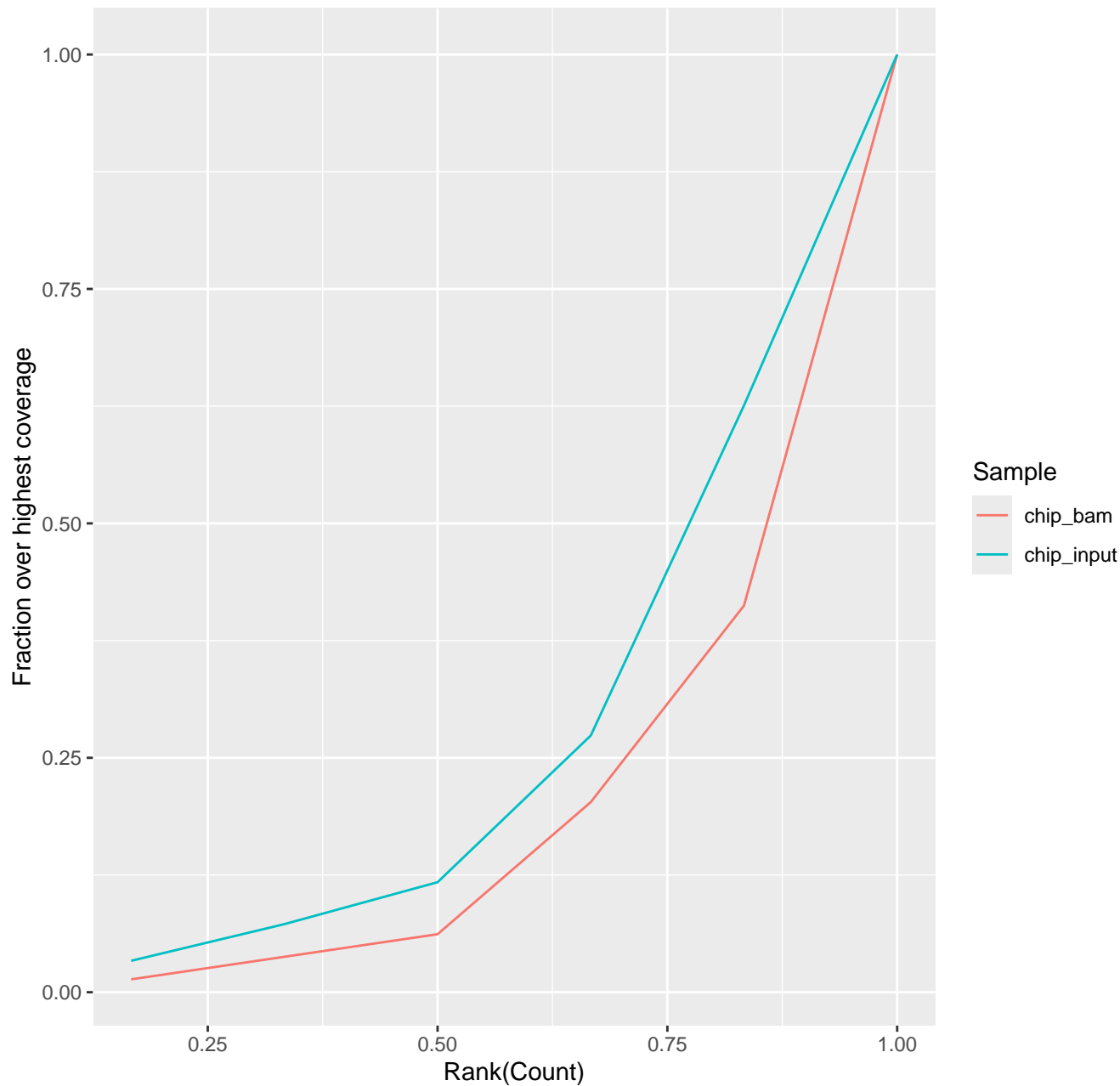
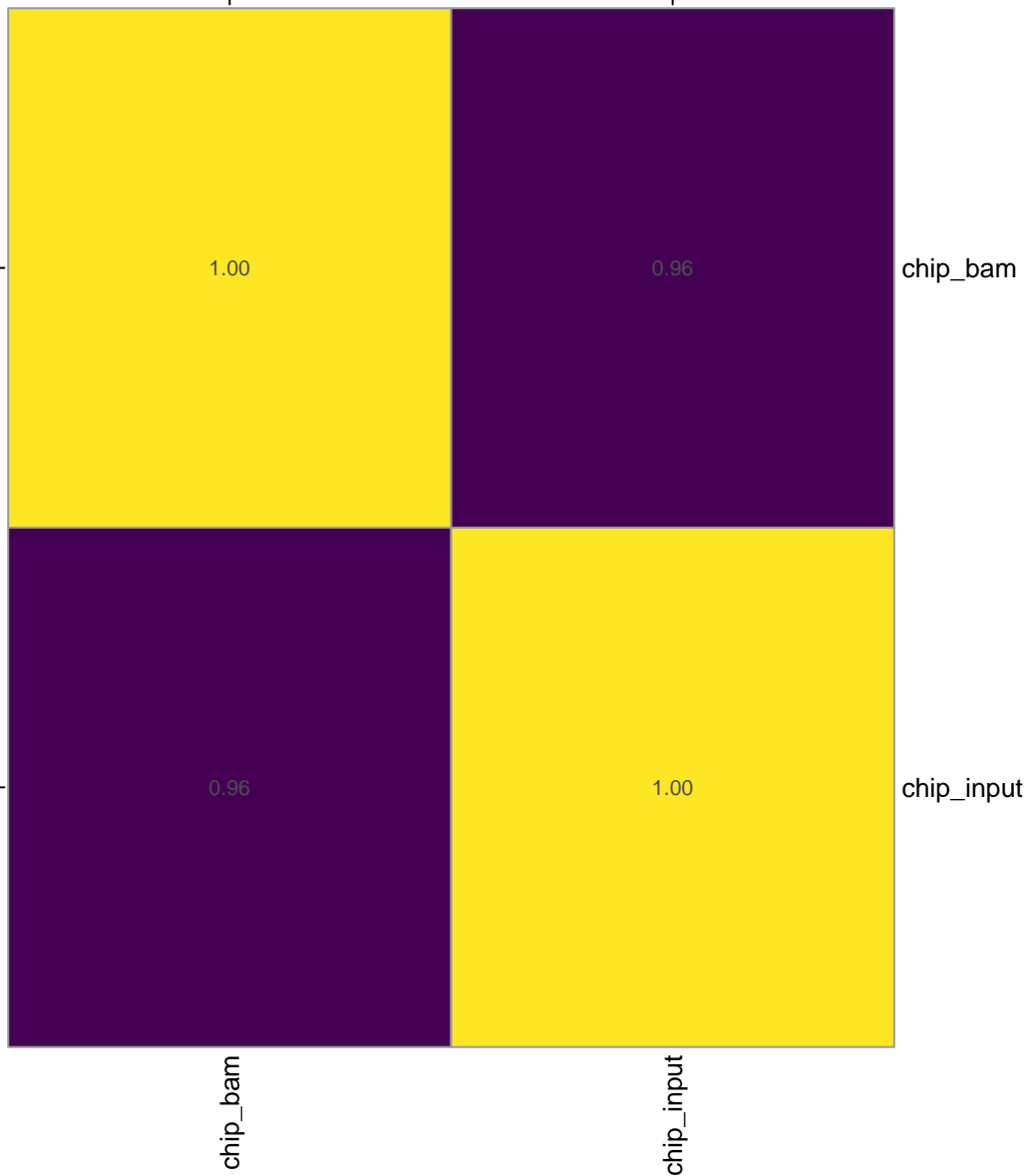


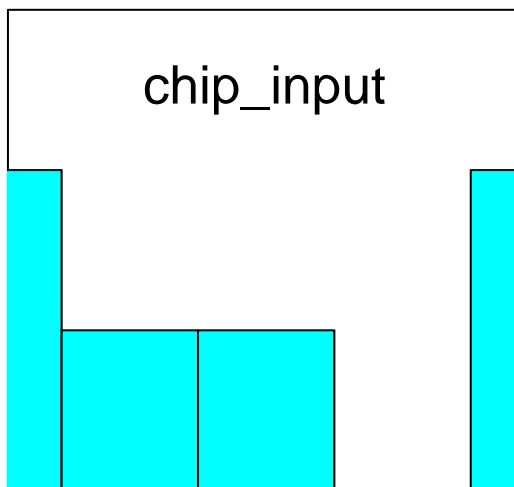
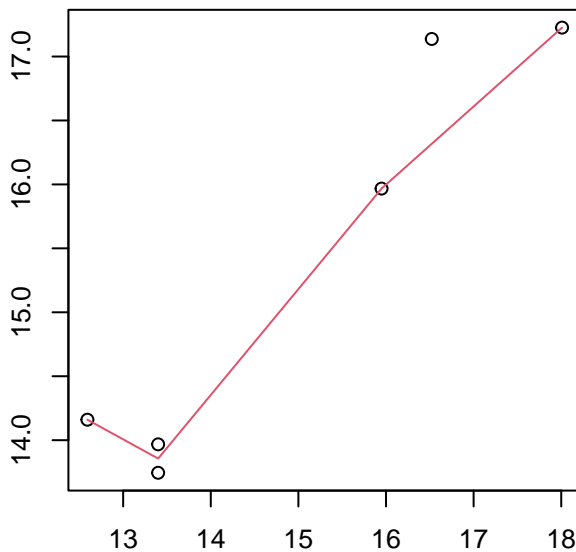
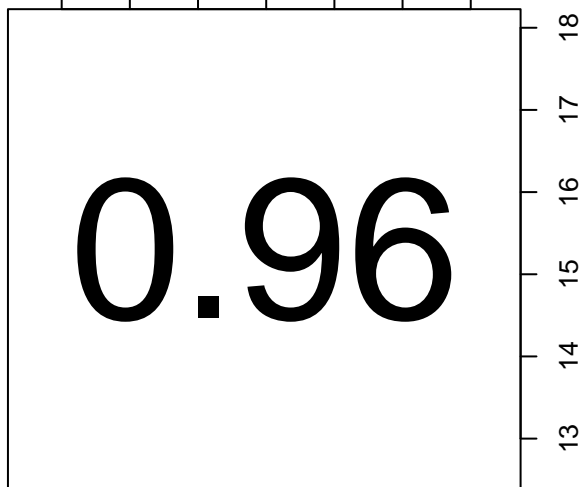
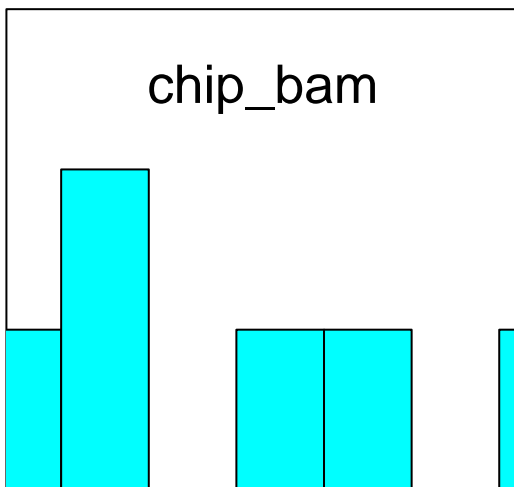
Binned read counts distribution: bin size = 1e+05

