

Estimated.Number.of.Cells

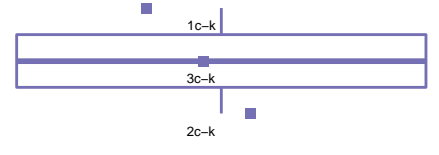
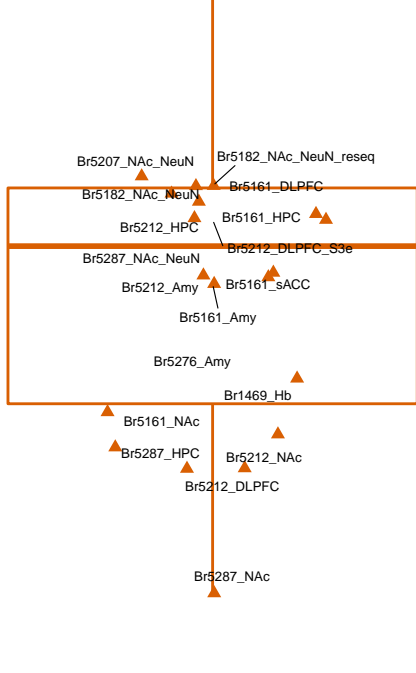
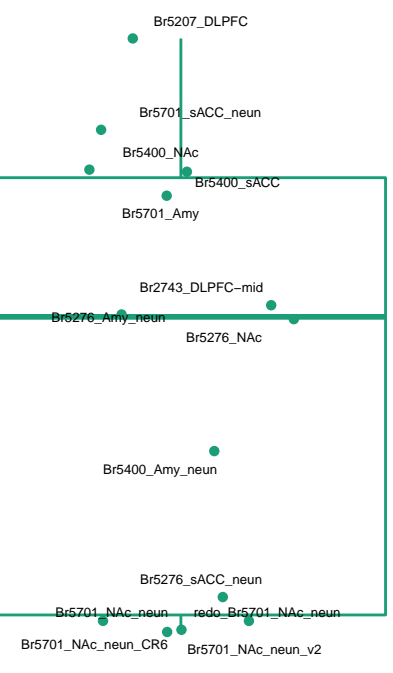
15000  
10000  
5000  
0

