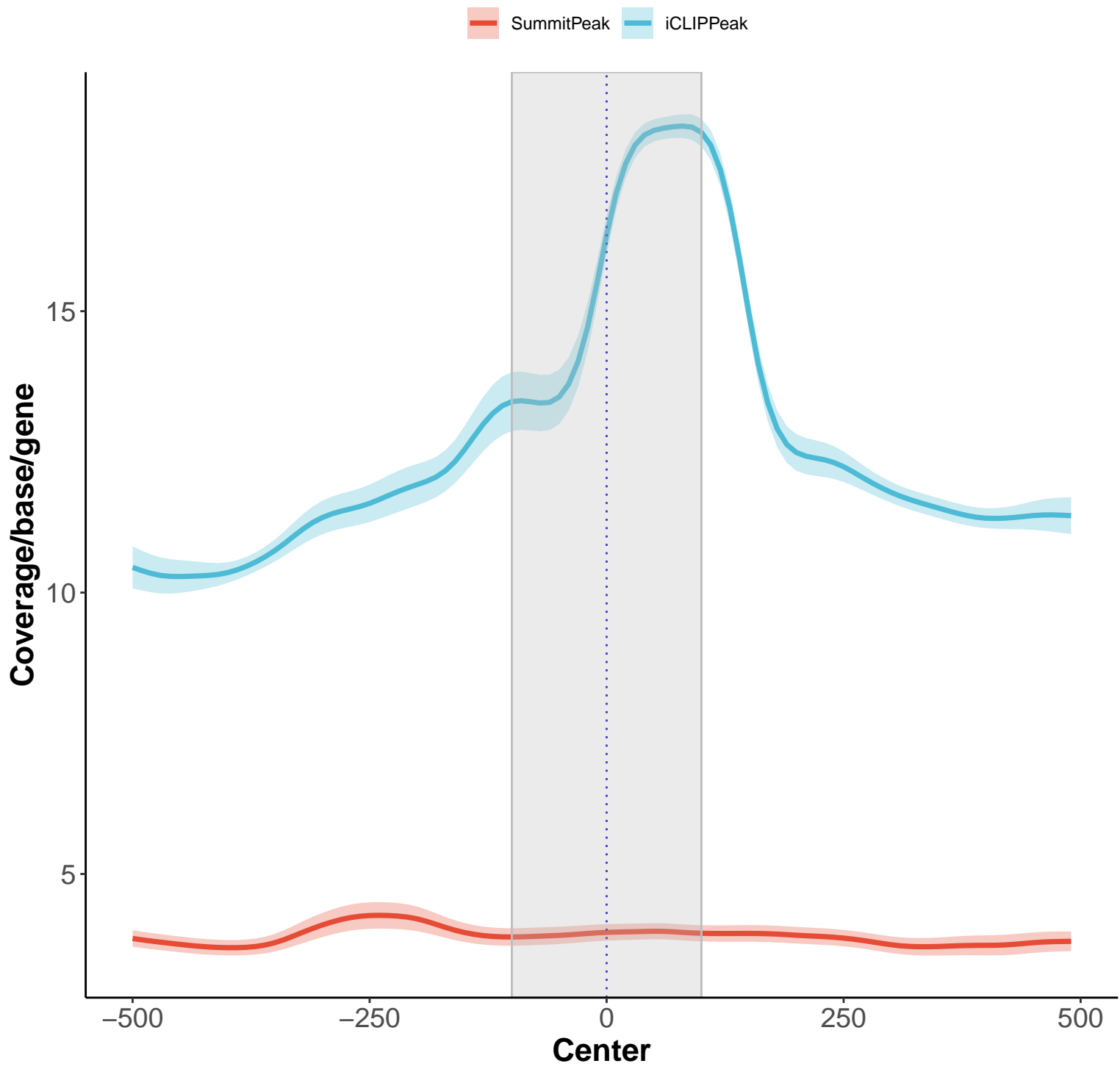
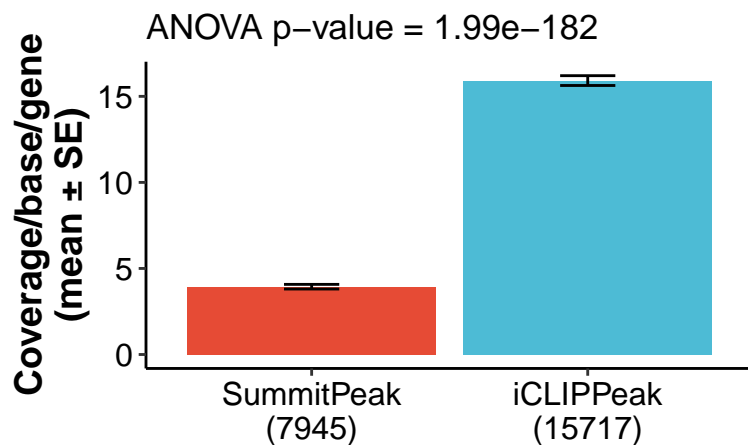
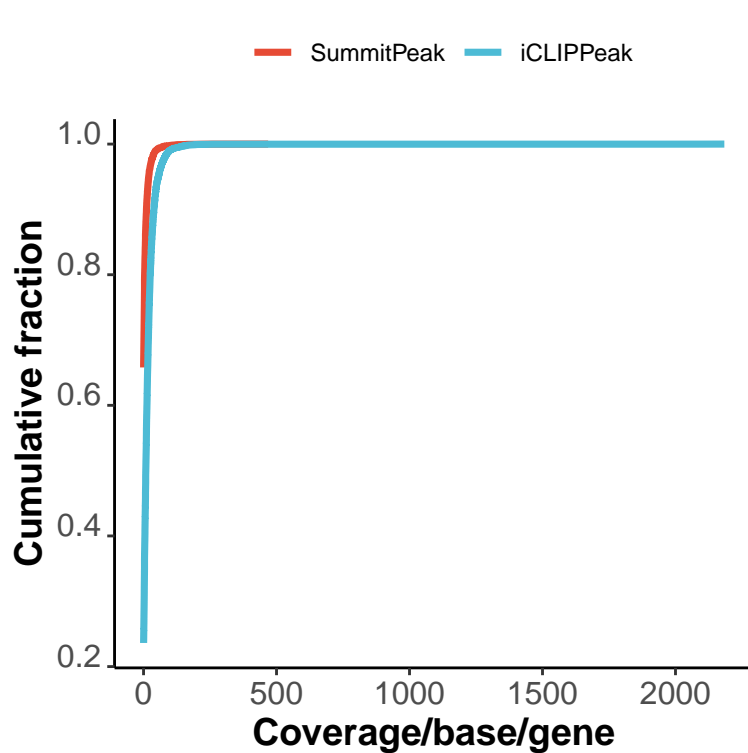
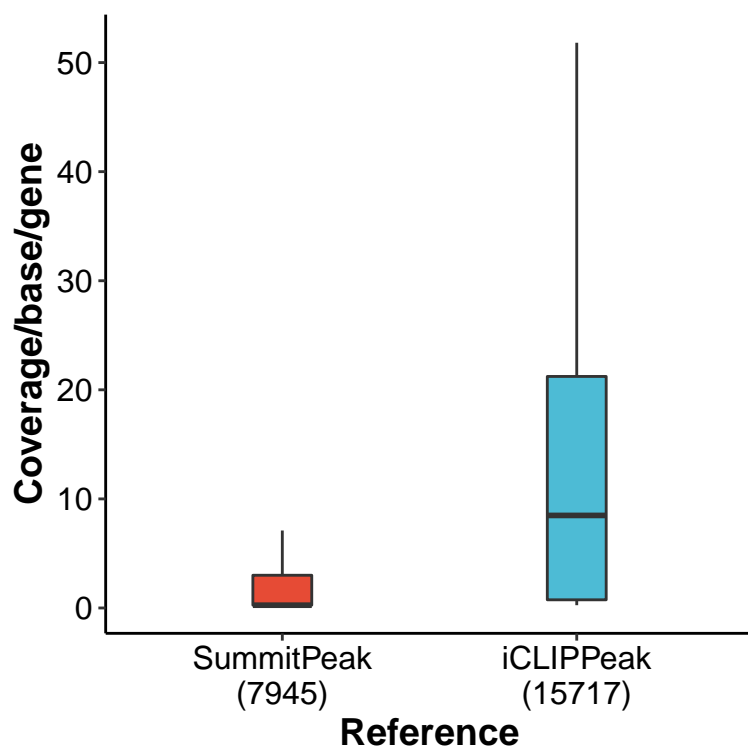
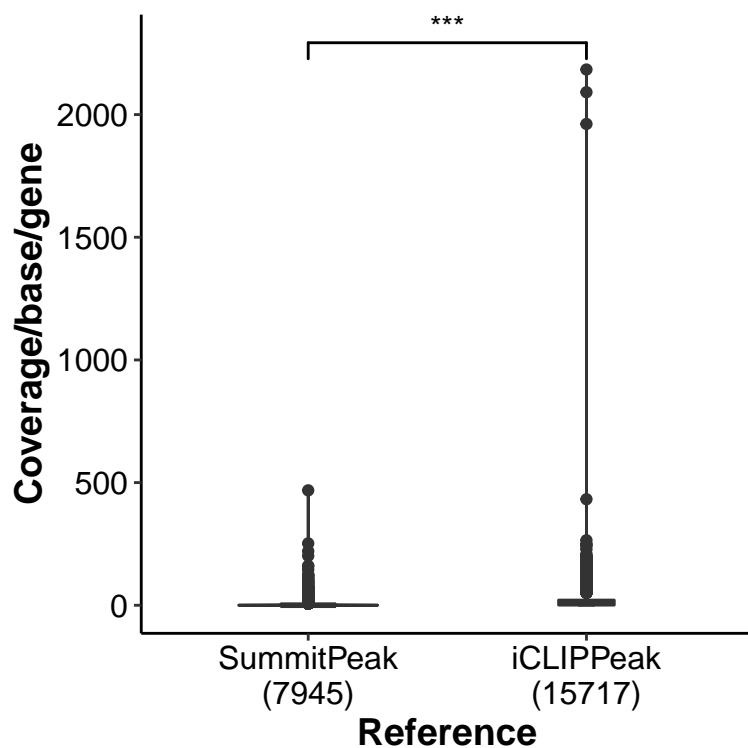