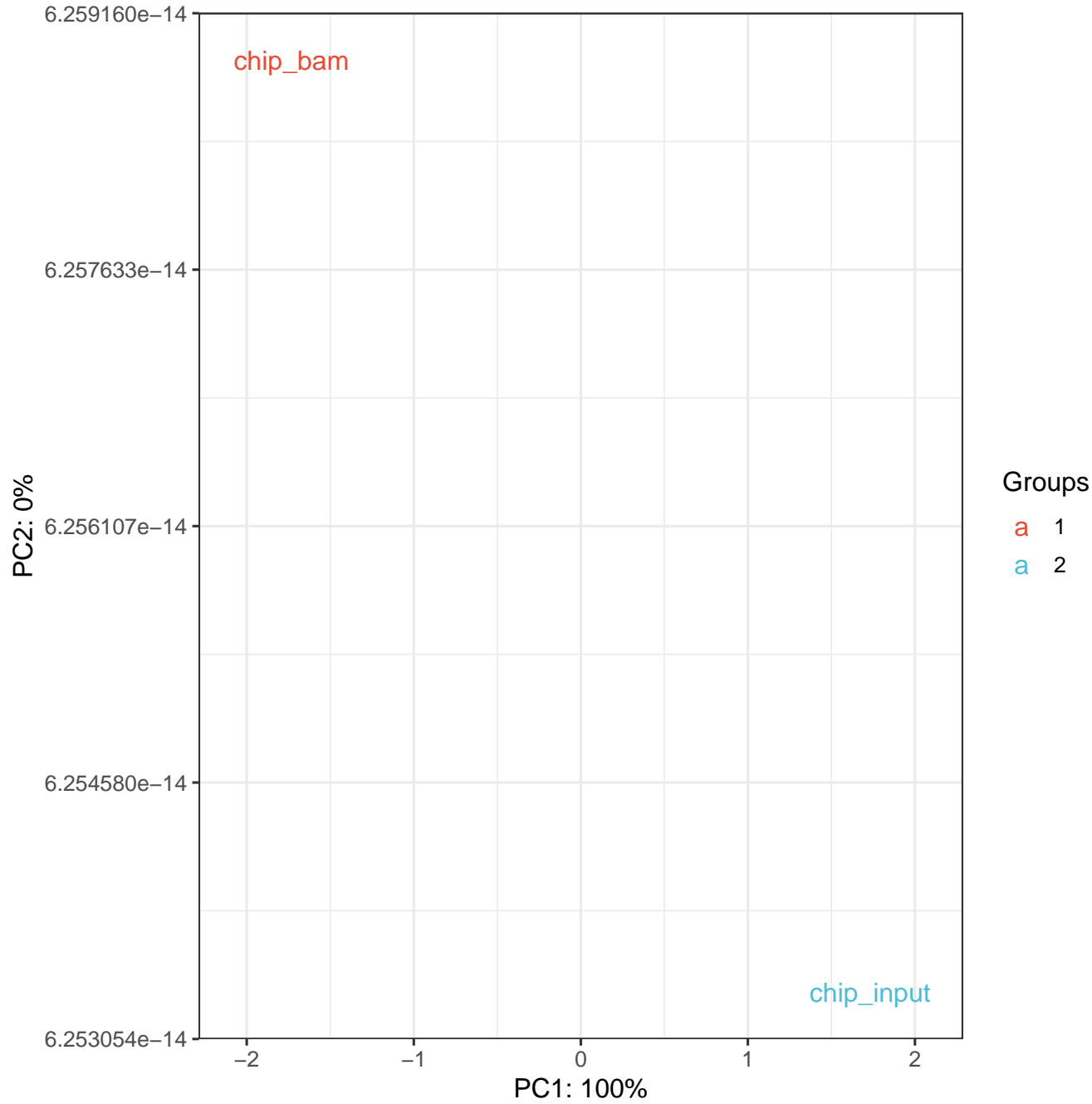




$\log_2(\text{CPM}/\text{bin})$, bin size = $1\text{e}+05$

14.0 15.0 16.0 17.0





SummitPeak

2

17

76

NarrowPeak

3

76

21

iCLIPPeak

51

2

2

iCLIPPeak

NarrowPeak

SummitPeak

NarrowPeak

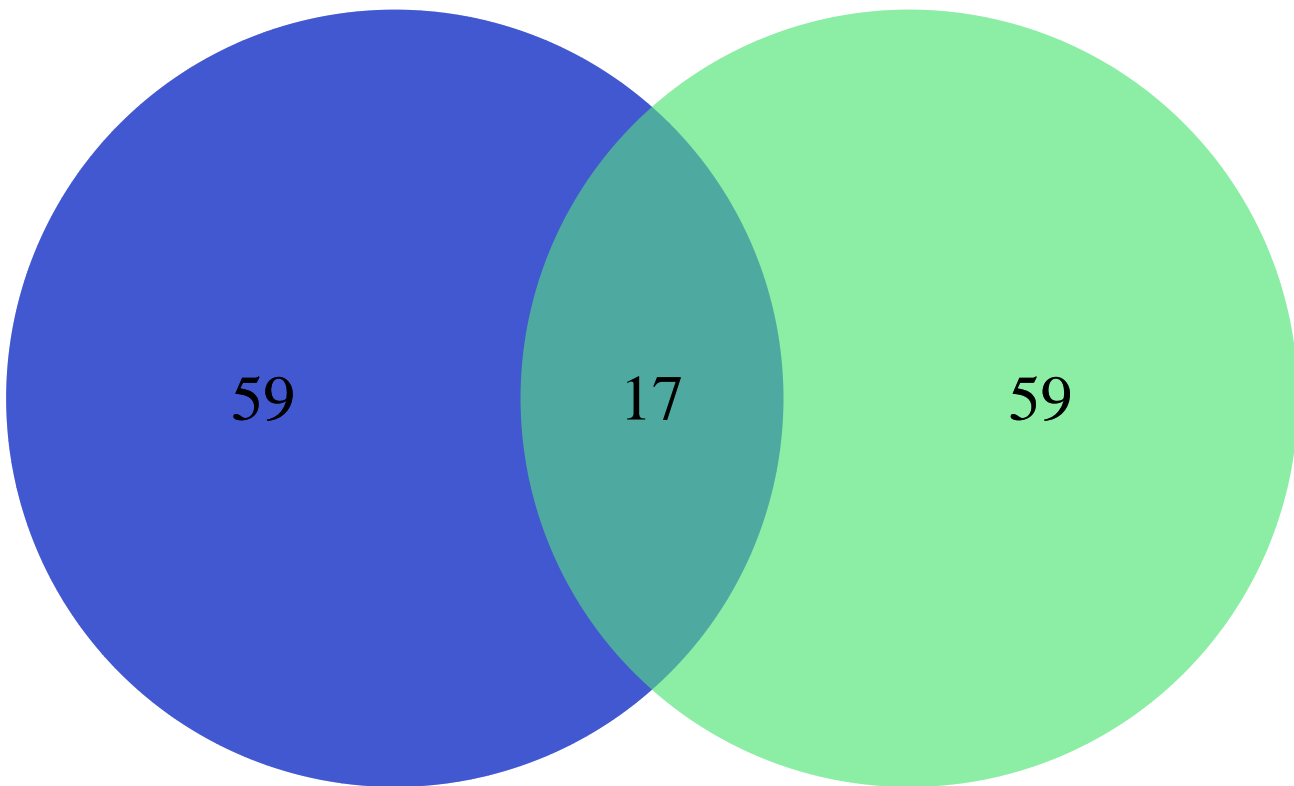
SummitPeak

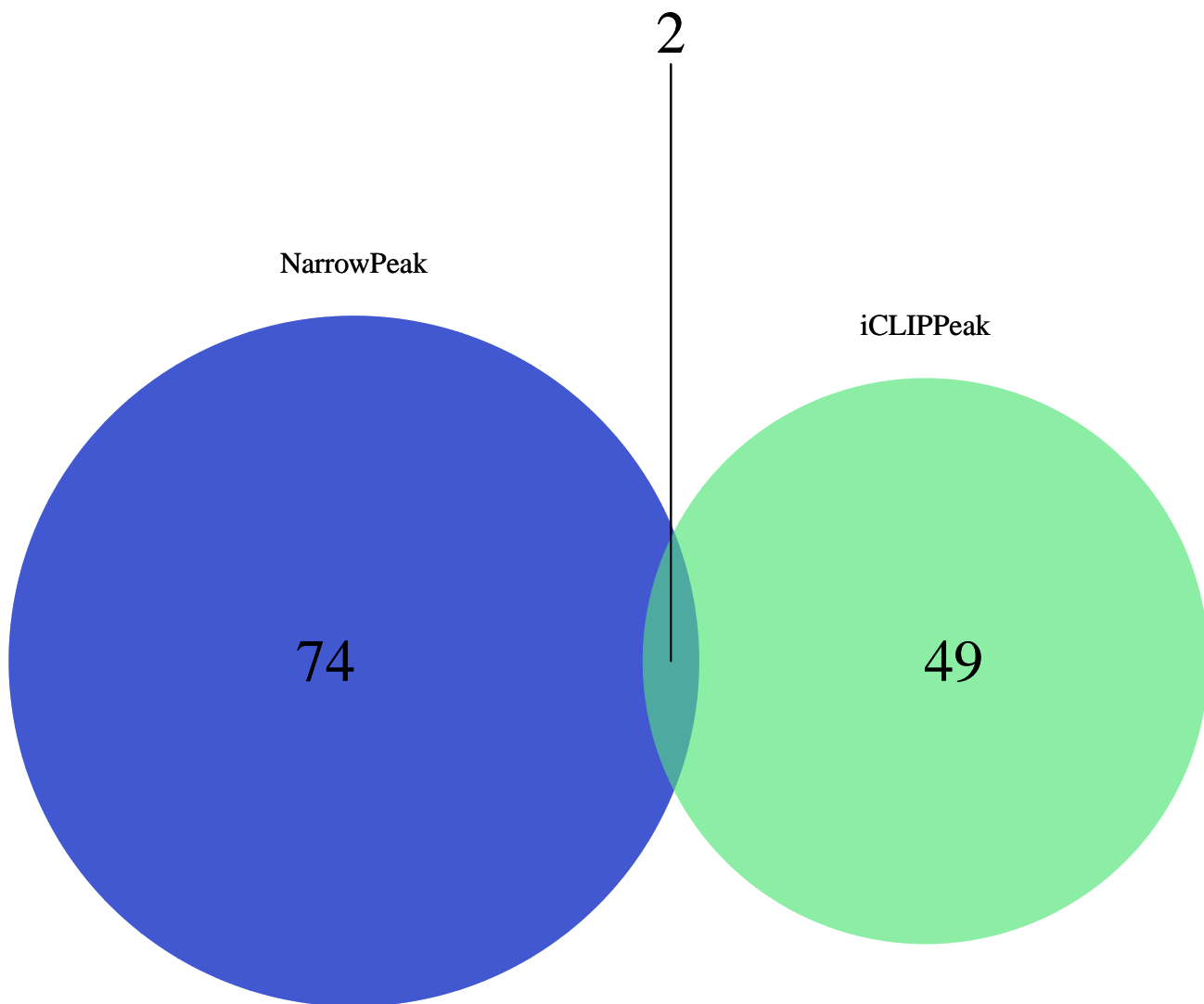
59

17

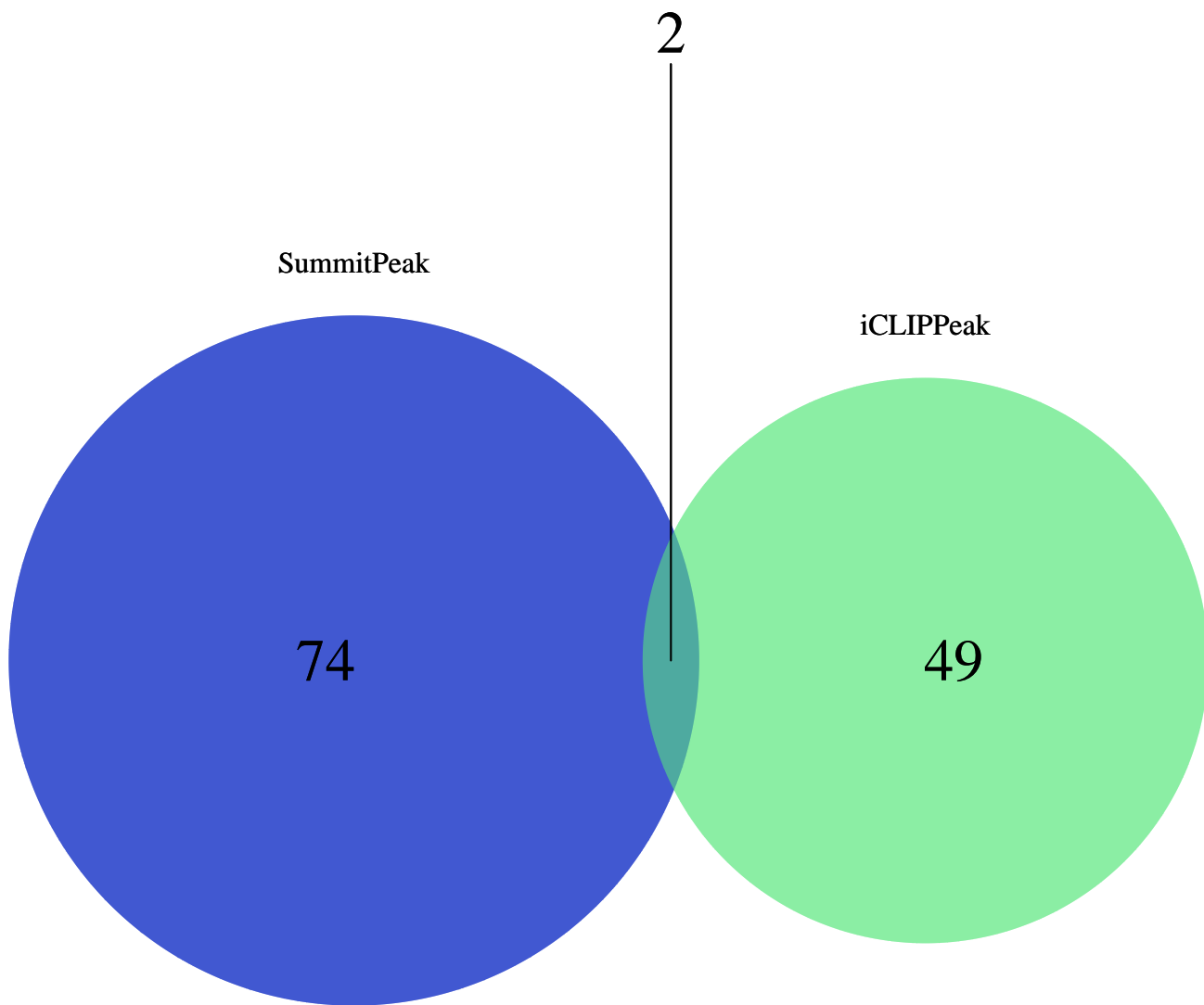
59

Jaccard: 0.12593





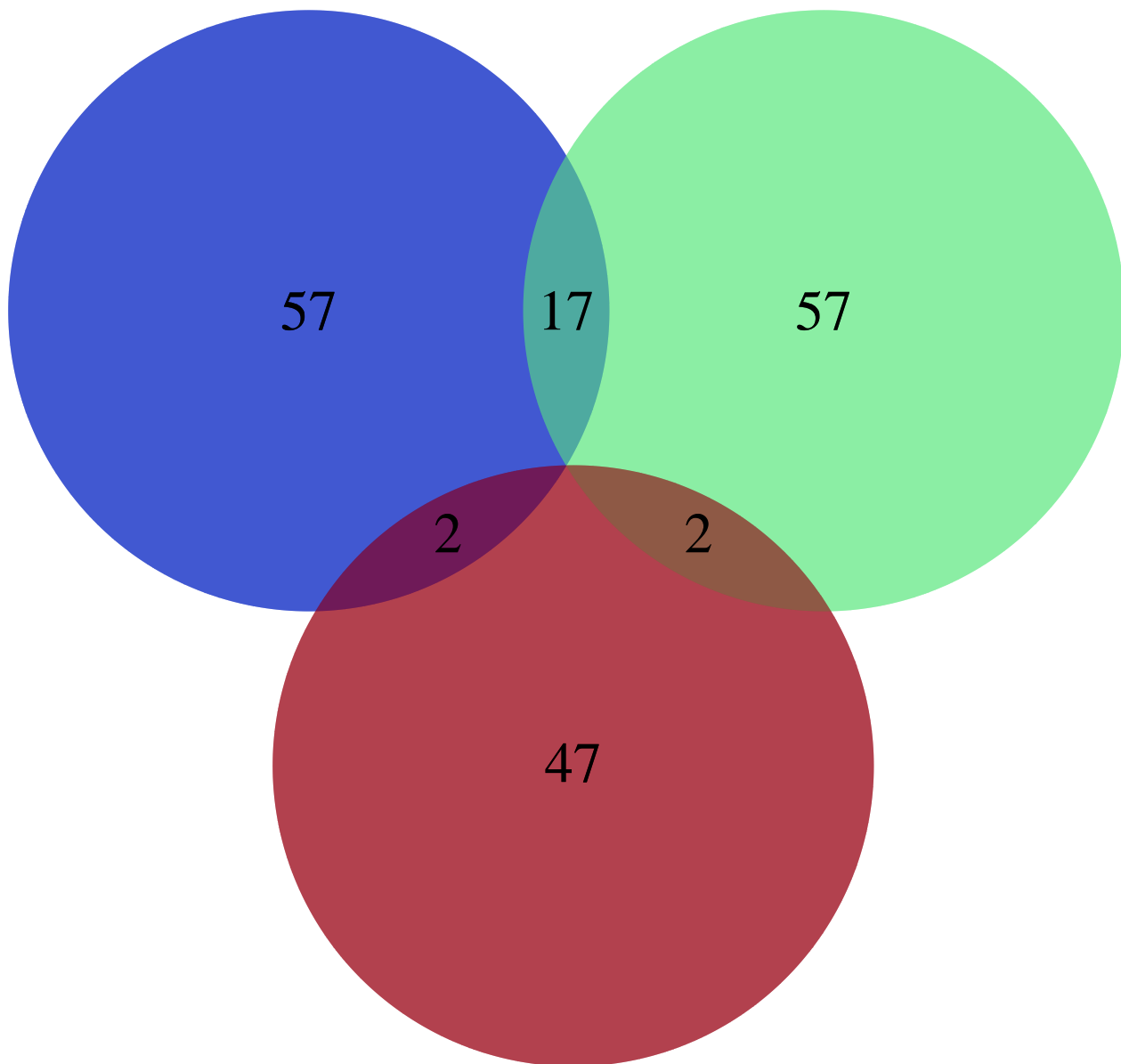
Jaccard: 0.016



Jaccard: 0.016

NarrowPeak

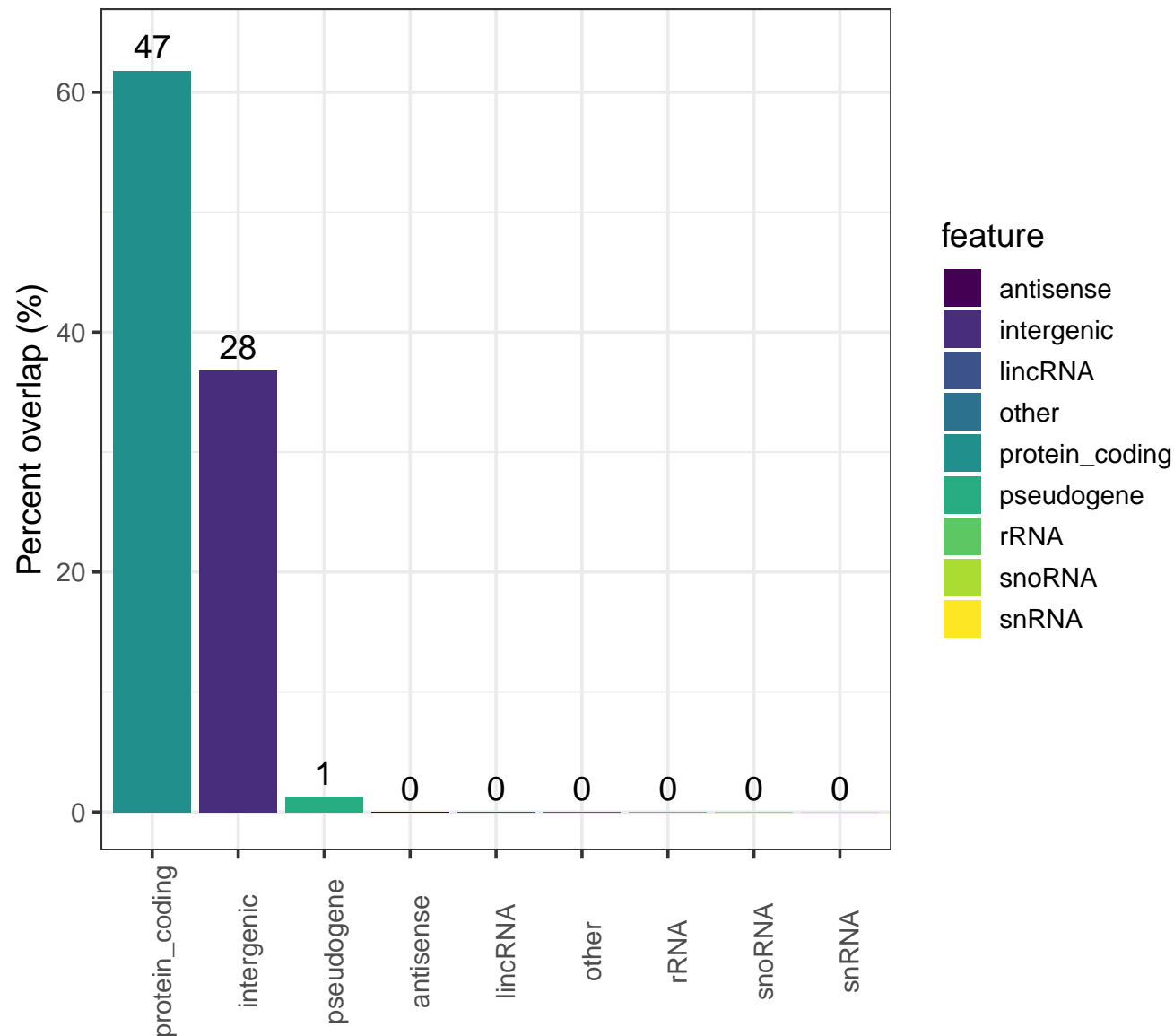
SummitPeak



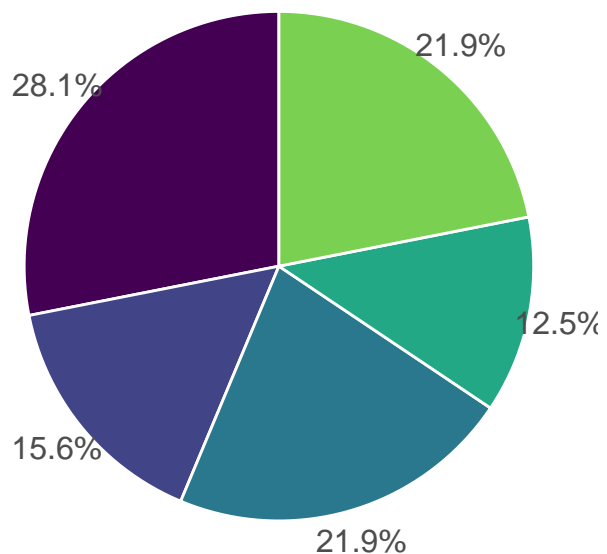
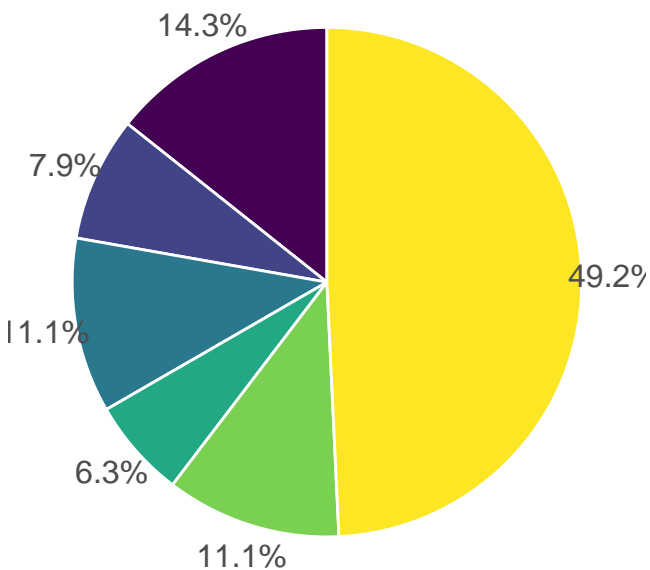
iCLIPPeak

Annotation of peaks to all type of genes

(Total number of peaks = 76)



