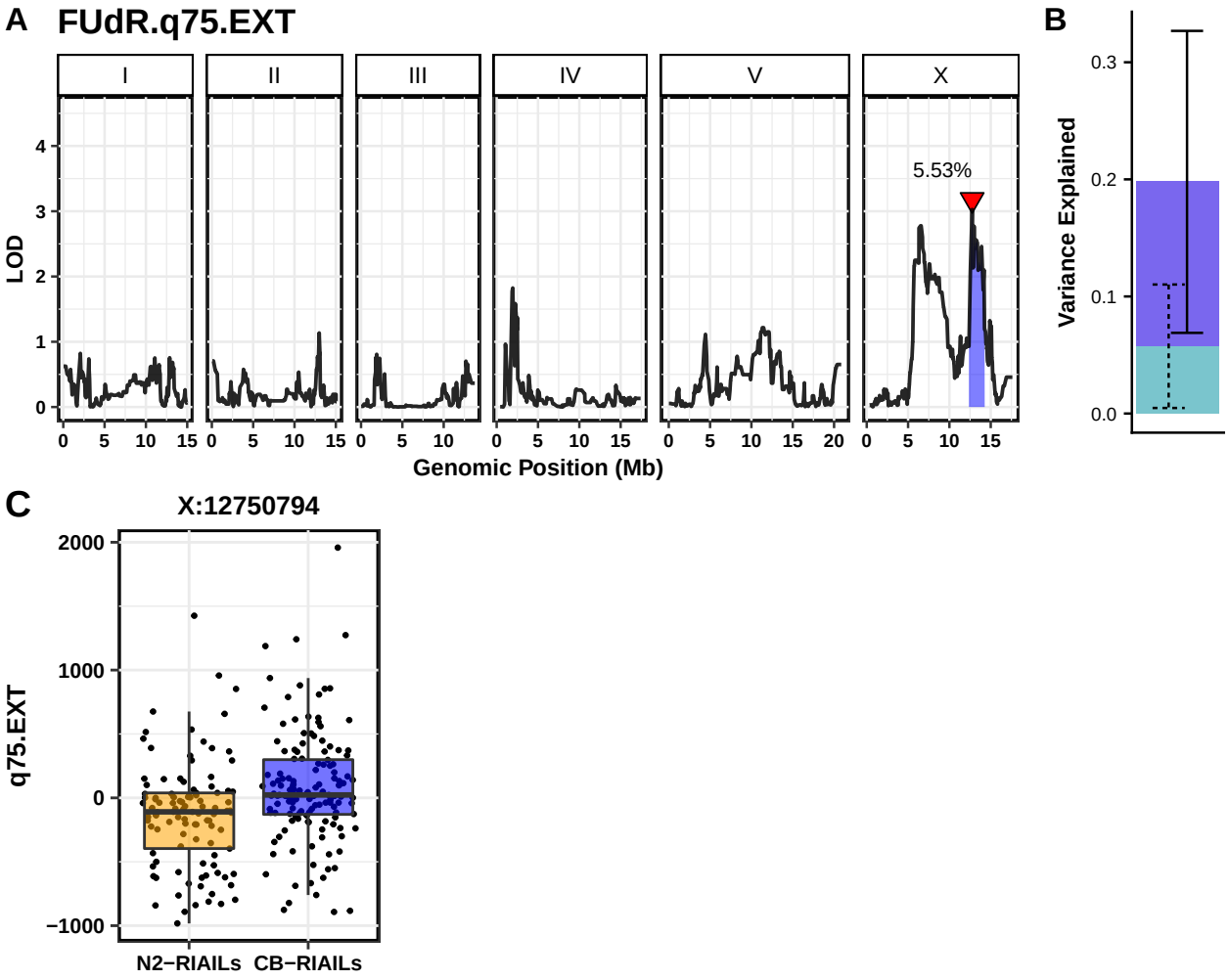

A
fluoxetine.q25.norm.EXT
I
II
III
IV
V
X
8.21%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:16277985
q25.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA241
ECA240
Chr IV
Genome

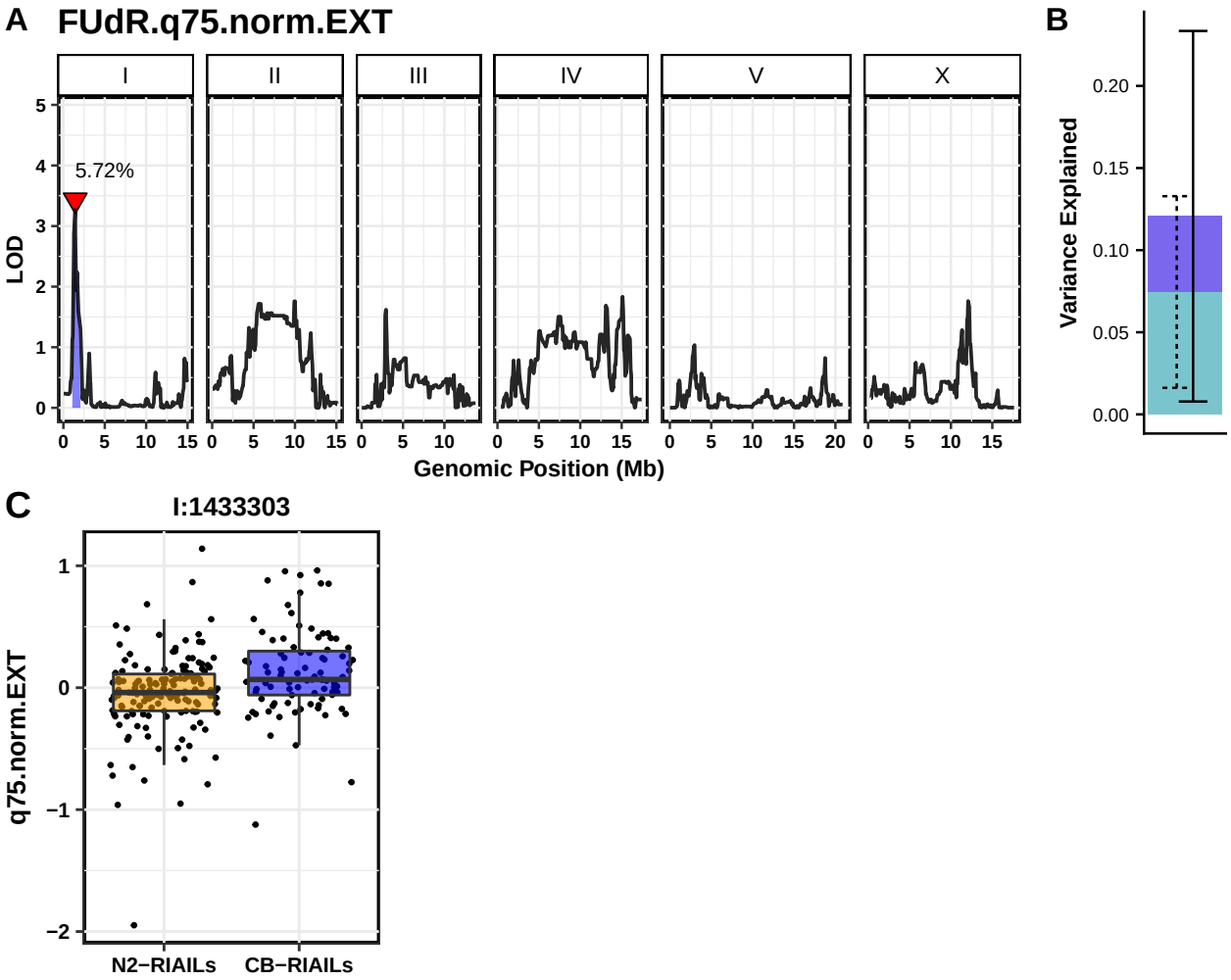

A
fluoxetine.q75.norm.EXT
I
II
III
IV
V
X
LOD
6.82%
Genomic Position (Mb)
B
Variance Explained
C
V:3819945
q75.norm.EXT
N2−RIAILs
CB−RIAILs

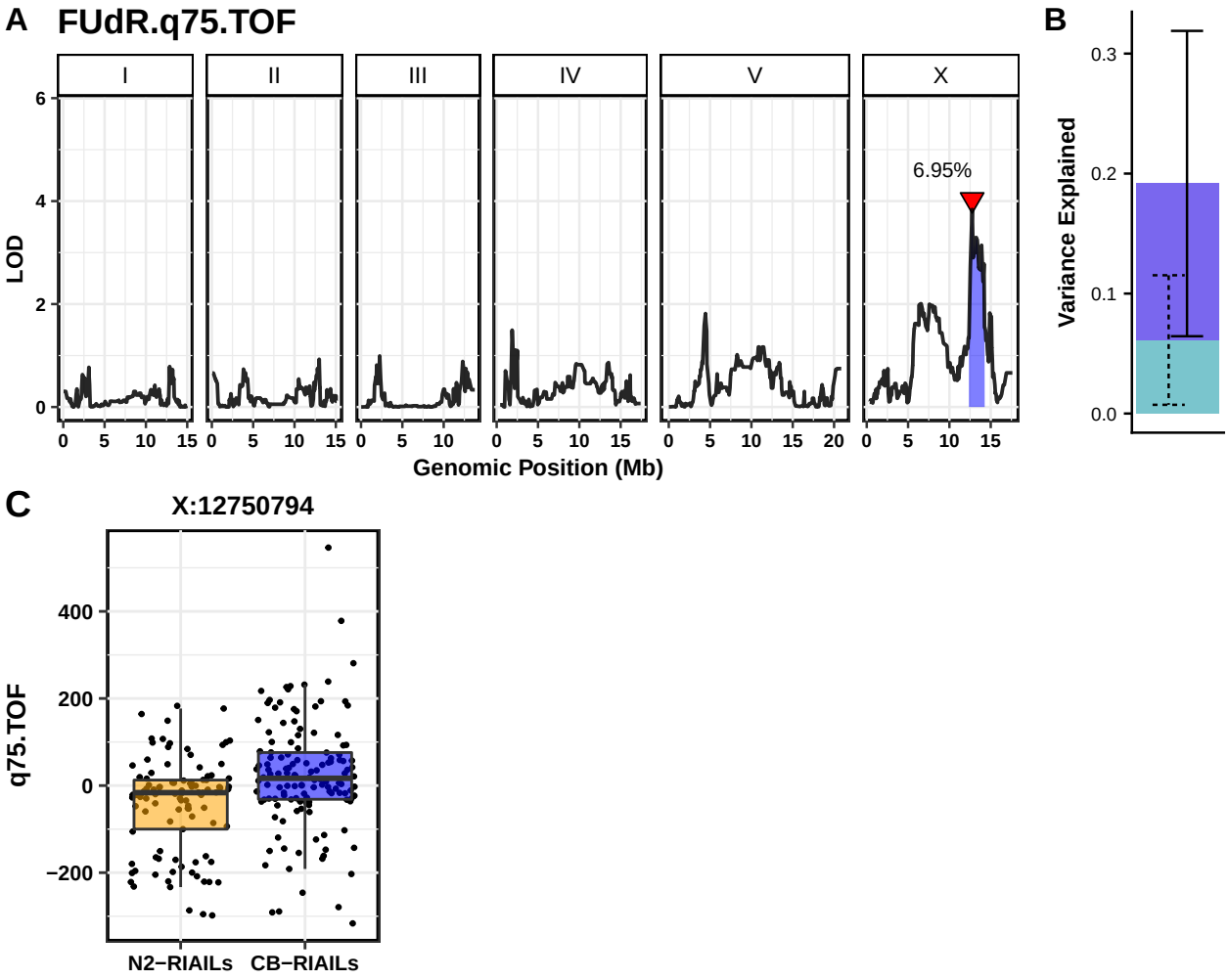

A
fluoxetine.var.EXT
I
II
III
IV
V
X
LOD
7.3%
Genomic Position (Mb)
B
Variance Explained
C
IV:14091495
var.EXT
N2−RIAILs
CB−RIAILs
NIL
a
b
ab
b
N2
CB4856
ECA241
ECA240
Chr IV
Genome

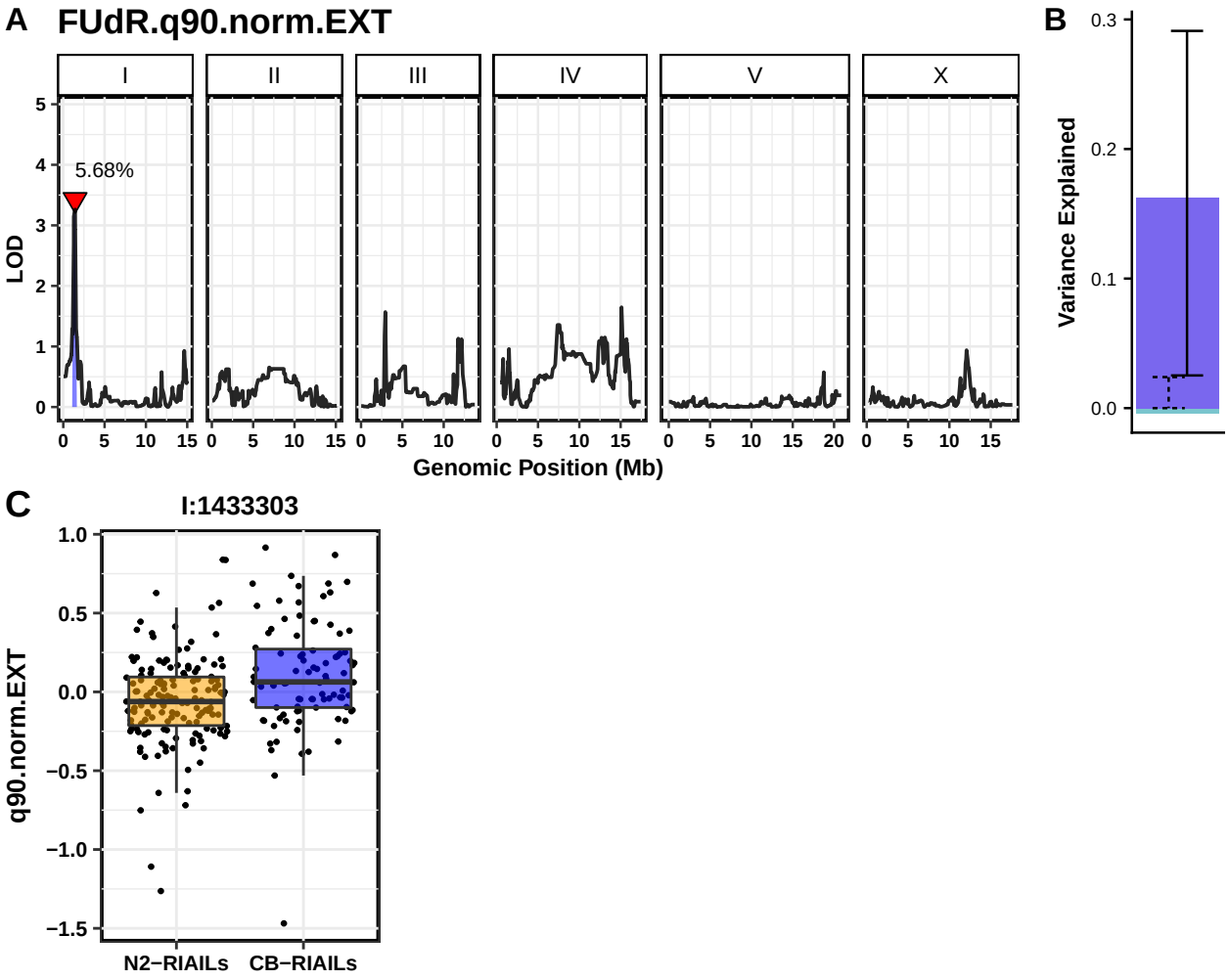

A
FUdR.mean.TOF
I
II
III
IV
V
X
LOD
5.67%
Genomic Position (Mb)
B
Variance Explained
C
X:12750794
mean.TOF
N2−RIAILs
CB−RIAILs

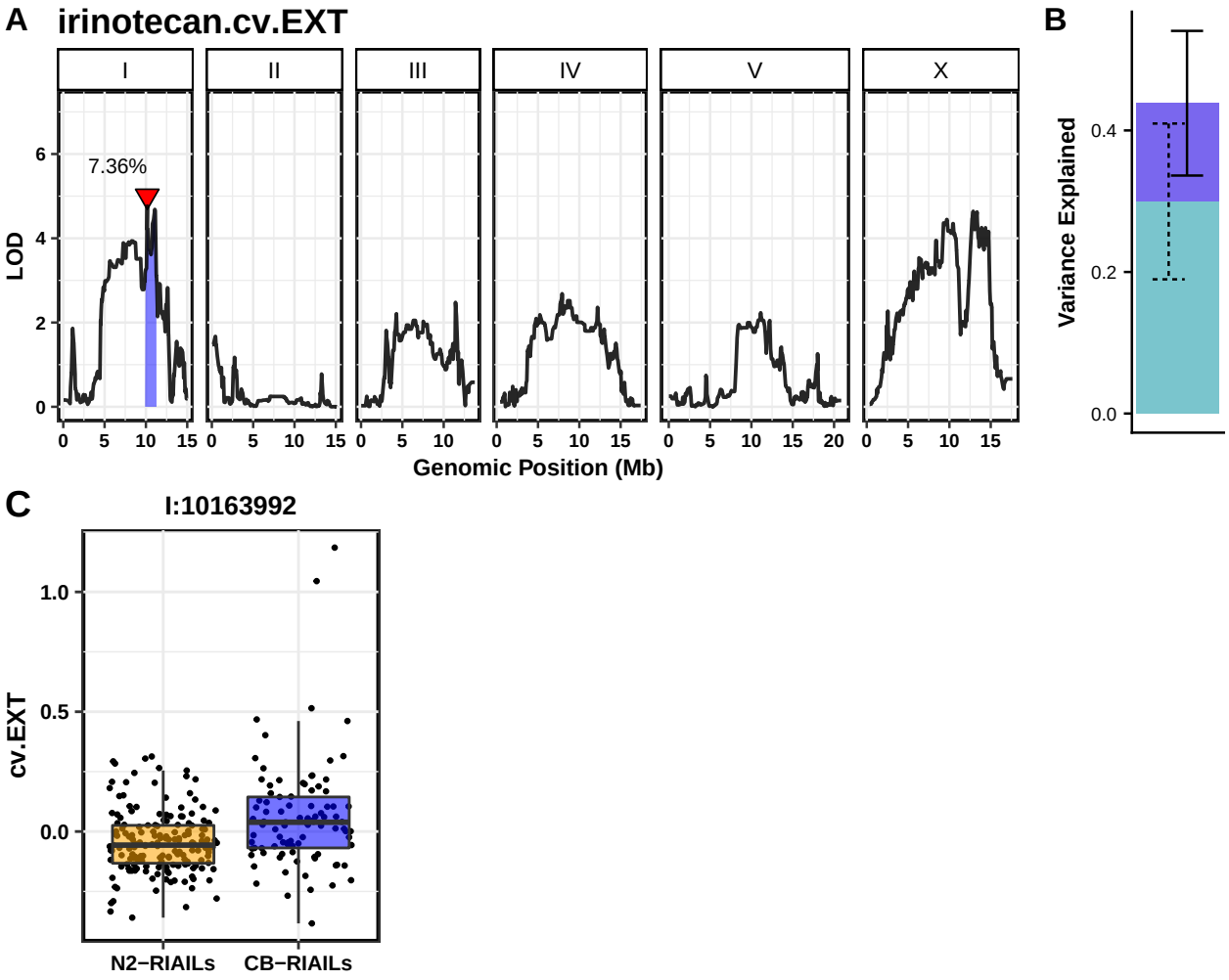

A
FUdR.median.EXT
I
II
III
IV
V
X
LOD
5.91%
Genomic Position (Mb)
B
Variance Explained
C
X:12750794
median.EXT
N2−RIAILs
CB−RIAILs

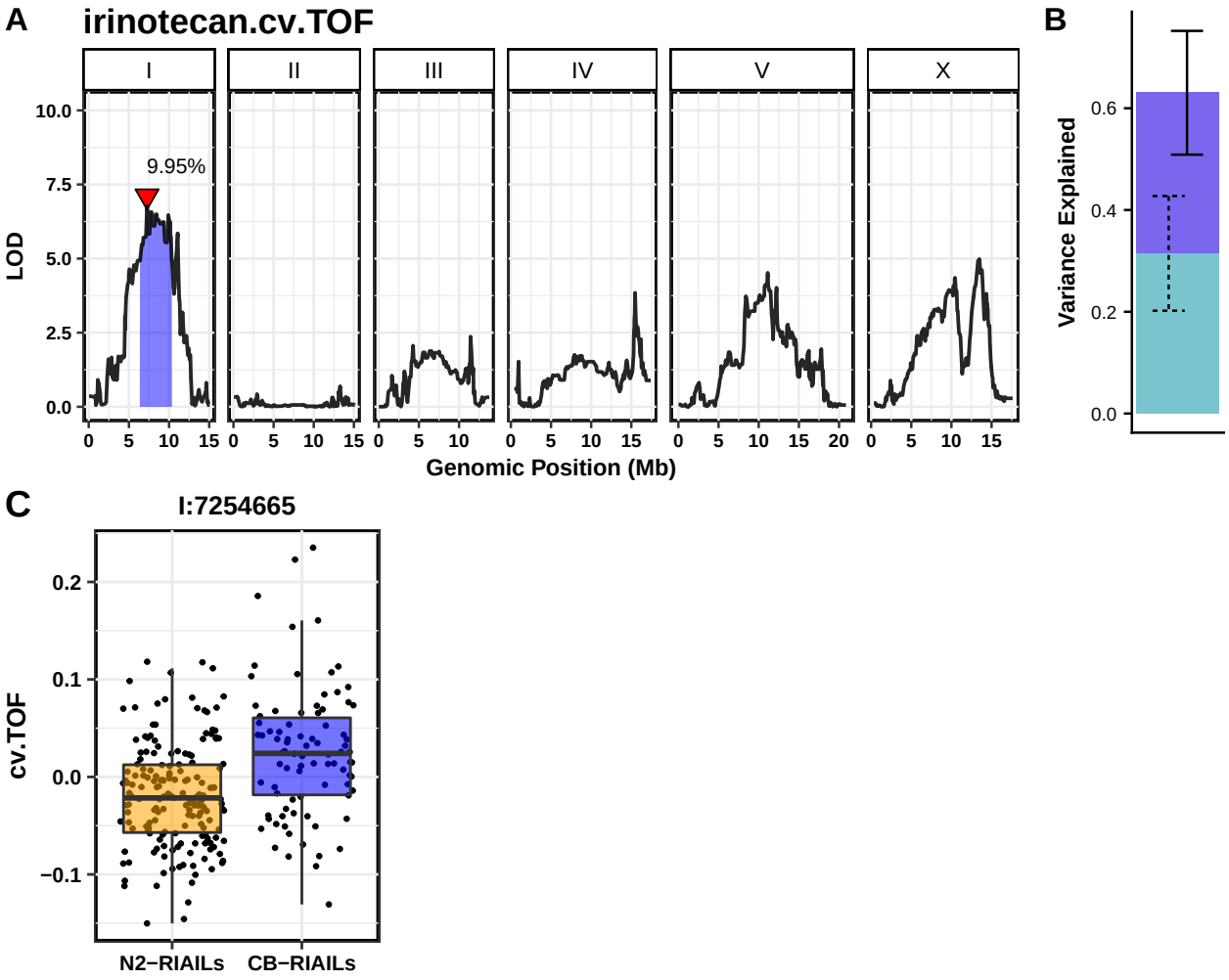

A
FUdR.q75.EXT
I
II
III
IV
V
X
5.53%
LOD
Genomic Position (Mb)
B
Variance Explained
C
X:12750794
q75.EXT
N2−RIAILs
CB−RIAILs

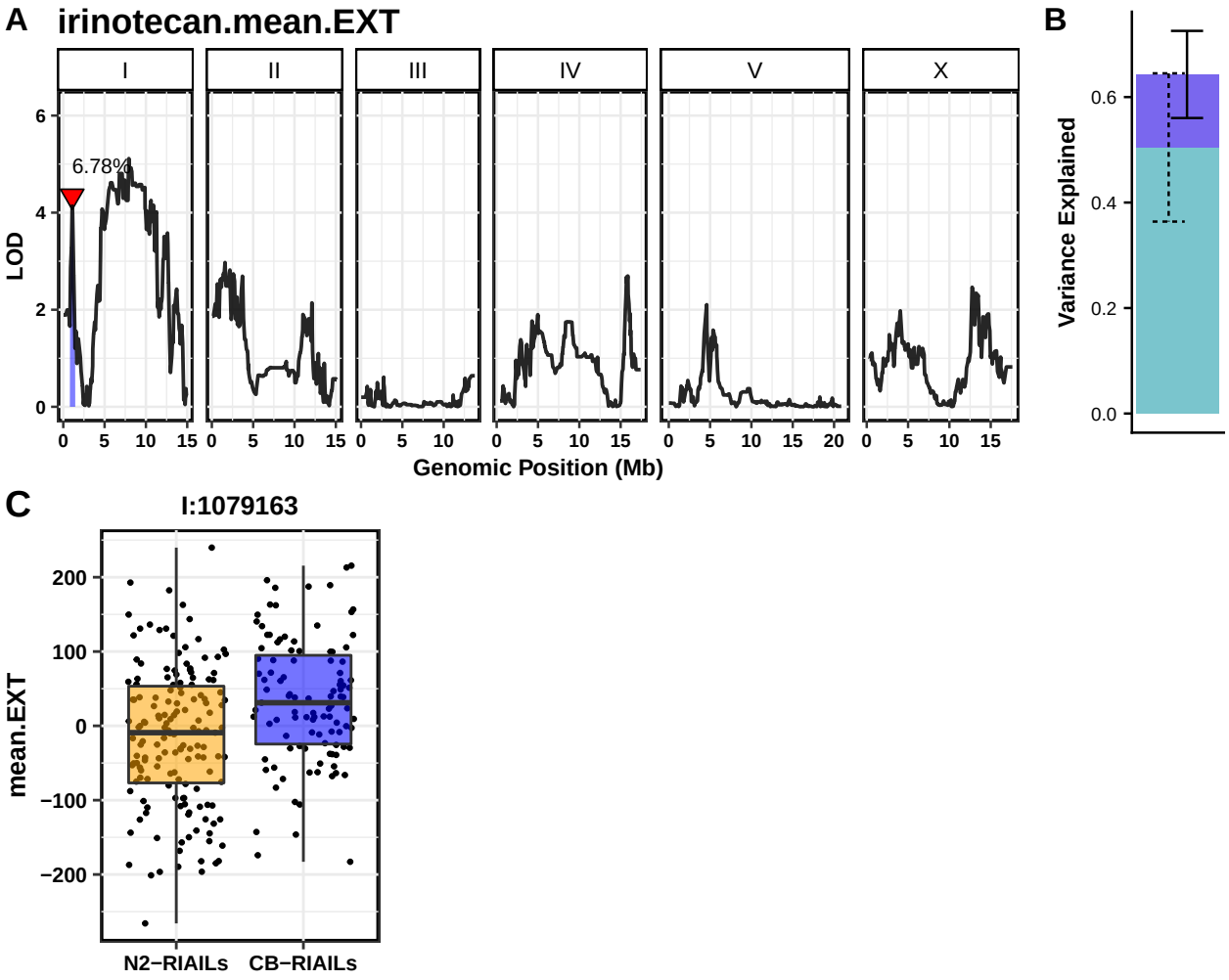

A
FUdR.q75.norm.EXT
I
II
III
IV
V
X
5.72%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:1433303
q75.norm.EXT
N2−RIAILs
CB−RIAILs

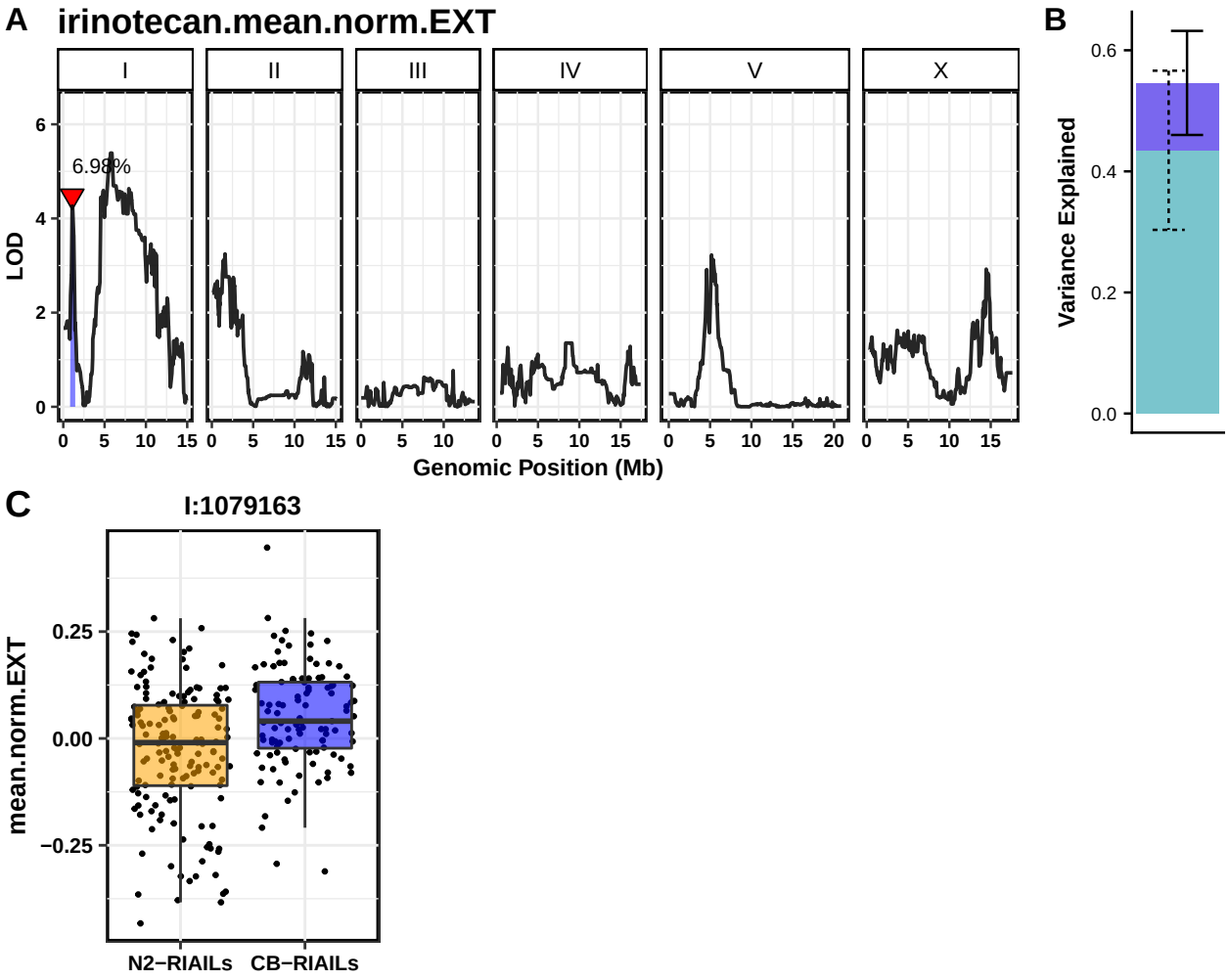

A
FUdR.q75.TOF
I
II
III
IV
V
X
6.95%
LOD
Genomic Position (Mb)
B
Variance Explained
C
X:12750794
q75.TOF
N2−RIAILs
CB−RIAILs

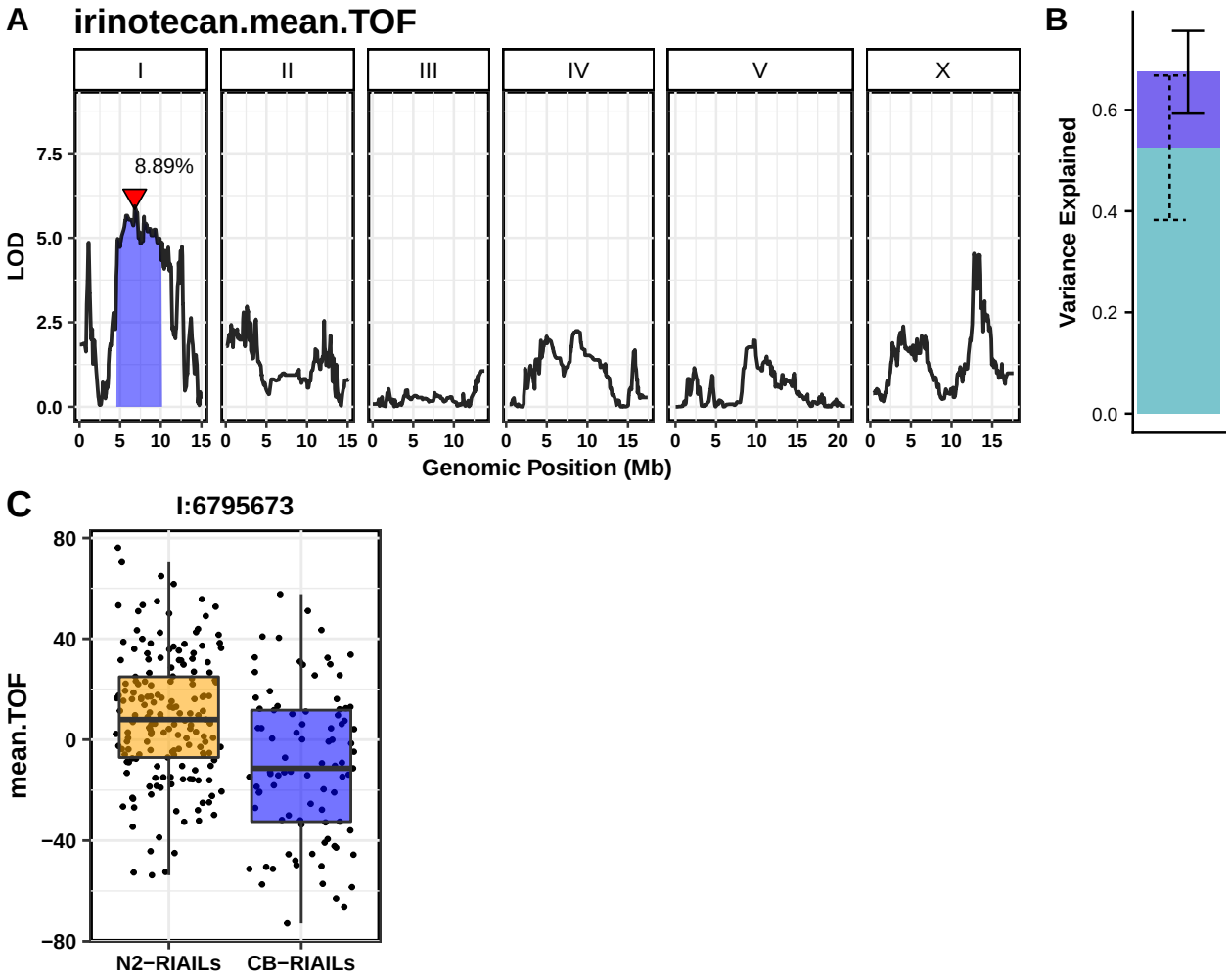

A
FUdR.q90.norm.EXT
I
II
III
IV
V
X
5.68%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:1433303
q90.norm.EXT
N2−RIAILs
CB−RIAILs

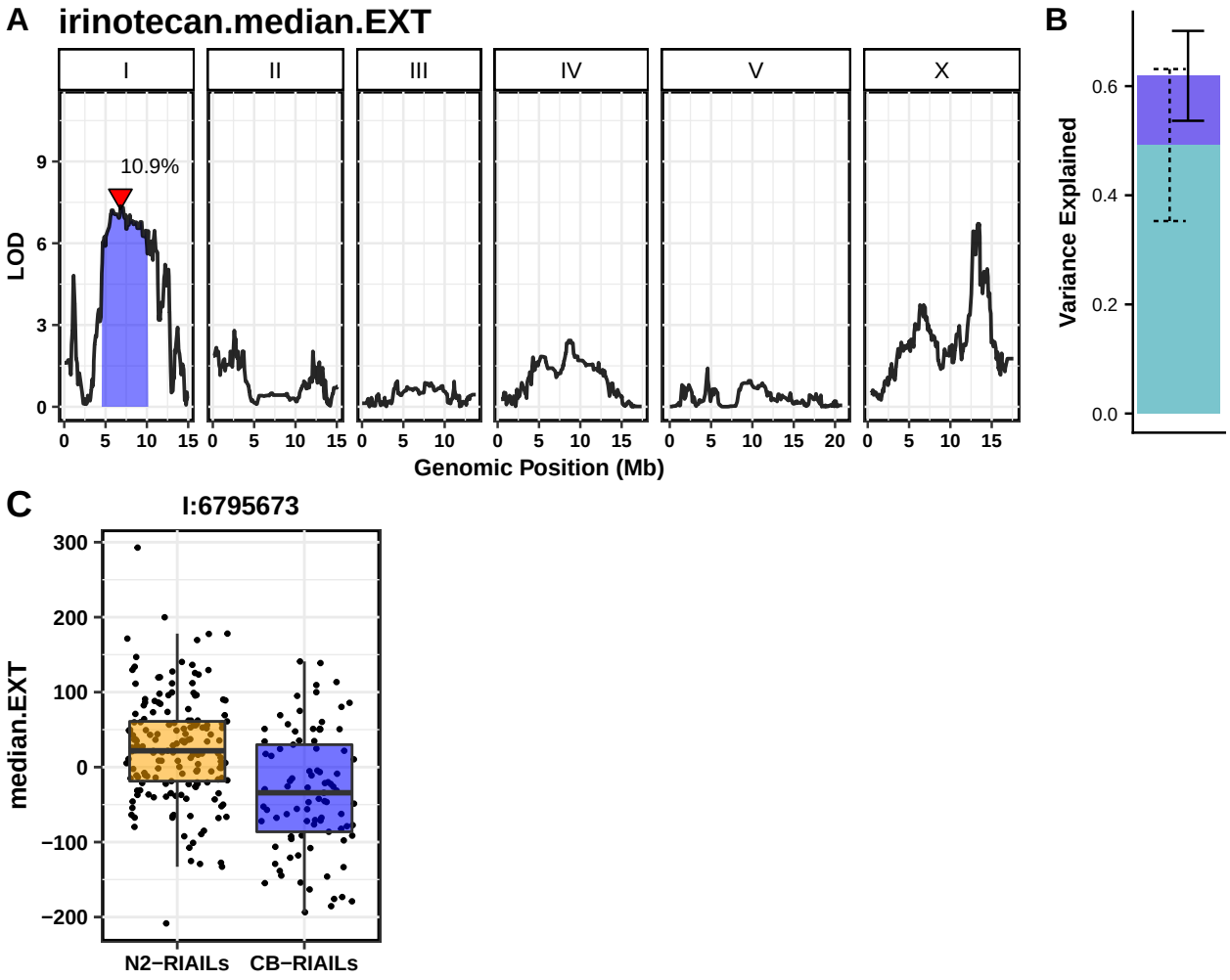

A
irinotecan.cv.EXT
I
II
III
IV
V
X
7.36%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:10163992
cv.EXT
N2−RIAILs
CB−RIAILs

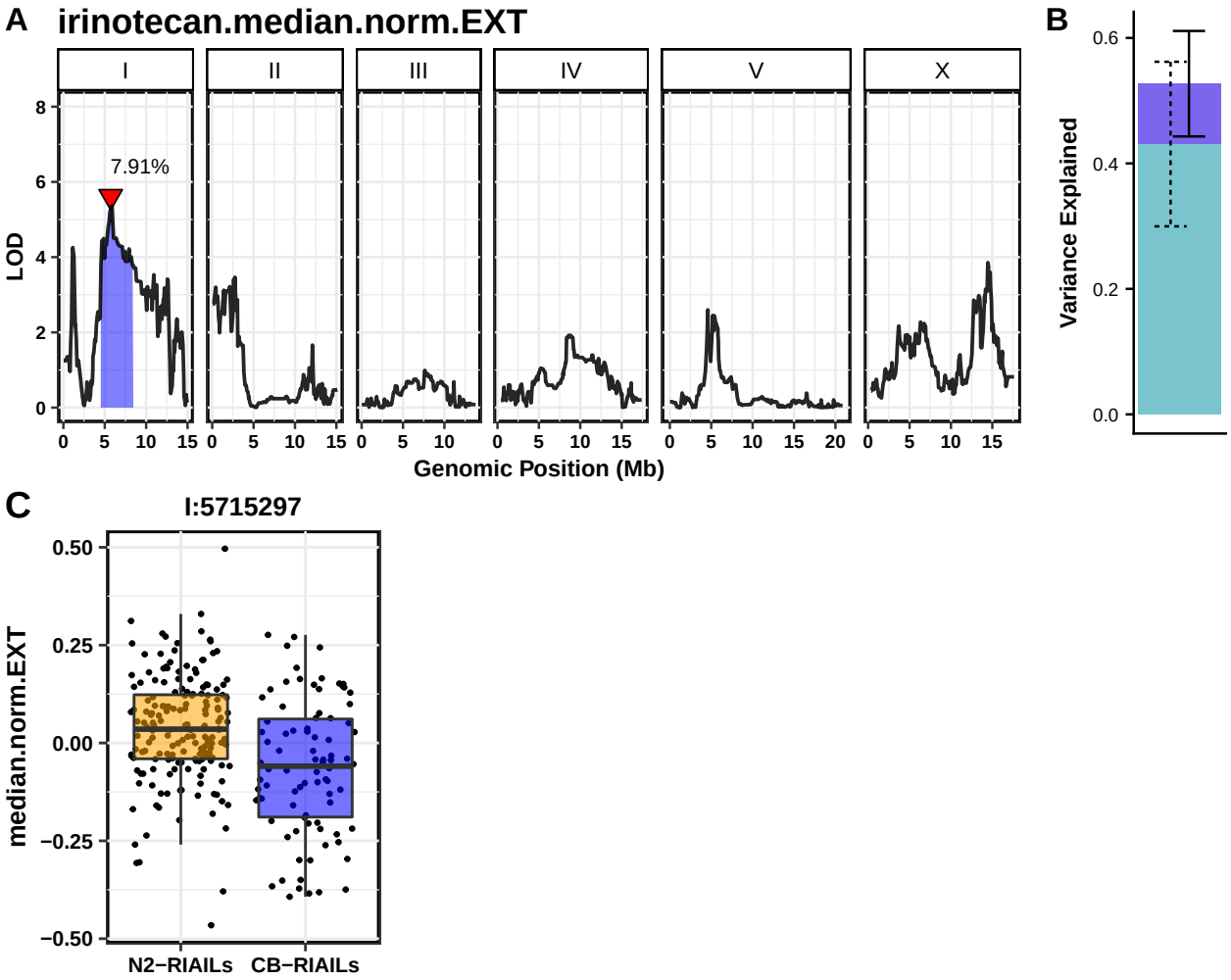

A
irinotecan.cv.TOF
I
II
III
IV
V
X
9.95%
LOD
10.0
7.5
5.0
2.5
0.0
0 5 10 15
0 5 10 15
0 5 10
0 5 10 15
0 5 10 15 20
0 5 10 15
Genomic Position (Mb)
B
Variance Explained
0.6
0.4
0.2
0.0
C
I:7254665
cv.TOF
0.2
0.1
0.0
−0.1
N2−RIAILs
CB−RIAILs

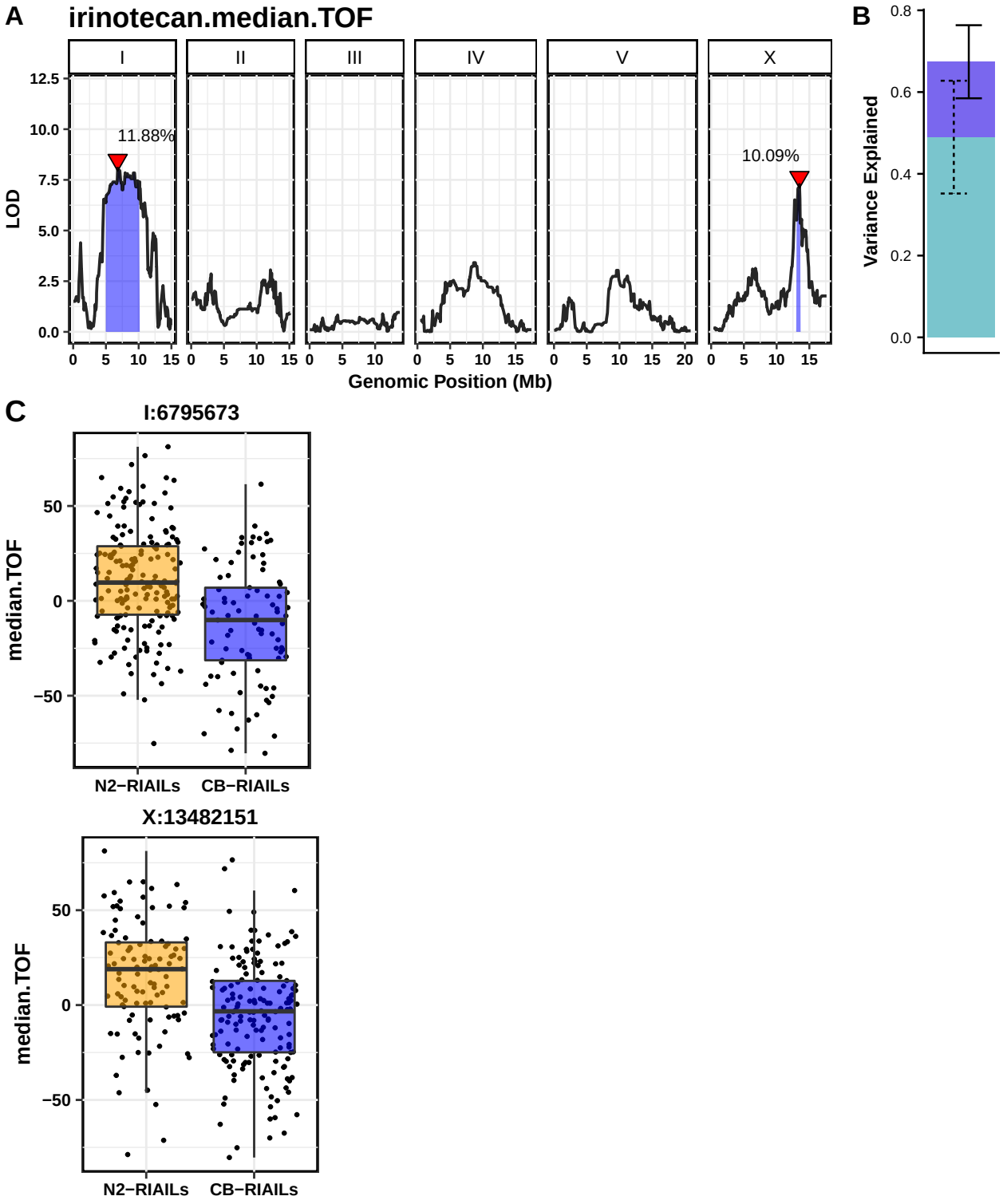

A
irinotecan.mean.EXT
I
II
III
IV
V
X
6.78%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:1079163
mean.EXT
N2−RIAILs
CB−RIAILs

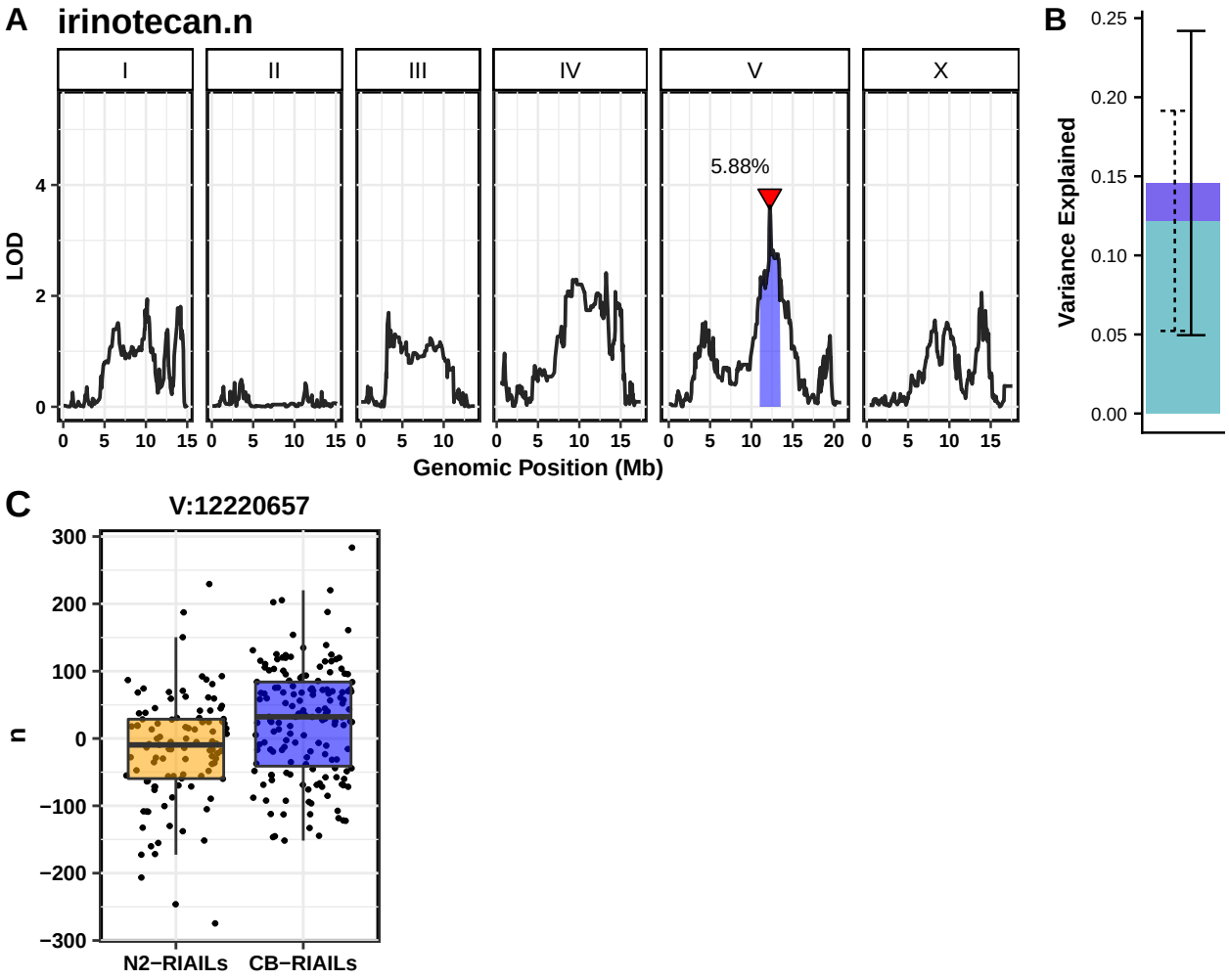

A
irinotecan.mean.norm.EXT
I
II
III
IV
V
X
6.98%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:1079163
mean.norm.EXT
N2−RIAILs
CB−RIAILs

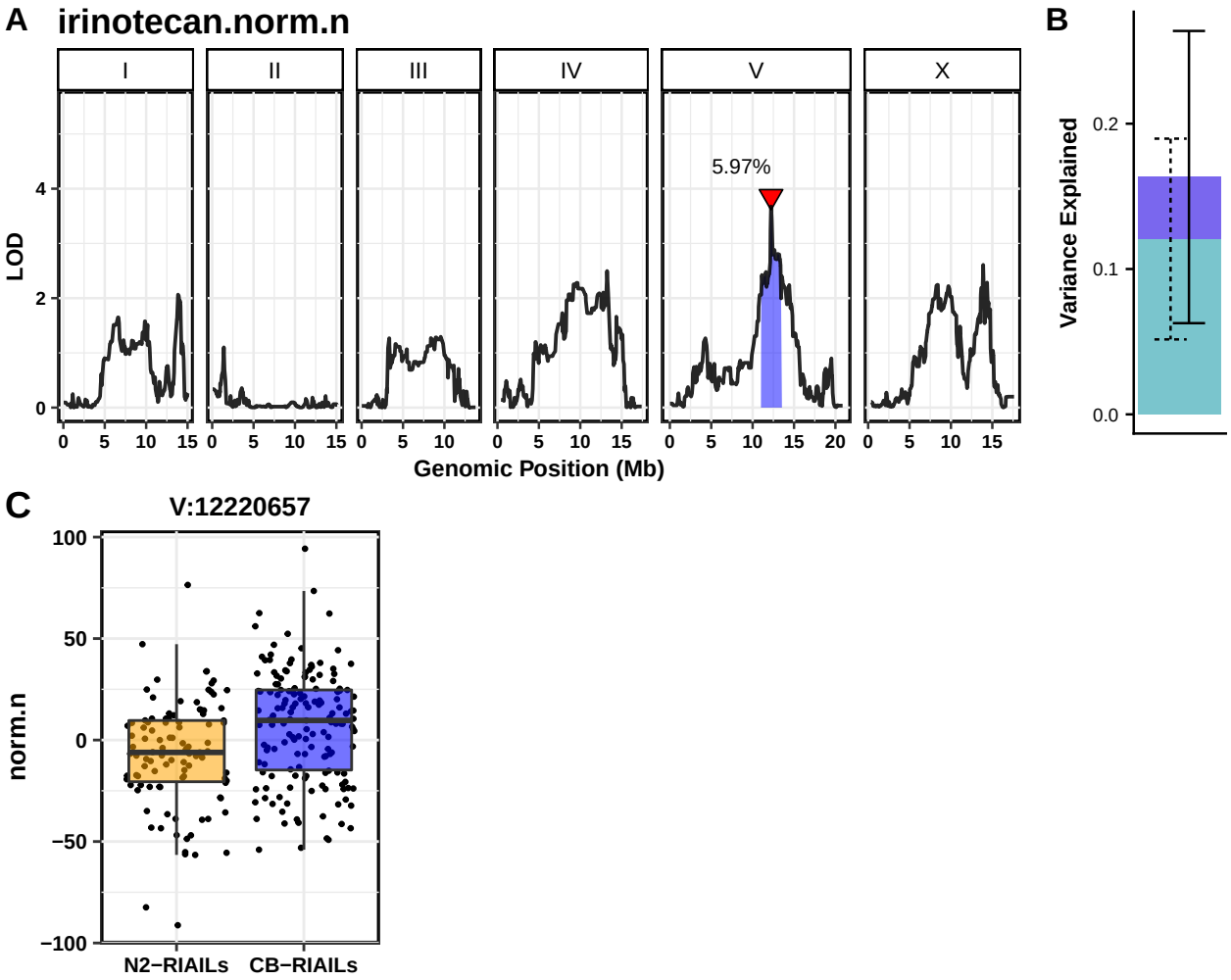

A
irinotecan.mean.TOF
I
II
III
IV
V
X
8.89%
LOD
7.5
5.0
2.5
0.0
0 5 10 15
0 5 10 15
0 5 10
0 5 10 15
0 5 10 15 20
0 5 10 15
Genomic Position (Mb)
B
Variance Explained
0.6
0.4
0.2
0.0
C
I:6795673
mean.TOF
80
40
0
−40
−80
N2−RIAILs
CB−RIAILs

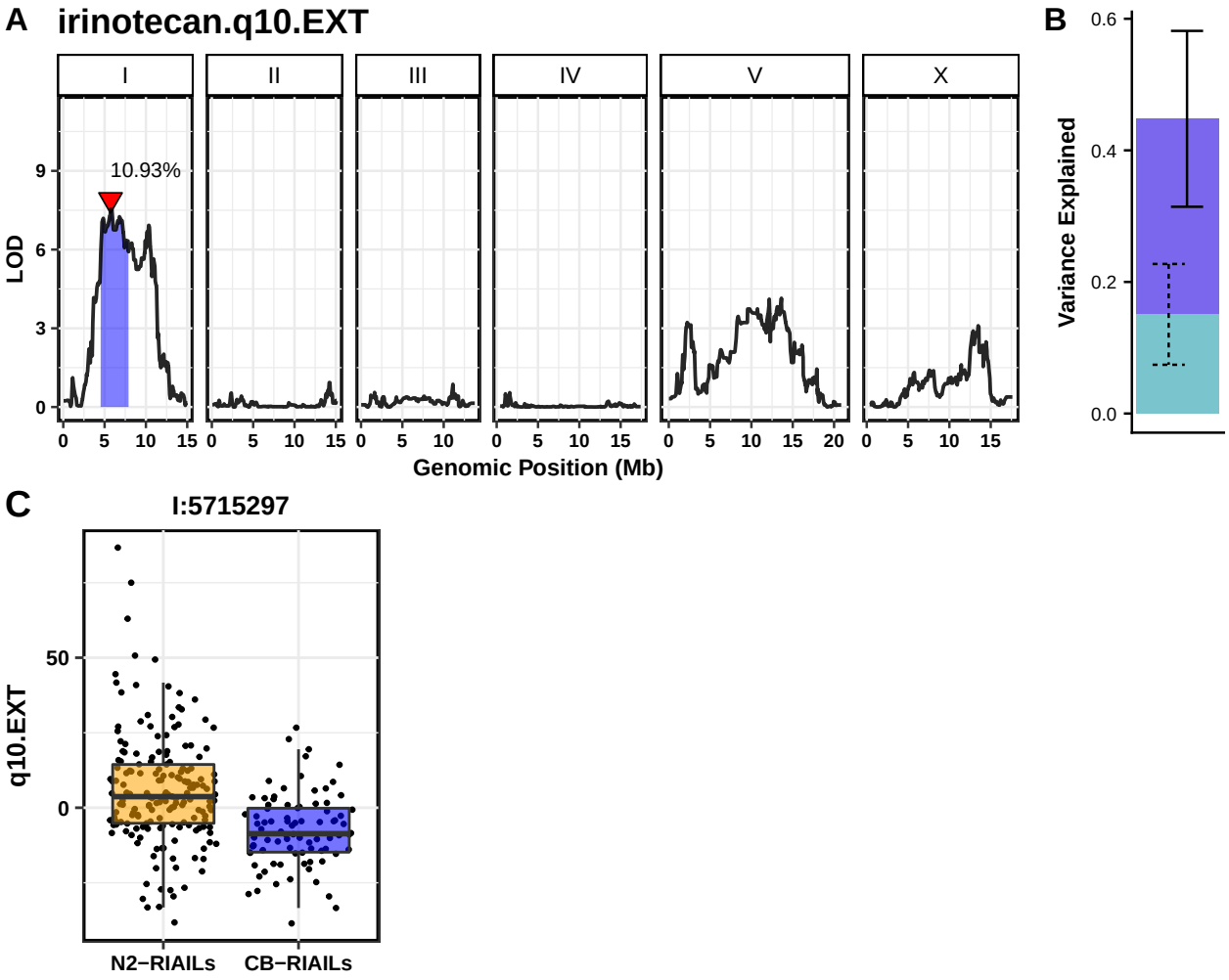

A
irinotecan.median.EXT
I
II
III
IV
V
X
10.9%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:6795673
median.EXT
N2−RIAILs
CB−RIAILs

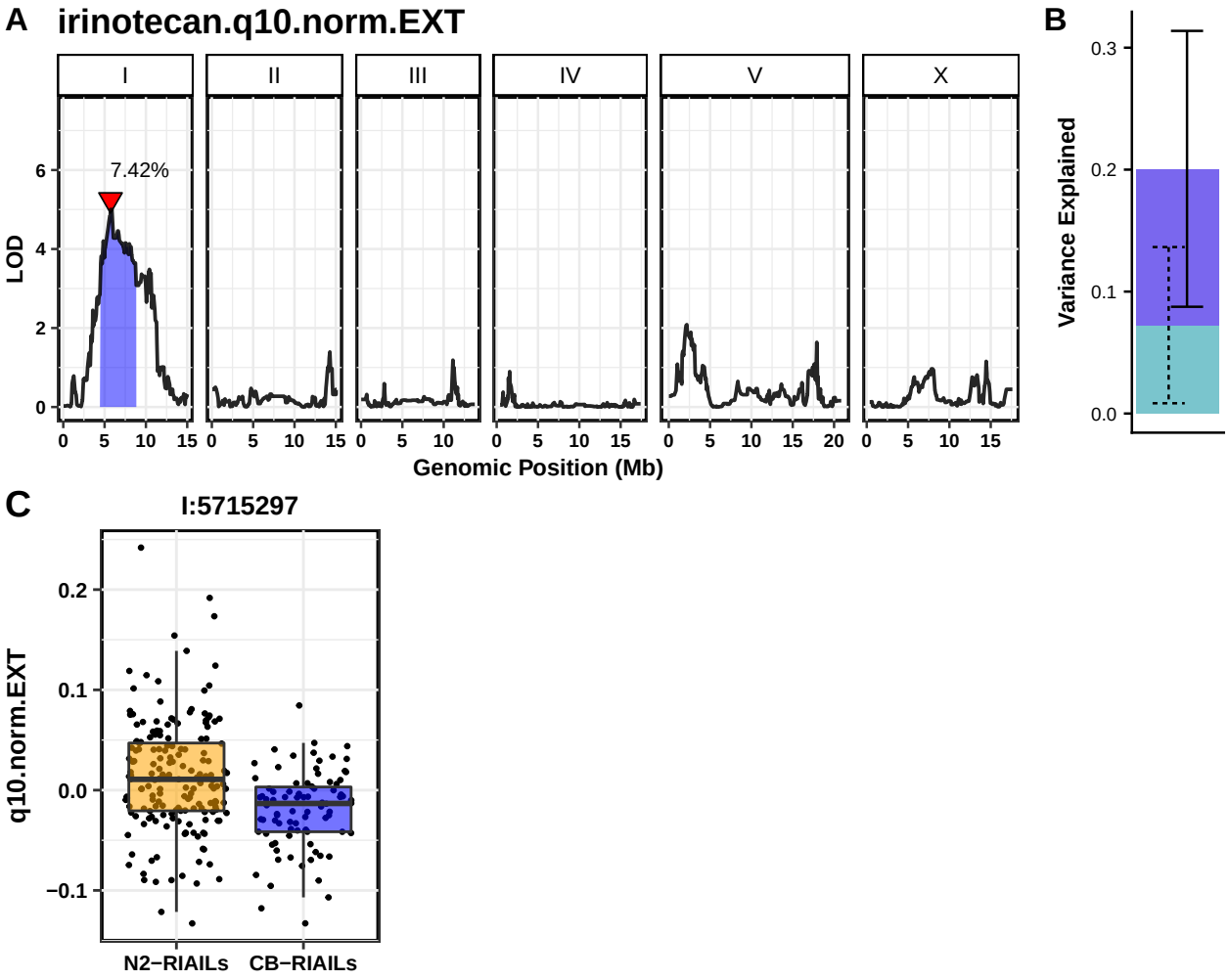

A
irinotecan.median.norm.EXT
I
II
III
IV
V
X
7.91%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:5715297
median.norm.EXT
N2−RIAILs
CB−RIAILs