clip_bam

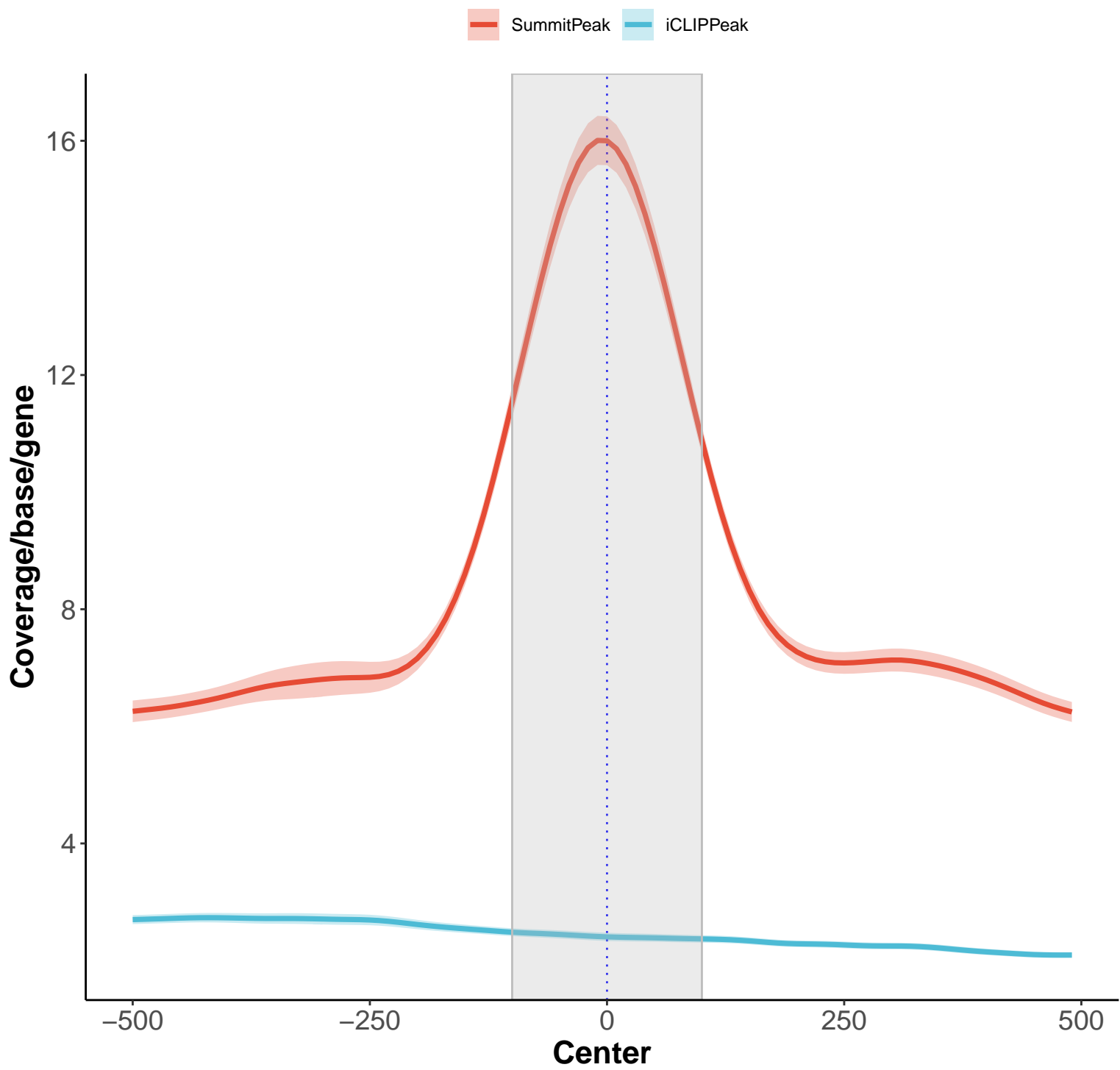


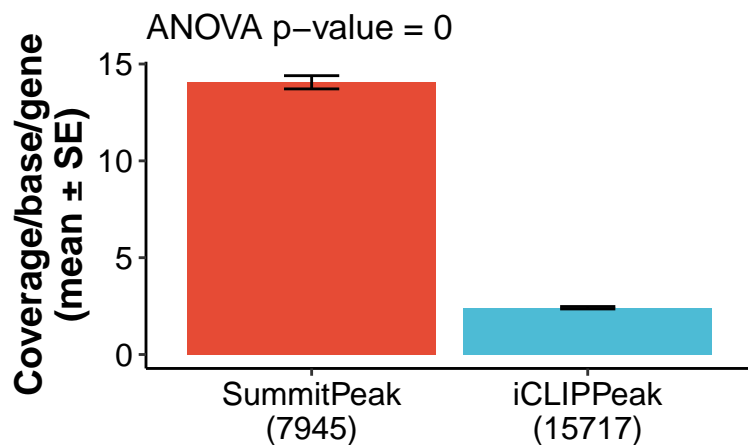
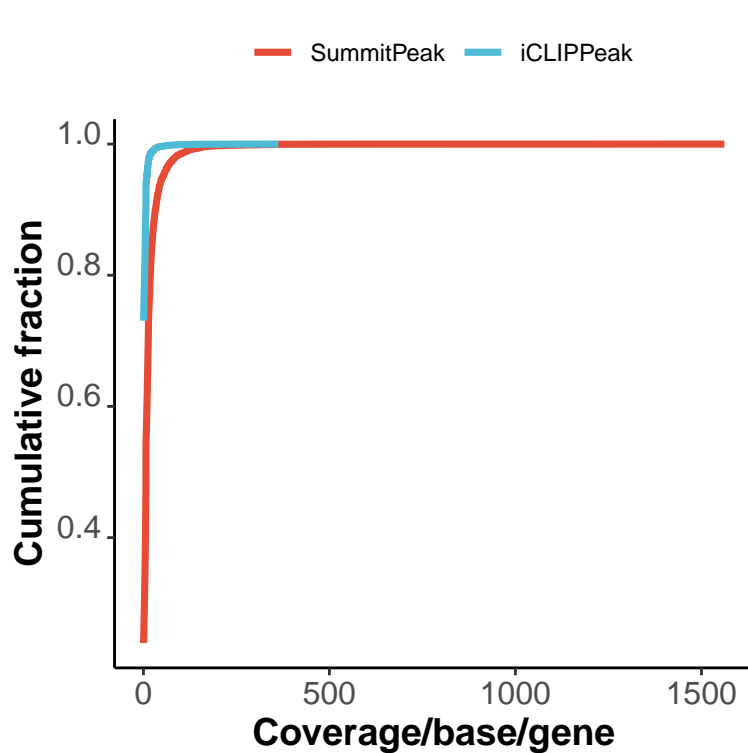
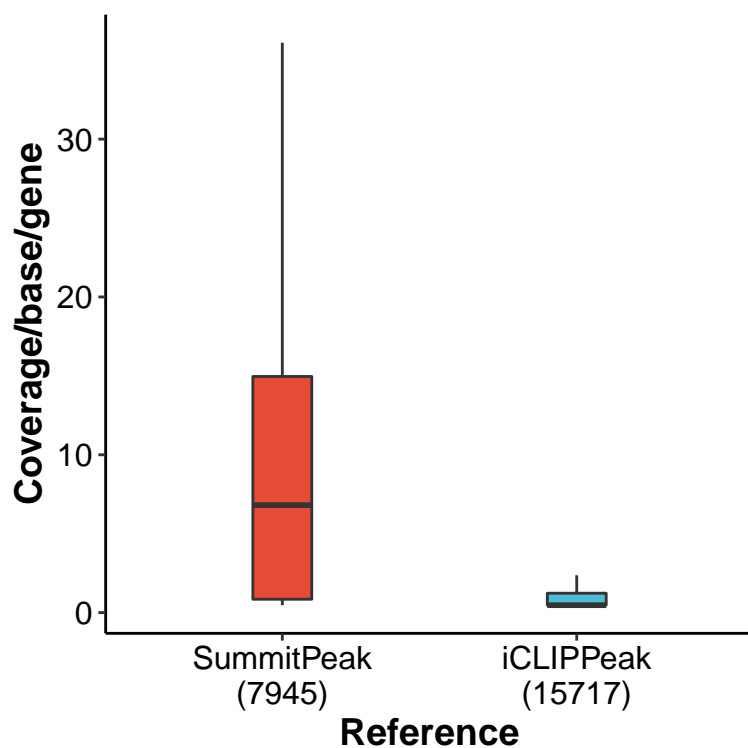
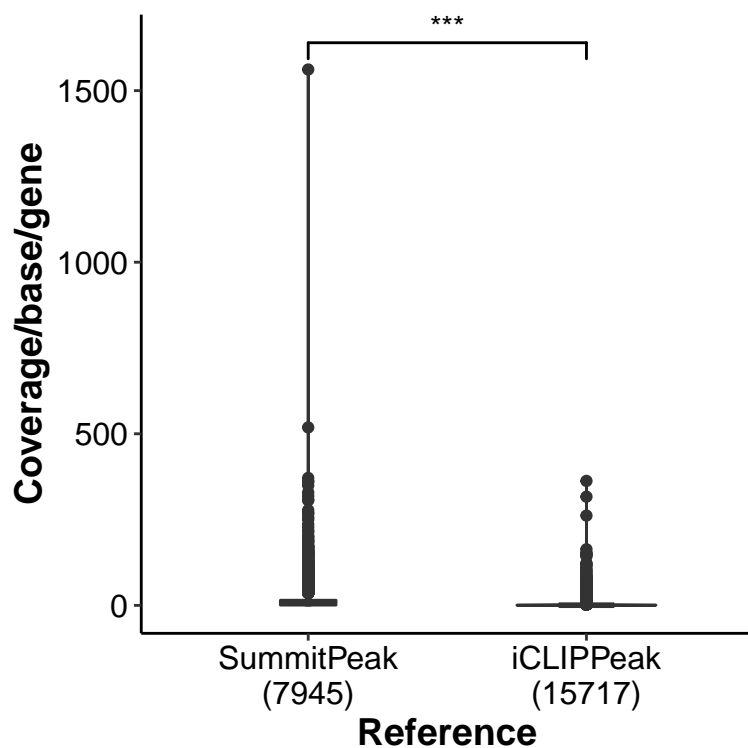