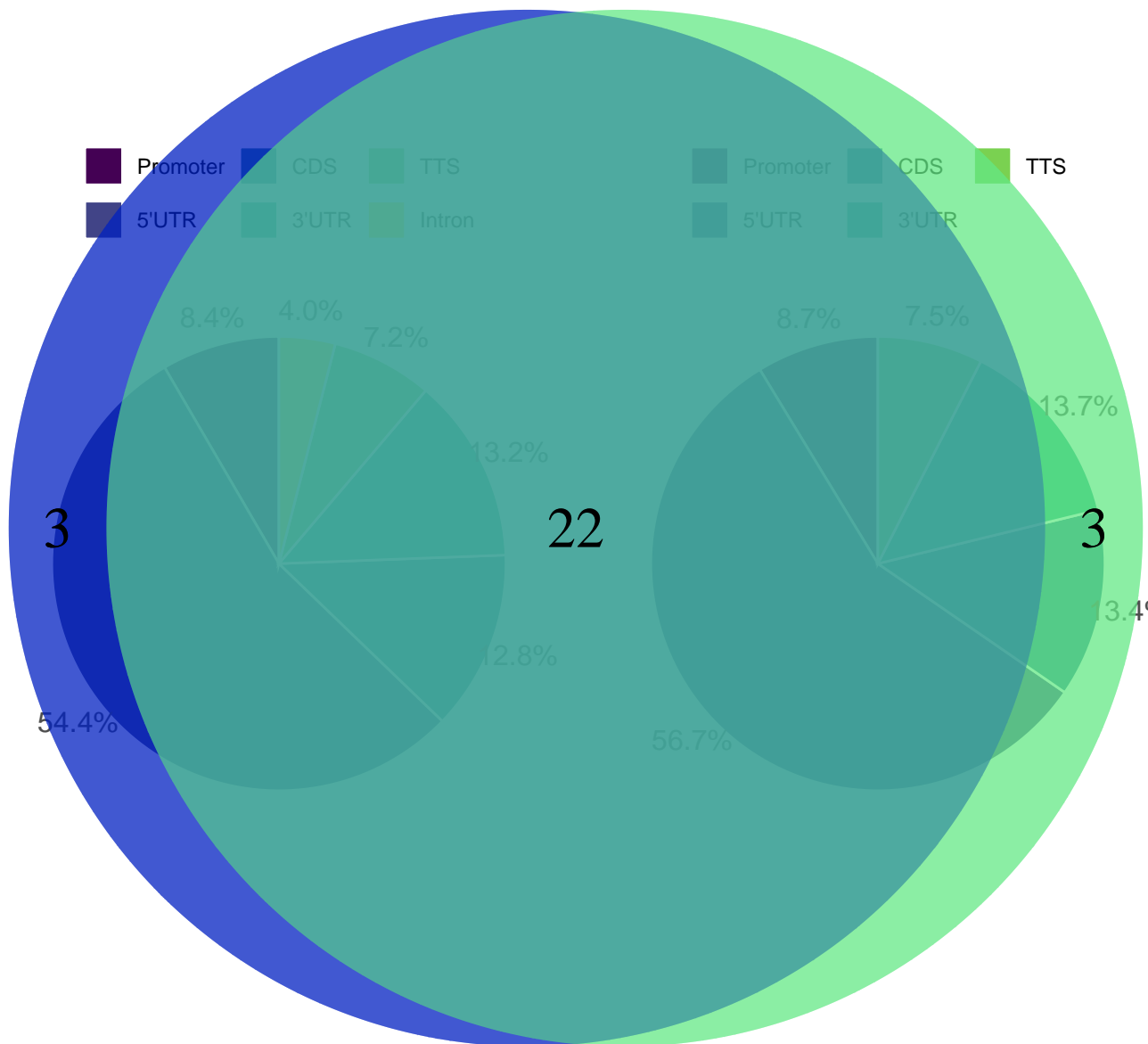
Absolute counts



Length-normalized counts

test1

test2



3

22

3

54.4%

56.7%

8.4%

4.0%

7.2%

13.2%

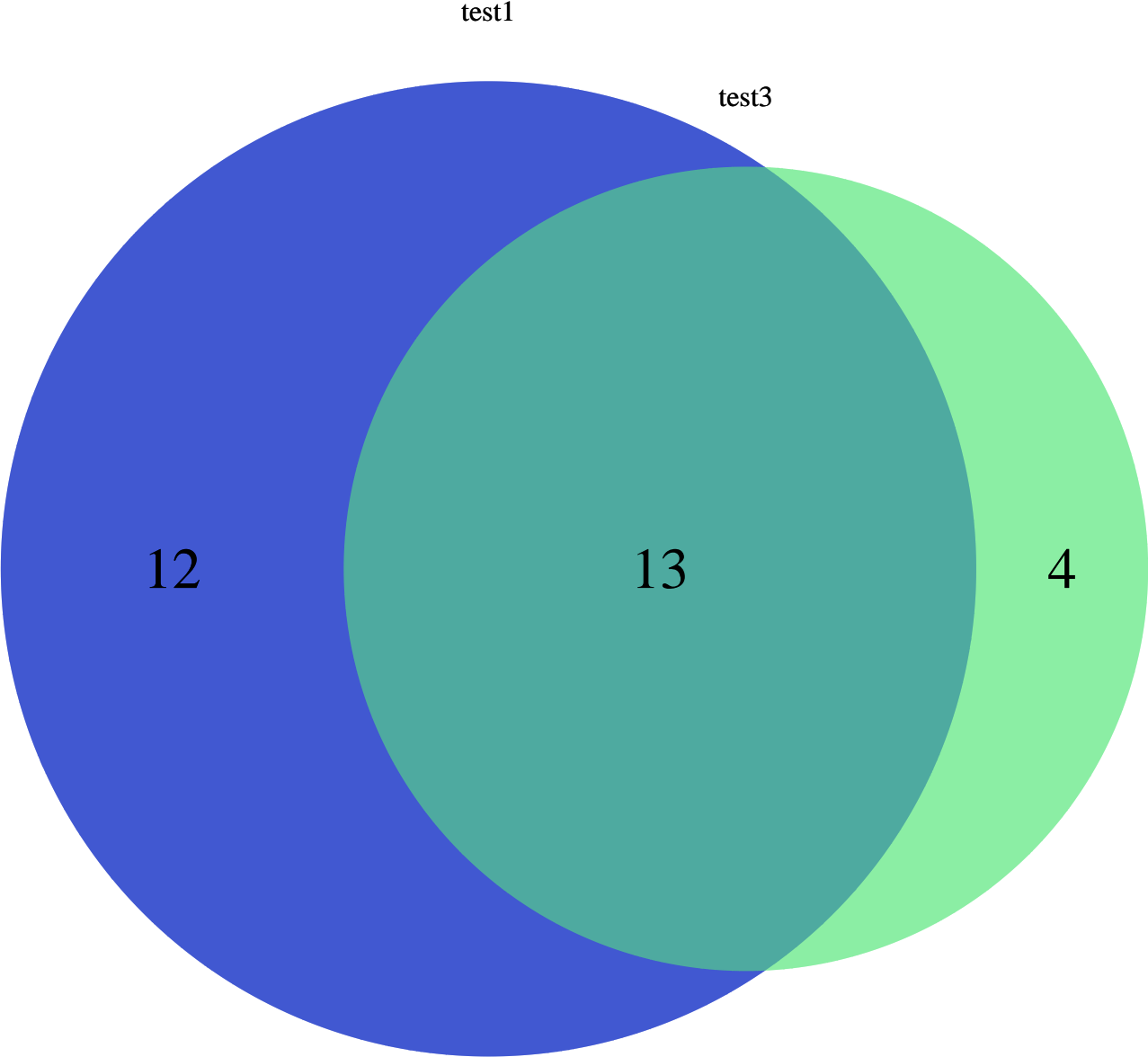
12.8%

8.7%

7.5%

13.7%

13.4%



test1

test3

12

13

4

Jaccard: 0.44828

test1

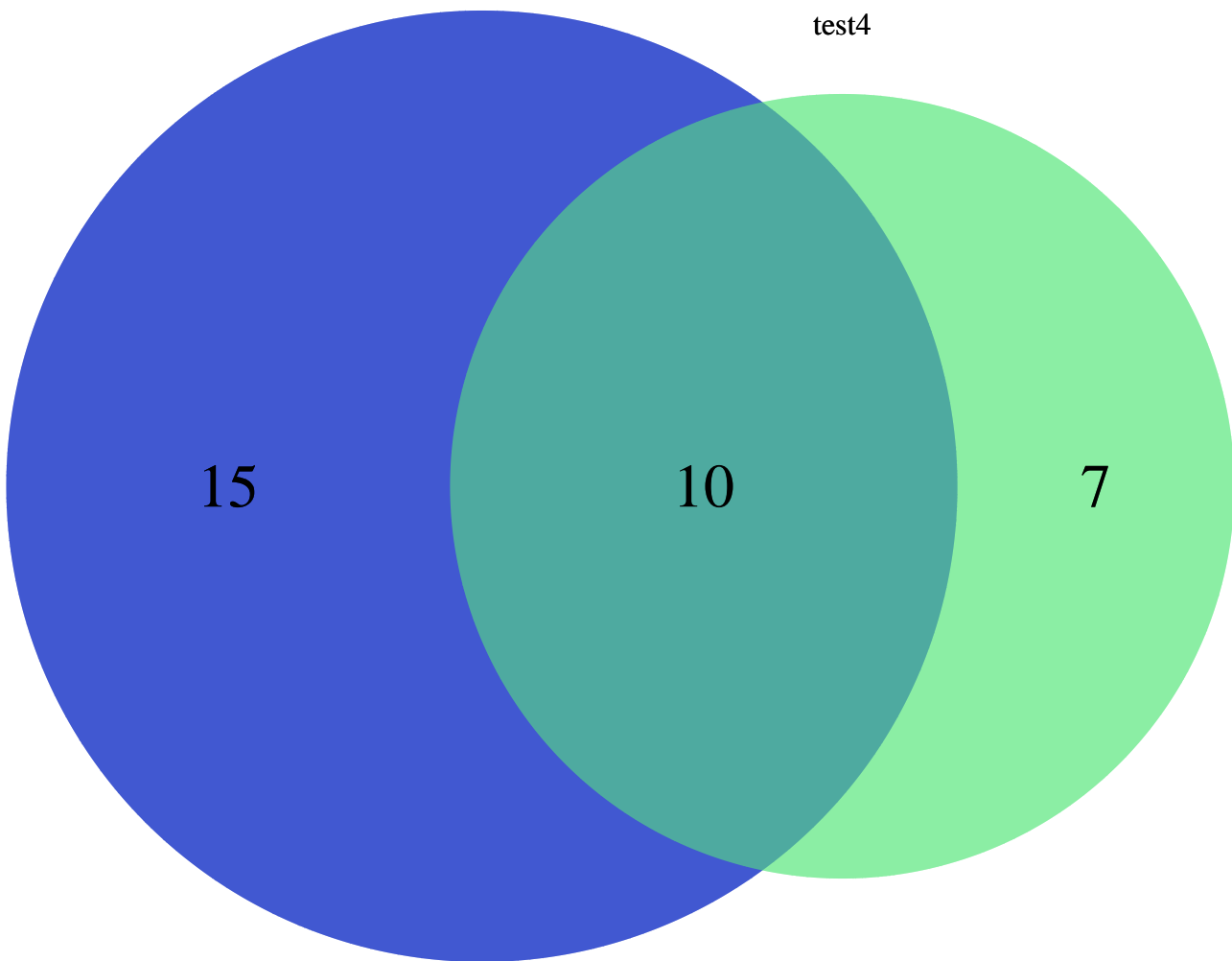
test4

15

10

7

Jaccard: 0.3125



test2

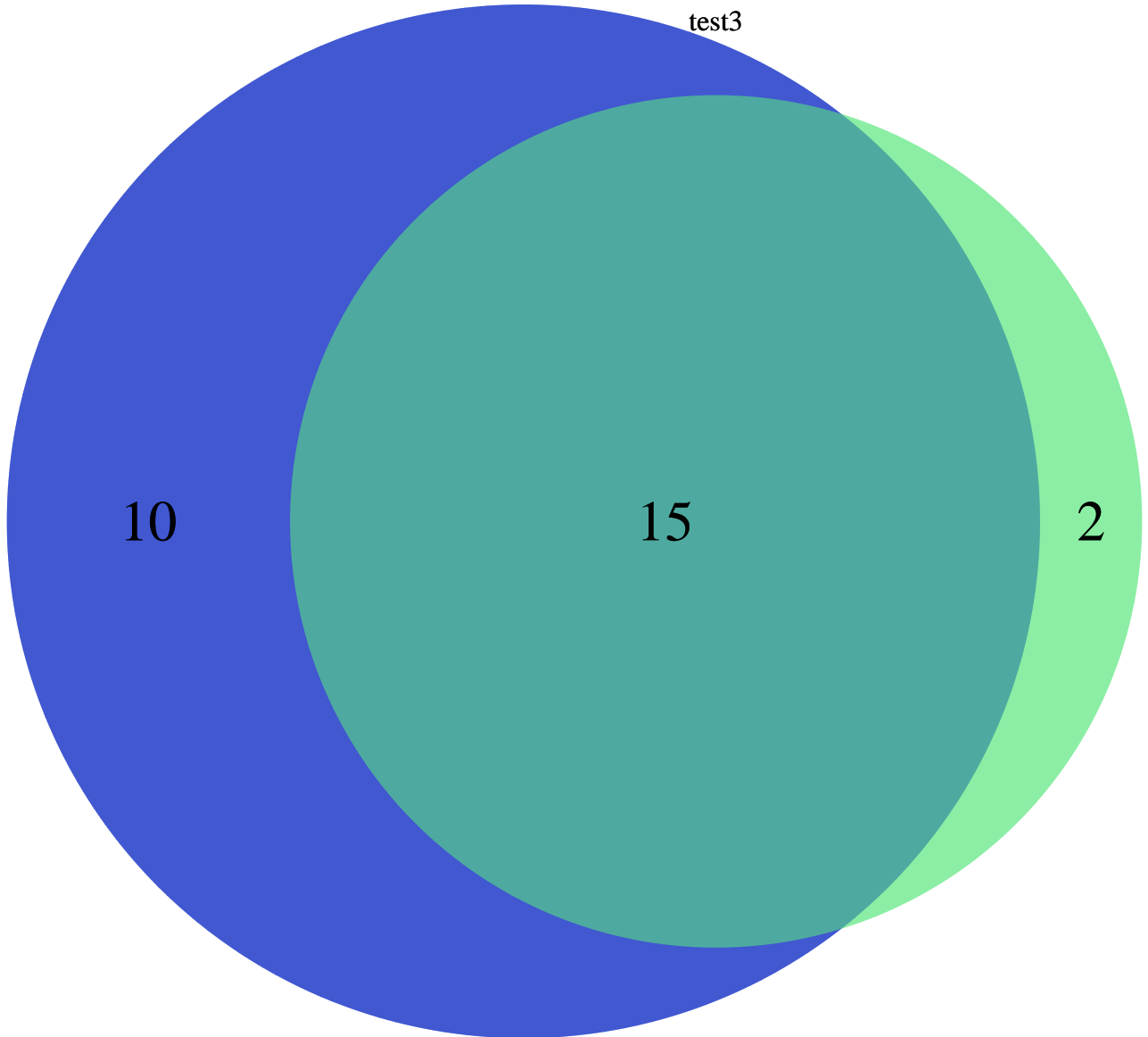
test3

10

15

2

Jaccard: 0.55556



test2

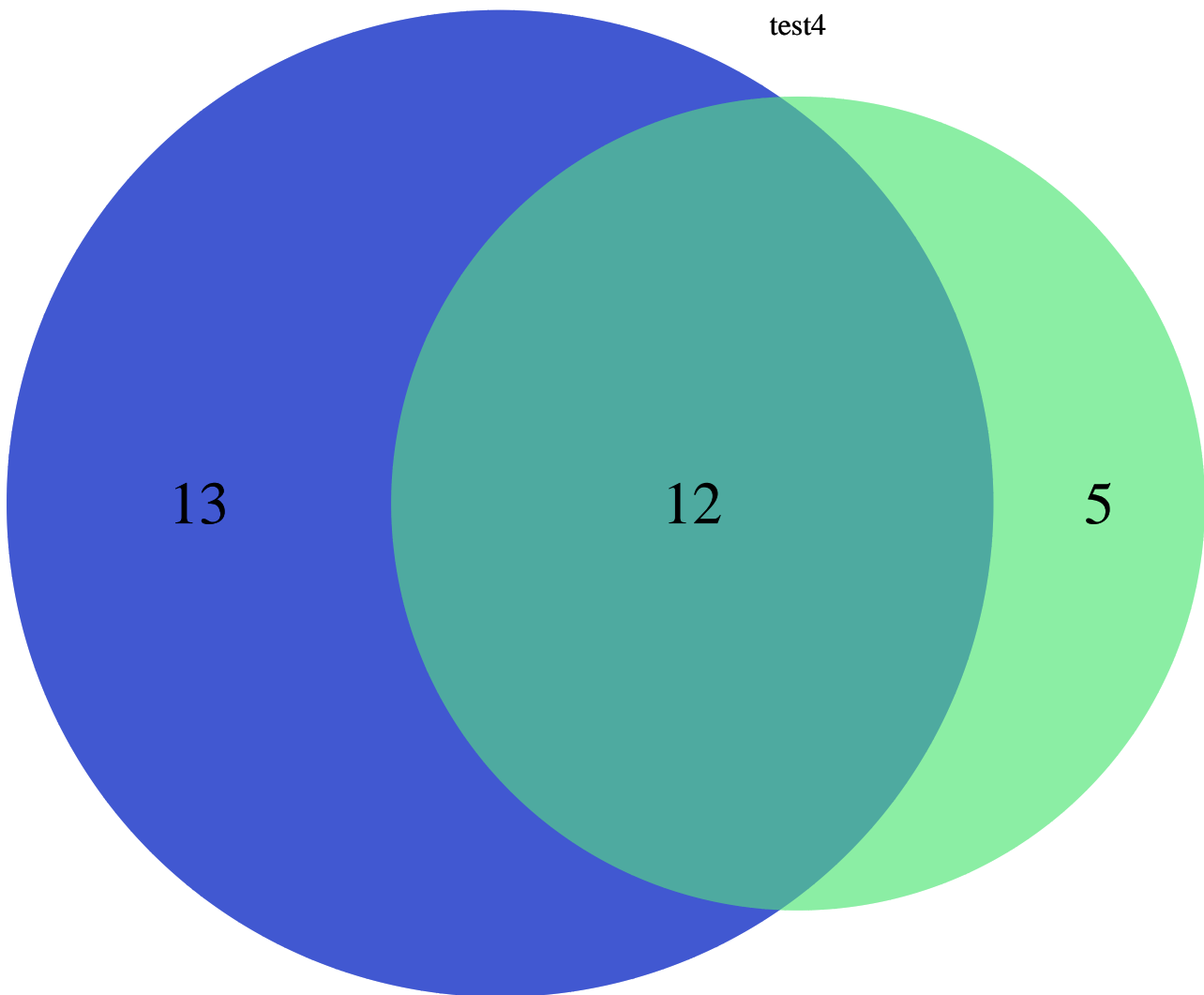
test4

13

12

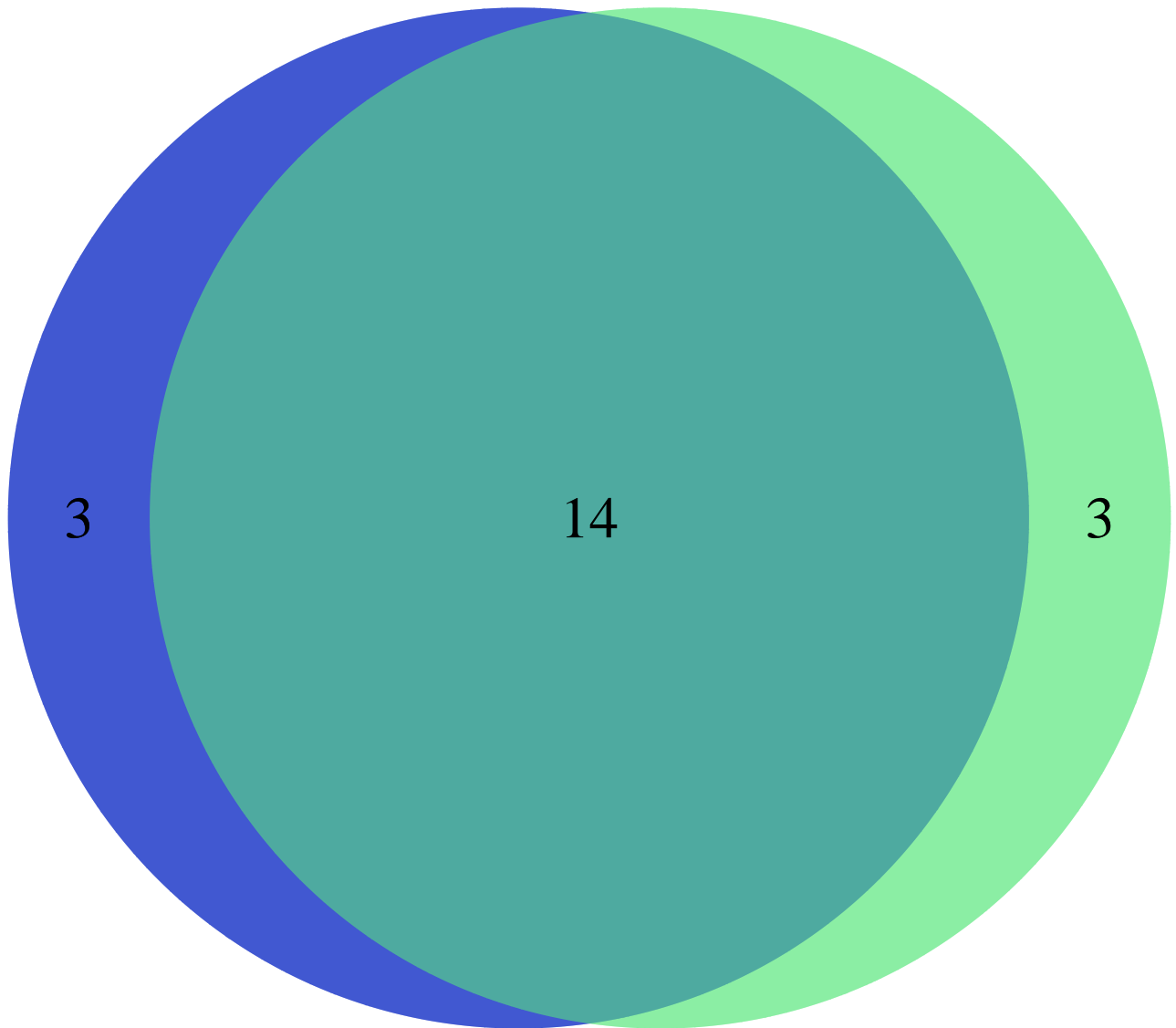
5

Jaccard: 0.4

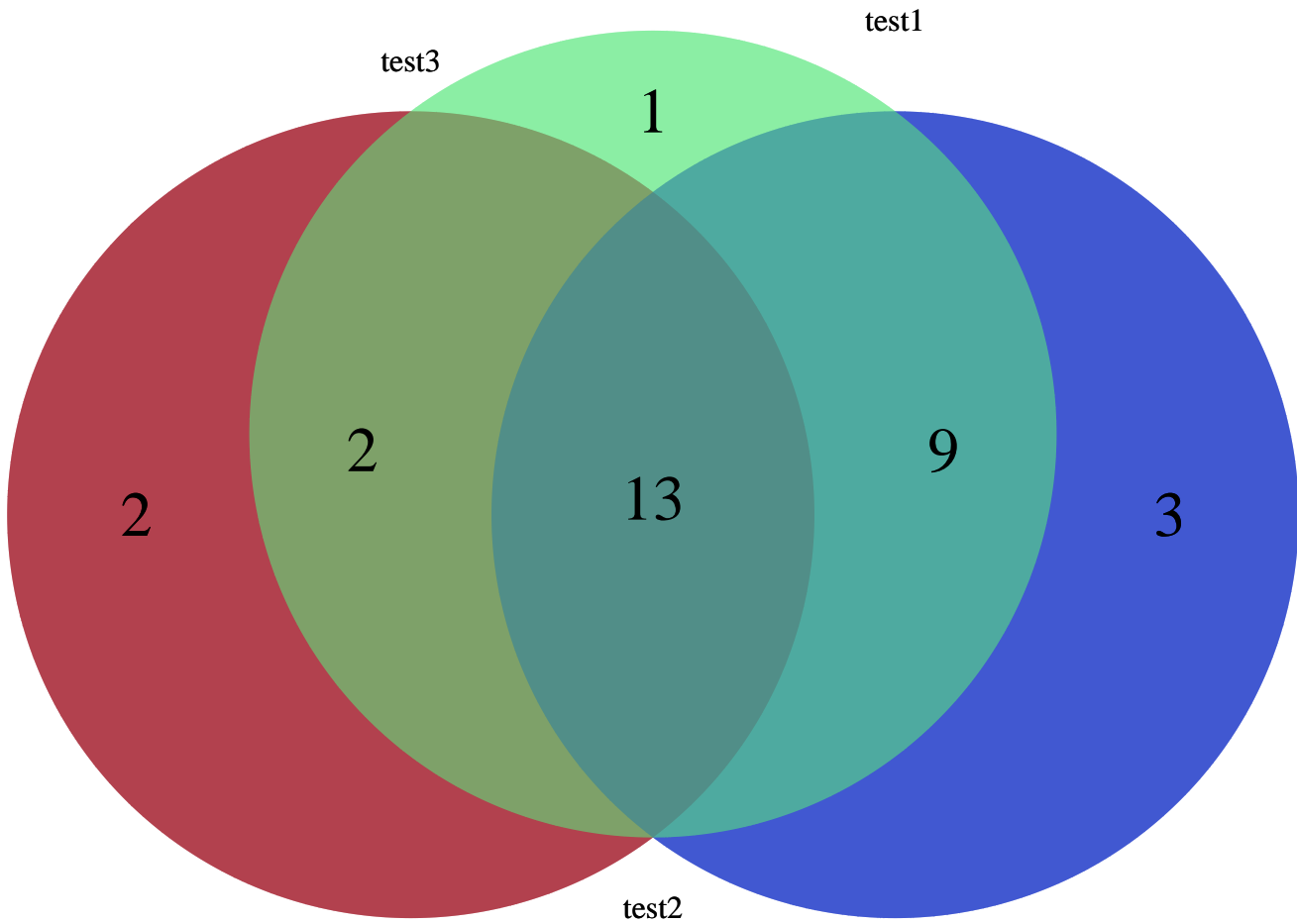


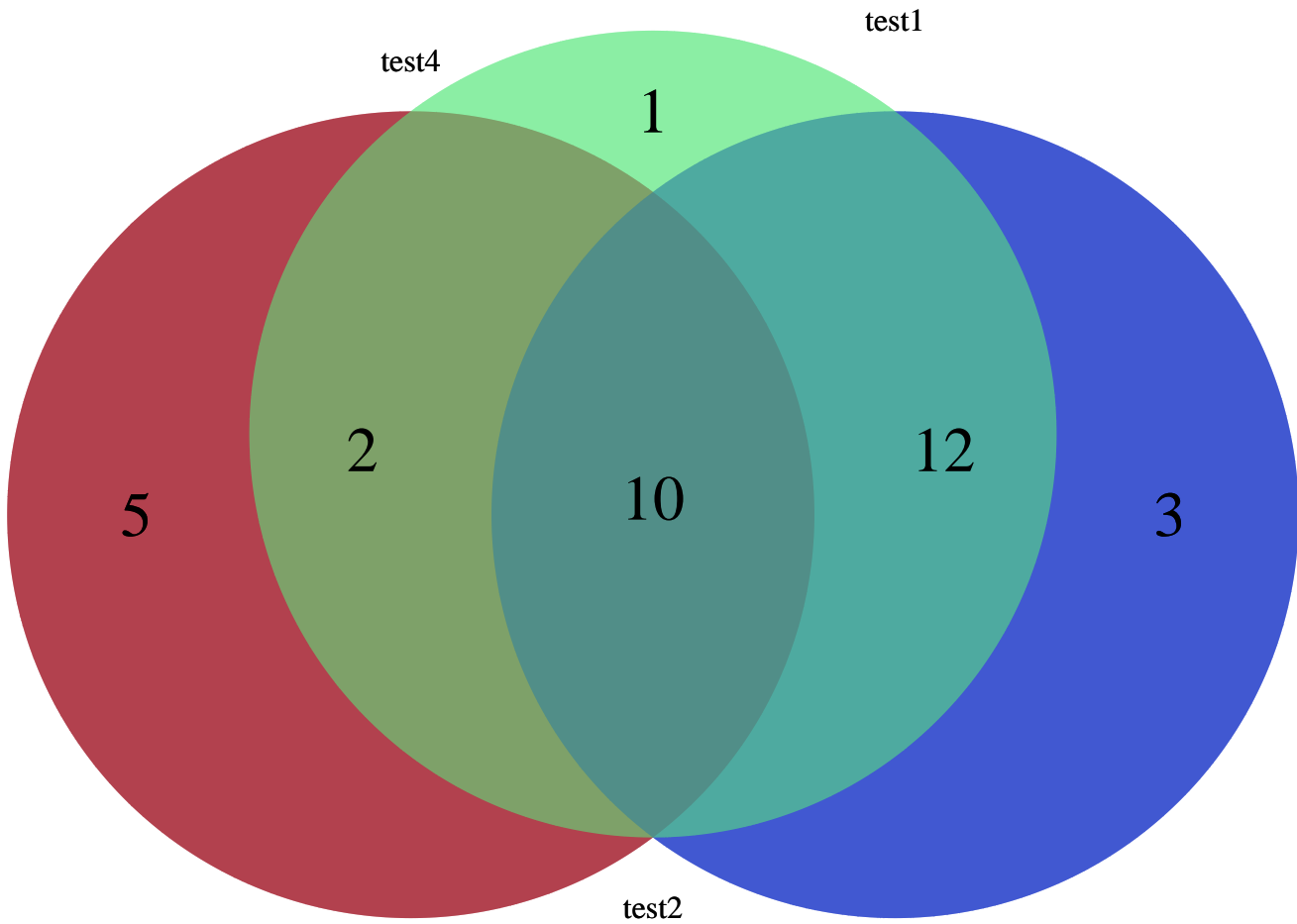
test3

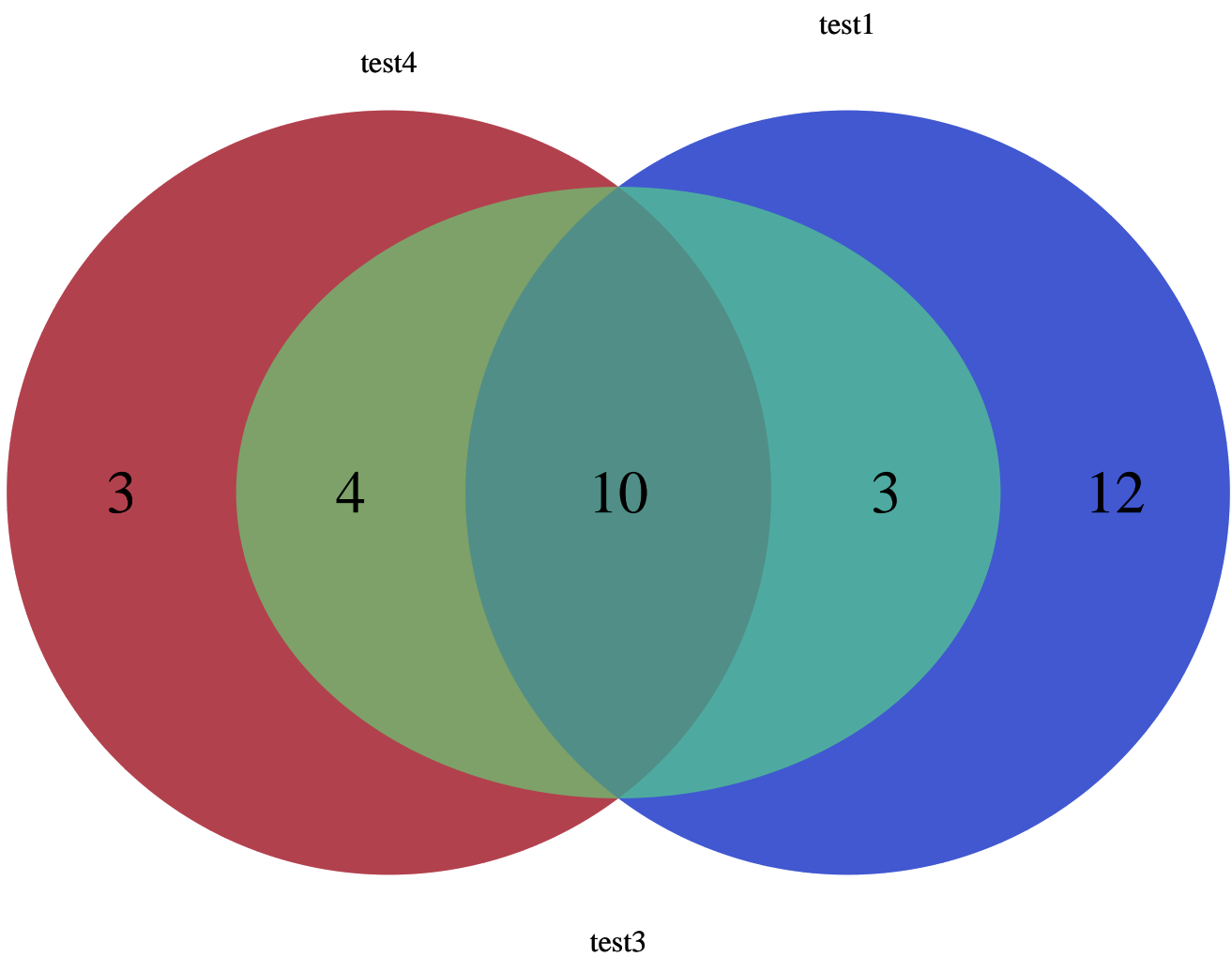
test4

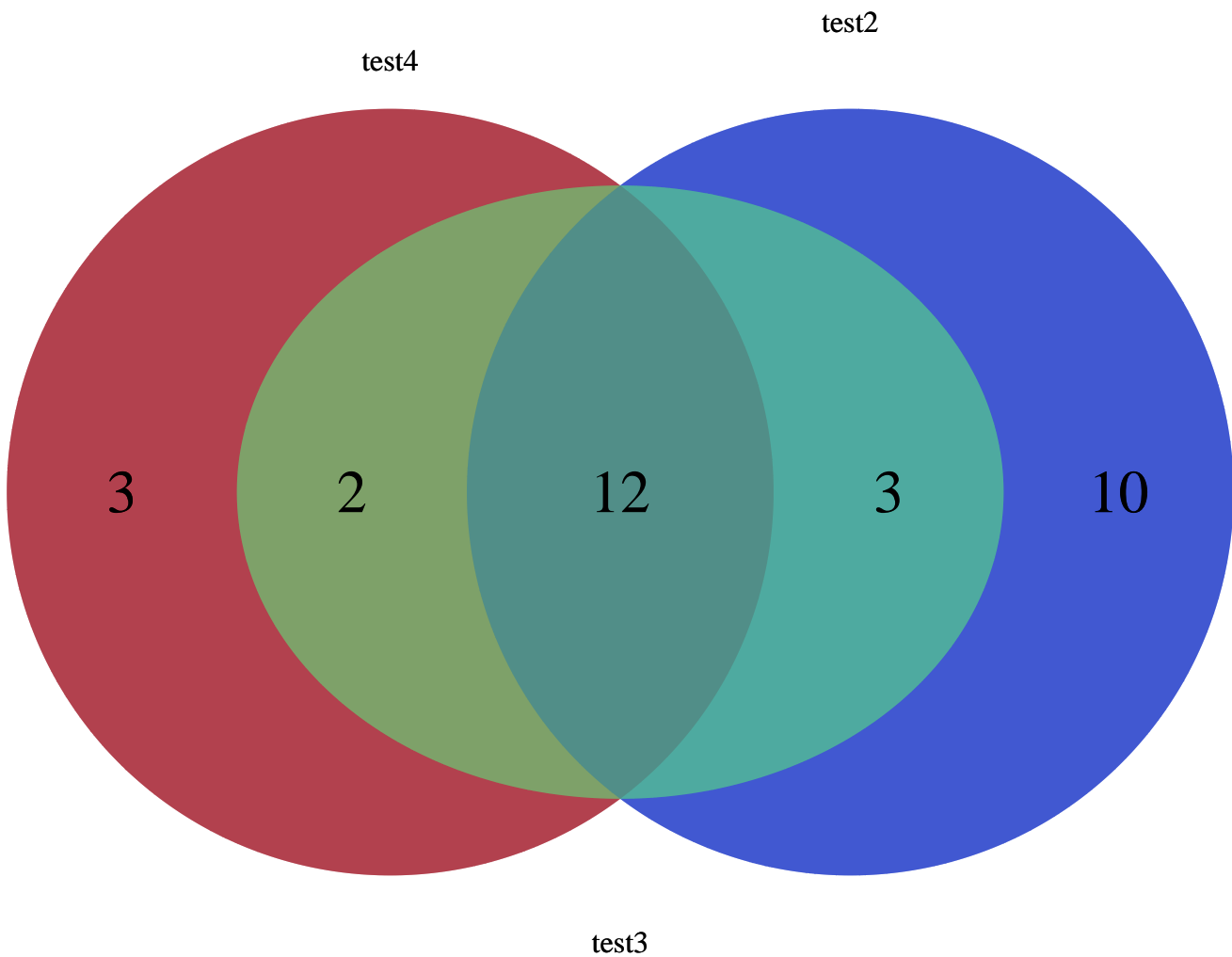


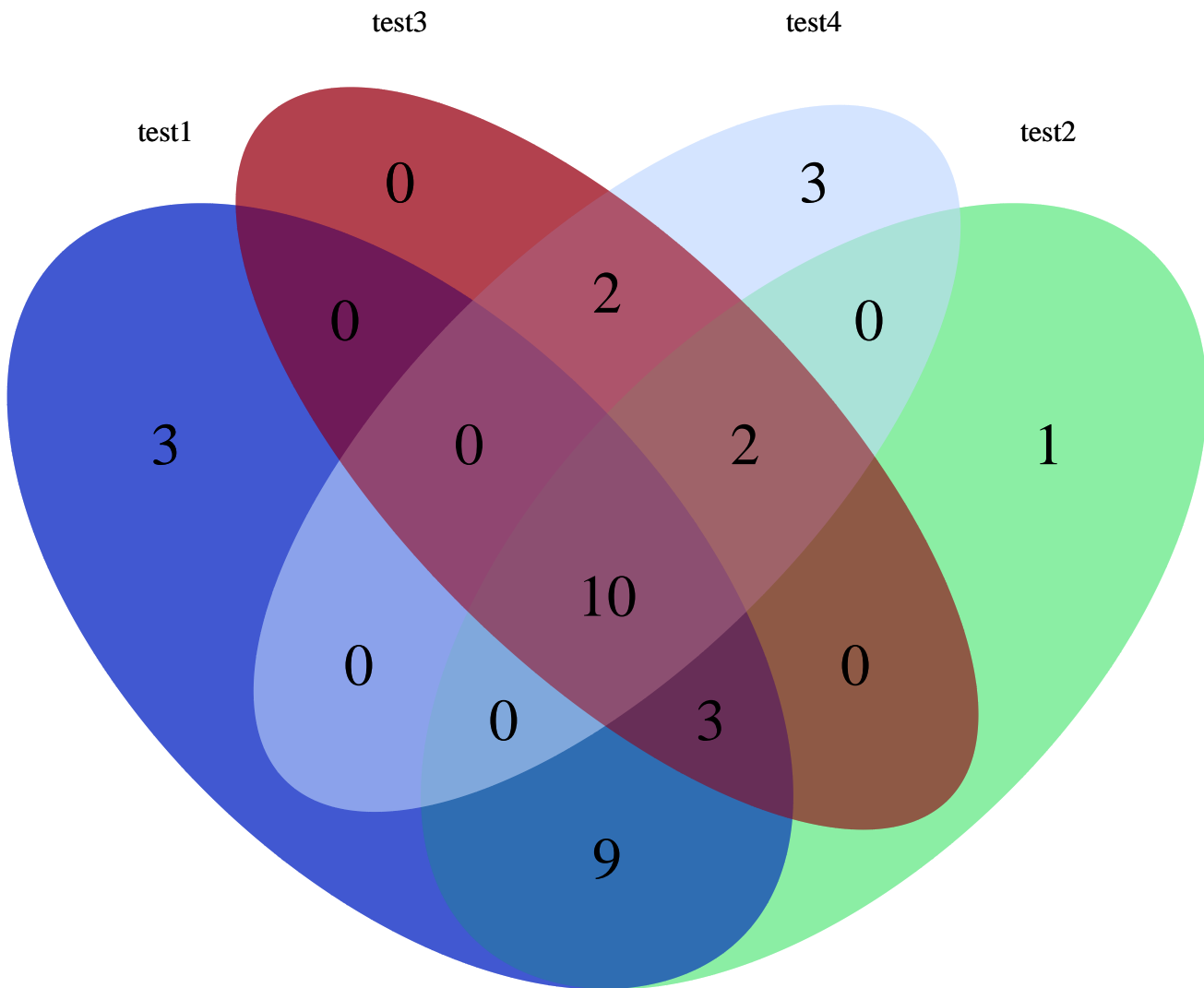
Jaccard: 0.7

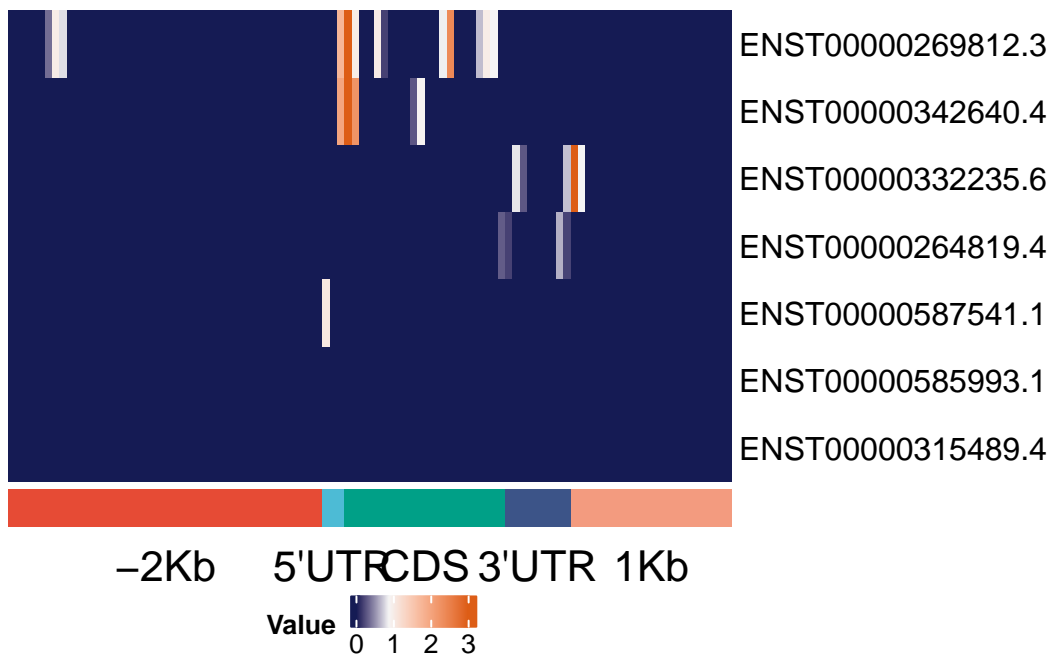
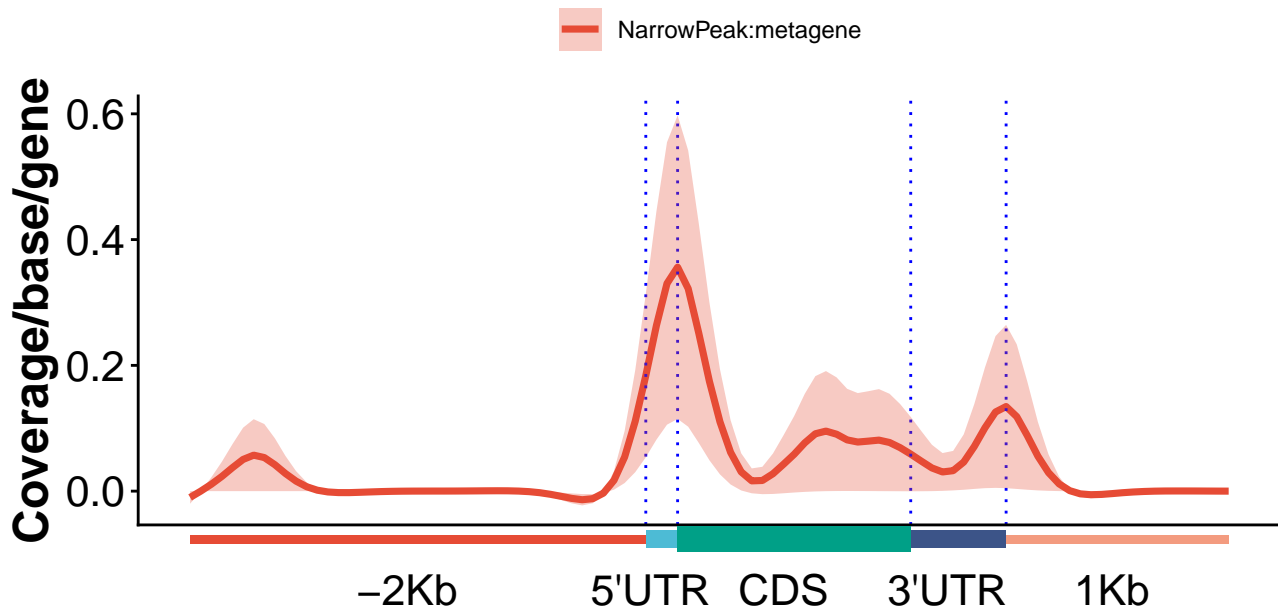


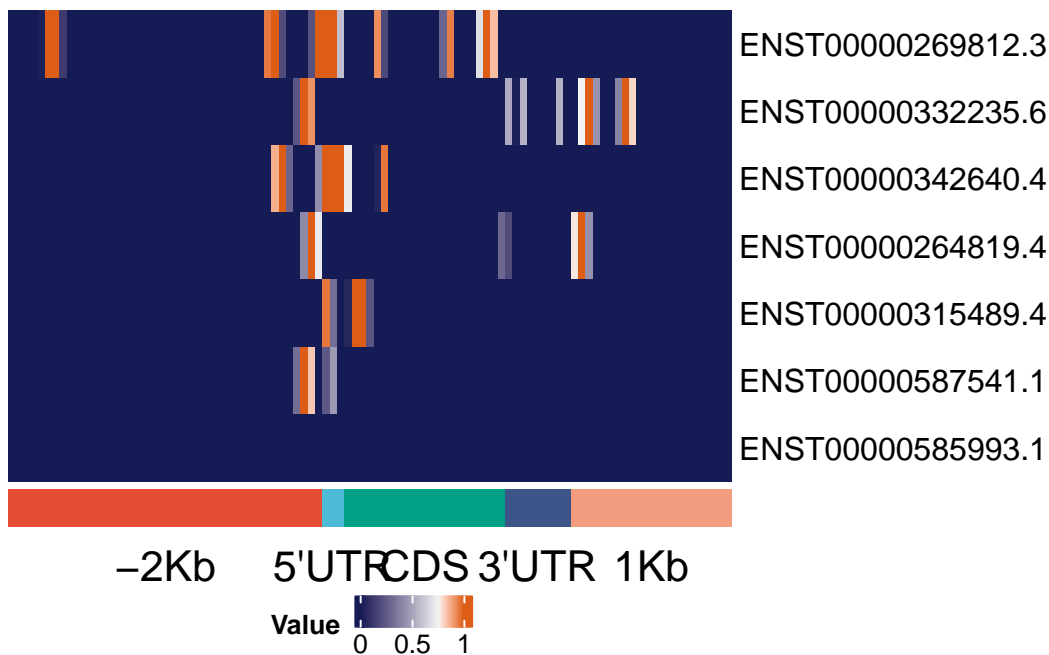
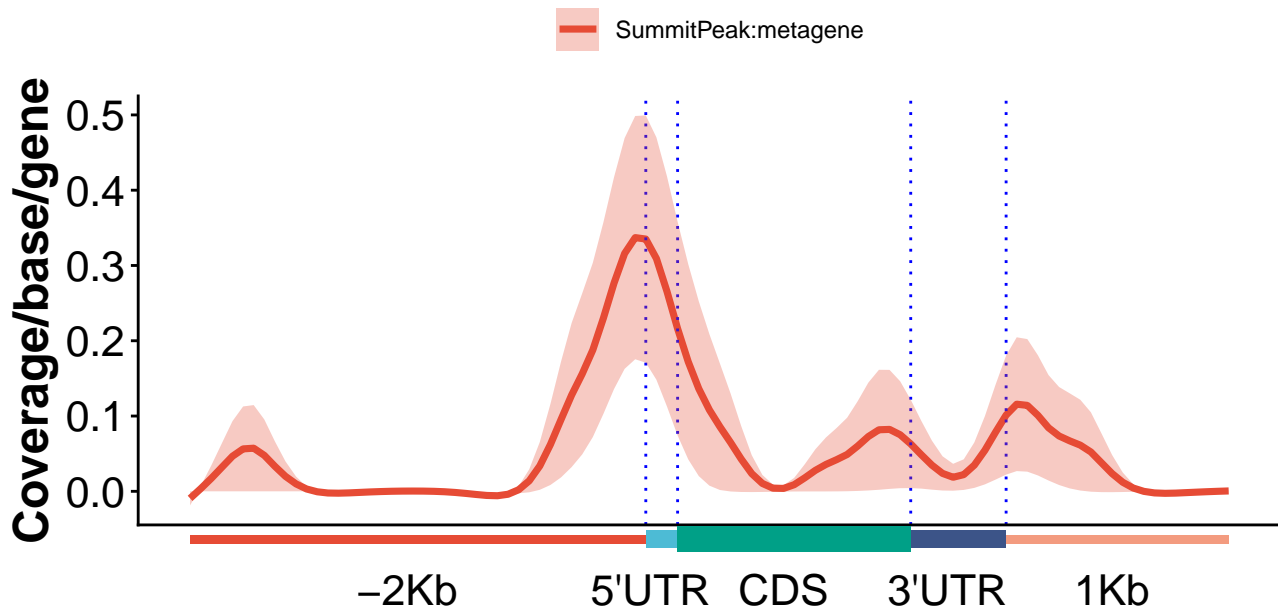