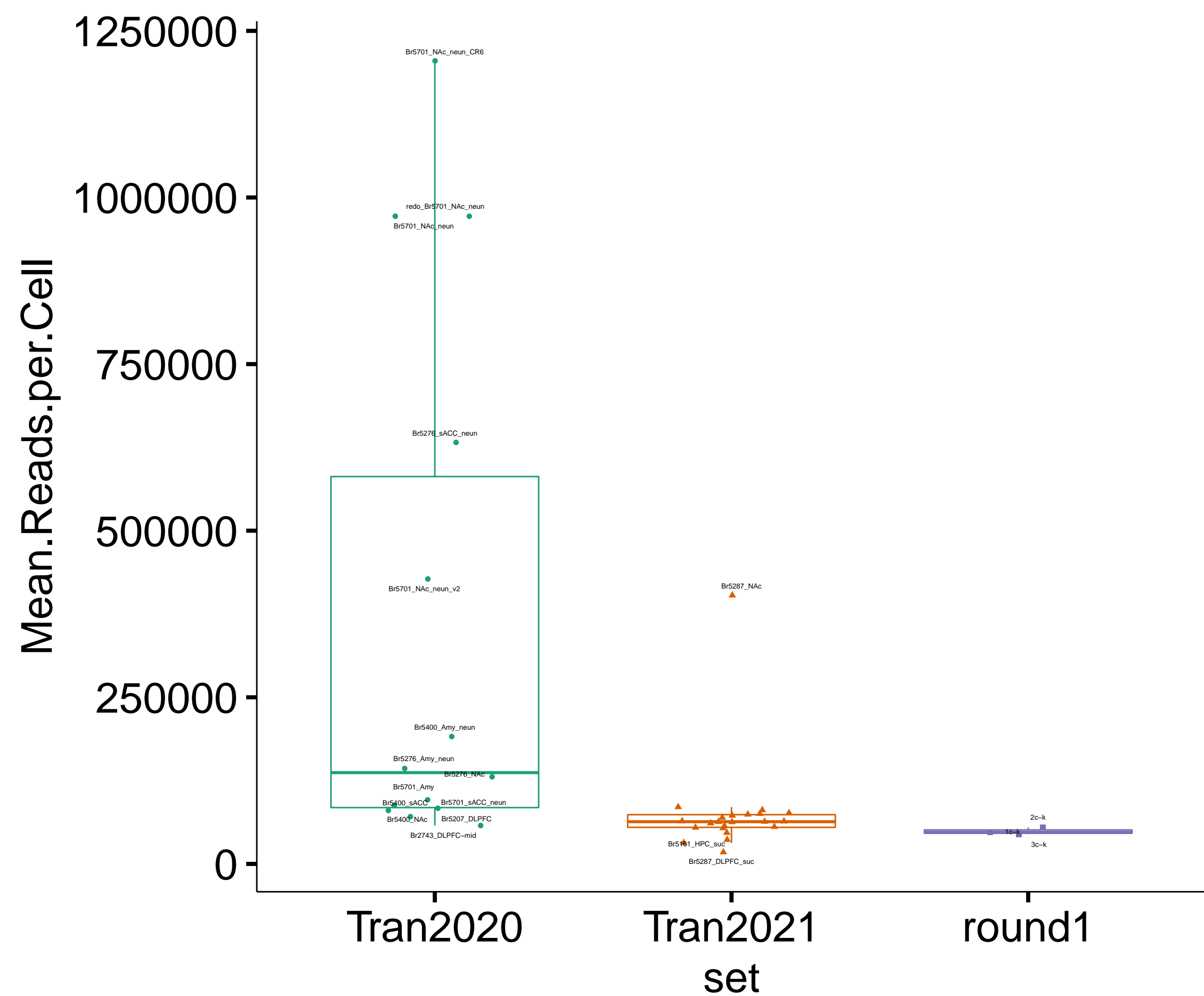
Tran2020

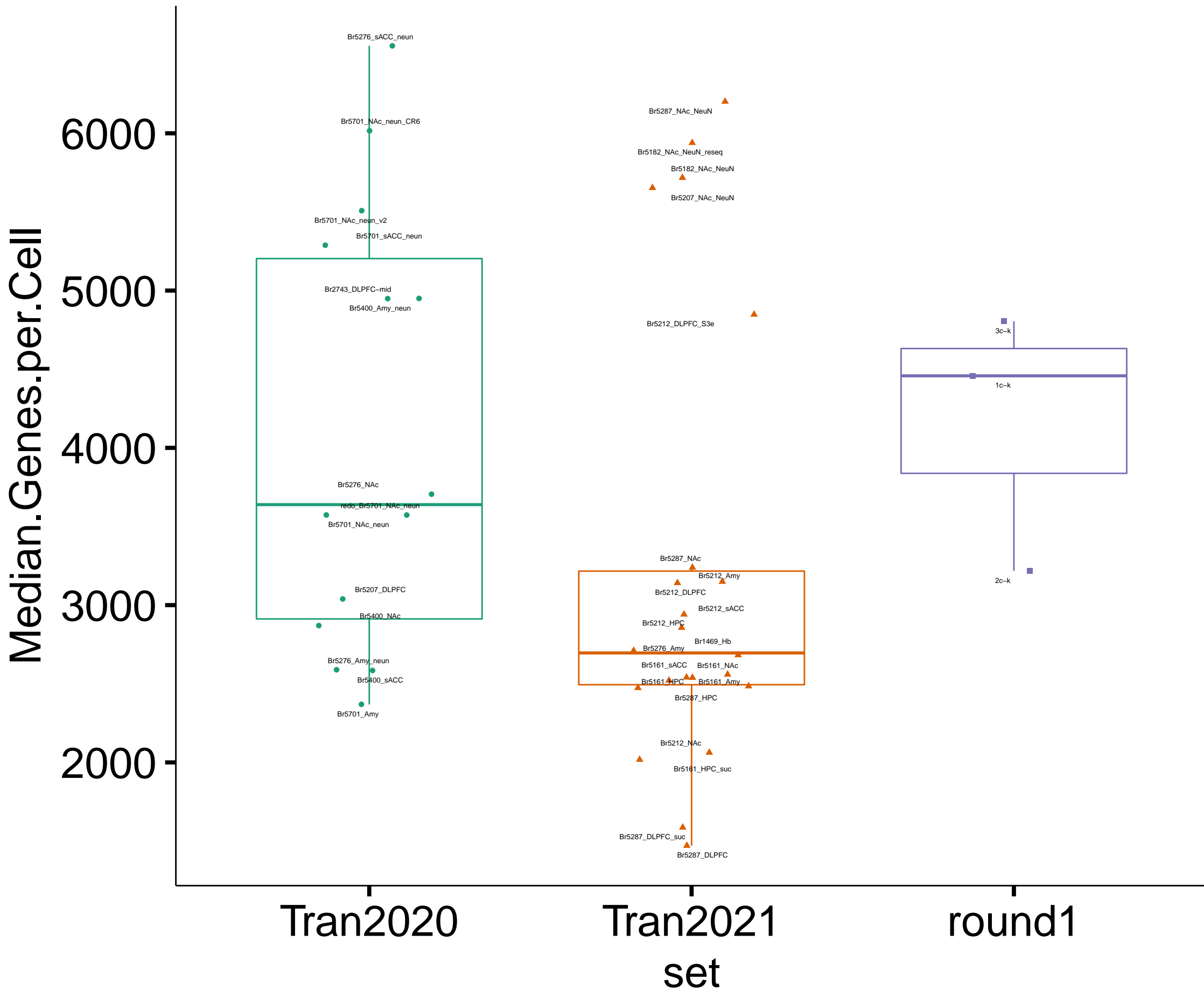
Tran2021

set

round1







Number.of.Reads

4e+08

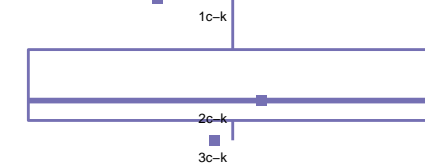
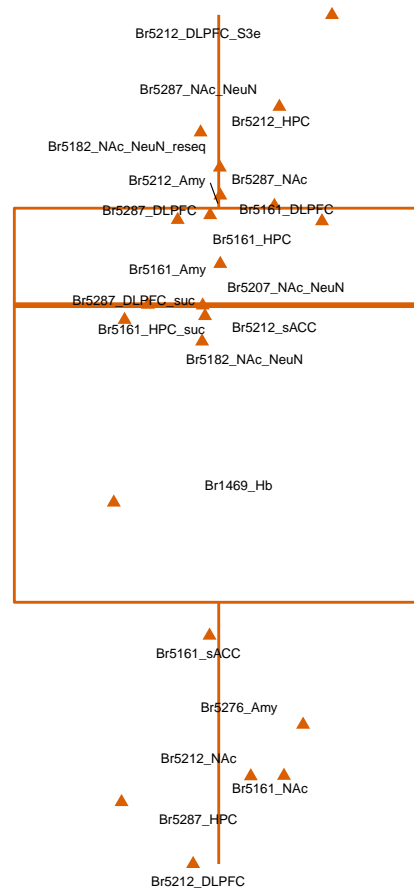
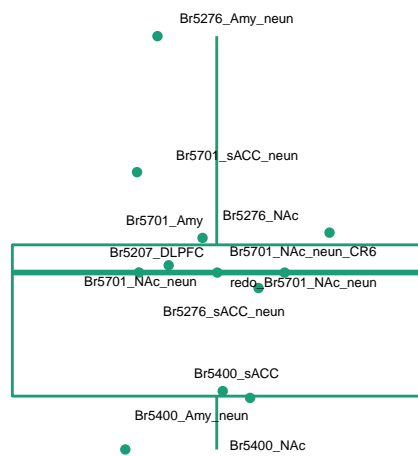
3e+08