post hoc TukeyHSD test

	diff	lwr	upr	p adj
iCLIPPeak-SummitPeak	11.974	11.167	12.782	0

chip_bam

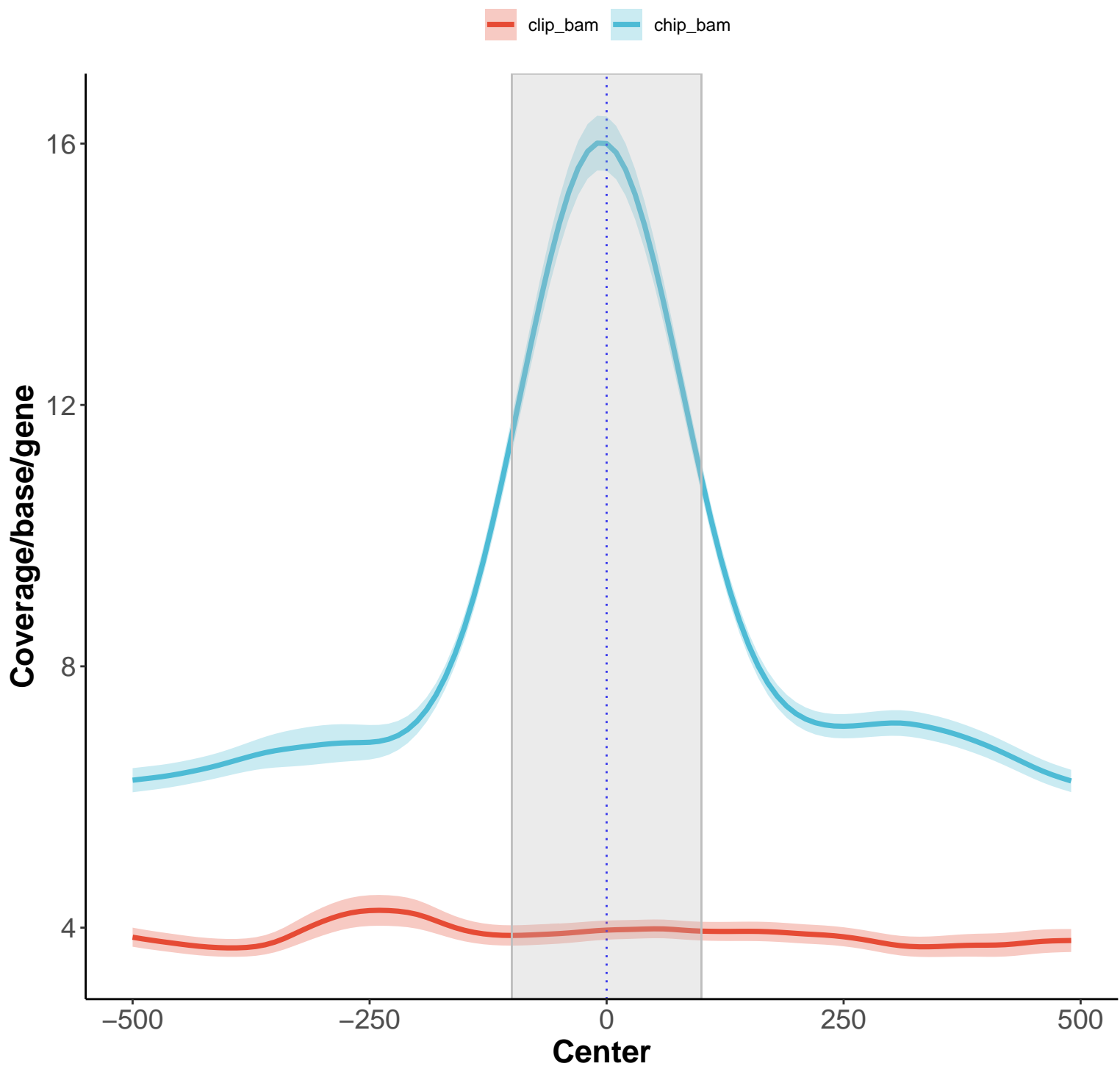


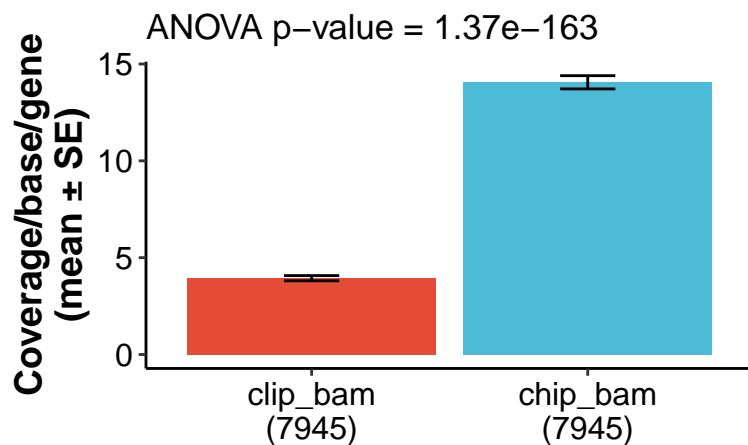
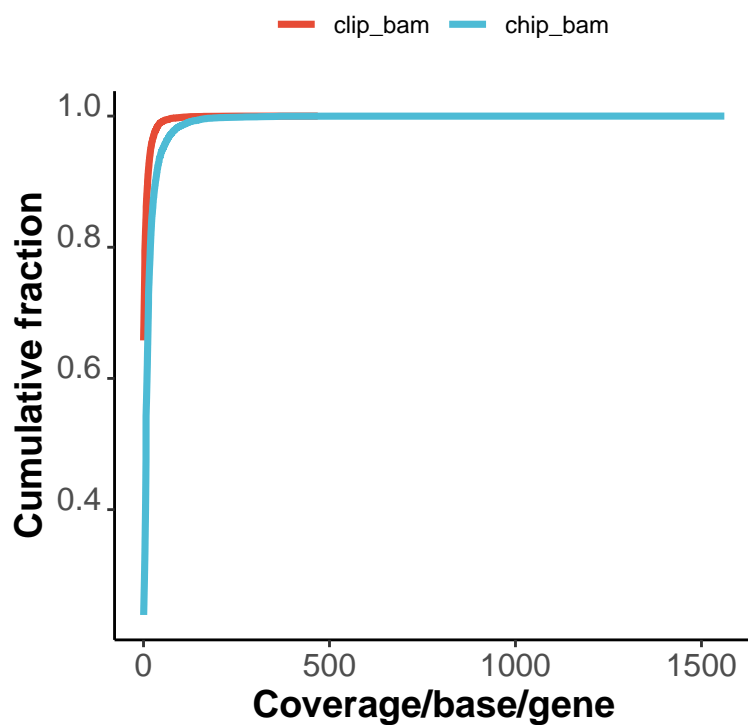
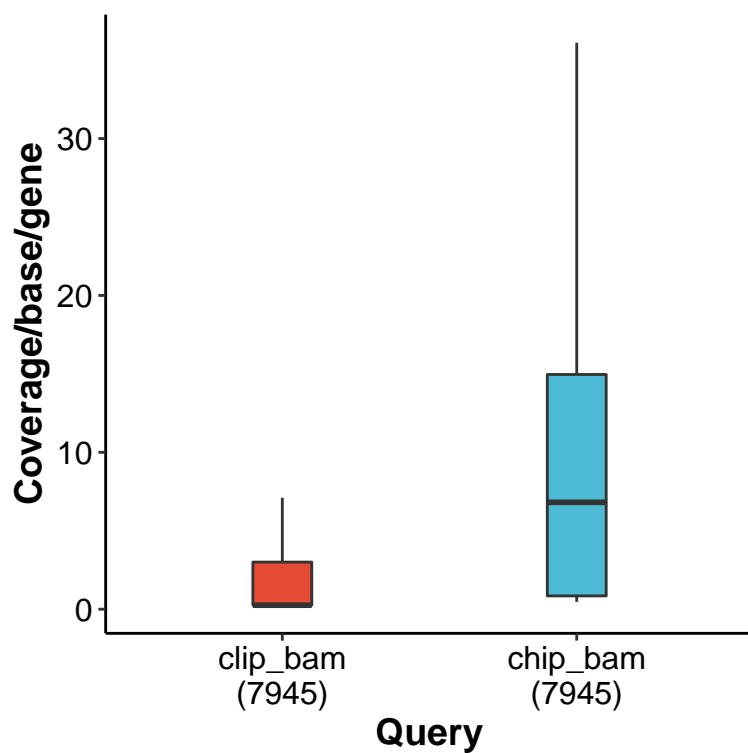
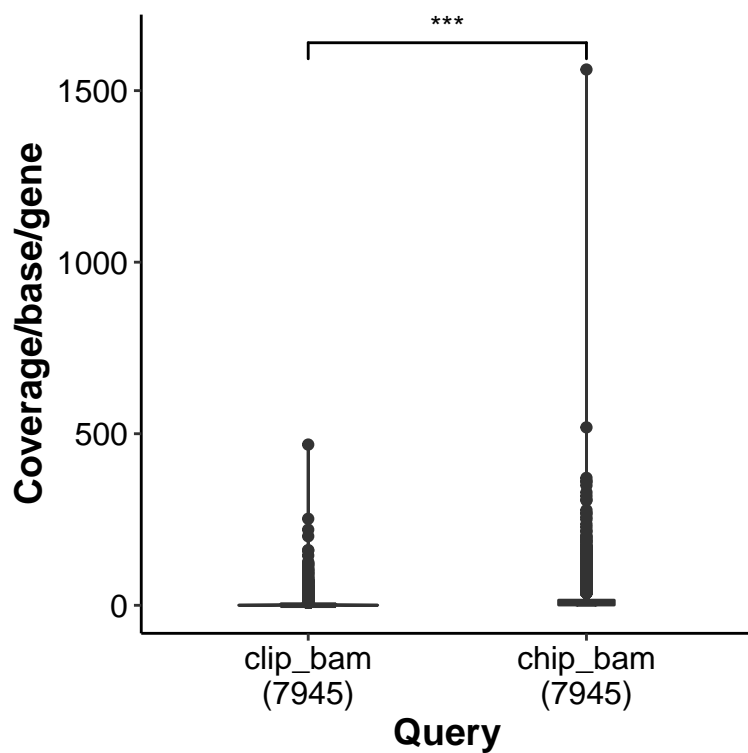