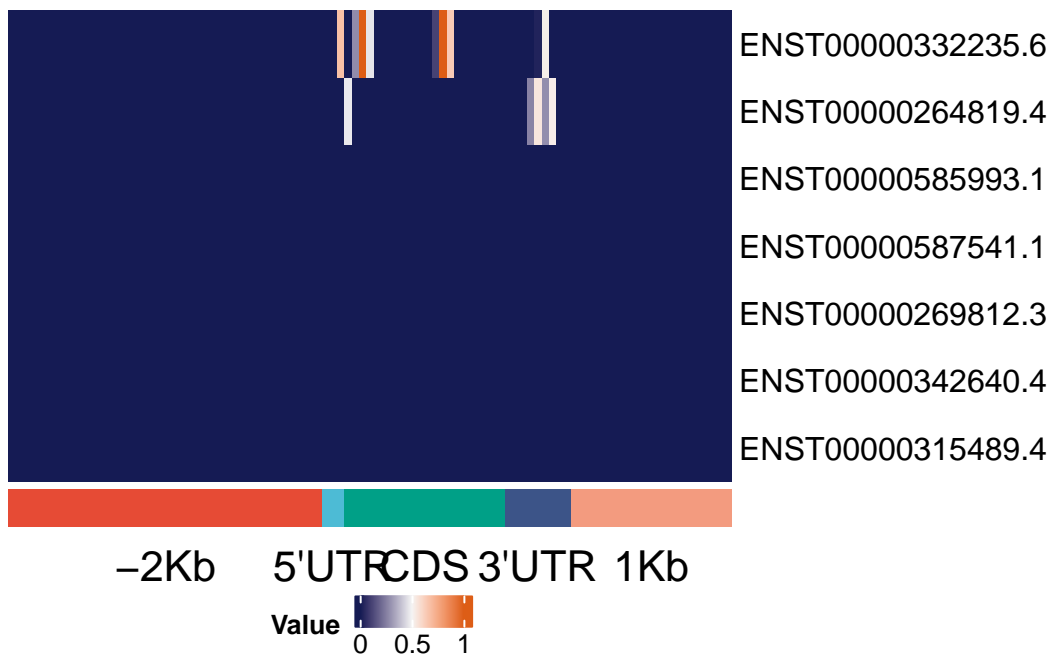
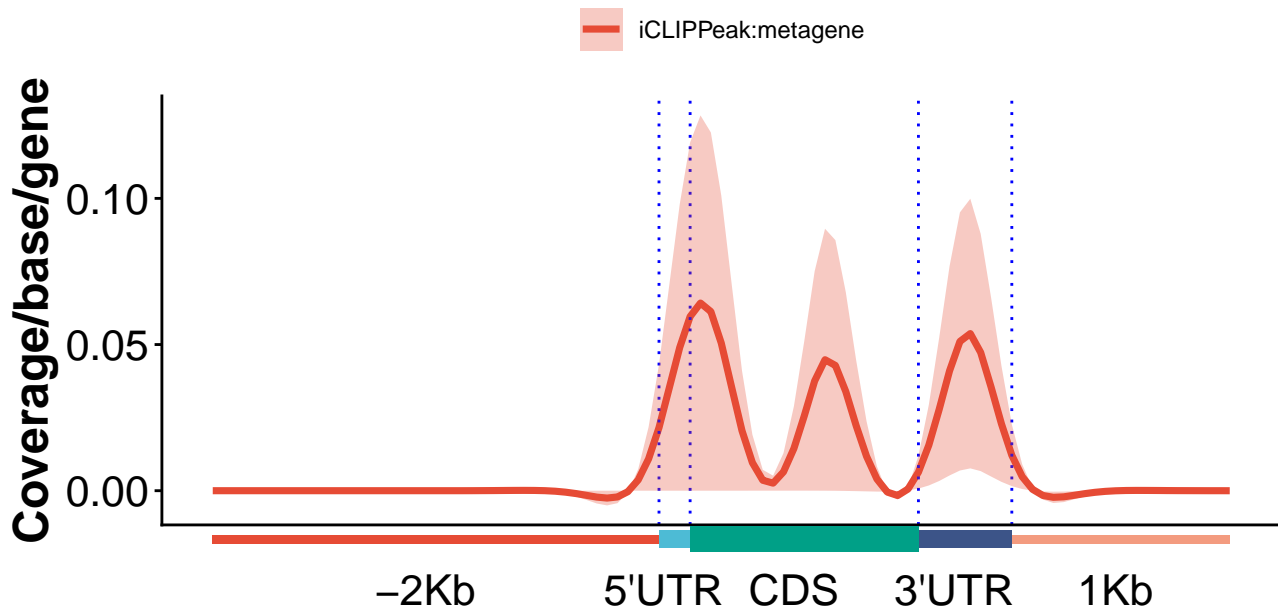




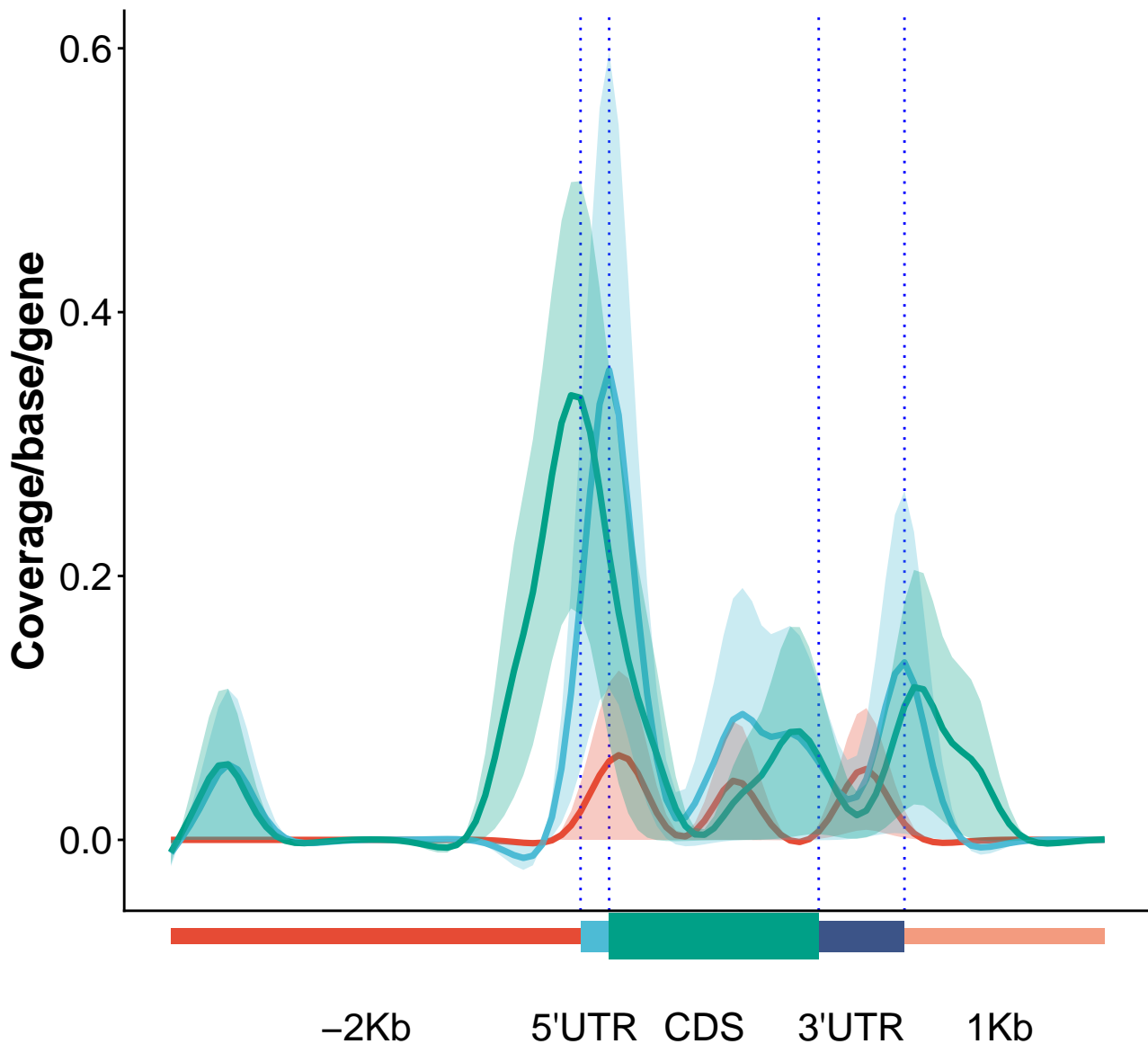


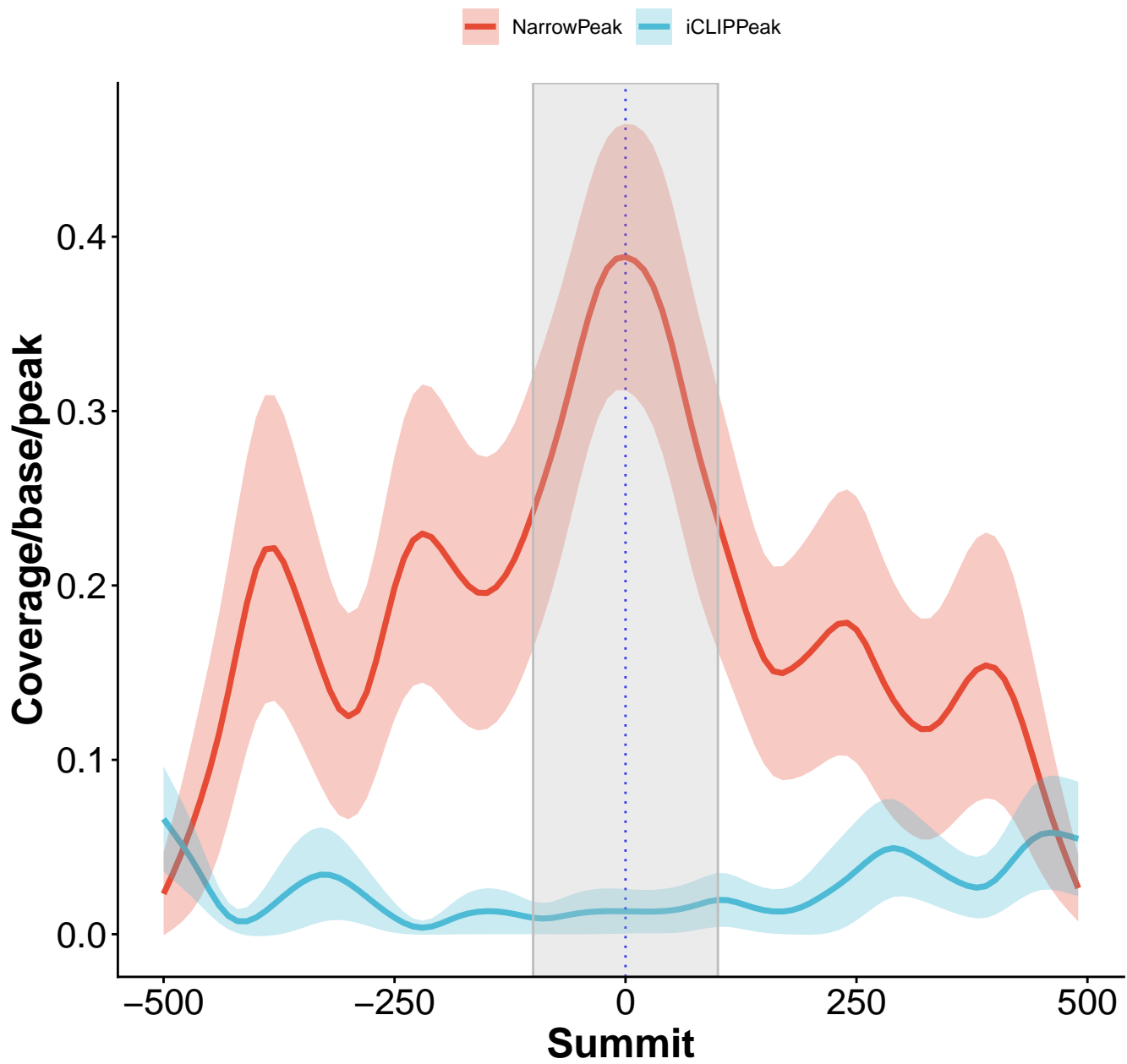


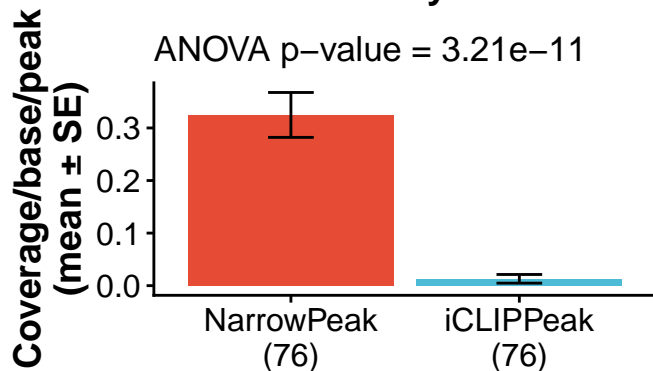
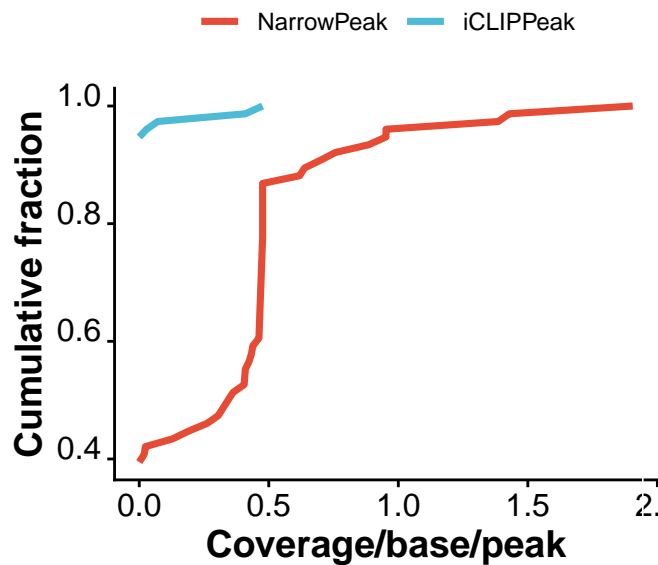
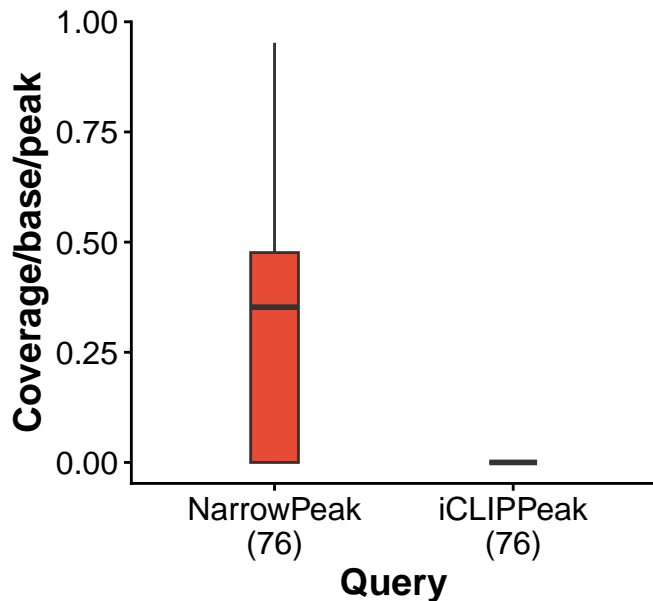
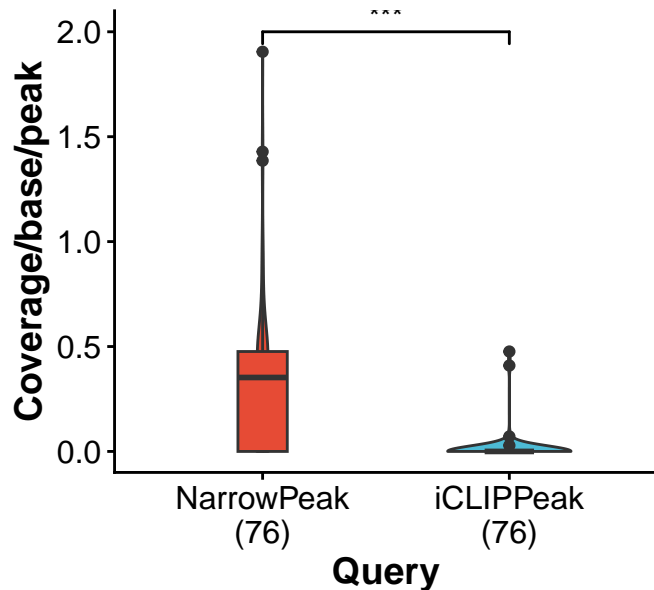




iCLIPPeak:metagene NarrowPeak:metagene SummitPeak:metagene



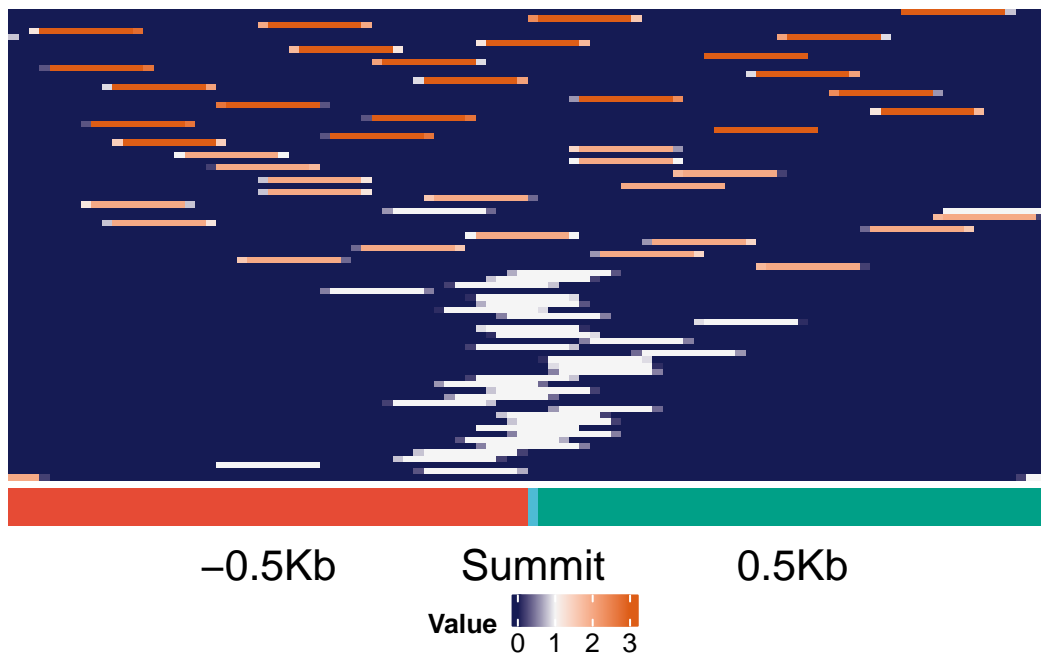
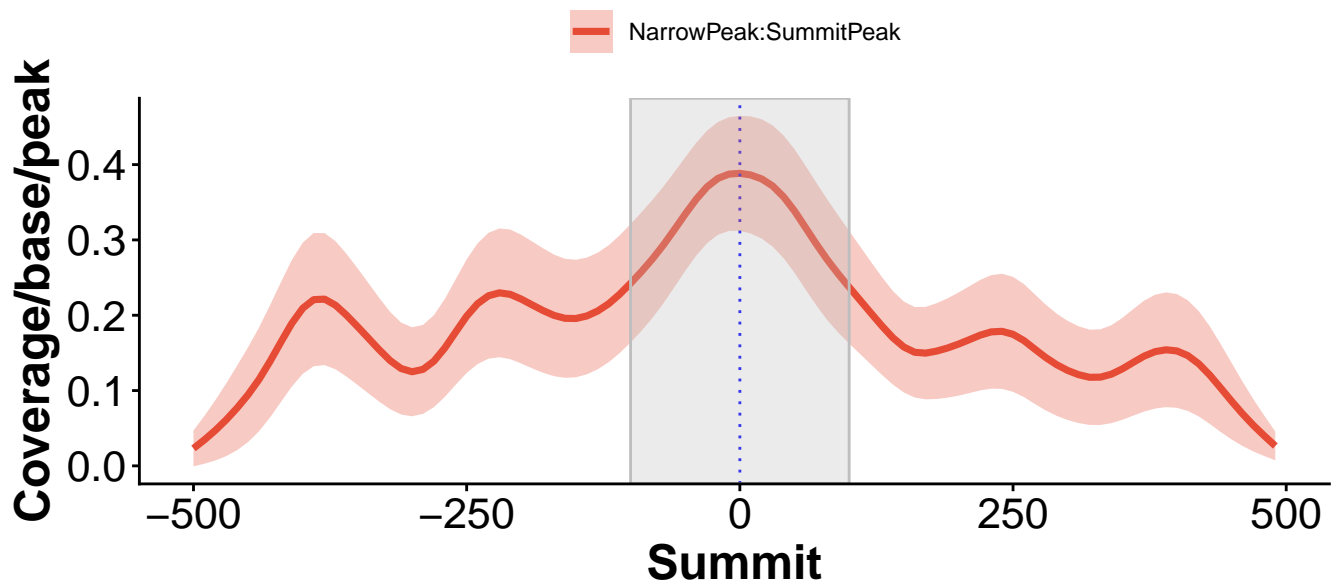




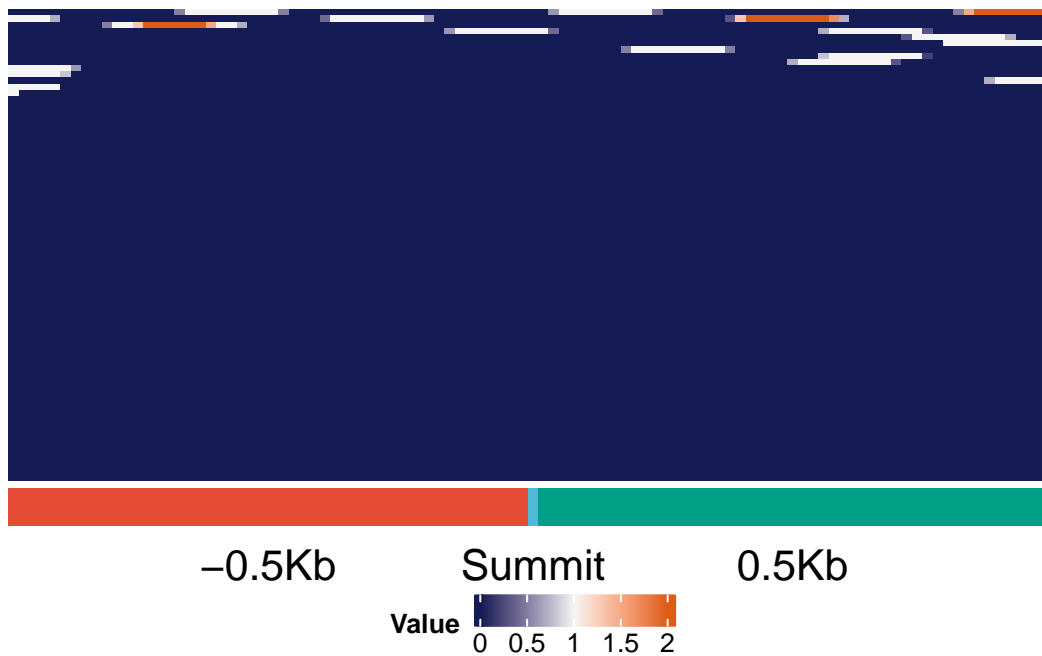
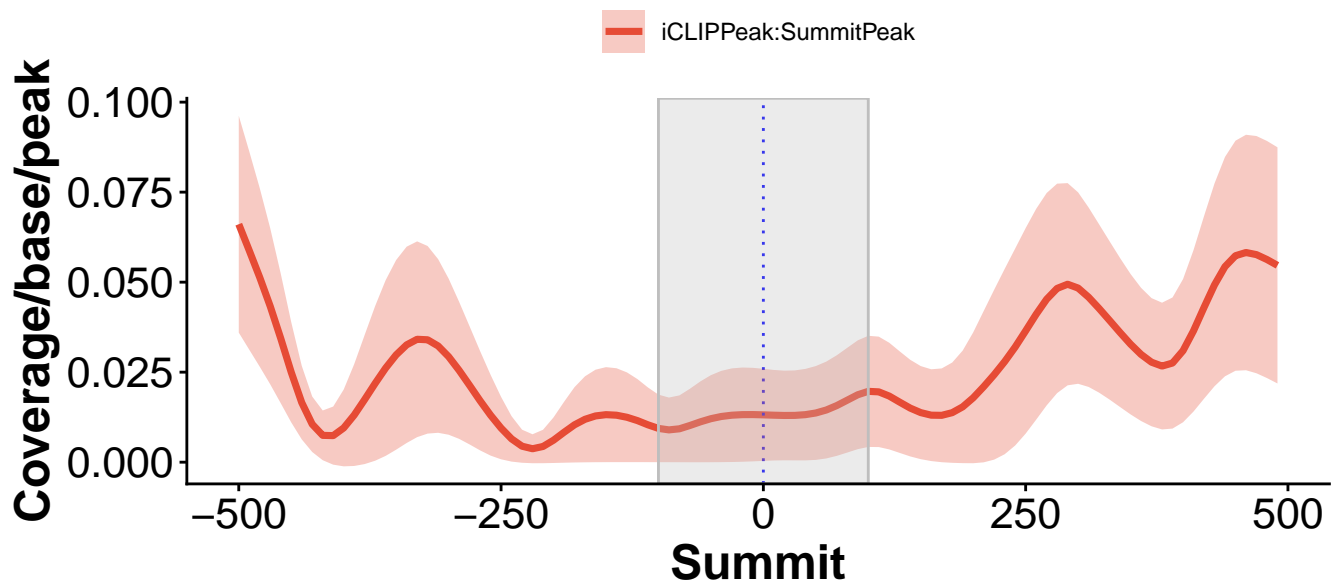
post hoc TukeyHSD test

	diff	lwr	upr	p adj
iCLIPPeak-NarrowPeak	-0.312	-0.398	-0.226	3.21e-11

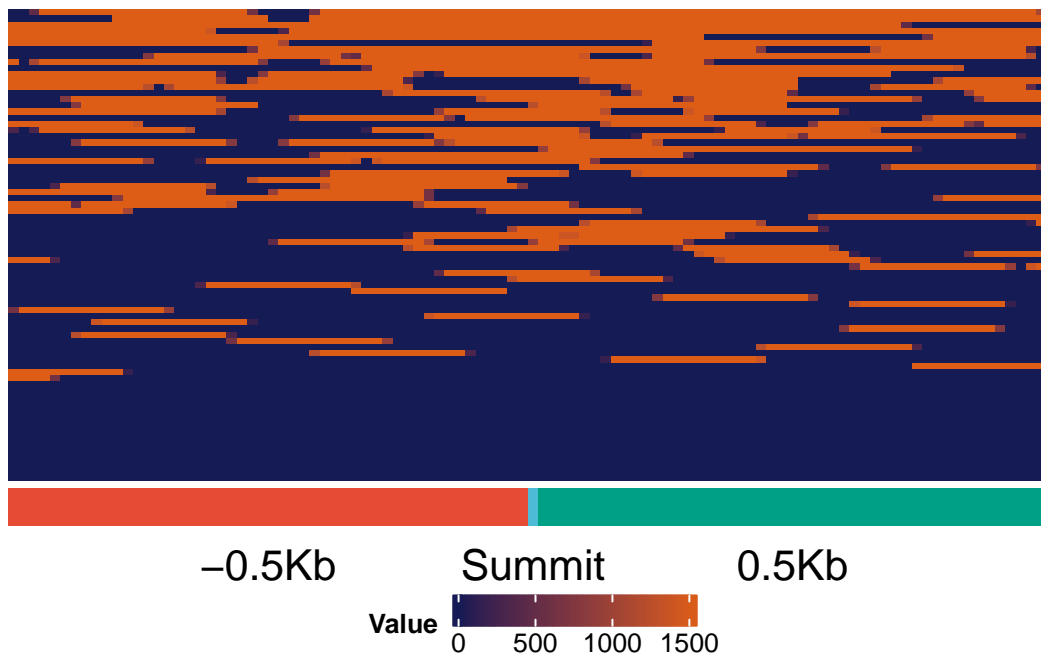
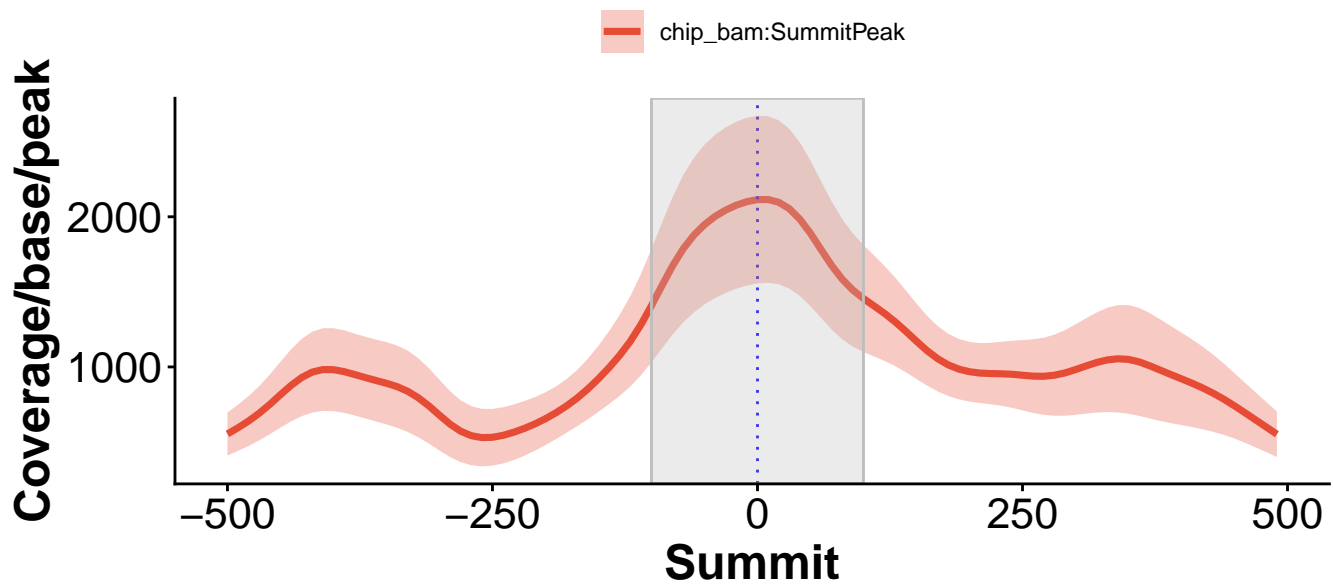
NarrowPeak:SummitPeak