2e+08

Tran2020

Tran2021  
set

round1



Valid.Barcode

98

97

96

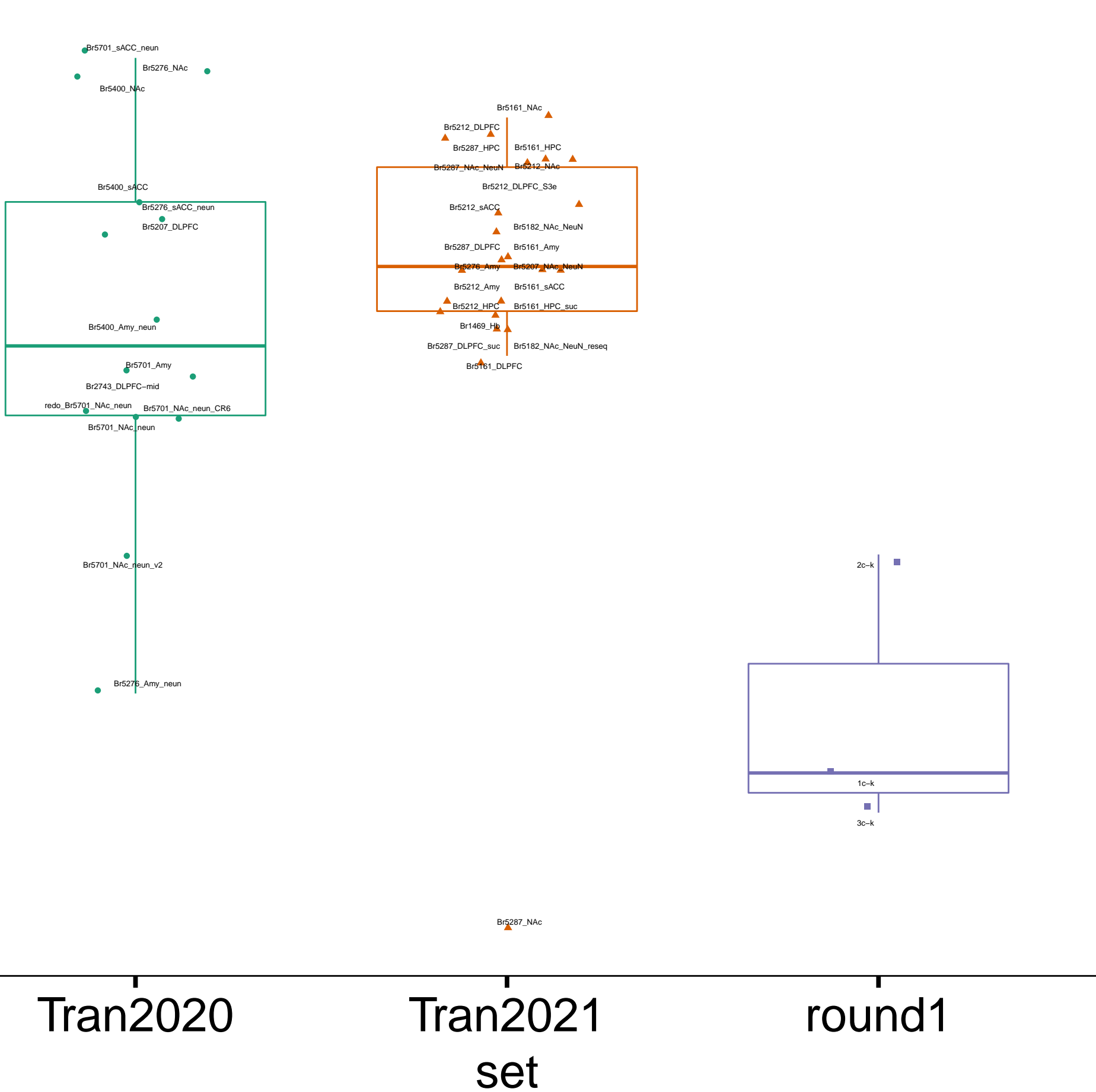
95

94

Tran2020

Tran2021  
set

round1



Sequencing.Saturation

80

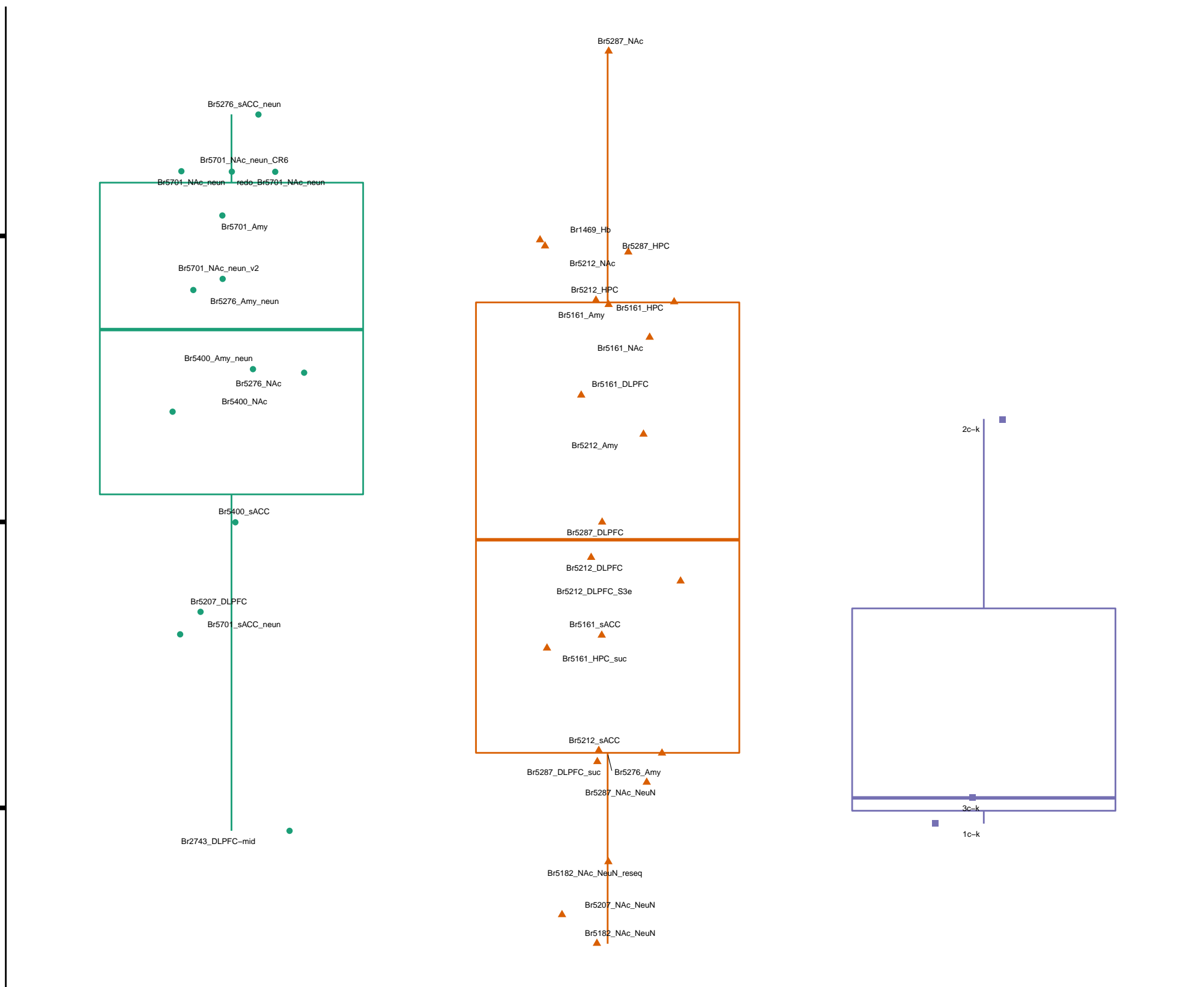
60

40

Tran2020

Tran2021  
set

round1



Q30.Bases.in.Barcode

97

96

95

94

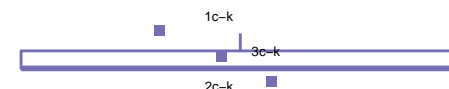
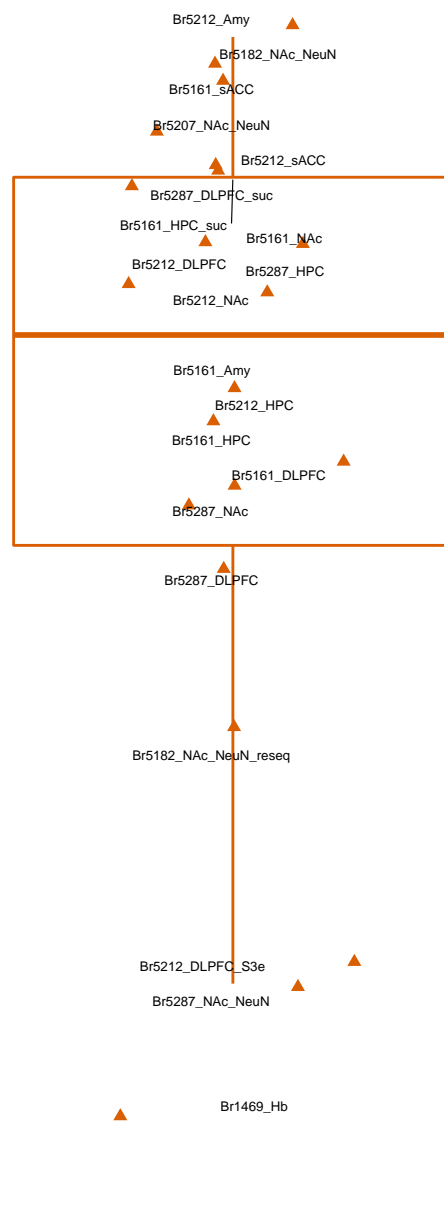
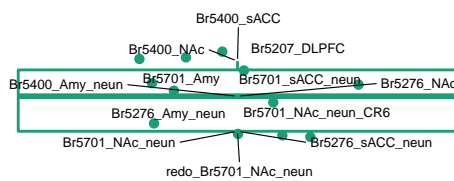
93