post hoc TukeyHSD test

	diff	lwr	upr	p adj
iCLIPPeak-SummitPeak	-11.64	-12.146	-11.135	0

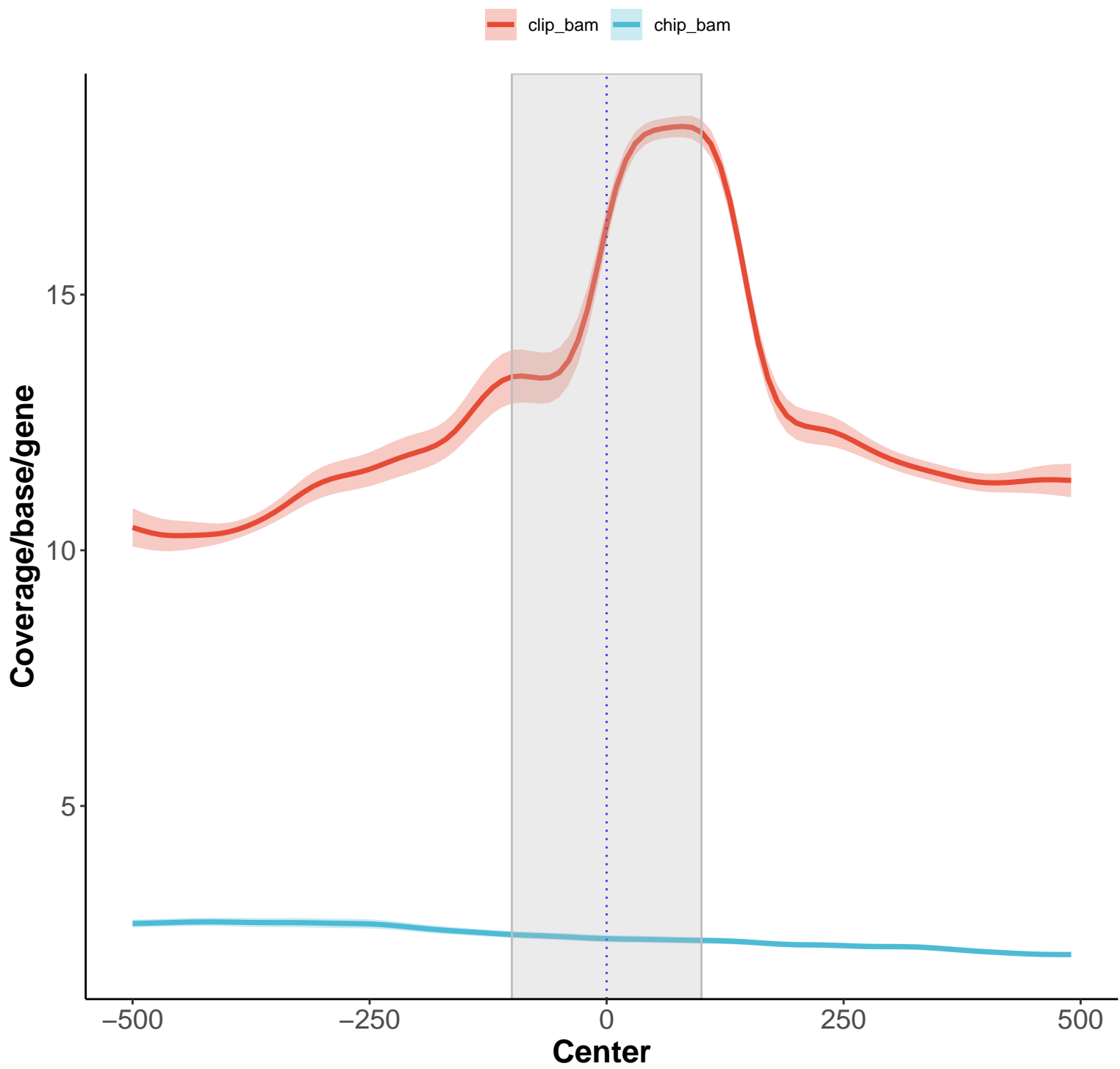
SummitPeak

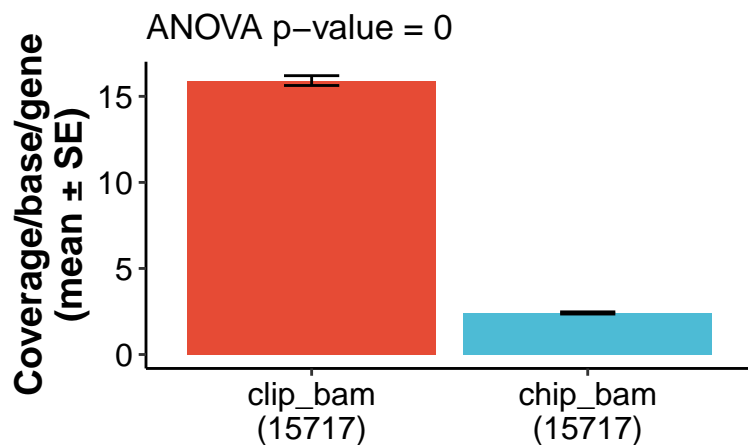
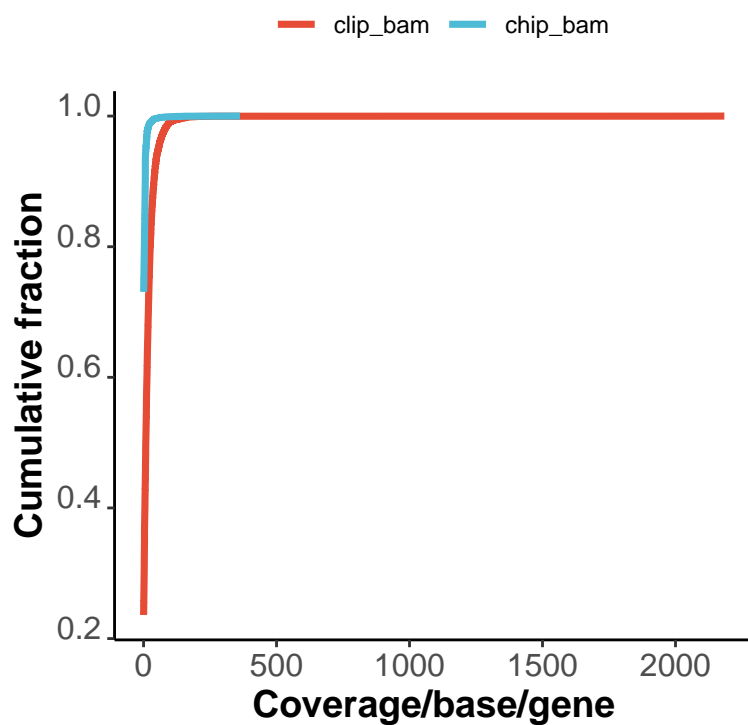
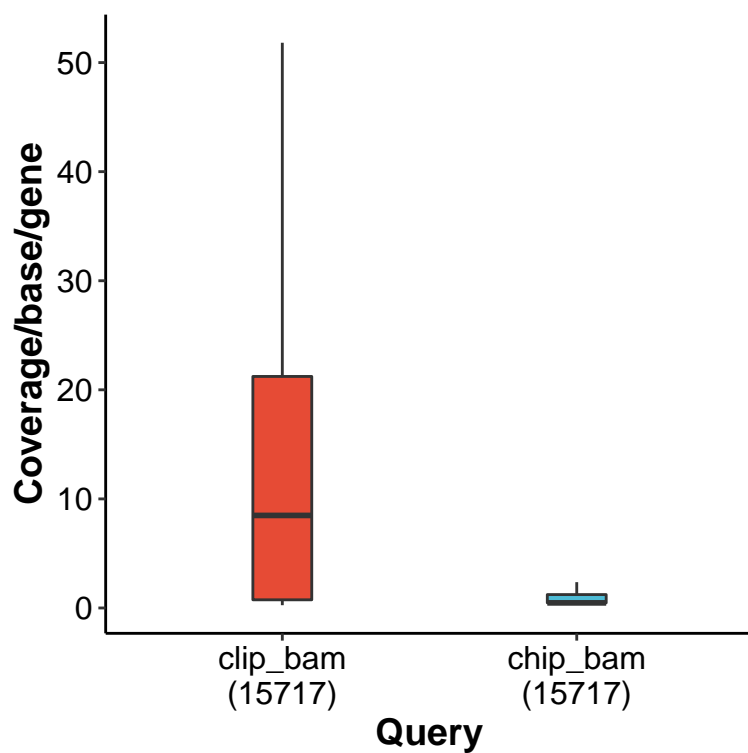
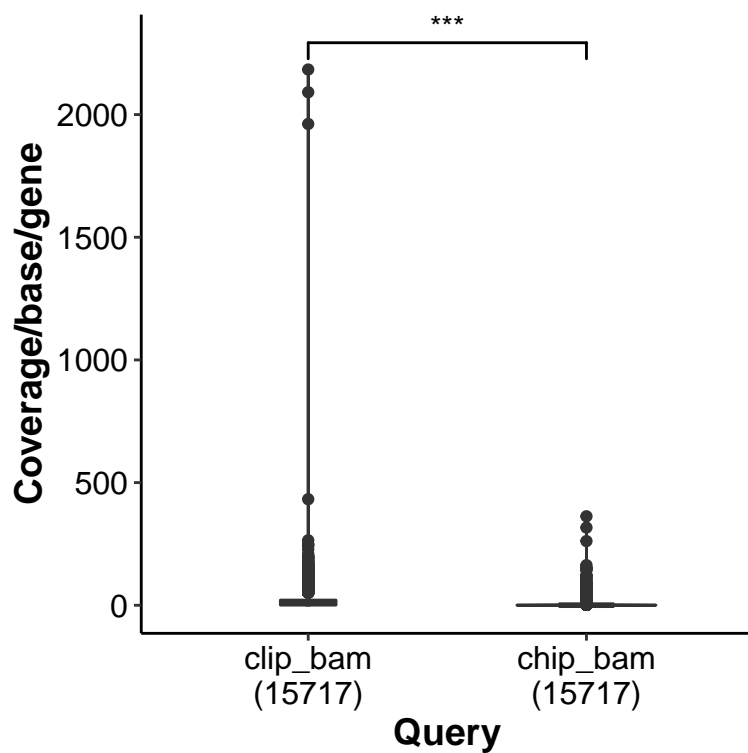