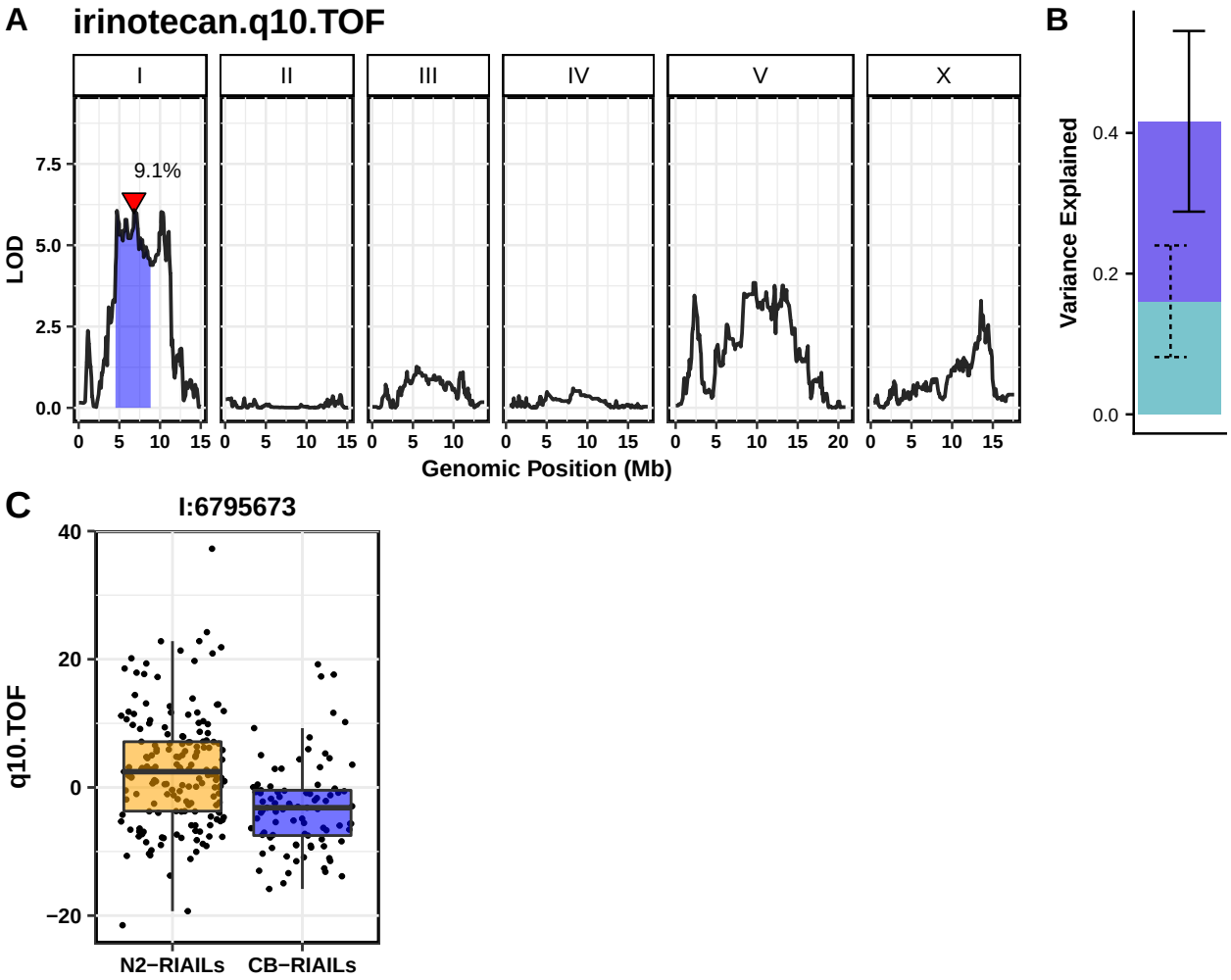

A
irinotecan.median.TOF
I
II
III
IV
V
X
11.88%
10.09%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:6795673
median.TOF
N2−RIAILs
CB−RIAILs
X:13482151

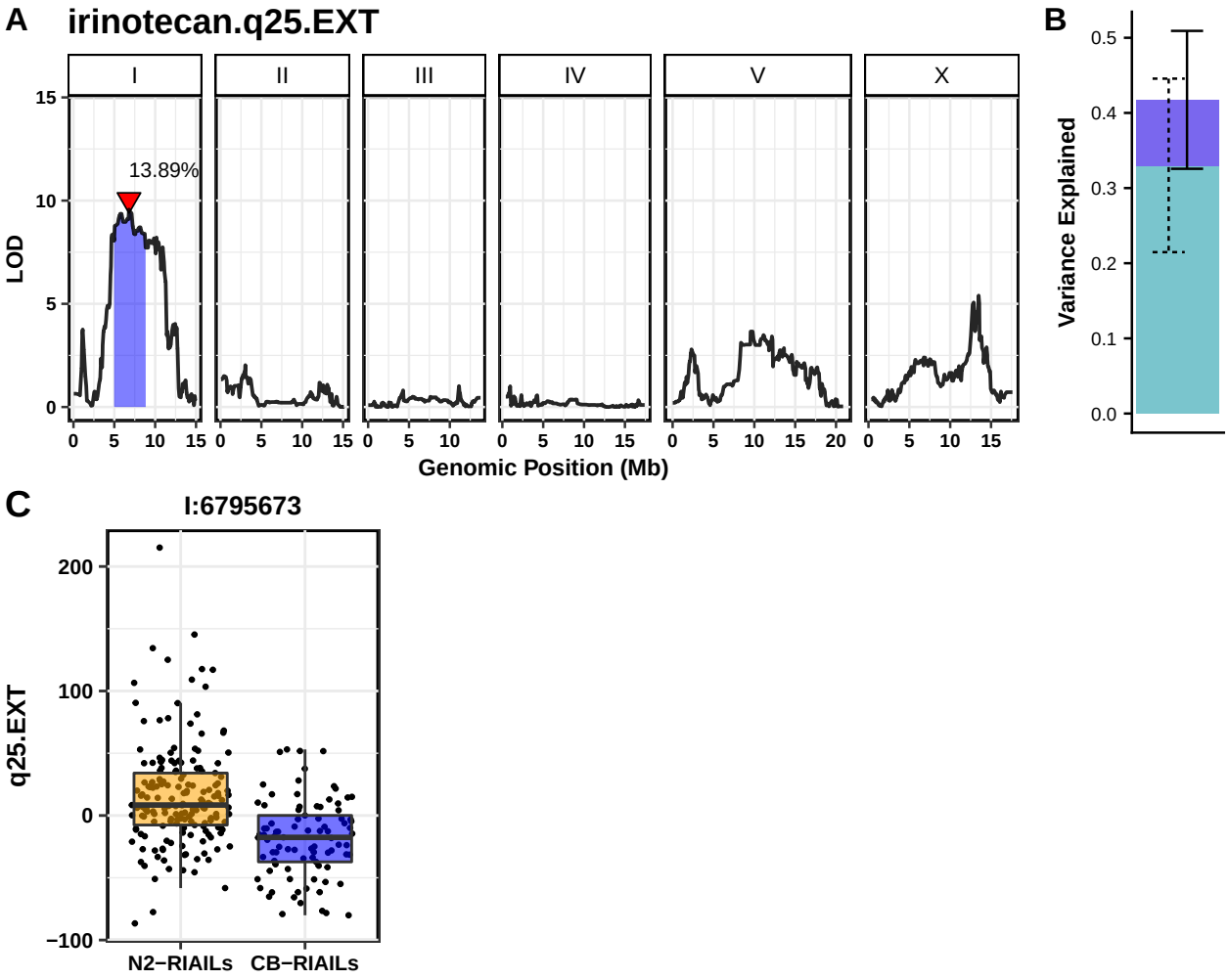

A
irinotecan.n
I
II
III
IV
V
X
5.88%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:12220657
n
N2−RIAILs
CB−RIAILs

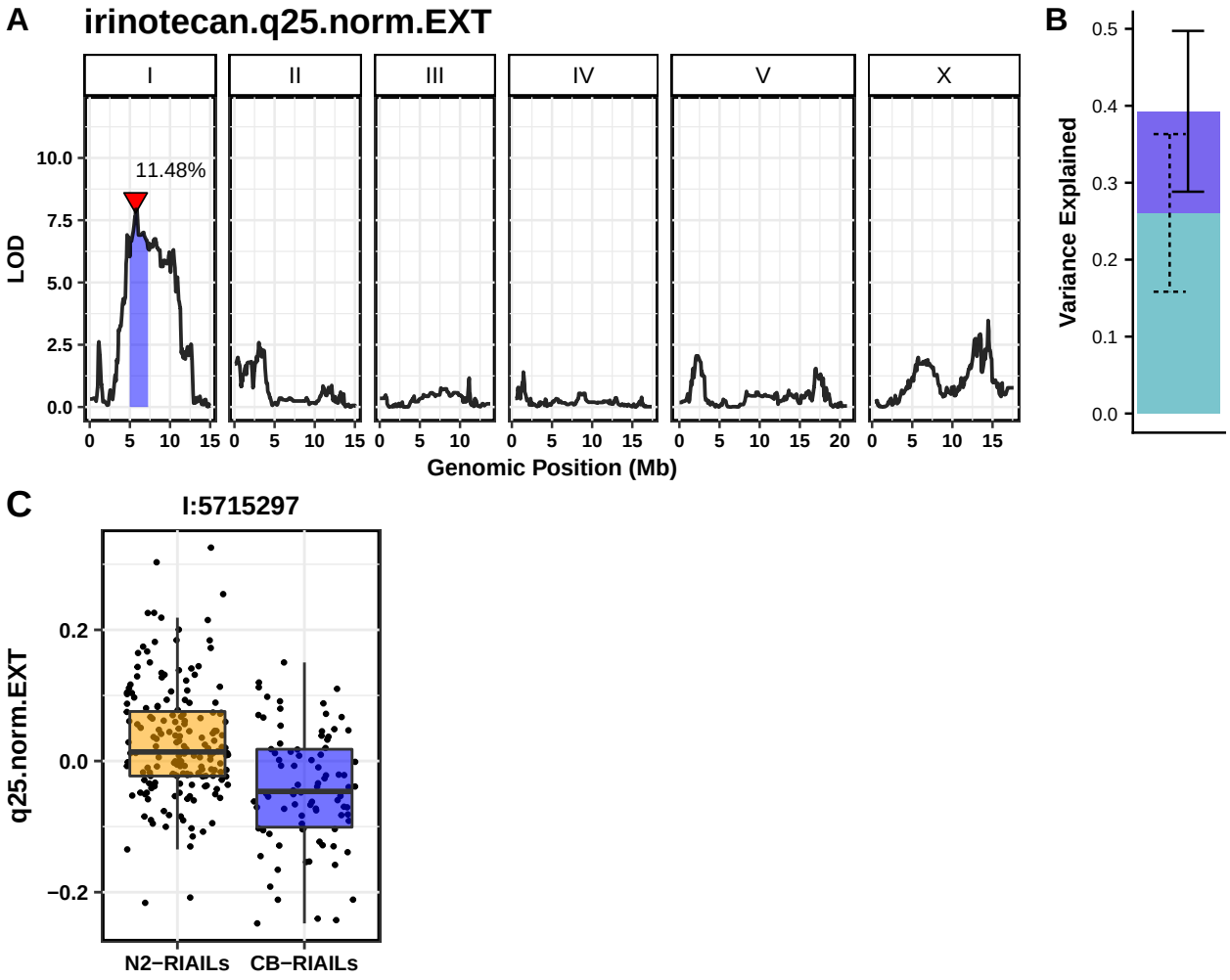

A
irinotecan.norm.n
I
II
III
IV
V
X
5.97%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:12220657
norm.n
N2−RIAILs
CB−RIAILs

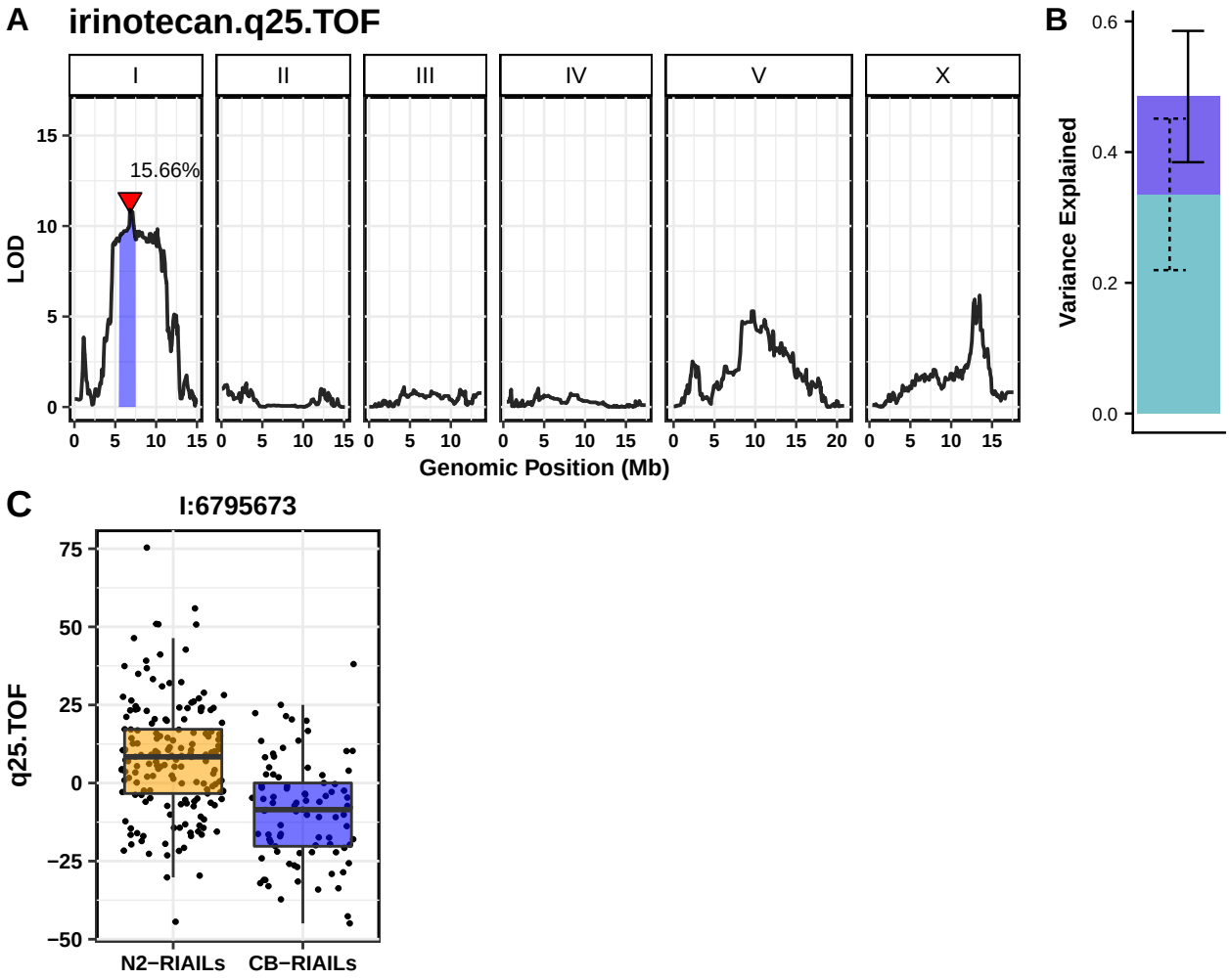

A
irinotecan.q10.EXT
I
II
III
IV
V
X
10.93%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:5715297
q10.EXT
N2−RIAILs
CB−RIAILs

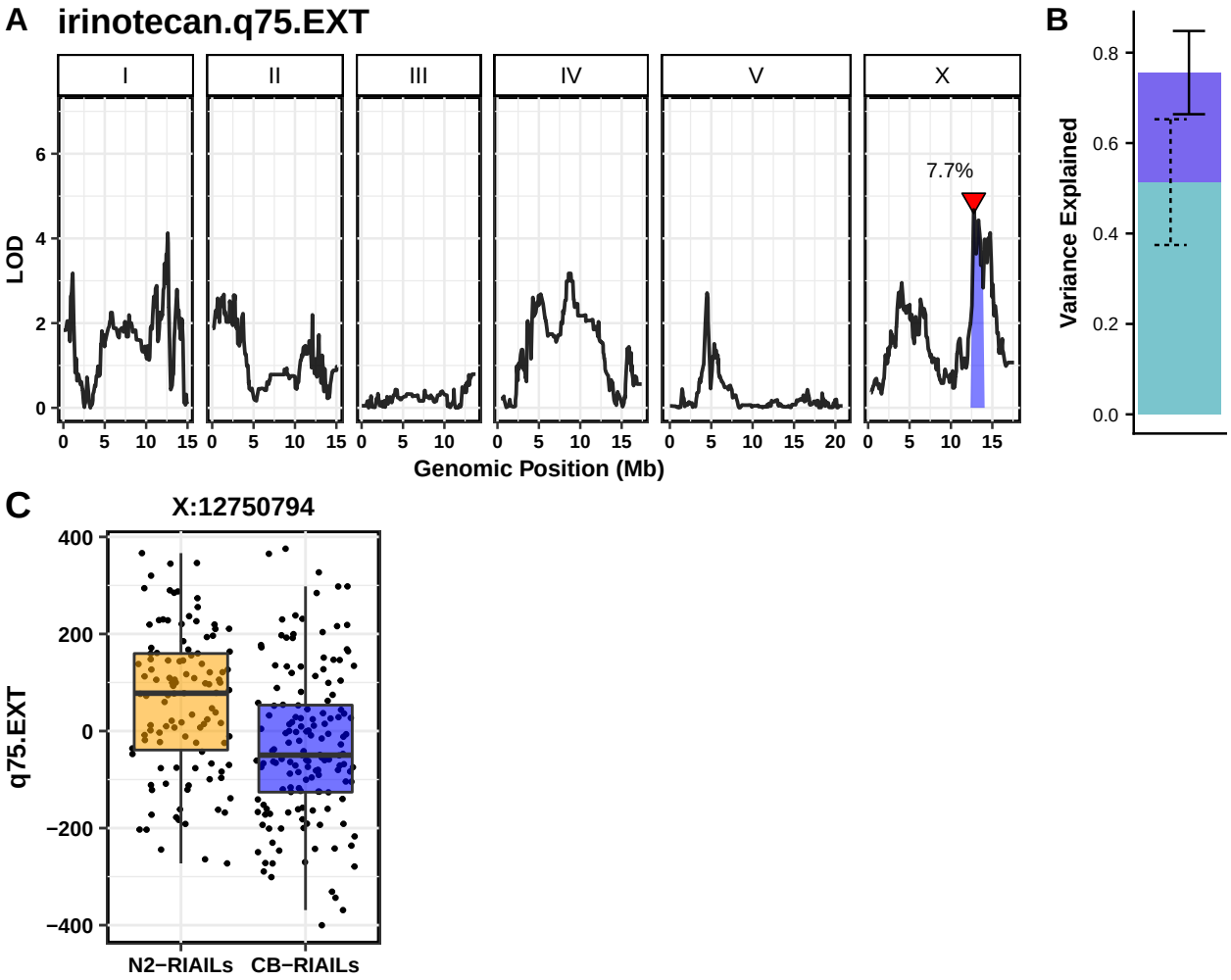

A
irinotecan.q10.norm.EXT
I
II
III
IV
V
X
7.42%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:5715297
q10.norm.EXT
N2−RIAILs
CB−RIAILs

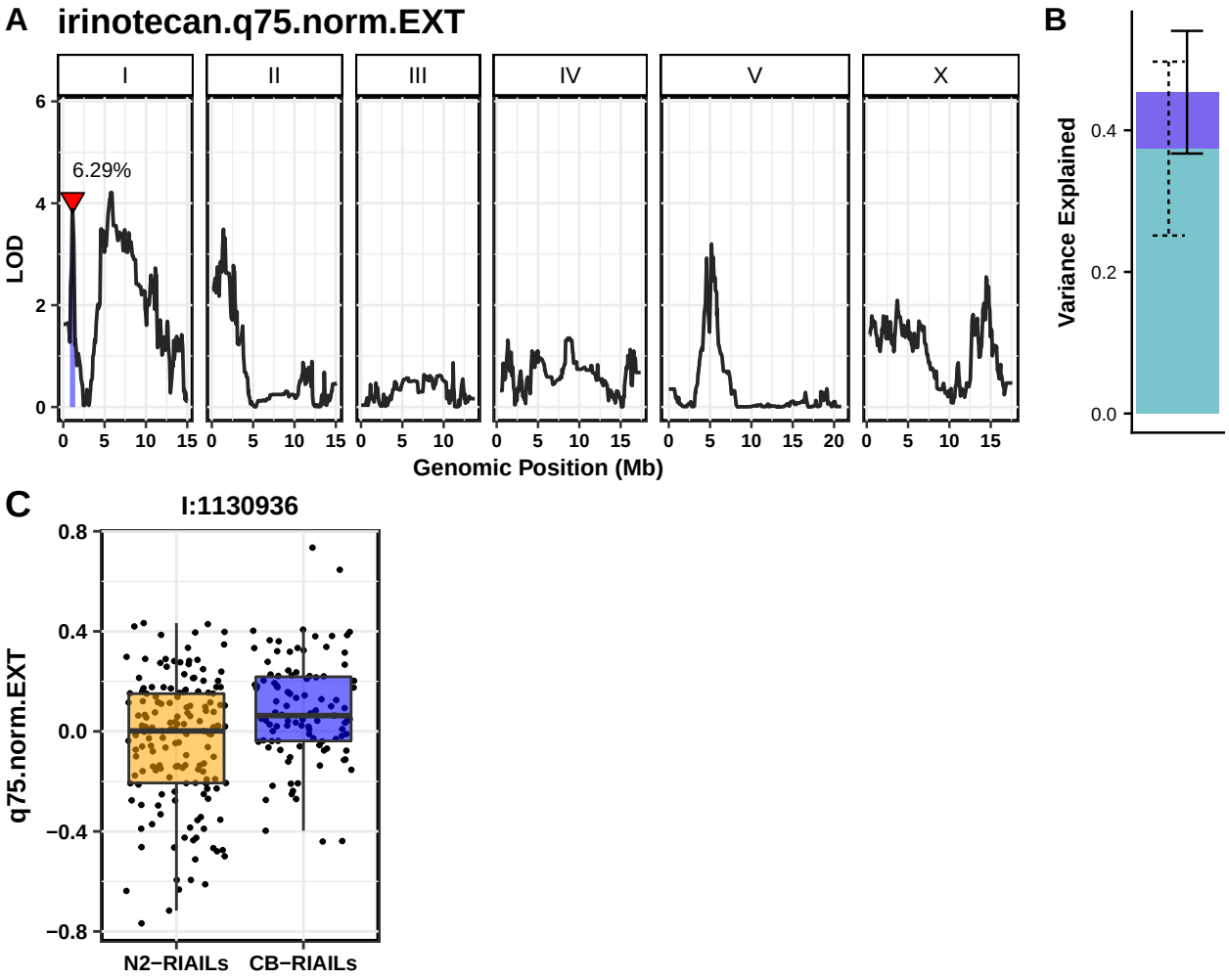

A
irinotecan.q10.TOF
I
II
III
IV
V
X
9.1%
LOD
7.5
5.0
2.5
0.0
0 5 10 15
0 5 10 15
0 5 10
0 5 10 15
0 5 10 15 20
0 5 10 15
Genomic Position (Mb)
B
Variance Explained
0.4
0.2
0.0
C
I:6795673
q10.TOF
40
20
0
−20
N2−RIAILs
CB−RIAILs

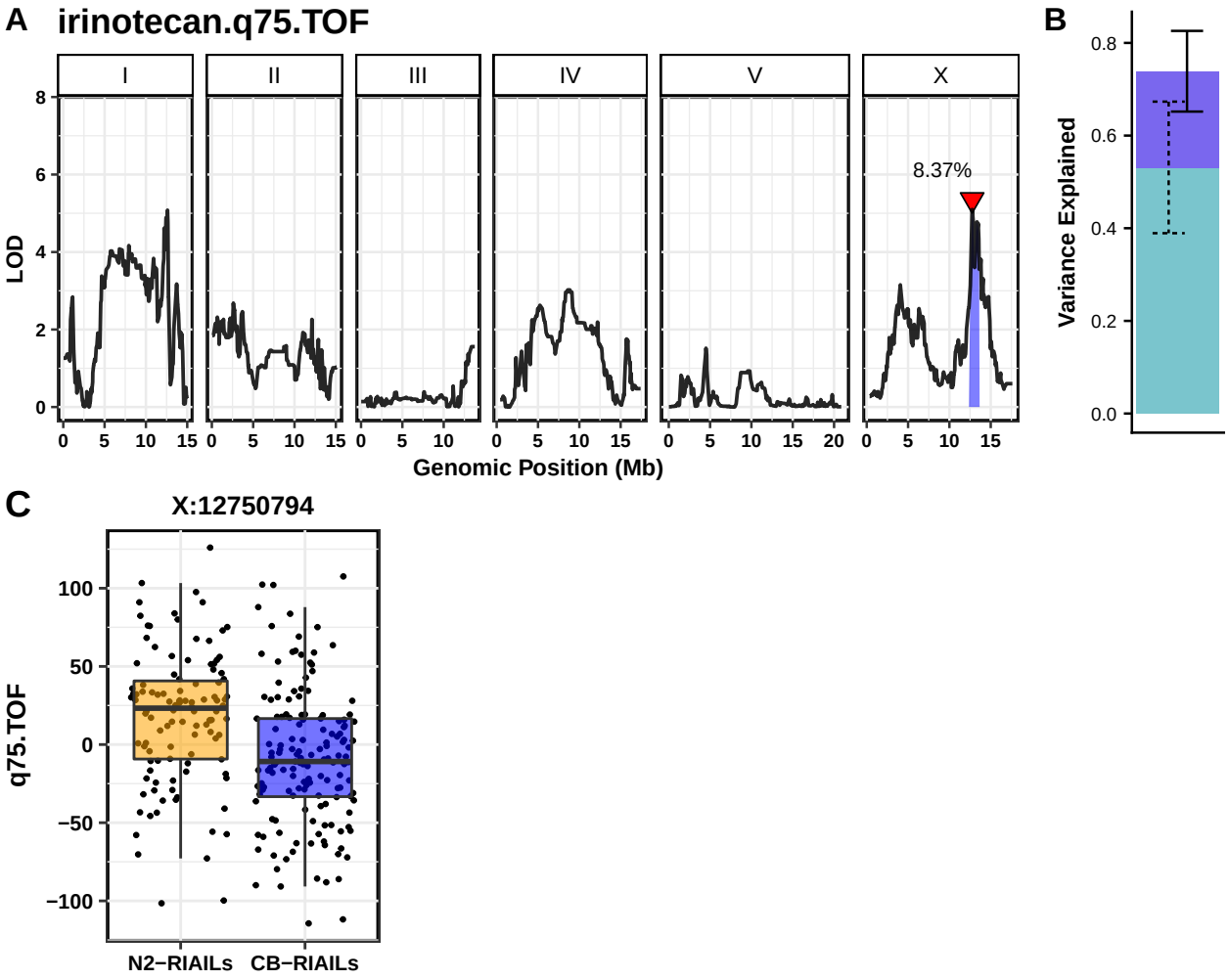

A
irinotecan.q25.EXT
I
II
III
IV
V
X
13.89%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:6795673
q25.EXT
N2−RIAILs
CB−RIAILs

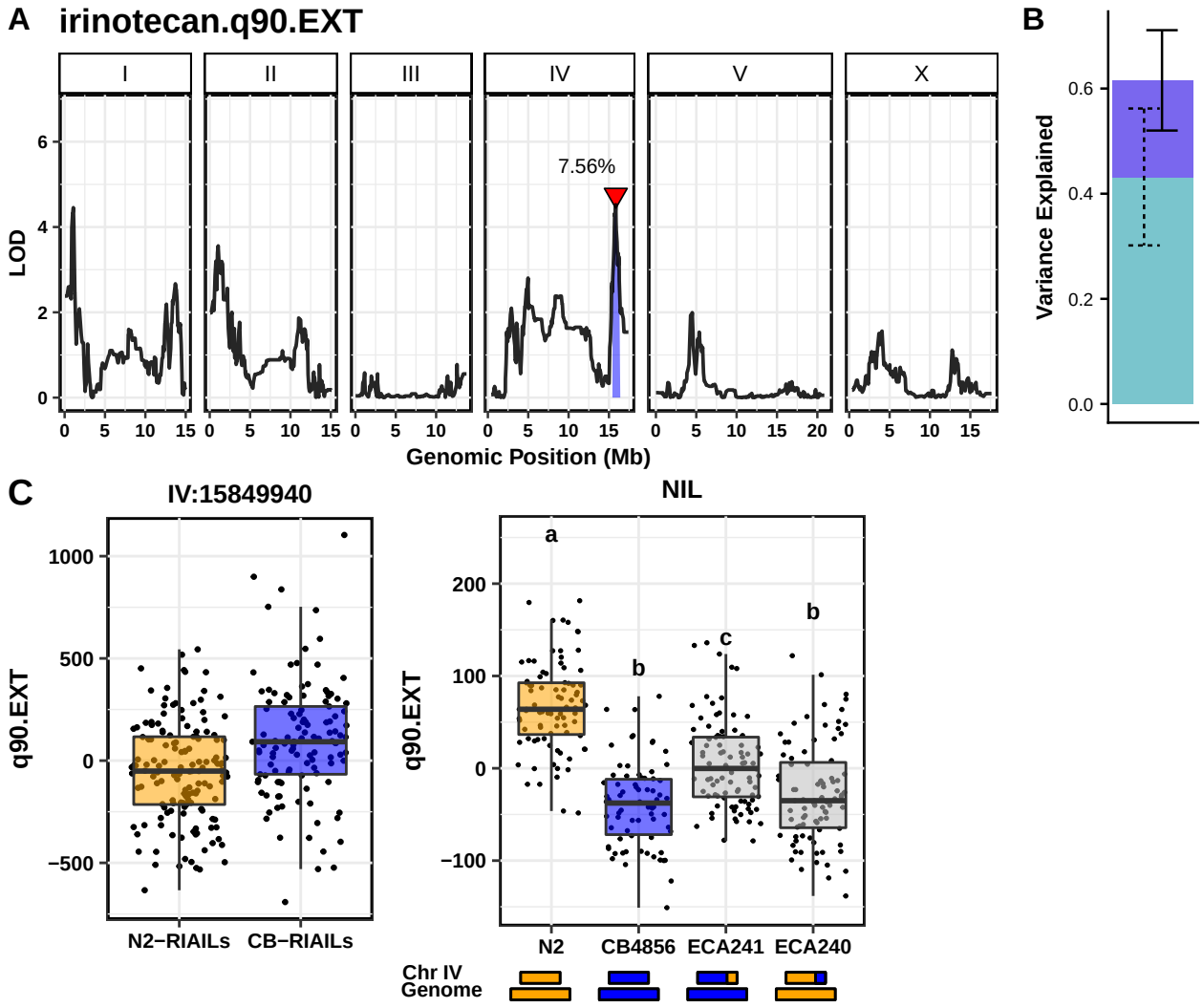

A
irinotecan.q25.norm.EXT
I
II
III
IV
V
X
11.48%
LOD
10.0
7.5
5.0
2.5
0.0
0 5 10 15
0 5 10 15
0 5 10
0 5 10 15
0 5 10 15 20
0 5 10 15
Genomic Position (Mb)
B
Variance Explained
0.5
0.4
0.3
0.2
0.1
0.0
C
I:5715297
q25.norm.EXT
0.2
0.0
−0.2
N2−RIAILs
CB−RIAILs

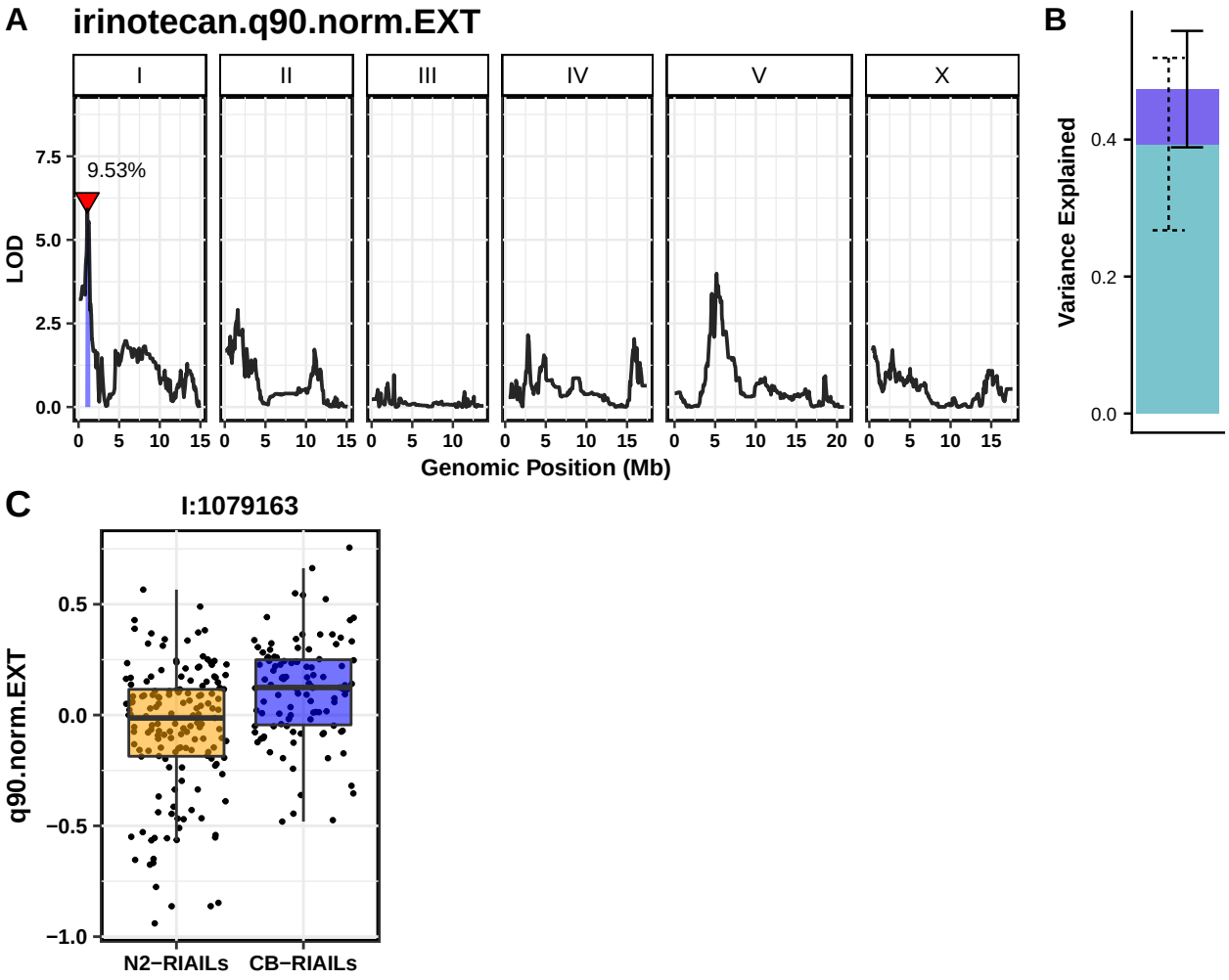

A
irinotecan.q25.TOF
I
II
III
IV
V
X
15.66%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:6795673
q25.TOF
N2−RIAILs
CB−RIAILs

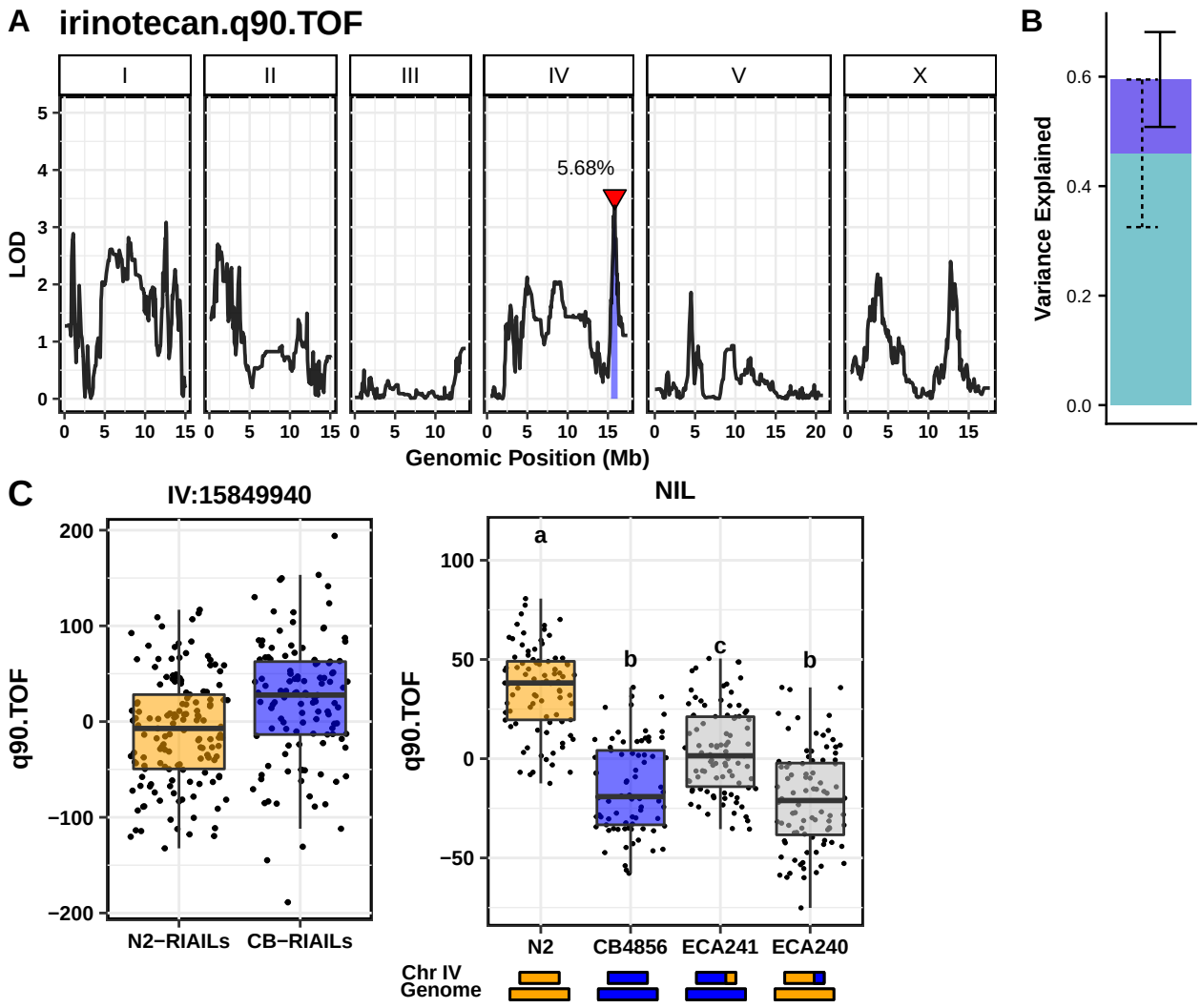

A
irinotecan.q75.EXT
I
II
III
IV
V
X
LOD
7.7%
Genomic Position (Mb)
B
Variance Explained
C
X:12750794
q75.EXT
N2−RIAILs
CB−RIAILs

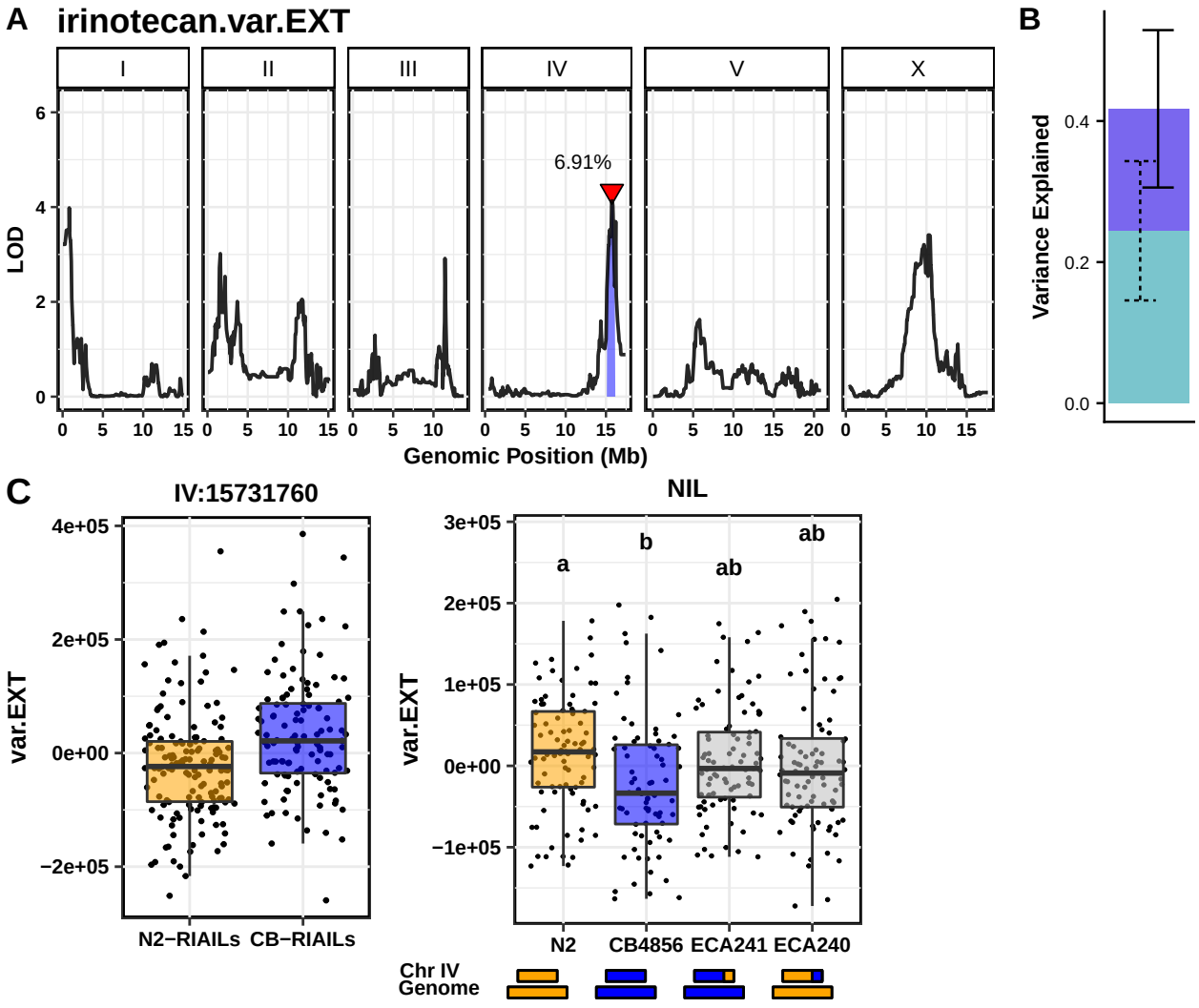

A
irinotecan.q75.norm.EXT
I
II
III
IV
V
X
6.29%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:1130936
q75.norm.EXT
N2−RIAILs
CB−RIAILs

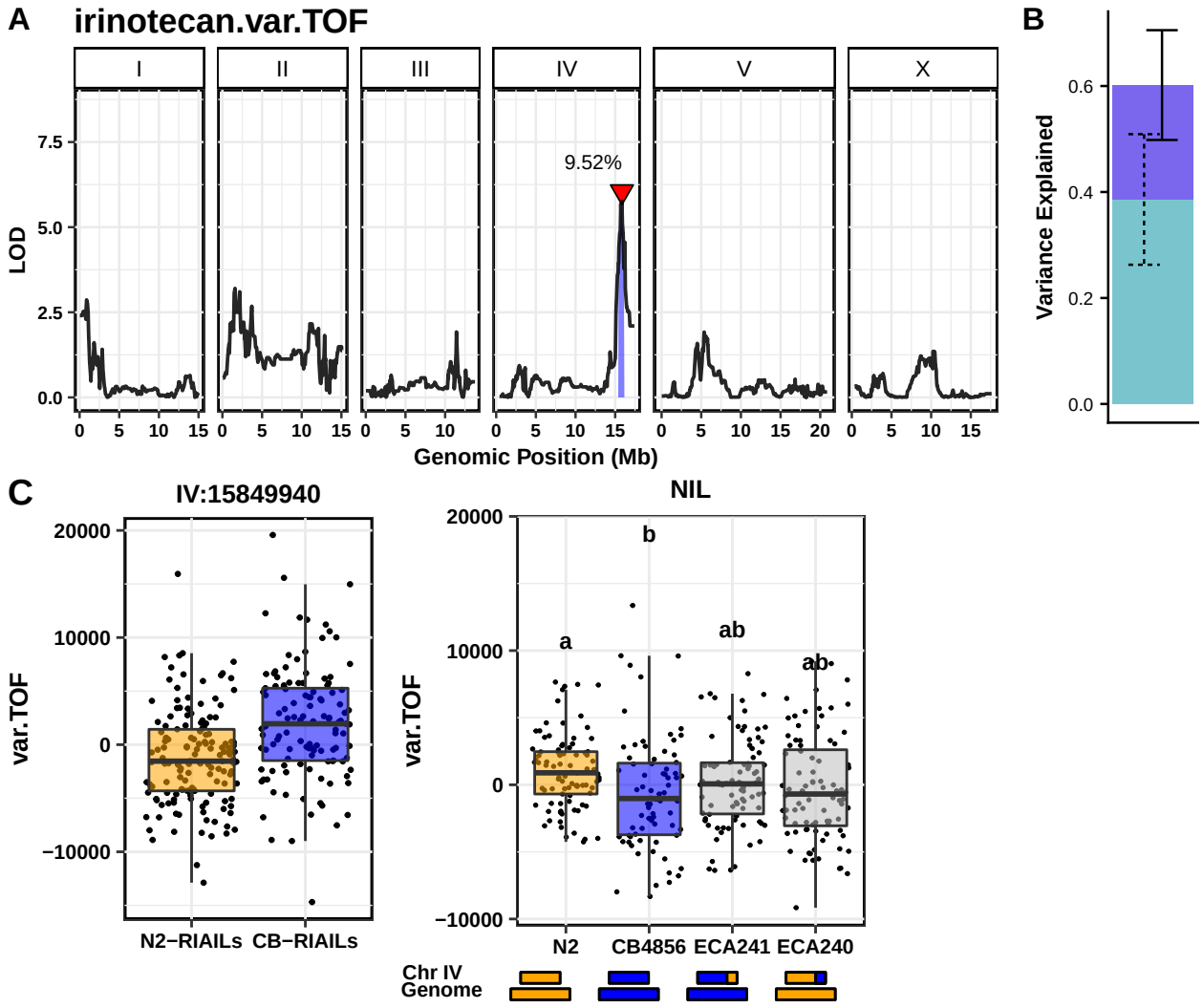

A
irinotecan.q75.TOF
I
II
III
IV
V
X
LOD
8.37%
Genomic Position (Mb)
B
Variance Explained
C
X:12750794
q75.TOF
N2−RIAILs
CB−RIAILs

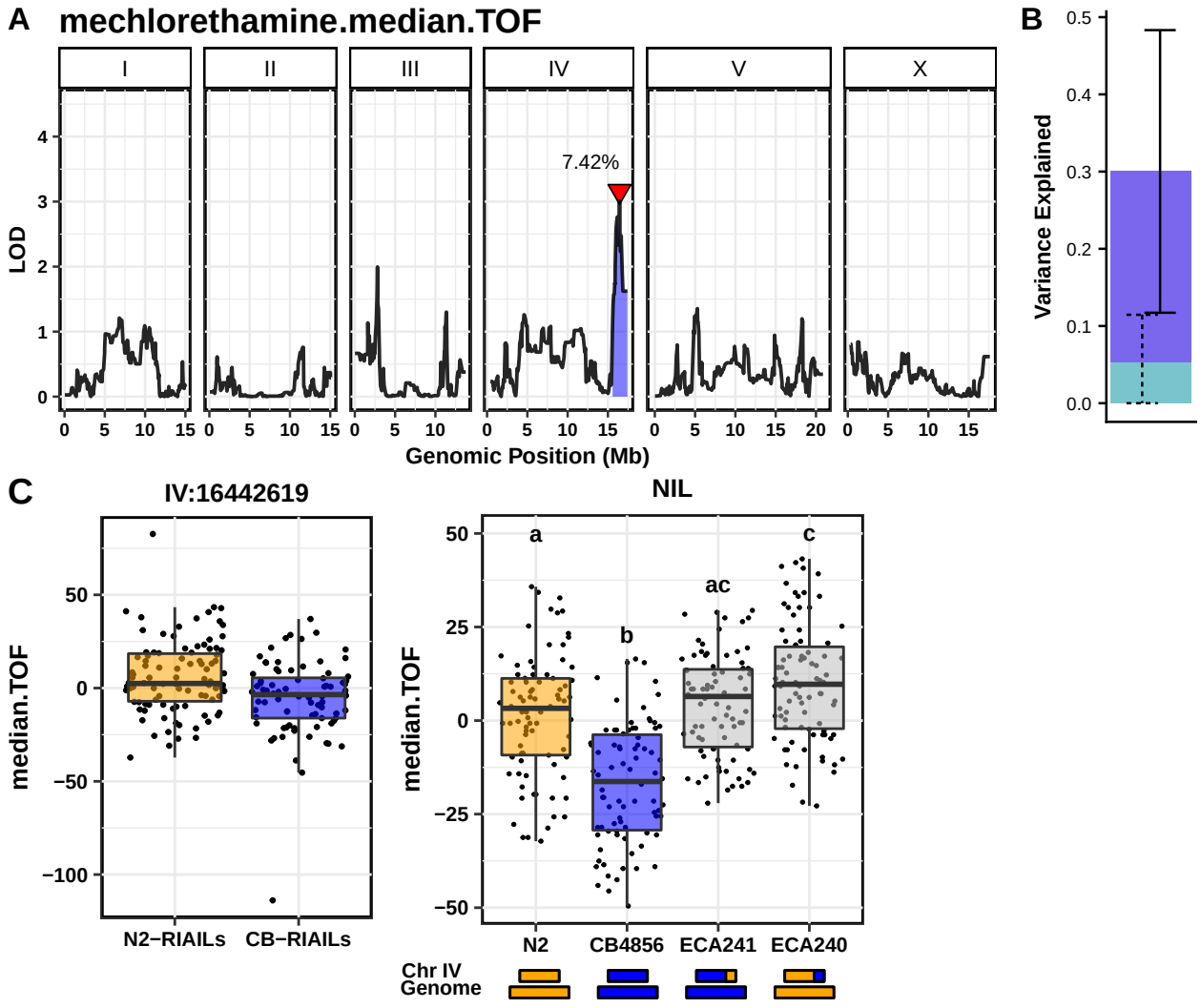

A
irinotecan.q90.EXT
I
II
III
IV
V
X
7.56%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:15849940
q90.EXT
N2−RIAILs
CB−RIAILs
NIL
a
b
c
b
N2
CB4856
ECA241
ECA240
Chr IV
Genome

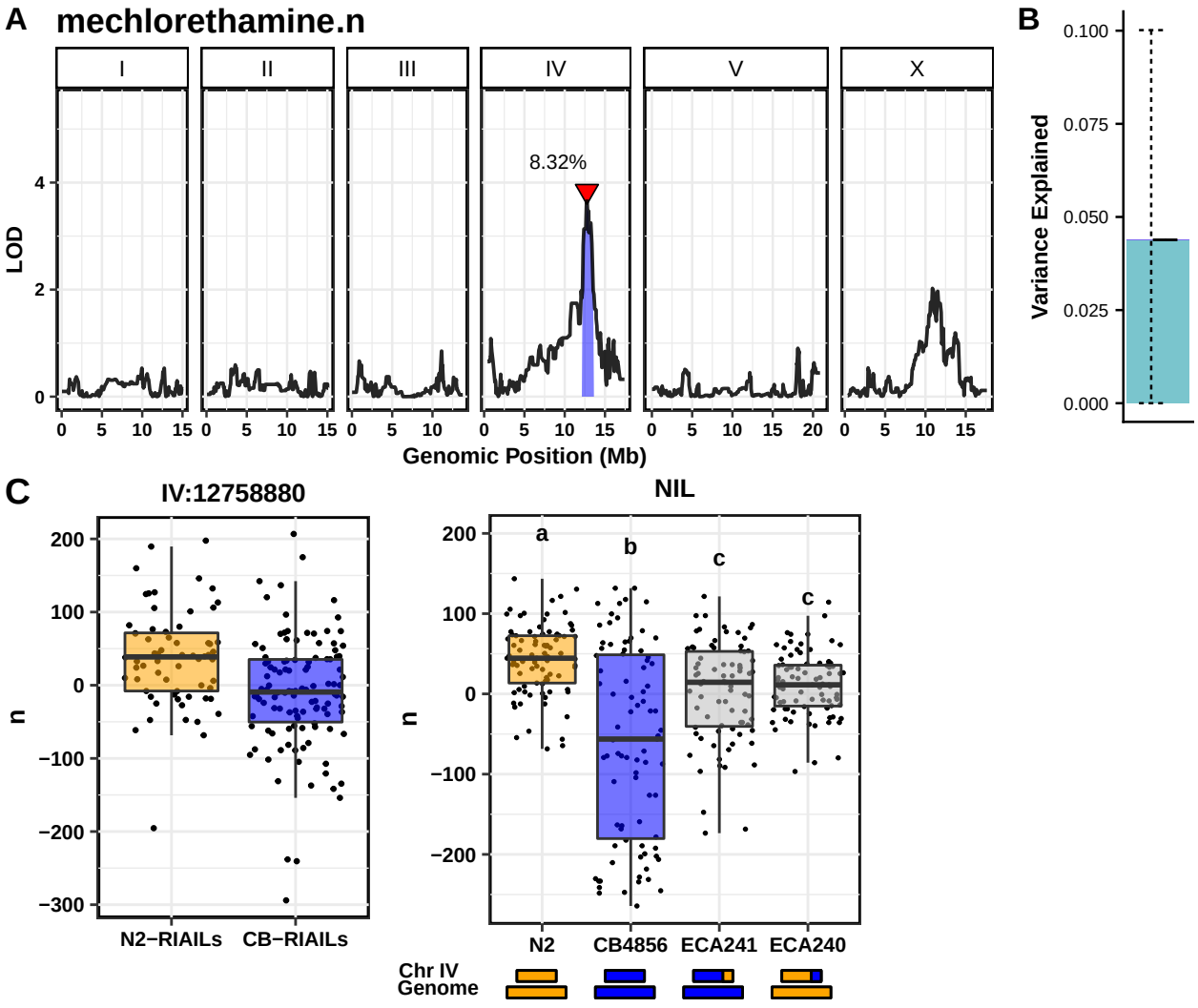

A
irinotecan.q90.norm.EXT
I
II
III
IV
V
X
9.53%
LOD
7.5
5.0
2.5
0.0
0 5 10 15
0 5 10 15
0 5 10
0 5 10 15
0 5 10 15 20
0 5 10 15
Genomic Position (Mb)
B
Variance Explained
0.4
0.2
0.0
C
I:1079163
q90.norm.EXT
0.5
0.0
−0.5
−1.0
N2−RIAILs
CB−RIAILs

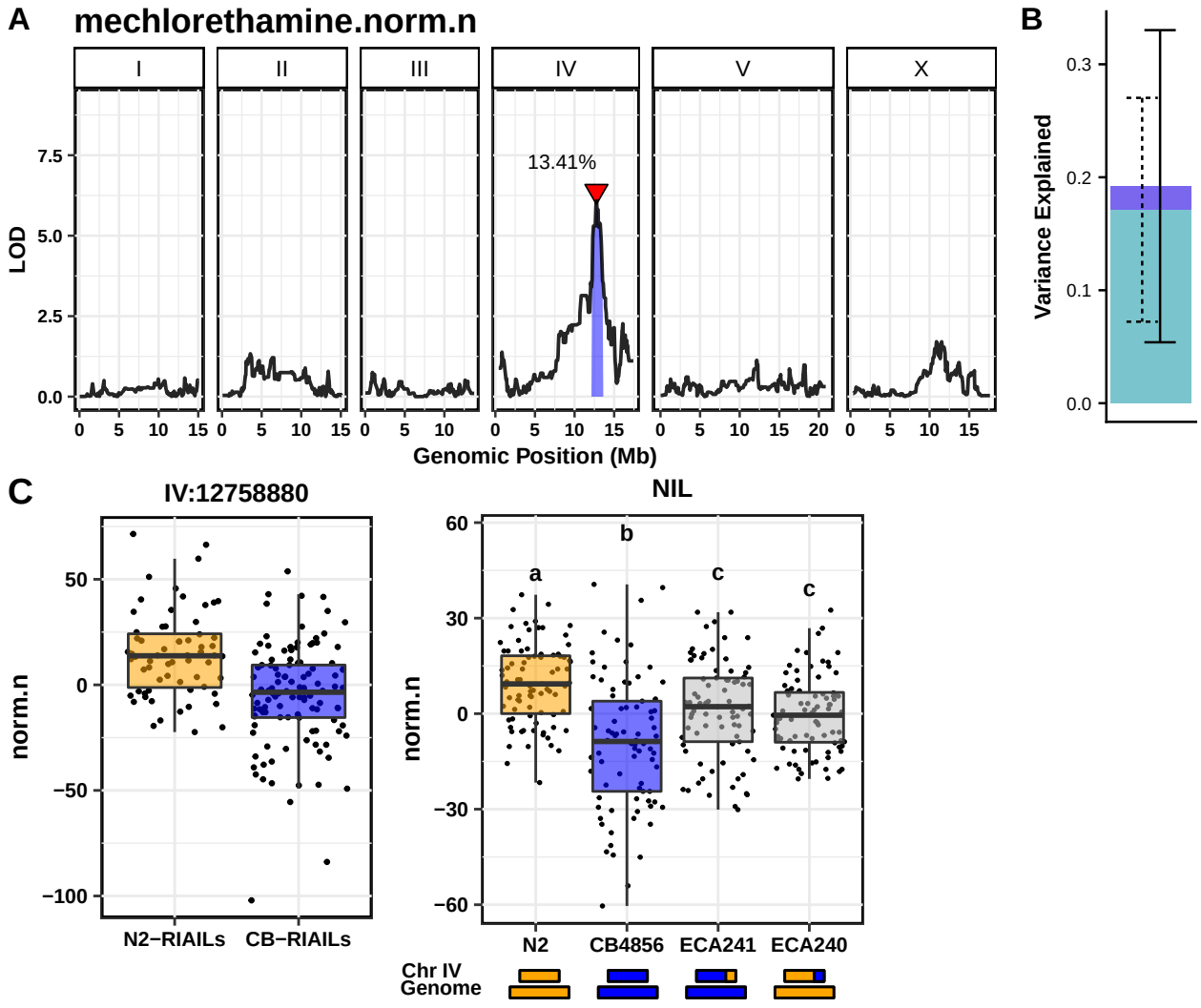

A
irinotecan.q90.TOF
I
II
III
IV
V
X
5.68%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:15849940
q90.TOF
N2−RIAILs
CB−RIAILs
NIL
a
b
c
b
N2
CB4856
ECA241
ECA240
Chr IV
Genome