Tran2020

Tran2021

set

round1



Q30.Bases.in.RNA.Read

95.0

92.5

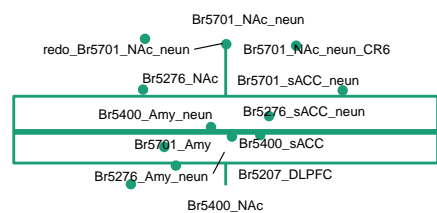
90.0

87.5

Tran2020

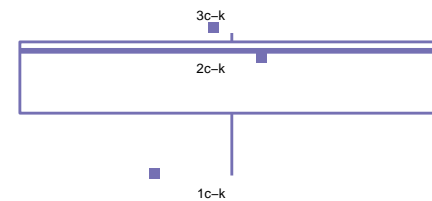
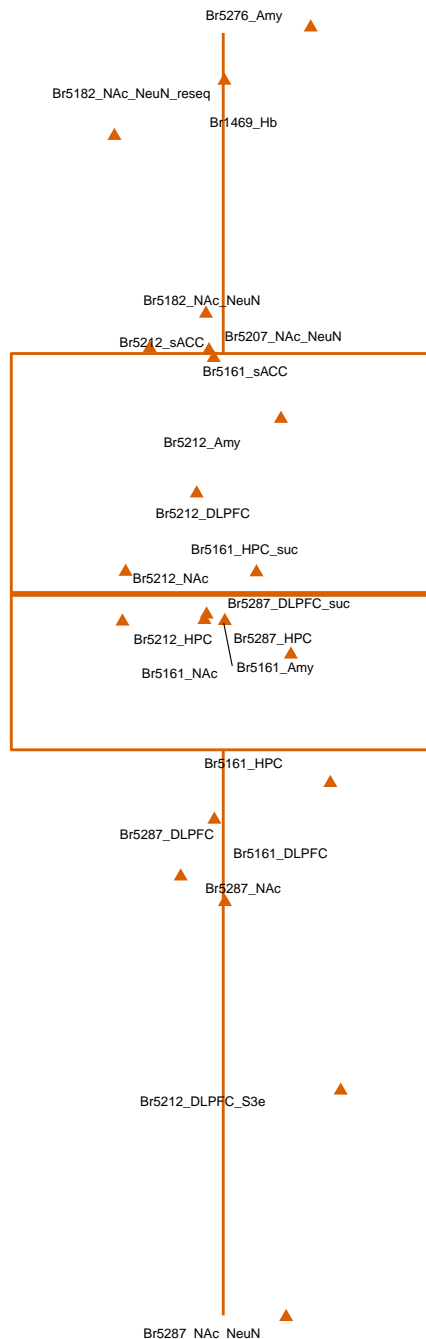
Tran2021  
set