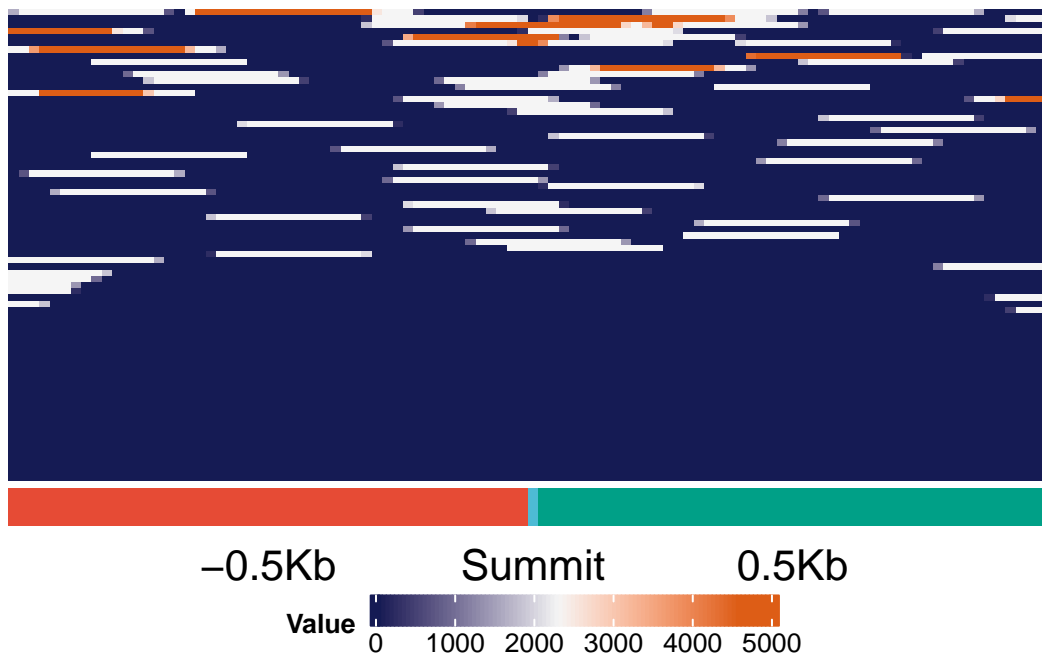
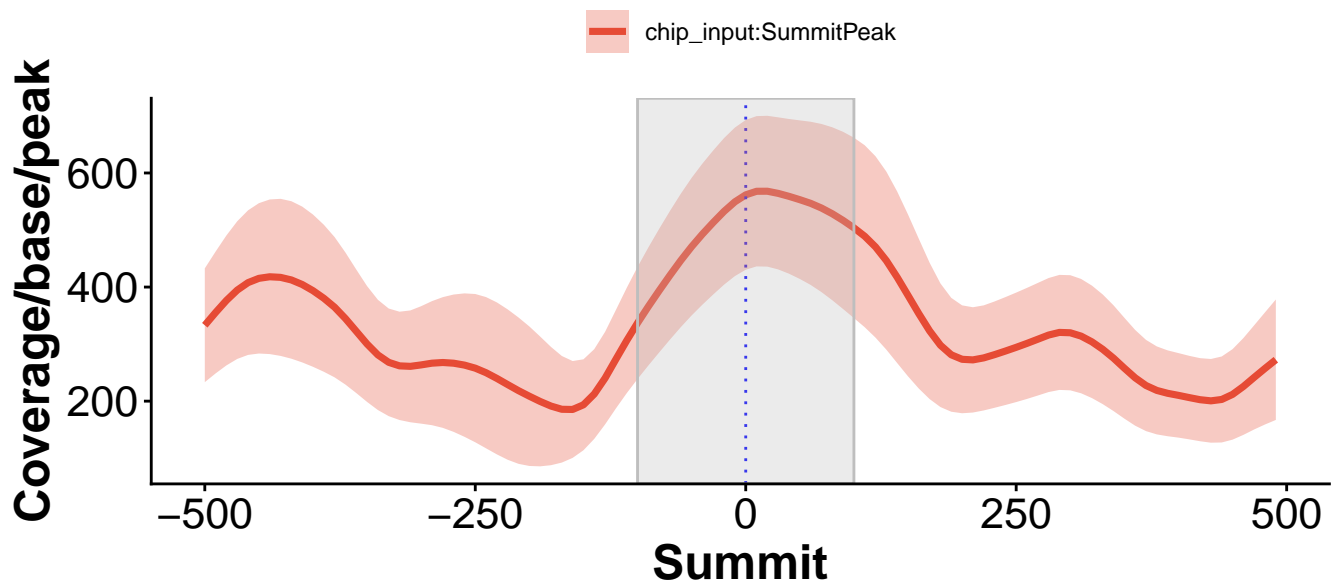
iCLIPPeak:SummitPeak



chip_bam:SummitPeak



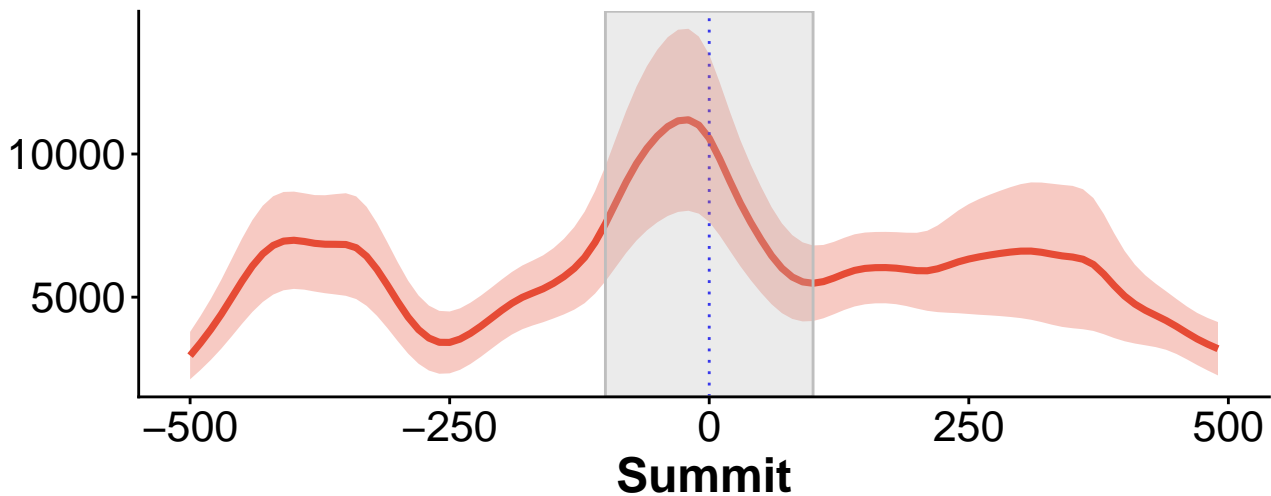
chip_input:SummitPeak



chip_bam:SummitPeak

chip_bam:SummitPeak

Ratio-over-Input



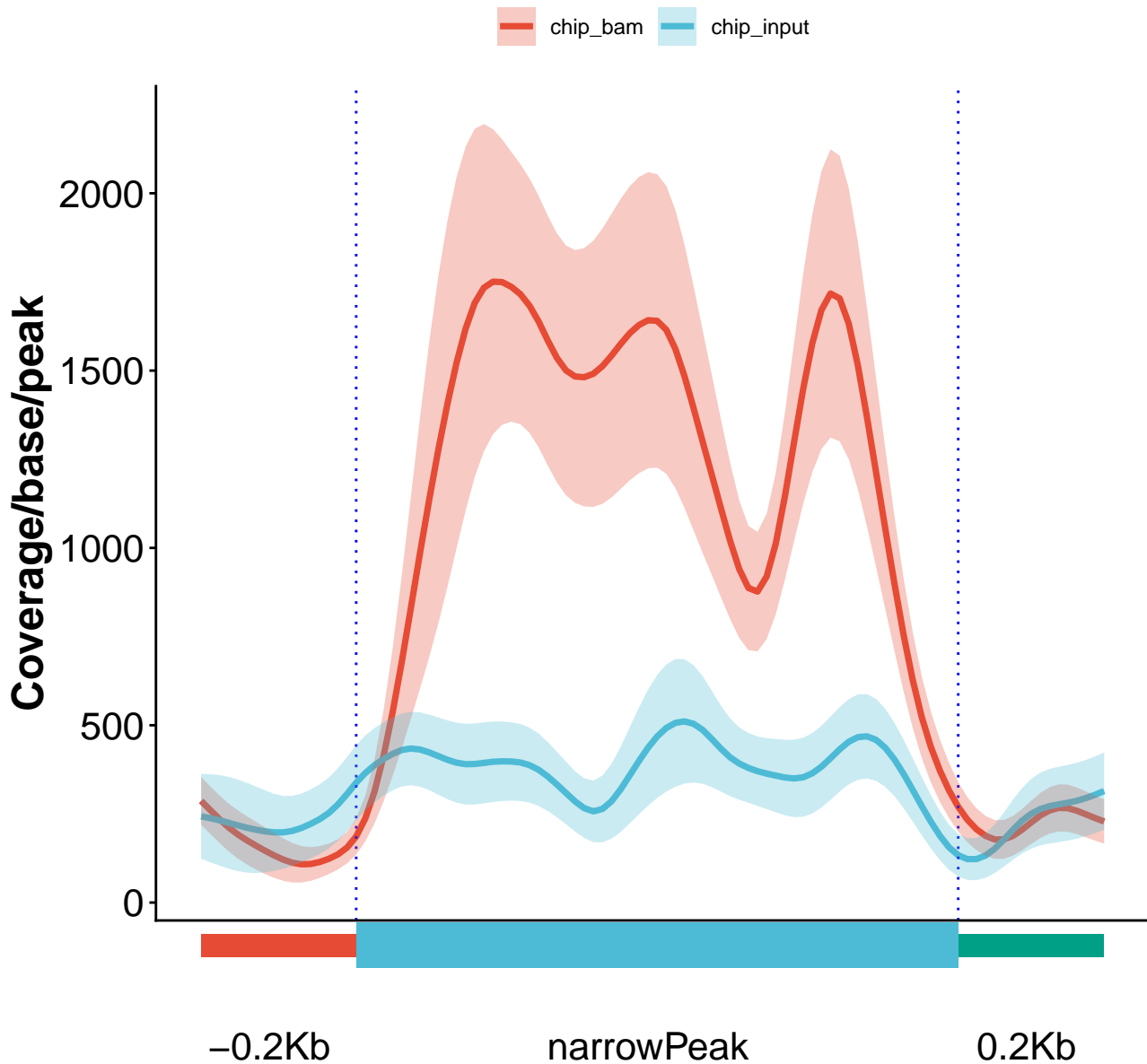
-0.5Kb

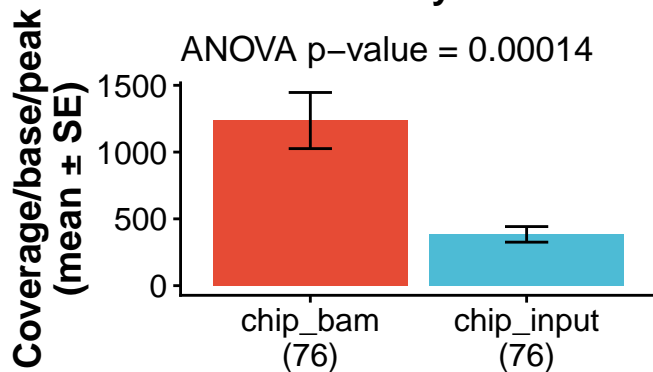
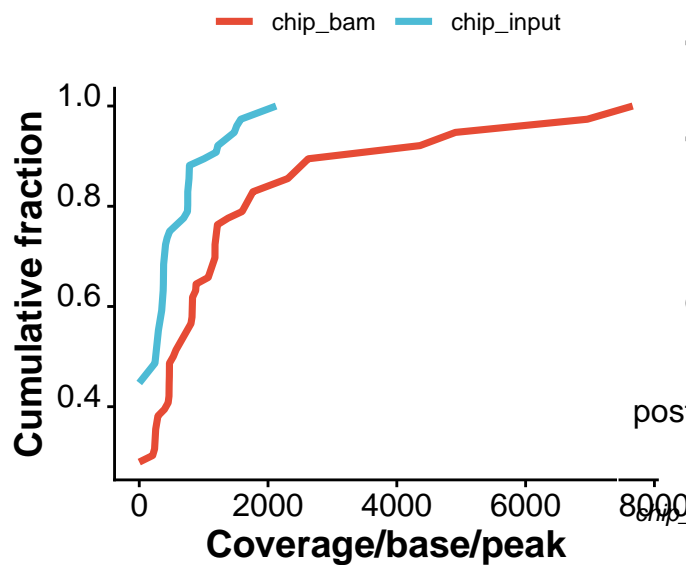
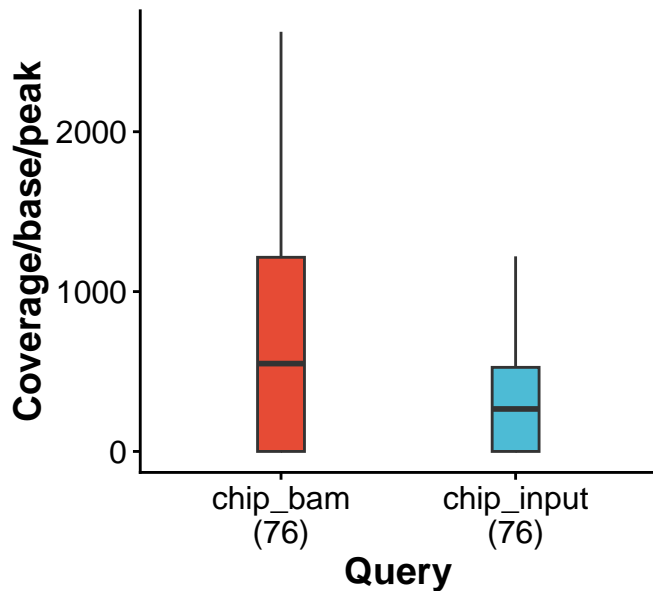
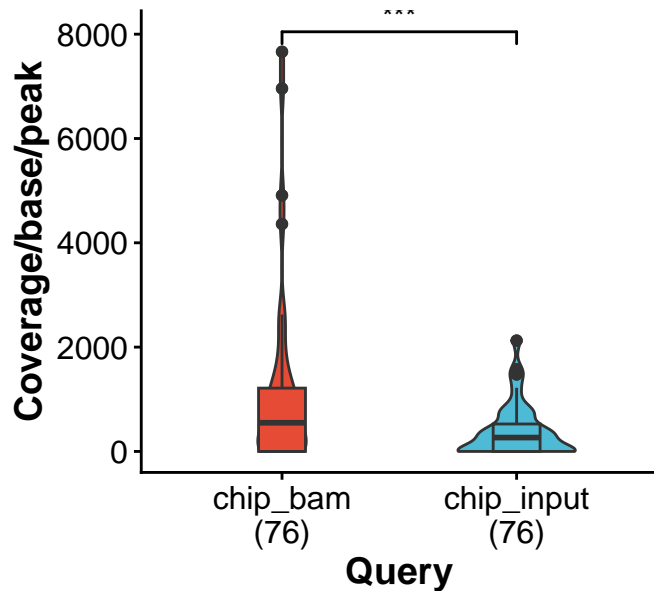
Summit

0.5Kb

Value
0 2 4 6 8

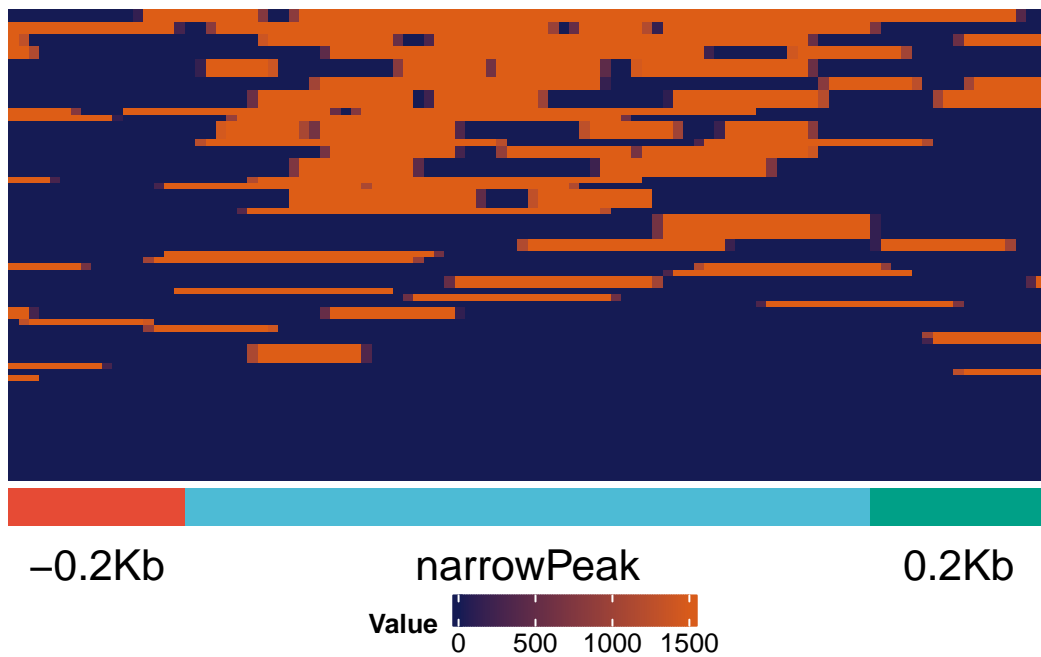
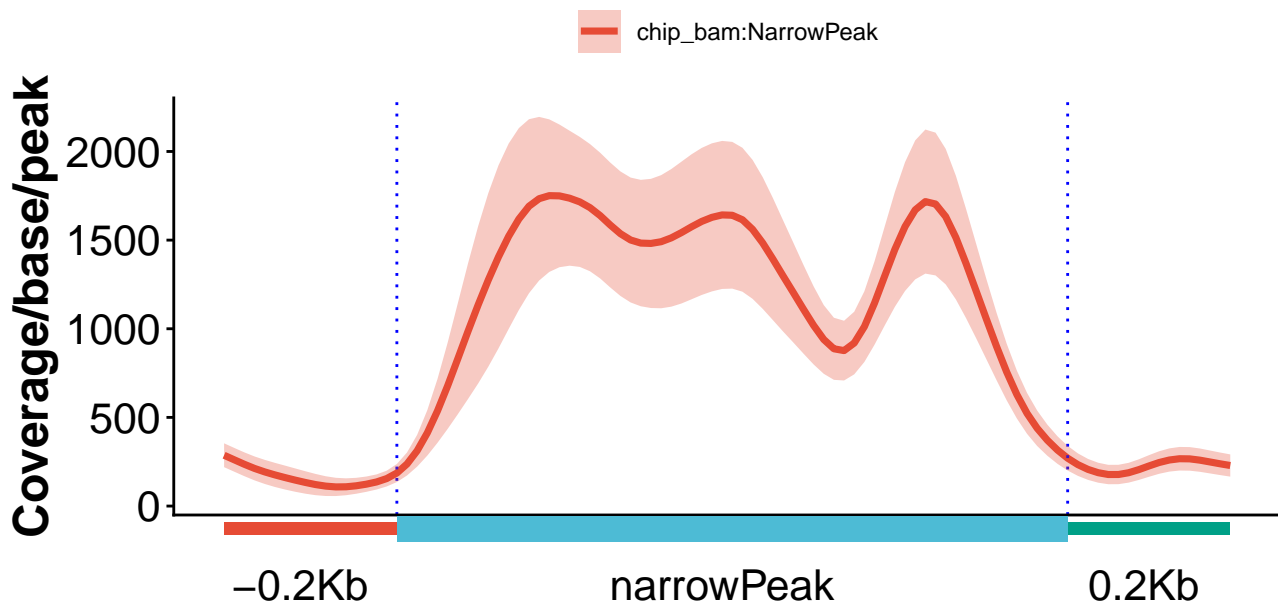
NarrowPeak

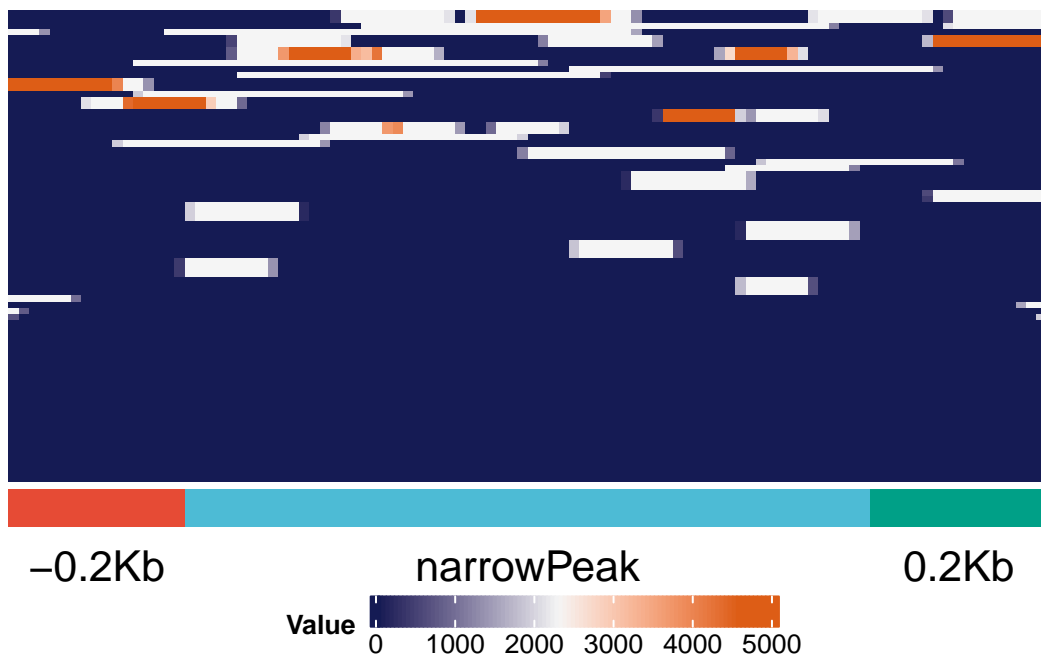
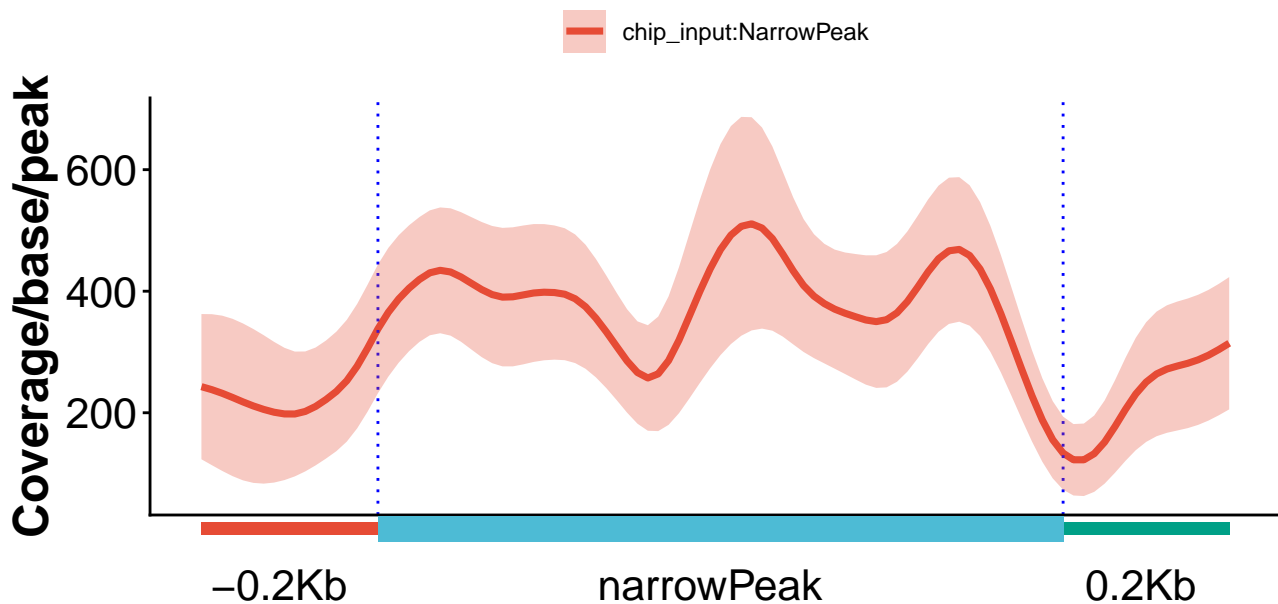


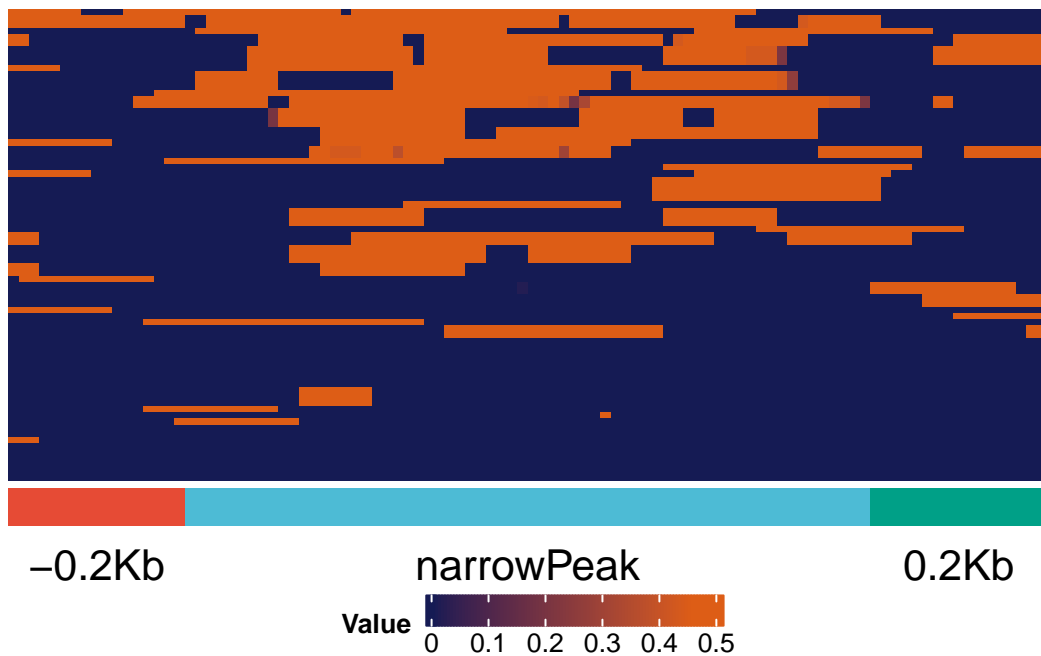
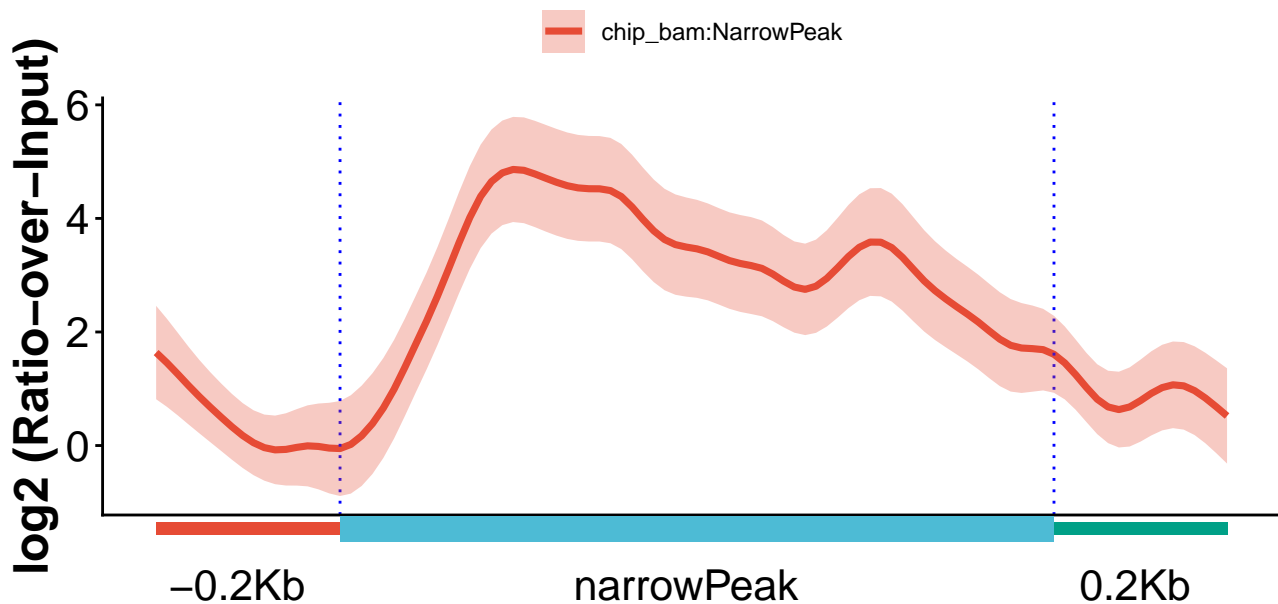