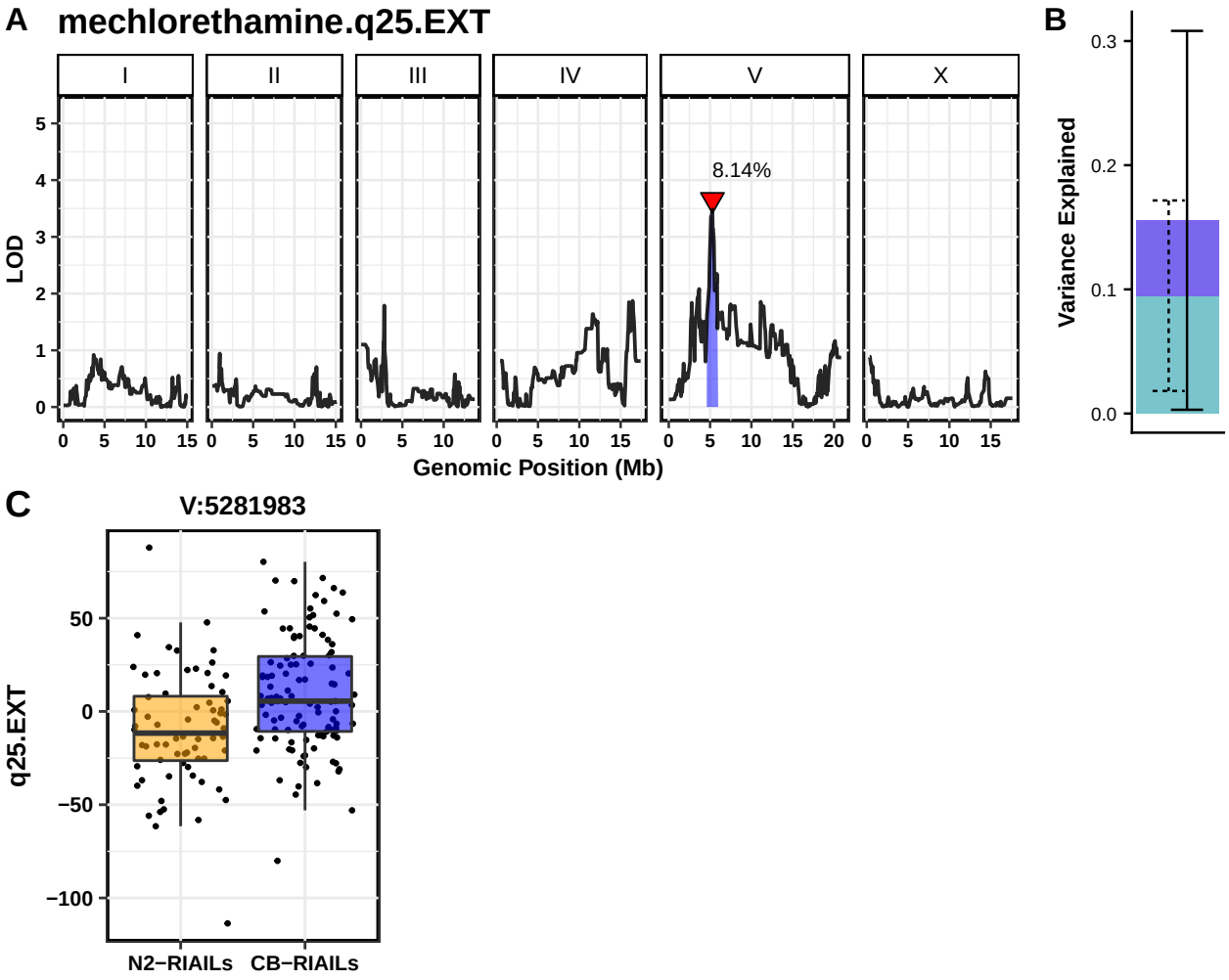

A
irinotecan.var.EXT
I
II
III
IV
V
X
6.91%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:15731760
var.EXT
N2−RIAILs
CB−RIAILs
NIL
a
b
ab
ab
N2
CB4856
ECA241
ECA240
Chr IV
Genome

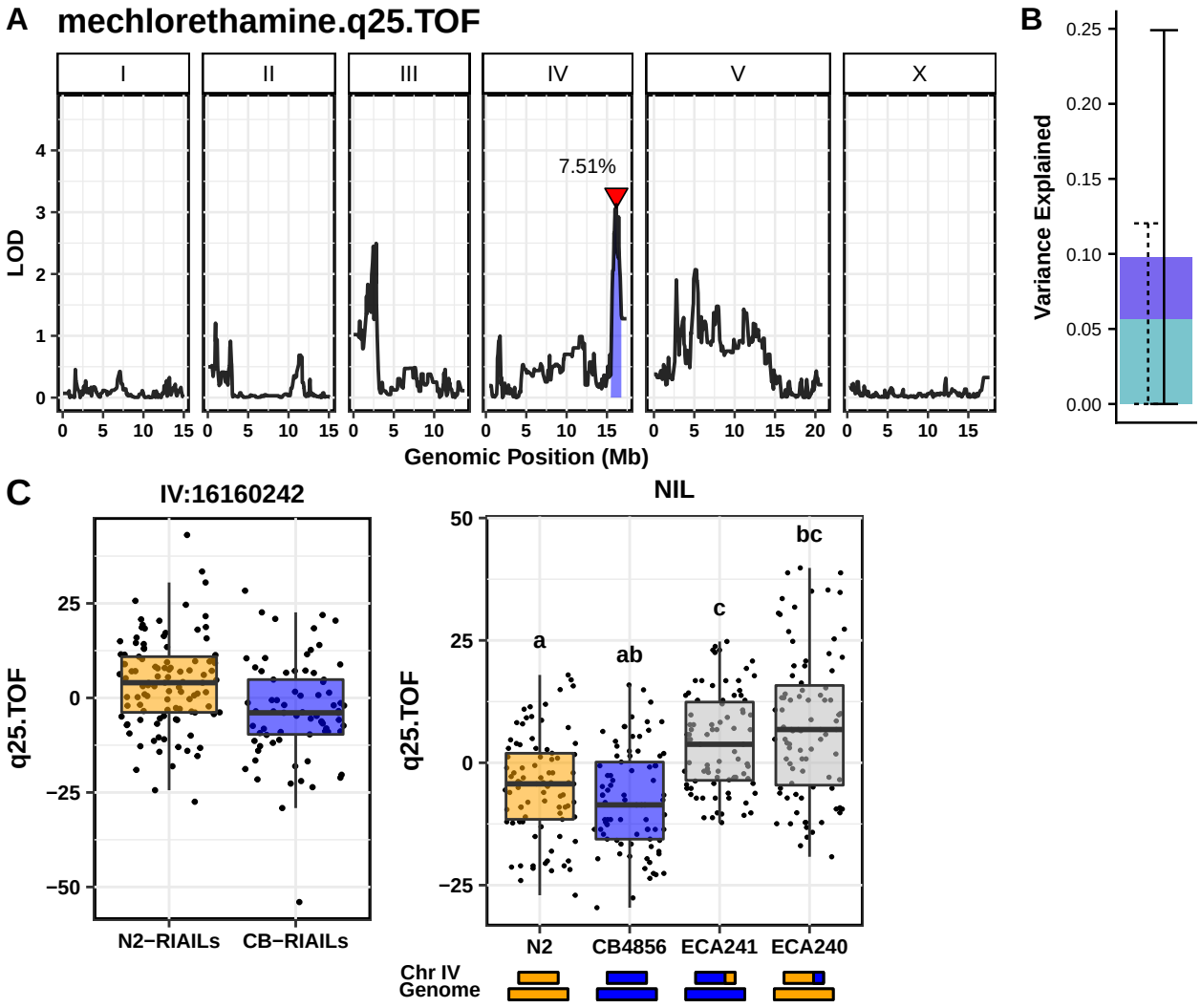

A
irinotecan.var.TOF
I
II
III
IV
V
X
LOD
9.52%
Genomic Position (Mb)
B
Variance Explained
C
IV:15849940
var.TOF
N2−RIAILs
CB−RIAILs
NIL
a
b
ab
ab
N2
CB4856
ECA241
ECA240
Chr IV
Genome

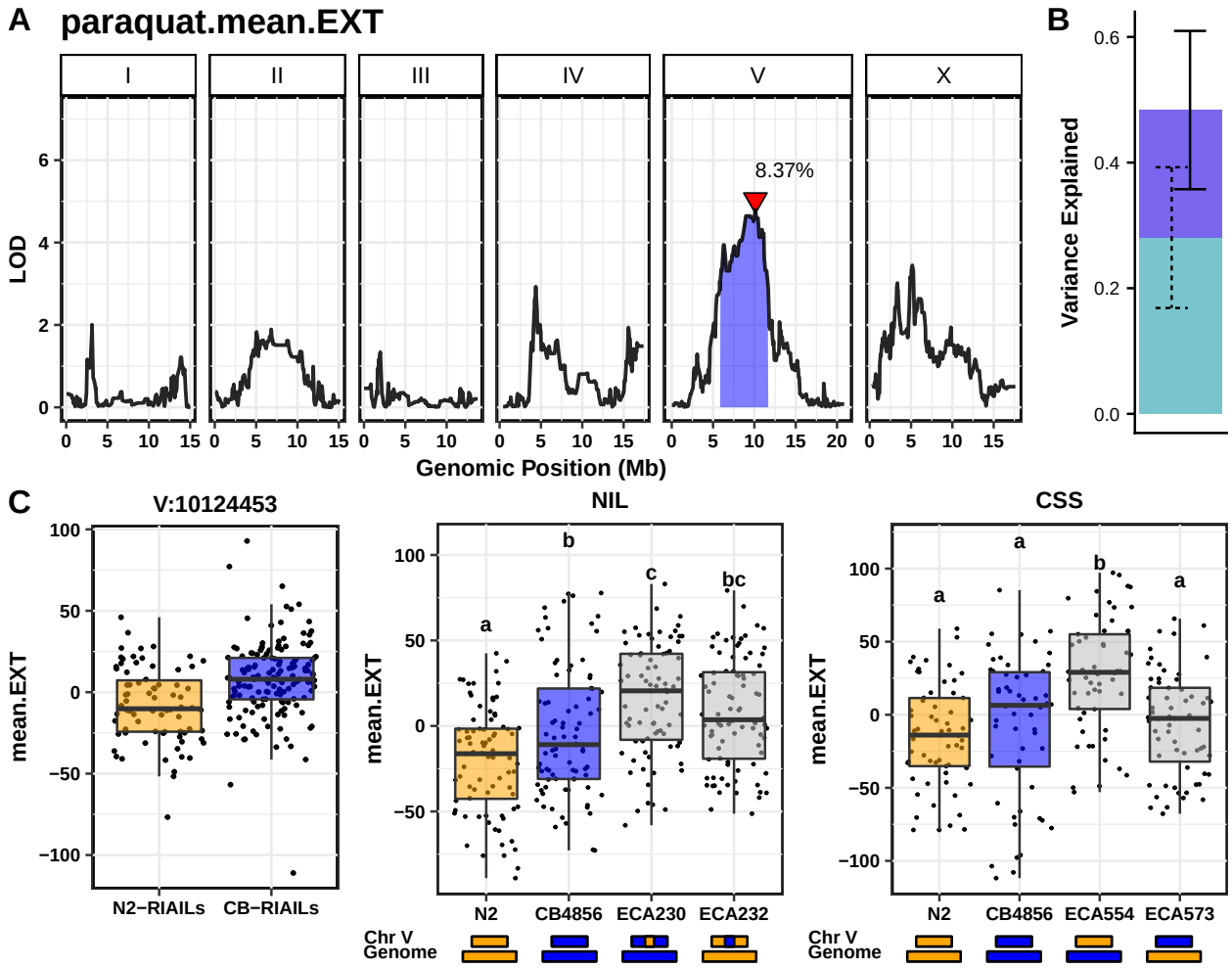

A
mechlorethamine.median.TOF
I
II
III
IV
V
X
7.42%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:16442619
median.TOF
N2−RIAILs
CB−RIAILs
NIL
a
b
ac
c
N2
CB4856
ECA241
ECA240
Chr IV
Genome

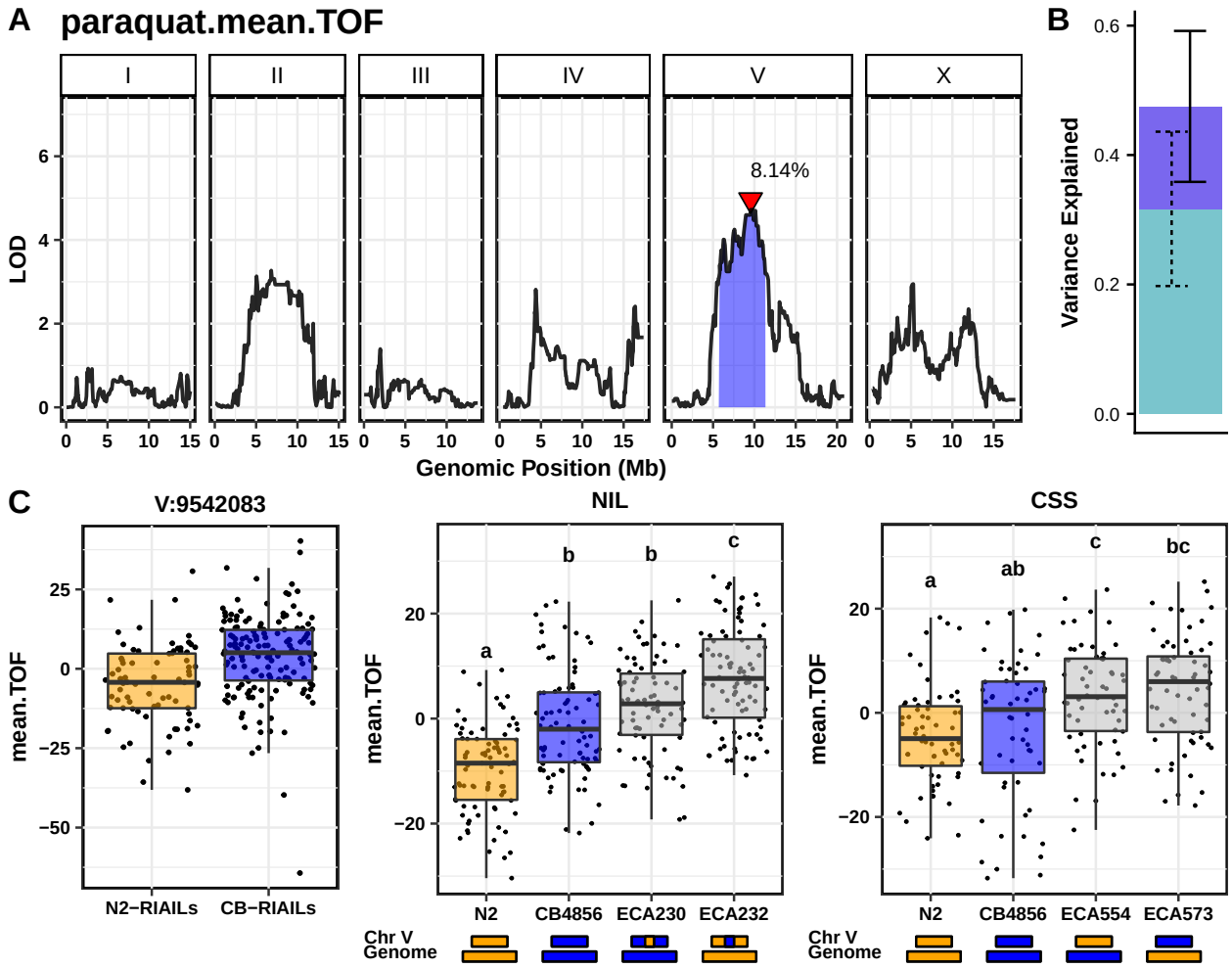

A
mechlorethamine.n
I
II
III
IV
V
X
8.32%
LOD
Genomic Position (Mb)
B
Variance Explained
0.100
0.075
0.050
0.025
0.000
C
IV:12758880
n
N2−RIAILs
CB−RIAILs
NIL
a
b
c
c
N2
CB4856
ECA241
ECA240
Chr IV
Genome

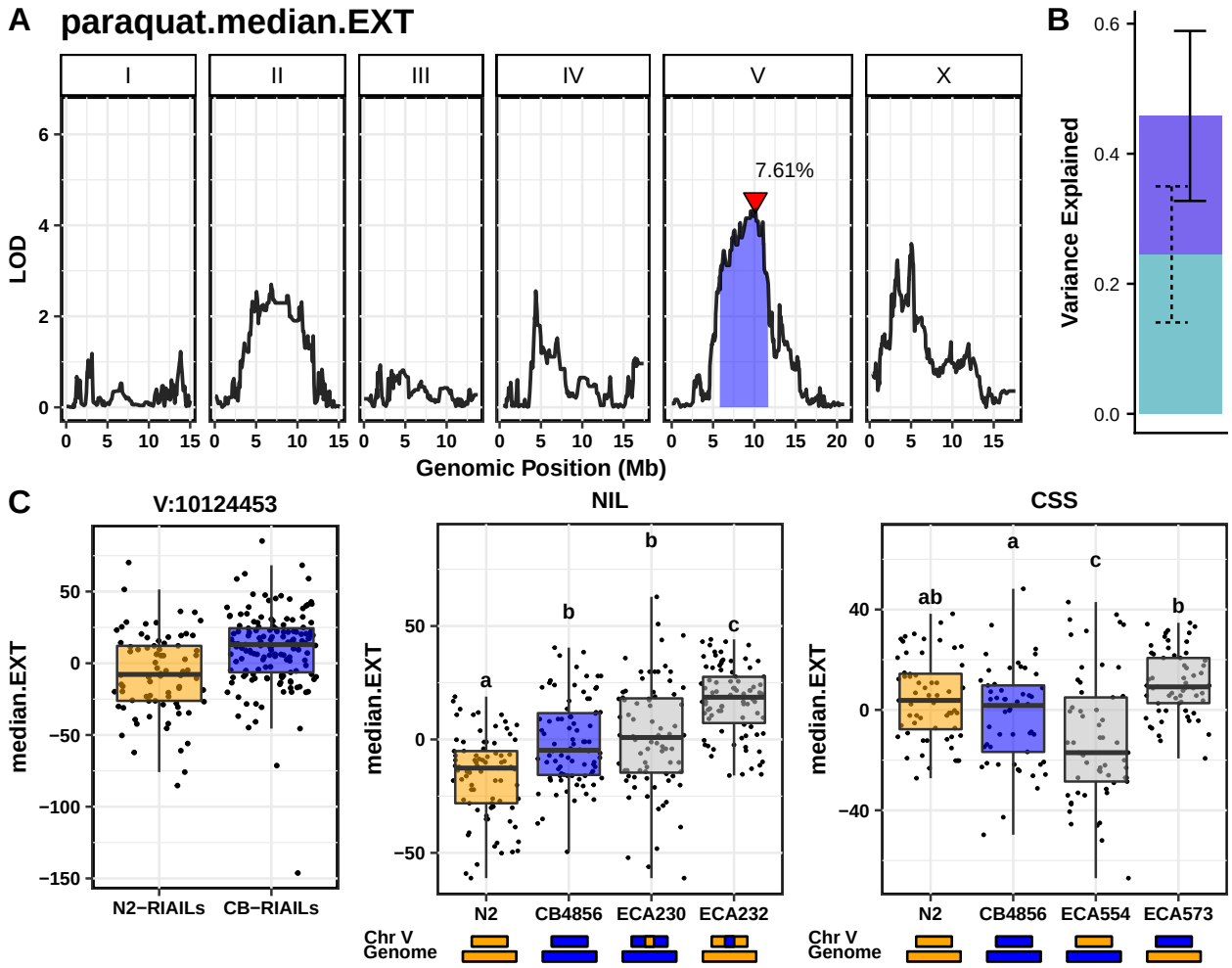

A
mechlorethamine.norm.n
I
II
III
IV
V
X
LOD
7.5
5.0
2.5
0.0
13.41%
0 5 10 15
0 5 10 15
0 5 10
0 5 10 15
0 5 10 15 20
0 5 10 15
Genomic Position (Mb)
B
Variance Explained
0.3
0.2
0.1
0.0
C
IV:12758880
norm.n
50
0
−50
−100
N2−RIAILs
CB−RIAILs
NIL
60
30
0
−30
−60
a
b
c
c
N2
CB4856
ECA241
ECA240
Chr IV
Genome

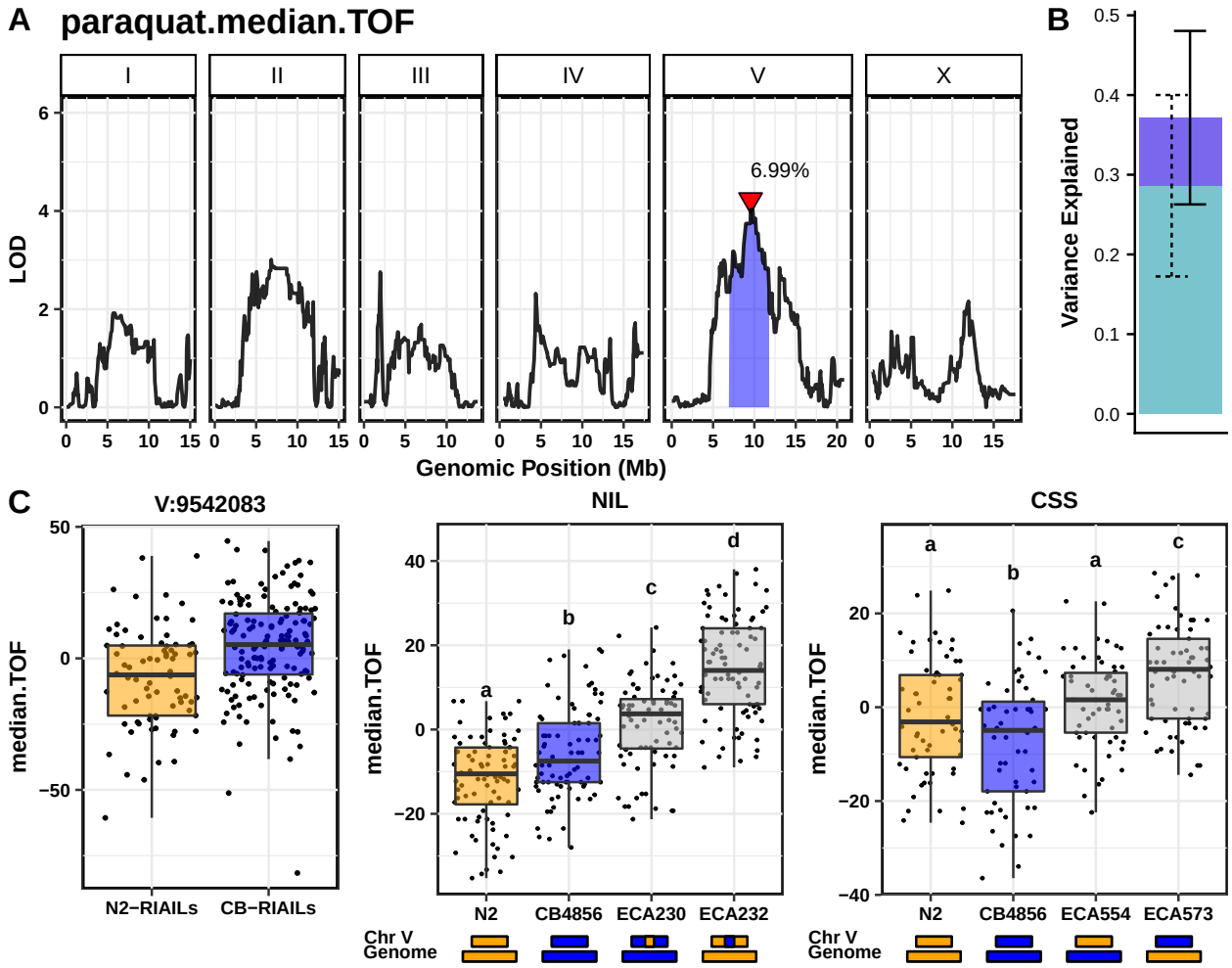

A
mechlorethamine.q25.EXT
I
II
III
IV
V
X
8.14%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:5281983
q25.EXT
N2−RIAILs
CB−RIAILs

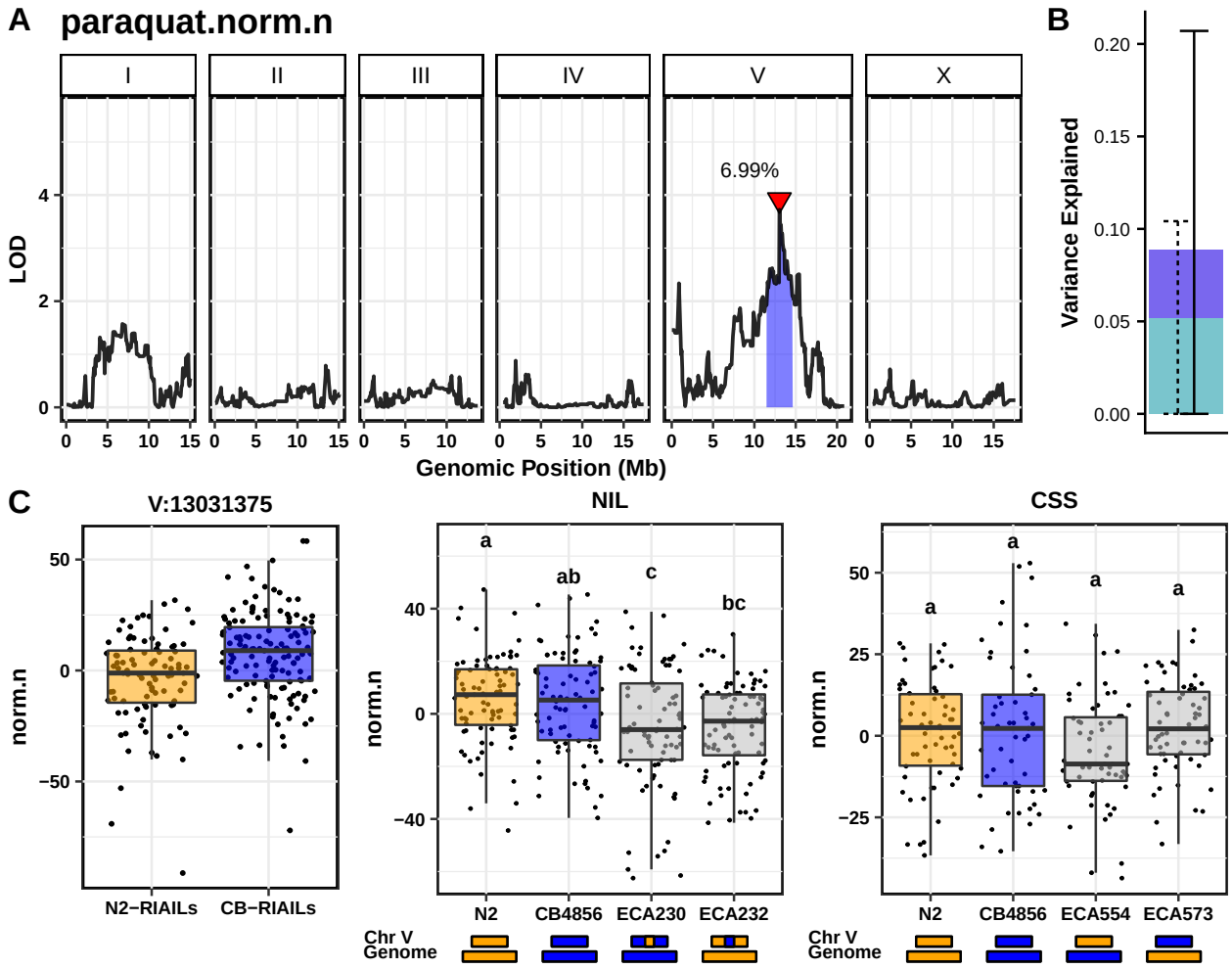

A
mechlorethamine.q25.TOF
I
II
III
IV
V
X
7.51%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:16160242
q25.TOF
N2−RIAILs
CB−RIAILs
NIL
a
ab
c
bc
N2
CB4856
ECA241
ECA240
Chr IV
Genome

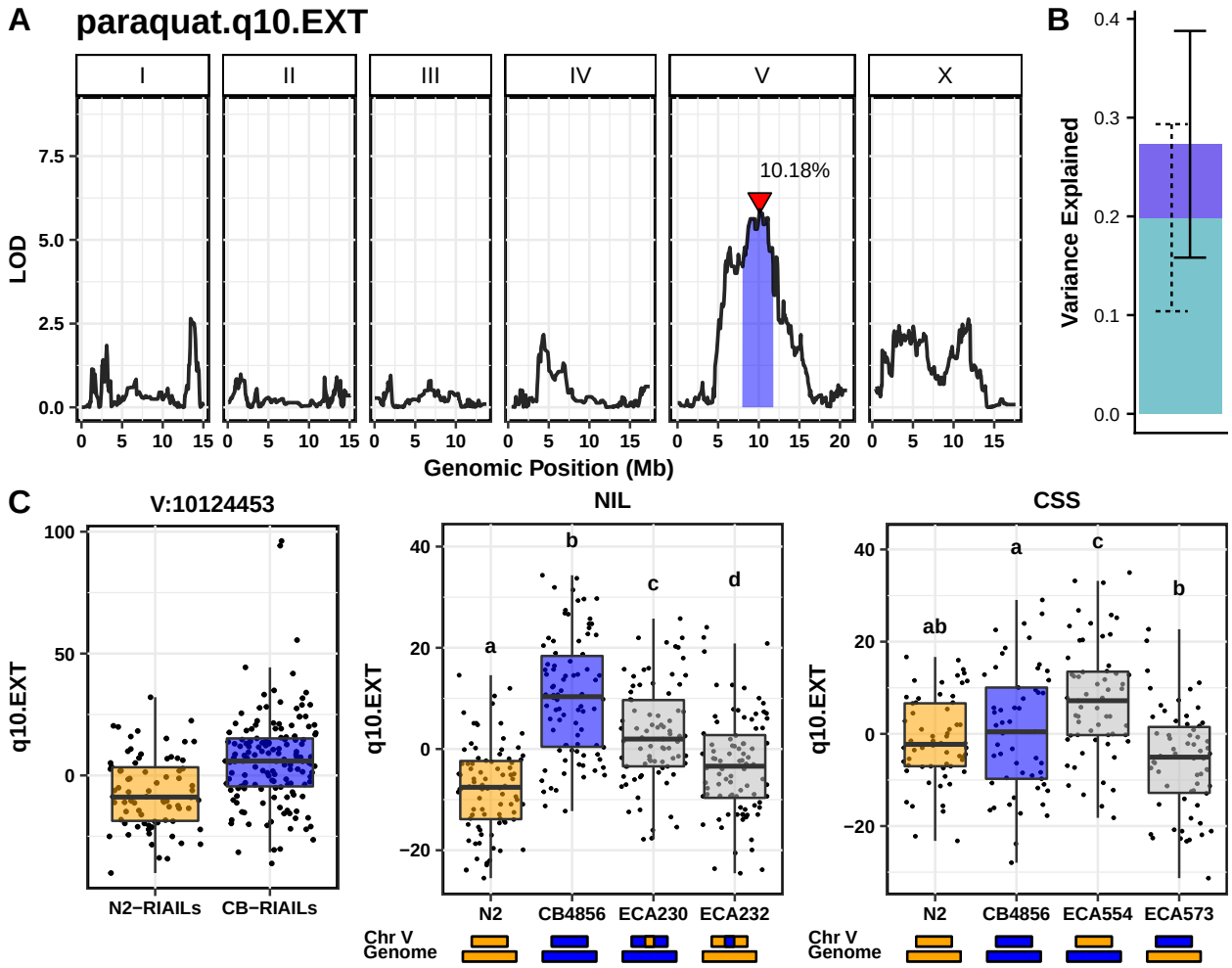

A
paraquat.mean.EXT
I
II
III
IV
V
X
8.37%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:10124453
mean.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573

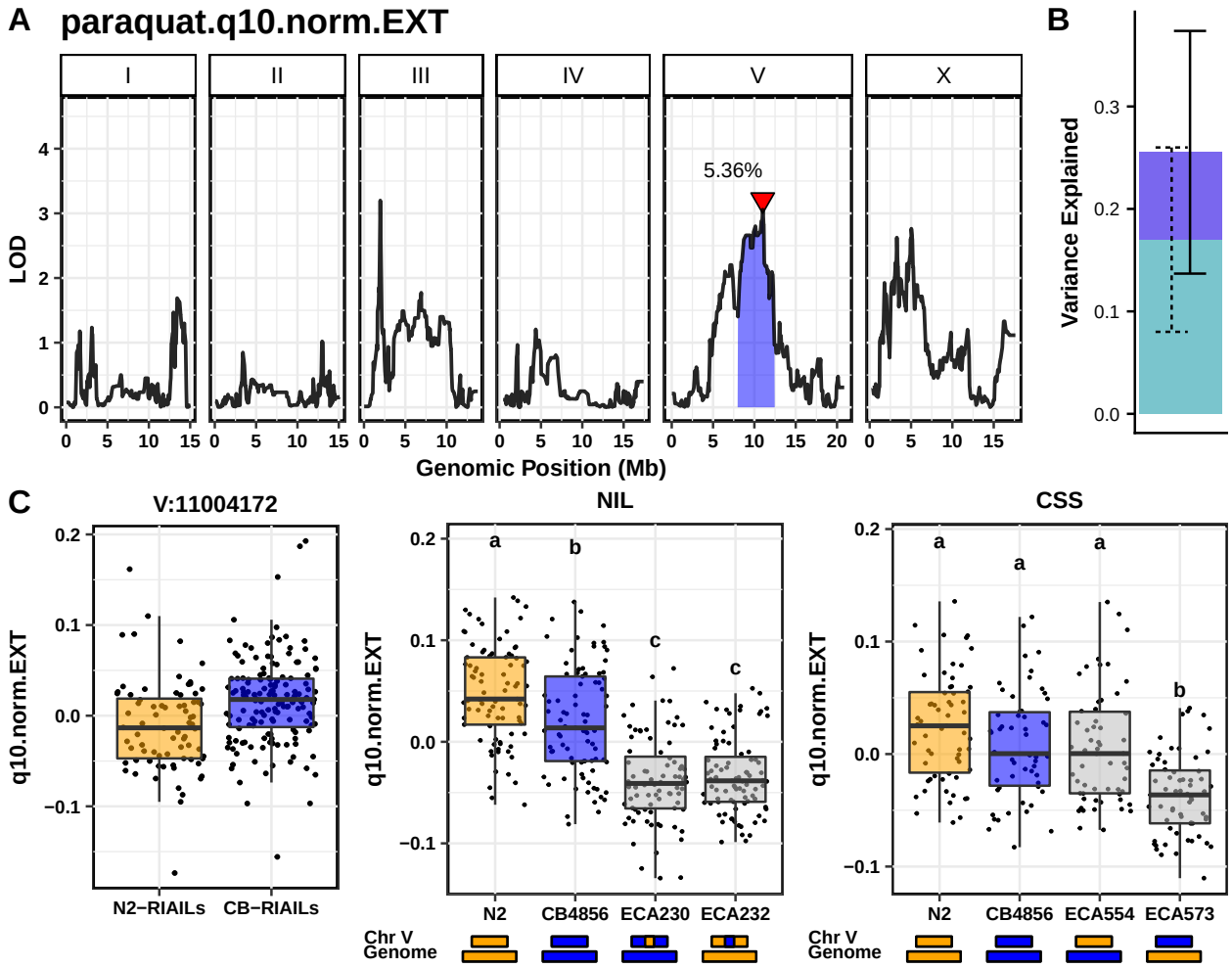

A
paraquat.mean.TOF
I
II
III
IV
V
X
LOD
8.14%
Genomic Position (Mb)
B
Variance Explained
C
V:9542083
mean.TOF
N2−RIAILs
CB−RIAILs
NIL
a
b
b
c
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
a
ab
c
bc
N2
CB4856
ECA554
ECA573
Chr V Genome

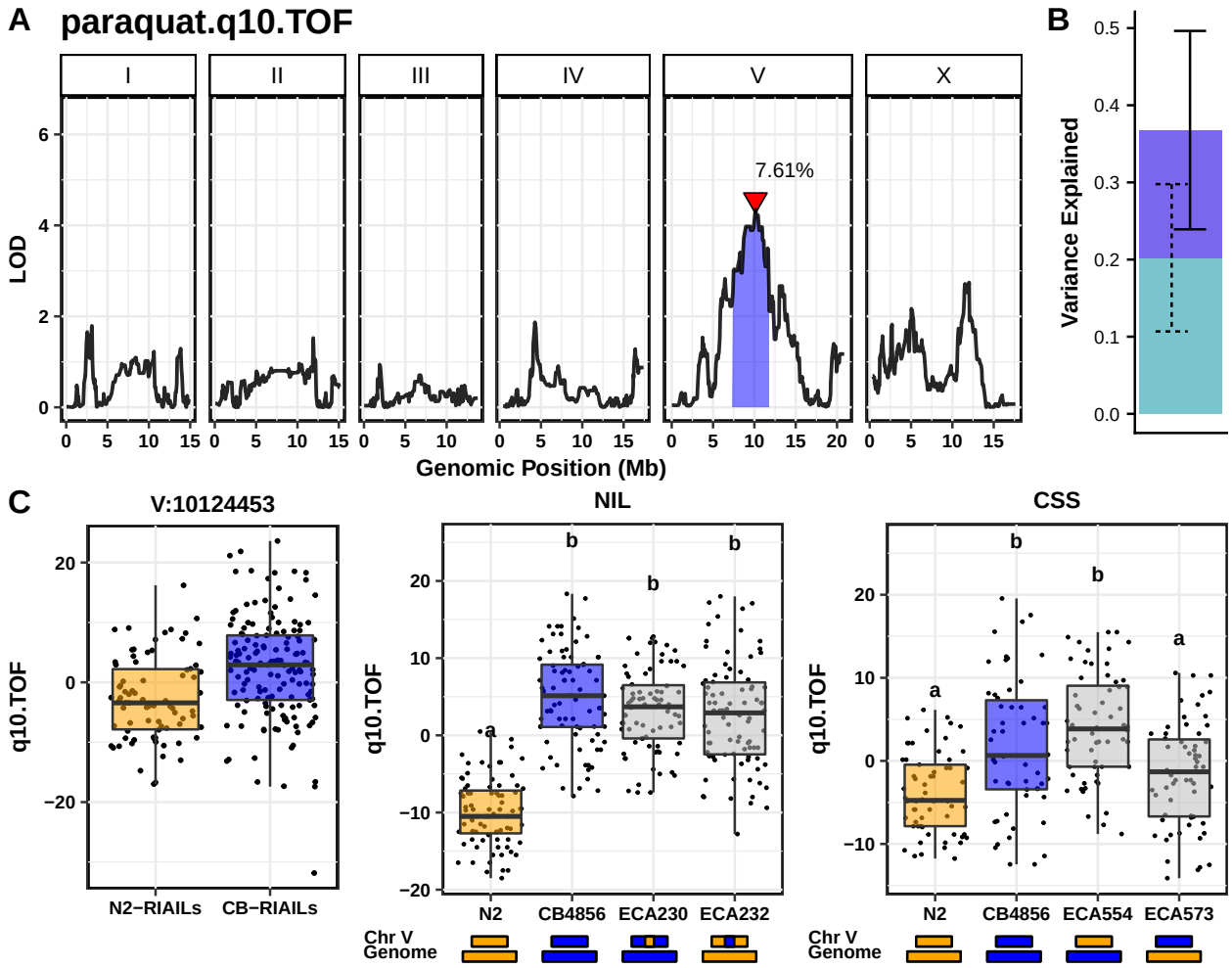

A
paraquat.median.EXT
I
II
III
IV
V
X
LOD
7.61%
Genomic Position (Mb)
B
Variance Explained
C
V:10124453
median.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
ECA554
ECA573

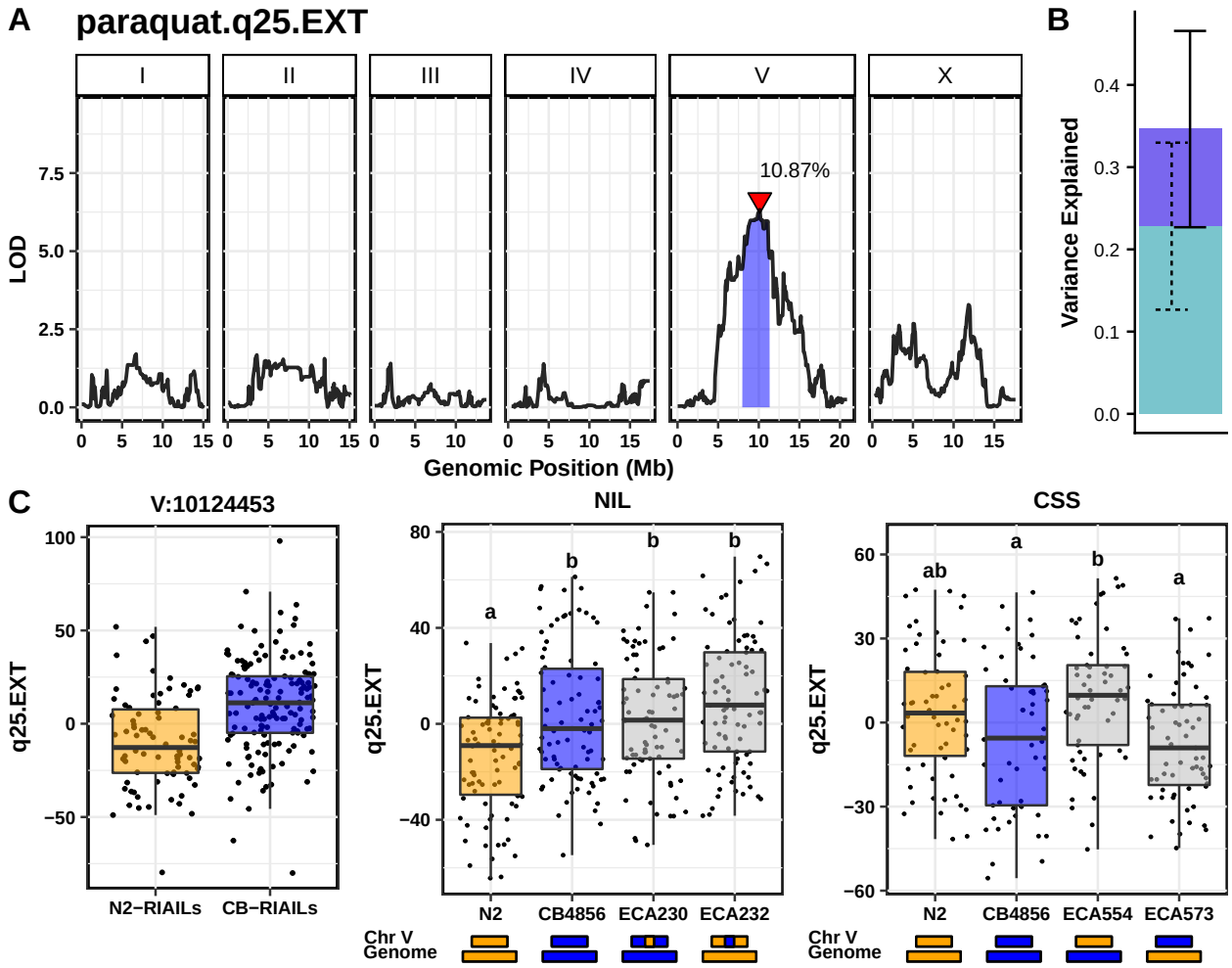

A
paraquat.median.TOF
I
II
III
IV
V
X
6.99%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:9542083
median.TOF
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

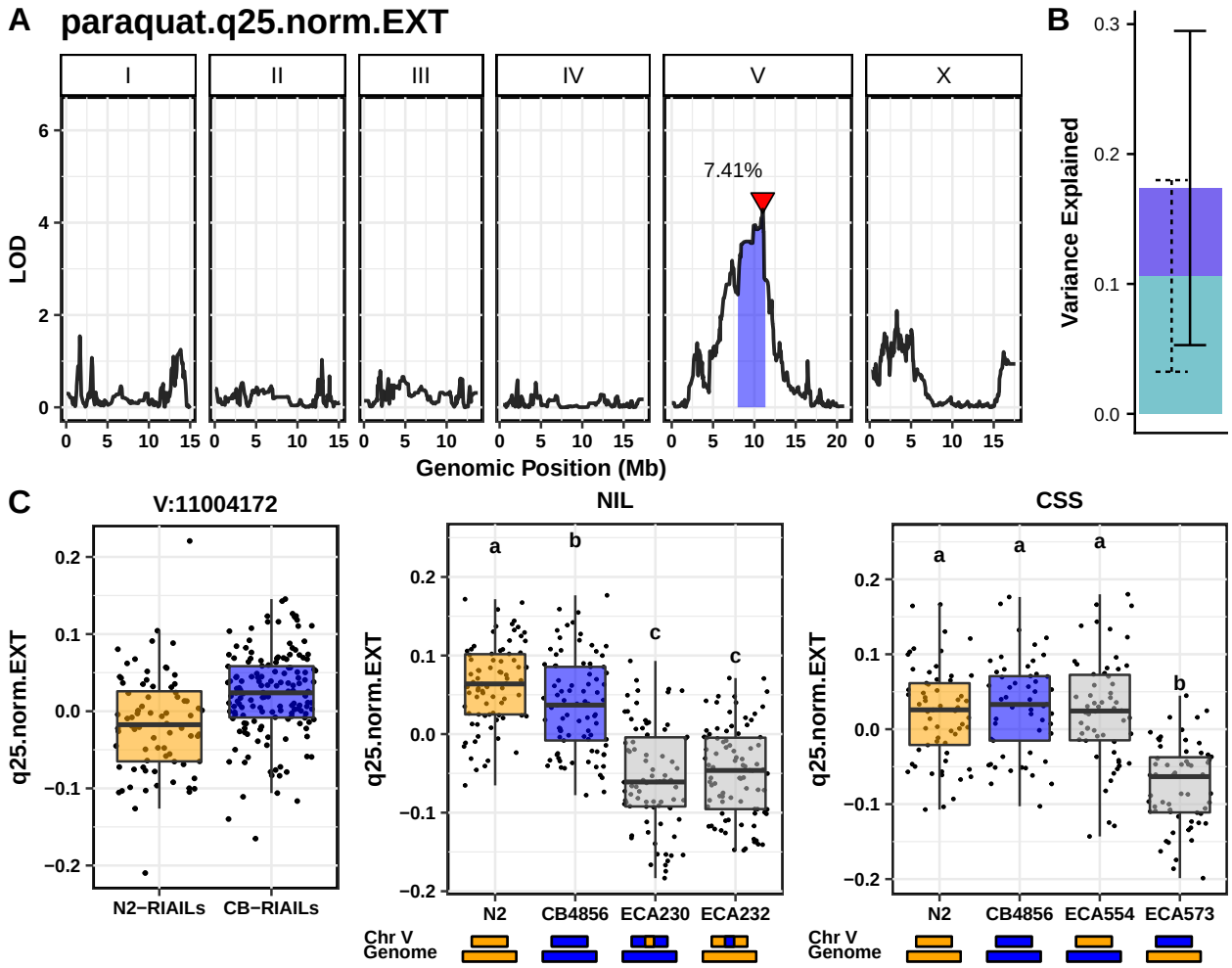

A
paraquat.norm.n
I
II
III
IV
V
X
6.99%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:13031375
norm.n
N2−RIAILs
CB−RIAILs
NIL
a
ab
c
bc
N2
CB4856
ECA230
ECA232
Chr V
Genome
CSS
a
a
a
a
N2
CB4856
ECA554
ECA573
Chr V
Genome

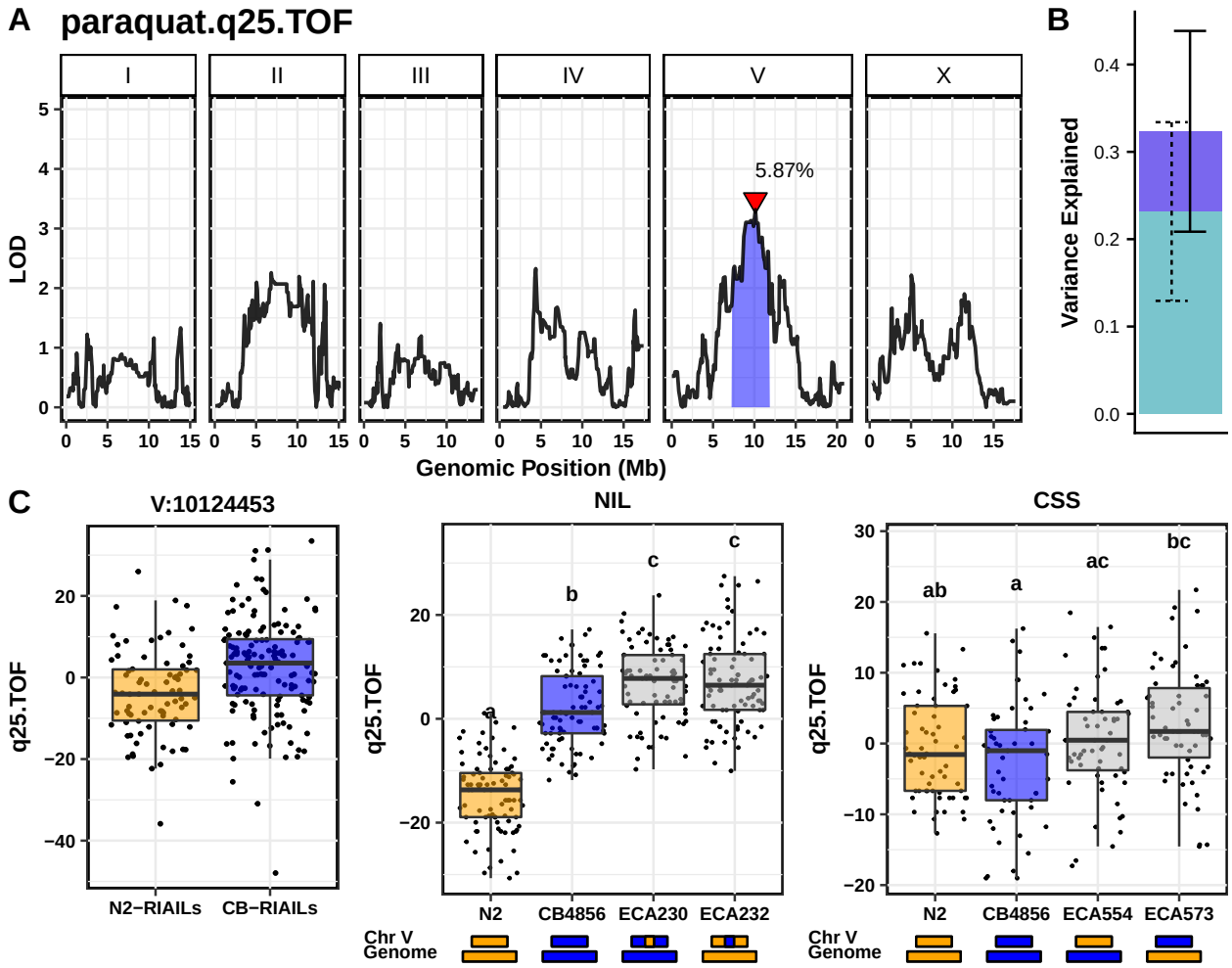

A
paraquat.q10.EXT
I
II
III
IV
V
X
LOD
10.18%
Genomic Position (Mb)
B
Variance Explained
C
V:10124453
q10.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

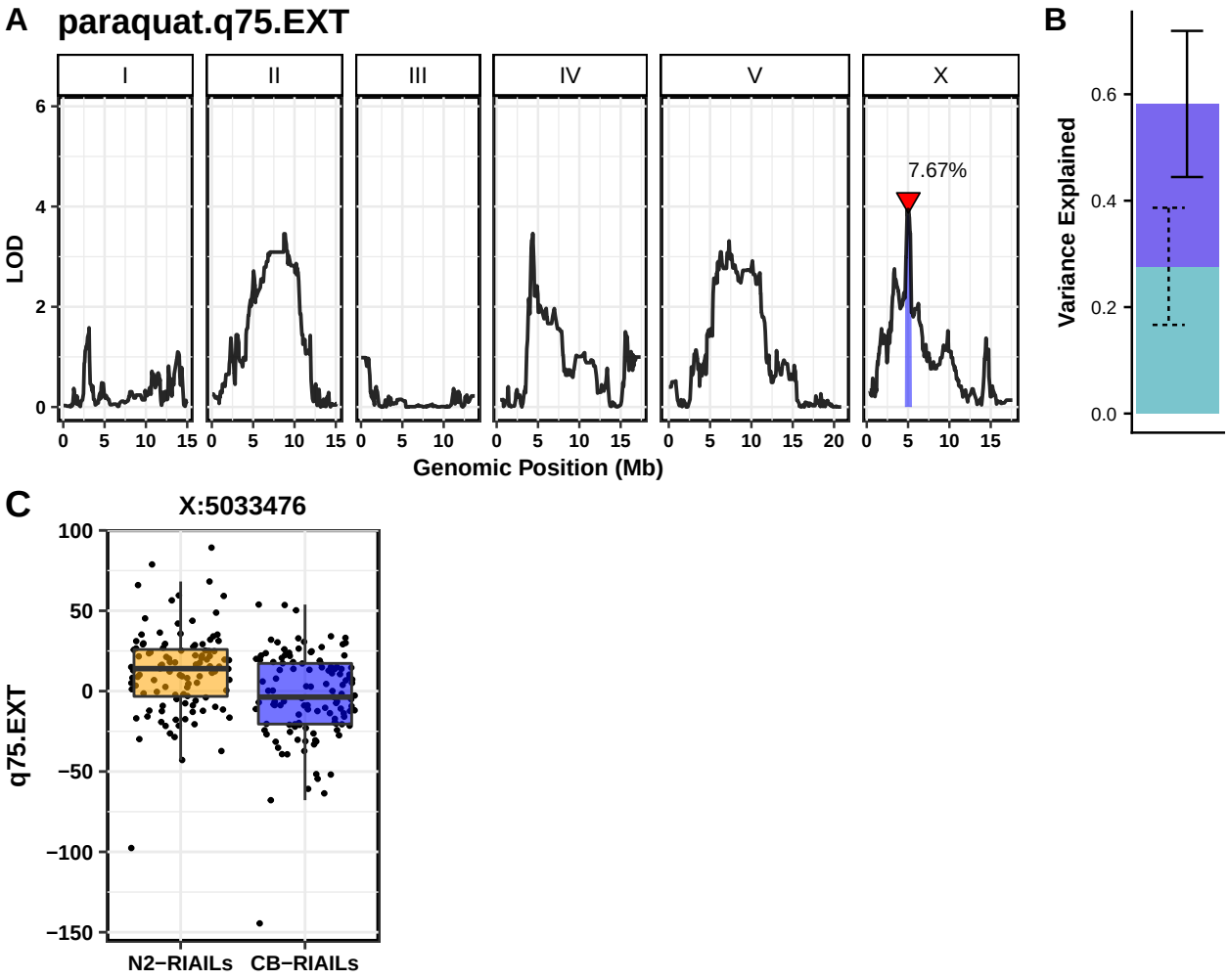

A
paraquat.q10.norm.EXT
I
II
III
IV
V
X
LOD
5.36%
Genomic Position (Mb)
B
Variance Explained
C
V:11004172
q10.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573

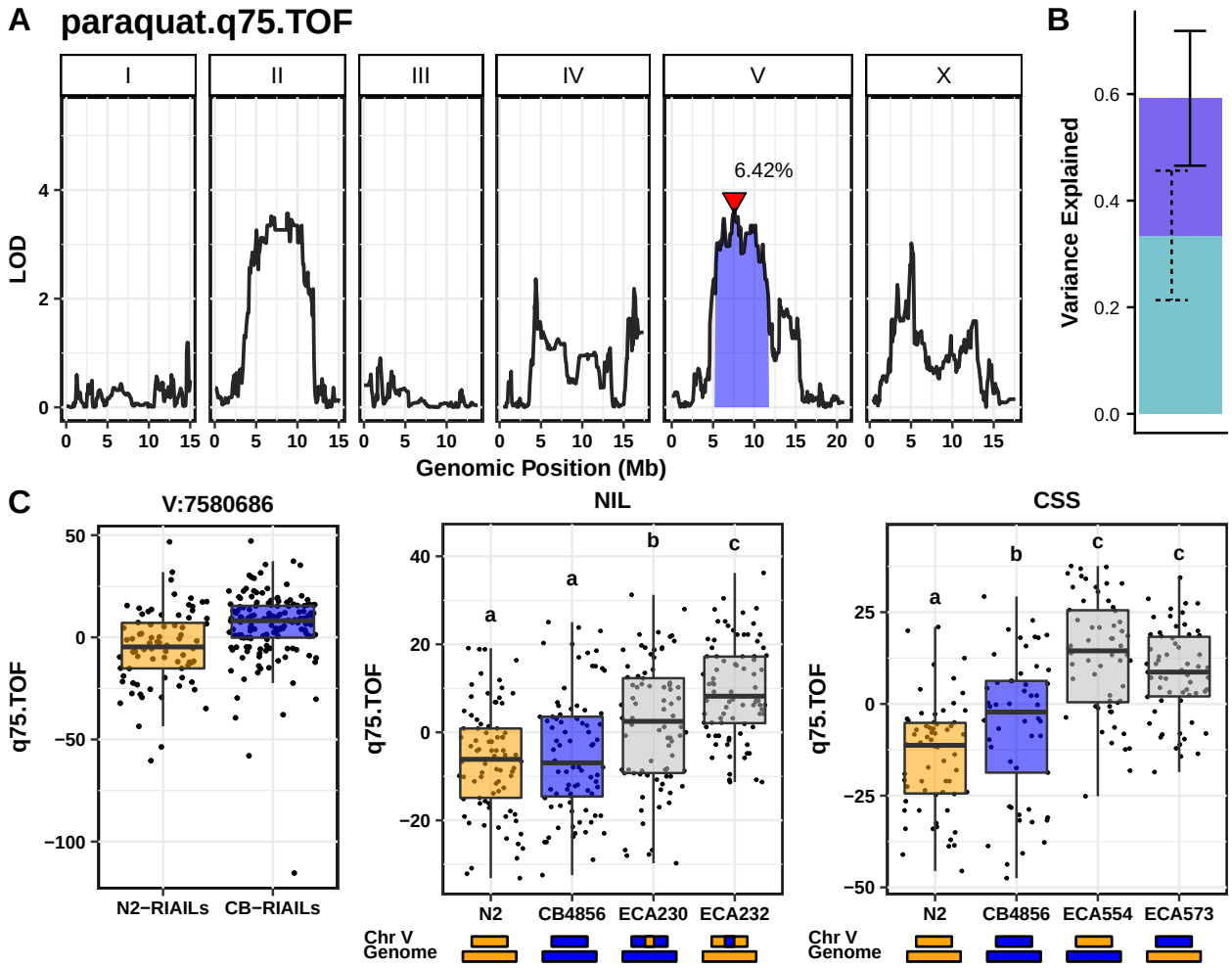

A
paraquat.q10.TOF
I
II
III
IV
V
X
LOD
7.61%
Genomic Position (Mb)
B
Variance Explained
C
V:10124453
q10.TOF
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

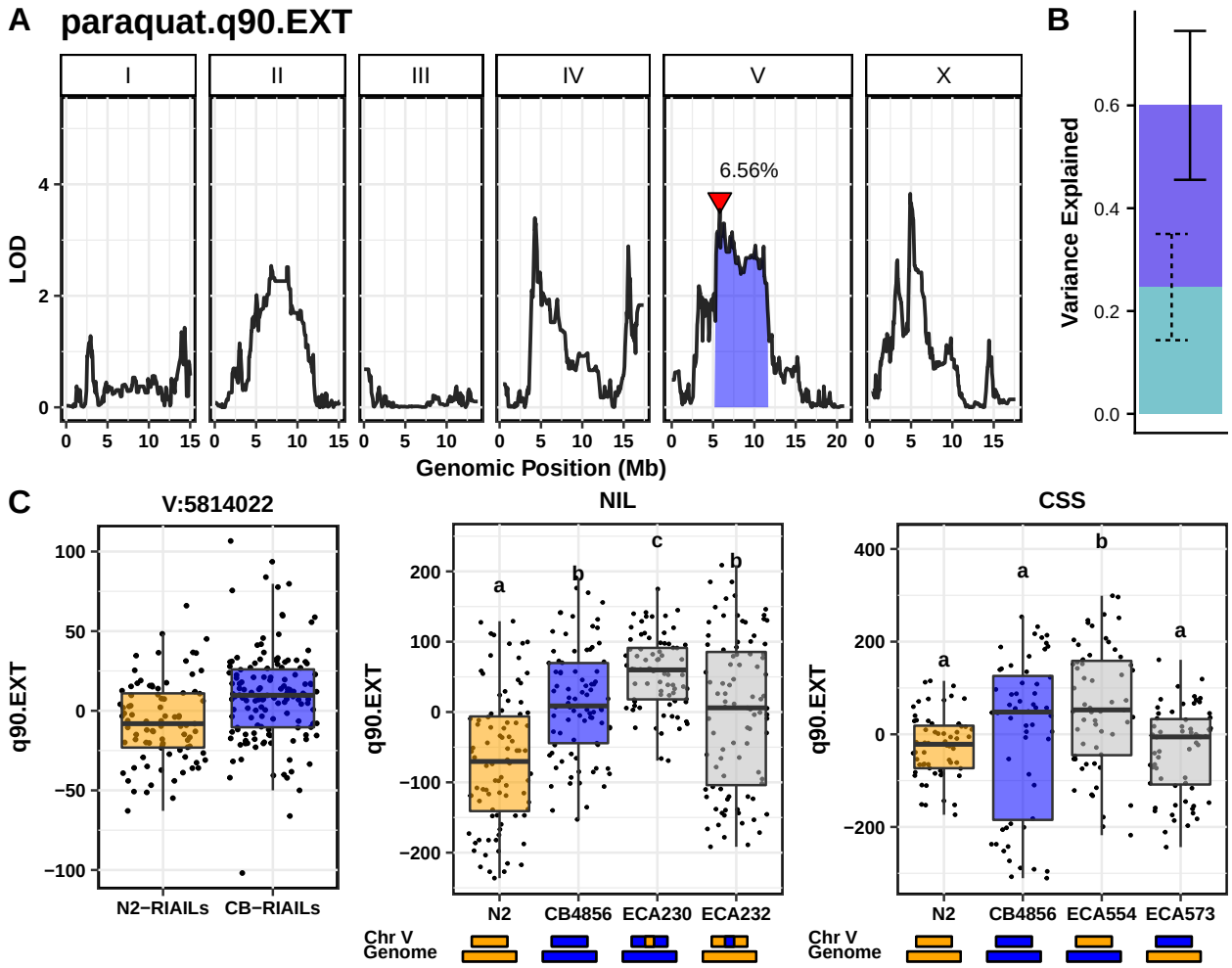

A
paraquat.q25.EXT
I
II
III
IV
V
X
10.87%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:10124453
q25.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