round1

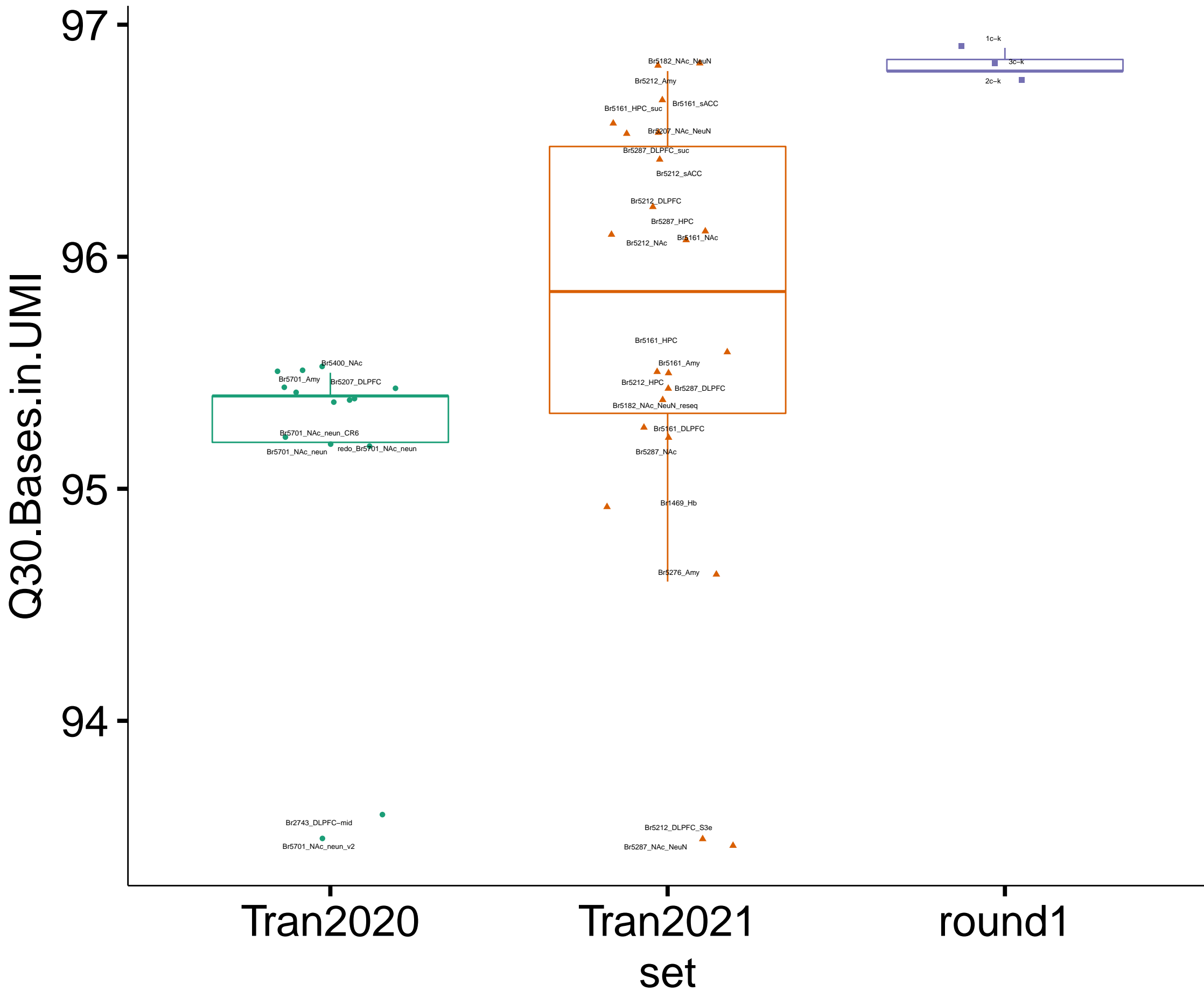


Br5701\_NAc\_neun\_v2

Br2743\_DLPFC--mid







Reads.Mapped.to.Genome

95

90

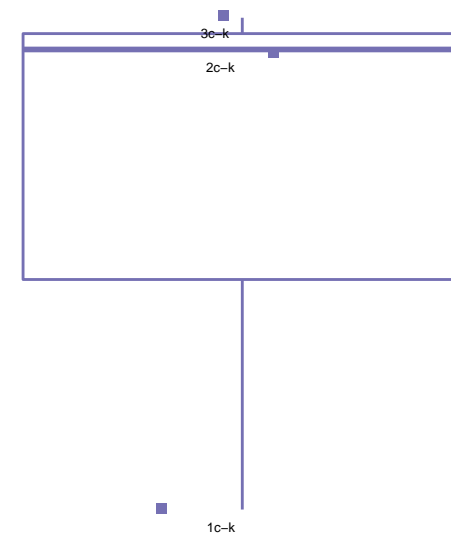
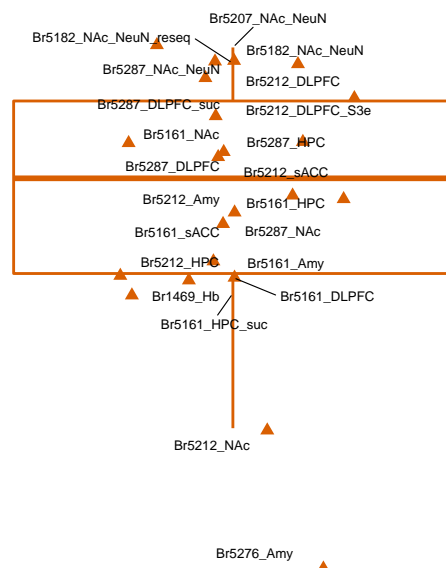
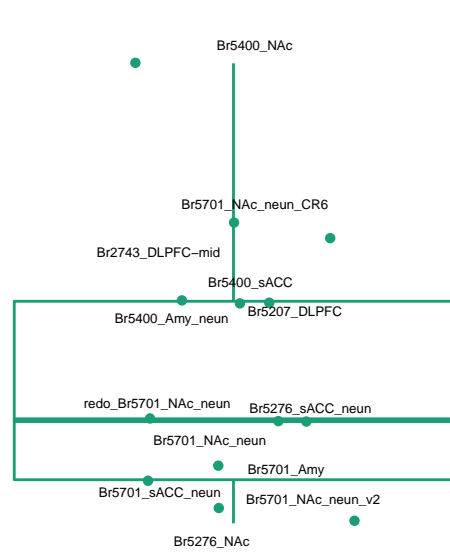
85