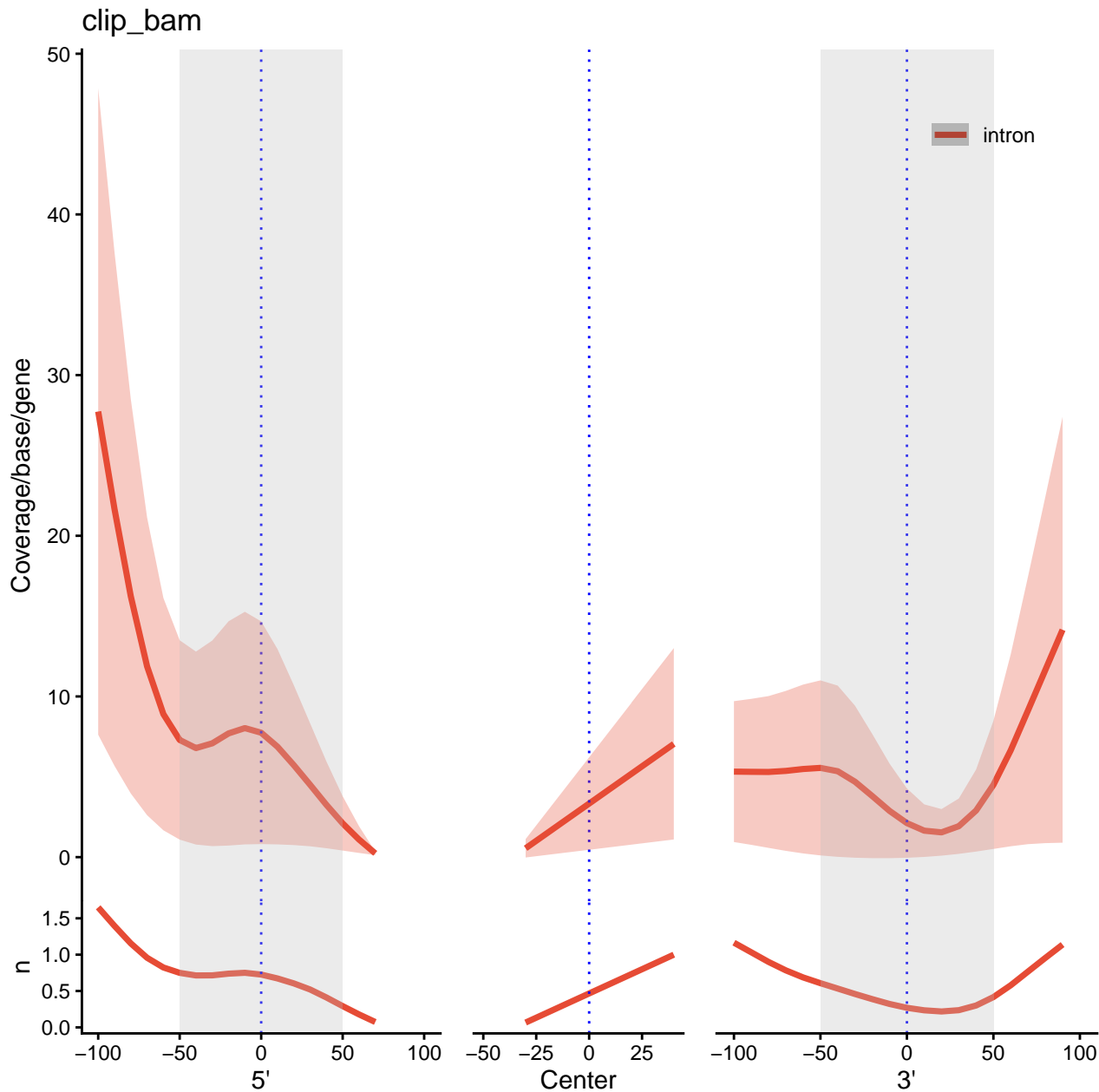
post hoc TukeyHSD test

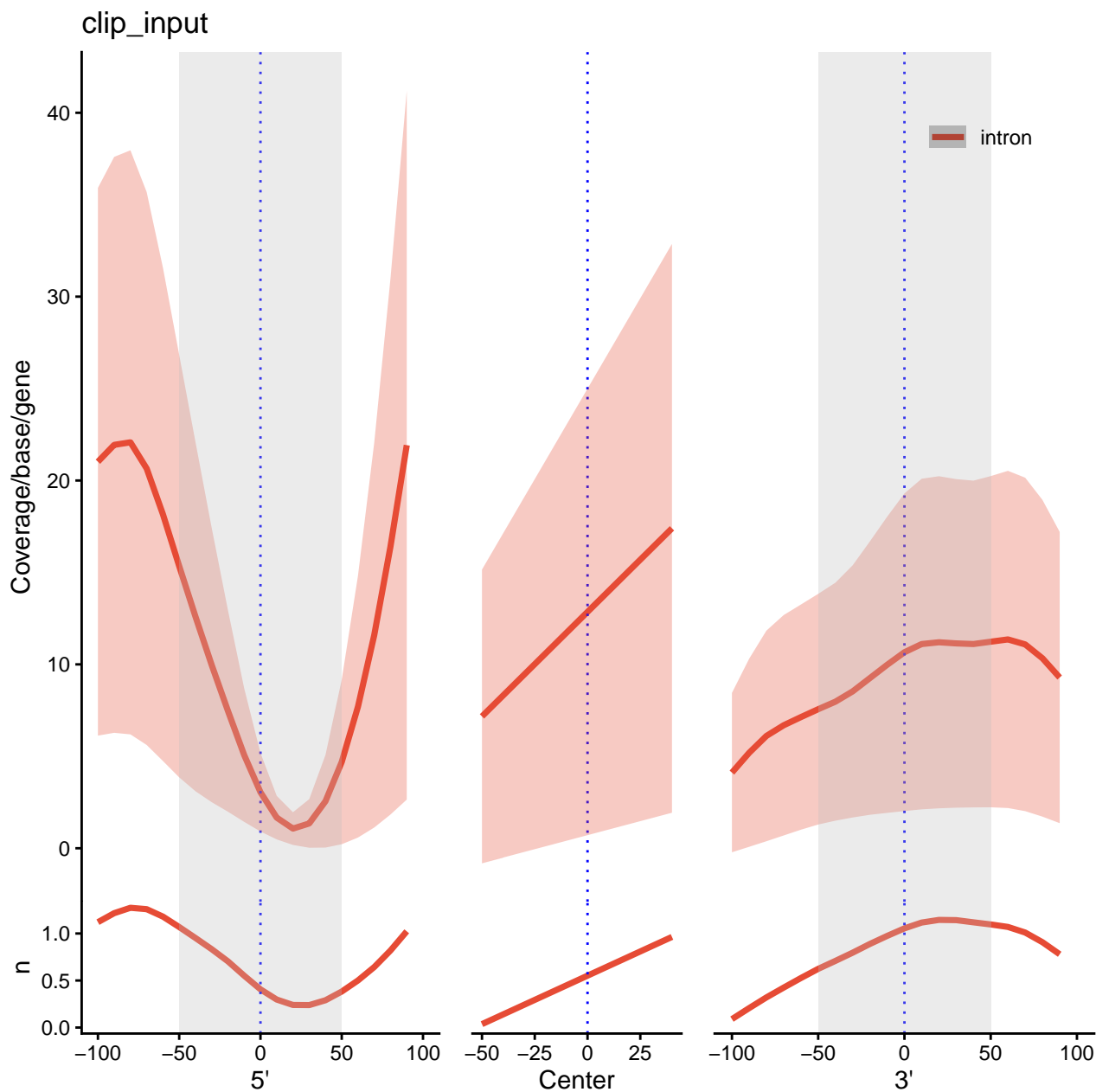
	diff	lwr	upr	p a
chip_input-chip_bam	-852.362	-1283.166	-421.557	0.00