post hoc TukeyHSD test

	diff	lwr	upr	p adj
chip_bam-clip_bam	10.115	9.396	10.834	2.04e-08



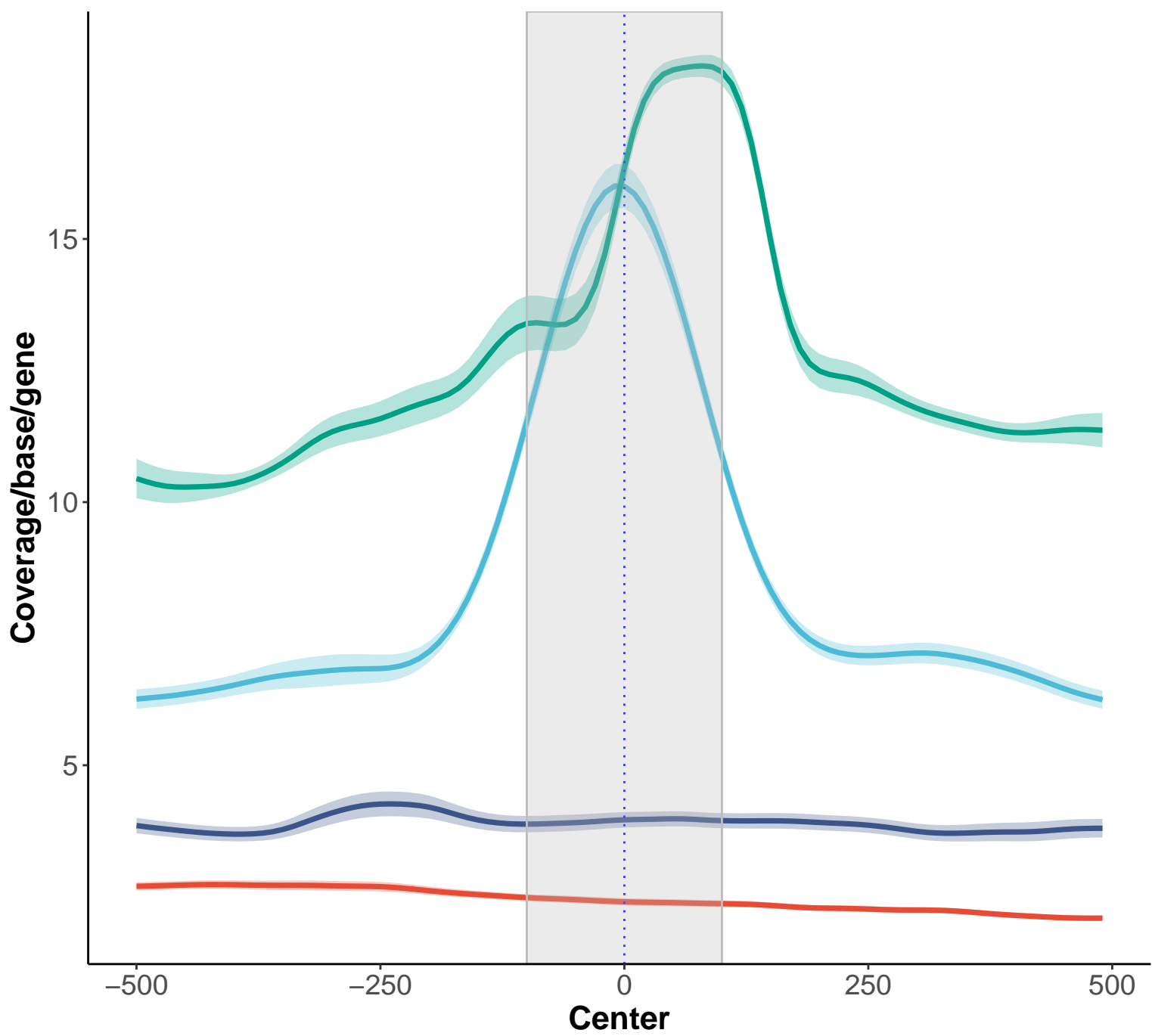


post hoc TukeyHSD test

	diff	lwr	upr	p adj
chip_bam-clip_bam	-13.5	-14.071	-12.928	0

clip_bam:SummitPeak, clip_bam:iCLIPPeak, chip_bam:SummitPeak, chip_bam:iCLIPPeak

chip_bam:iCLIPPeak chip_bam:SummitPeak clip_bam:iCLIPPeak clip_bam:SummitPeak



clip_bam:Summ

clip_bam:iCLIPPe

chip_bam:Summ

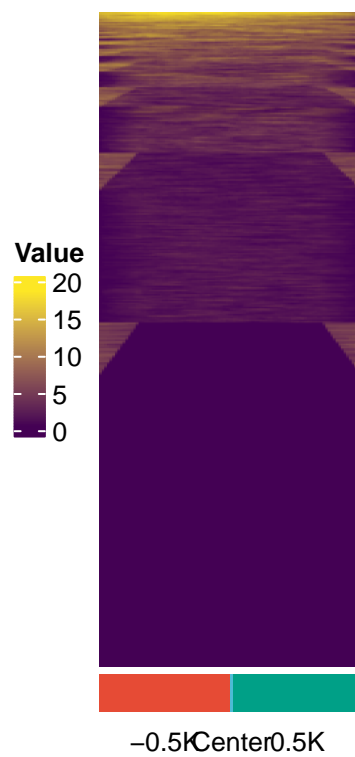
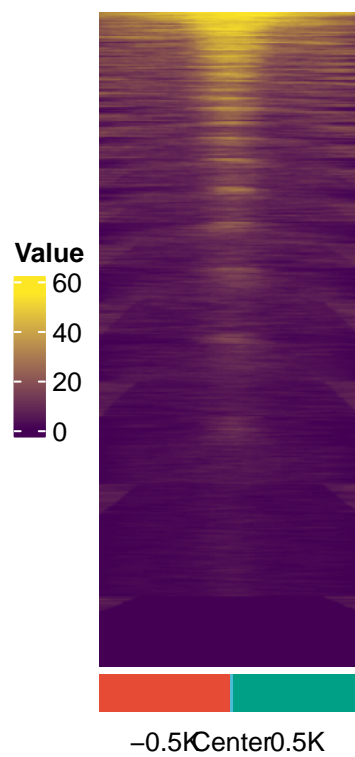
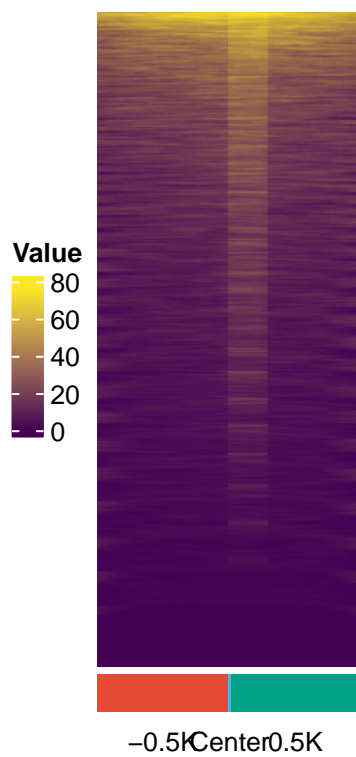
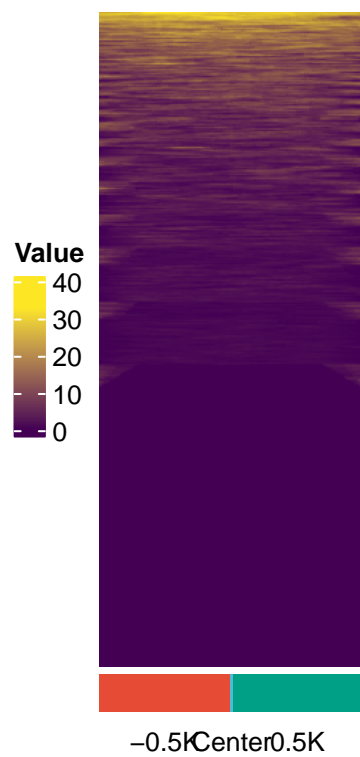
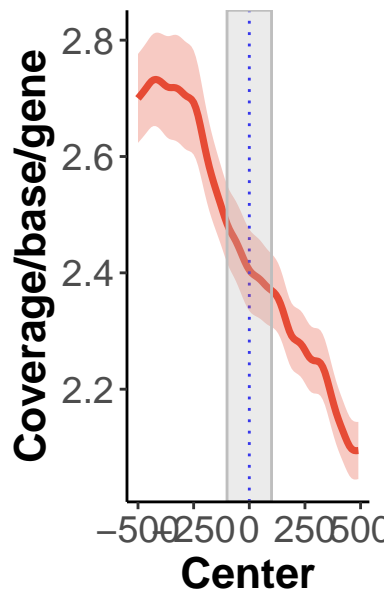
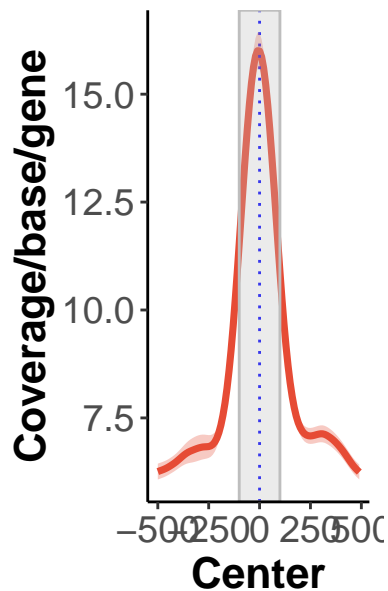
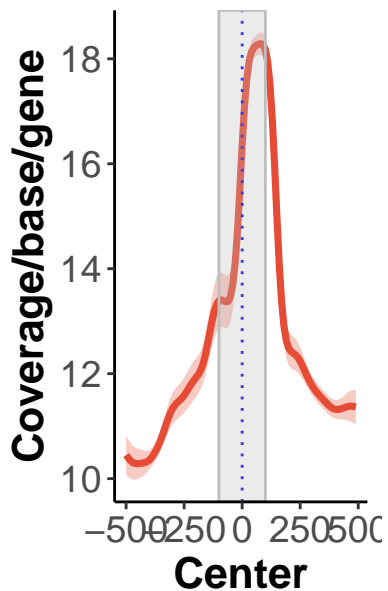
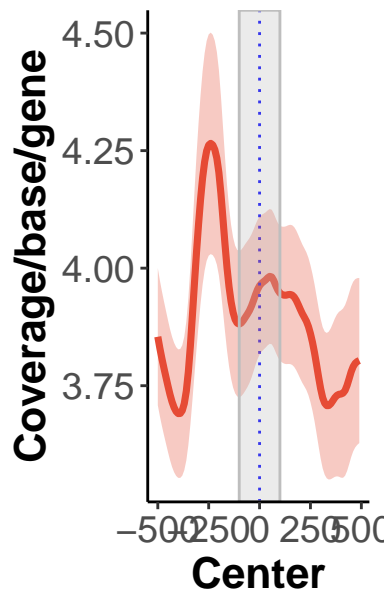
chip_bam:iCLIPPe