80

Tran2020

Tran2021  
set

round1



Reads.Mapped.Confidently.to.Genome

80

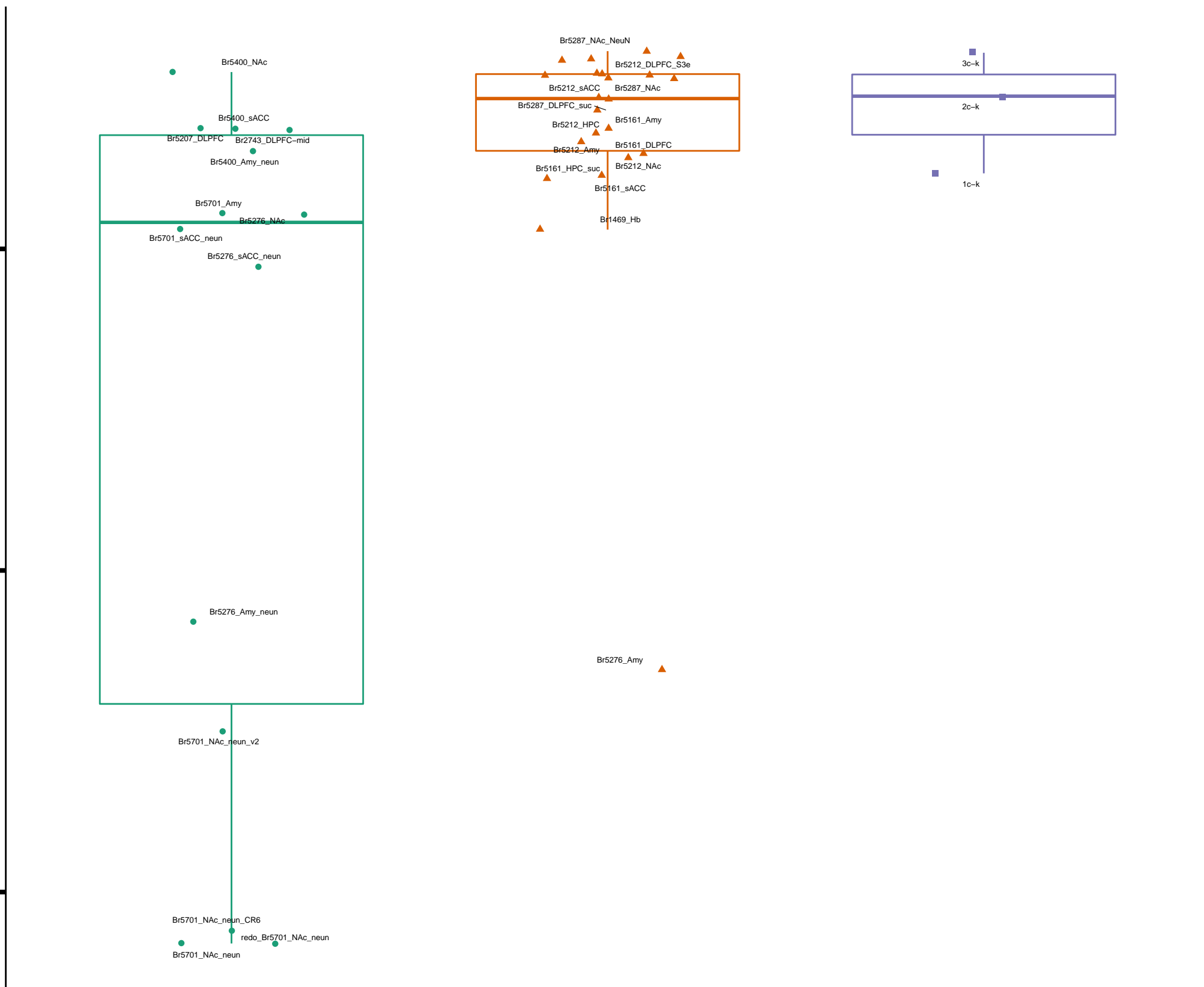
60

40

Tran2020

Tran2021  
set

round1



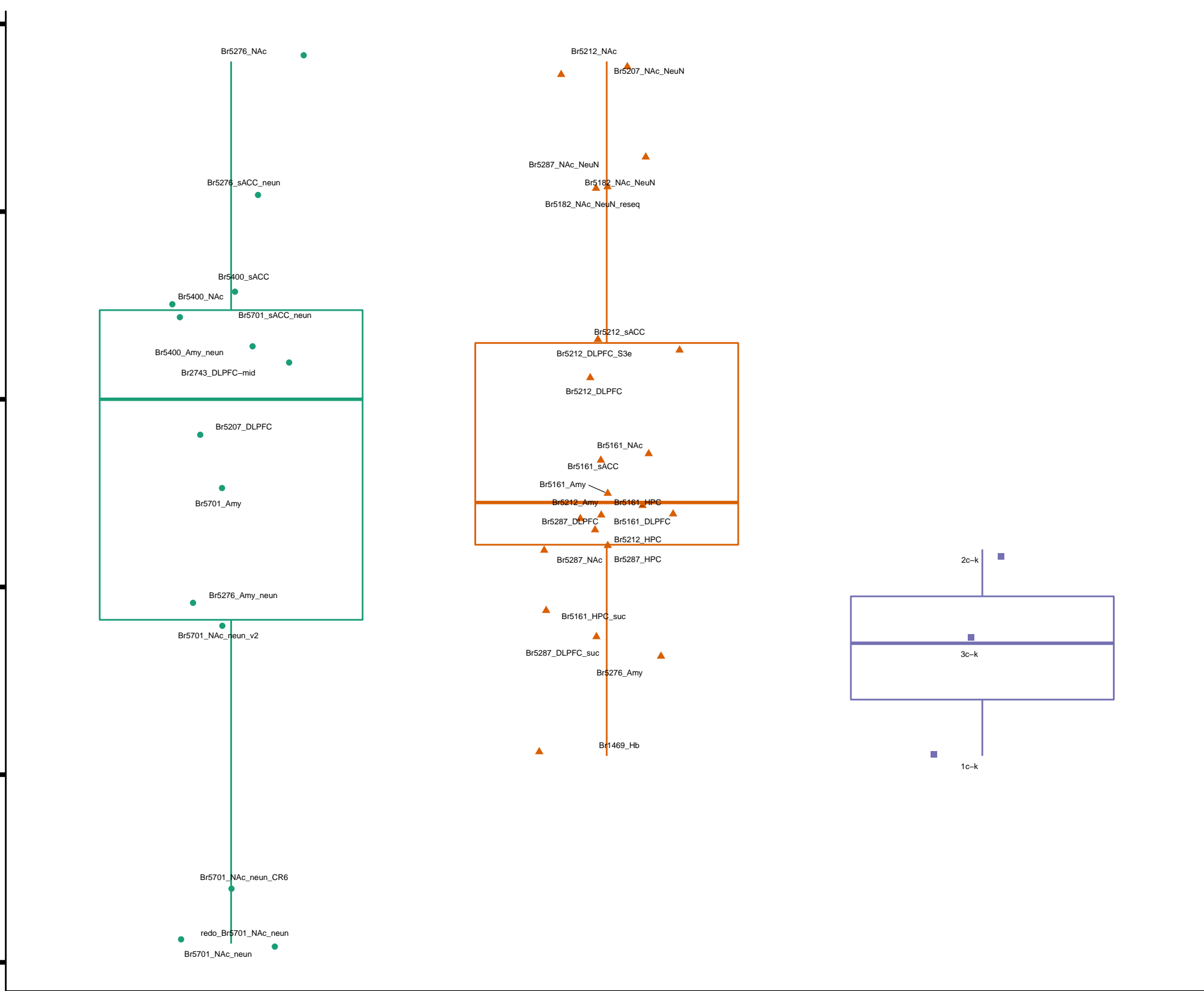
Reads.Mapped.Confidently.to.Intergenic.Regions