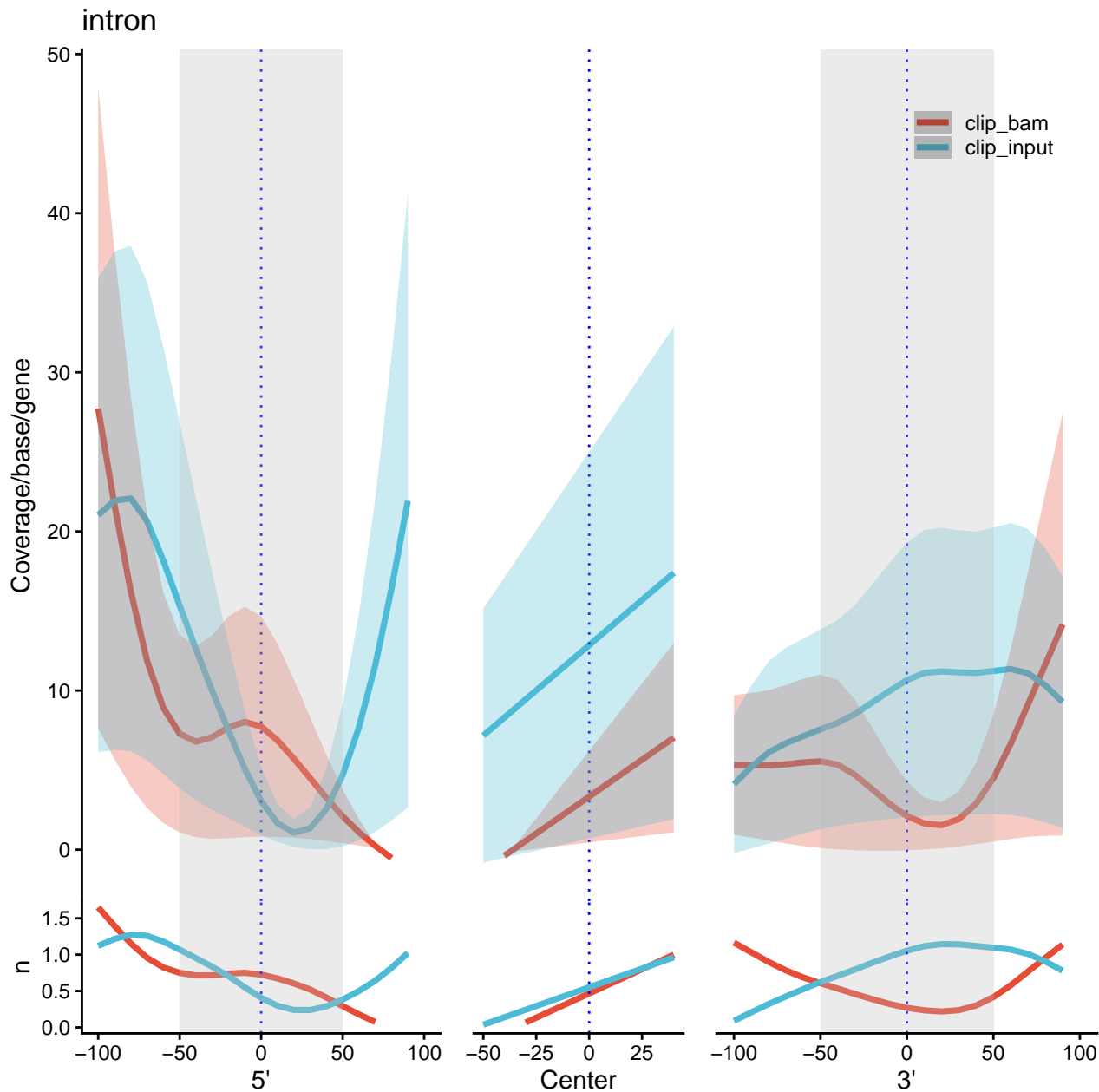


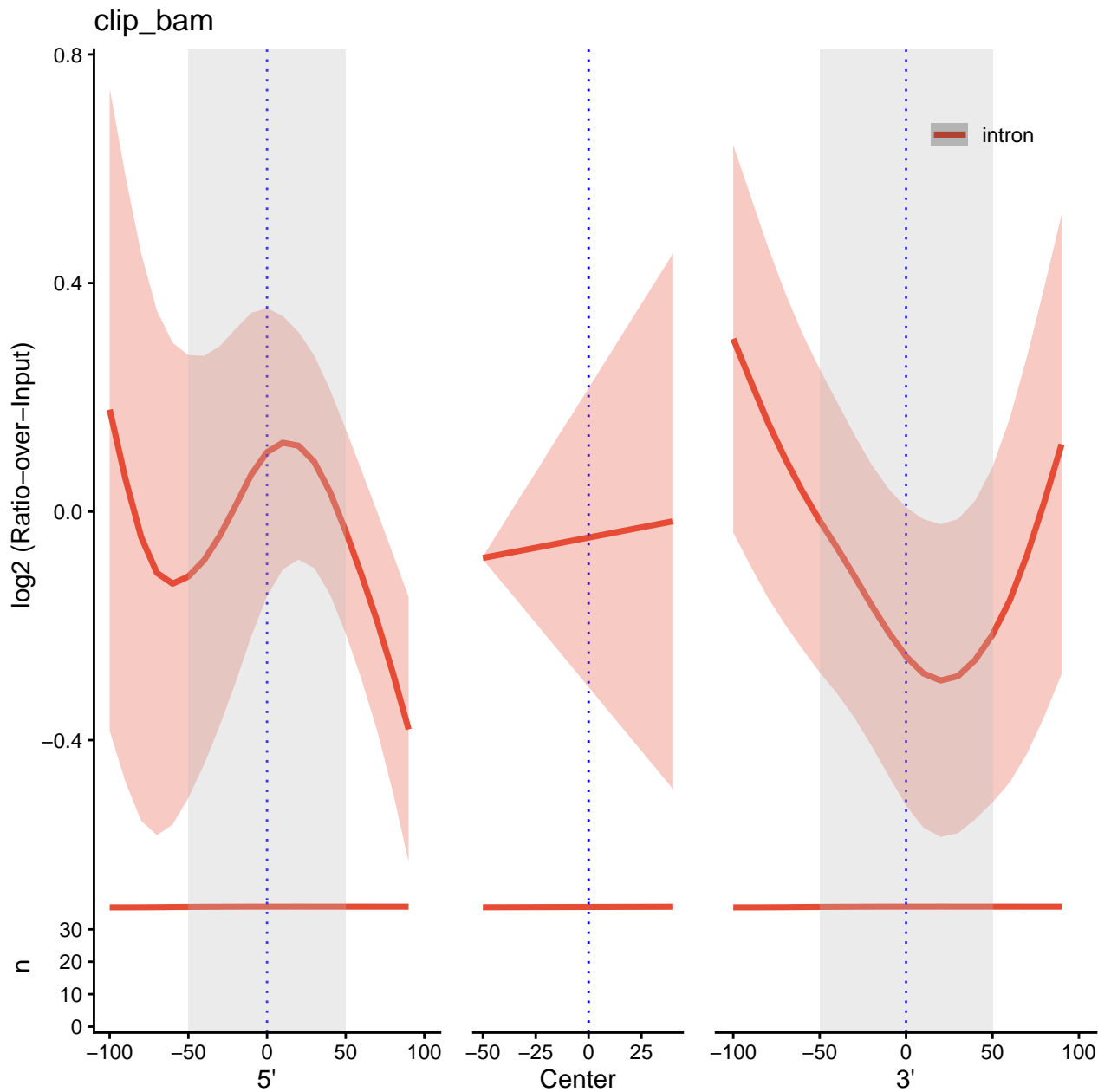


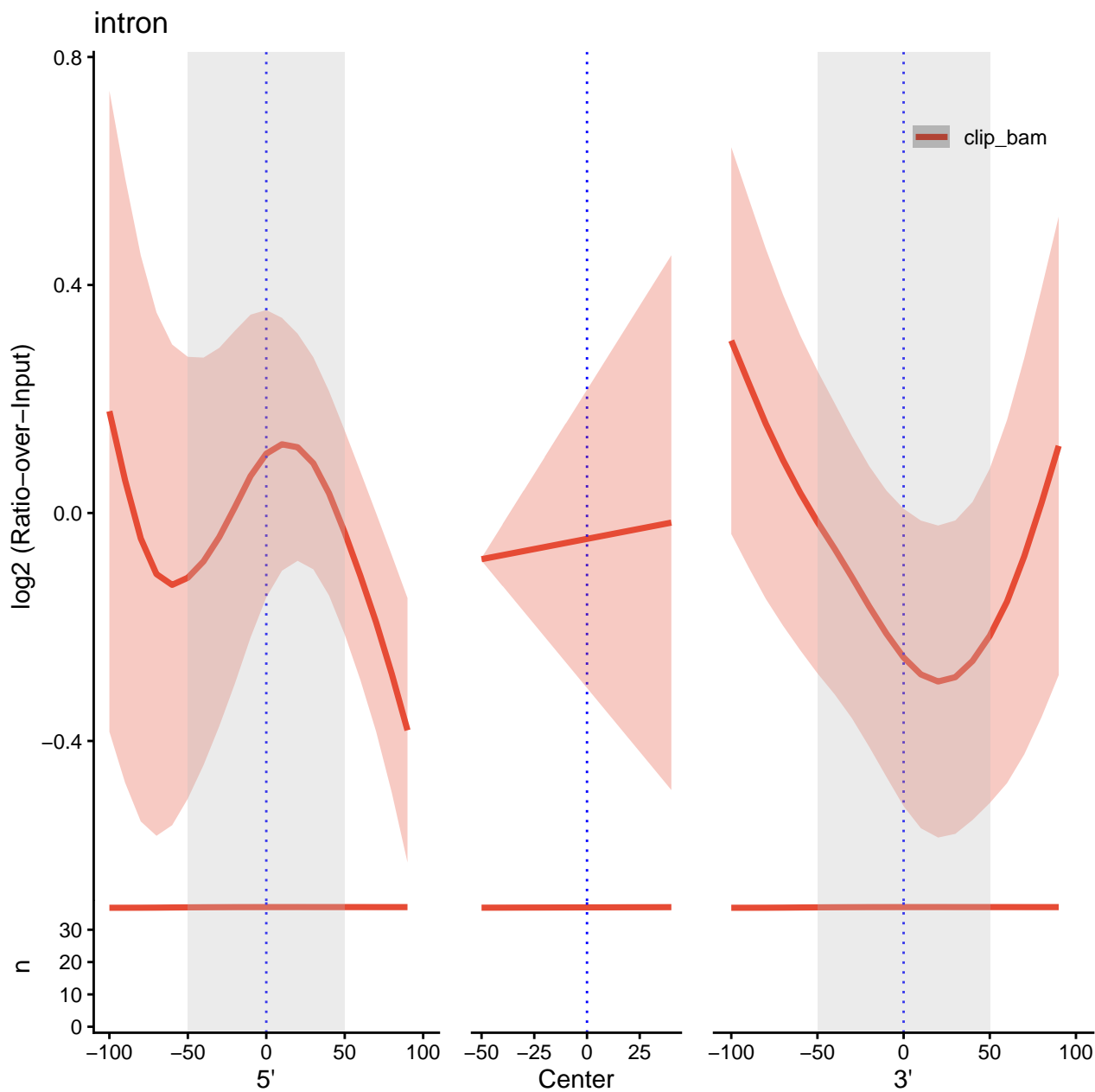


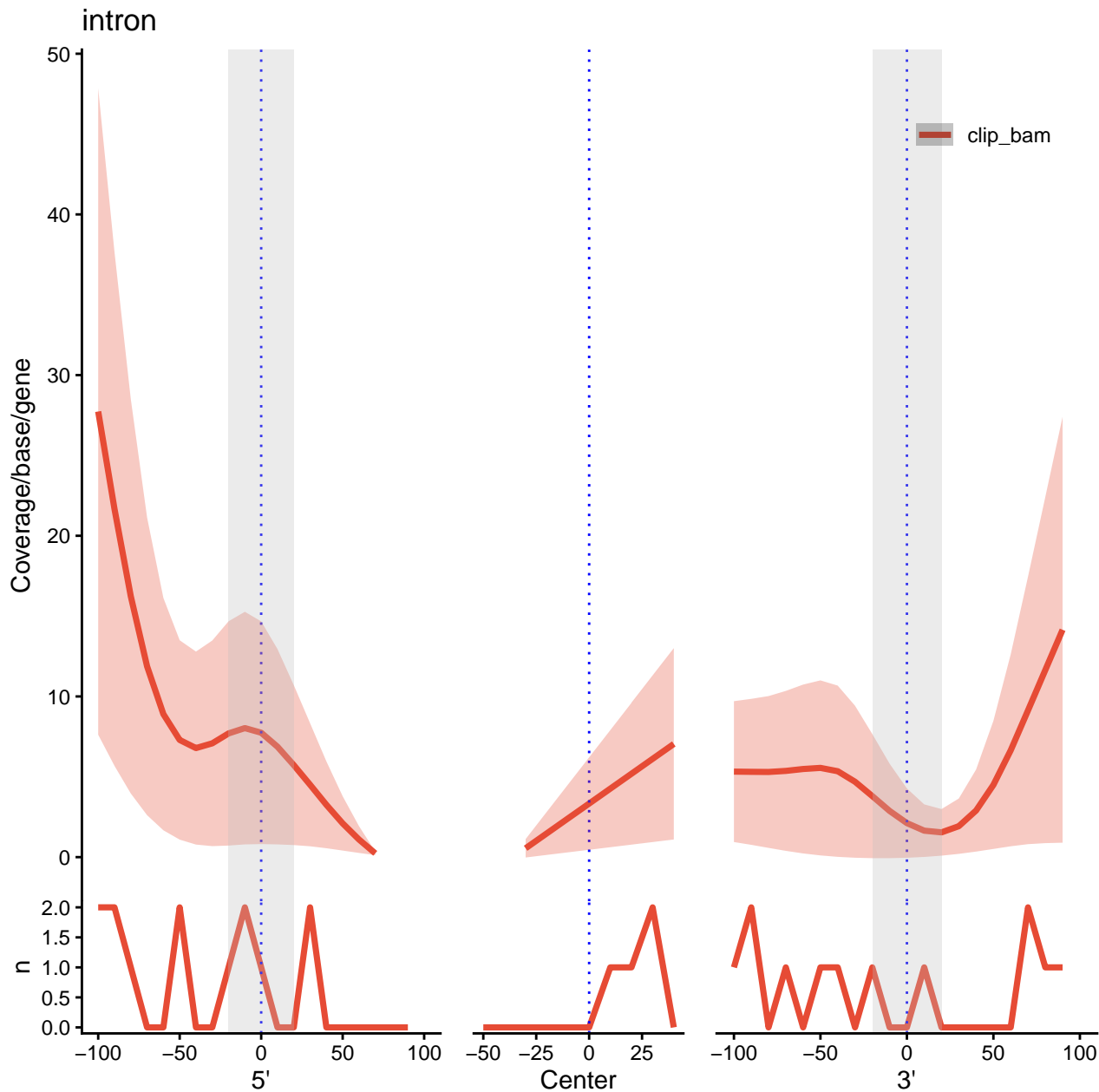


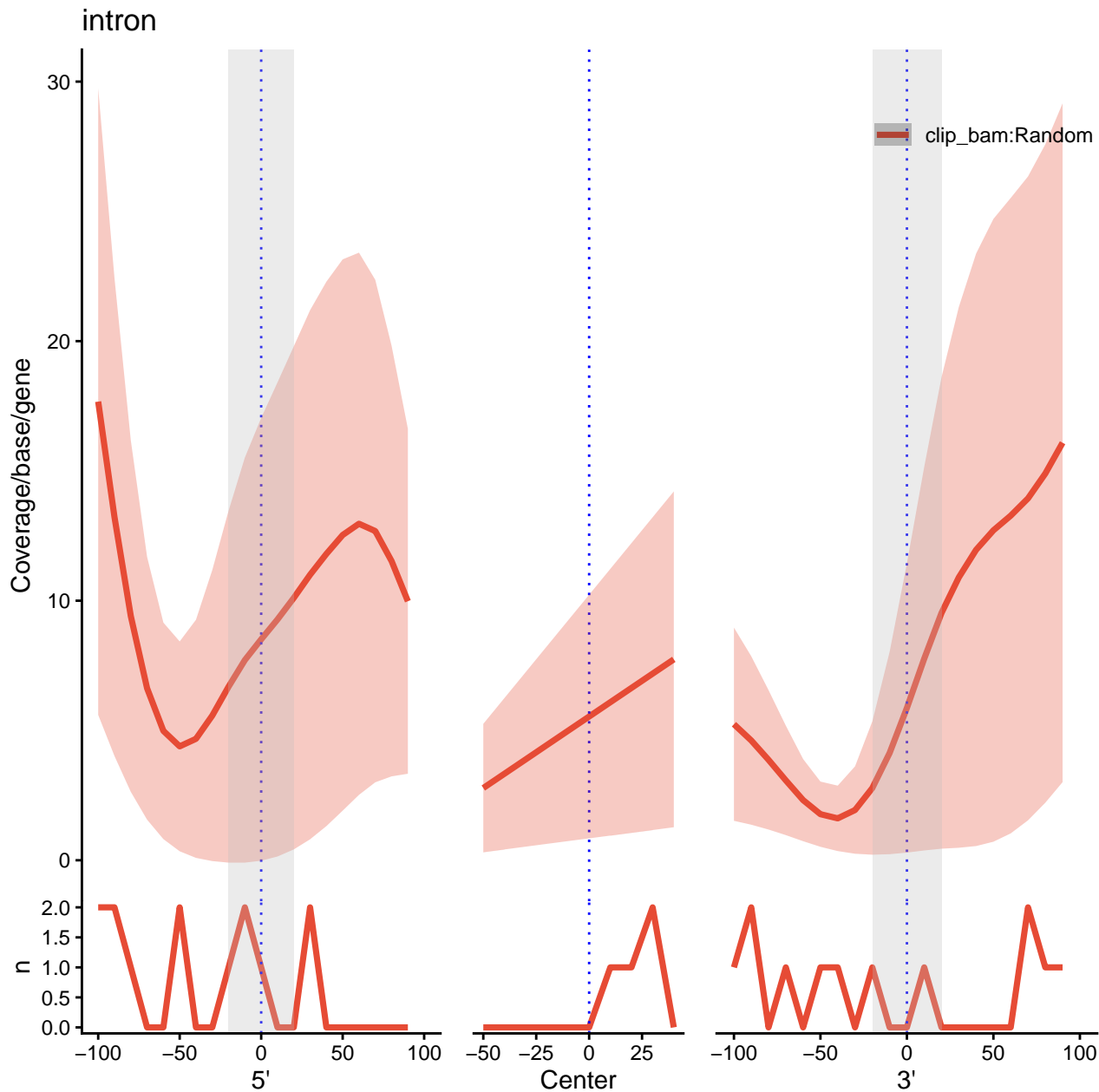




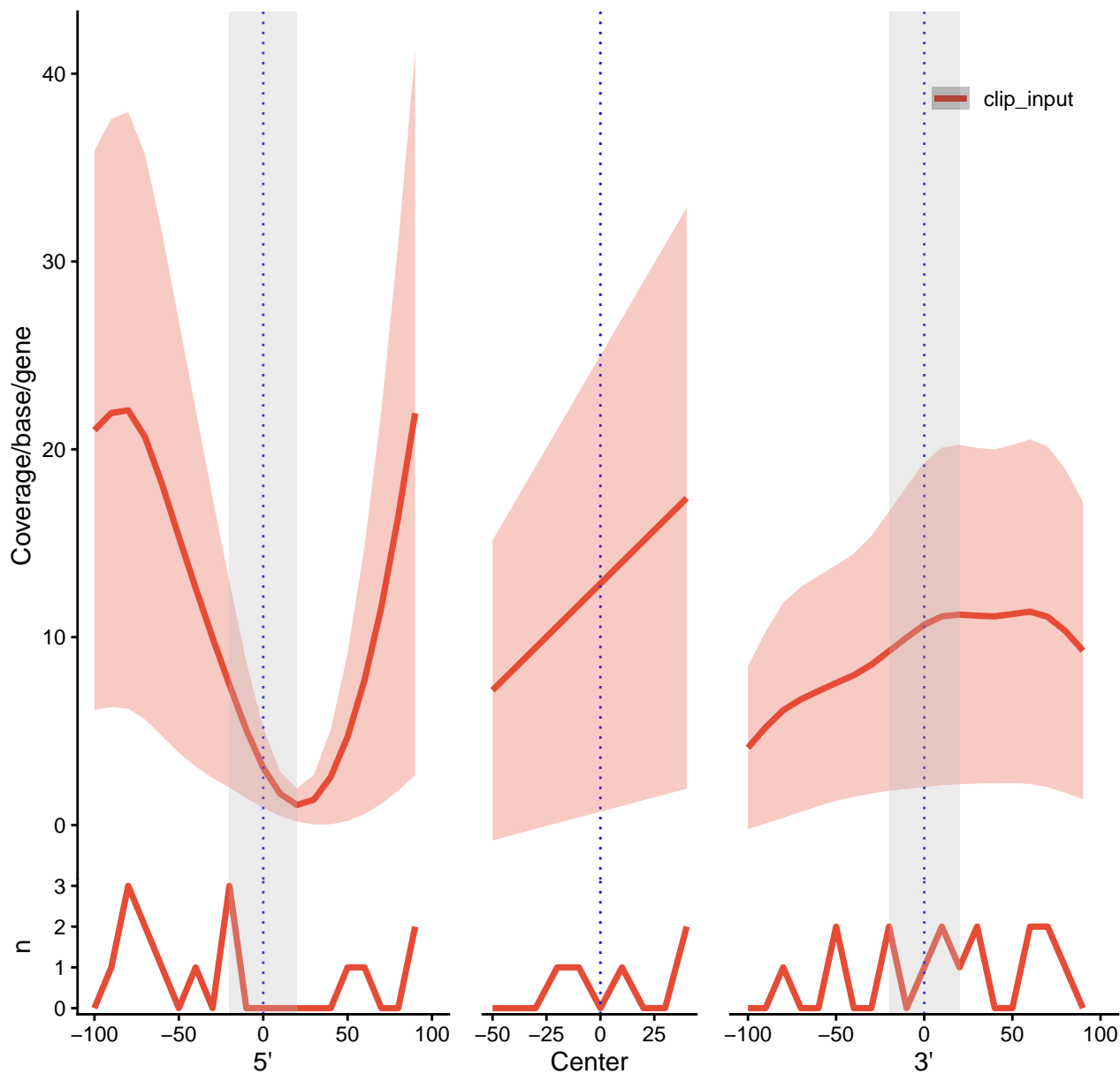




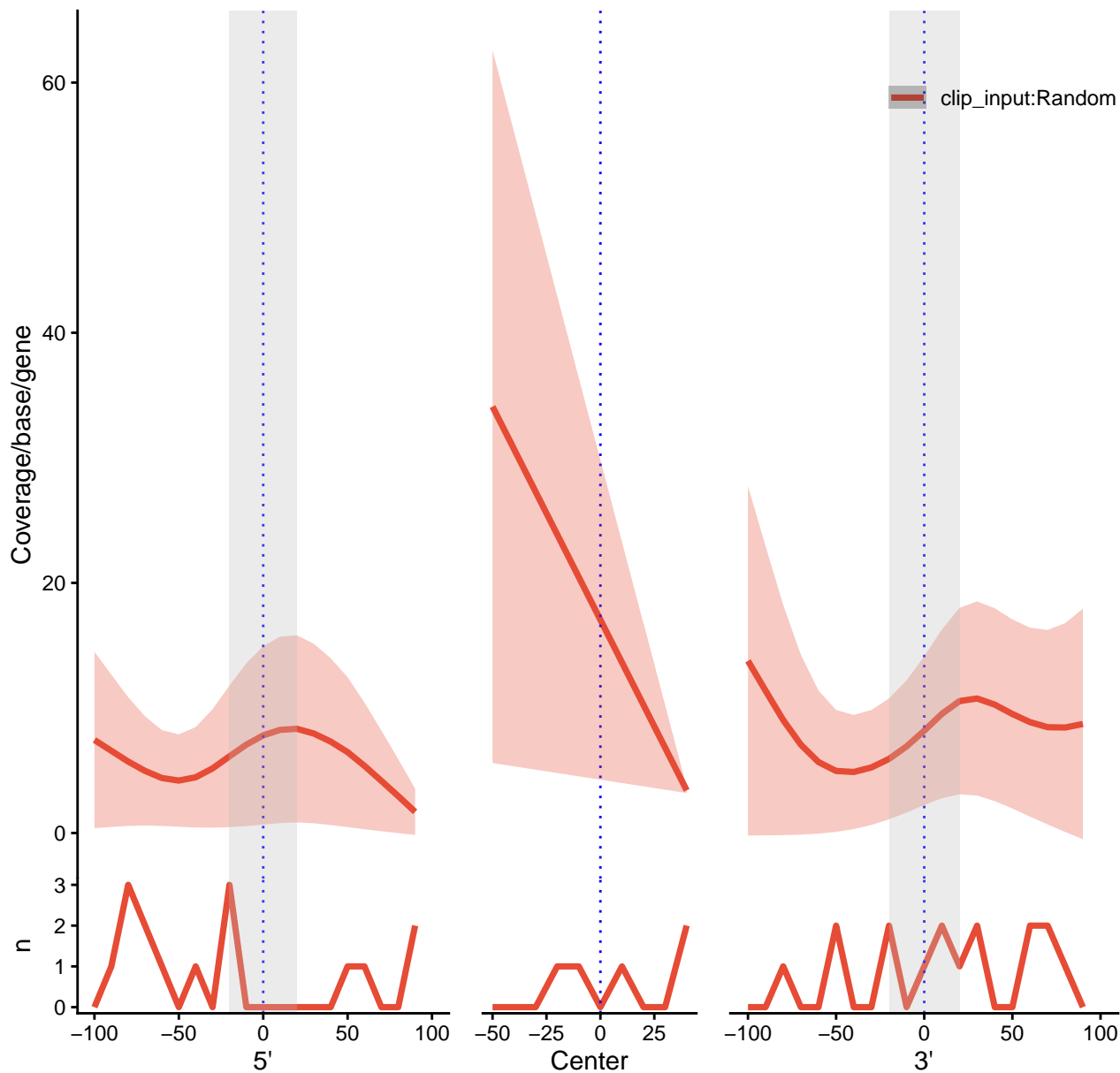




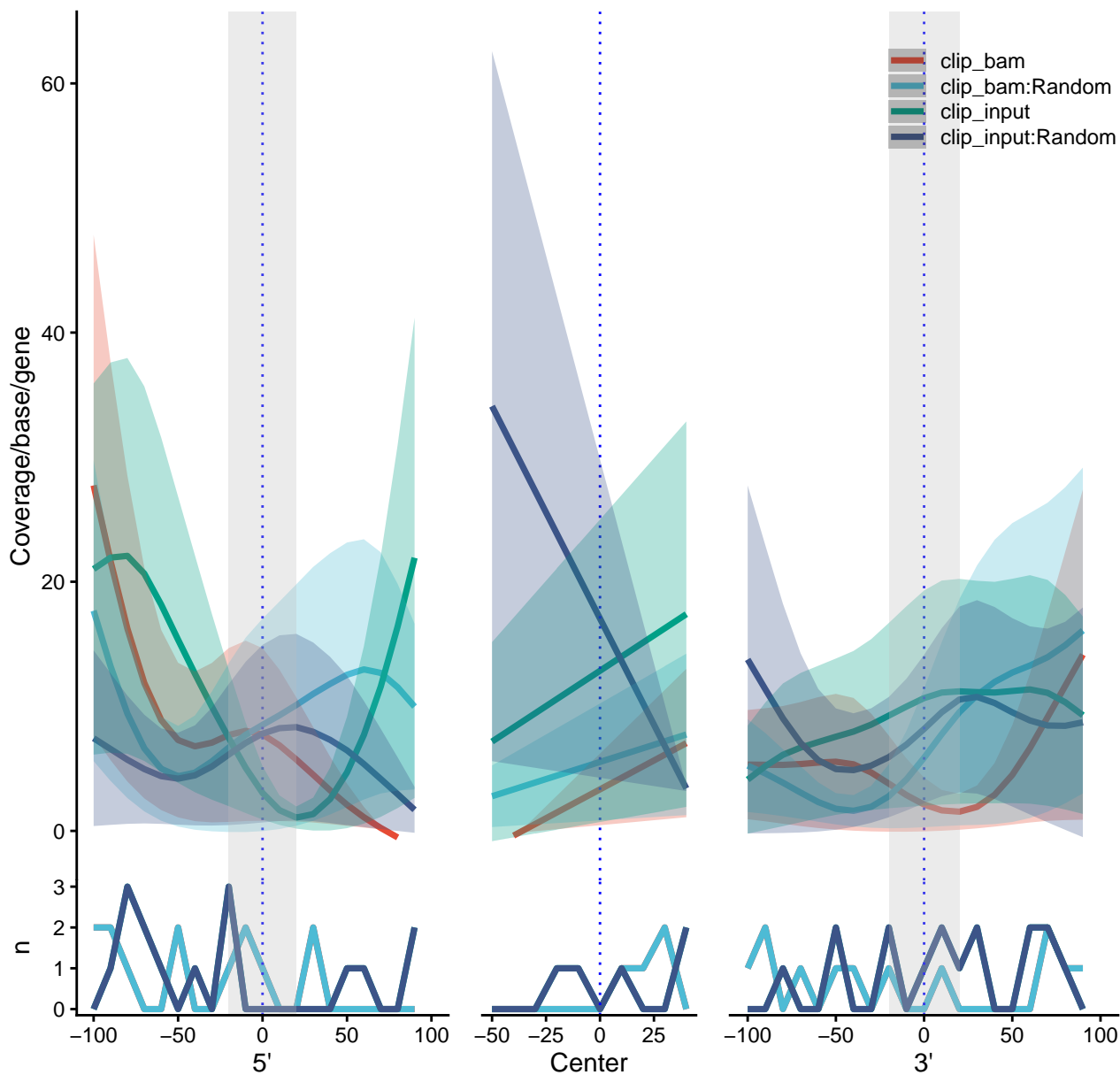
intron

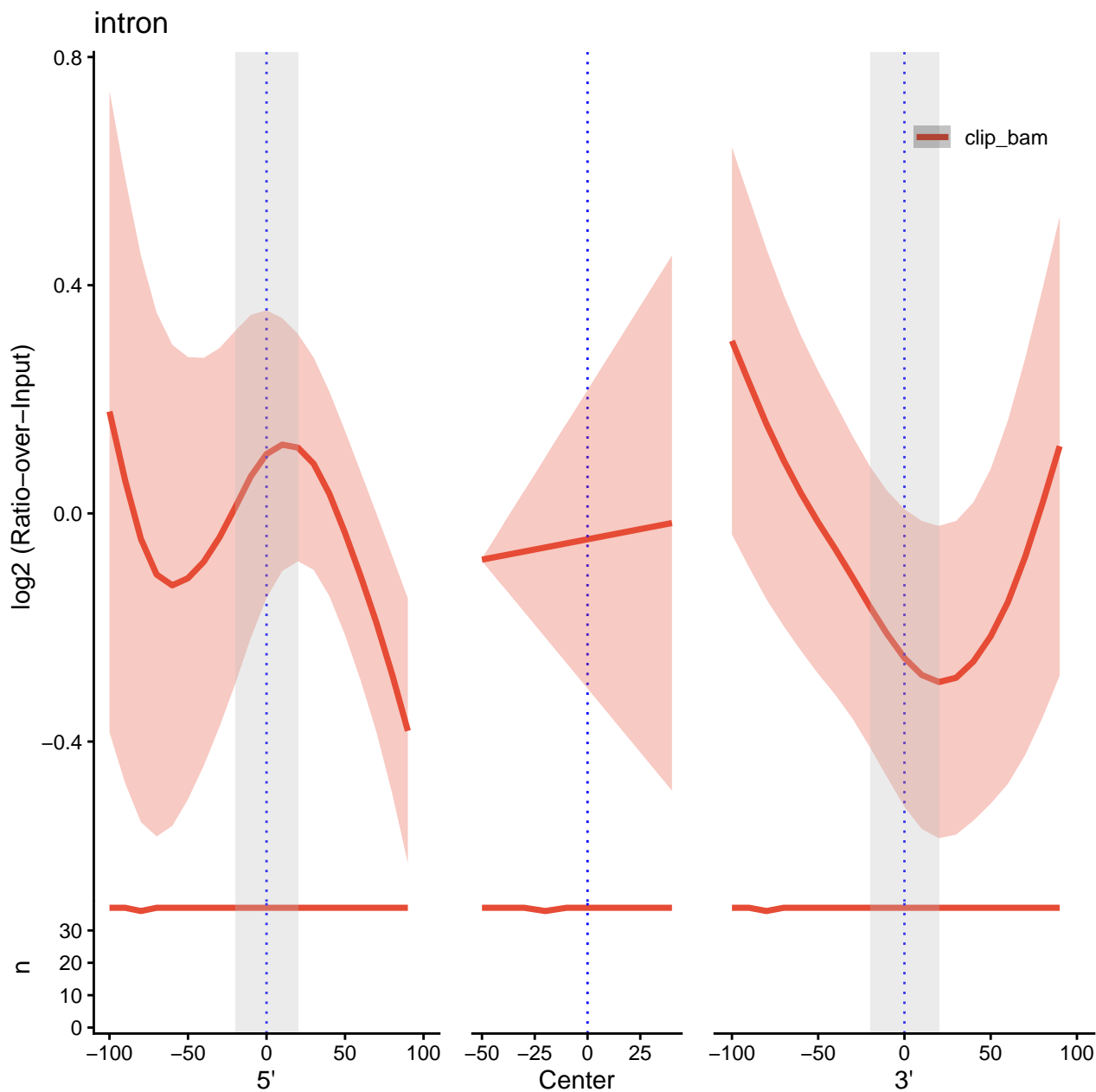


intron

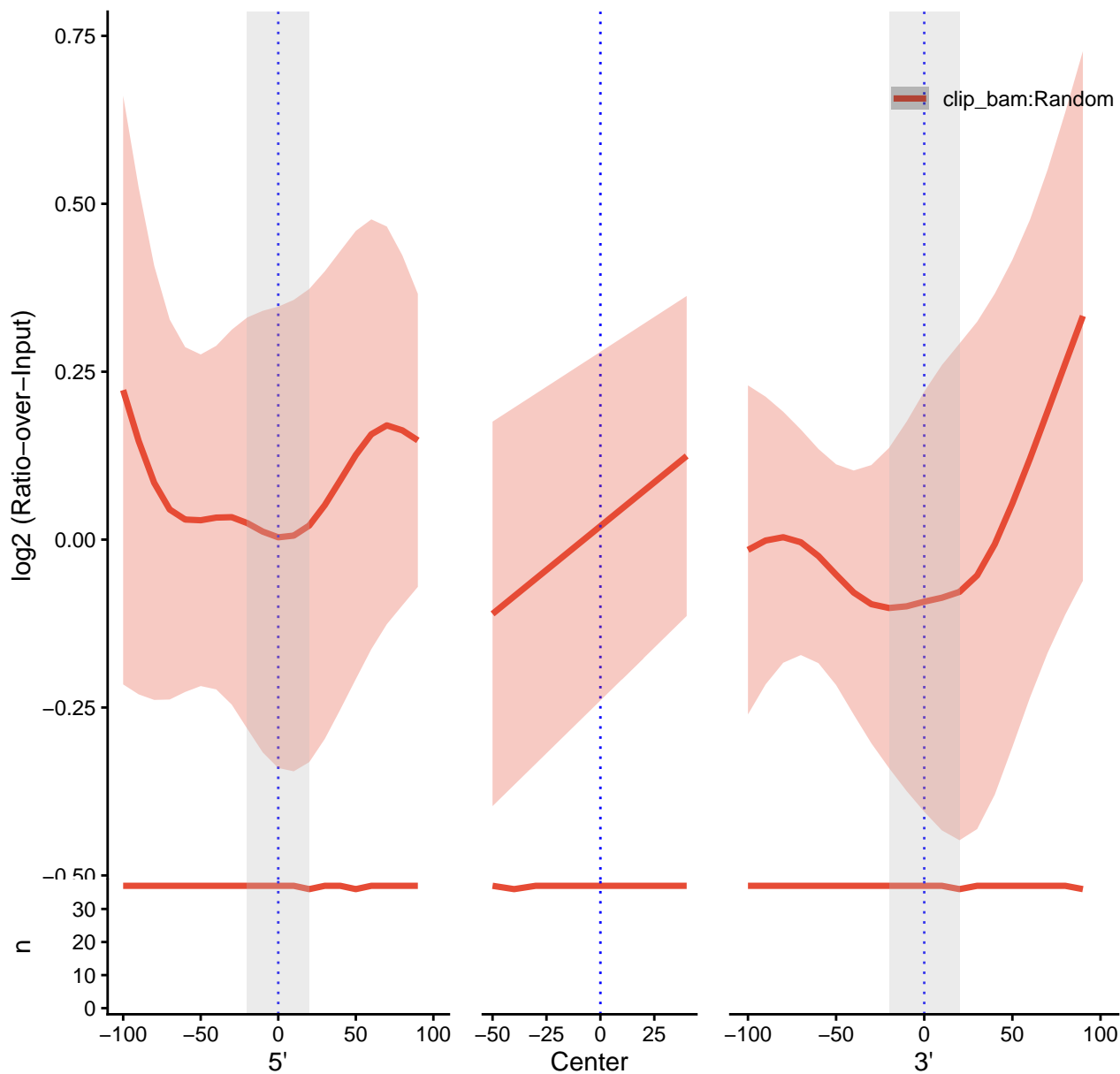


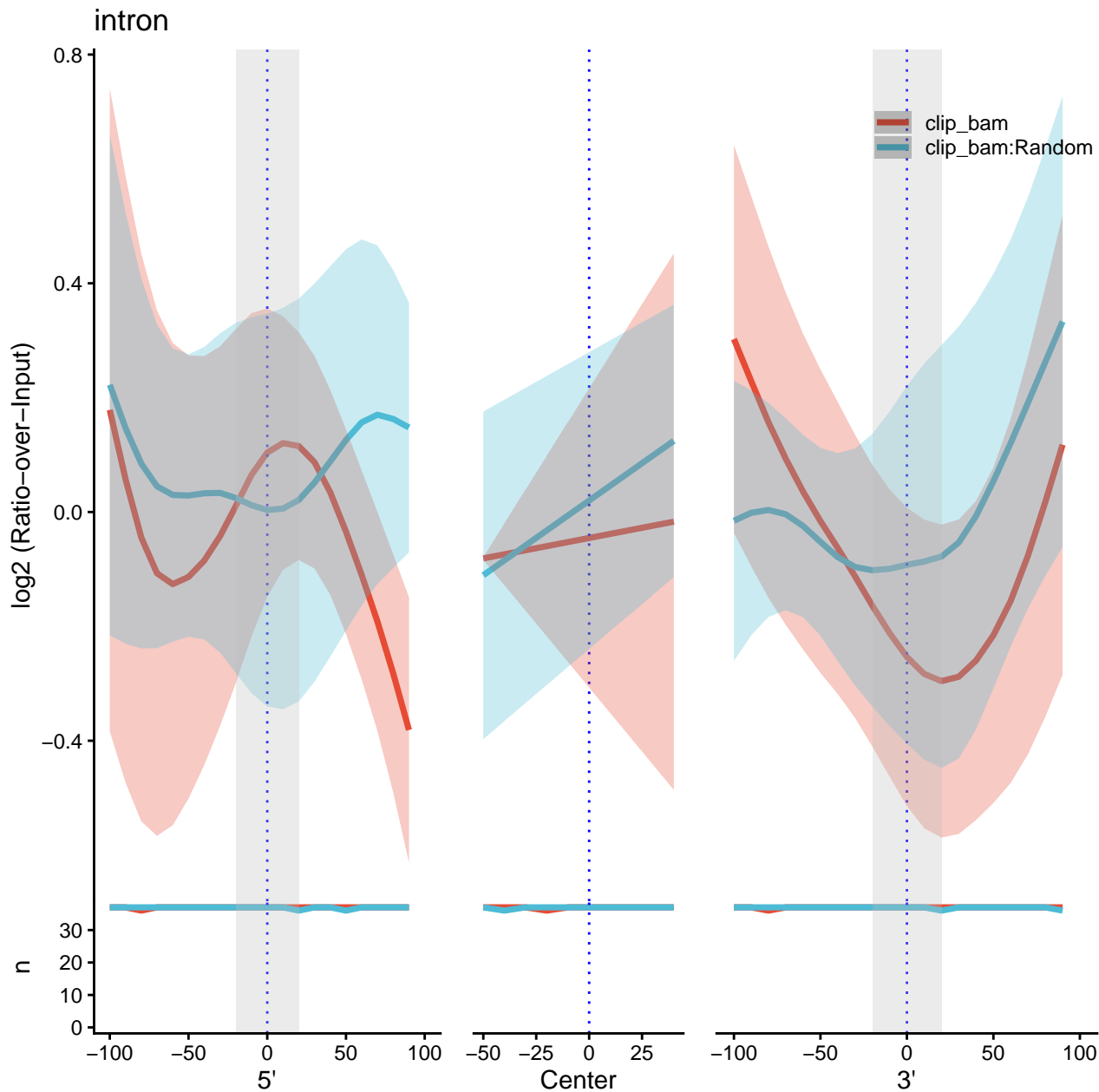
intron



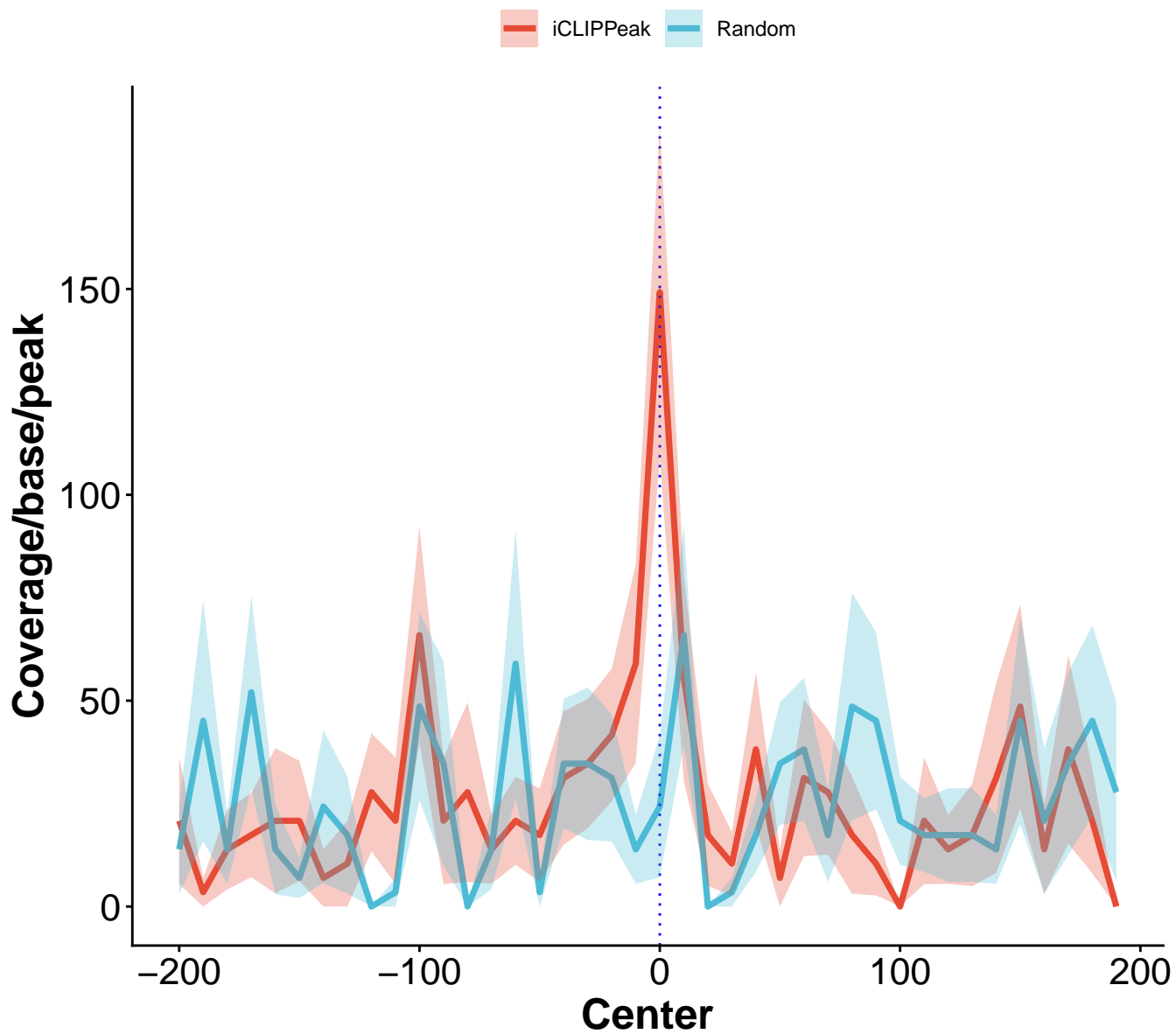


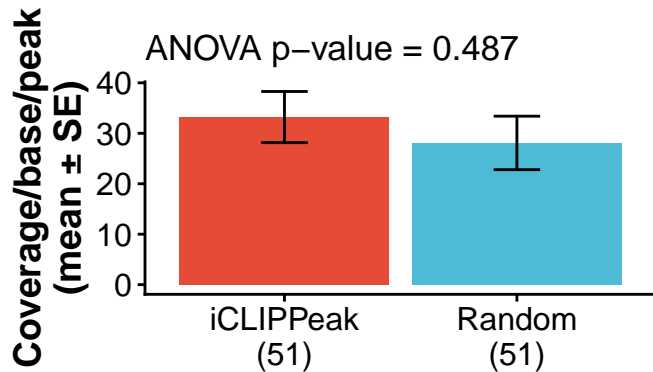
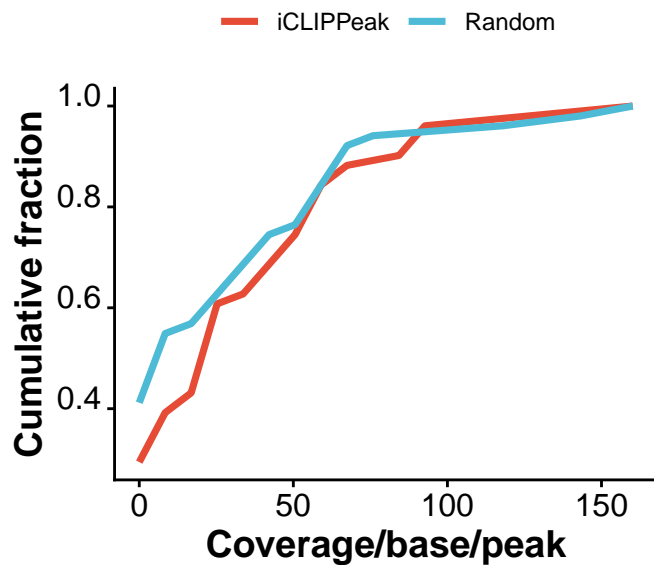
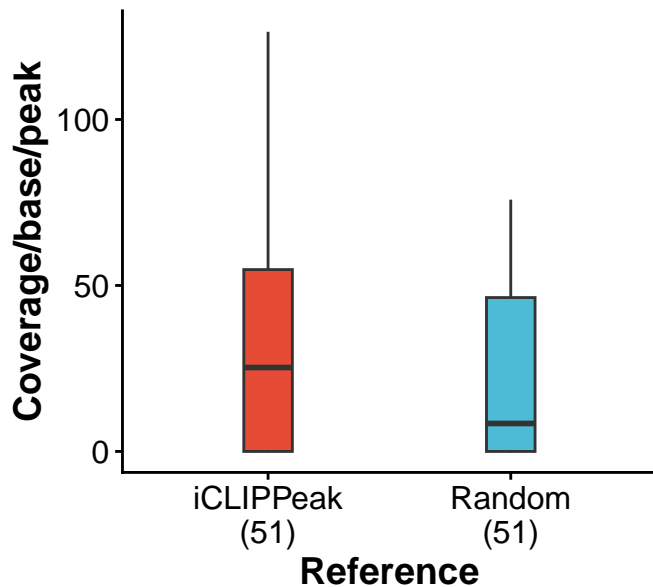
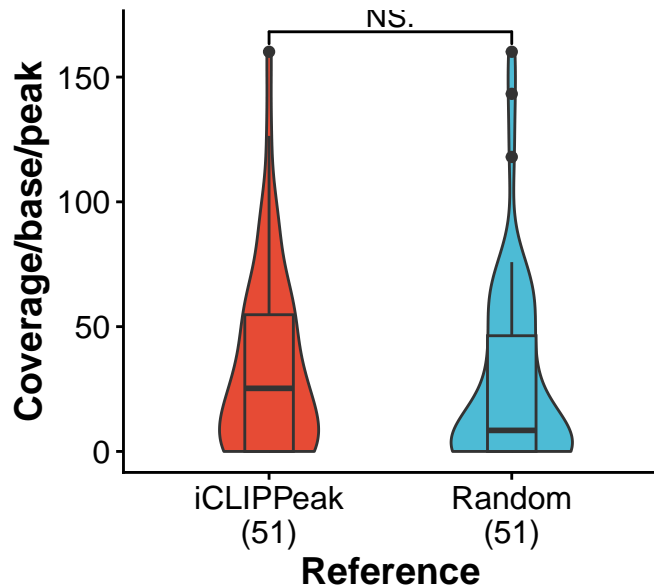
intron