clip_bam:SummitPe

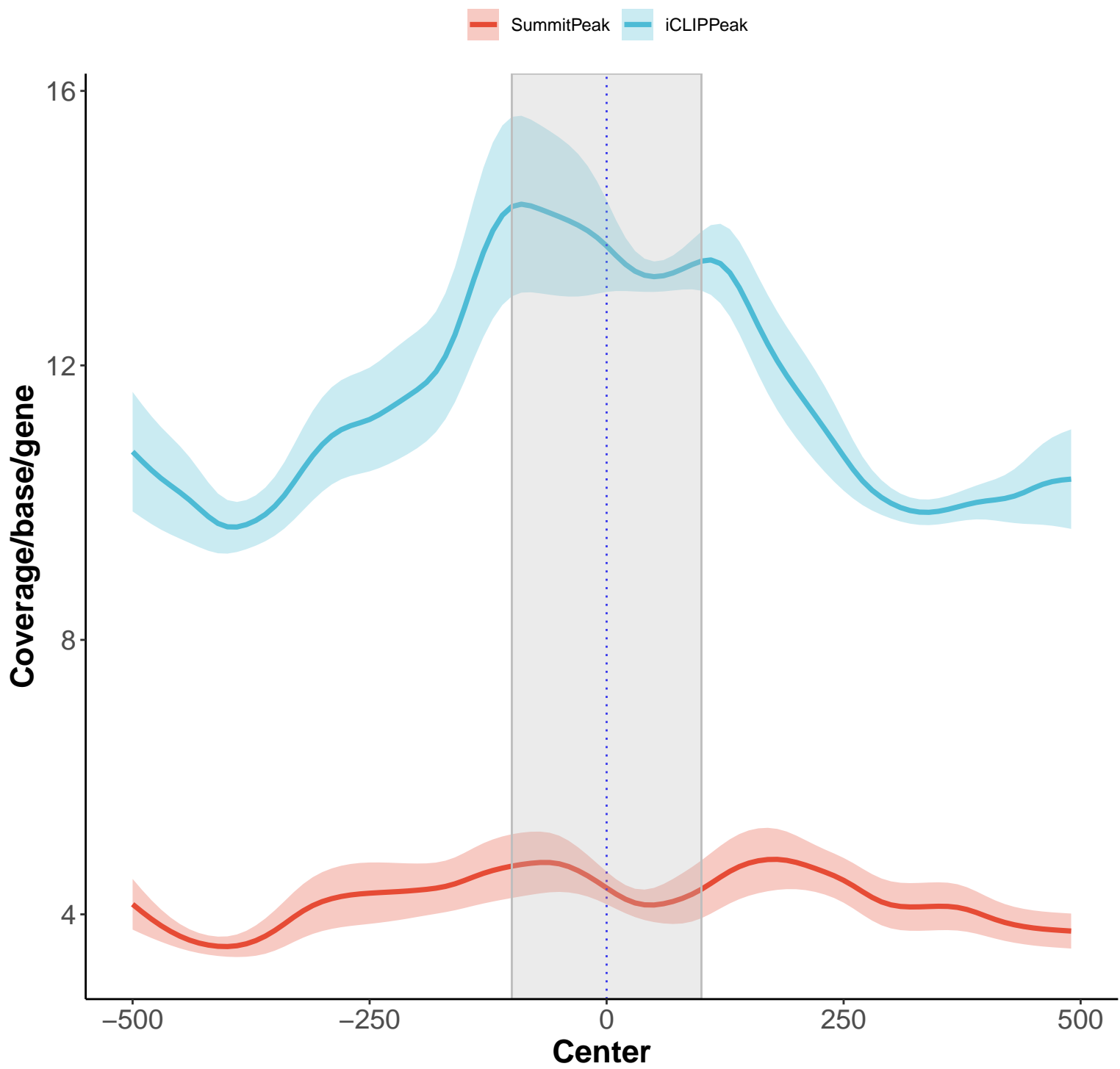
clip_bam:iCLIPPeak

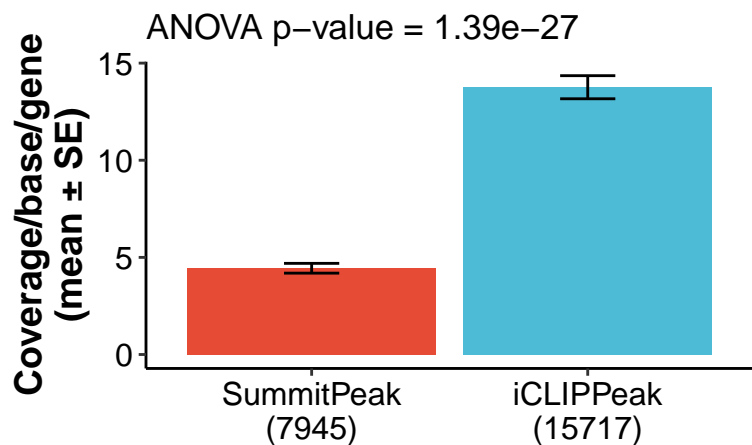
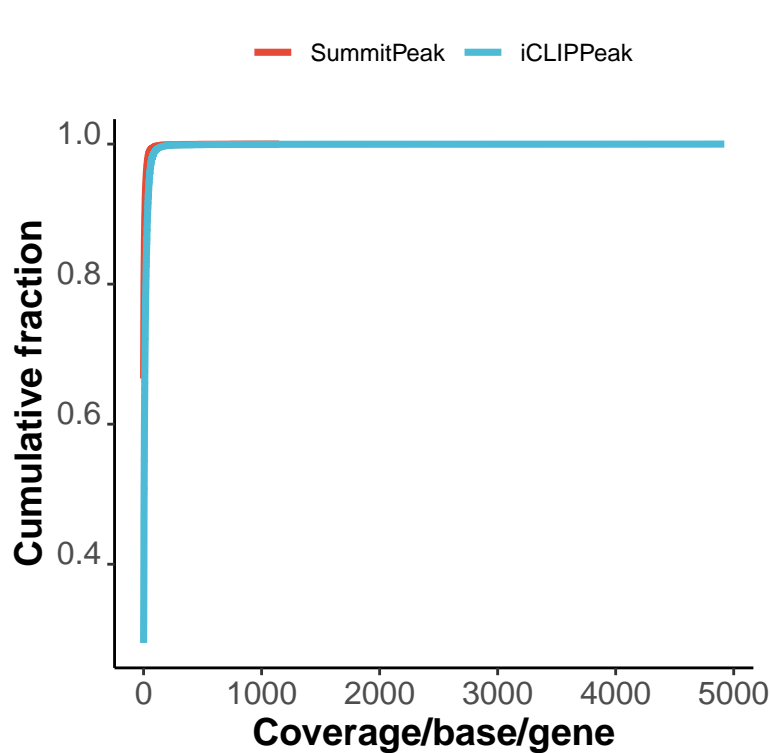
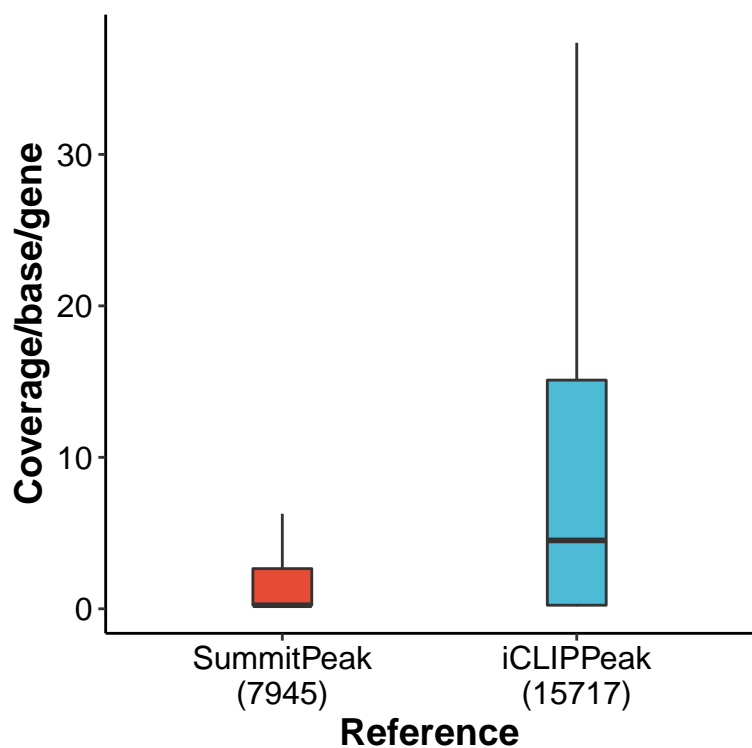
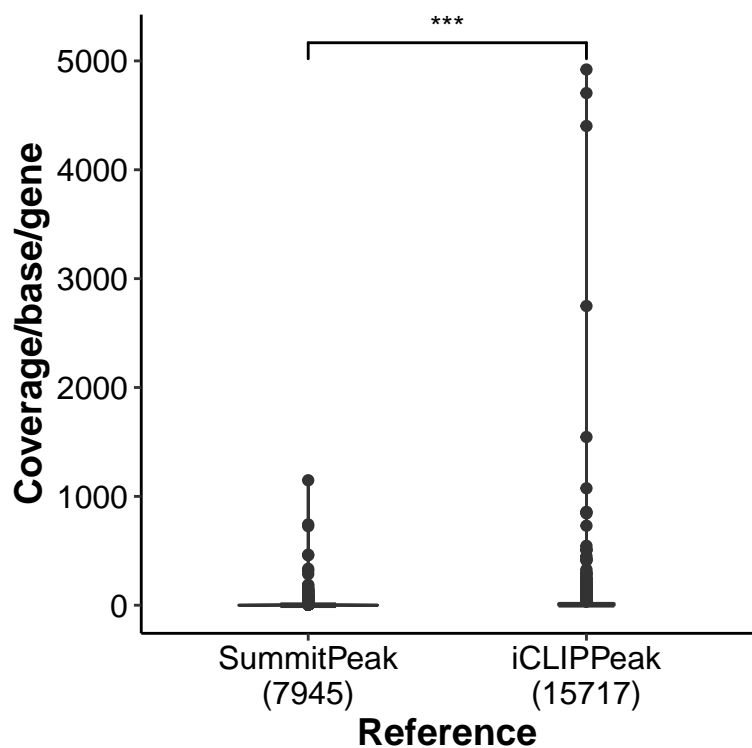
chip_bam:SummitPe