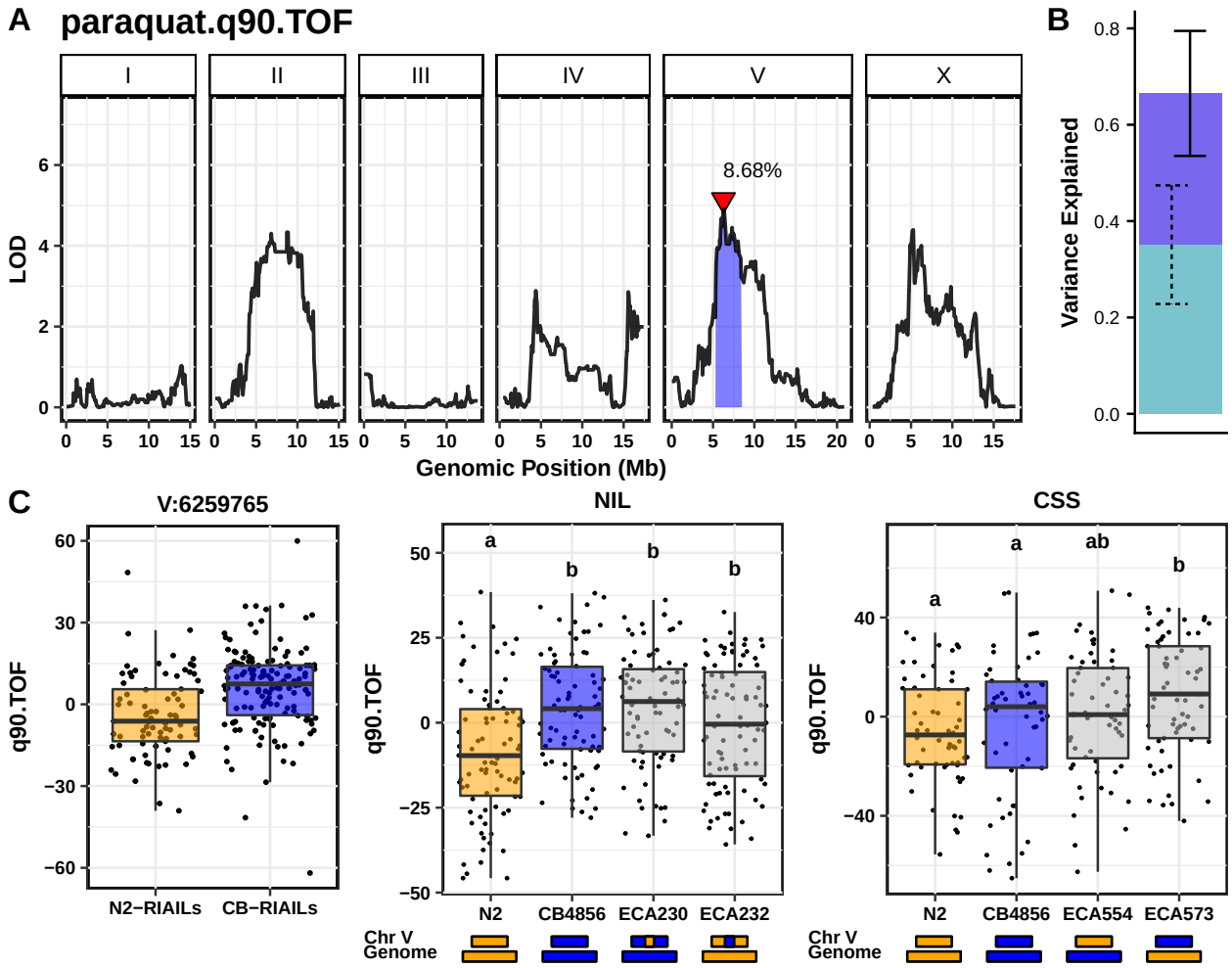

A
paraquat.q25.norm.EXT
I
II
III
IV
V
X
7.41%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:11004172
q25.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

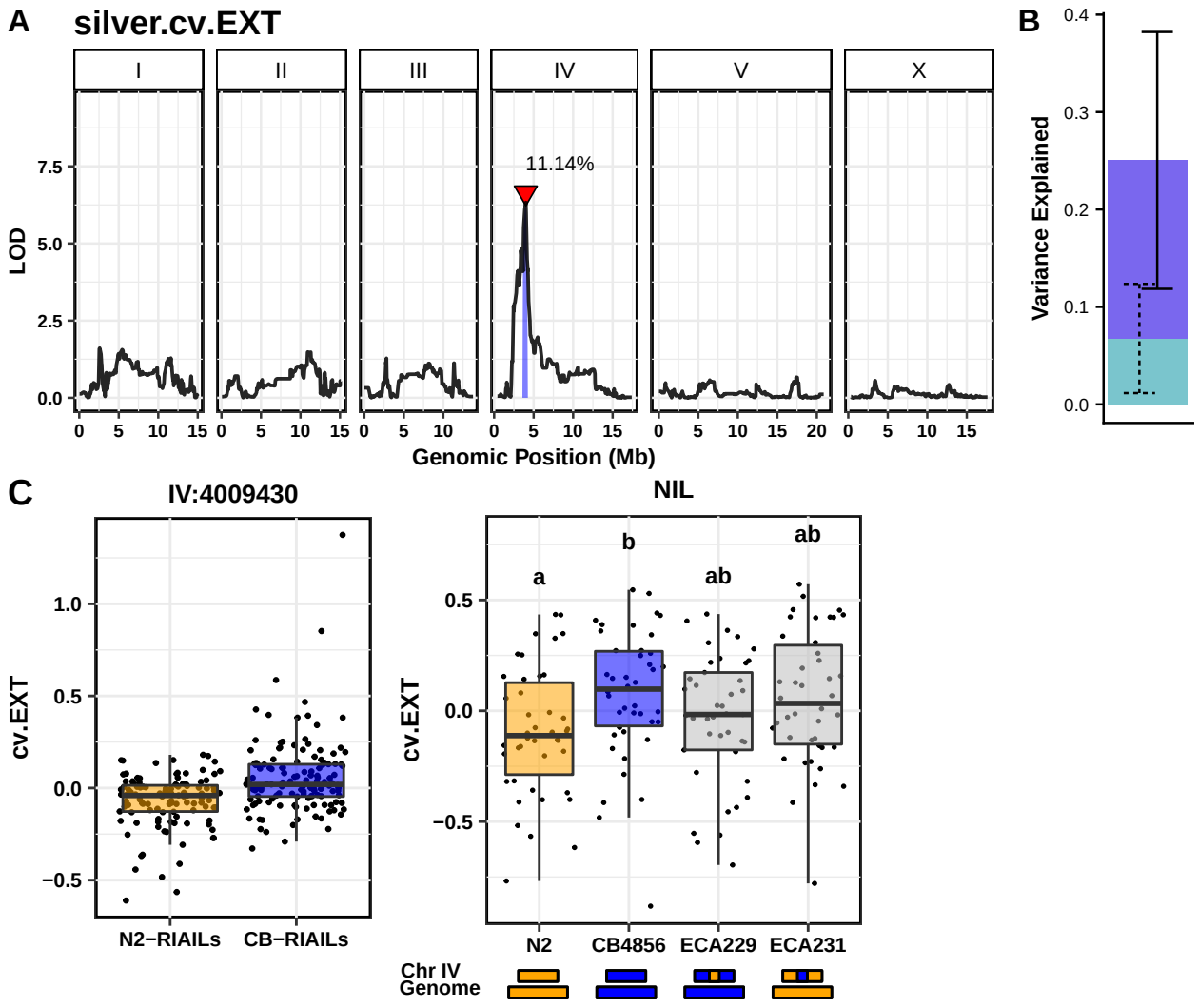

A
paraquat.q25.TOF
I
II
III
IV
V
X
5.87%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:10124453
q25.TOF
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
ab
a
ac
bc
ECA554
ECA573

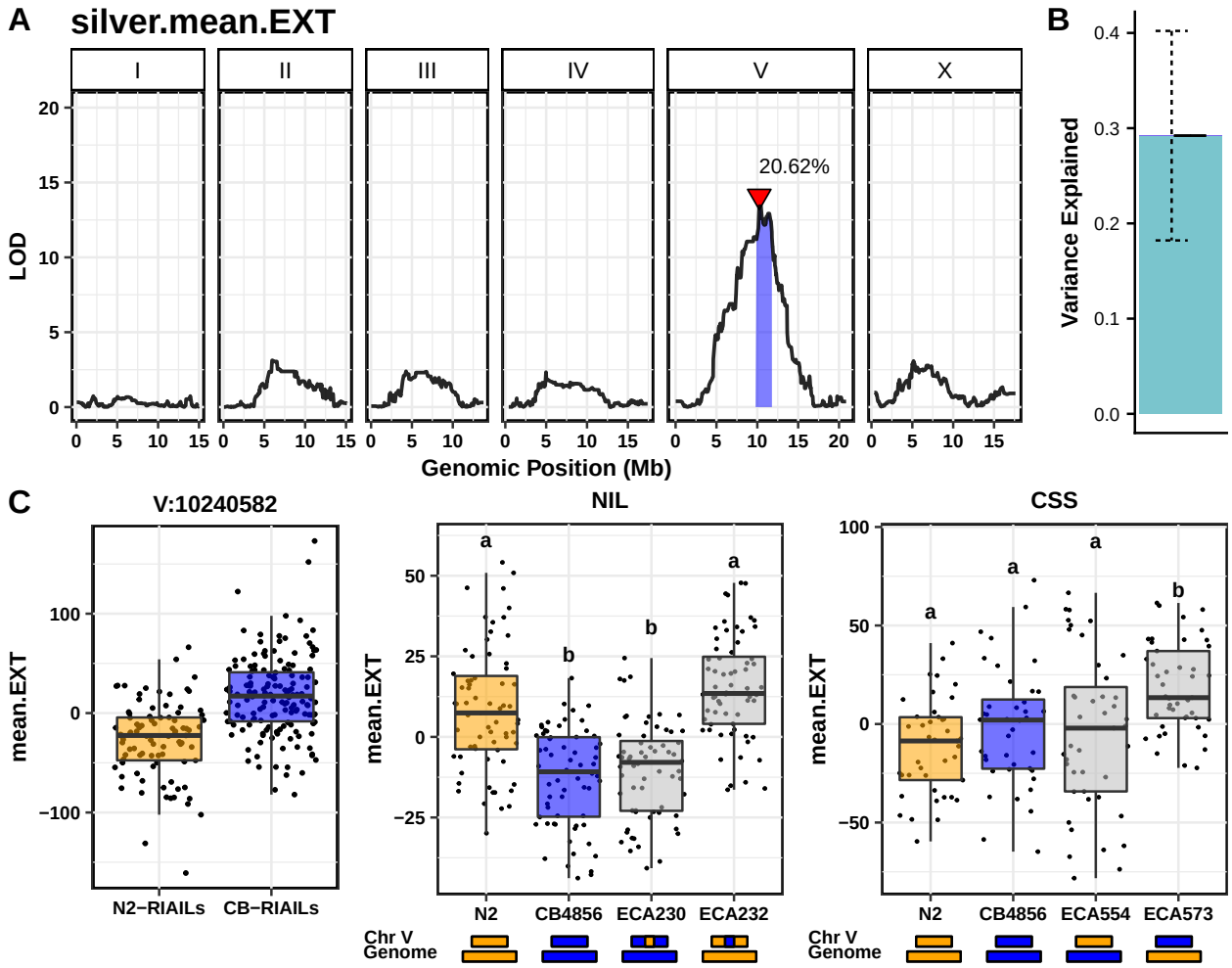

A
paraquat.q75.EXT
I
II
III
IV
V
X
LOD
7.67%
Genomic Position (Mb)
B
Variance Explained
C
X:5033476
q75.EXT
N2−RIAILs
CB−RIAILs

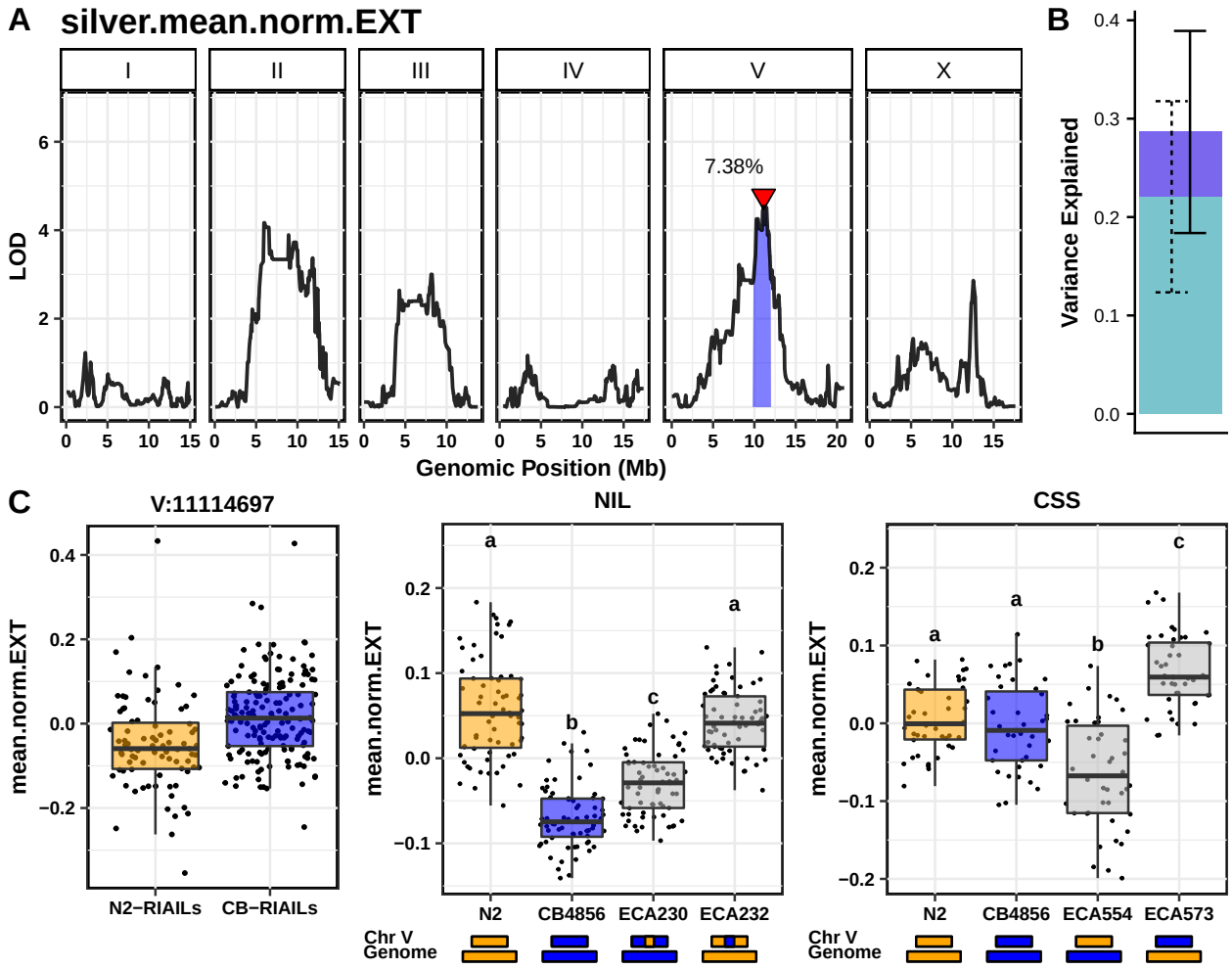

A
paraquat.q75.TOF
I
II
III
IV
V
X
6.42%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:7580686
q75.TOF
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
ECA554
ECA573

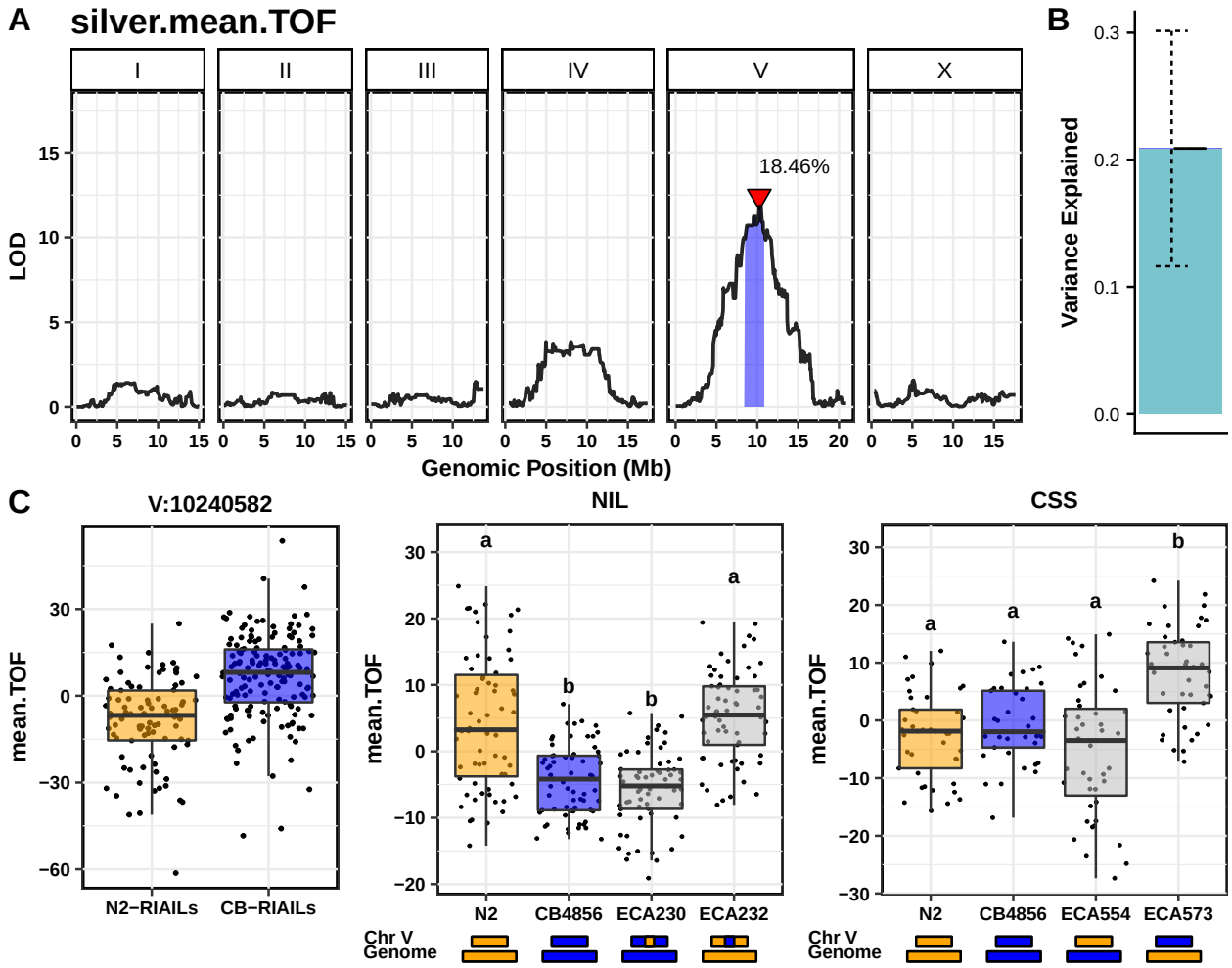

A
paraquat.q90.EXT
I
II
III
IV
V
X
6.56%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:5814022
q90.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

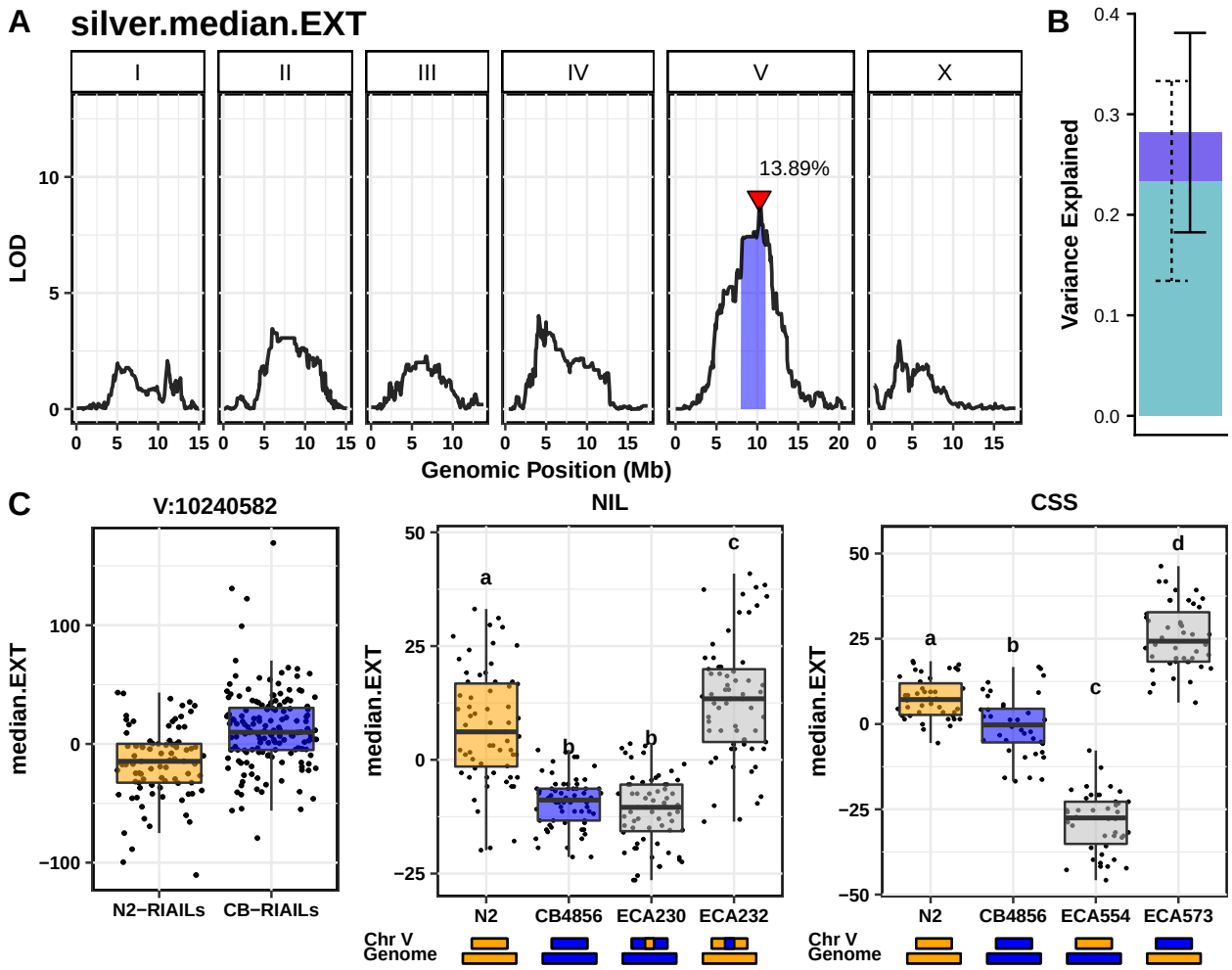

A
paraquat.q90.TOF
I
II
III
IV
V
X
8.68%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:6259765
q90.TOF
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
ECA554
ECA573

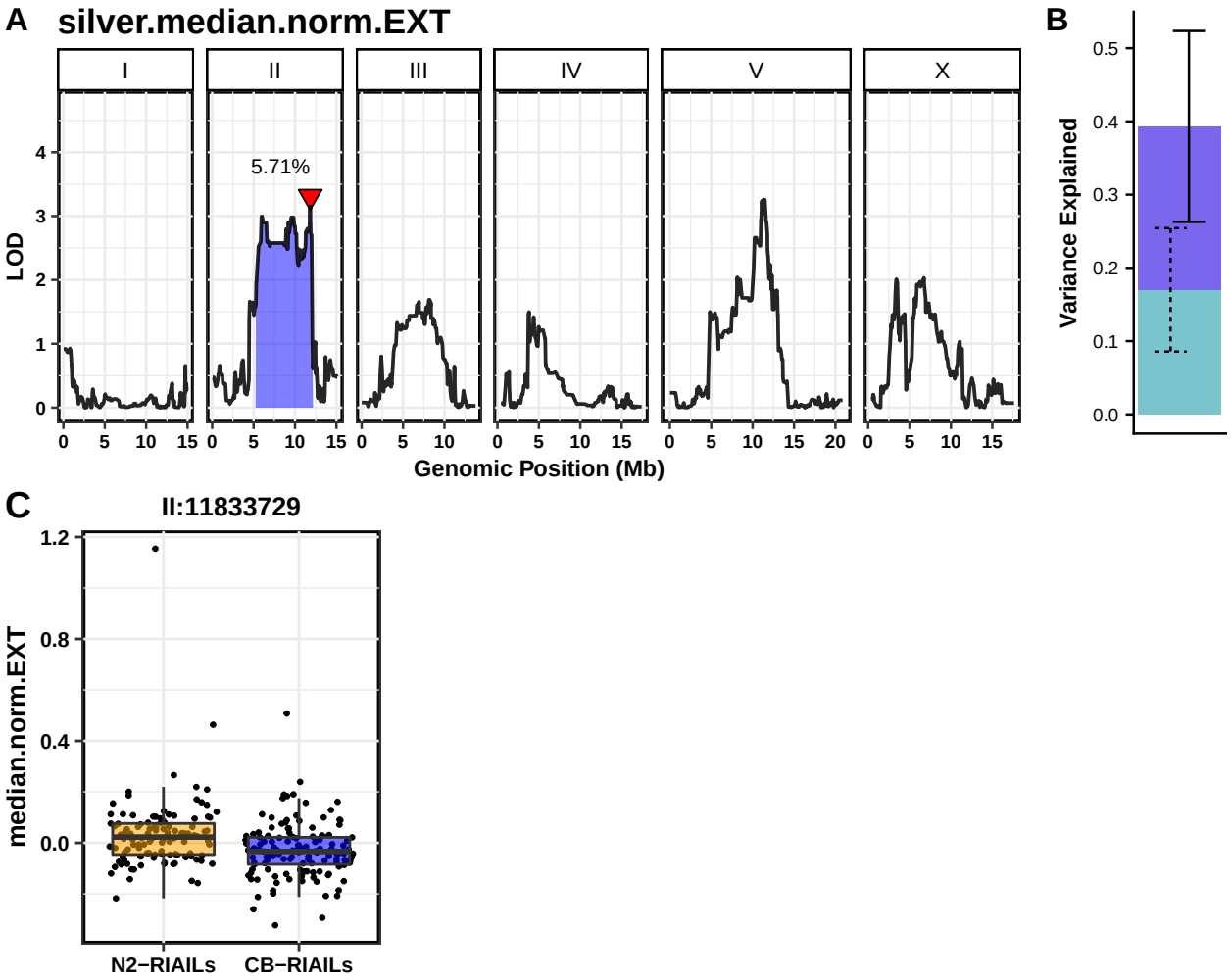

A
silver.cv.EXT
I
II
III
IV
V
X
11.14%
LOD
7.5
5.0
2.5
0.0
0 5 10 15
0 5 10 15
0 5 10
0 5 10 15
0 5 10 15 20
0 5 10 15
Genomic Position (Mb)
B
Variance Explained
0.4
0.3
0.2
0.1
0.0
C
IV:4009430
cv.EXT
1.0
0.5
0.0
−0.5
N2−RIAILs
CB−RIAILs
NIL
a
b
ab
ab
0.5
0.0
−0.5
N2
CB4856
ECA229
ECA231
Chr IV
Genome

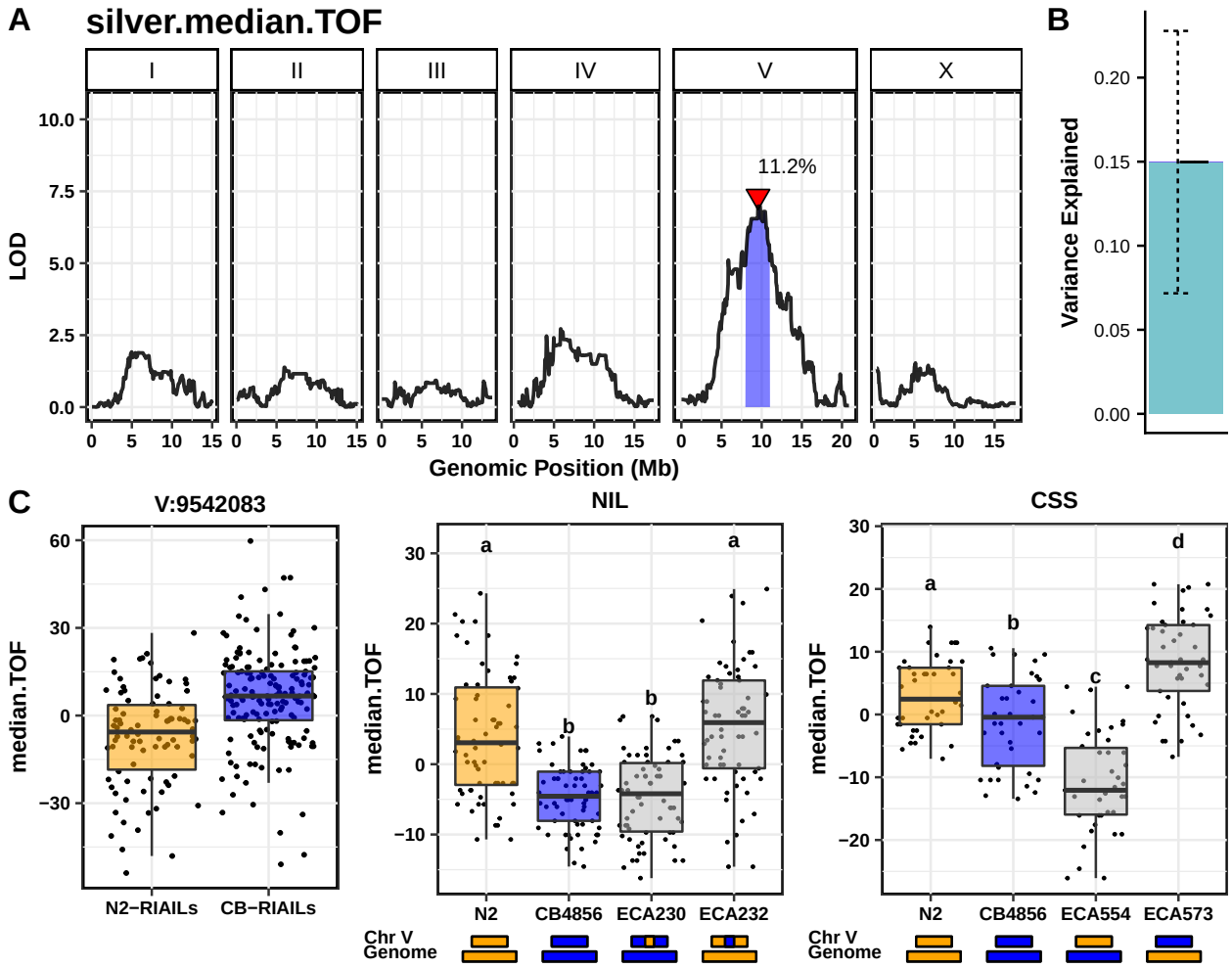

A
silver.mean.EXT
I
II
III
IV
V
X
LOD
20.62%
Genomic Position (Mb)
B
Variance Explained
C
V:10240582
mean.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

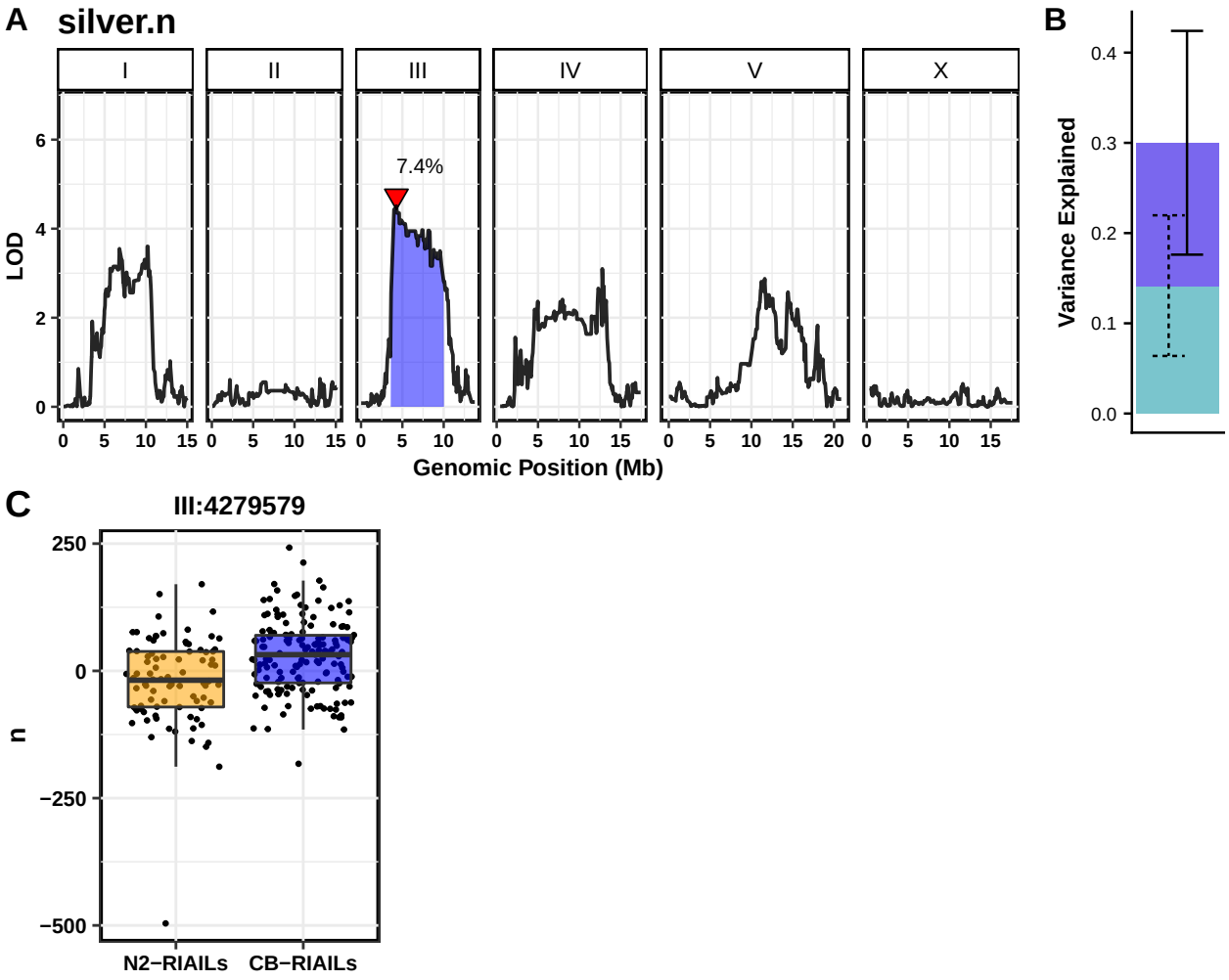

A
silver.mean.norm.EXT
I
II
III
IV
V
X
7.38%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:11114697
mean.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

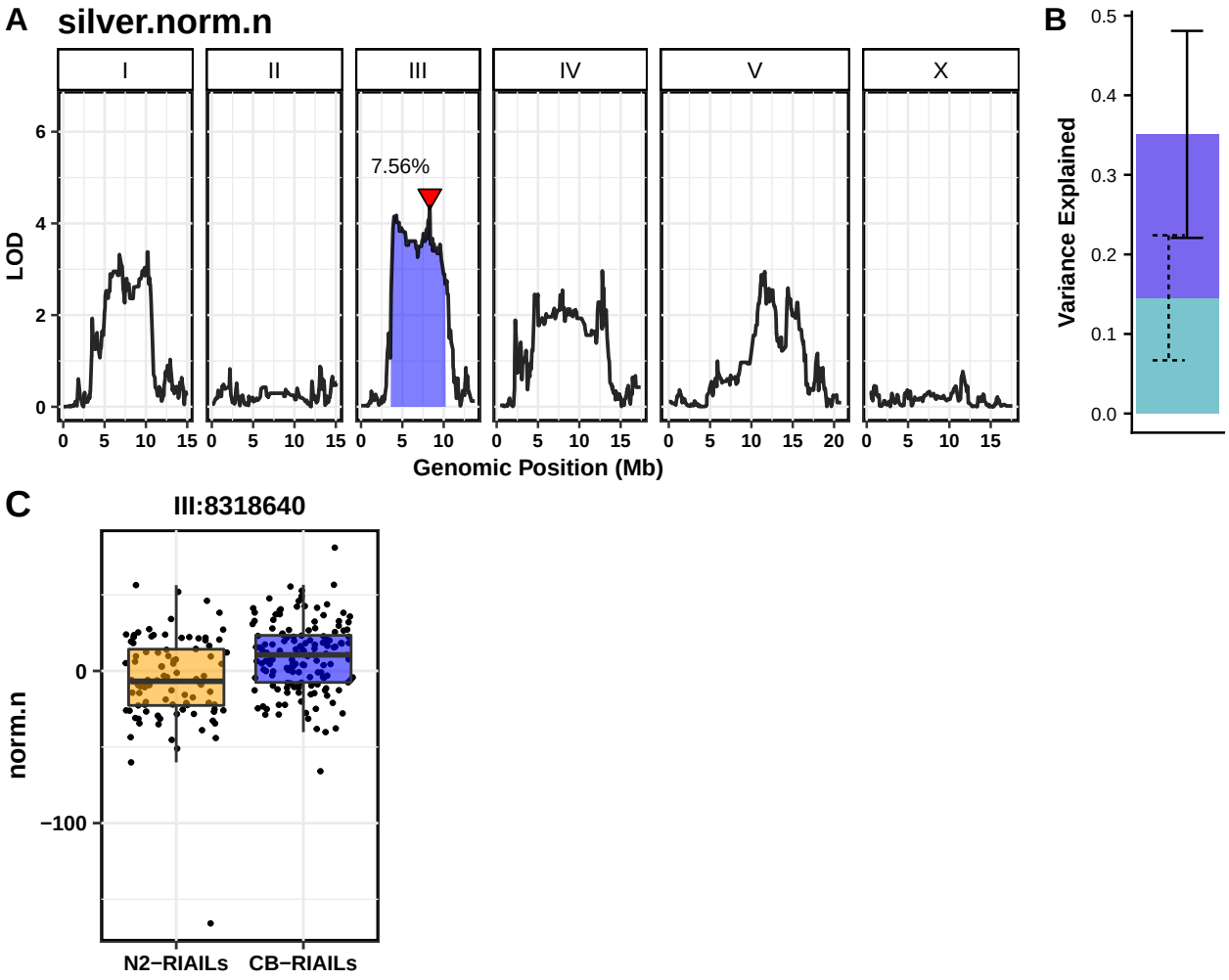

A
silver.mean.TOF
I
II
III
IV
V
X
LOD
18.46%
Genomic Position (Mb)
B
Variance Explained
C
V:10240582
mean.TOF
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V
Genome
CSS
ECA554
ECA573

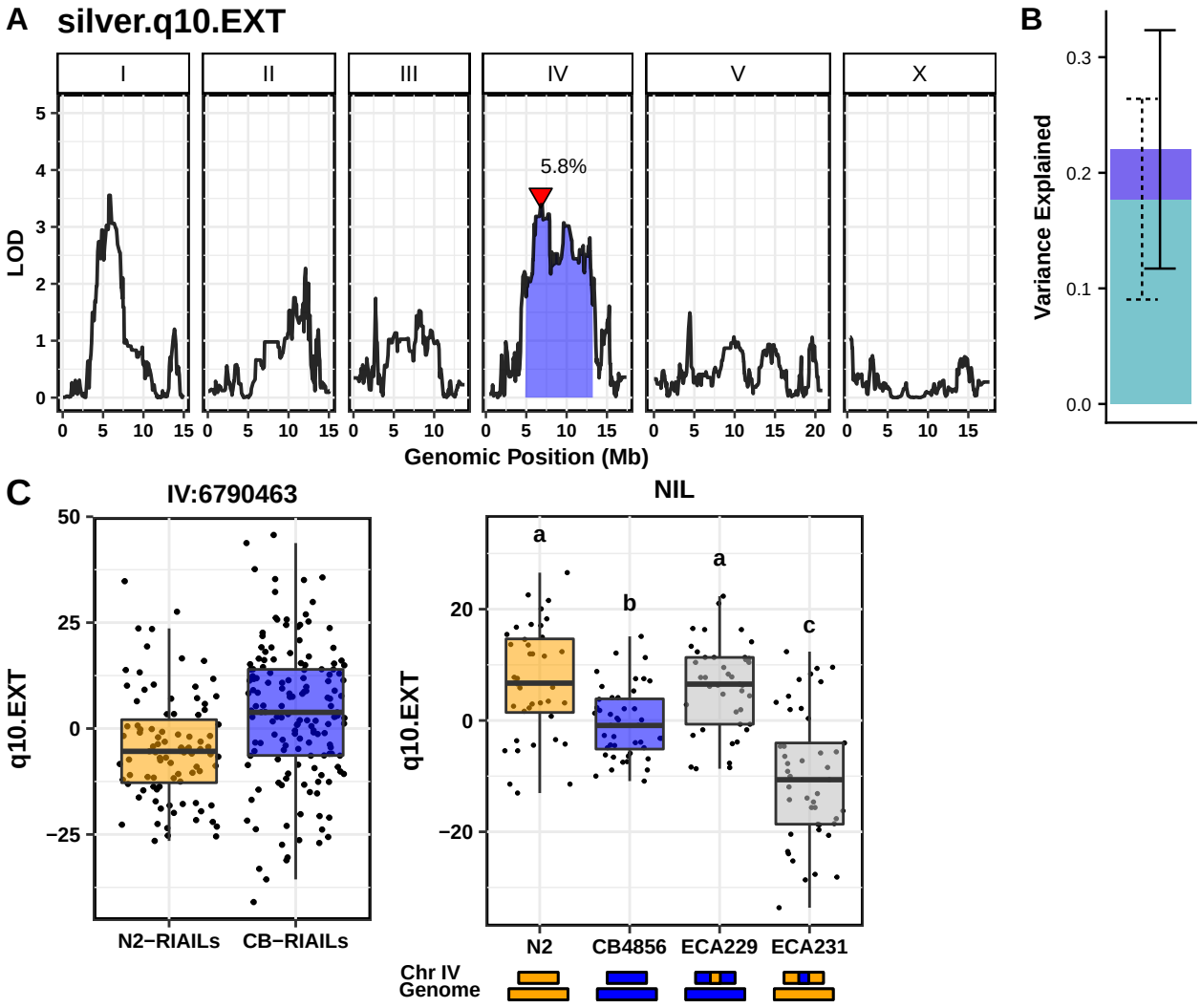

A
silver.median.EXT
I
II
III
IV
V
X
LOD
13.89%
Genomic Position (Mb)
B
Variance Explained
C
V:10240582
median.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

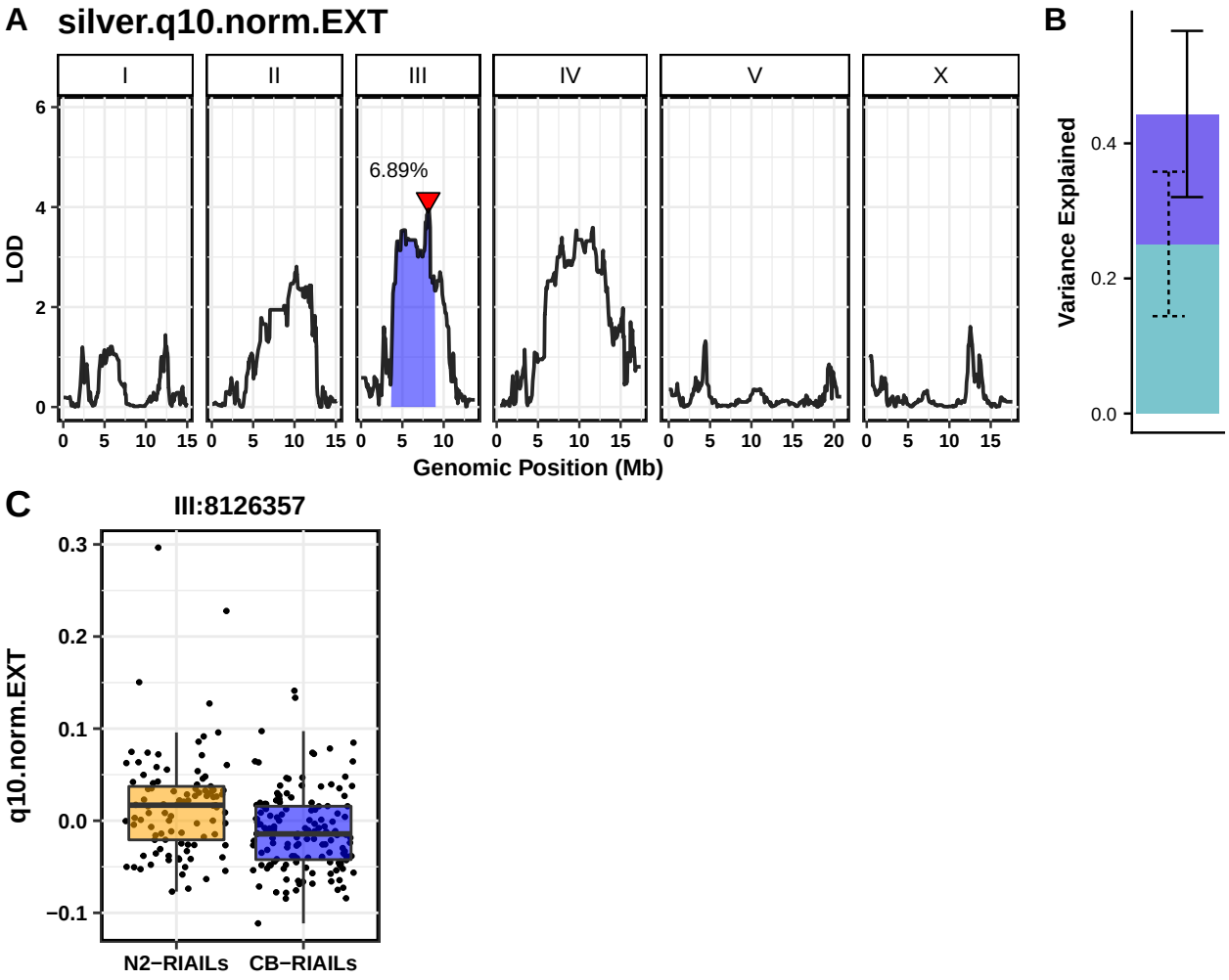

A
silver.median.norm.EXT
I
II
III
IV
V
X
5.71%
LOD
Genomic Position (Mb)
B
Variance Explained
C
II:11833729
median.norm.EXT
N2−RIAILs
CB−RIAILs

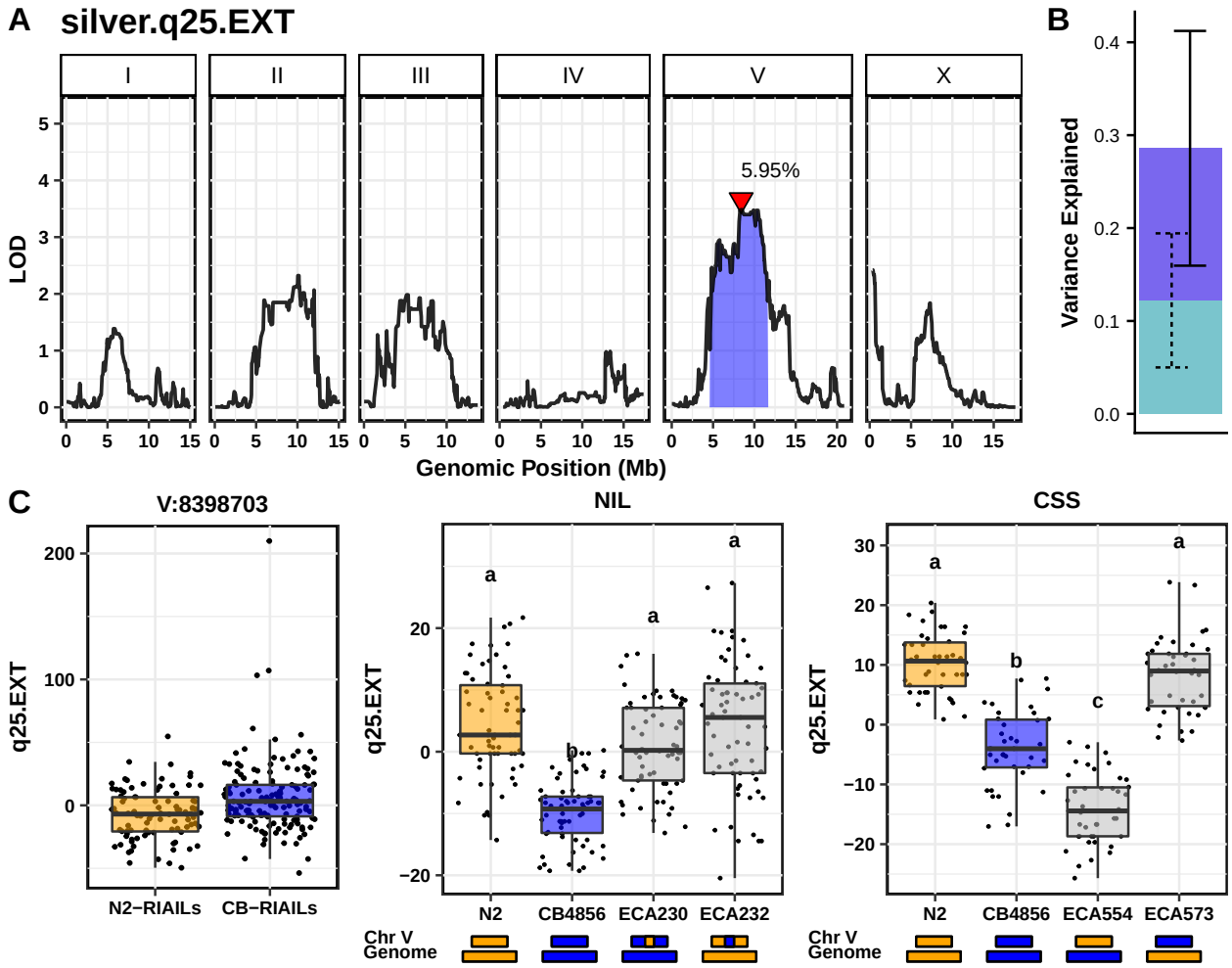

A
silver.median.TOF
I
II
III
IV
V
X
LOD
11.2%
Genomic Position (Mb)
B
Variance Explained
C
V:9542083
median.TOF
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

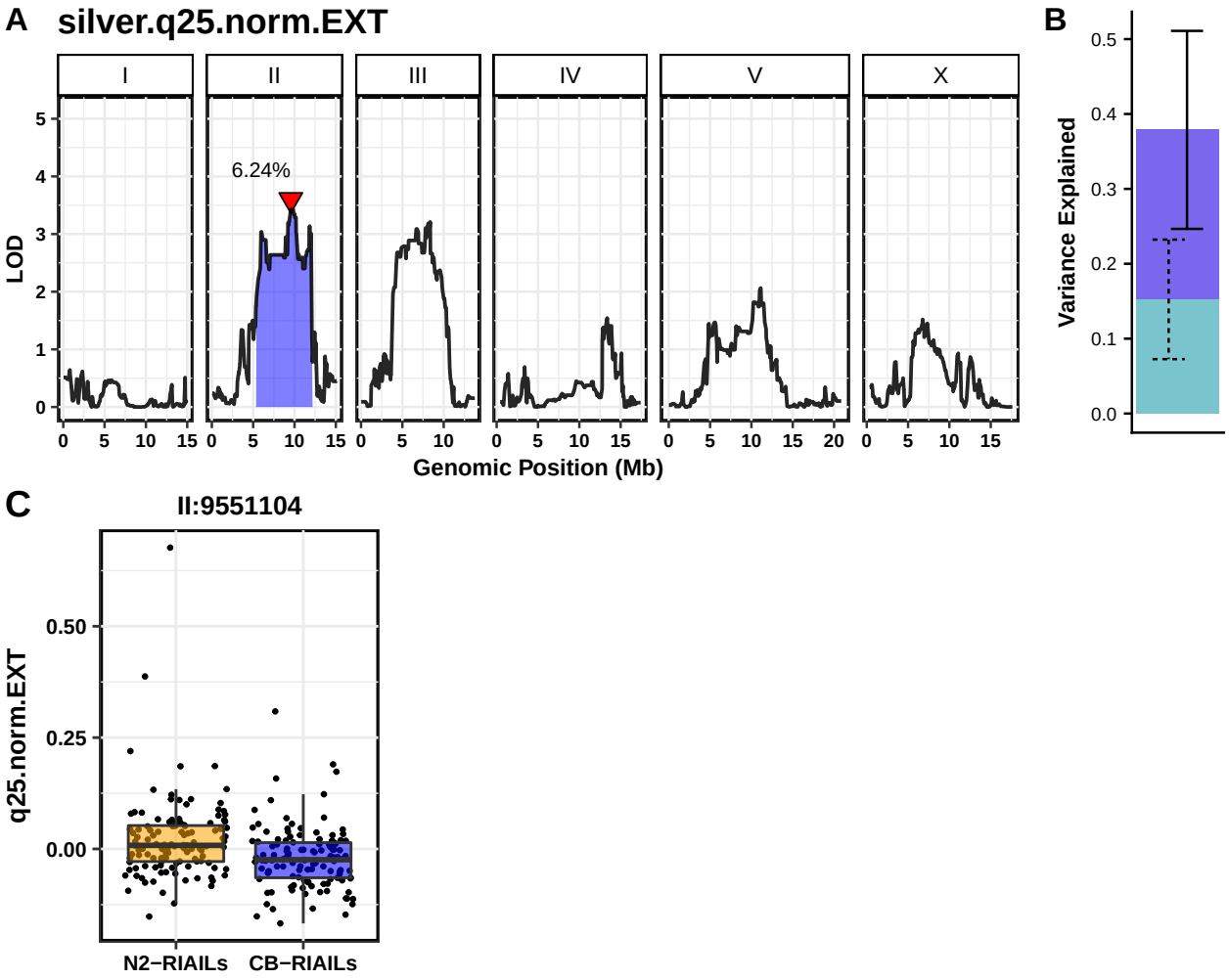

A
silver.n
I
II
III
IV
V
X
7.4%
LOD
Genomic Position (Mb)
B
Variance Explained
C
III:4279579
n
N2−RIAILs
CB−RIAILs

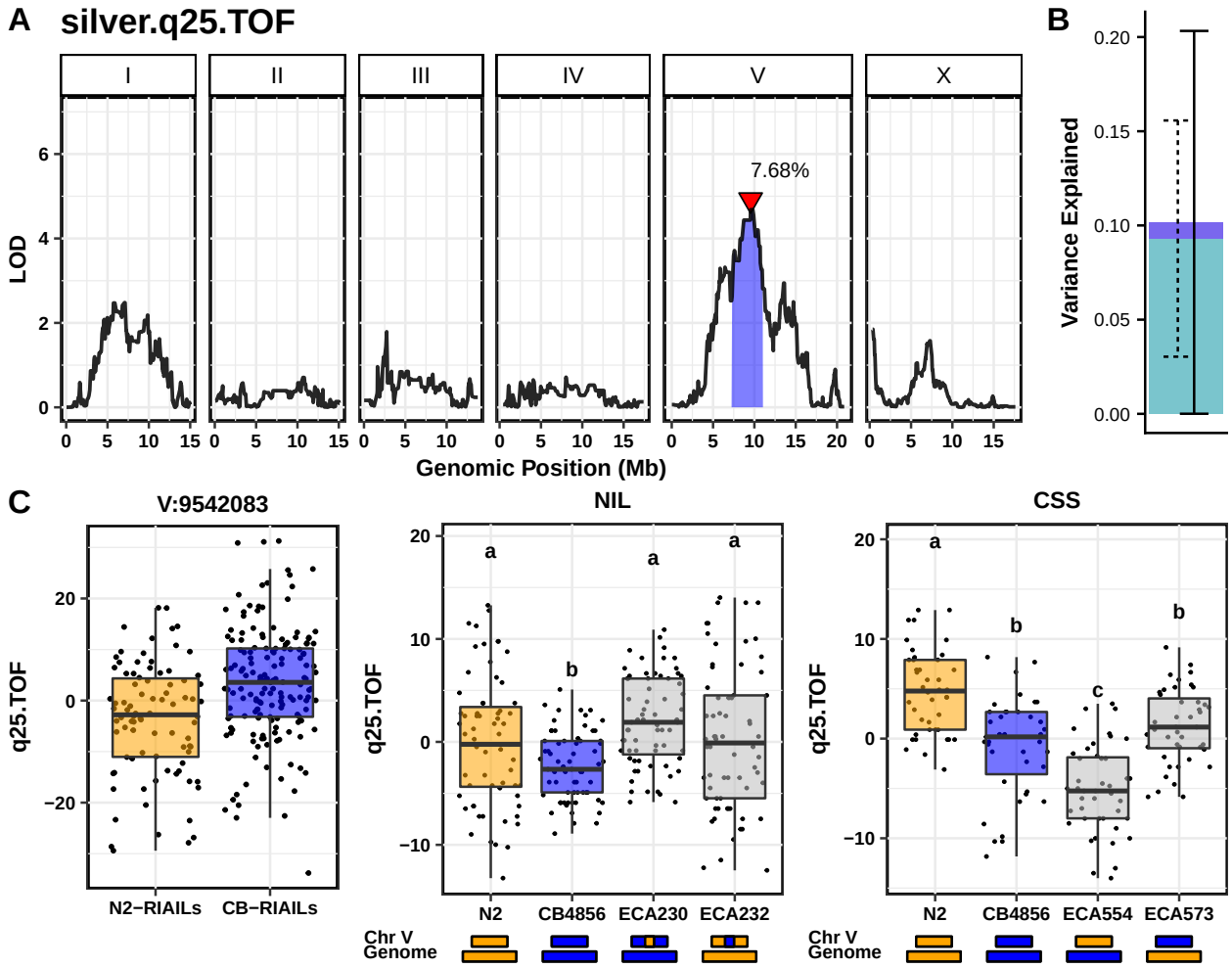

A
silver.norm.n
I
II
III
IV
V
X
7.56%
LOD
Genomic Position (Mb)
B
Variance Explained
C
III:8318640
norm.n
N2−RIAILs
CB−RIAILs

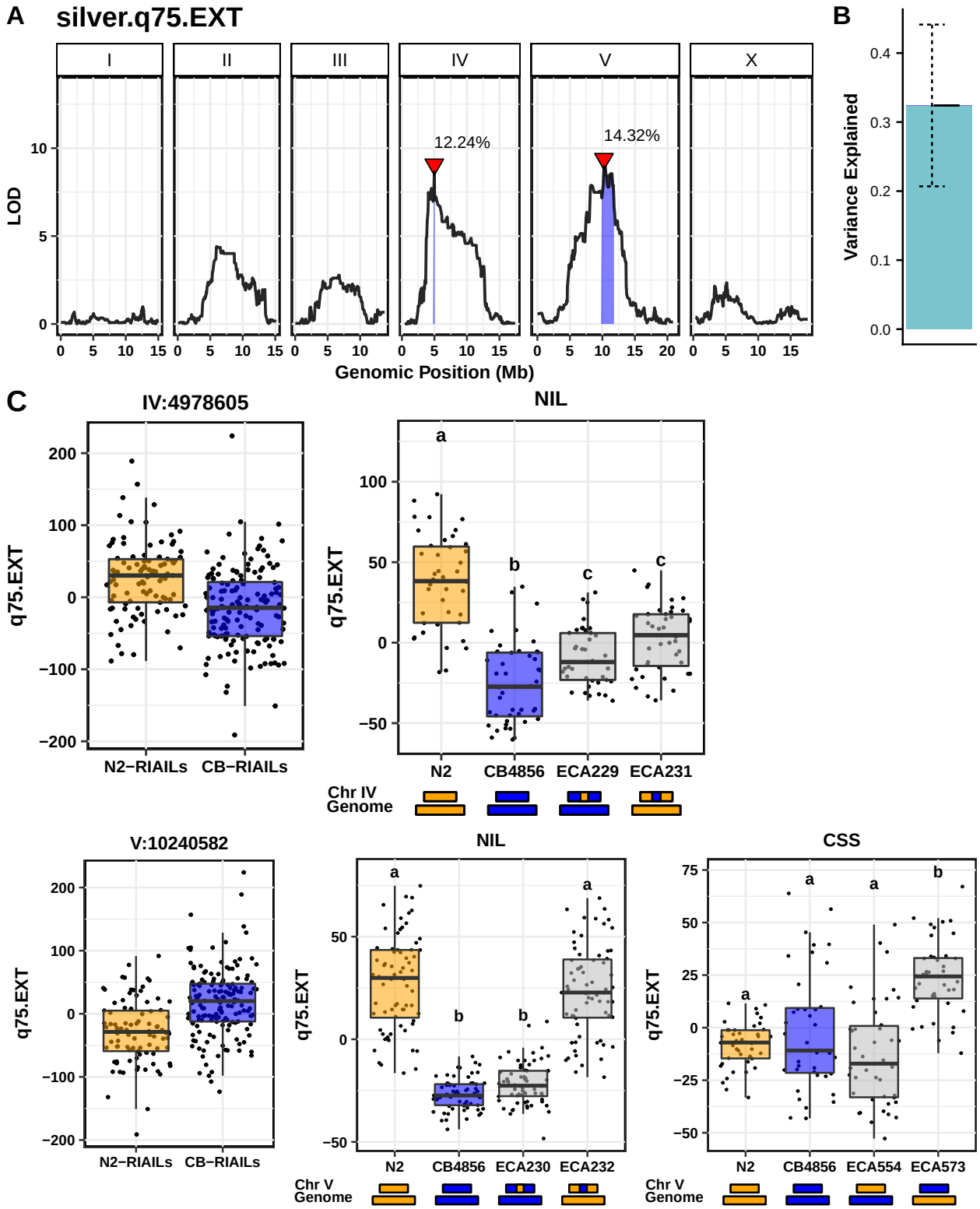

A
silver.q10.EXT
I
II
III
IV
V
X
5.8%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:6790463
q10.EXT
N2−RIAILs
CB−RIAILs
NIL
a
b
a
c
N2
CB4856
ECA229
ECA231
Chr IV
Genome