Feature: unrestricted
Reference size: 51
Sample name: clip_bam

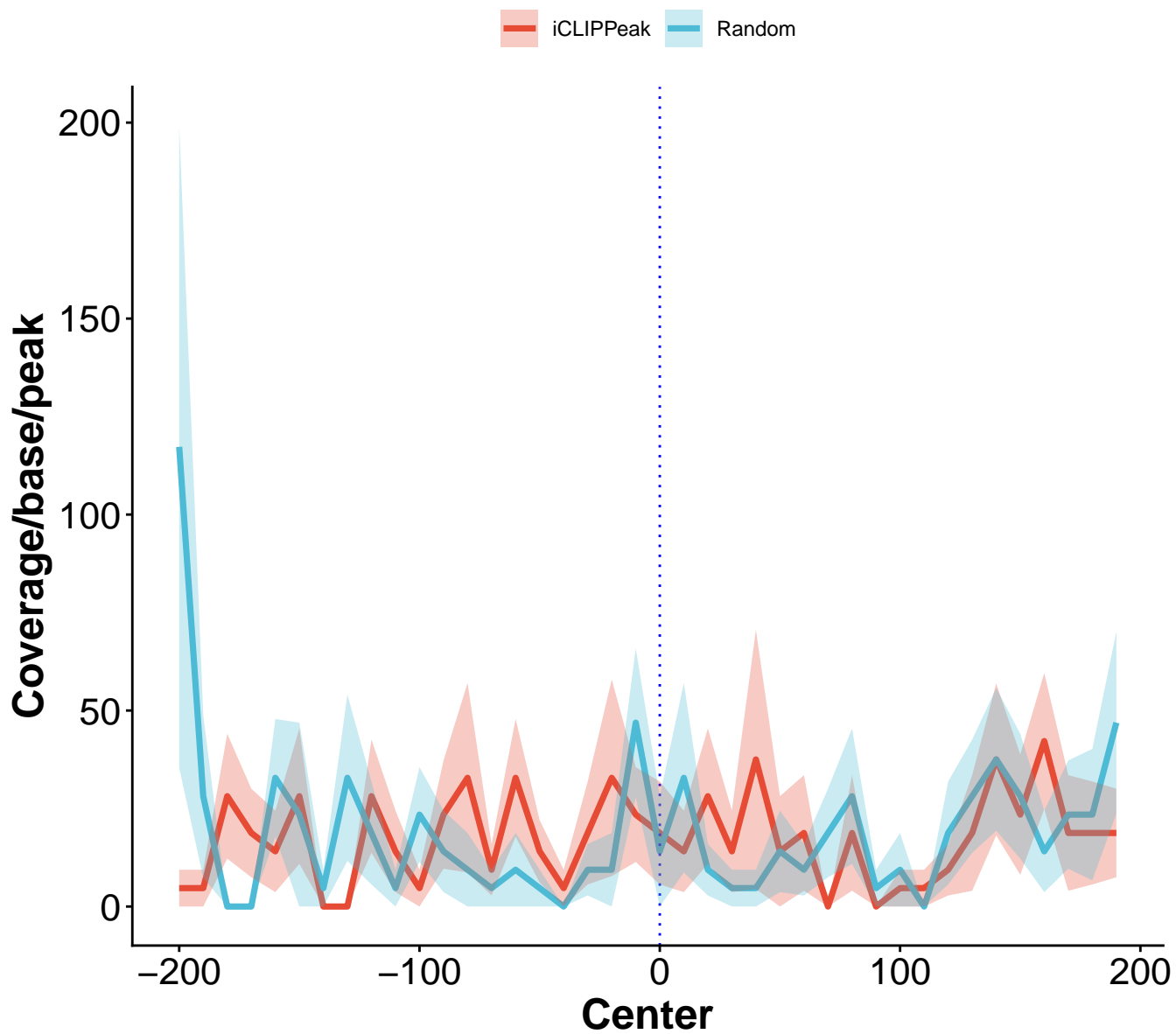


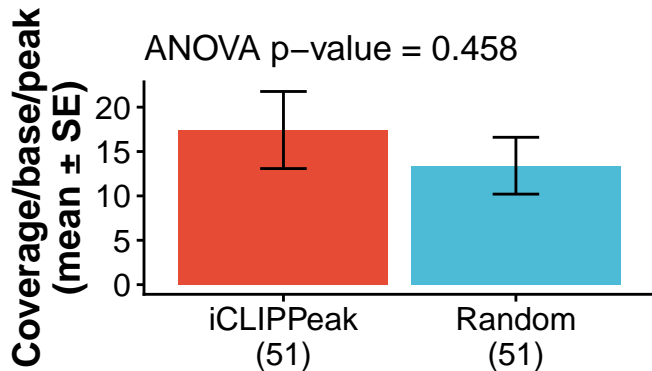
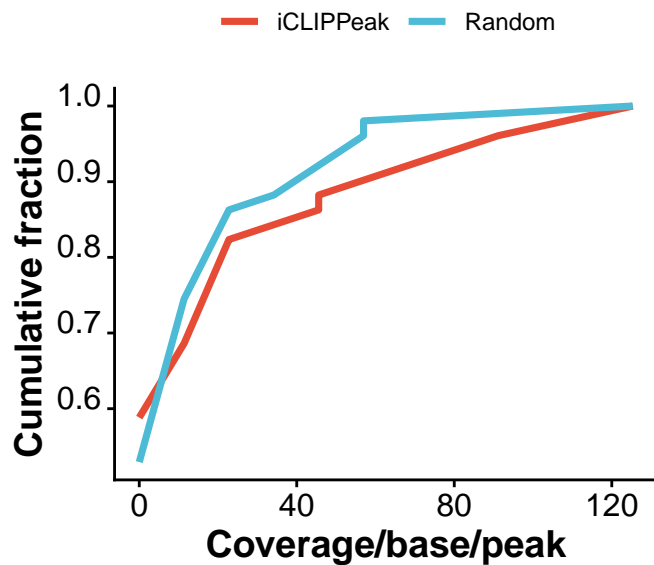
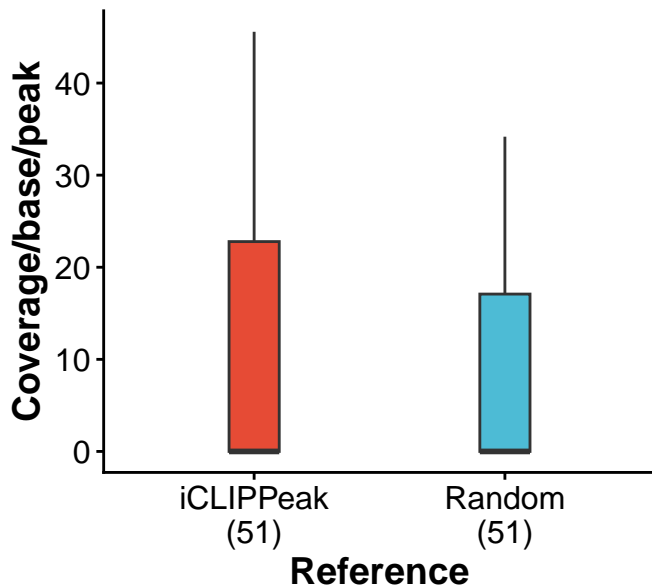
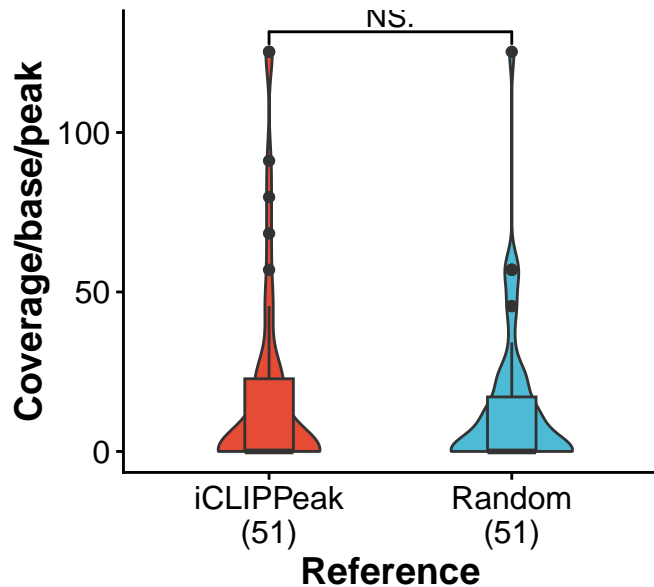


post hoc TukeyHSD test

	diff	lwr	upr	p adj
<i>Random-iCLIPPeak</i>	-5.123	-19.678	9.432	0.487

Feature: unrestricted
Reference size: 51
Sample name: clip_input



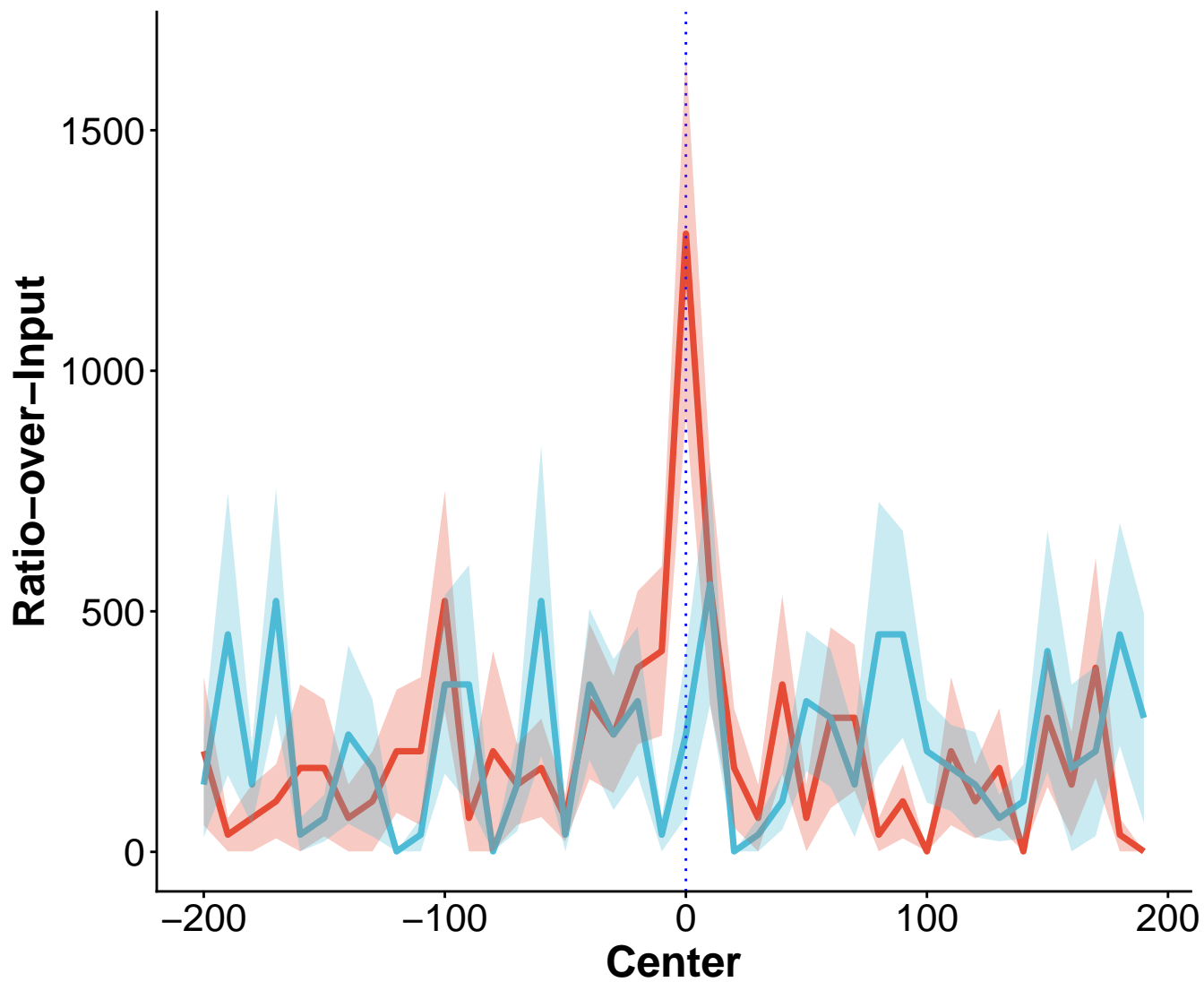


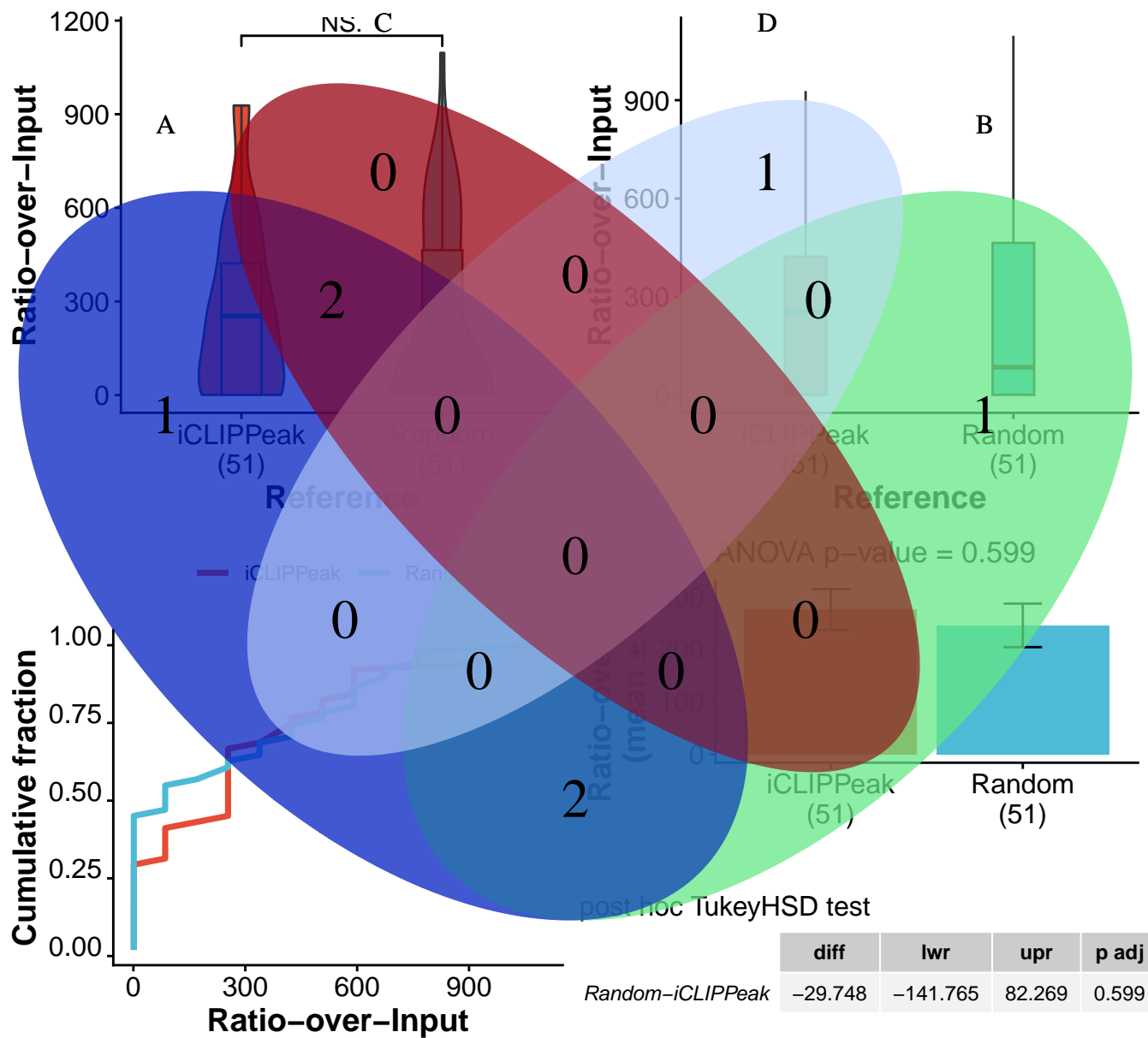
post hoc TukeyHSD test

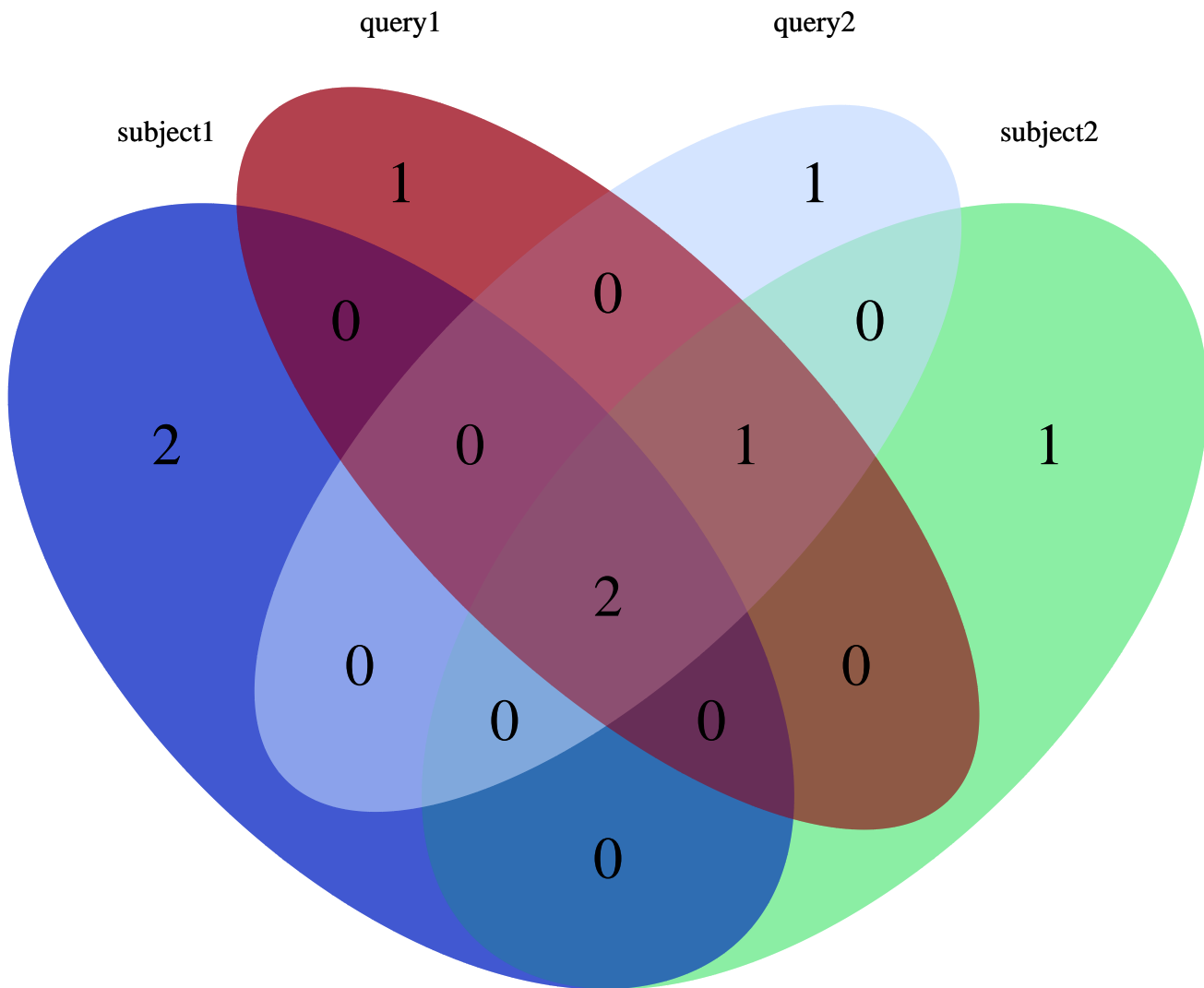
	diff	lwr	upr	p adj
Random-iCLIPPeak	-4.021	-14.726	6.685	0.458

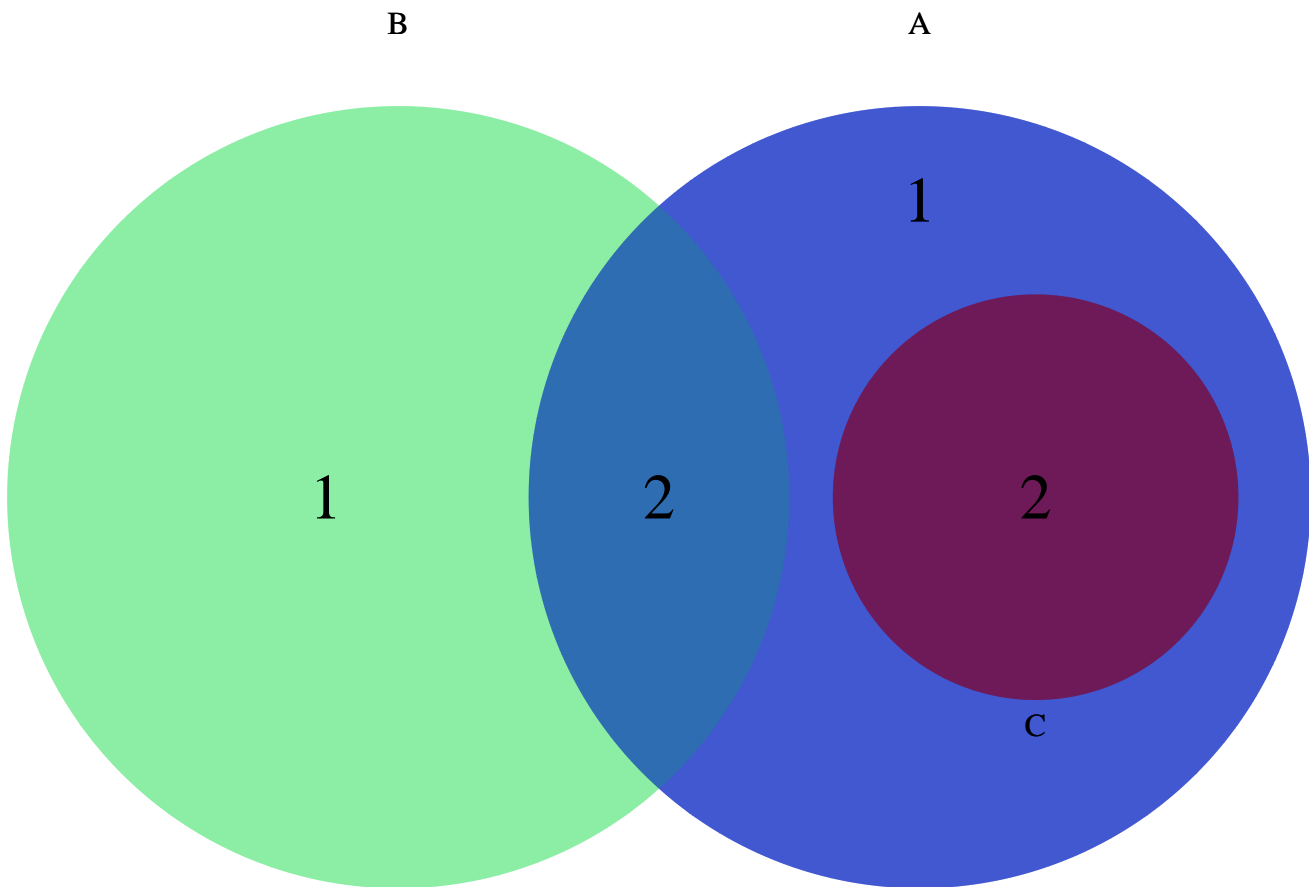
Feature: unrestricted
Reference size: 51
Sample name: clip_bam

iCLIPPeak Random



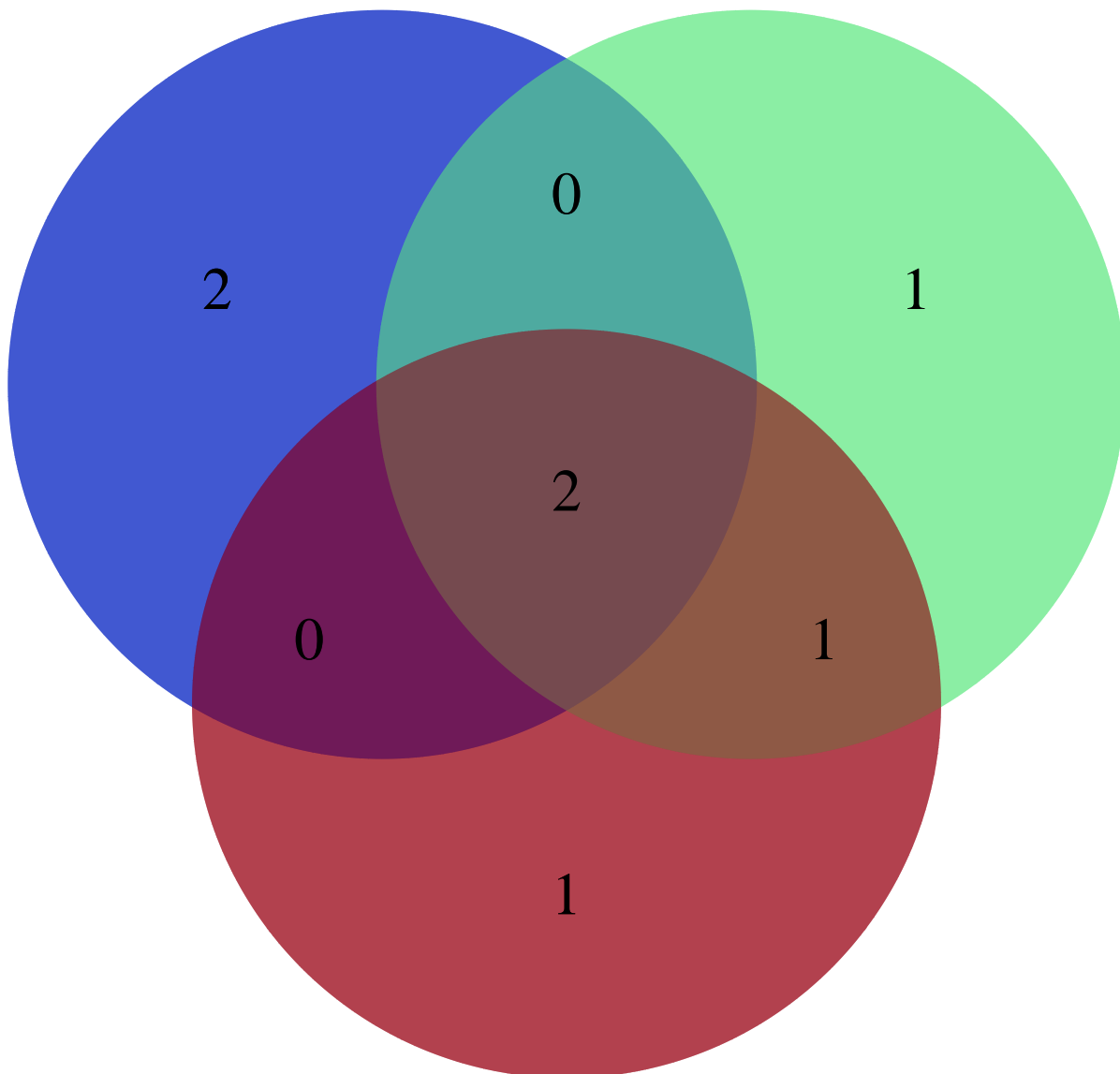




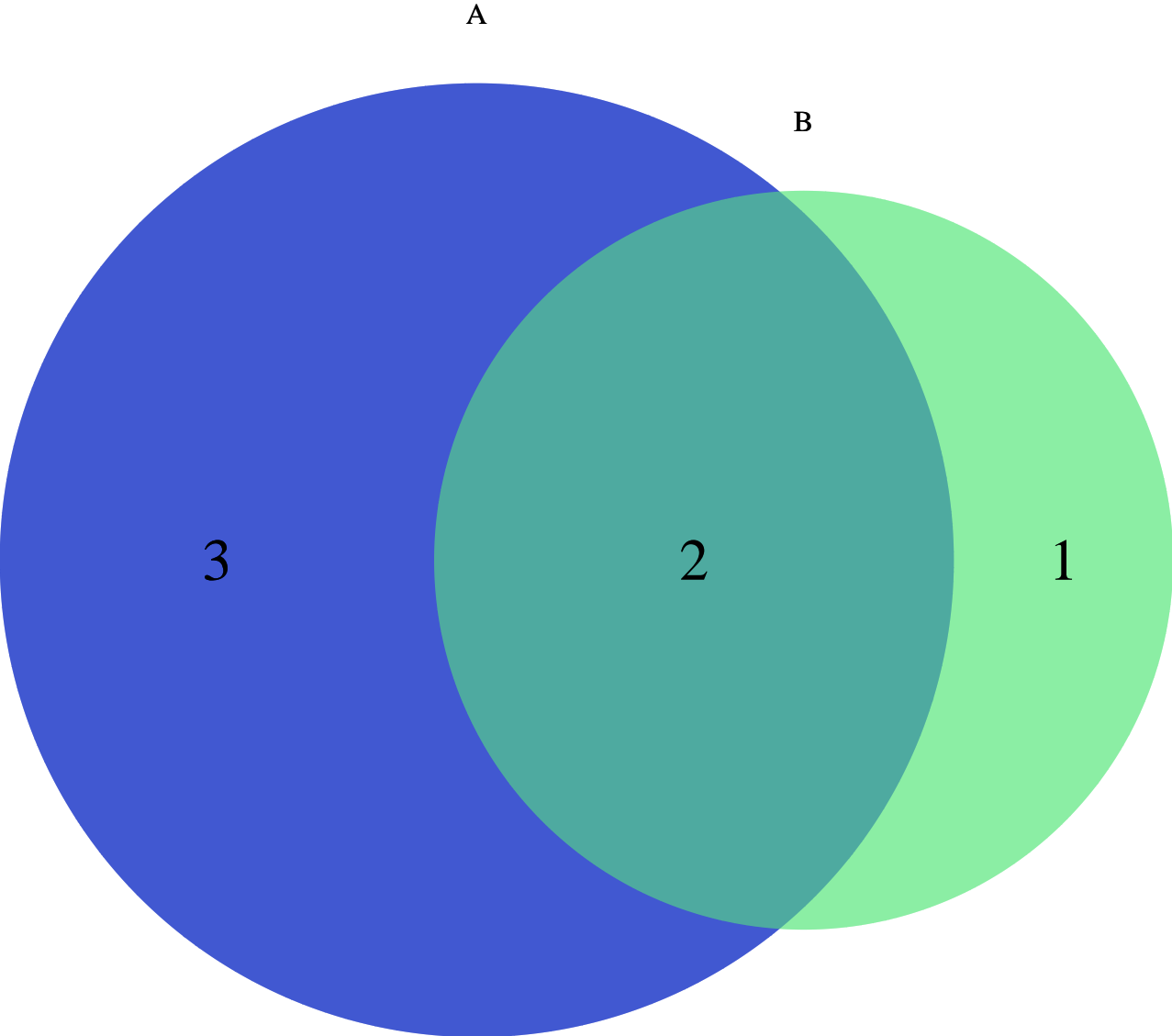


subject1

subject2



query



A

B

3

2

1

Jaccard: 0.33333

query

subject

2

2

2

Jaccard: 0.33333