chip_bam:iCLIPPeak



clip_input

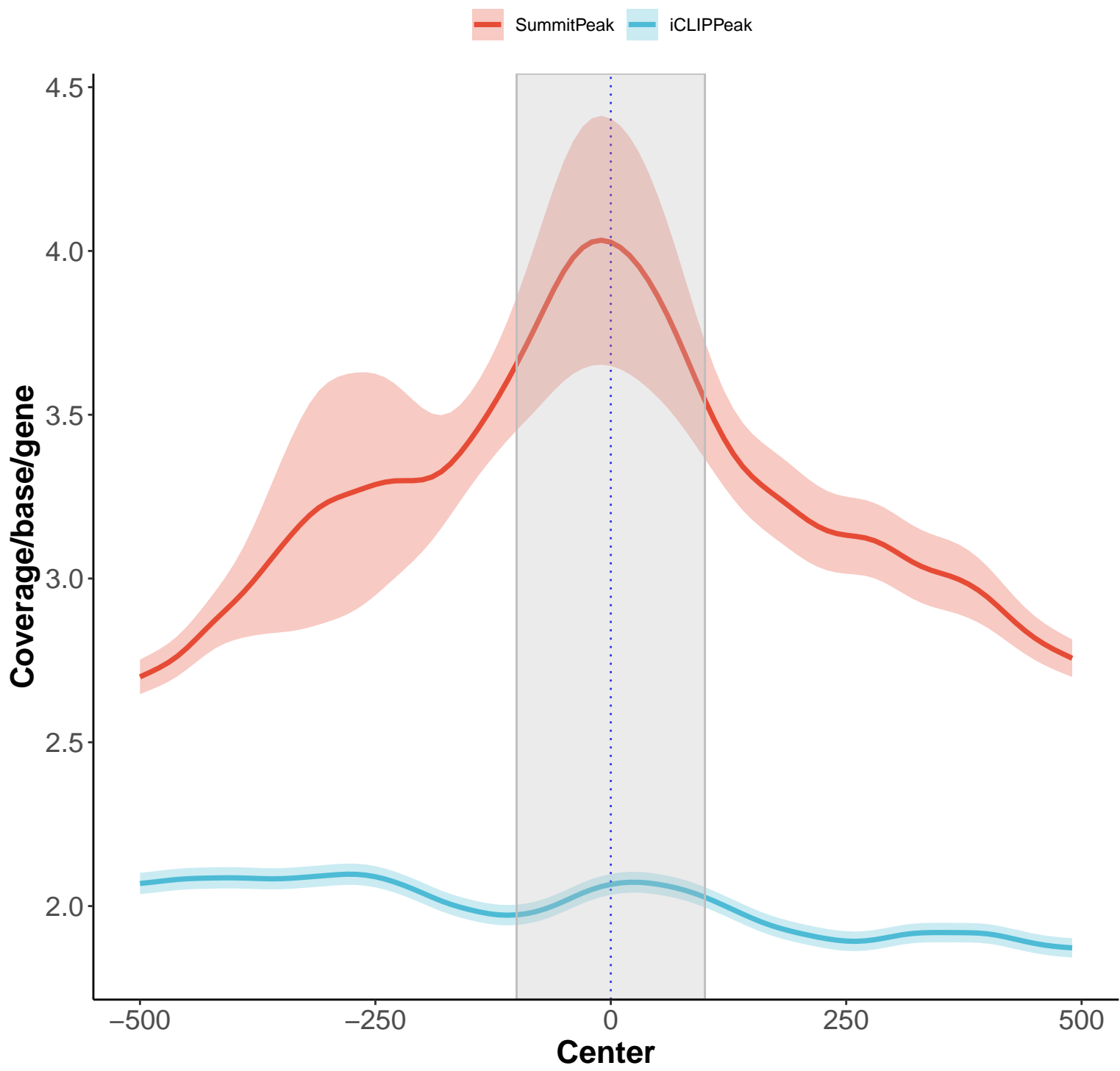


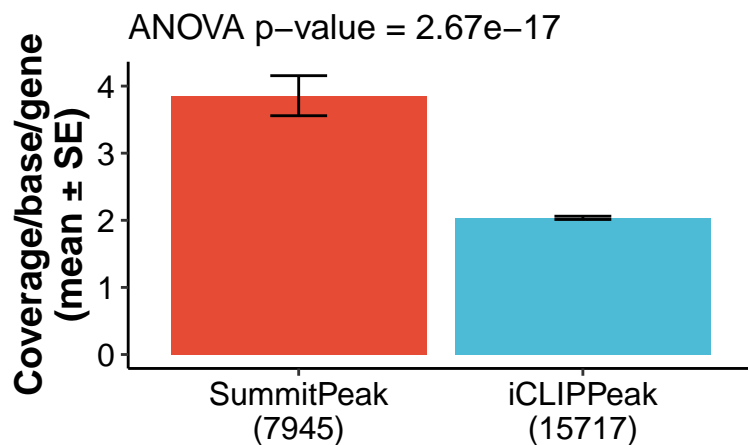
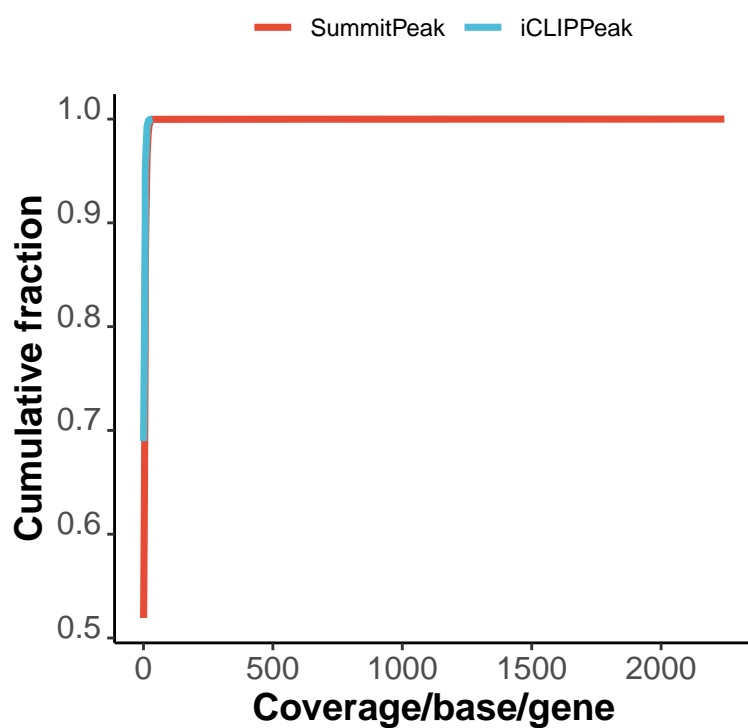
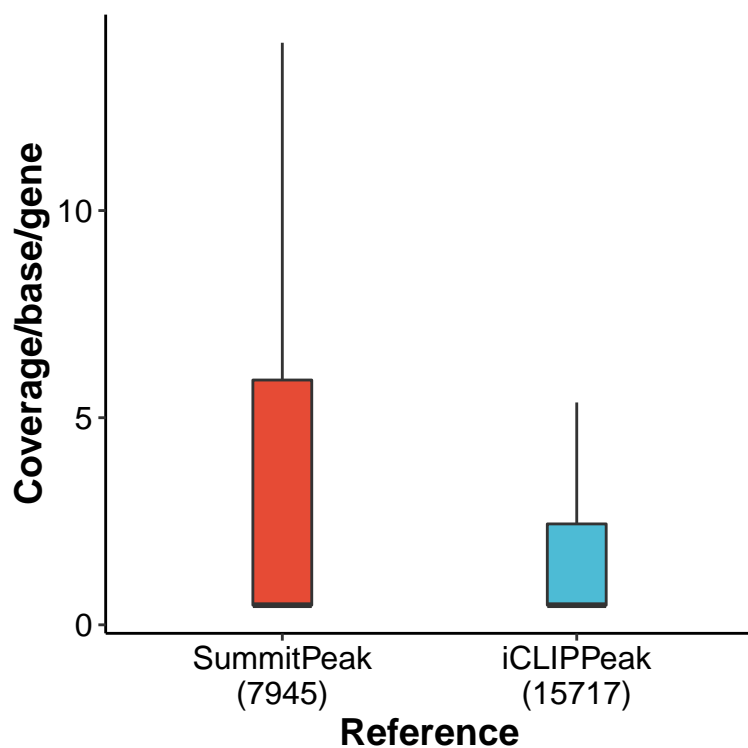
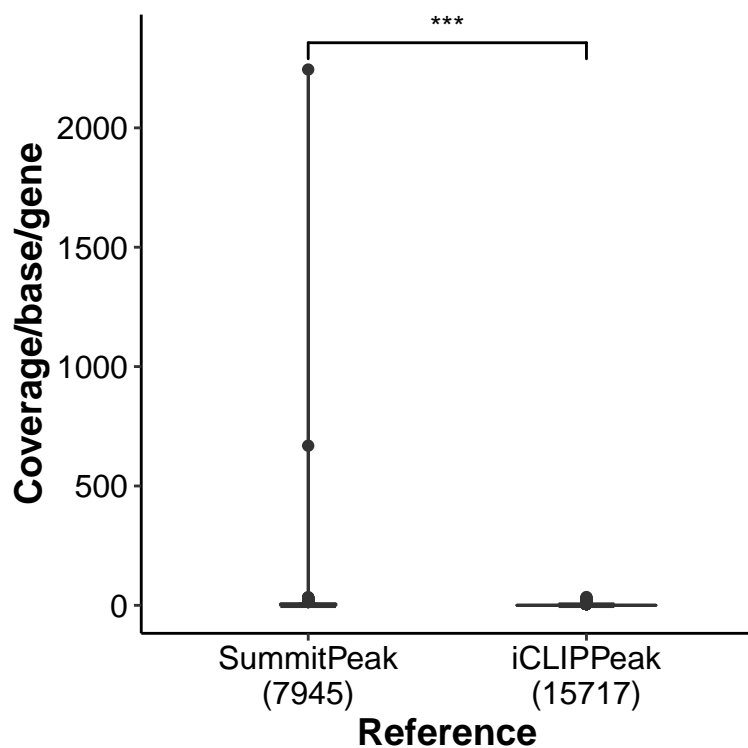