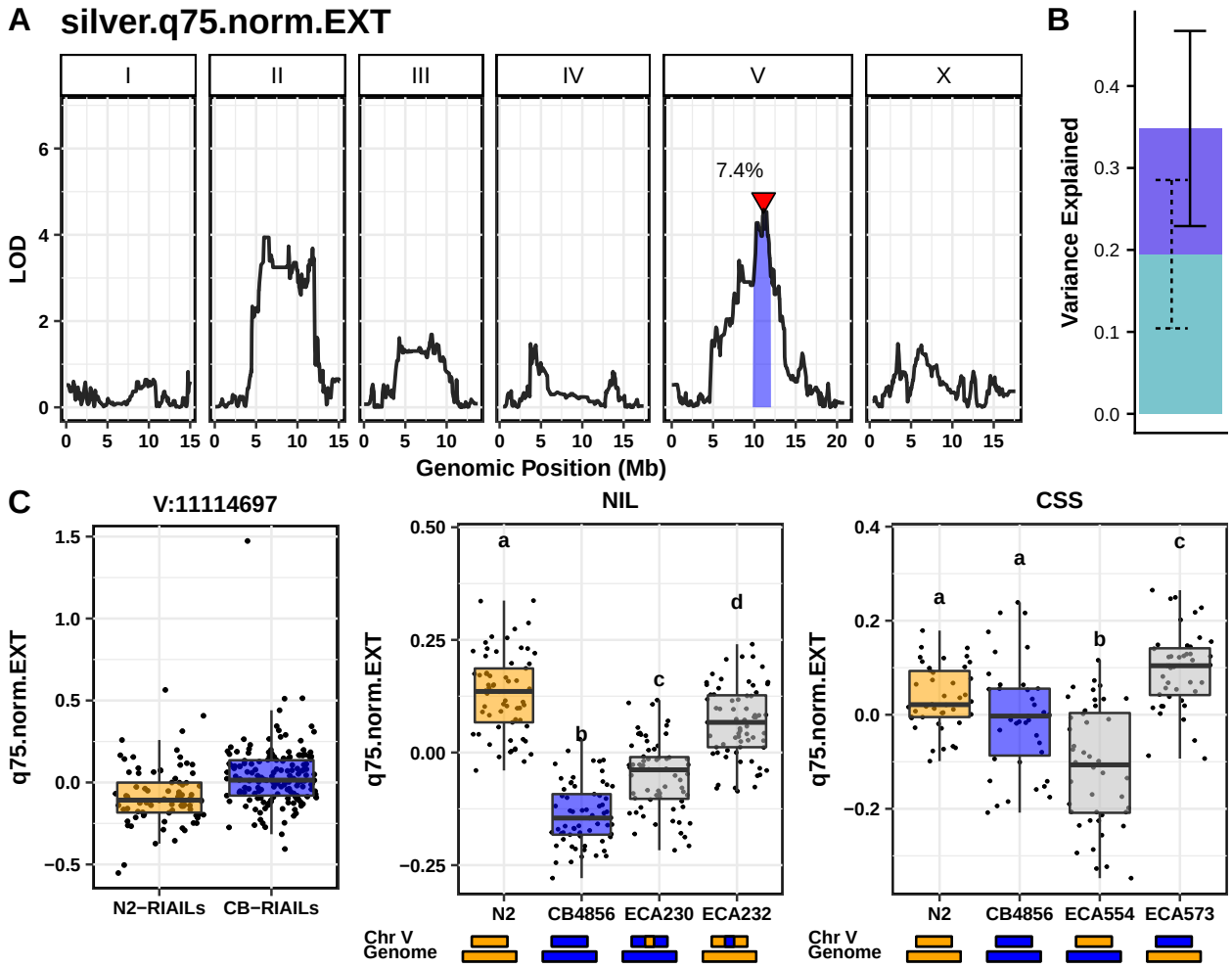

A
silver.q10.norm.EXT
I
II
III
IV
V
X
6.89%
LOD
Genomic Position (Mb)
B
Variance Explained
C
III:8126357
q10.norm.EXT
N2−RIAILs
CB−RIAILs

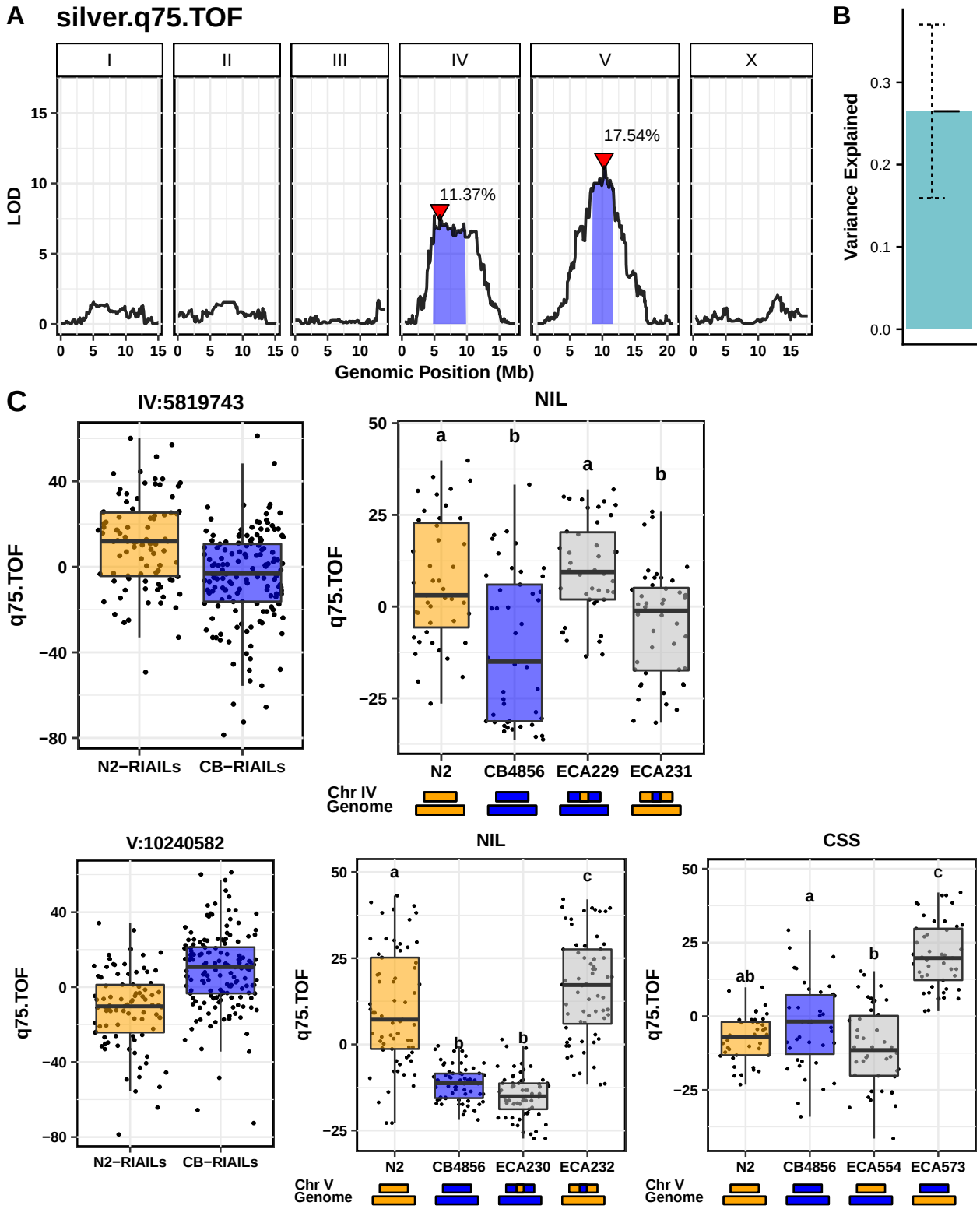

A
silver.q25.EXT
I
II
III
IV
V
X
LOD
5.95%
Genomic Position (Mb)
B
Variance Explained
C
V:8398703
q25.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

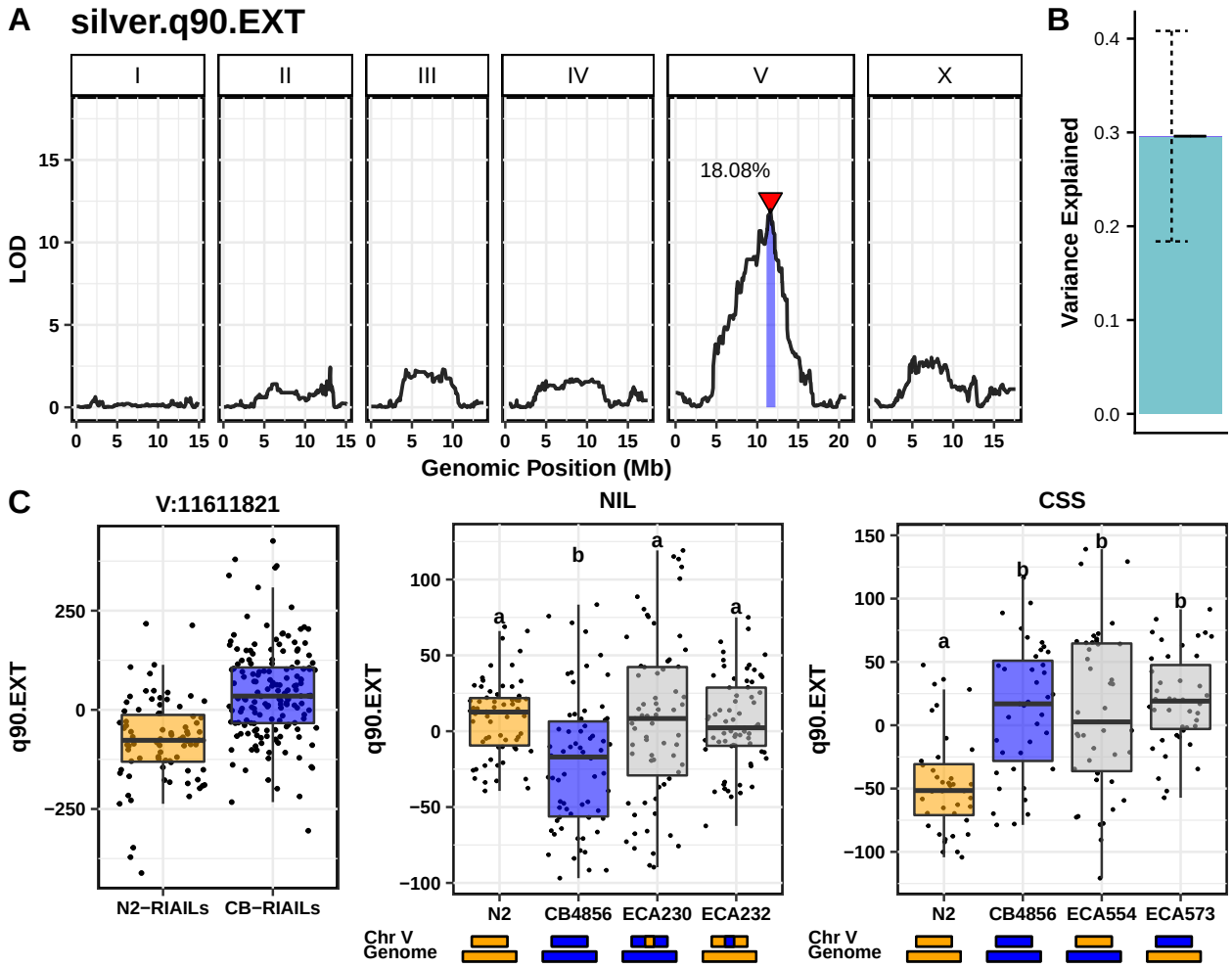

A
silver.q25.norm.EXT
I
II
III
IV
V
X
6.24%
LOD
Genomic Position (Mb)
B
Variance Explained
C
II:9551104
q25.norm.EXT
N2−RIAILs
CB−RIAILs

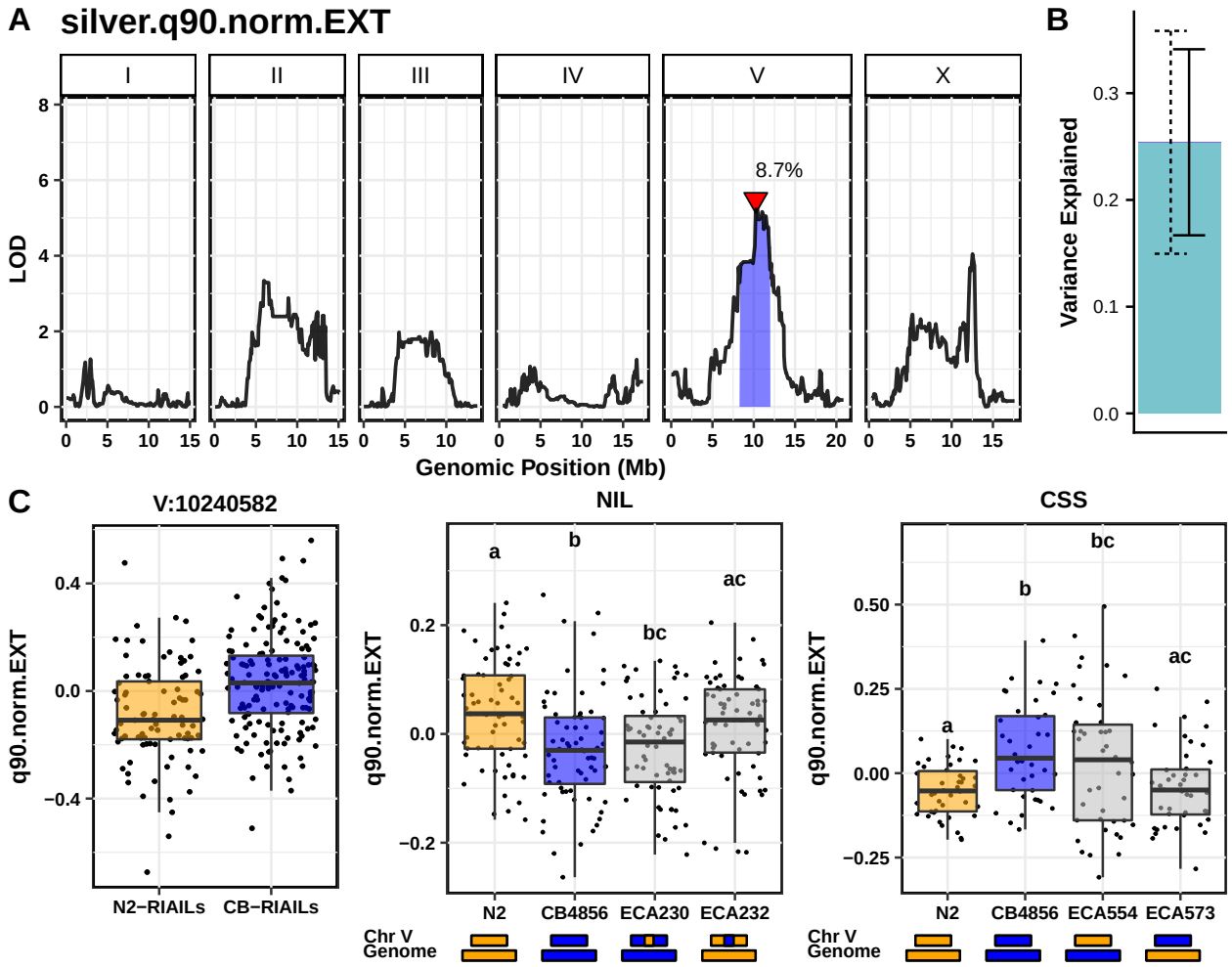

A
silver.q25.TOF
I
II
III
IV
V
X
7.68%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:9542083
q25.TOF
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

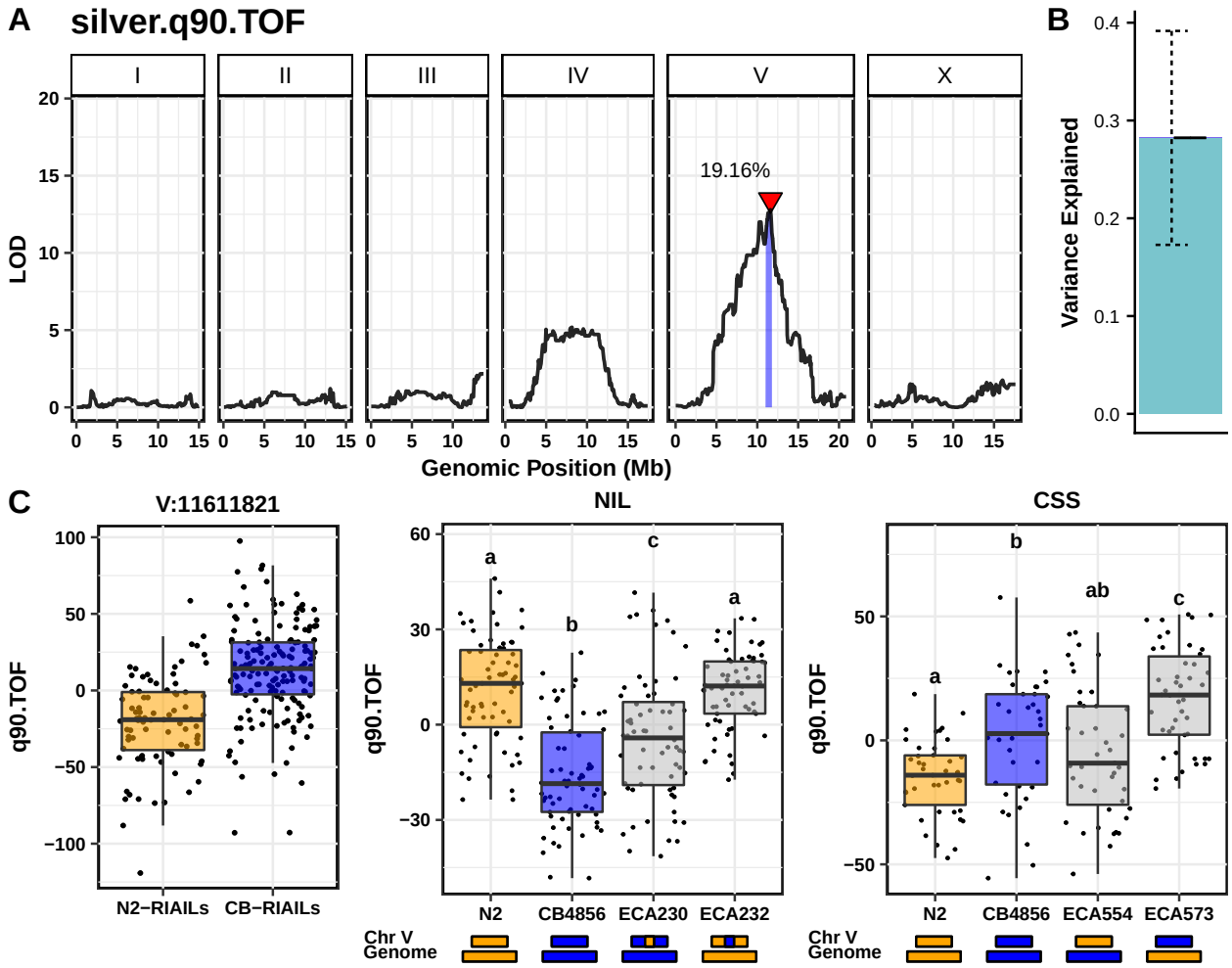

A
silver.q75.EXT
I
II
III
IV
V
X
12.24%
14.32%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:4978605
q75.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA229
ECA231
Chr IV Genome
V:10240582
ECA230
ECA232
CSS
ECA554
ECA573
Chr V Genome

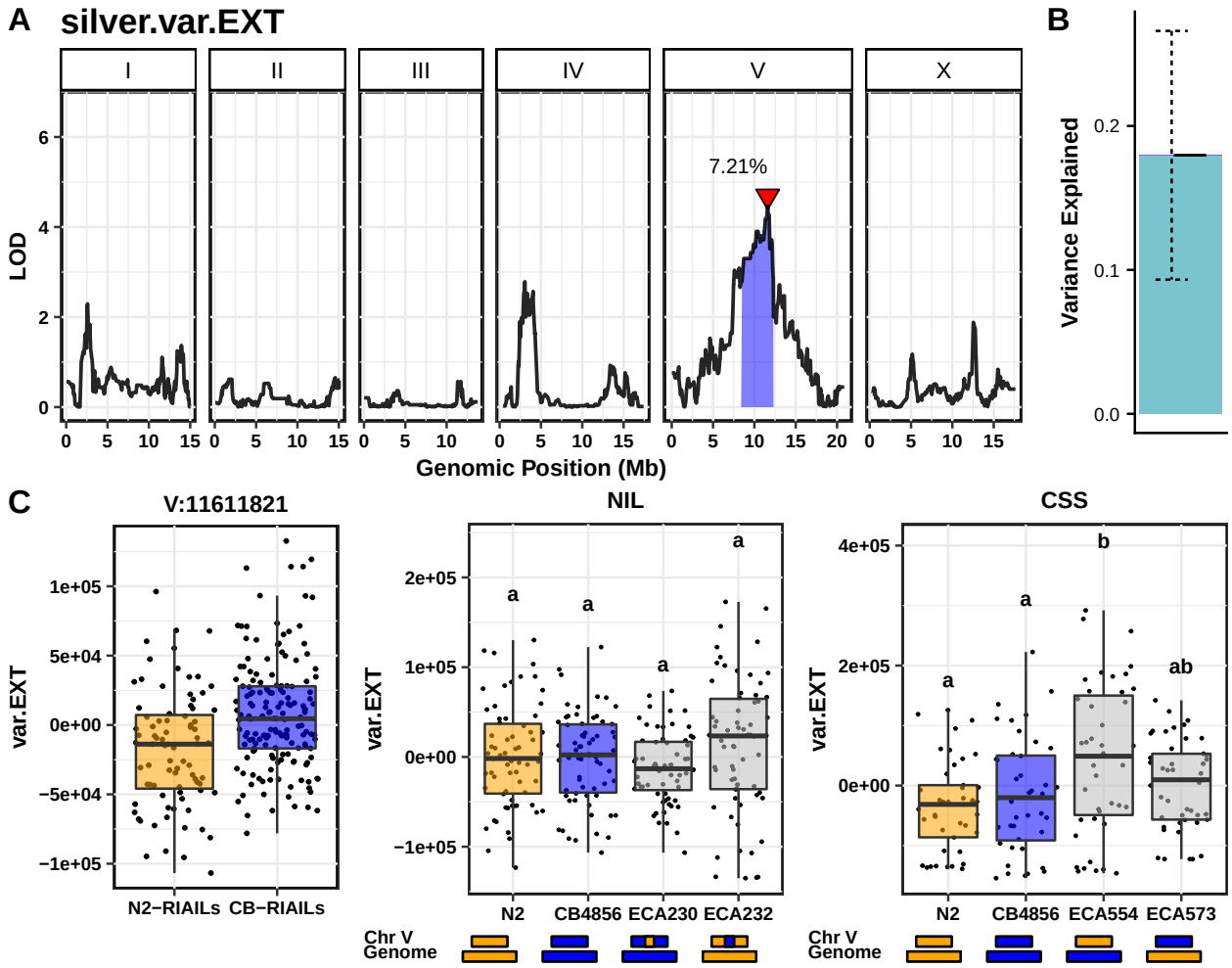

A
silver.q75.norm.EXT
I
II
III
IV
V
X
LOD
7.4%
Genomic Position (Mb)
B
Variance Explained
C
V:11114697
q75.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
ECA554
ECA573

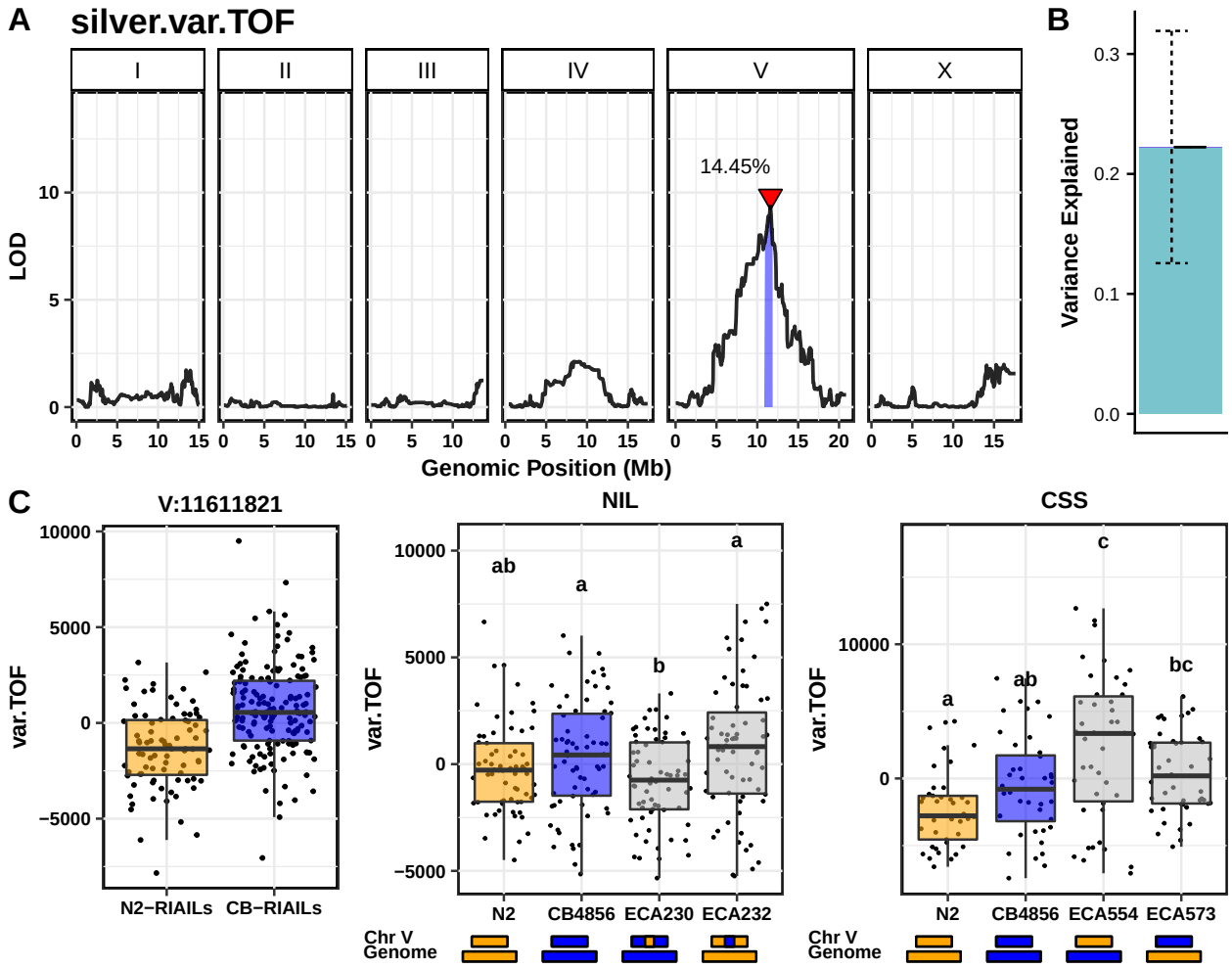

A
silver.q75.TOF
I
II
III
IV
V
X
LOD
11.37%
17.54%
Genomic Position (Mb)
B
Variance Explained
C
IV:5819743
q75.TOF
N2−RIAILs
CB−RIAILs
NIL
a
b
a
b
N2
CB4856
ECA229
ECA231
Chr IV
Genome
V:10240582
N2−RIAILs
CB−RIAILs
NIL
a
b
b
c
N2
CB4856
ECA230
ECA232
Chr V
Genome
CSS
ab
a
b
c
N2
CB4856
ECA554
ECA573
Chr V
Genome

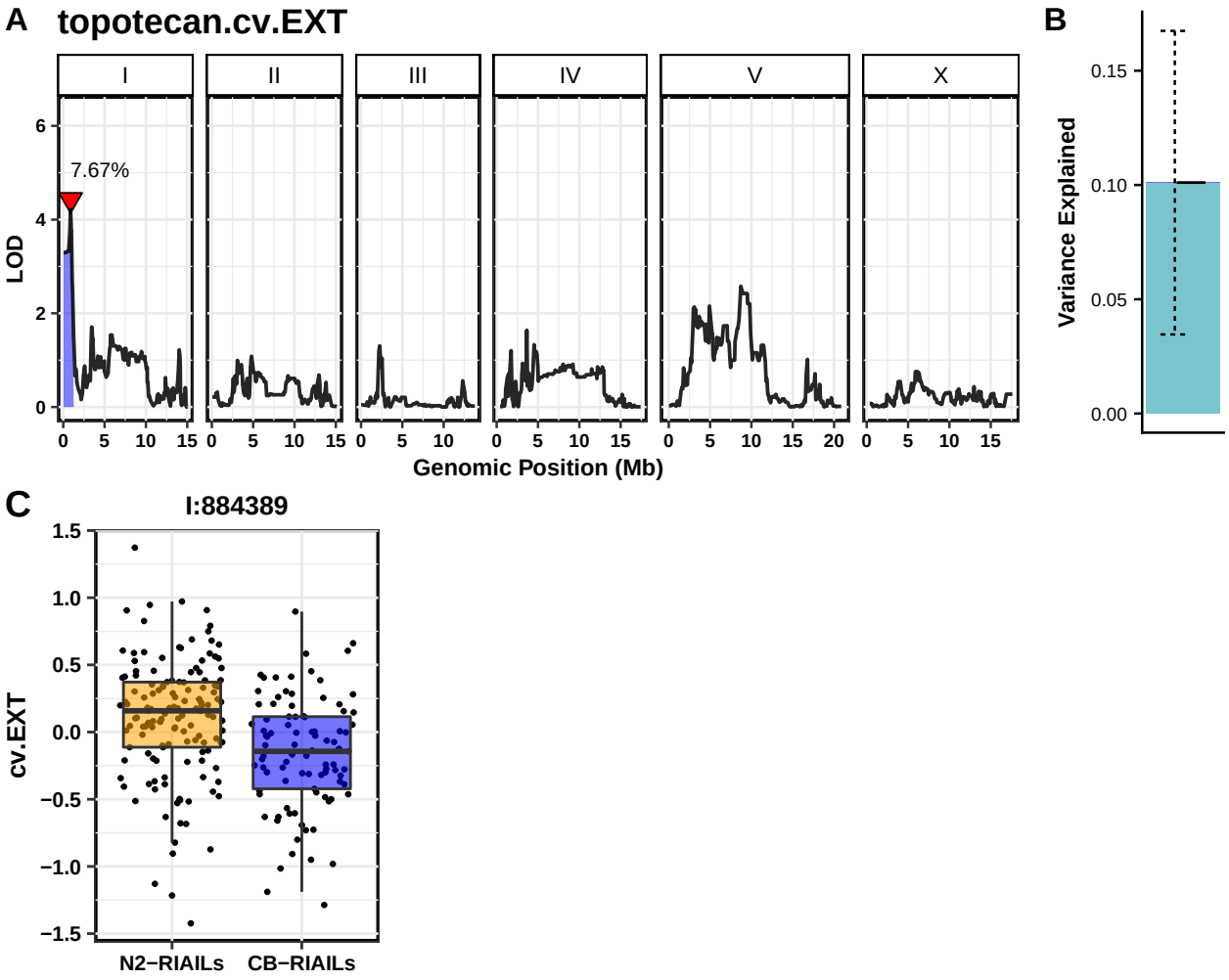

A
silver.q90.EXT
I
II
III
IV
V
X
18.08%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:11611821
q90.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

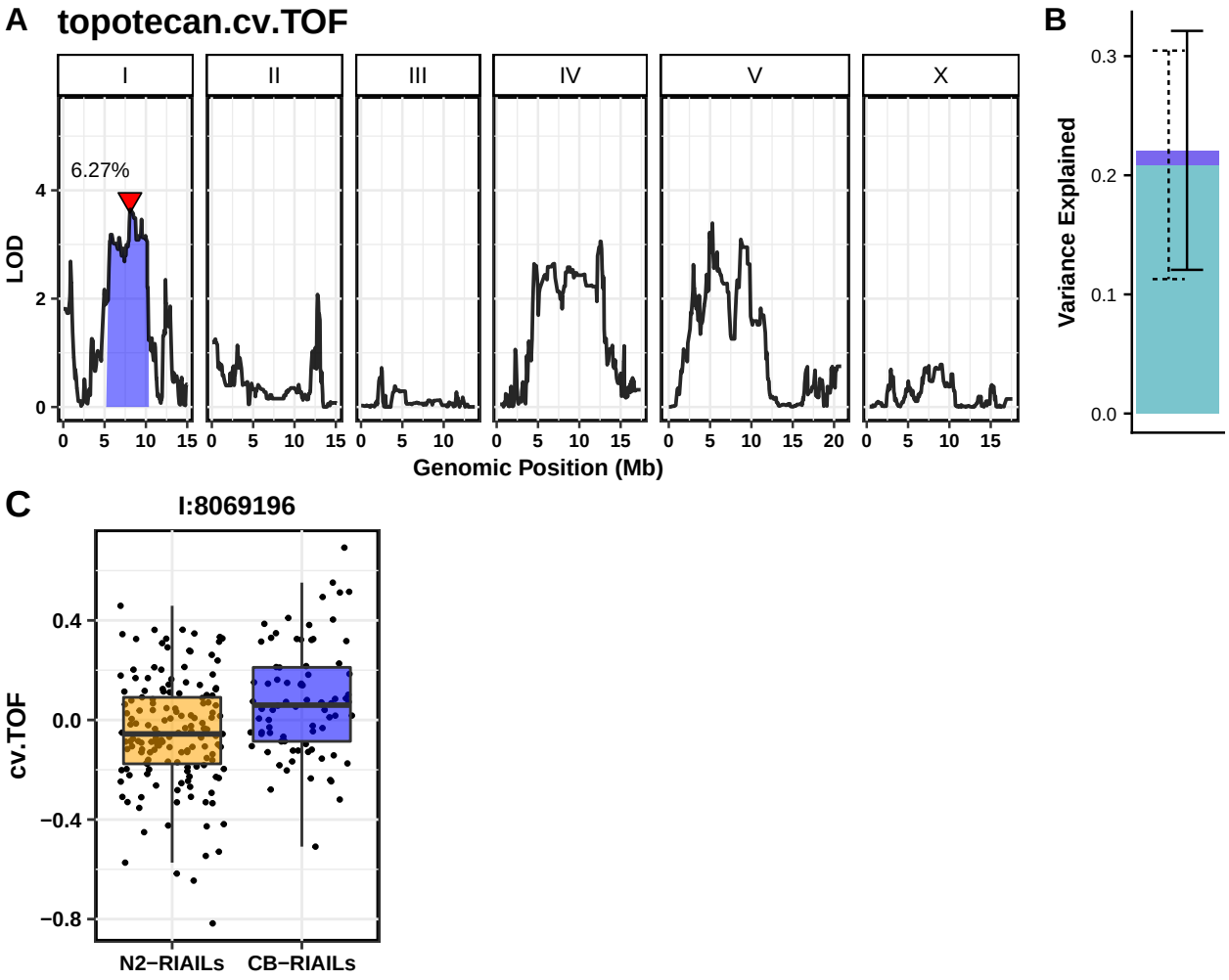

A
silver.q90.norm.EXT
I
II
III
IV
V
X
8.7%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:10240582
q90.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
a
b
bc
ac
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
bc
b
a
ac
N2
CB4856
ECA554
ECA573
Chr V Genome

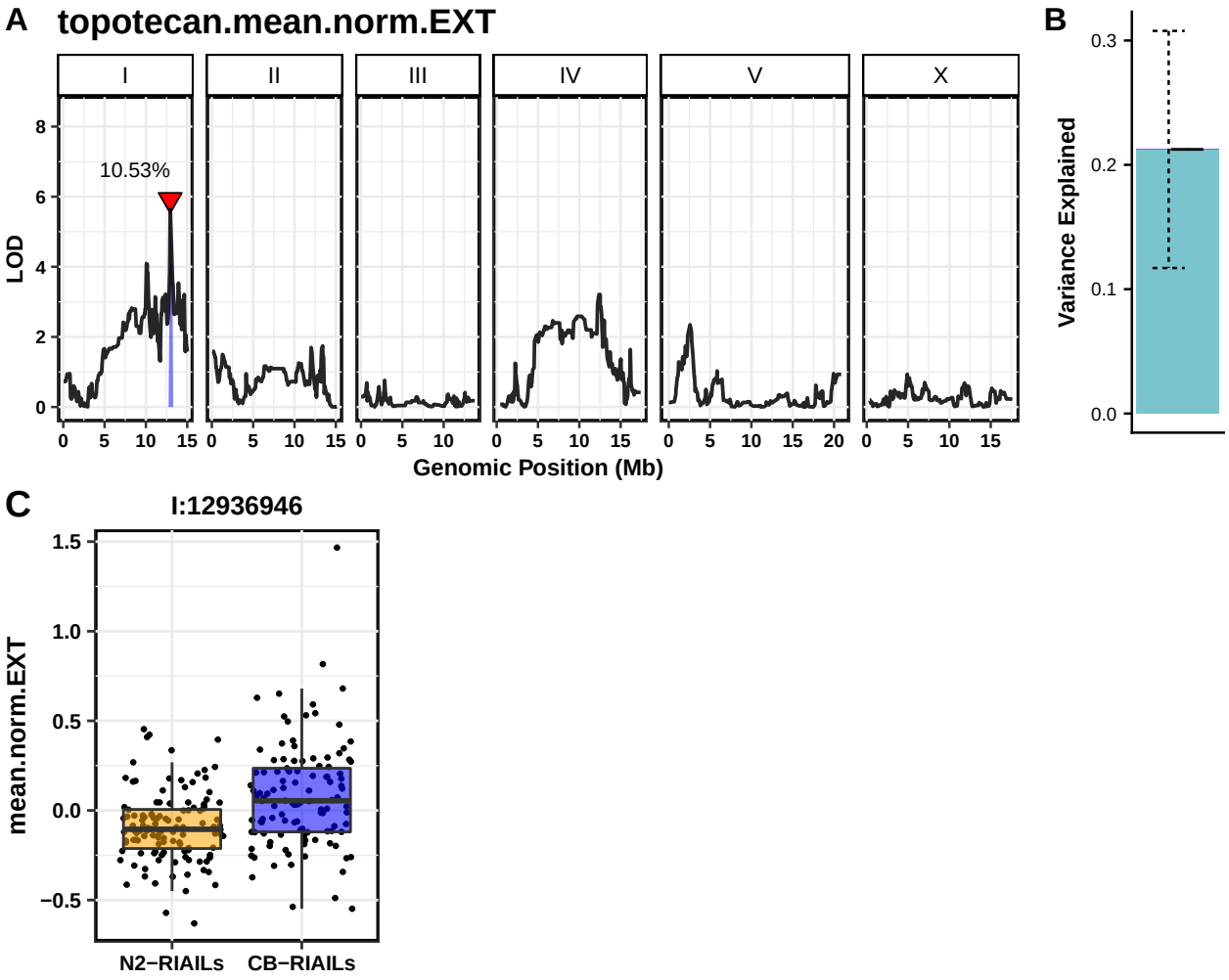

A
silver.q90.TOF
I
II
III
IV
V
X
LOD
19.16%
Genomic Position (Mb)
B
Variance Explained
C
V:11611821
q90.TOF
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
N2
CB4856
ECA554
ECA573
Chr V Genome

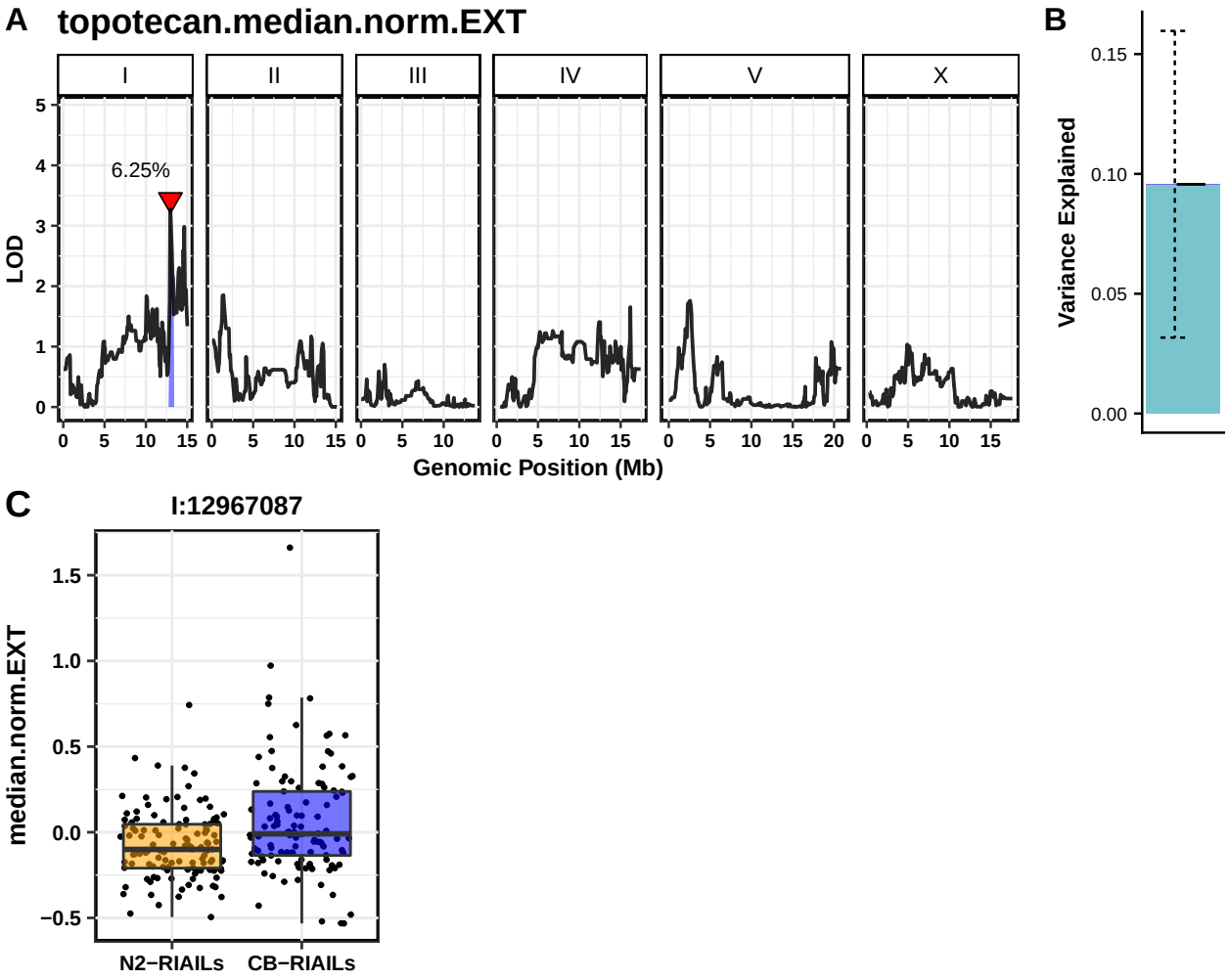

A
silver.var.EXT
I
II
III
IV
V
X
7.21%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:11611821
var.EXT
N2−RIAILs
CB−RIAILs
NIL
N2
CB4856
ECA230
ECA232
CSS
ECA554
ECA573
Chr V
Genome

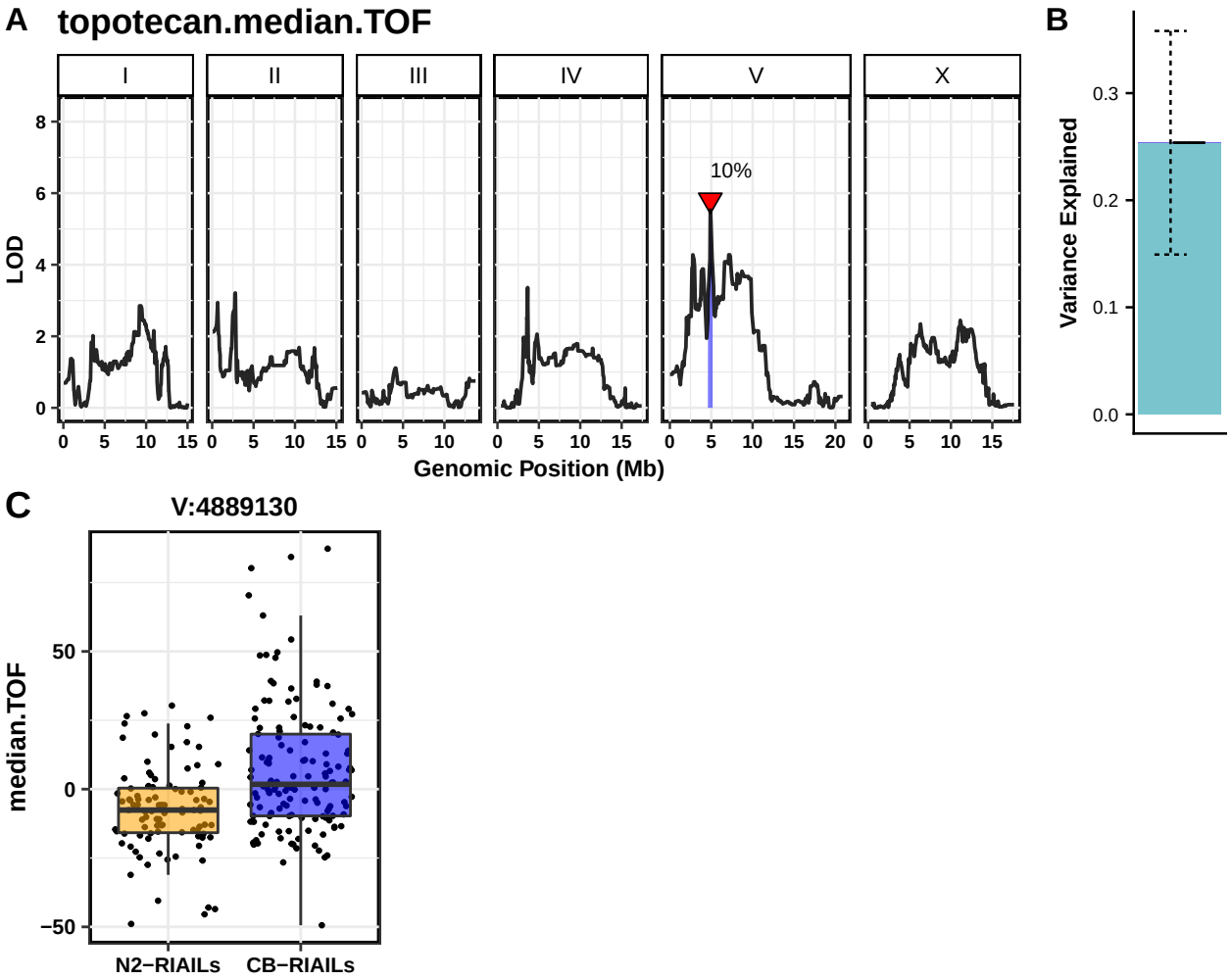

A
silver.var.TOF
I
II
III
IV
V
X
14.45%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:11611821
var.TOF
N2−RIAILs
CB−RIAILs
NIL
ab
a
b
a
N2
CB4856
ECA230
ECA232
Chr V Genome
CSS
a
ab
c
bc
N2
CB4856
ECA554
ECA573
Chr V Genome

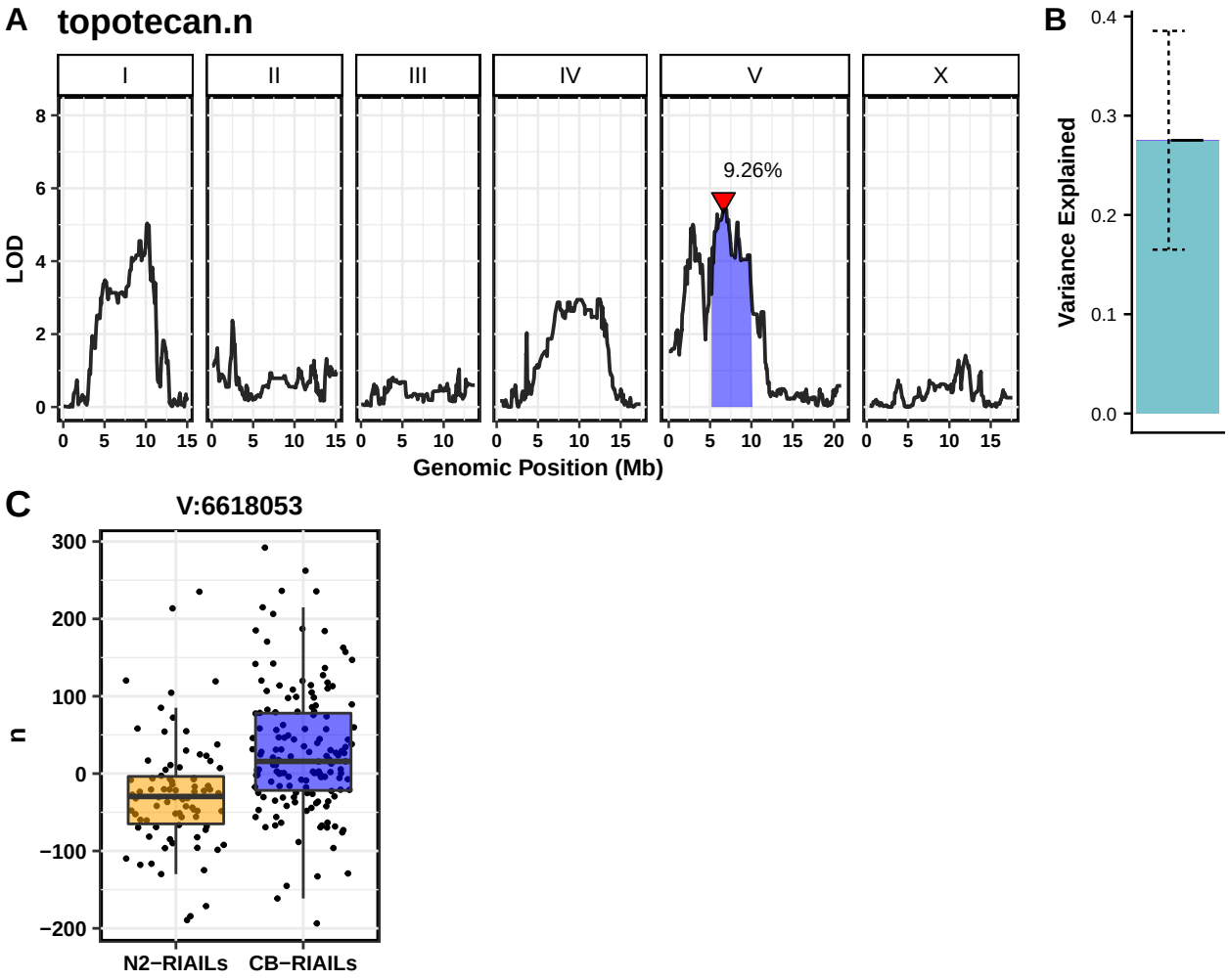

A
topotecan.cv.EXT
I
II
III
IV
V
X
7.67%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:884389
cv.EXT
N2−RIAILs
CB−RIAILs

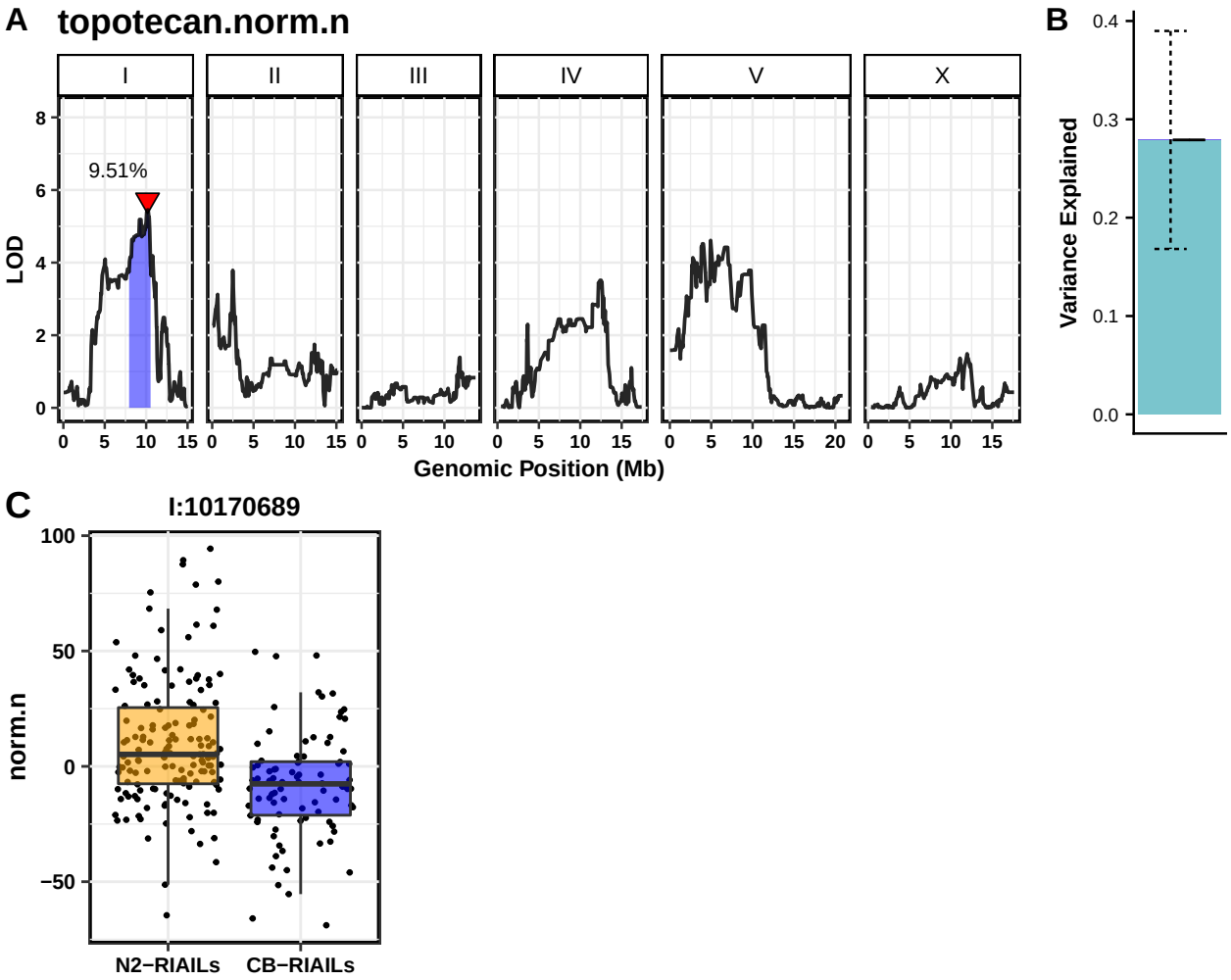

A
topotecan.cv.TOF
I
II
III
IV
V
X
6.27%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:8069196
cv.TOF
N2−RIAILs
CB−RIAILs

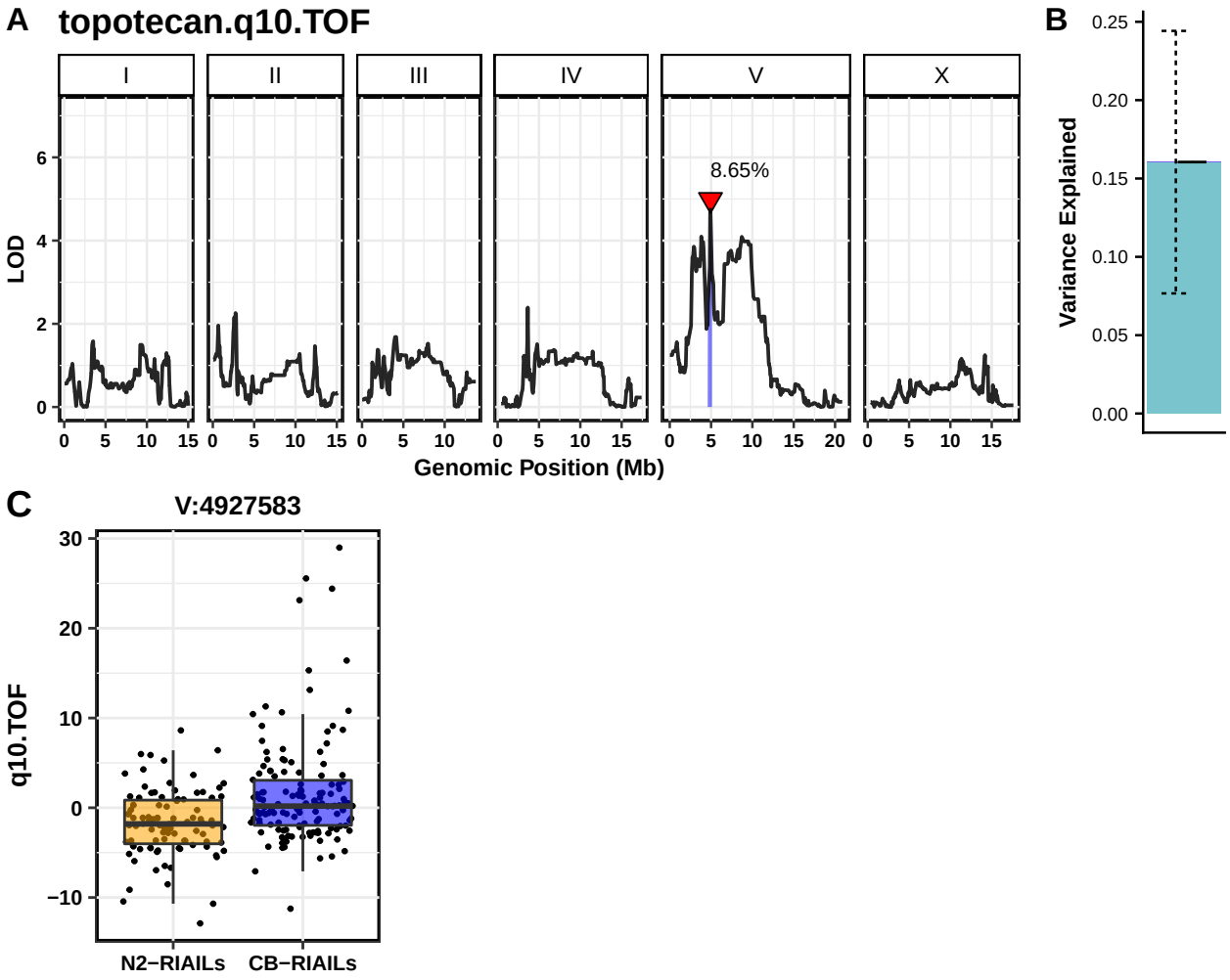

A
topotecan.mean.norm.EXT
I
II
III
IV
V
X
10.53%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:12936946
mean.norm.EXT
N2−RIAILs
CB−RIAILs

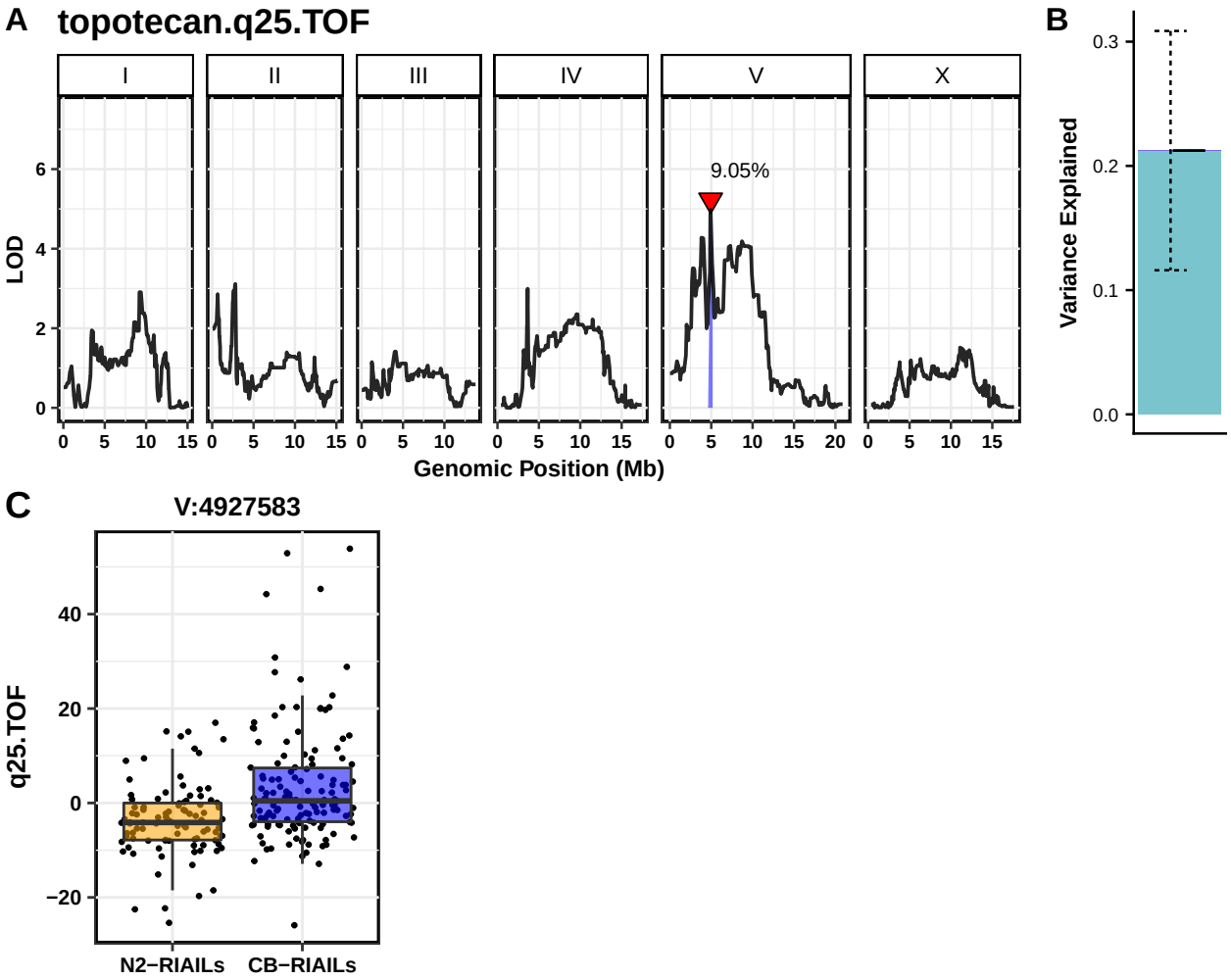

A
topotecan.median.norm.EXT
I
II
III
IV
V
X
6.25%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:12967087
median.norm.EXT
N2−RIAILs
CB−RIAILs