10  
9  
8  
7  
6  
5

Tran2020

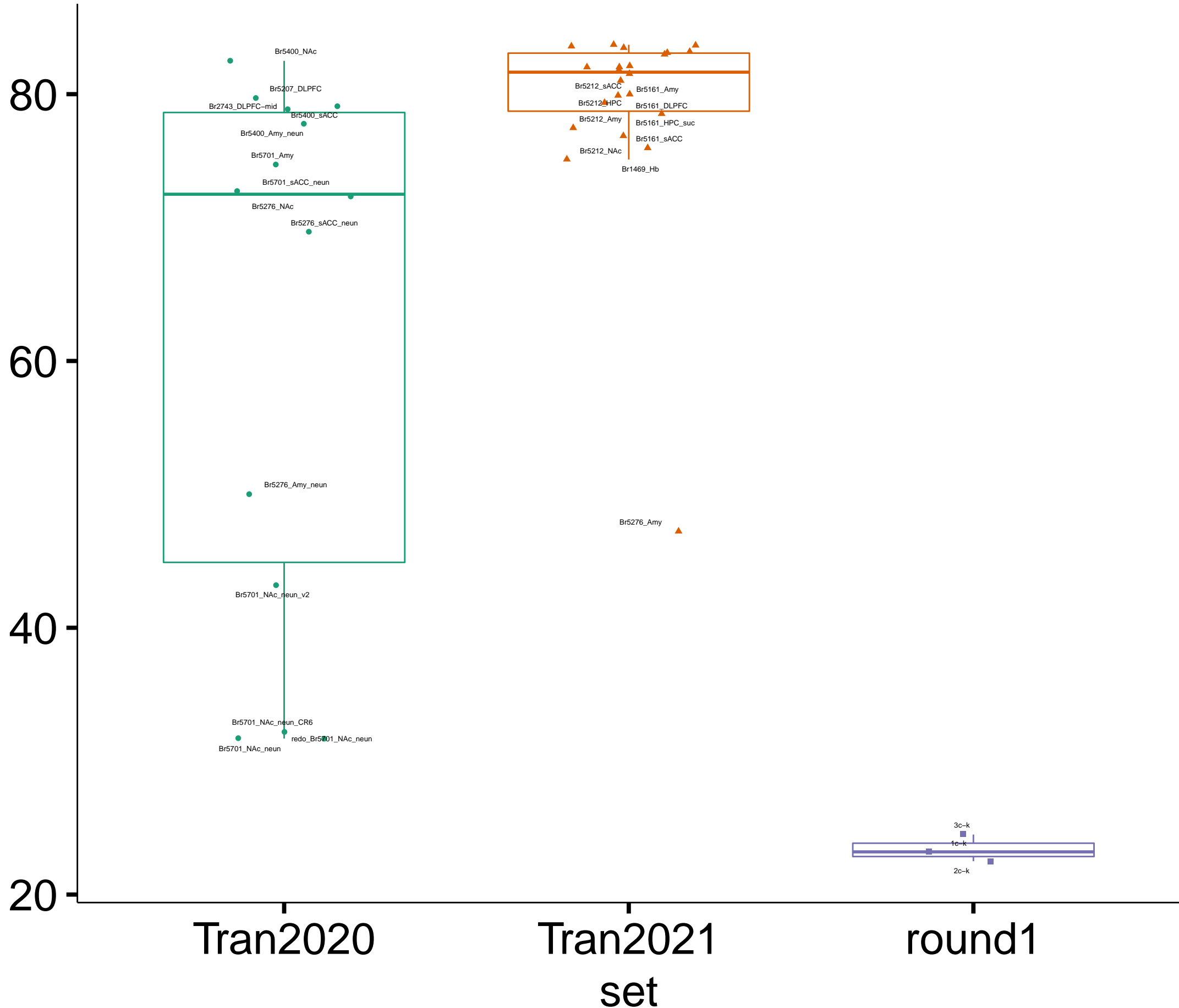
Tran2021  
set

round1





Reads.Mapped.Confidently.to.Exonic.Regions



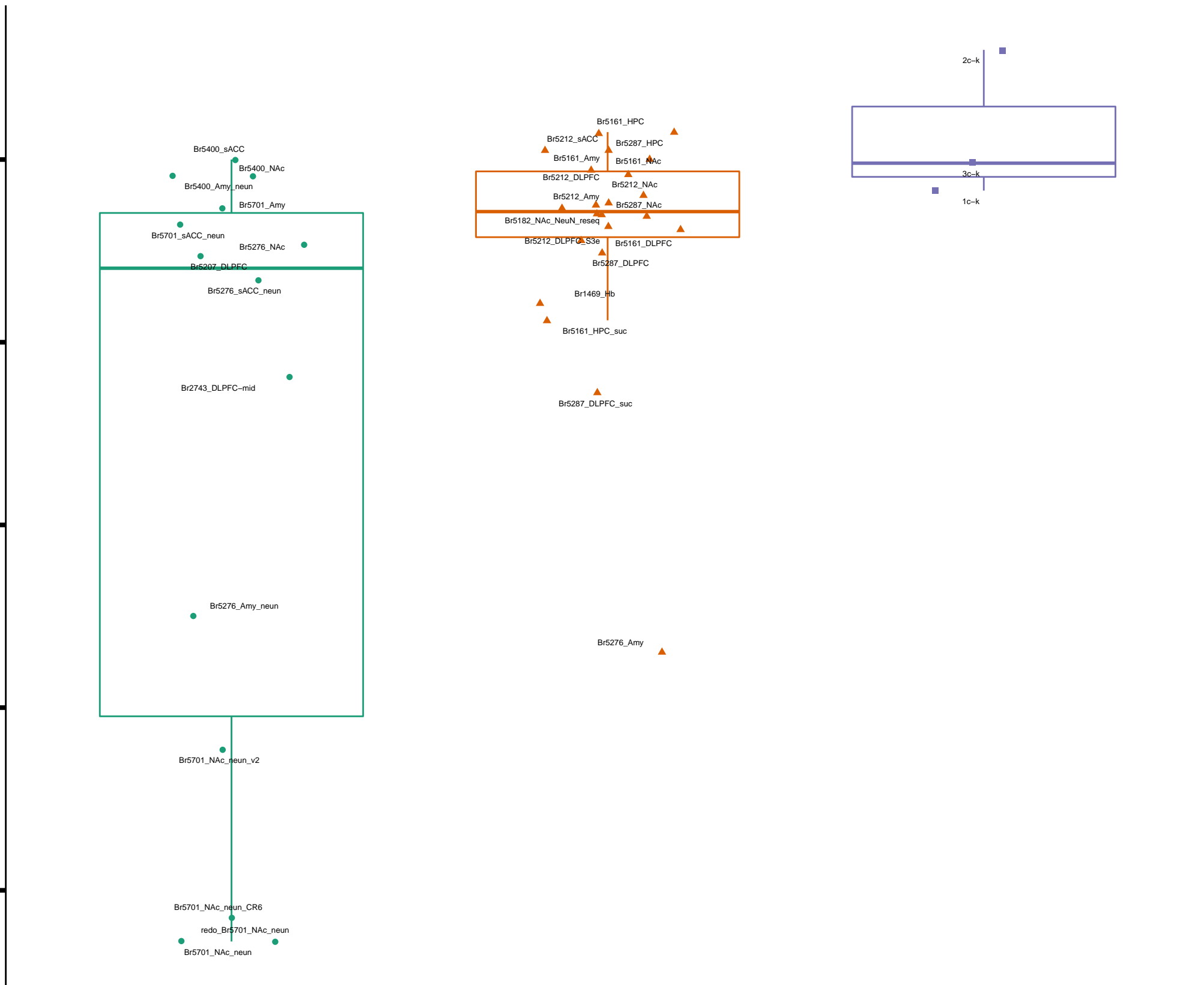
Reads.Mapped.Confidently.to.Transcriptome