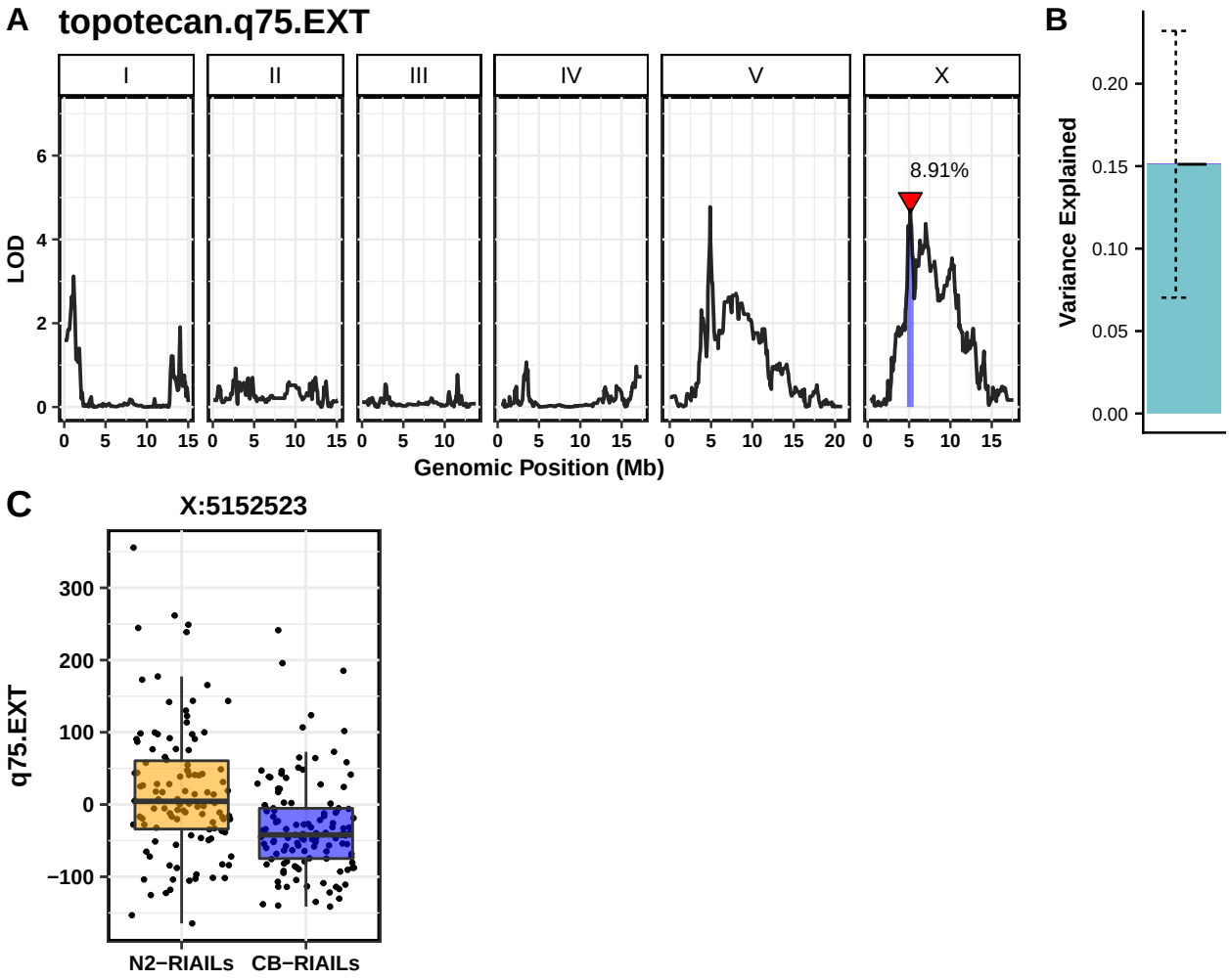

A
topotecan.median.TOF
I
II
III
IV
V
X
LOD
10%
Genomic Position (Mb)
B
Variance Explained
C
V:4889130
median.TOF
N2−RIAILs
CB−RIAILs

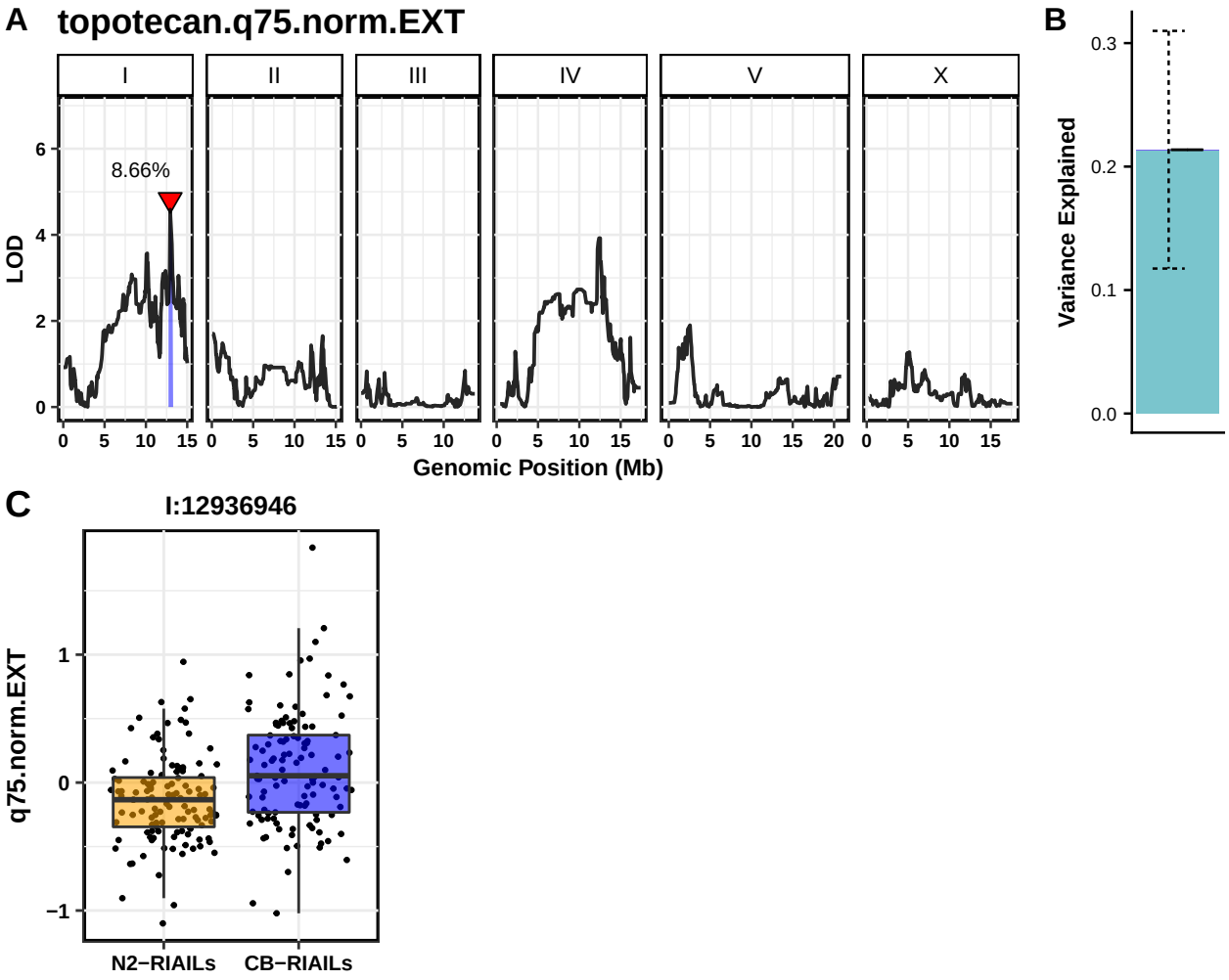

A
topotecan.n
I
II
III
IV
V
X
LOD
9.26%
Genomic Position (Mb)
B
Variance Explained
C
V:6618053
n
N2−RIAILs
CB−RIAILs

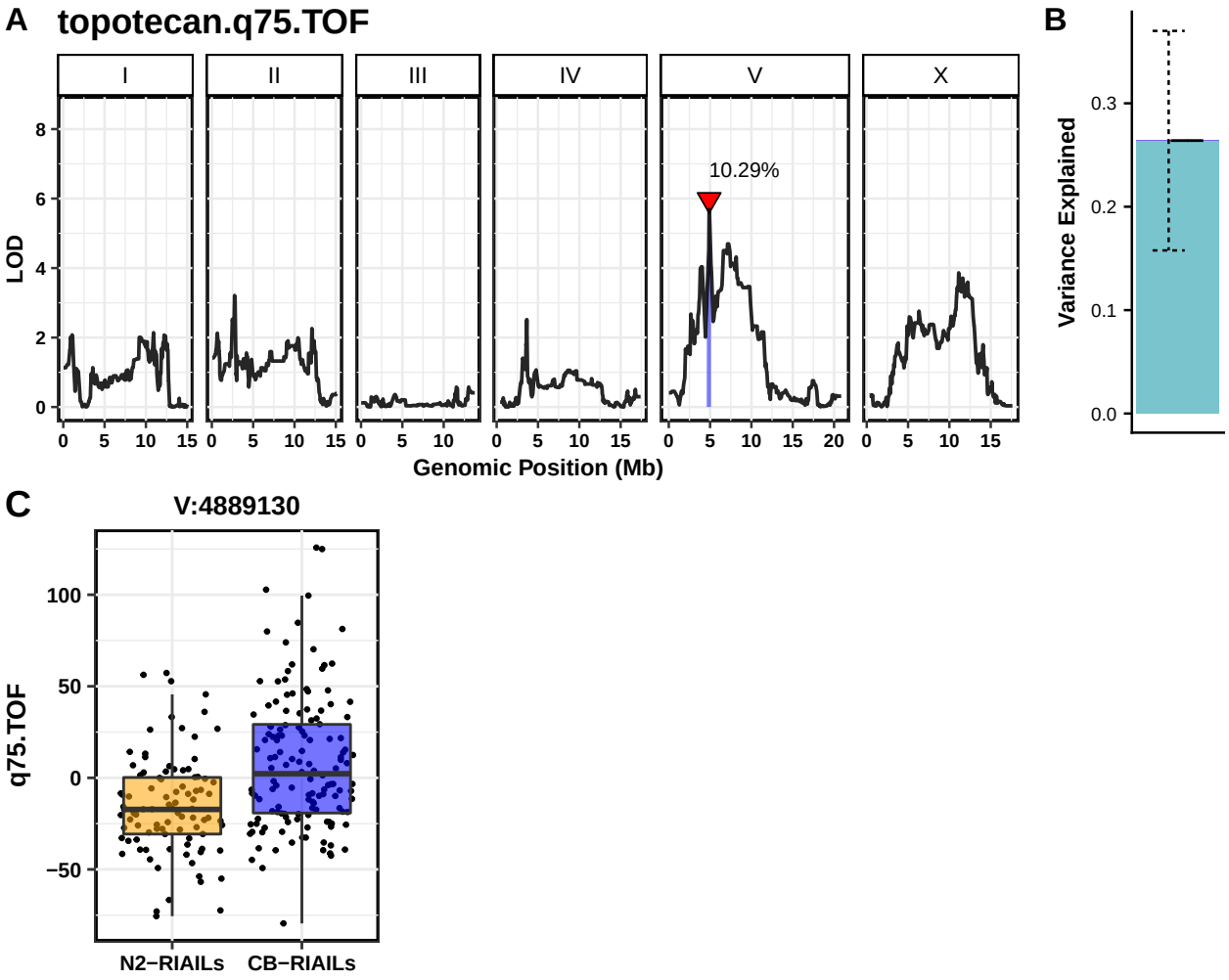

A
topotecan.norm.n
I
II
III
IV
V
X
9.51%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:10170689
norm.n
N2−RIAILs
CB−RIAILs

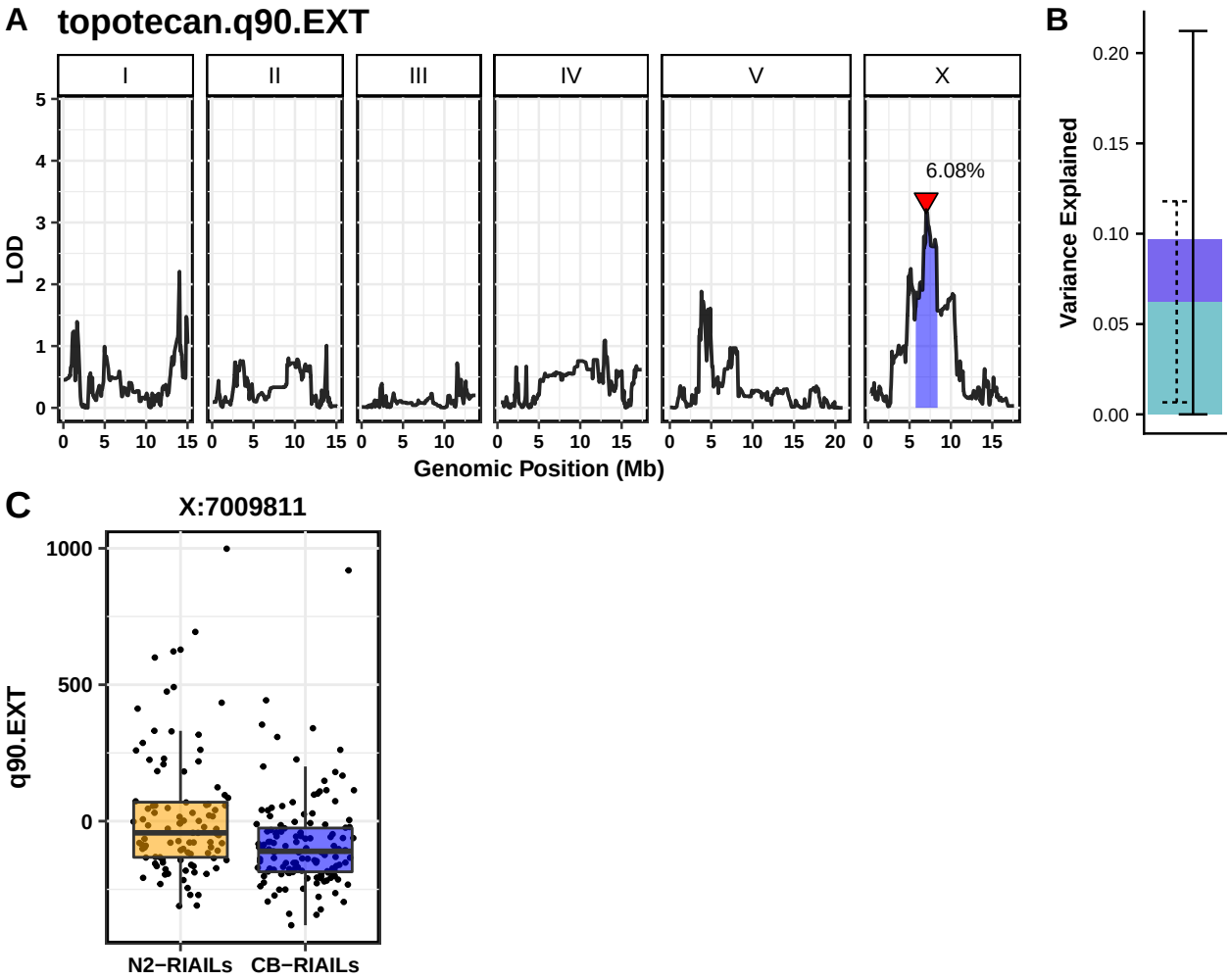

A
topotecan.q10.TOF
I
II
III
IV
V
X
8.65%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:4927583
q10.TOF
N2−RIAILs
CB−RIAILs

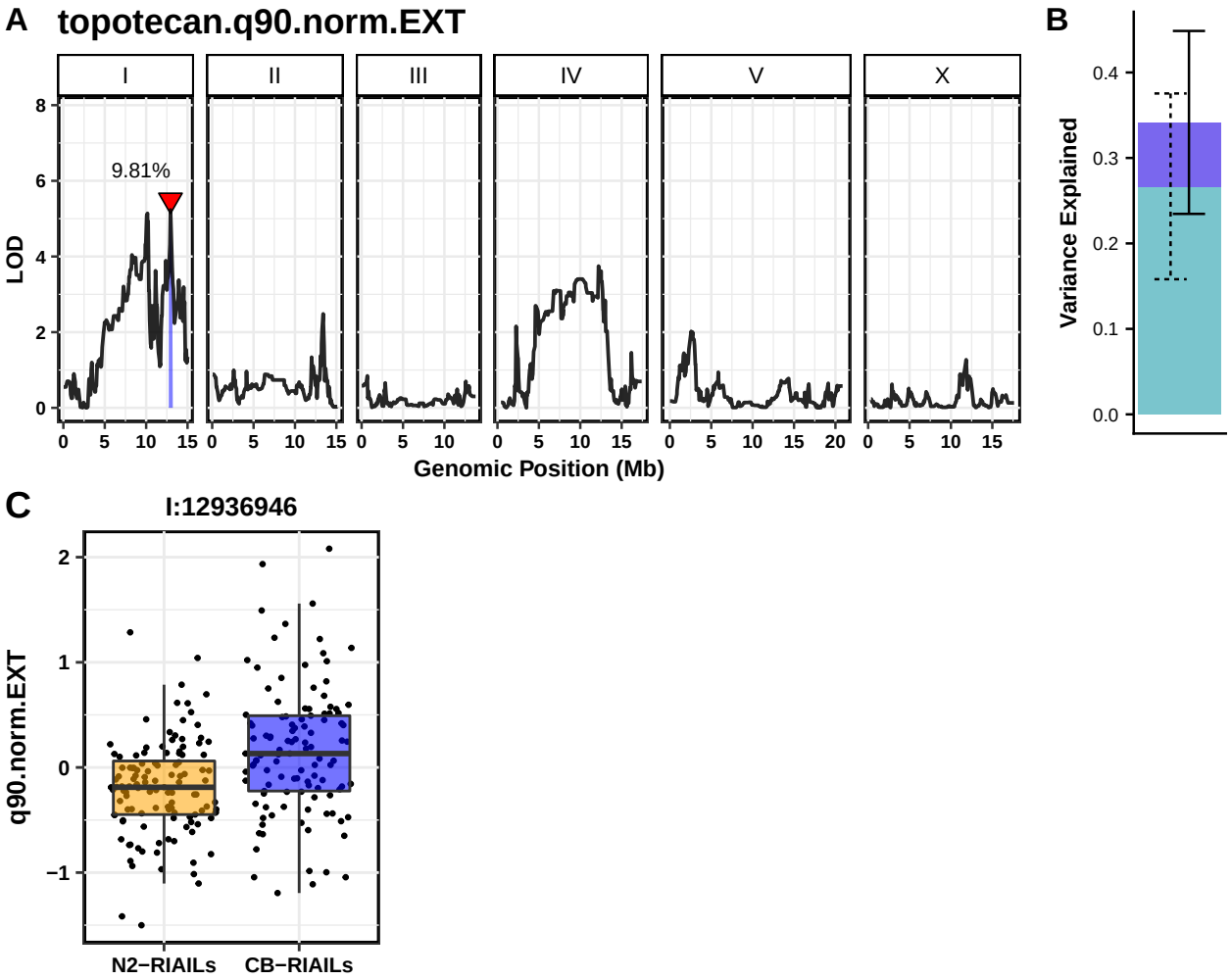

A
topotecan.q25.TOF
I
II
III
IV
V
X
9.05%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:4927583
q25.TOF
N2−RIAILs
CB−RIAILs

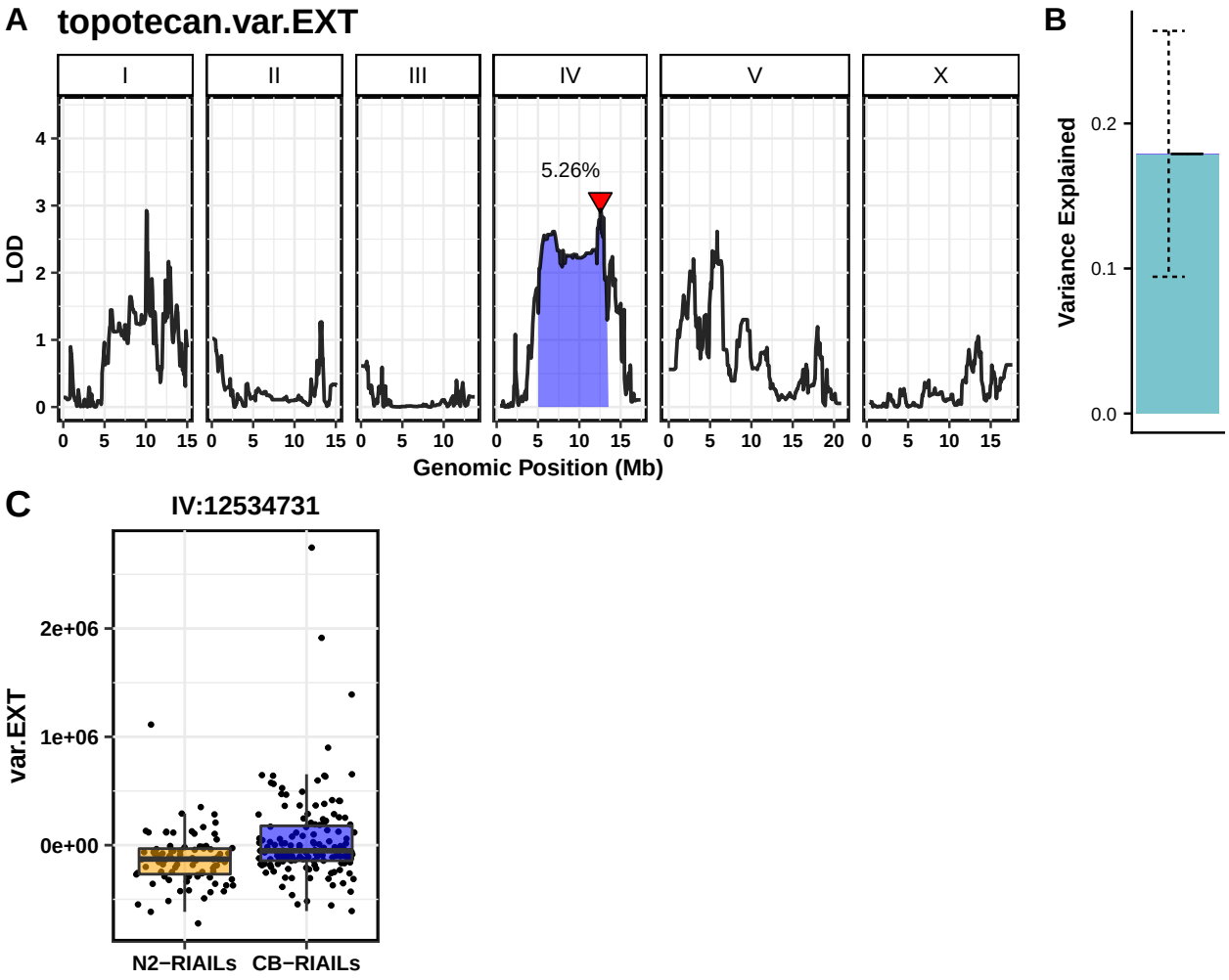

A
topotecan.q75.EXT
I
II
III
IV
V
X
LOD
8.91%
Genomic Position (Mb)
B
Variance Explained
C
X:5152523
q75.EXT
N2−RIAILs
CB−RIAILs

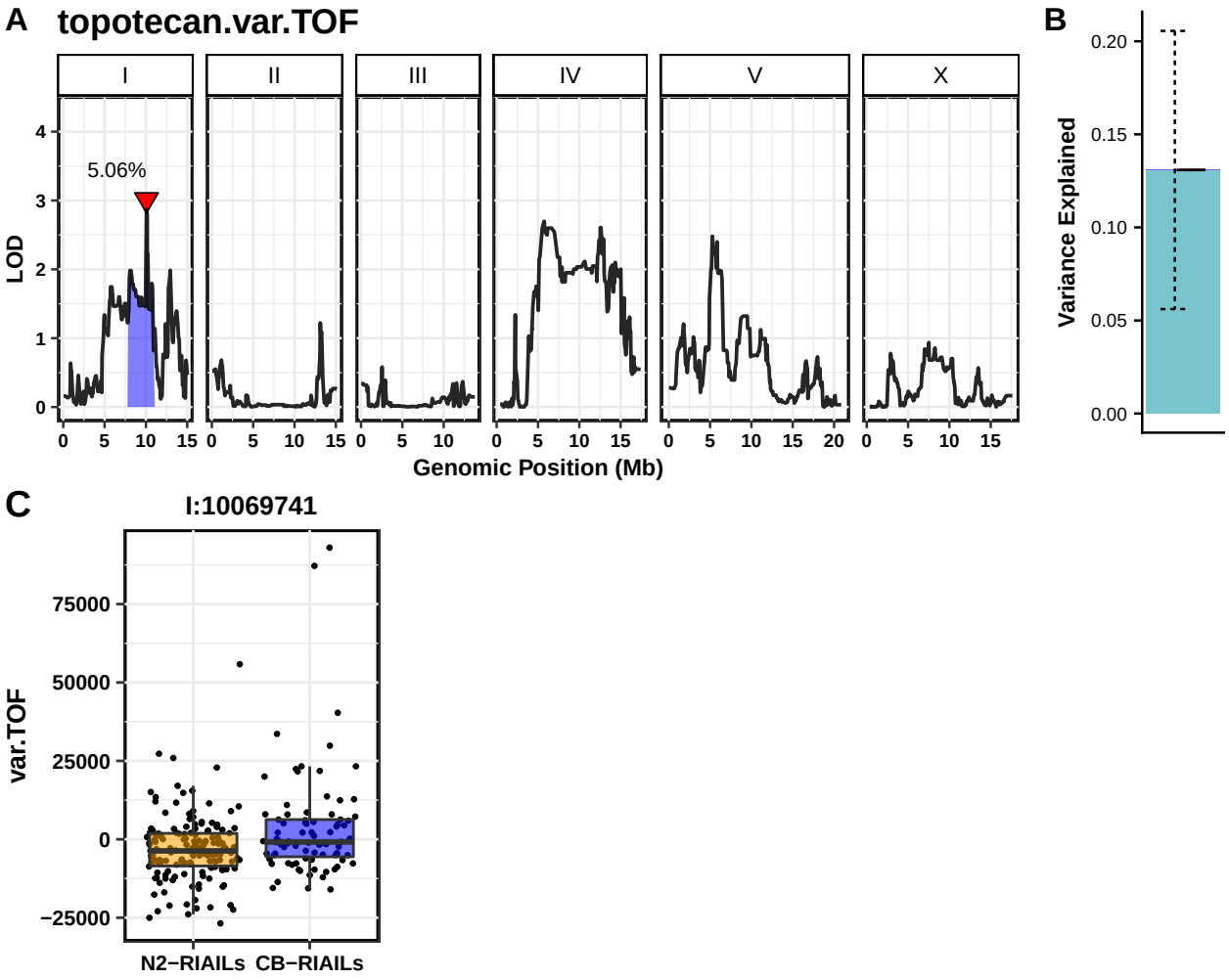

A
topotecan.q75.norm.EXT
I
II
III
IV
V
X
8.66%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:12936946
q75.norm.EXT
N2−RIAILs
CB−RIAILs

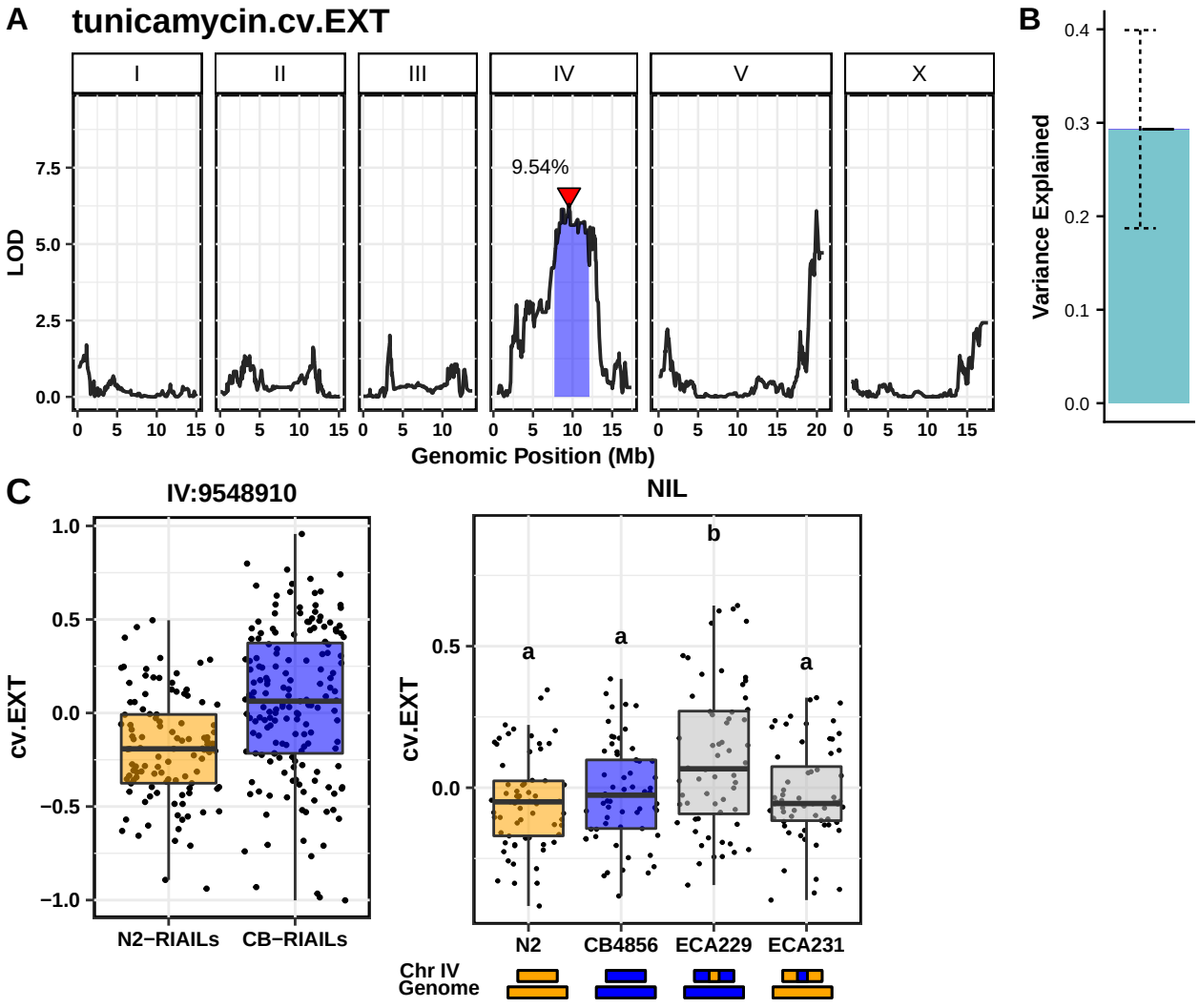

A
topotecan.q75.TOF
I
II
III
IV
V
X
10.29%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:4889130
q75.TOF
N2−RIAILs
CB−RIAILs

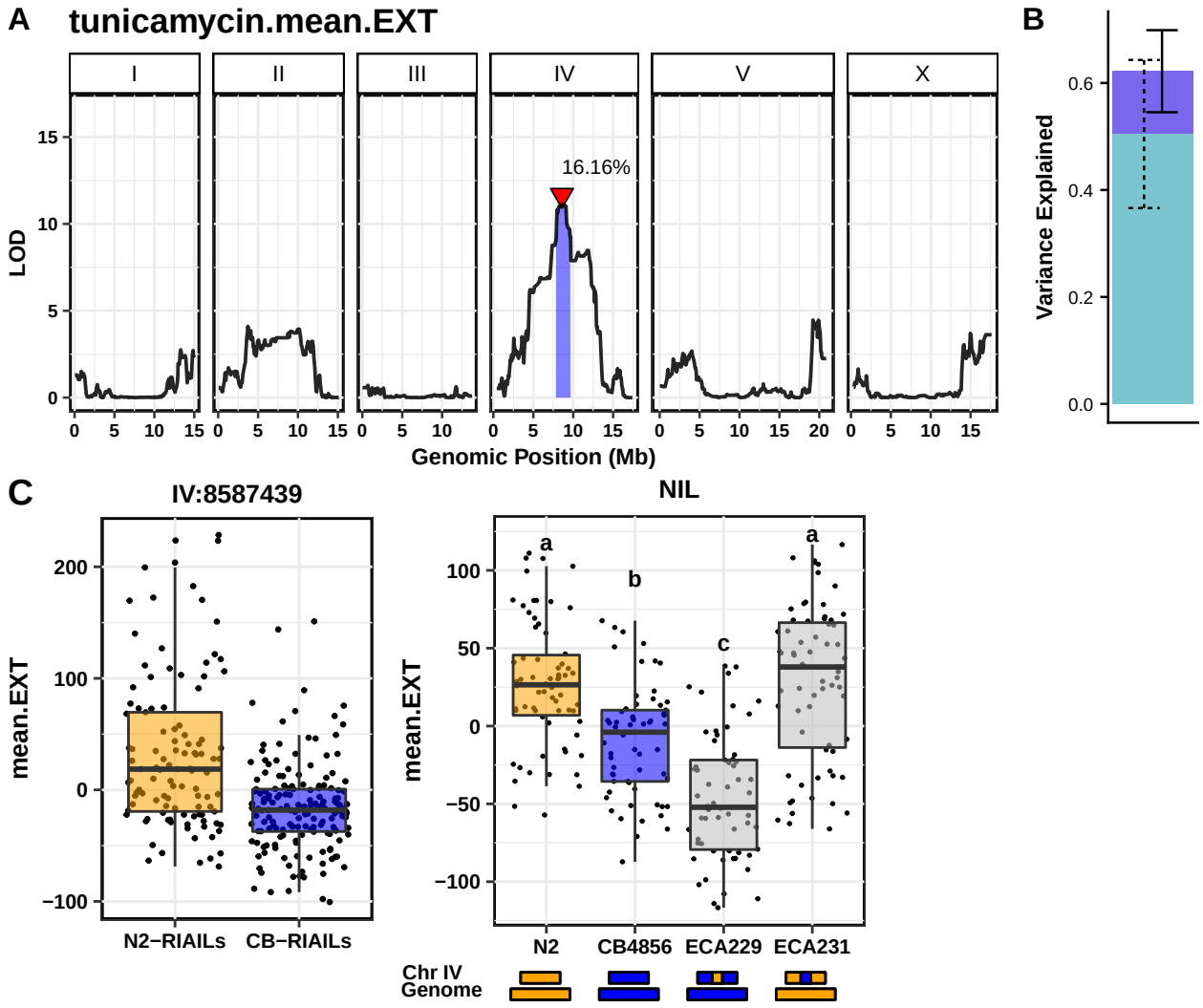

A
topotecan.q90.EXT
I
II
III
IV
V
X
6.08%
LOD
Genomic Position (Mb)
B
Variance Explained
C
X:7009811
q90.EXT
N2−RIAILs
CB−RIAILs

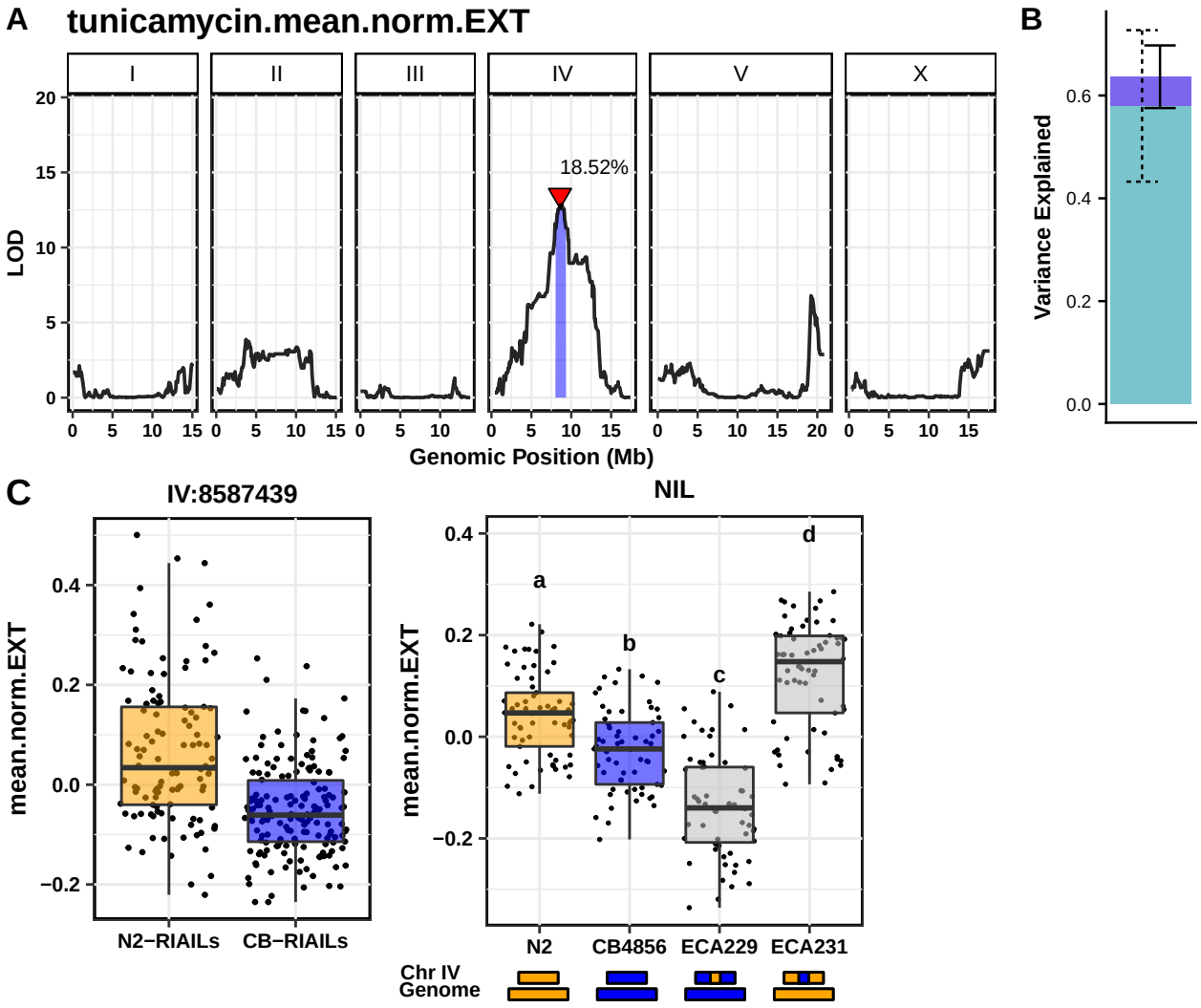

A
topotecan.q90.norm.EXT
I
II
III
IV
V
X
9.81%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:12936946
q90.norm.EXT
N2−RIAILs
CB−RIAILs

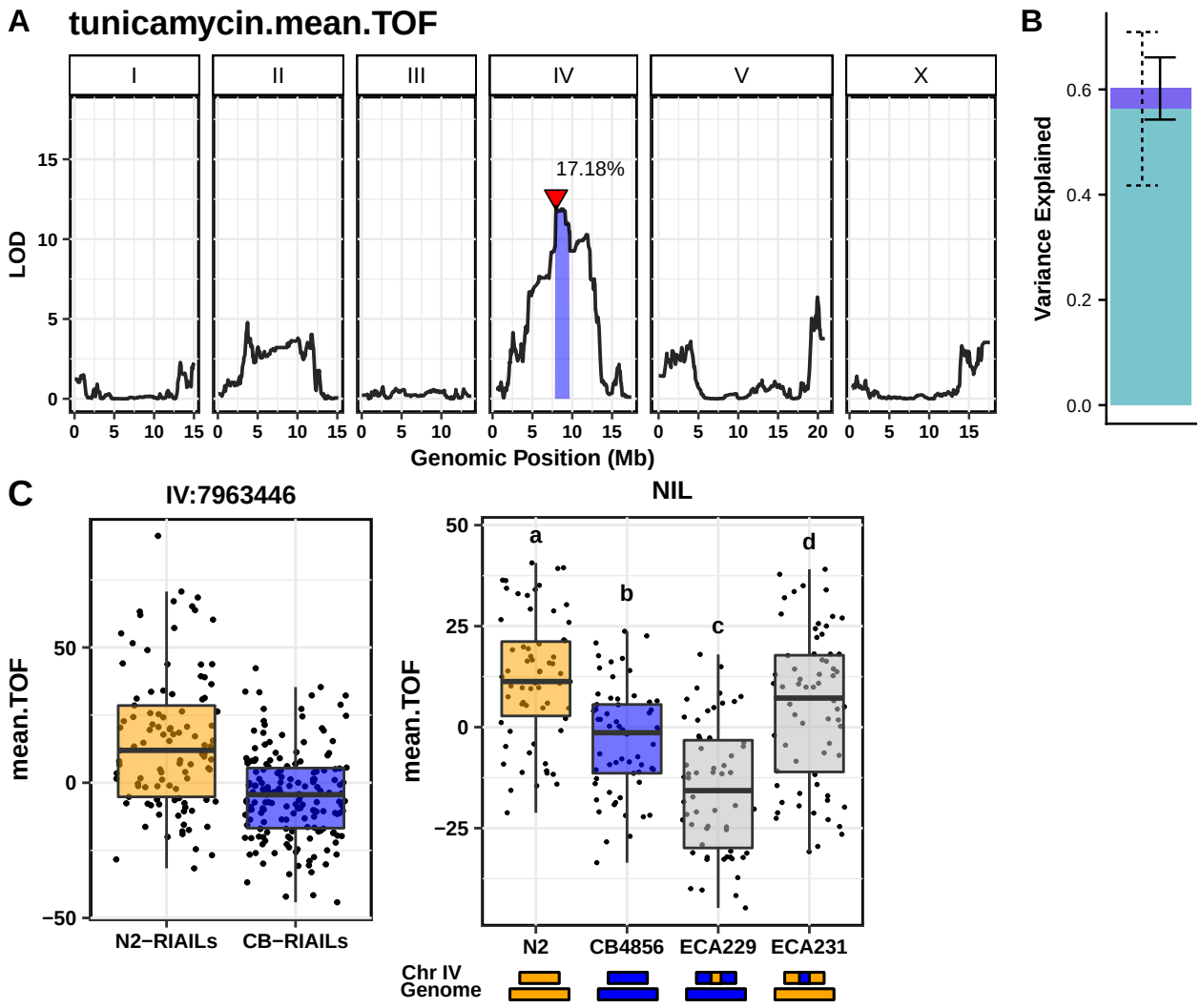

A
topotecan.var.EXT
I
II
III
IV
V
X
5.26%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:12534731
var.EXT
N2−RIAILs
CB−RIAILs

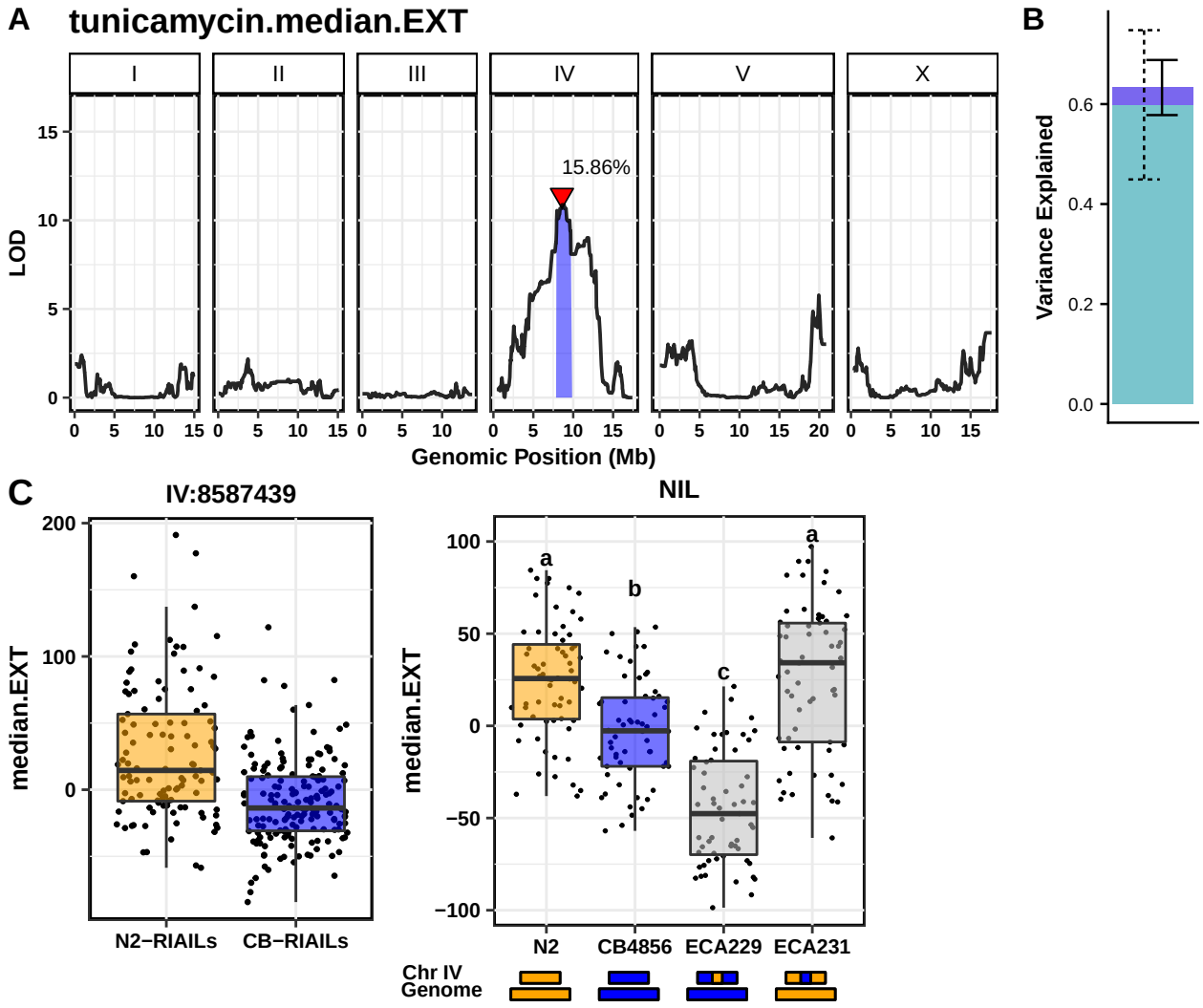

A
topotecan.var.TOF
I
II
III
IV
V
X
5.06%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:10069741
var.TOF
N2−RIAILs
CB−RIAILs

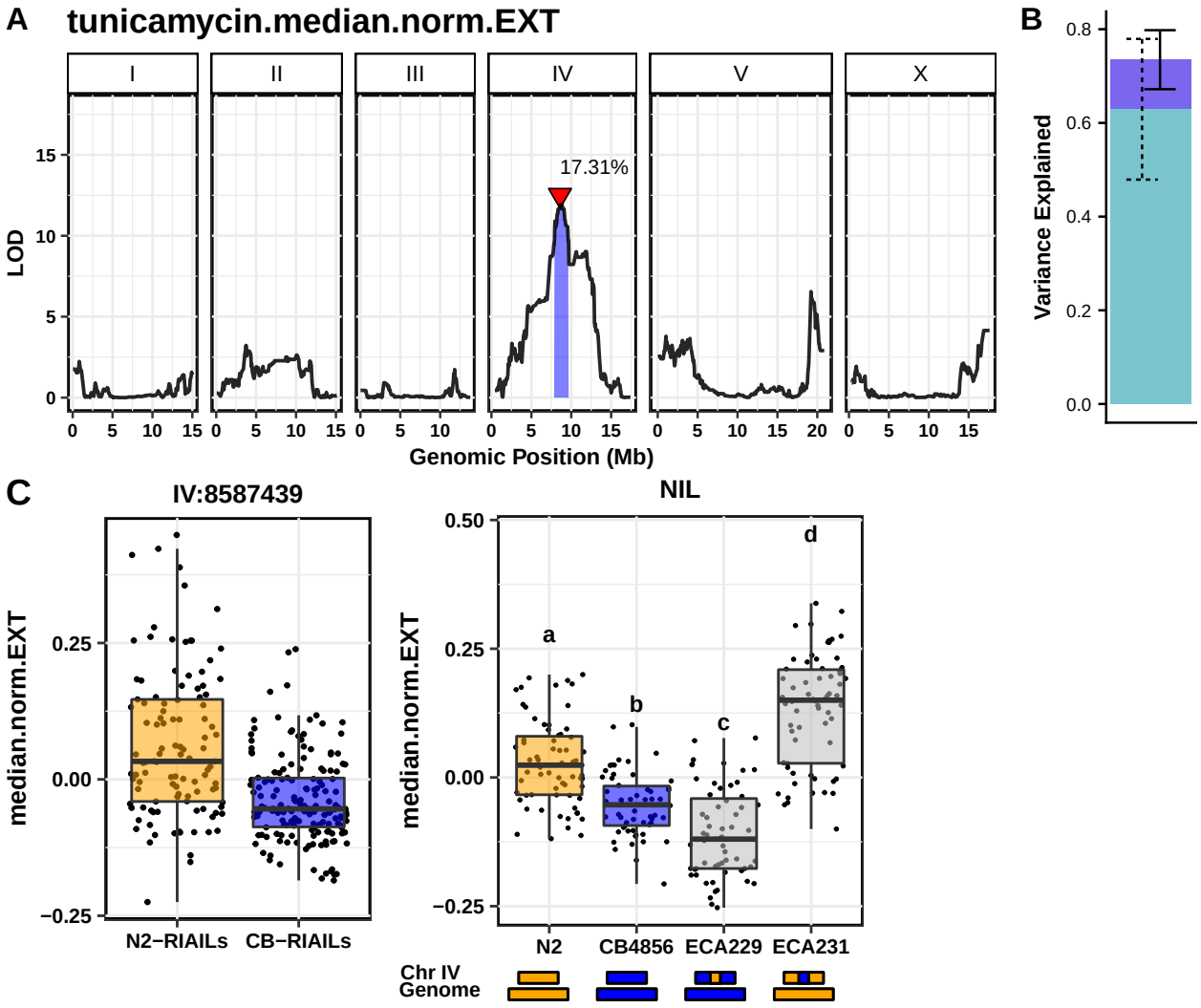

A
tunicamycin.cv.EXT
I
II
III
IV
V
X
9.54%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:9548910
cv.EXT
N2−RIAILs
CB−RIAILs
NIL
a
a
b
a
N2
CB4856
ECA229
ECA231
Chr IV
Genome

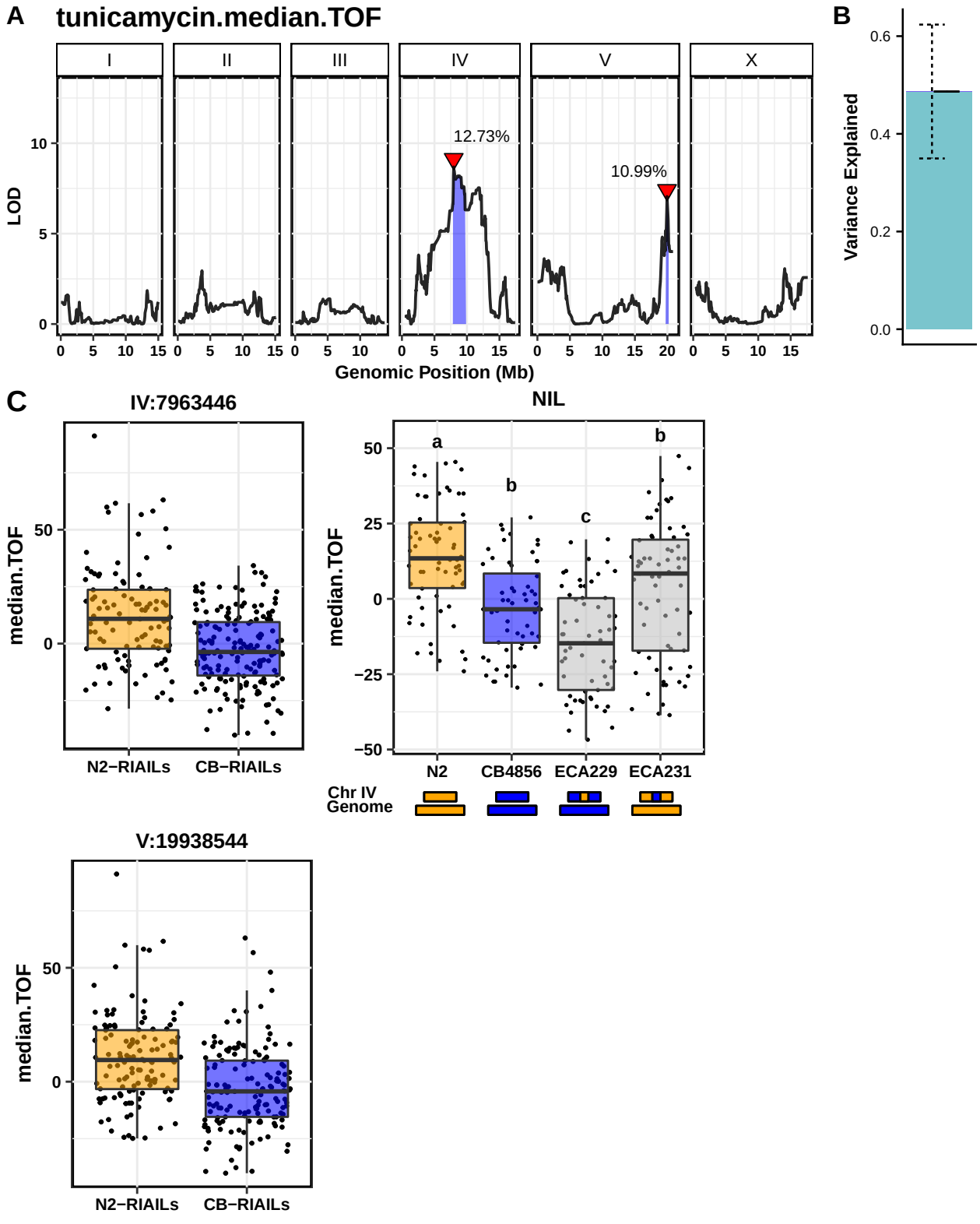

A
tunicamycin.mean.EXT
I
II
III
IV
V
X
16.16%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:8587439
mean.EXT
N2−RIAILs
CB−RIAILs
NIL
a
b
c
a
N2
CB4856
ECA229
ECA231
Chr IV
Genome

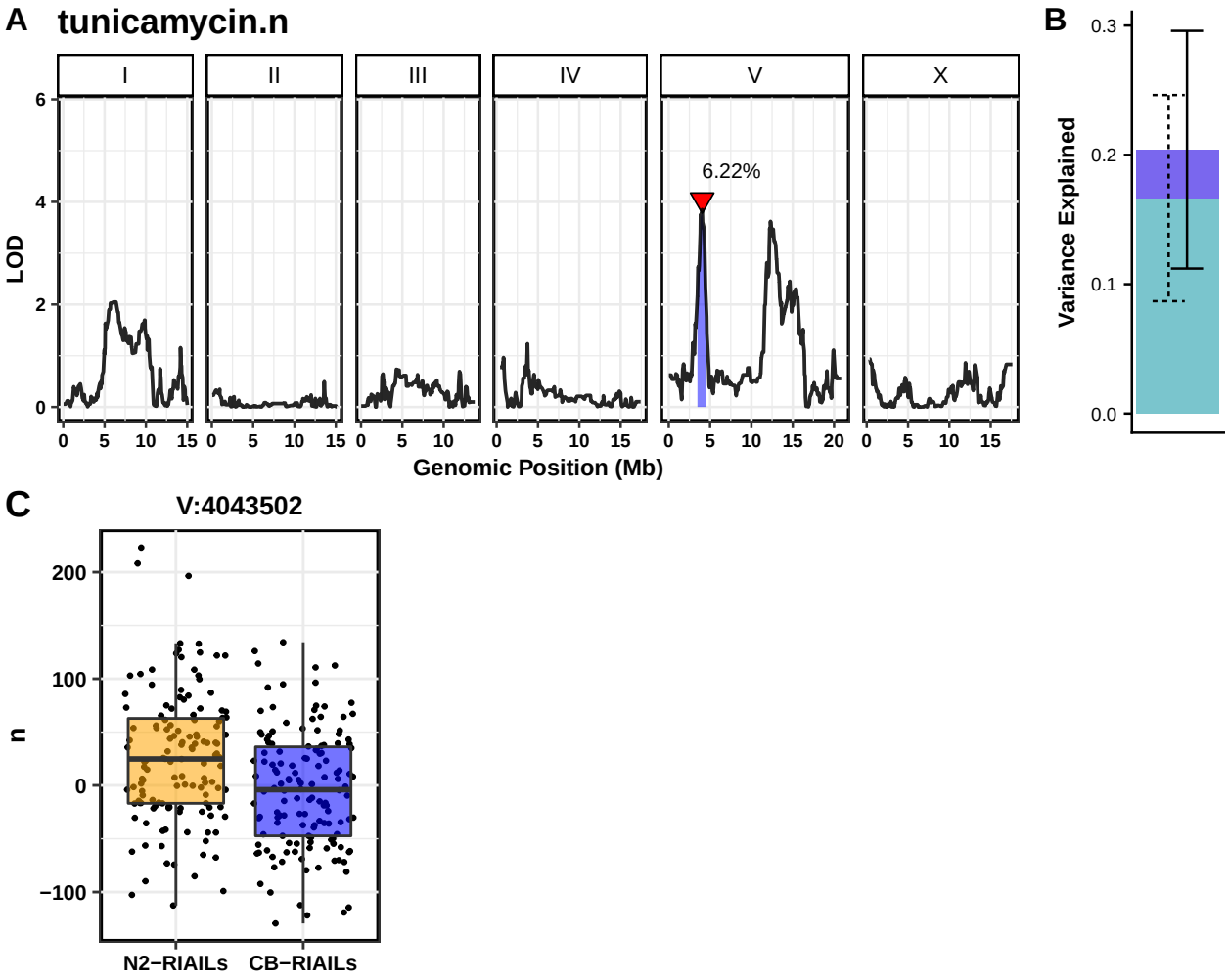

A
tunicamycin.mean.norm.EXT
I
II
III
IV
V
X
18.52%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:8587439
mean.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
a
b
c
d
N2
CB4856
ECA229
ECA231
Chr IV
Genome

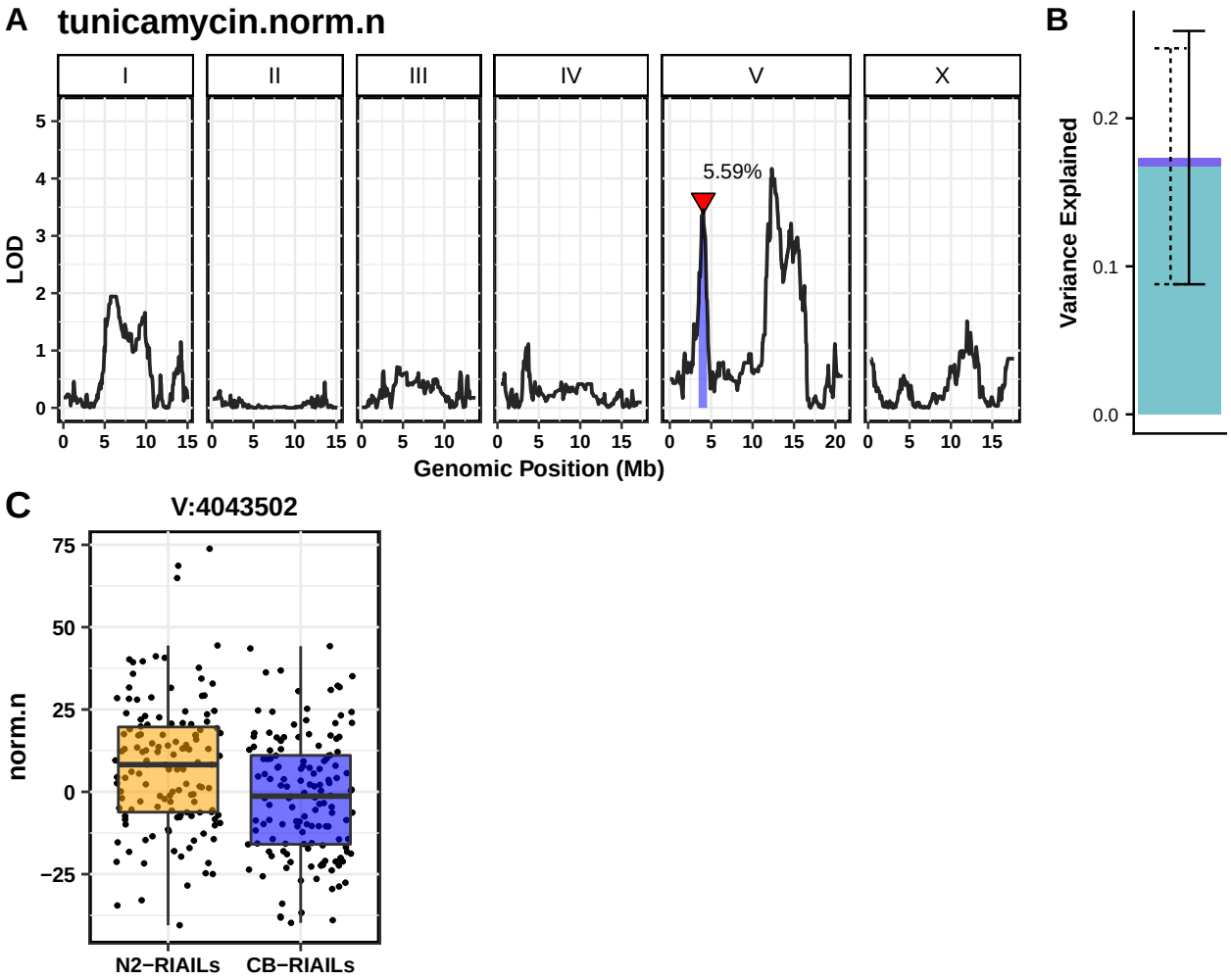

A
tunicamycin.mean.TOF
I
II
III
IV
V
X
17.18%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:7963446
mean.TOF
N2−RIAILs
CB−RIAILs
NIL
a
b
c
d
N2
CB4856
ECA229
ECA231
Chr IV
Genome

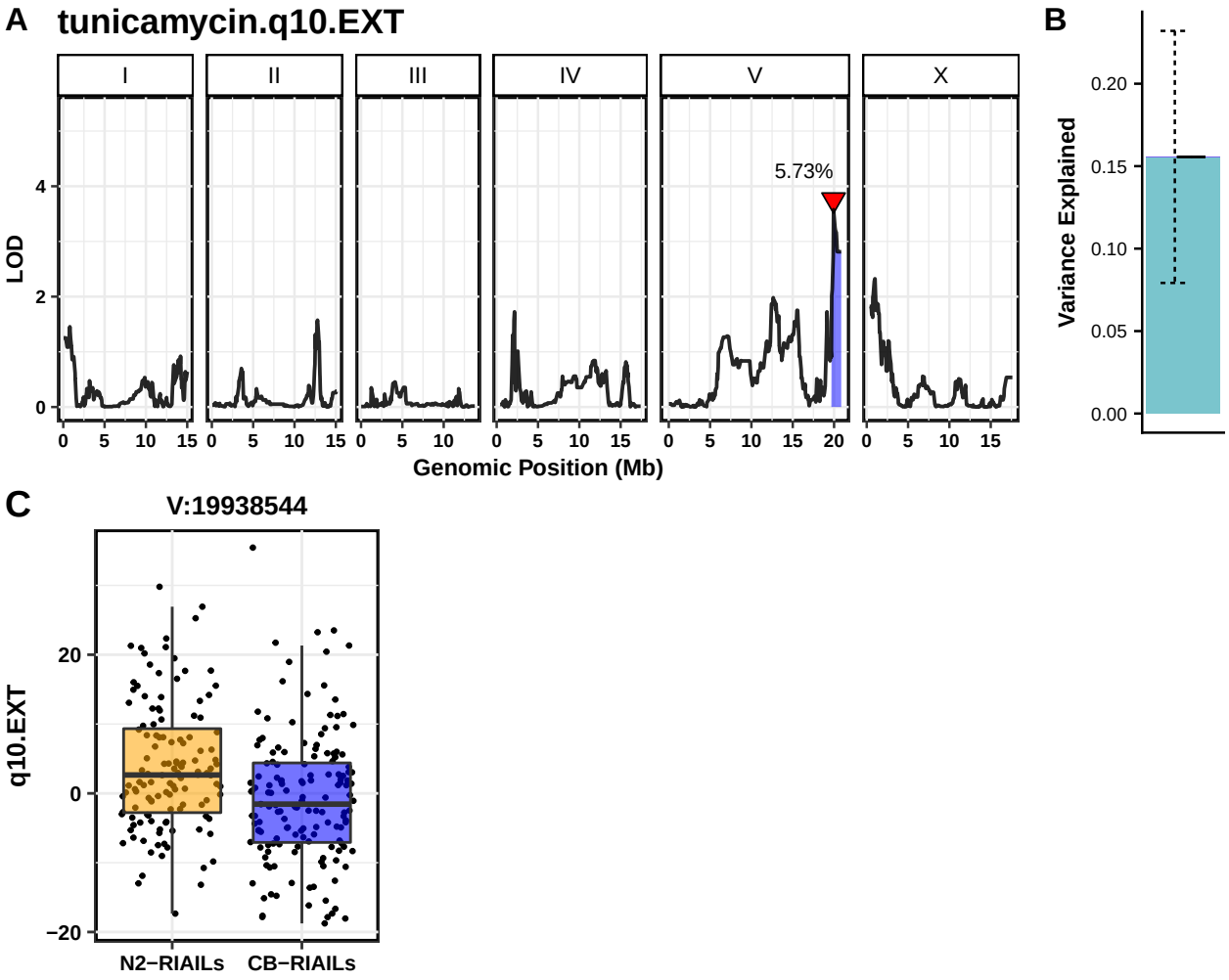

A
tunicamycin.median.EXT
I
II
III
IV
V
X
15.86%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:8587439
median.EXT
N2−RIAILs
CB−RIAILs
NIL
a
b
c
a
N2
CB4856
ECA229
ECA231
Chr IV
Genome

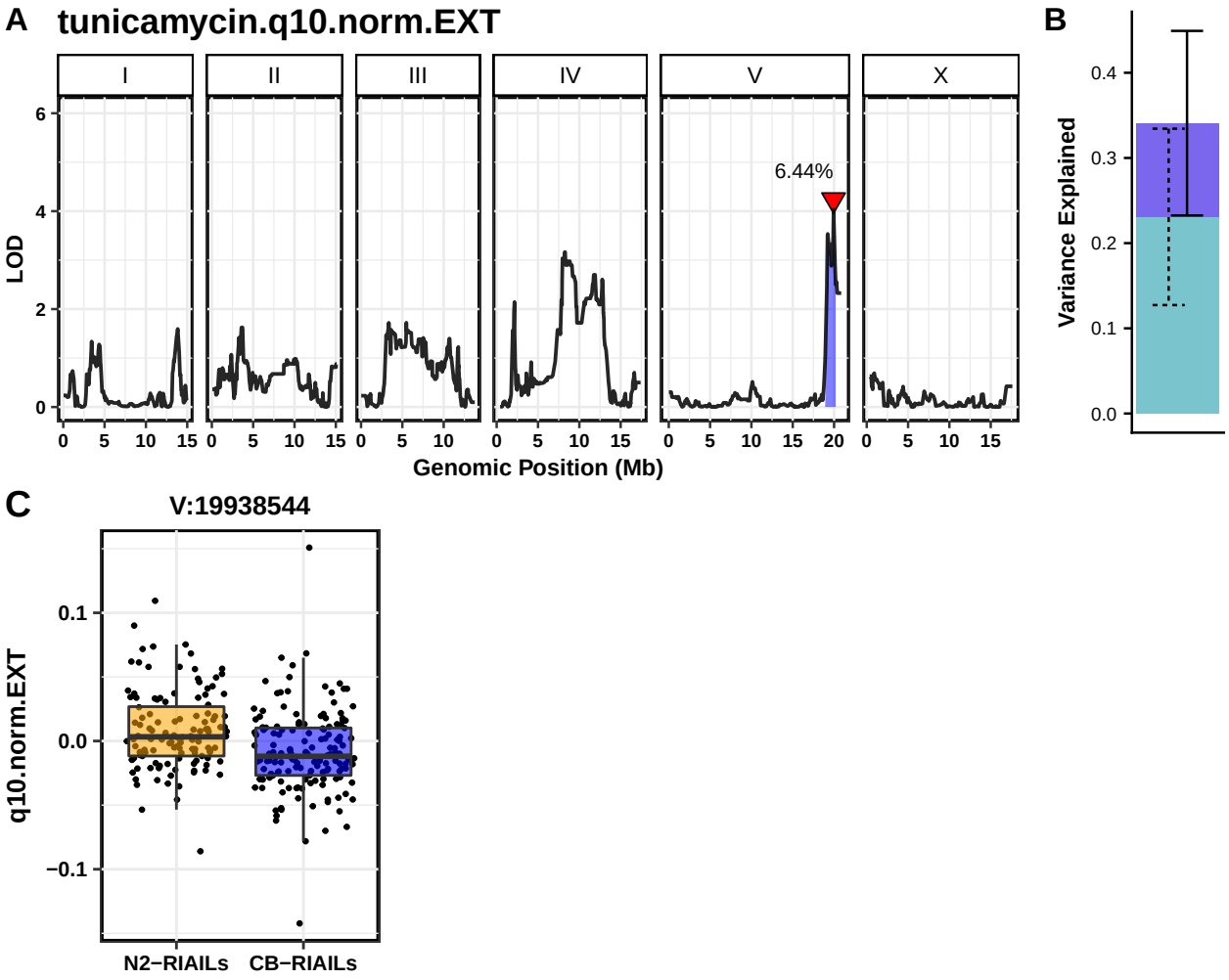

A
tunicamycin.median.norm.EXT
I
II
III
IV
V
X
LOD
17.31%
Genomic Position (Mb)
B
Variance Explained
C
IV:8587439
median.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
a
b
c
d
N2
CB4856
ECA229
ECA231
Chr IV
Genome

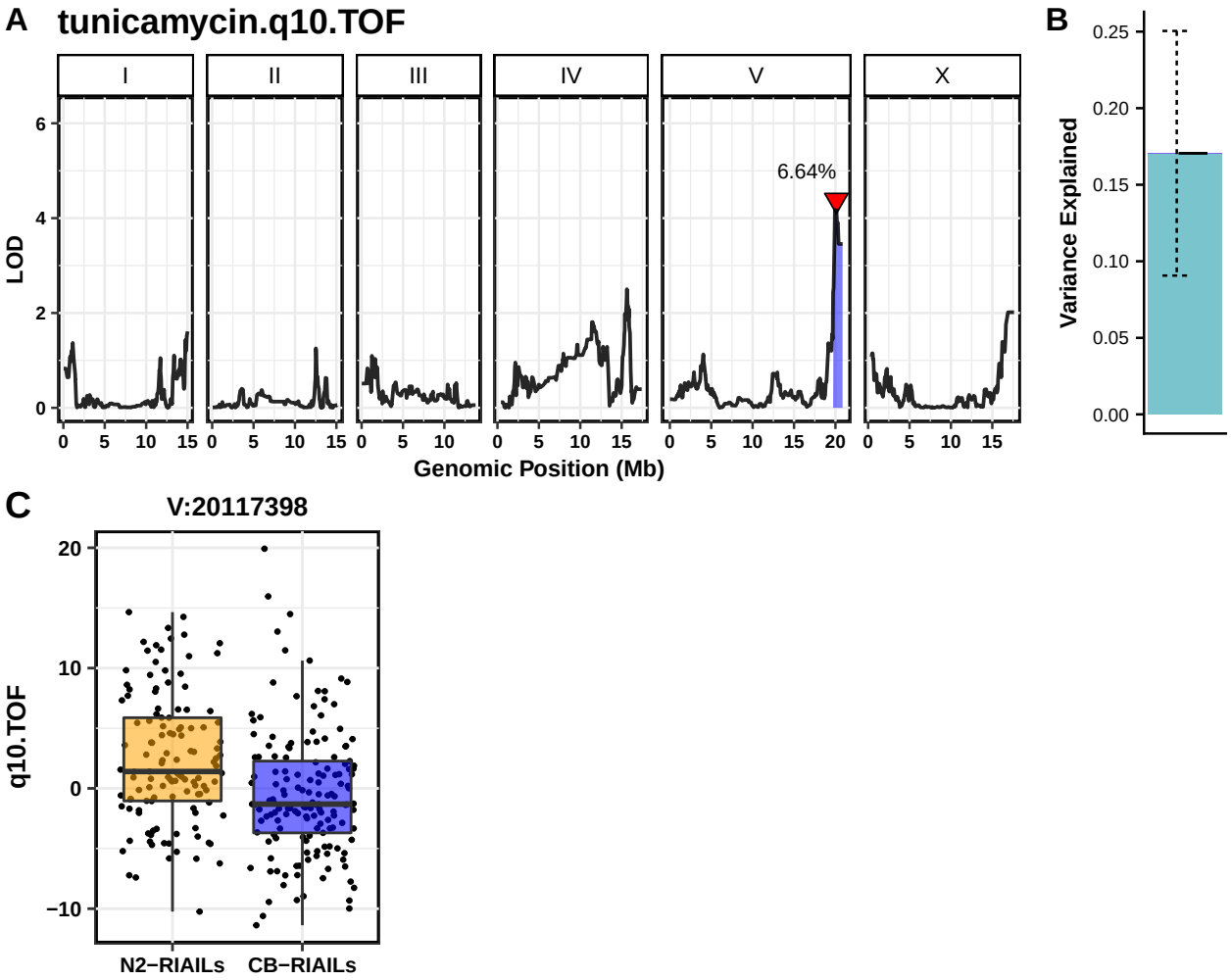

A
tunicamycin.median.TOF
I
II
III
IV
V
X
LOD
12.73%
10.99%
Genomic Position (Mb)
B
Variance Explained
C
IV:7963446
median.TOF
N2−RIAILs
CB−RIAILs
NIL
a
b
c
b
N2
CB4856
ECA229
ECA231
Chr IV
Genome
V:19938544

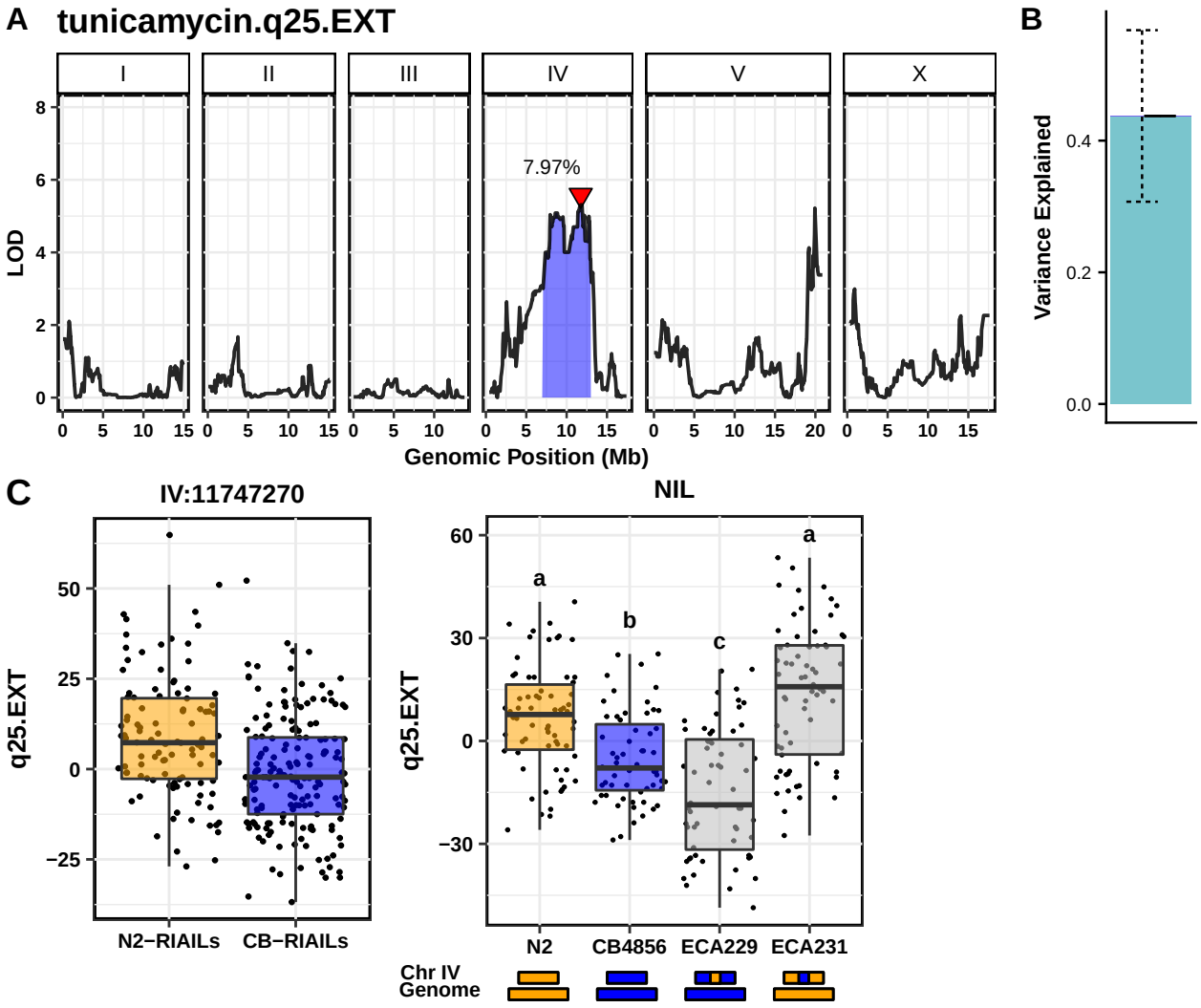

A
tunicamycin.n
I
II
III
IV
V
X
6.22%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:4043502
n
N2−RIAILs
CB−RIAILs

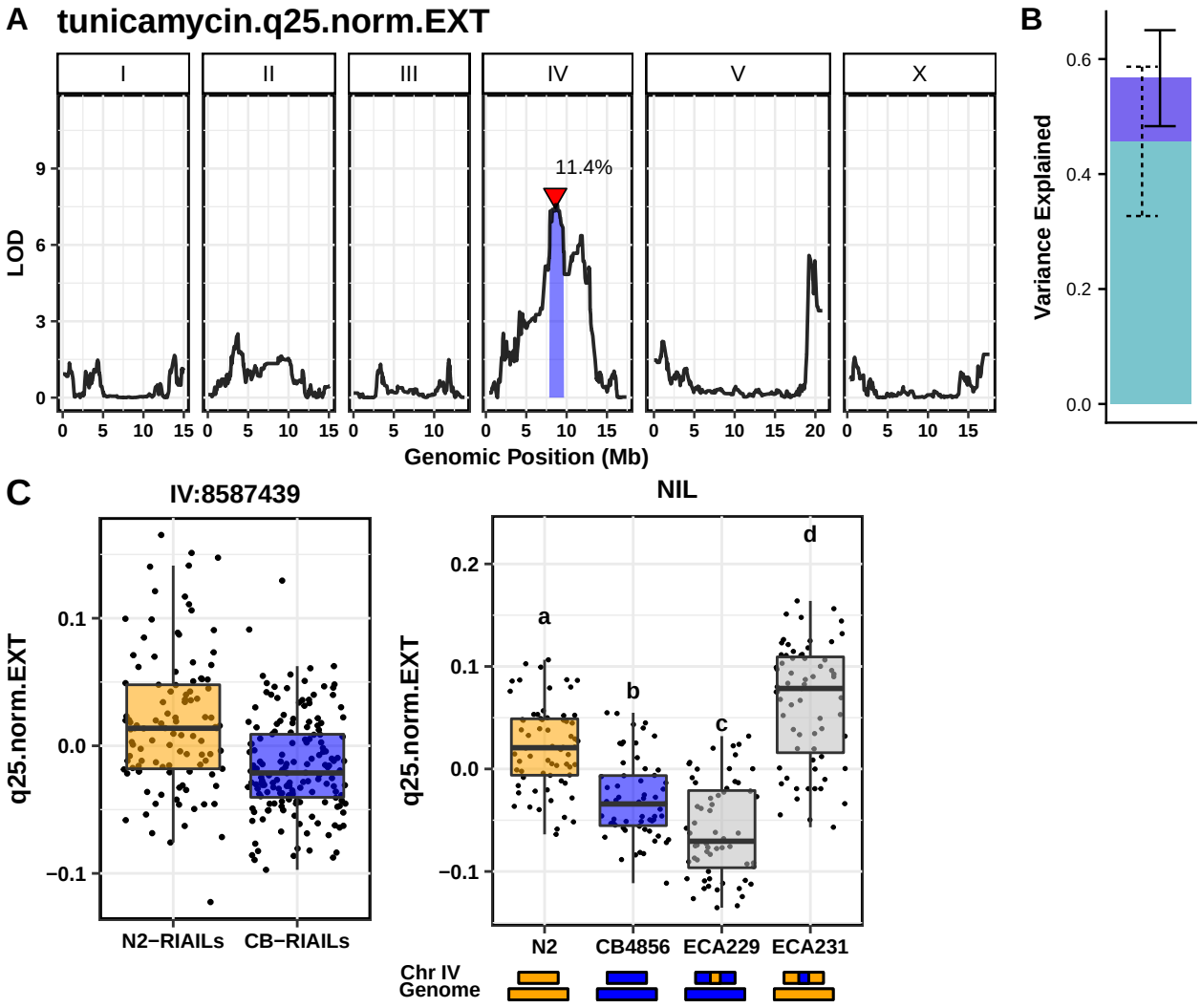

A
tunicamycin.norm.n
I
II
III
IV
V
X
LOD
5.59%
Genomic Position (Mb)
B
Variance Explained
C
V:4043502
norm.n
N2−RIAILs
CB−RIAILs

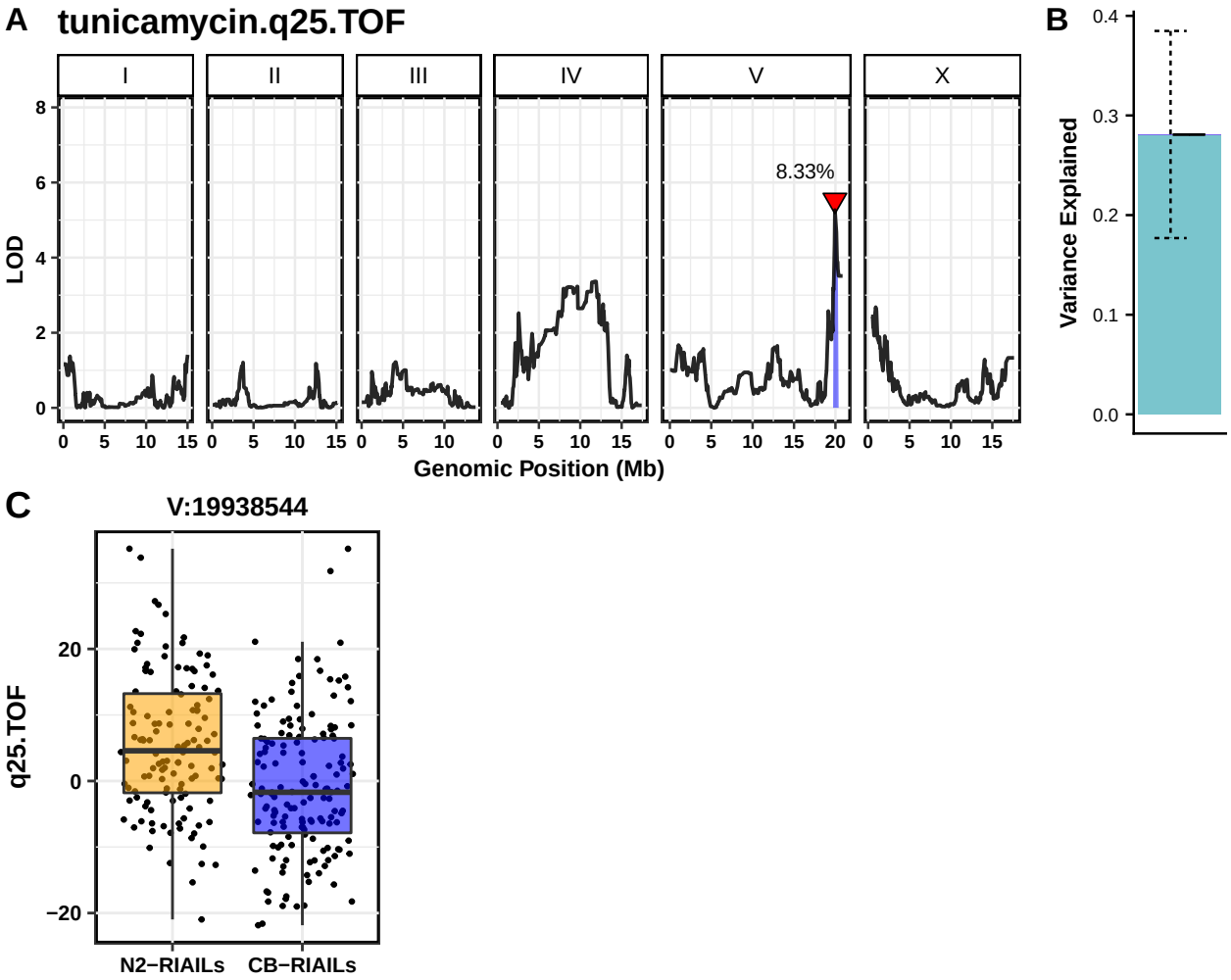

A
tunicamycin.q10.EXT
I
II
III
IV
V
X
5.73%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:19938544
q10.EXT
N2−RIAILs
CB−RIAILs

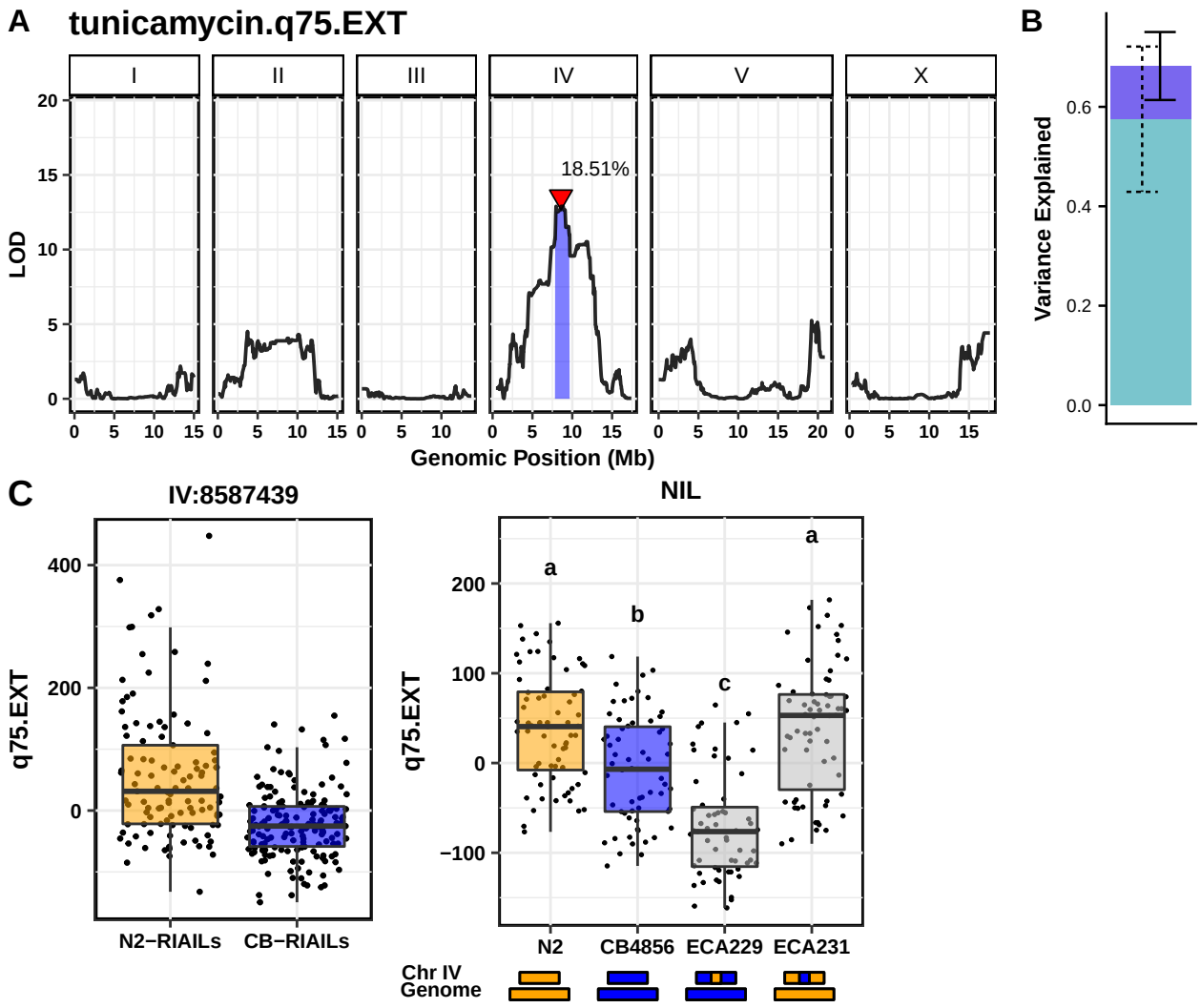

A
tunicamycin.q10.norm.EXT
I
II
III
IV
V
X
6.44%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:19938544
q10.norm.EXT
N2−RIAILs
CB−RIAILs

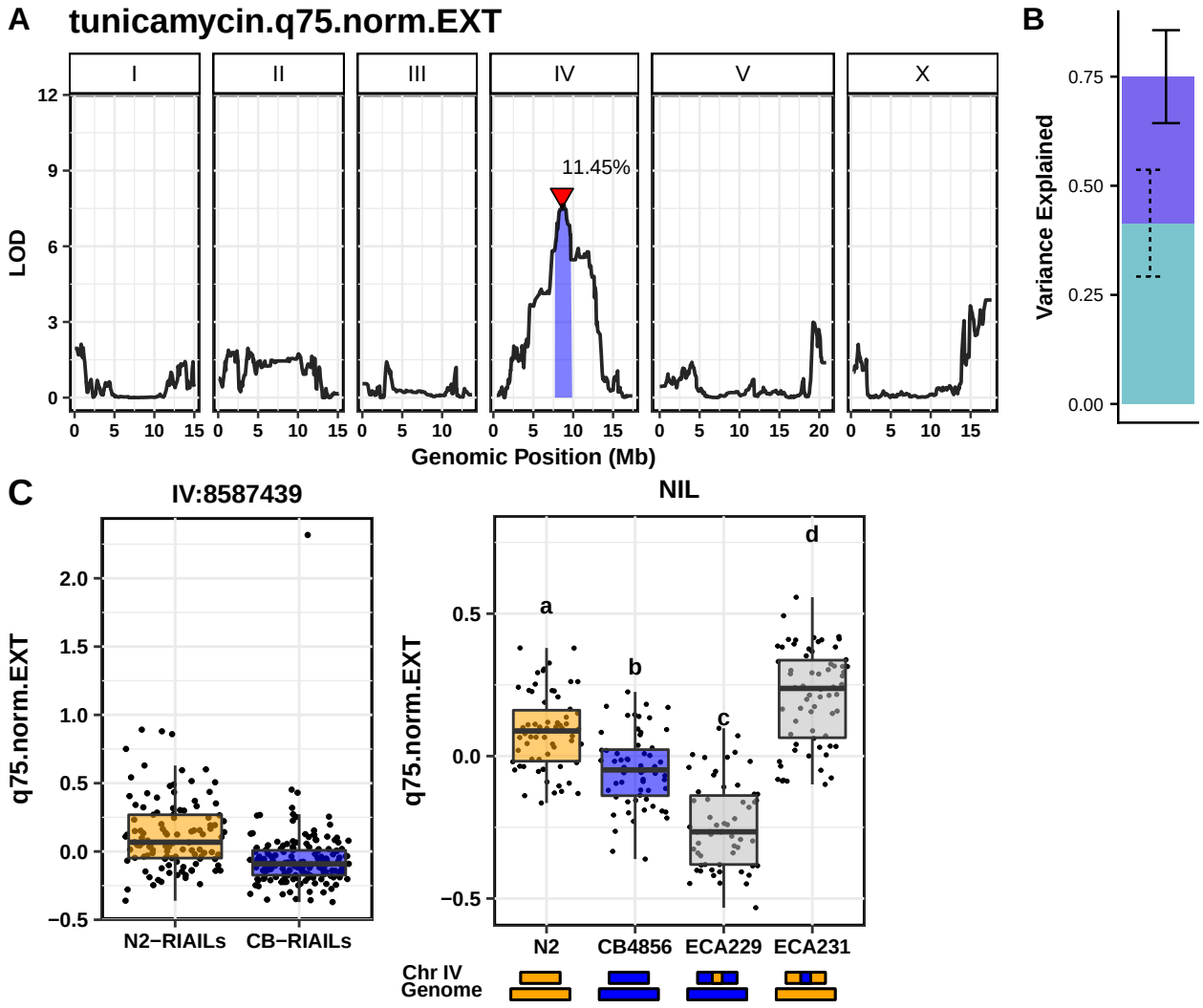

A
tunicamycin.q10.TOF
I
II
III
IV
V
X
6.64%
LOD
Genomic Position (Mb)
B
Variance Explained
C
V:20117398
q10.TOF
N2−RIAILs
CB−RIAILs

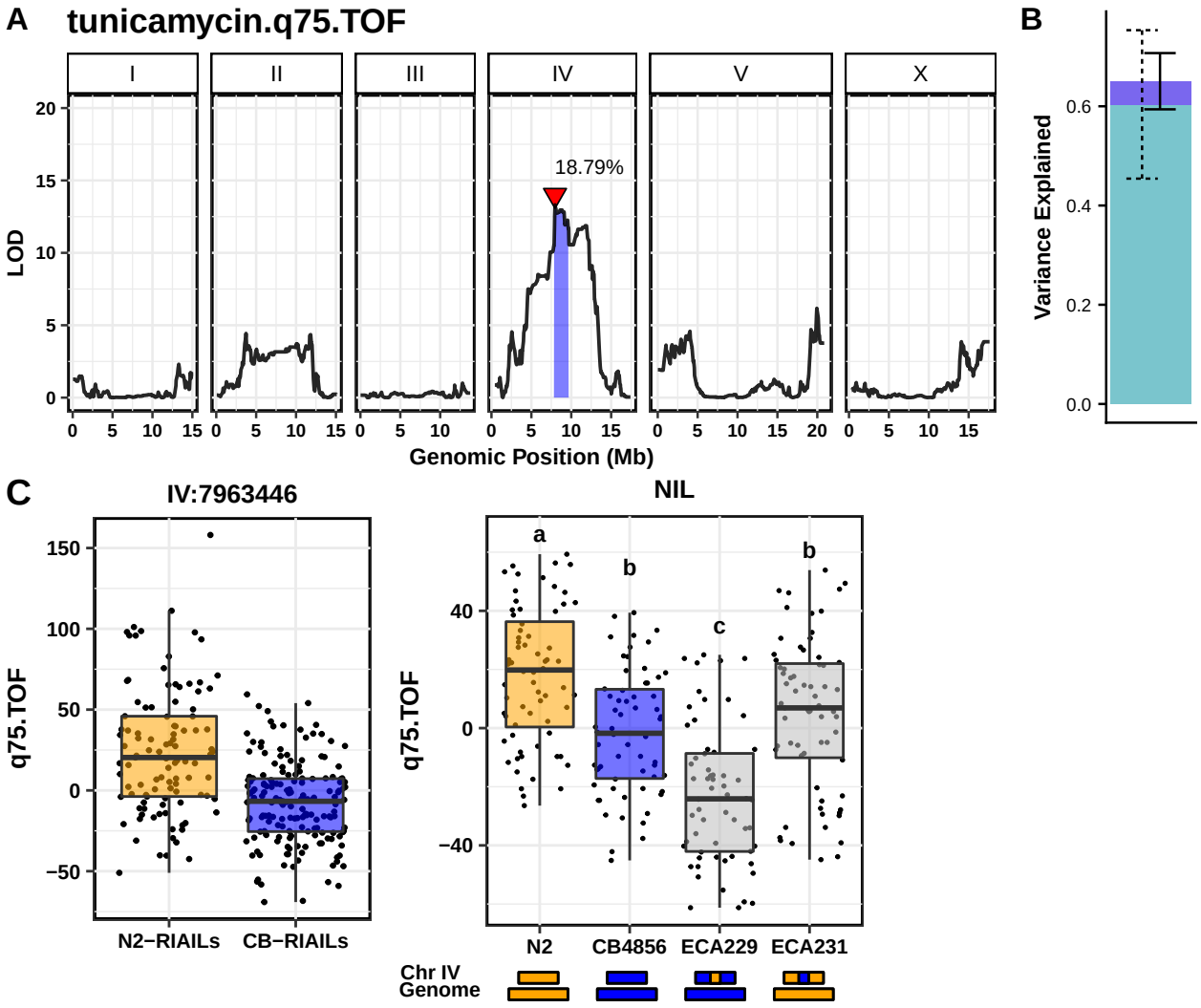

A
tunicamycin.q25.EXT
I
II
III
IV
V
X
7.97%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:11747270
q25.EXT
N2−RIAILs
CB−RIAILs
NIL
a
b
c
a
N2
CB4856
ECA229
ECA231
Chr IV
Genome

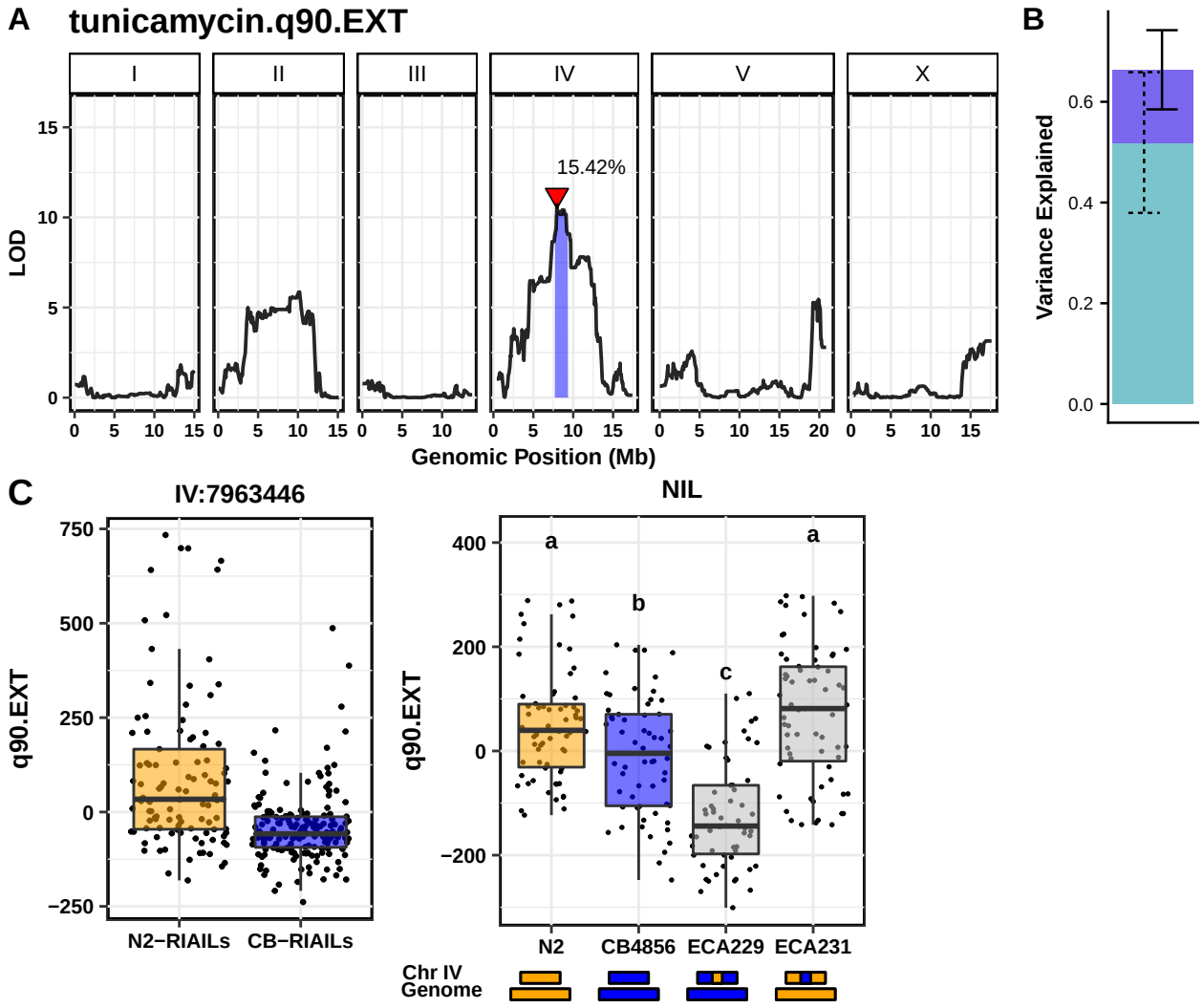

A
tunicamycin.q25.norm.EXT
I
II
III
IV
V
X
11.4%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:8587439
q25.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
a
b
c
d
N2
CB4856
ECA229
ECA231
Chr IV
Genome

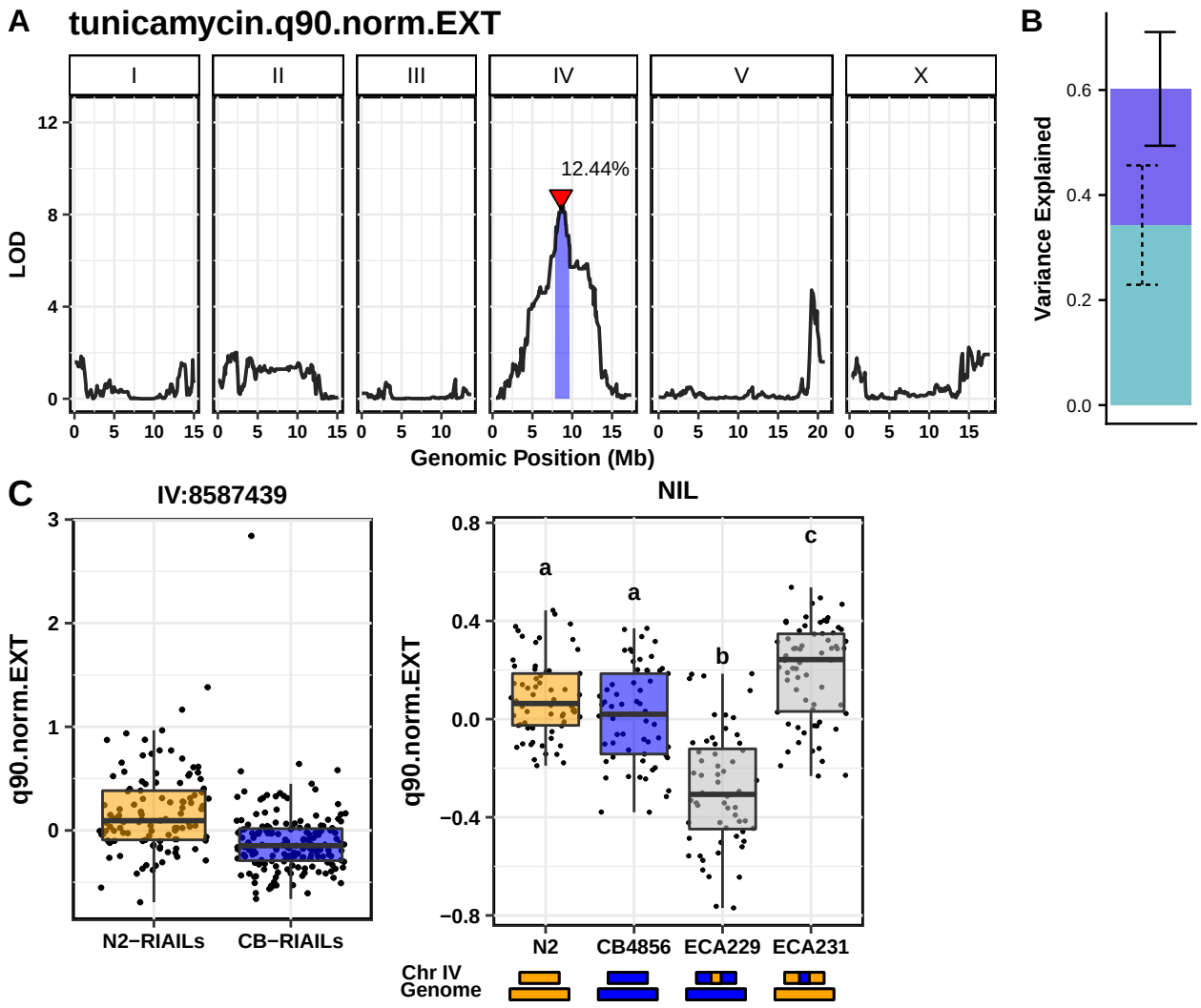

A
tunicamycin.q25.TOF
I
II
III
IV
V
X
LOD
8.33%
Genomic Position (Mb)
B
Variance Explained
C
V:19938544
q25.TOF
N2−RIAILs
CB−RIAILs

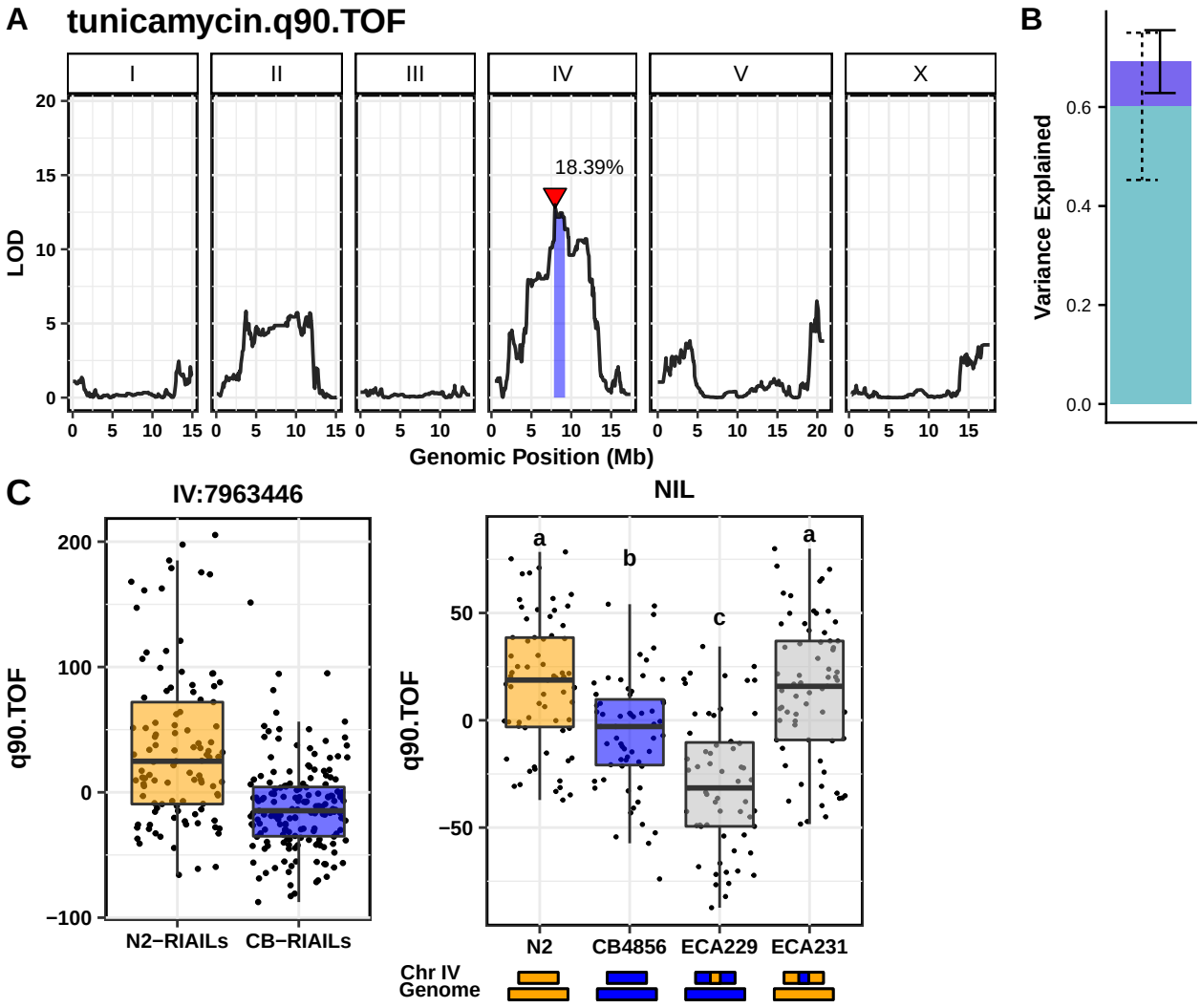

A
tunicamycin.q75.EXT
I
II
III
IV
V
X
18.51%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:8587439
q75.EXT
N2−RIAILs
CB−RIAILs
NIL
a
b
c
a
N2
CB4856
ECA229
ECA231
Chr IV
Genome

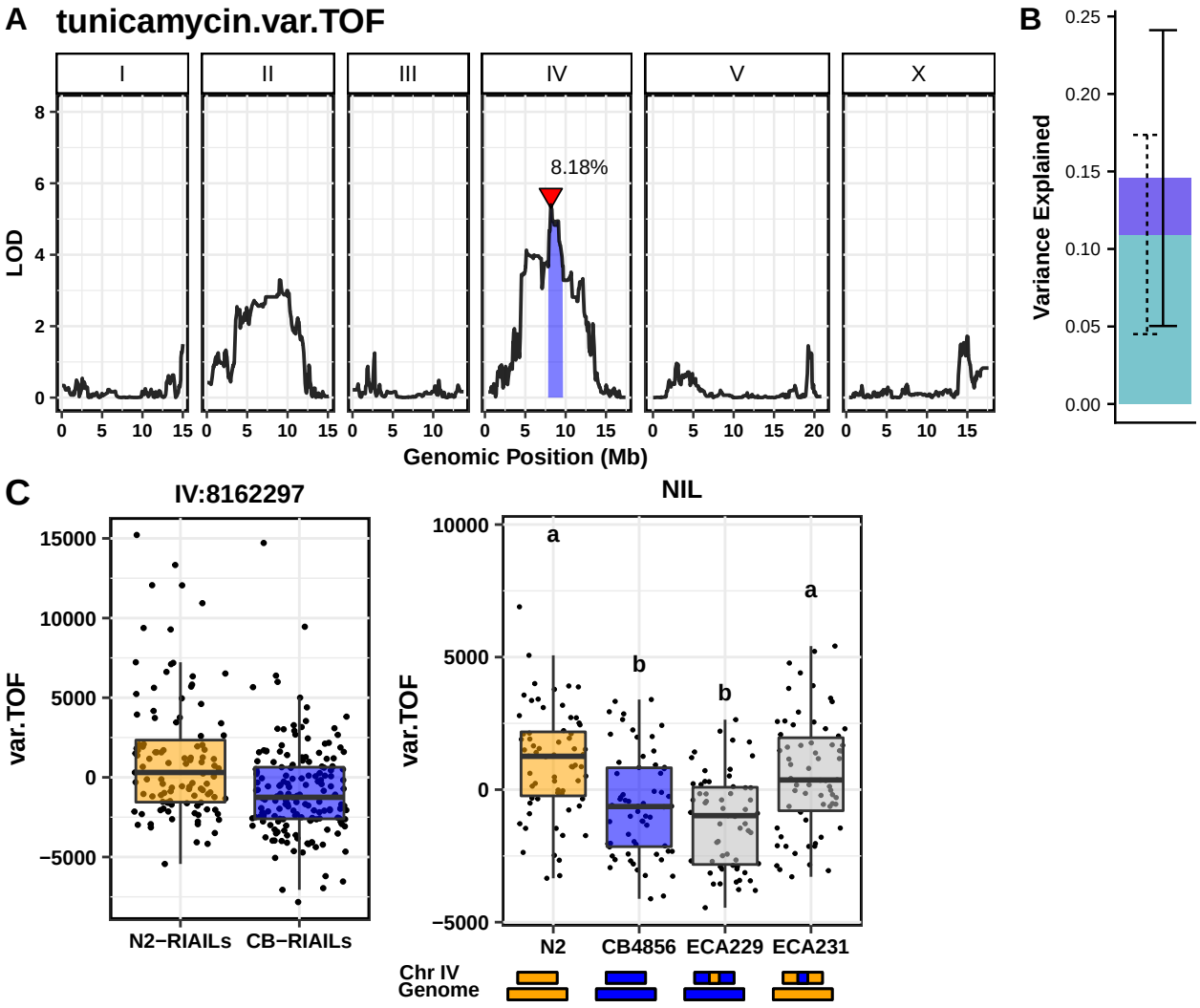

A
tunicamycin.q75.norm.EXT
I
II
III
IV
V
X
LOD
11.45%
Genomic Position (Mb)
B
Variance Explained
C
IV:8587439
q75.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
a
b
c
d
N2
CB4856
ECA229
ECA231
Chr IV
Genome

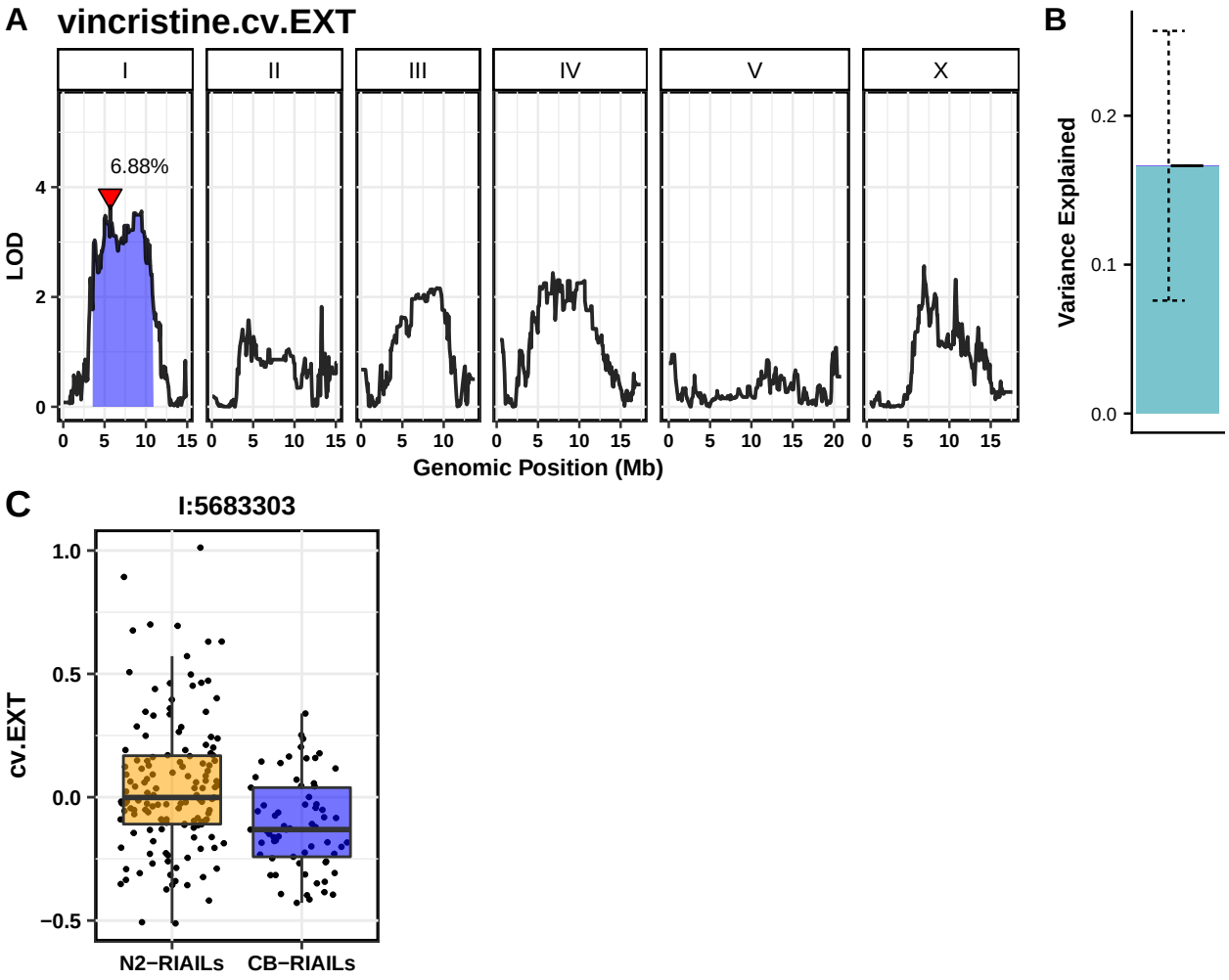

A
tunicamycin.q75.TOF
I
II
III
IV
V
X
LOD
18.79%
Genomic Position (Mb)
B
Variance Explained
C
IV:7963446
q75.TOF
N2−RIAILs
CB−RIAILs
NIL
a
b
c
b
N2
CB4856
ECA229
ECA231
Chr IV
Genome

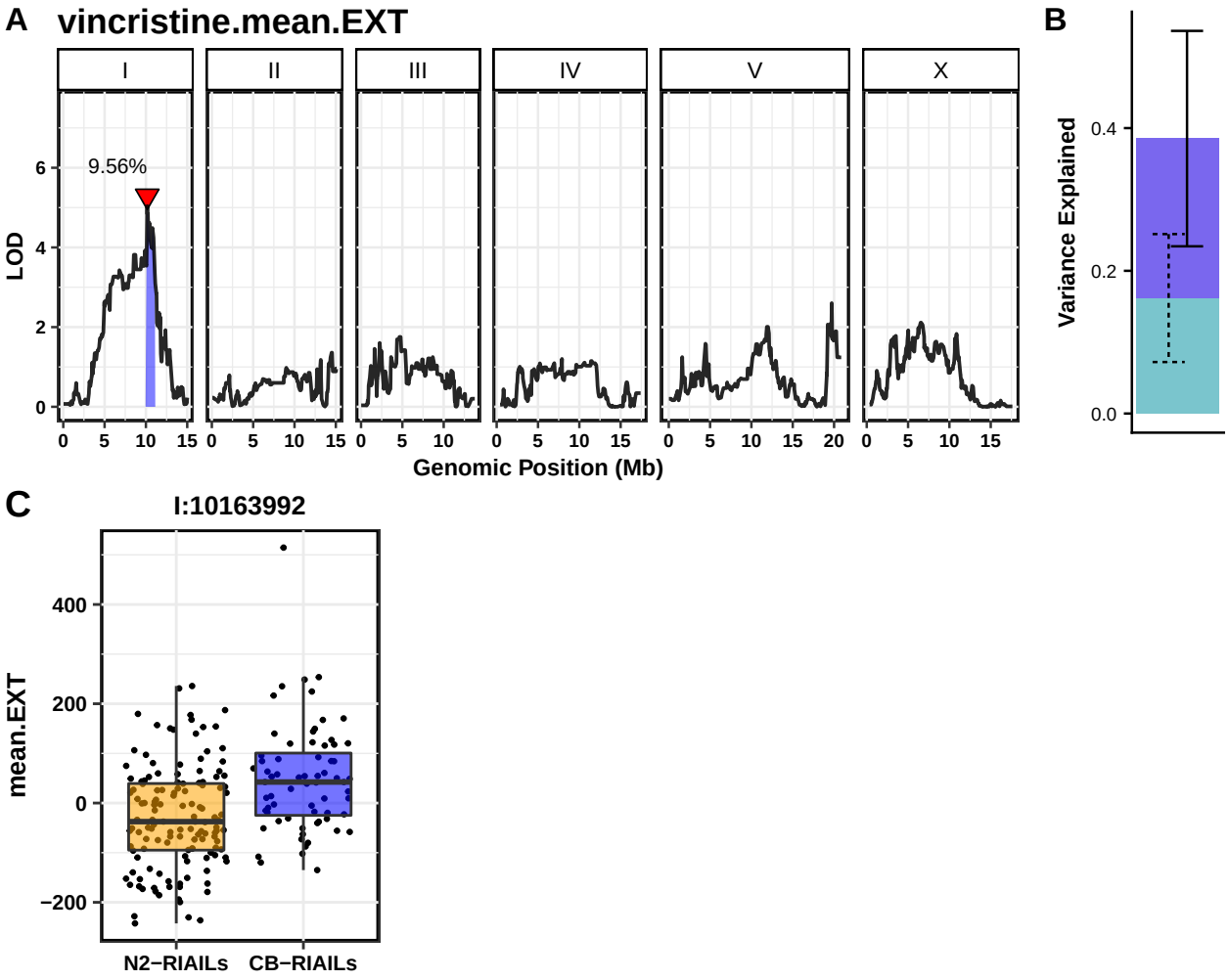

A
tunicamycin.q90.EXT
I
II
III
IV
V
X
15.42%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:7963446
q90.EXT
N2−RIAILs
CB−RIAILs
NIL
a
b
c
a
N2
CB4856
ECA229
ECA231
Chr IV
Genome

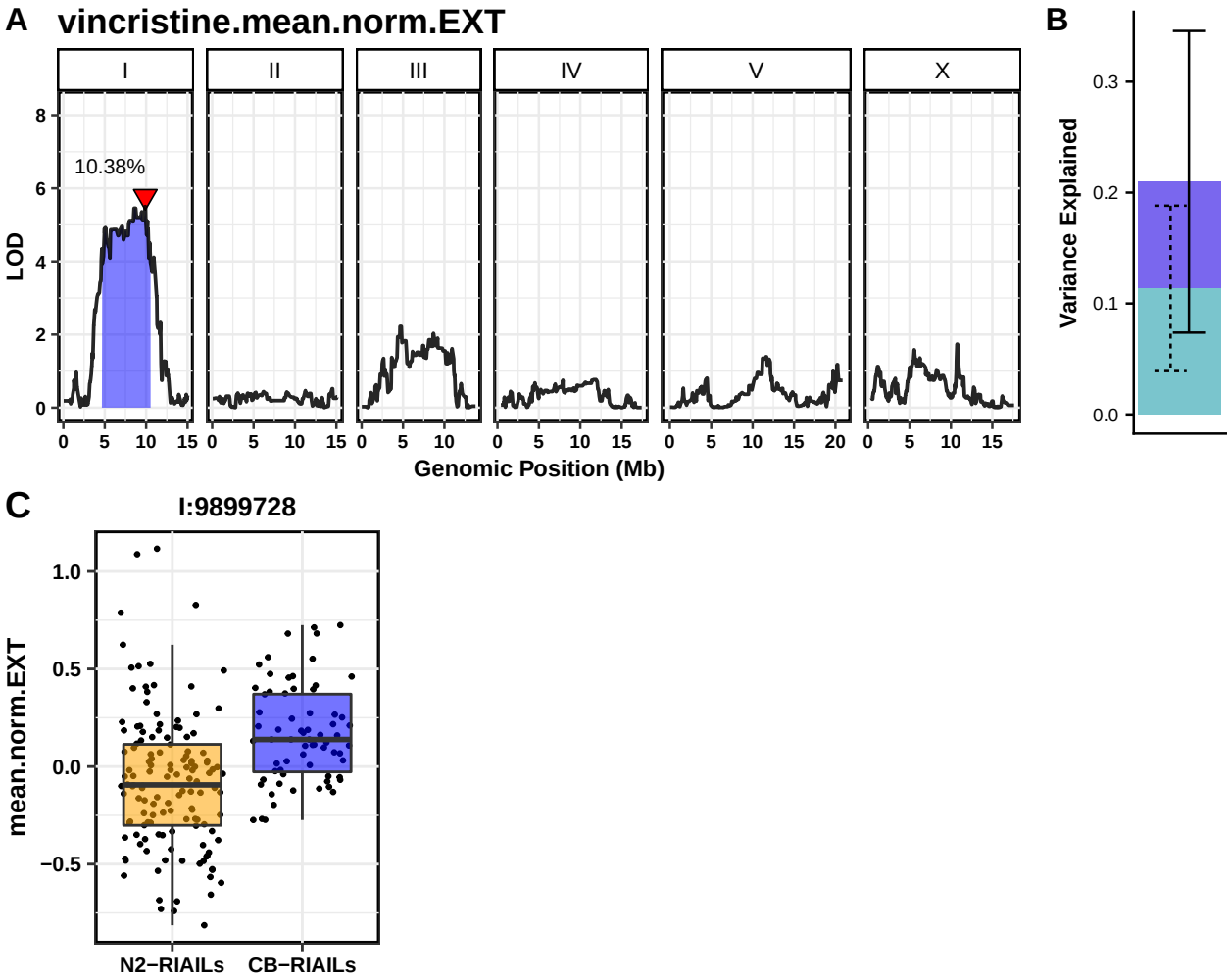

A
tunicamycin.q90.norm.EXT
I
II
III
IV
V
X
12.44%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:8587439
q90.norm.EXT
N2−RIAILs
CB−RIAILs
NIL
a
a
b
c
N2
CB4856
ECA229
ECA231
Chr IV
Genome