70  
60  
50  
40  
30

Tran2020

Tran2021  
set

round1



Reads.Mapped.Antisense.to.Gene

15

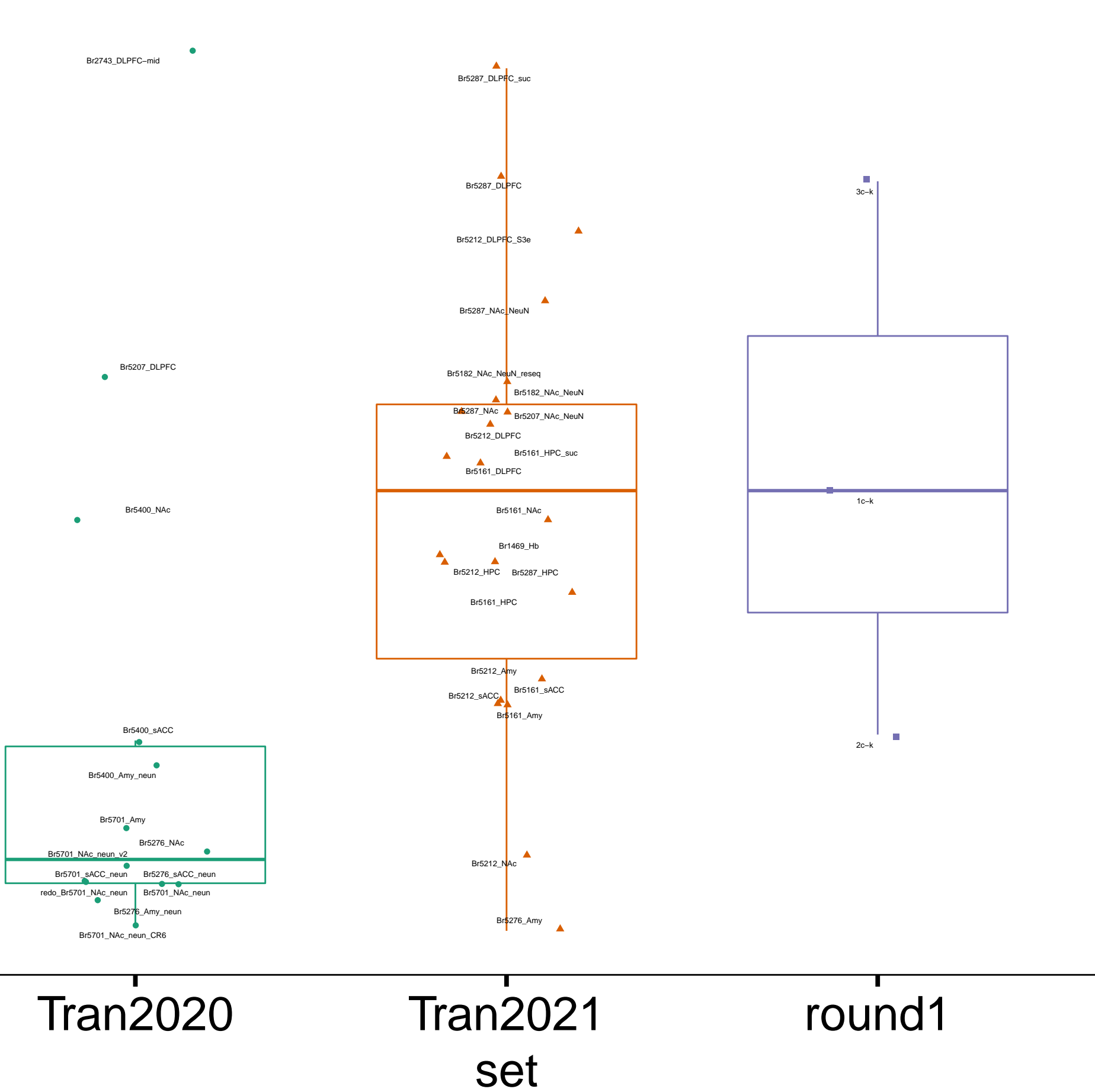
10

5

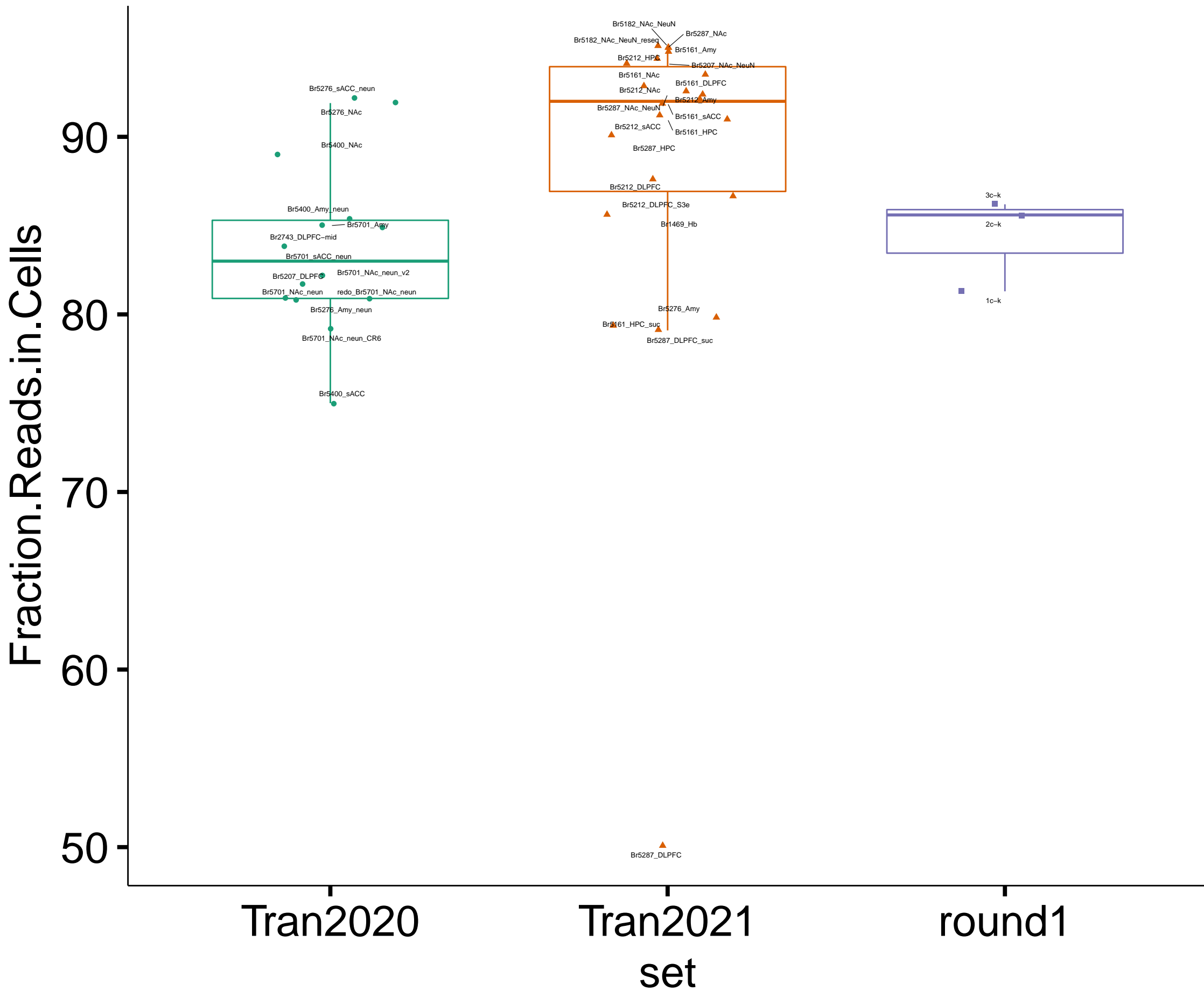
Tran2020

Tran2021  
set

round1







Total.Genes.Detected

30000

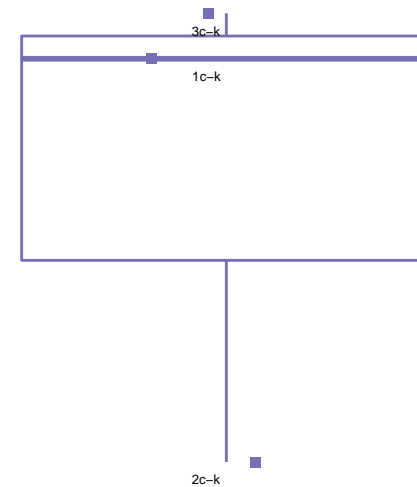
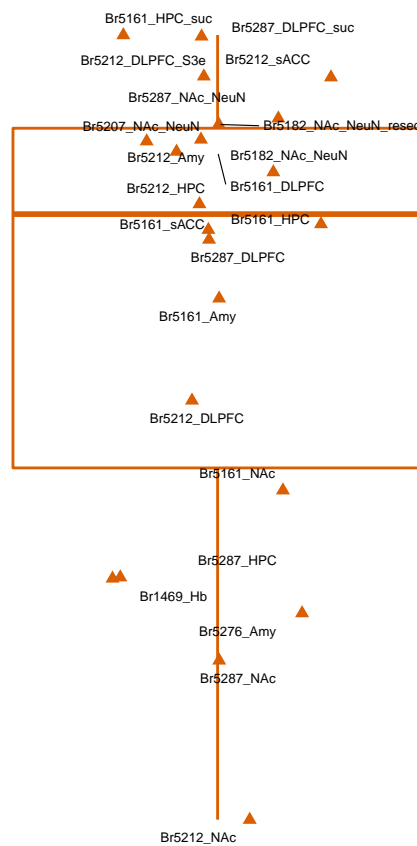
28000

26000

Tran2020

Tran2021  
set

round1



Median.UMI.Counts.per.Cell

30000

20000

10000

Tran2020

Tran2021  
set

round1