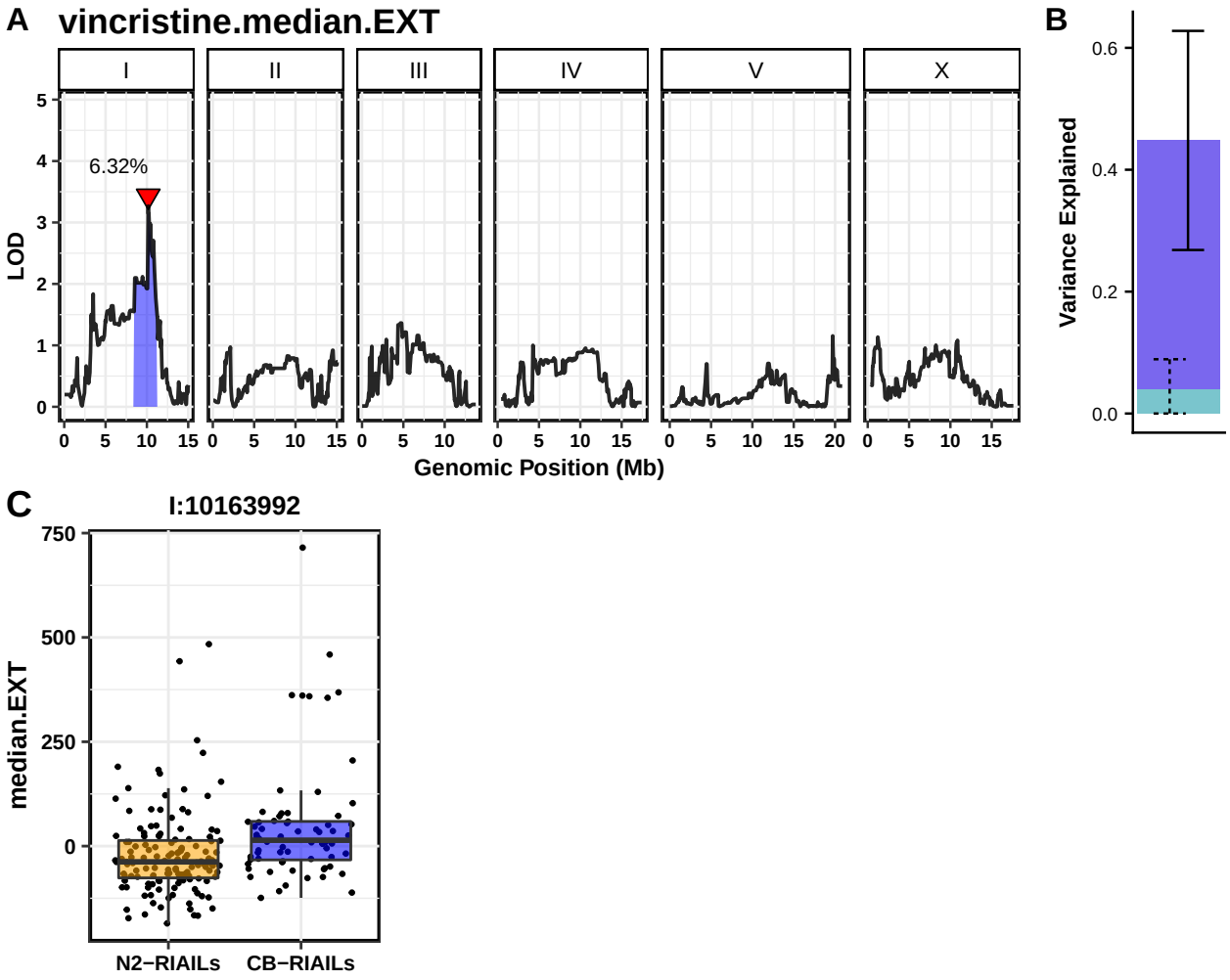

A
tunicamycin.q90.TOF
I
II
III
IV
V
X
LOD
18.39%
Genomic Position (Mb)
B
Variance Explained
C
IV:7963446
q90.TOF
N2−RIAILs
CB−RIAILs
NIL
a
b
c
a
N2
CB4856
ECA229
ECA231
Chr IV
Genome

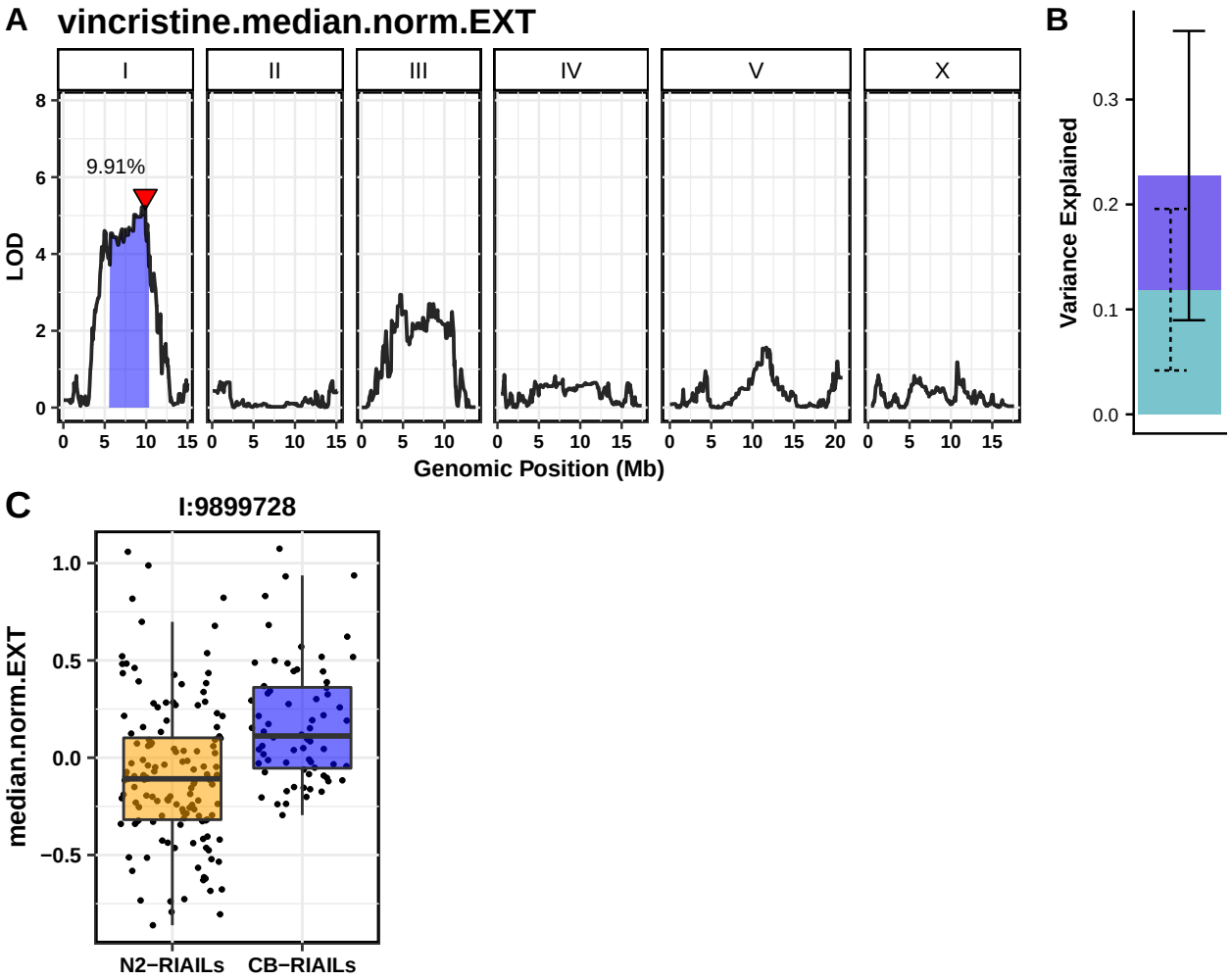

A
tunicamycin.var.TOF
I
II
III
IV
V
X
LOD
8.18%
Genomic Position (Mb)
B
Variance Explained
C
IV:8162297
var.TOF
N2−RIAILs
CB−RIAILs
NIL
a
b
b
a
N2
CB4856
ECA229
ECA231
Chr IV
Genome

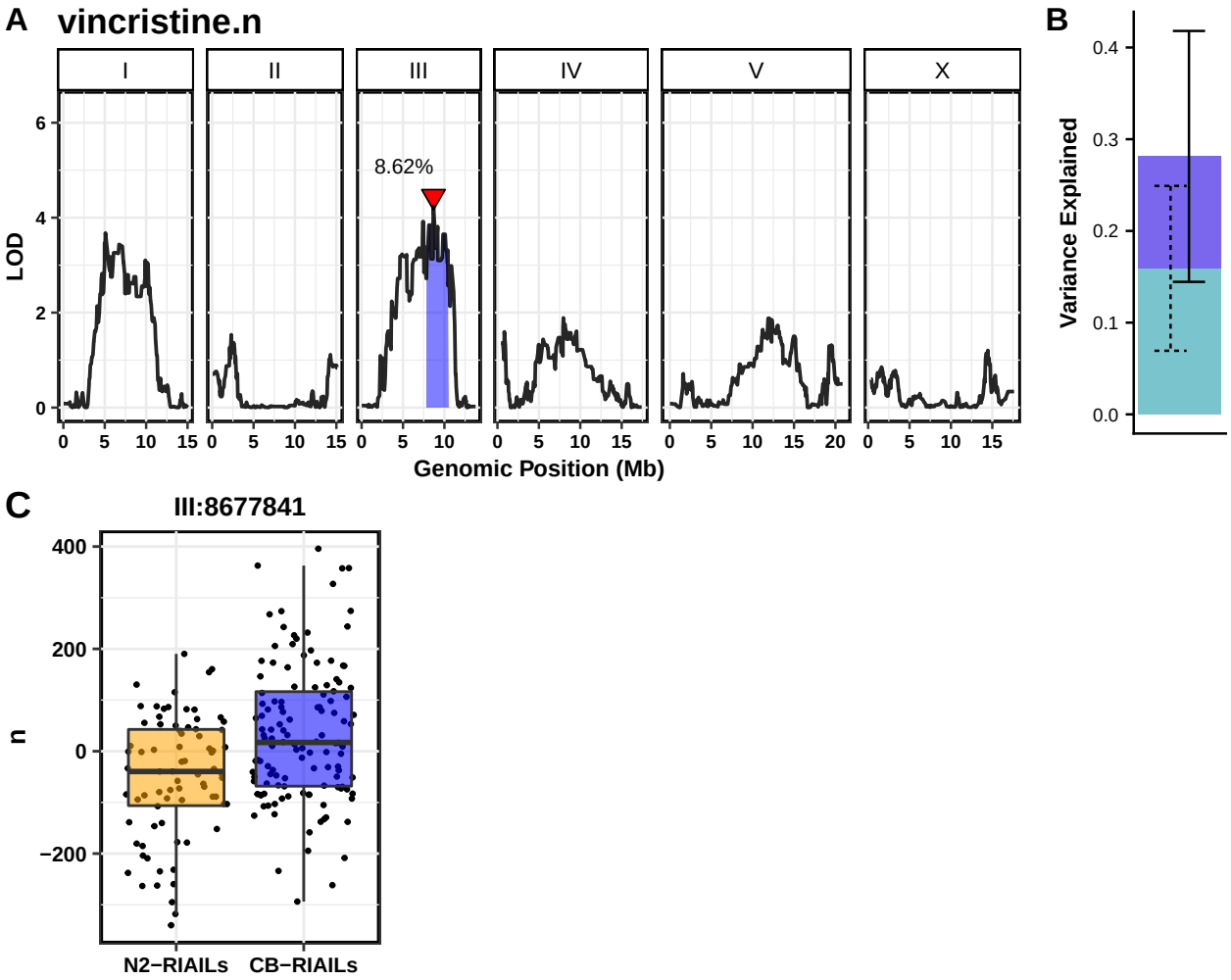

A
vincristine.cv.EXT
I
II
III
IV
V
X
6.88%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:5683303
cv.EXT
N2−RIAILs
CB−RIAILs

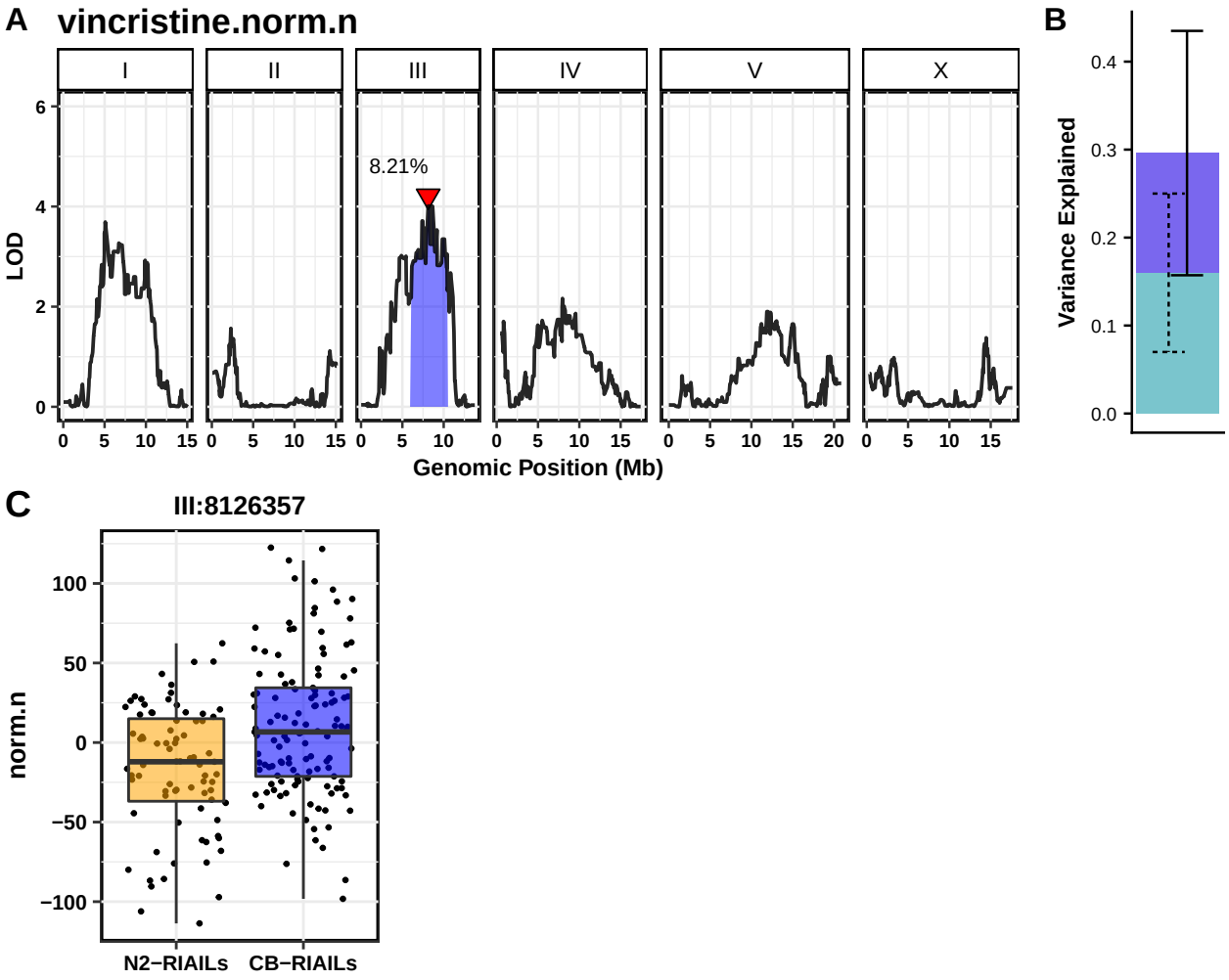

A
vincristine.mean.EXT
I
II
III
IV
V
X
9.56%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:10163992
mean.EXT
N2−RIAILs
CB−RIAILs

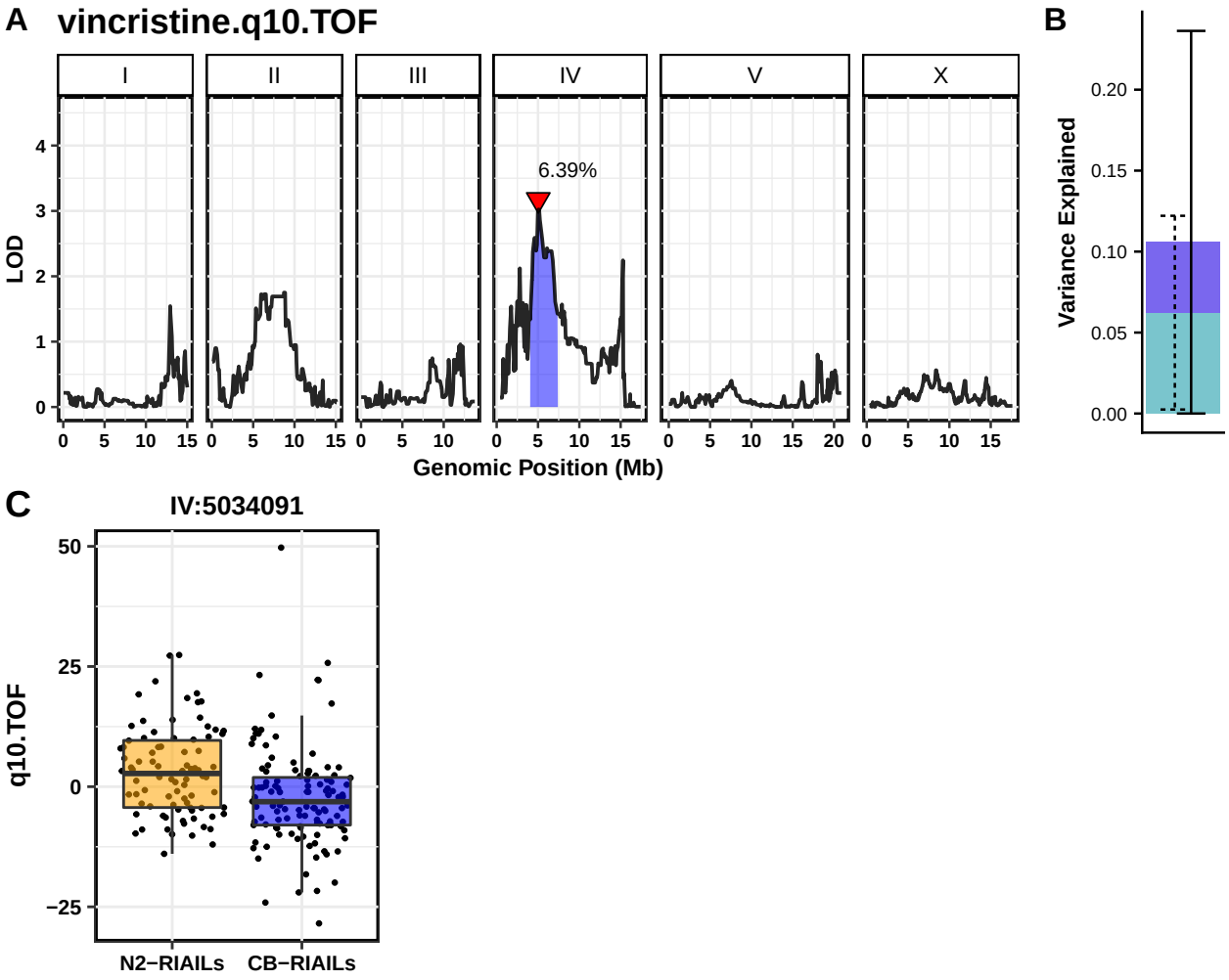

A
vincristine.mean.norm.EXT
I
II
III
IV
V
X
10.38%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:9899728
mean.norm.EXT
N2−RIAILs
CB−RIAILs

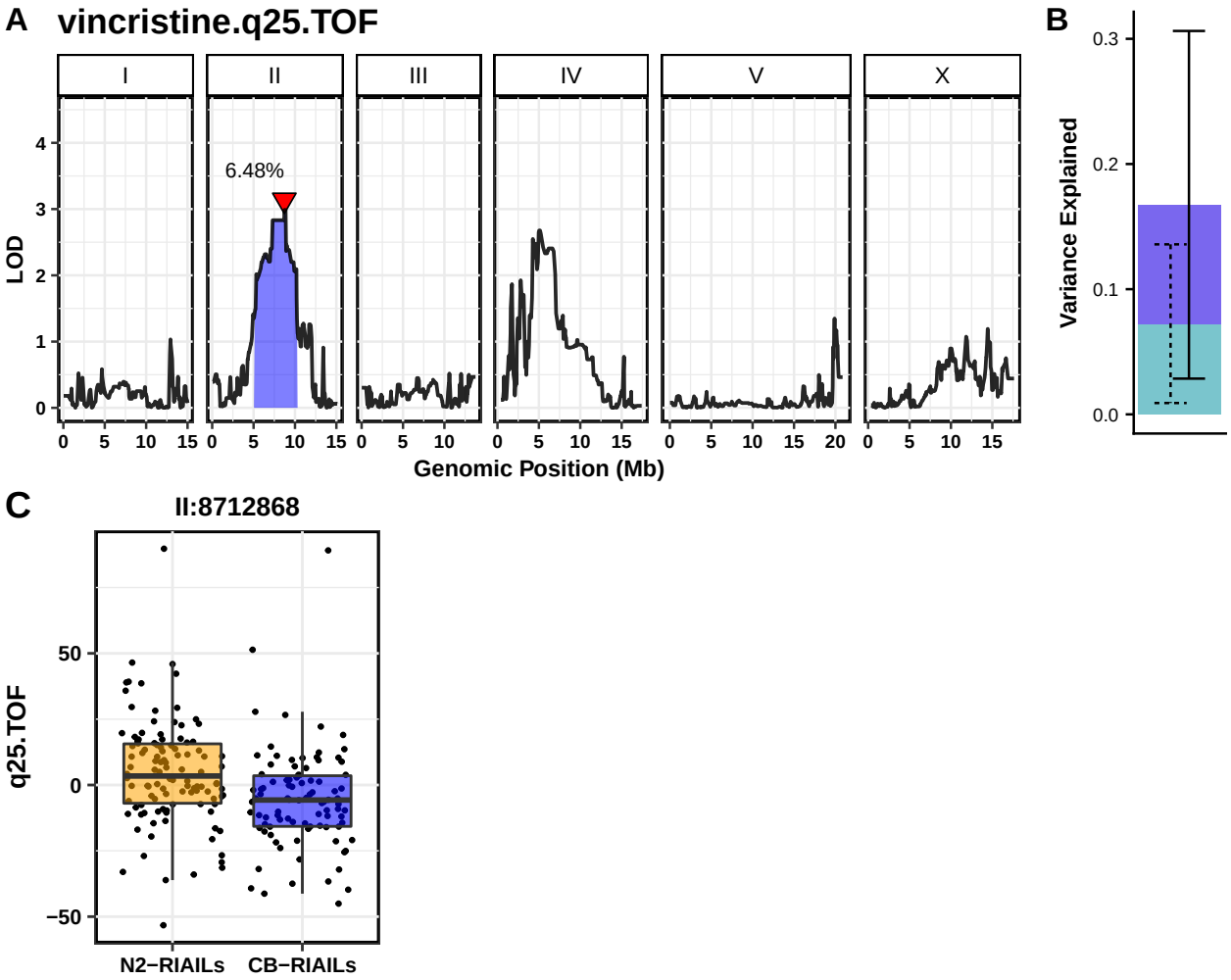

A
vincristine.median.EXT
I
II
III
IV
V
X
6.32%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:10163992
median.EXT
N2−RIAILs
CB−RIAILs

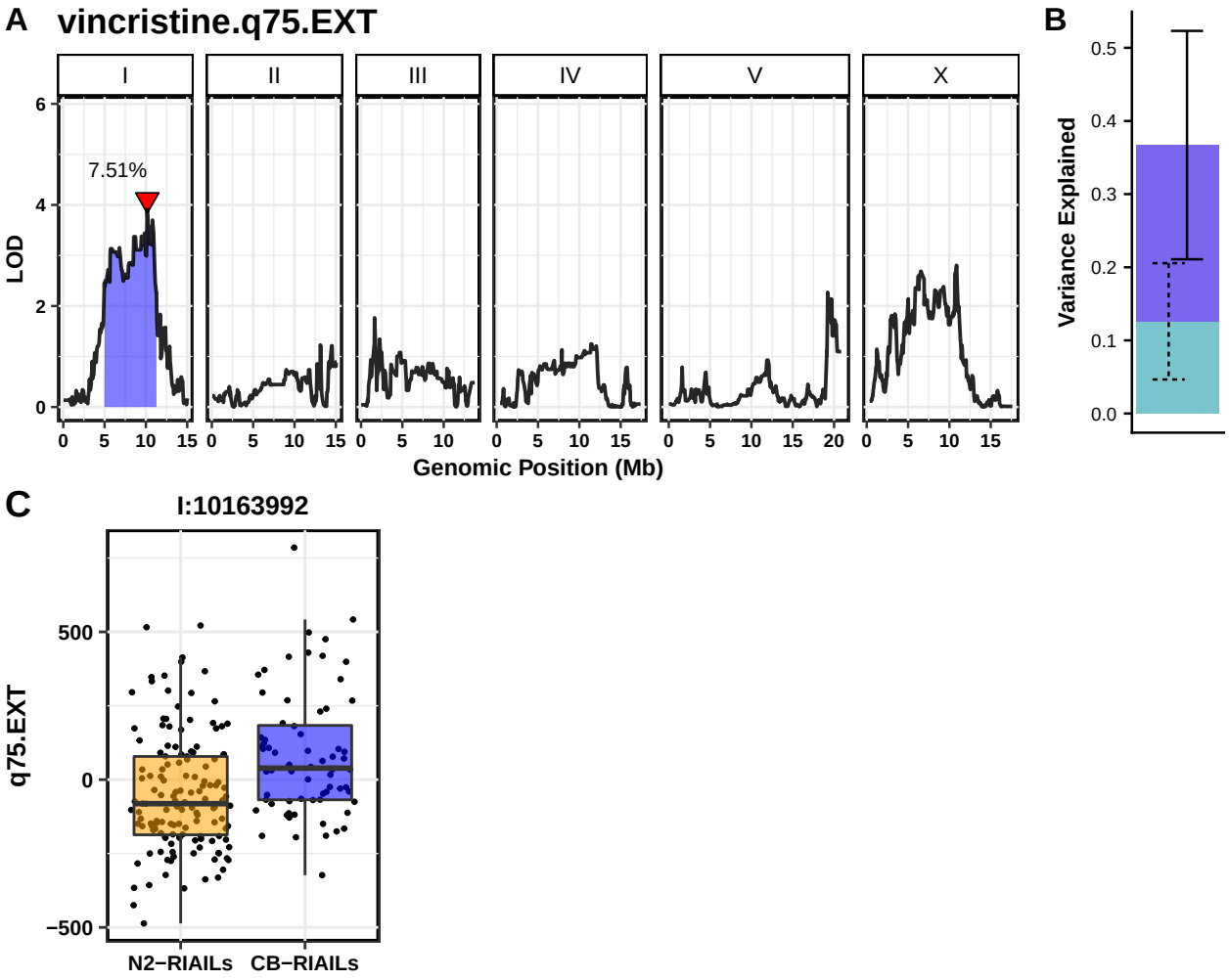

A
vincristine.median.norm.EXT
I
II
III
IV
V
X
9.91%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:9899728
median.norm.EXT
N2−RIAILs
CB−RIAILs

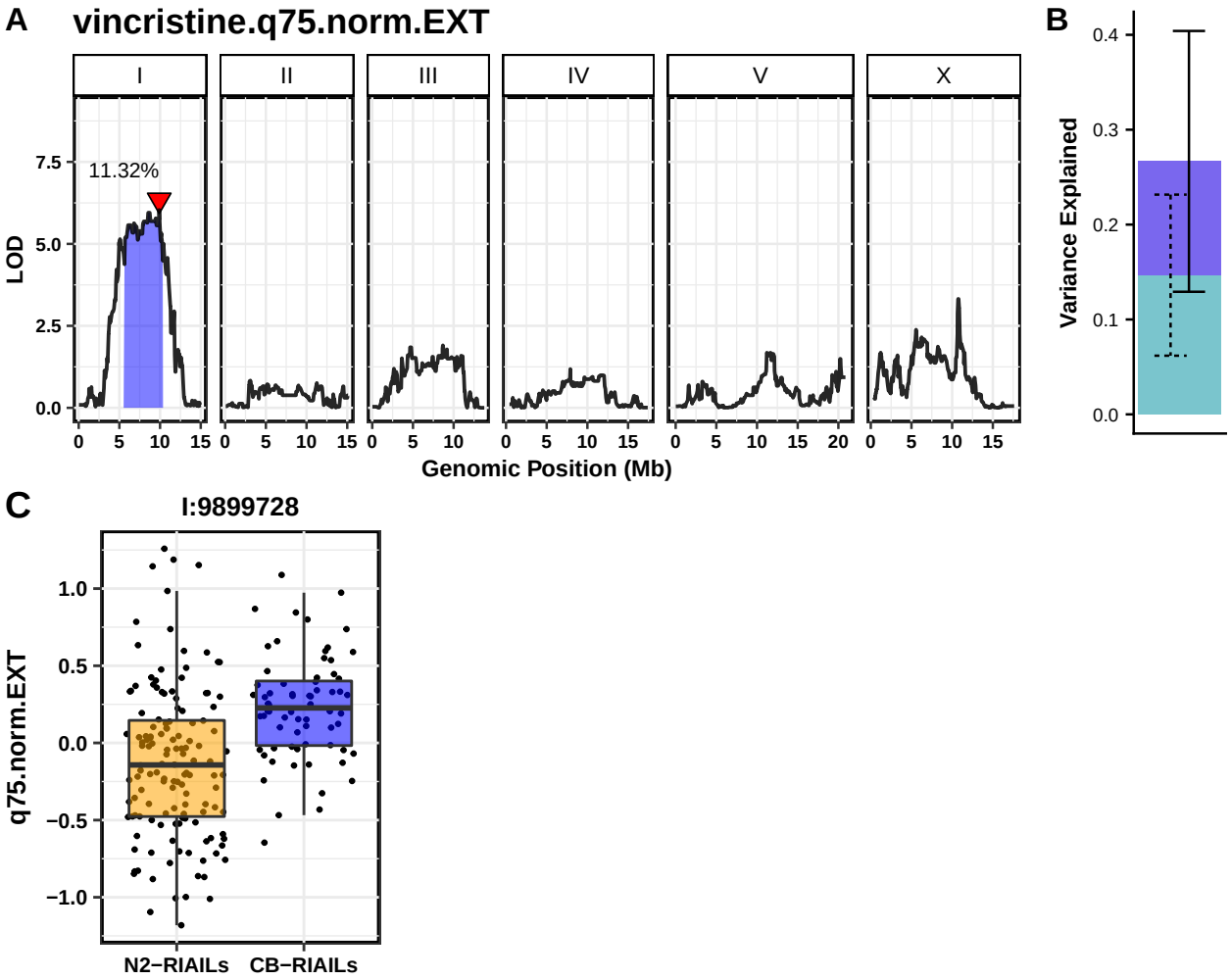

A
vincristine.n
I
II
III
IV
V
X
8.62%
LOD
Genomic Position (Mb)
B
Variance Explained
C
III:8677841
n
N2−RIAILs
CB−RIAILs

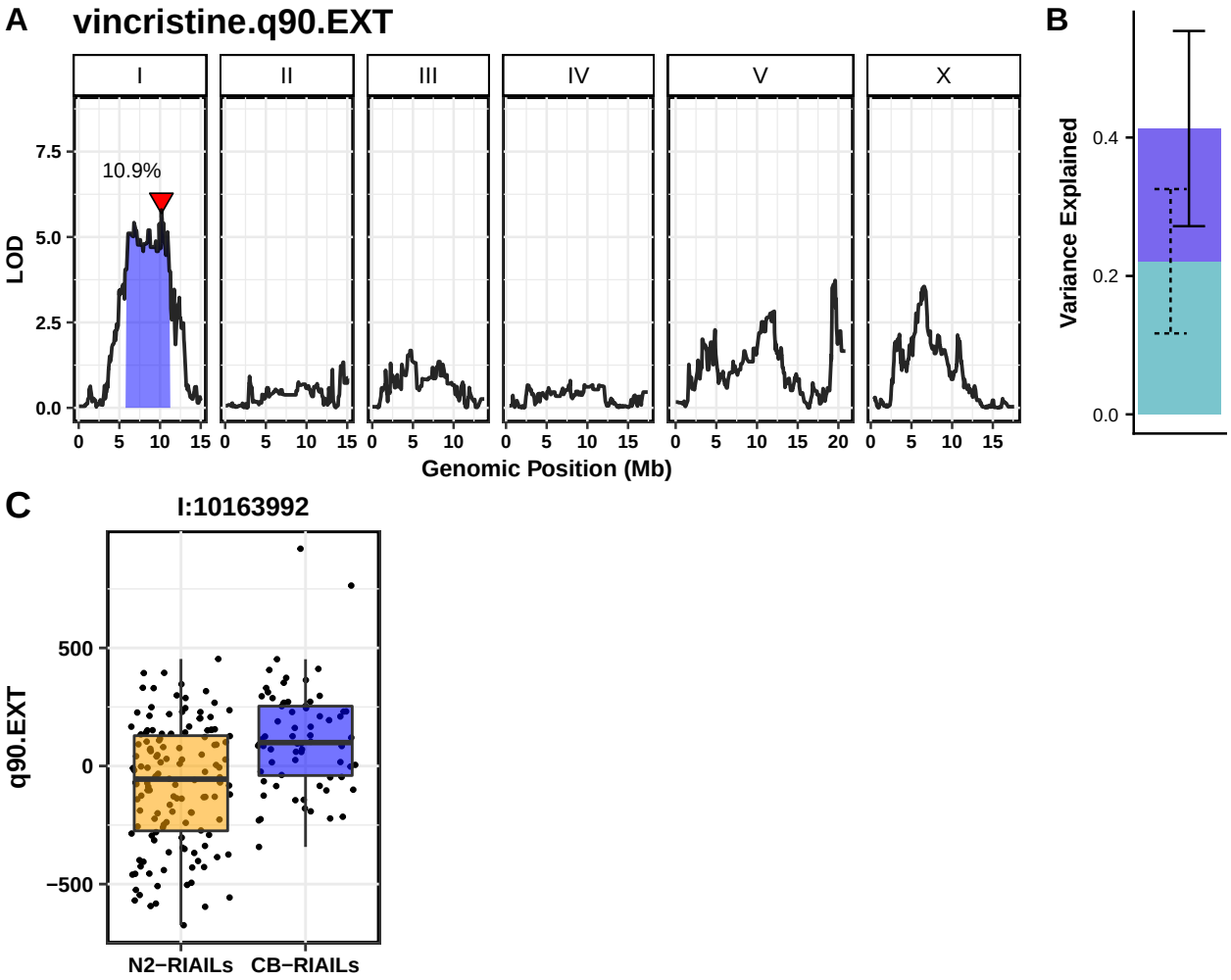

A
vincristine.norm.n
I
II
III
IV
V
X
8.21%
LOD
Genomic Position (Mb)
B
Variance Explained
C
III:8126357
norm.n
N2−RIAILs
CB−RIAILs

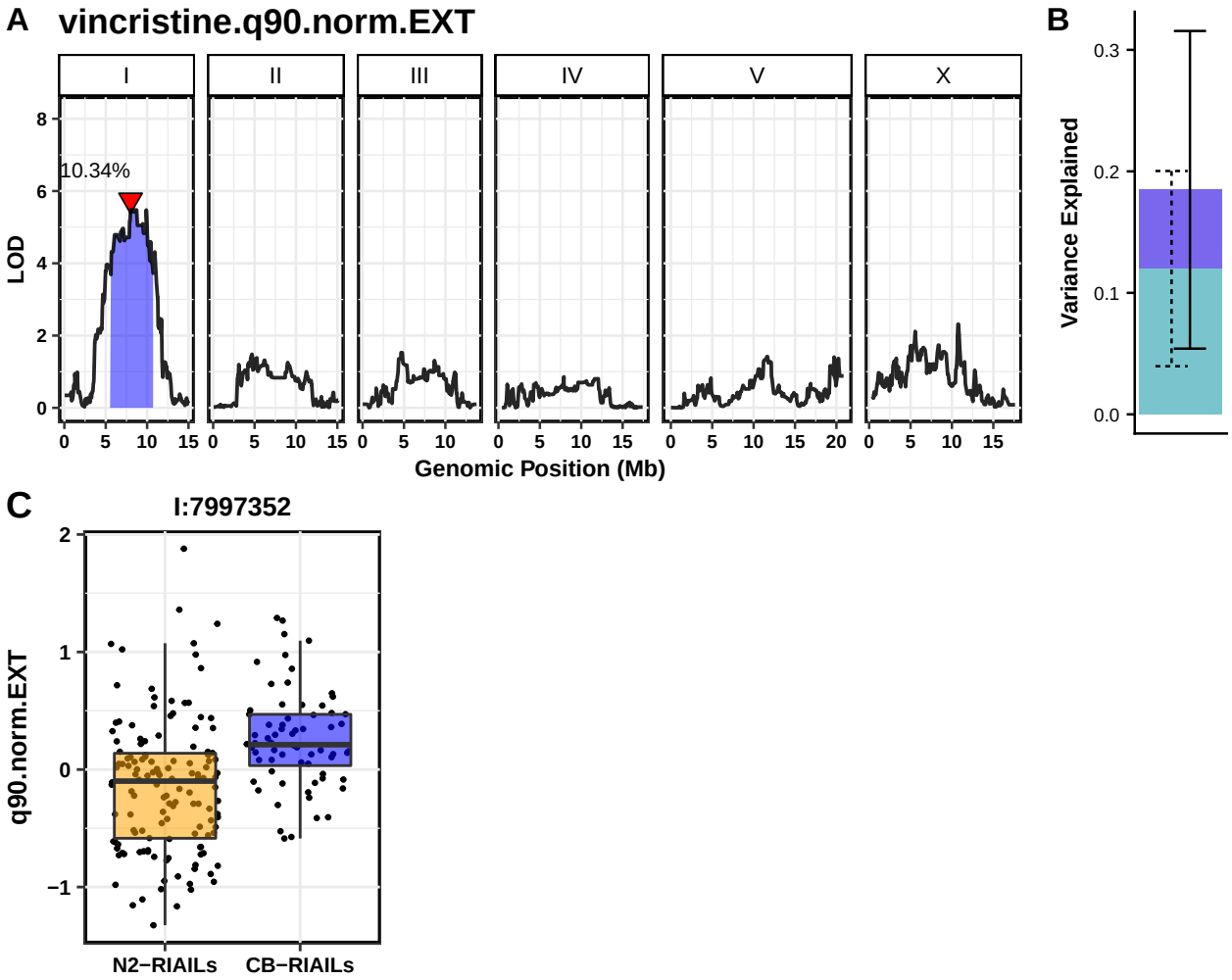

A
vincristine.q10.TOF
I
II
III
IV
V
X
6.39%
LOD
Genomic Position (Mb)
B
Variance Explained
C
IV:5034091
q10.TOF
N2−RIAILs
CB−RIAILs


A
vincristine.q25.TOF
I
II
III
IV
V
X
6.48%
LOD
Genomic Position (Mb)
B
Variance Explained
C
II:8712868
q25.TOF
N2−RIAILs
CB−RIAILs


A
vincristine.q75.EXT
I
II
III
IV
V
X
7.51%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:10163992
q75.EXT
N2−RIAILs
CB−RIAILs


A
vincristine.q75.norm.EXT
I
II
III
IV
V
X
11.32%
LOD
7.5
5.0
2.5
0.0
0 5 10 15
0 5 10 15
0 5 10
0 5 10 15
0 5 10 15 20
0 5 10 15
Genomic Position (Mb)
B
Variance Explained
0.4
0.3
0.2
0.1
0.0
C
I:9899728
q75.norm.EXT
1.0
0.5
0.0
−0.5
−1.0
N2−RIAILs
CB−RIAILs


A
vincristine.q90.EXT
I
II
III
IV
V
X
10.9%
LOD
7.5
5.0
2.5
0.0
0 5 10 15
0 5 10 15
0 5 10
0 5 10 15
0 5 10 15 20
0 5 10 15
Genomic Position (Mb)
B
Variance Explained
0.4
0.2
0.0
C
I:10163992
q90.EXT
500
0
−500
N2−RIAILs
CB−RIAILs


A
vincristine.q90.norm.EXT
I
II
III
IV
V
X
10.34%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:7997352
q90.norm.EXT
N2−RIAILs
CB−RIAILs

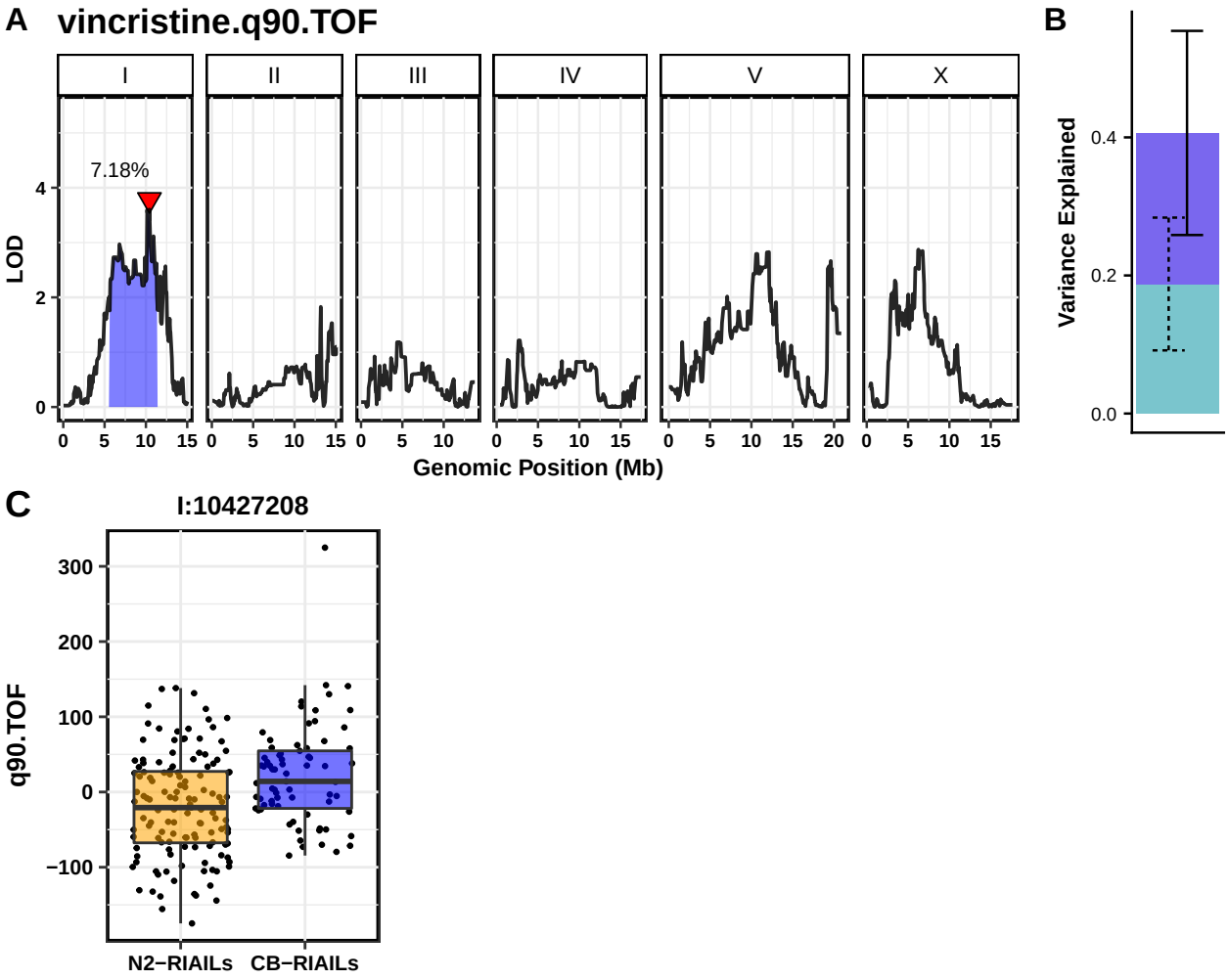

A
vincristine.q90.TOF
I
II
III
IV
V
X
7.18%
LOD
Genomic Position (Mb)
B
Variance Explained
C
I:10427208
q90.TOF
N2−RIAILs
CB−RIAILs

Figure S2 QTL linkage mapping, CSS and NIL results, and variance component contributions. (**A**) The maximum LOD score (y-axis) for each marker across the genome (x-axis), split by chromosome, is plotted as a black line. Significant QTL are indicated by a red triangle at the marker with the maximum LOD score and a light blue ribbon spanning the 95% confidence interval. The estimated phenotypic variation in the RIAILs explained by each QTL is indicated above each peak. (**B**) The proportion of phenotypic variation across the RIAILs caused by additive (light blue) and interactive (dark blue) genetic components are indicated. Solid and dashed error bars show the standard error around additive and interactive component estimates, respectively. (**C**) For each QTL plotted in A, the residual phenotypes (y-axis) of RIAILs split by genotype at the marker with the maximum LOD score (x-axis) are plotted as Tukey box plots. Data from RIAILs with the N2 or the CB4856 allele at the QTL peak marker are colored in orange and blue, respectively. (**D** and **E**) For traits in which CSSs and NILs were assayed, the residual phenotypic values (y-axis) of N2, CB4856, and reciprocal introgressed CSSs (**D**) or NILs (**E**) are plotted as Tukey box plots. Different letters represent significant differences ($p<0.05$) between strains (Tukey HSD). The genotype of each strain on the x-axis is modeled by the colored rectangles beneath the plots (N2 genotypes are orange, CB4856 genotypes are blue).

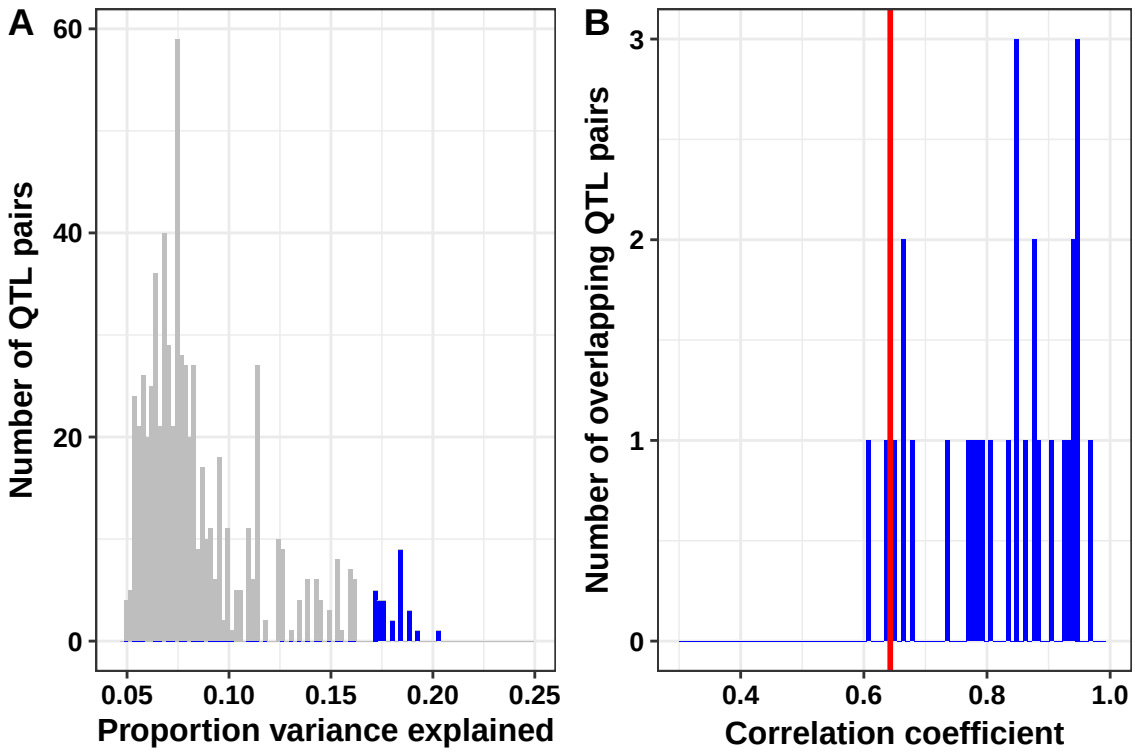


Figure S3 Determining a threshold for identifying distinct QTL. (**A**) Within each condition, pairs of traits with overlapping QTL confidence intervals are plotted as a histogram. The phenotypic variation explained by the lowest effect-size QTL per pair of overlapping confidence intervals is shown on the x-axis. Pairs of QTL with a variance explained estimate above the 95$^{\text{th}}$ percentile of this distribution are colored in blue. (**B**) A histogram of all pairs of traits with overlapping confidence intervals containing a QTL with a variance explained estimate above the cutoff from (A). The correlation coefficient of each of pair of traits, calculated from the dose-response data, is shown on the x-axis. The 5$^{\text{th}}$ percentile of this distribution is indicated by the red line at a correlation coefficient of 0.642.

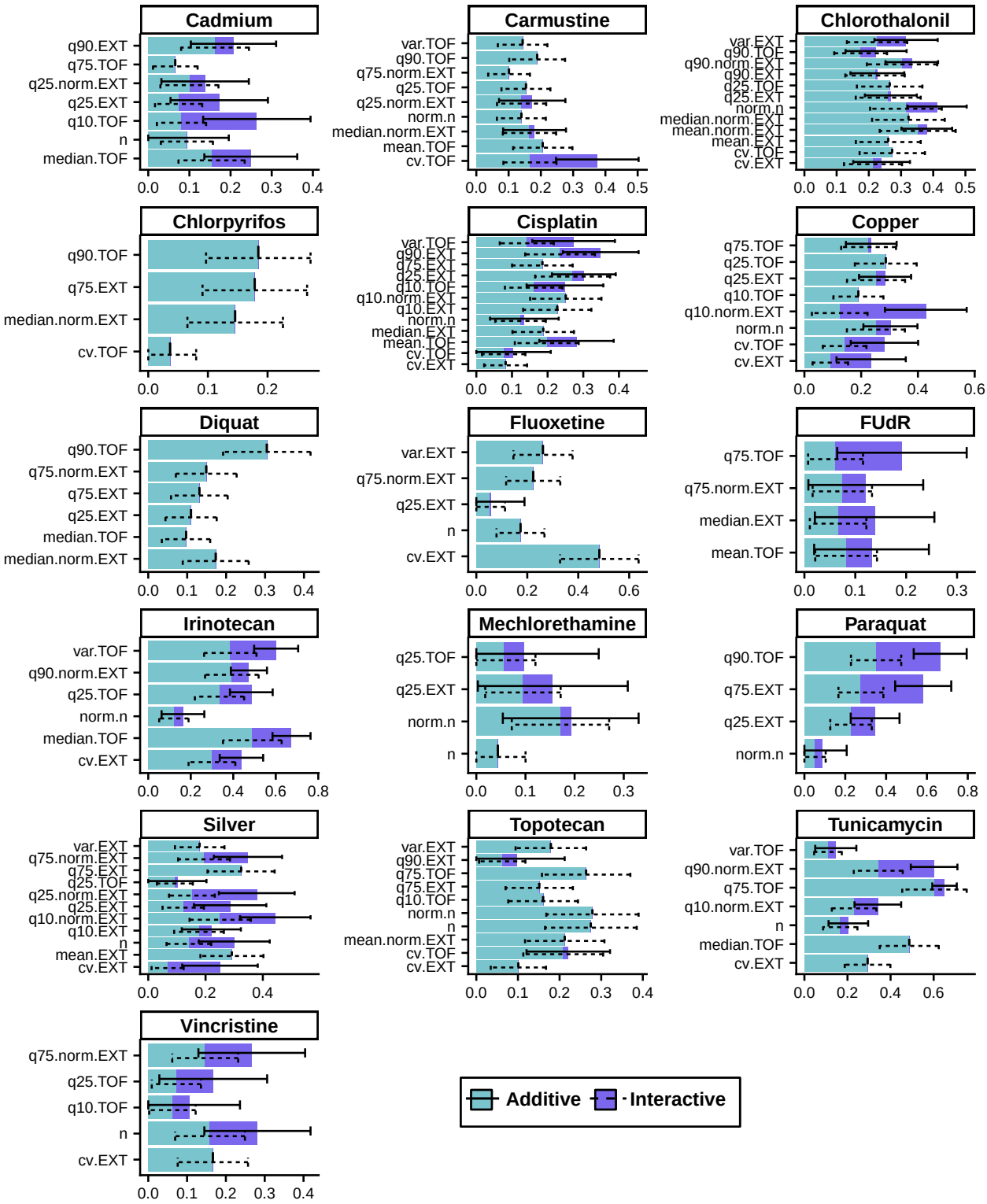
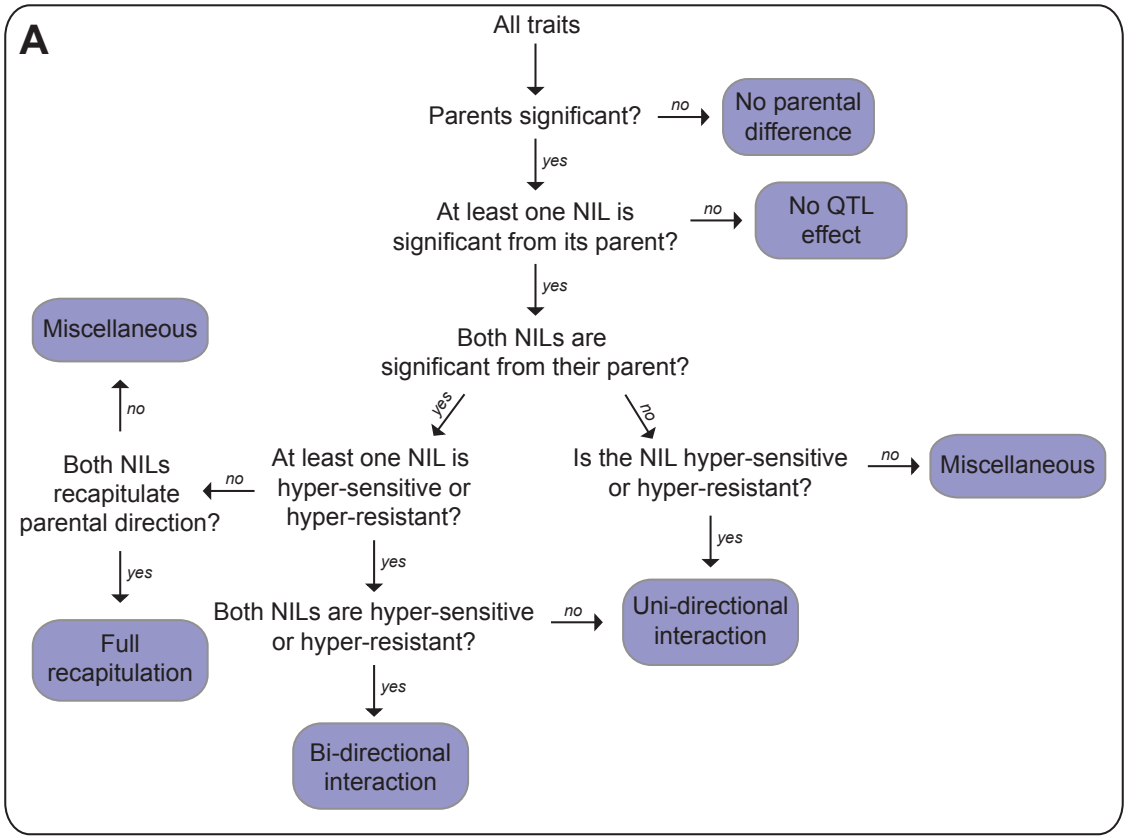


Figure S4 Additive and interactive genetic components. The proportion of phenotypic variation predicted to be caused by additive and interactive genetic components is shown for each trait that represents one of the 114 distinct QTL identified by linkage mapping. For each toxin, the fraction of phenotypic variation (x-axis) in a given trait (y-axis) that is attributable to additive (light blue) versus interactive (dark blue) genetic components is shown as a stacked bar plot. Solid and dashed error bars show the standard error around the mean of additive and interactive components, respectively.



B

Category	CSS	NIL
Full recapitulation	Full recapitulation	Full recapitulation
No parental effect	No parental difference	No parental difference
No QTL effect	No QTL effect	No QTL effect
Inter-chromosomal external interaction	Uni-directional or bi-directional interaction	Full recapitulation or no QTL effect
Inter-chromosomal internal interaction	Uni-directional or bi-directional interaction	Uni-directional or bi-directional interaction
Intra-chromosomal interaction	Full recapitulation or no QTL effect	Uni-directional or bi-directional interaction

Figure S5 NIL and CSS trait categorizations. (**A**) Flowchart for categorizing traits from the NIL or CSS phenotyping assays. (**B**) Six categories across both CSS and NIL assays for traits on chromosome V. The miscellaneous category is not depicted, but encompasses any other combination of NIL and CSS assay results.

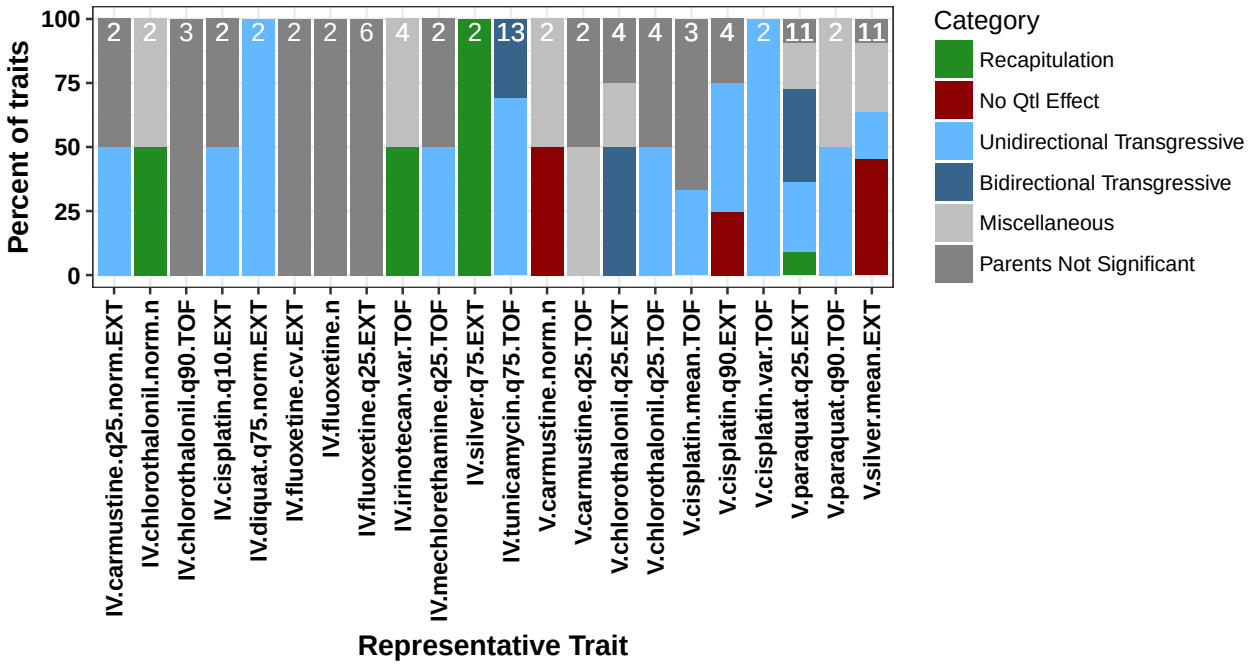


Figure S6 Categorization of correlated traits. The x-axis shows the representative trait (the trait with the highest LOD score) of a cluster of correlated traits with overlapping QTL confidence intervals. Each color represents the NIL assay categorization for each trait within a correlation cluster - either recapitulation (green), no QTL effect (red), unidirectional transgressive phenotype (light blue), bidirectional transgressive phenotype (dark blue), miscellaneous (light grey) or no significant parental difference (dark grey). The percent of all traits within the correlation cluster that falls within a given category is shown on the y-axis. Numbers above each bar indicate the number of traits within a correlation cluster.