post hoc TukeyHSD test

	diff	lwr	upr	p adj
iCLIPPeak-SummitPeak	9.317	7.641	10.993	0

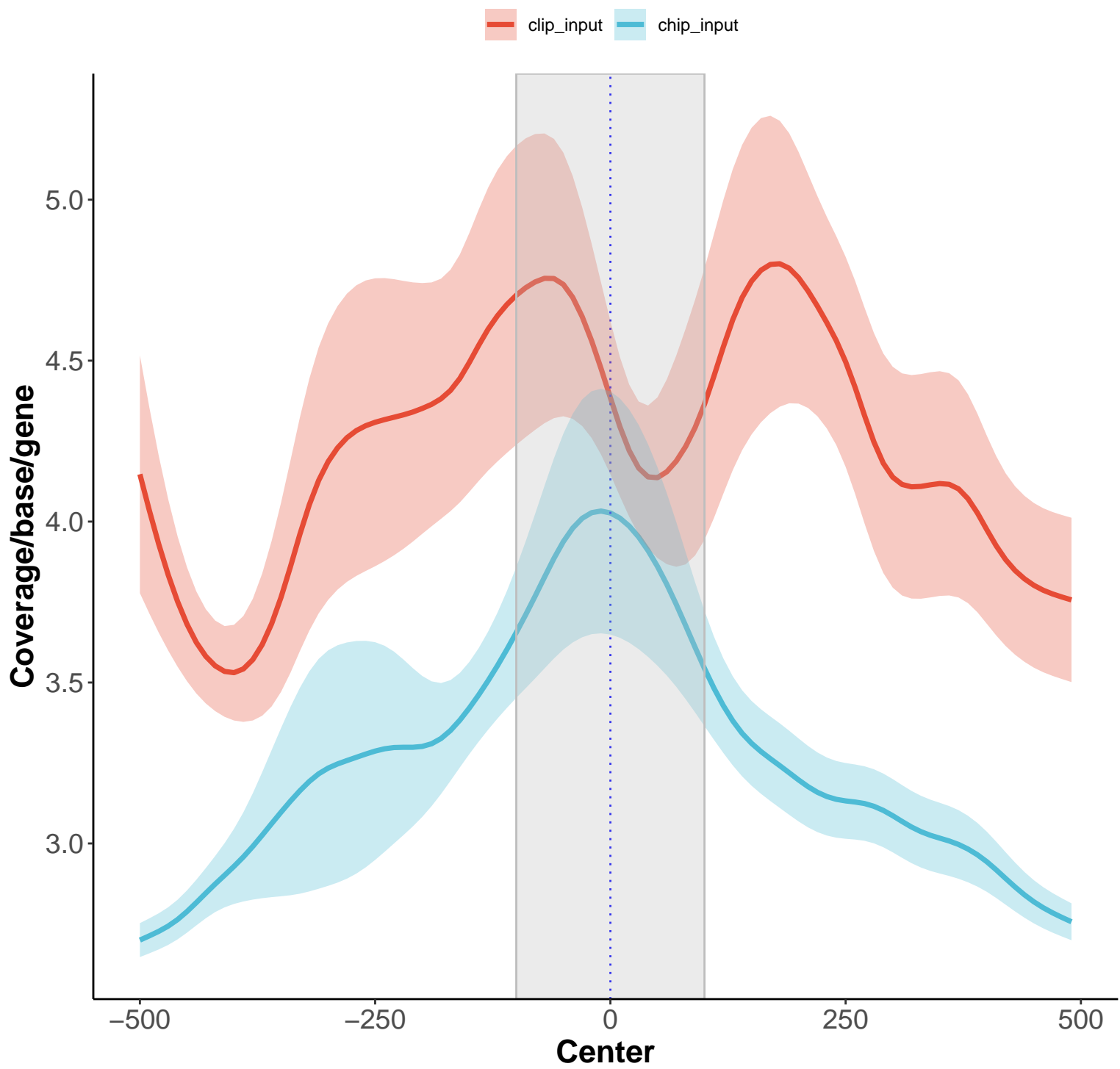
chip_input

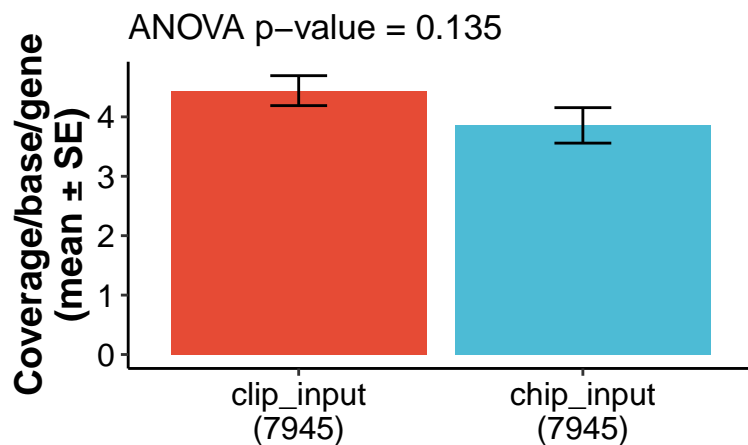
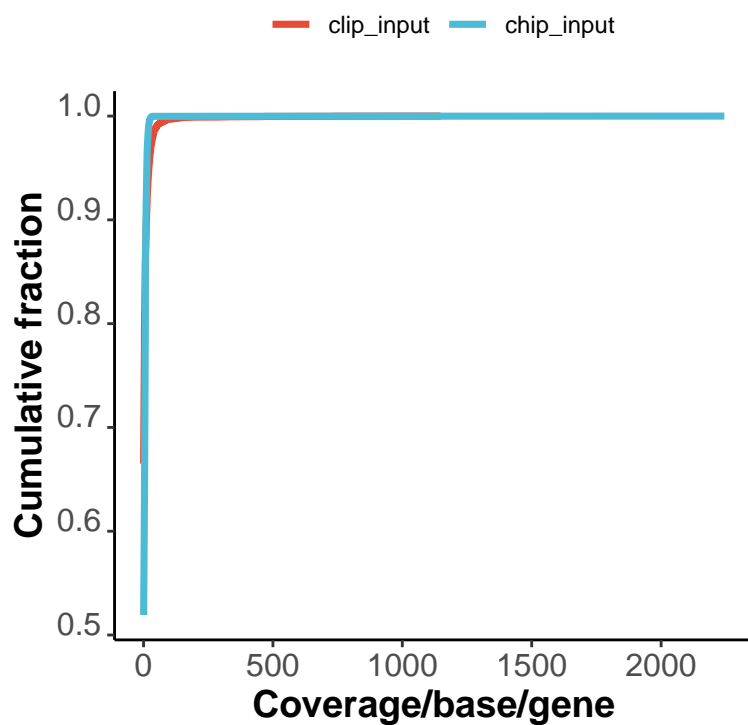
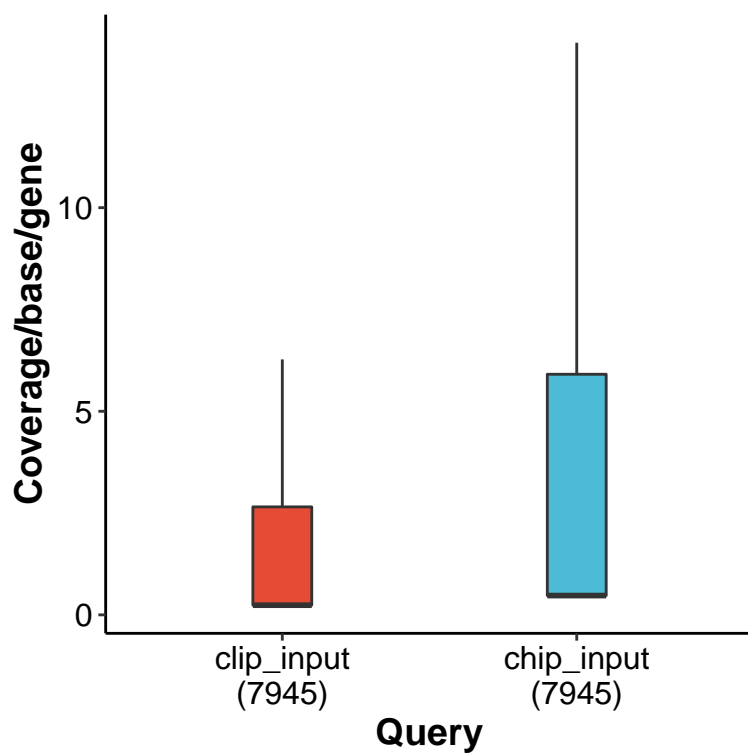
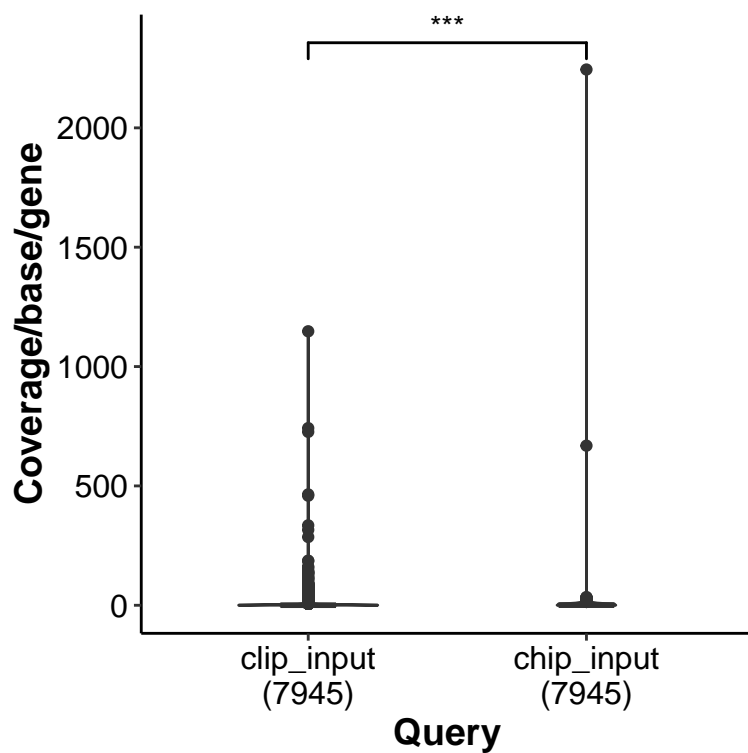




post hoc TukeyHSD test

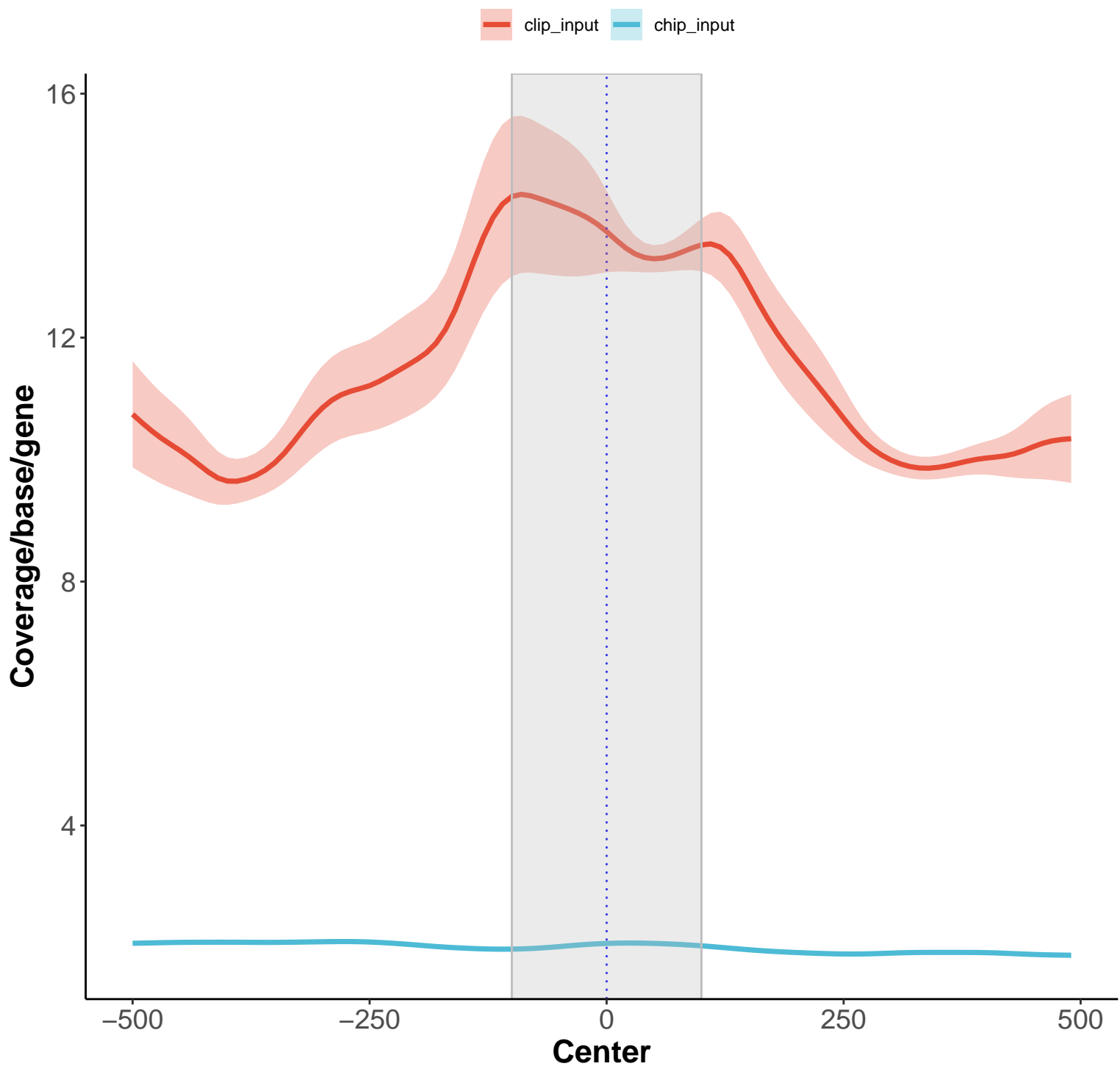
	diff	lwr	upr	p adj
iCLIPPeak-SummitPeak	-1.82	-2.241	-1.398	0

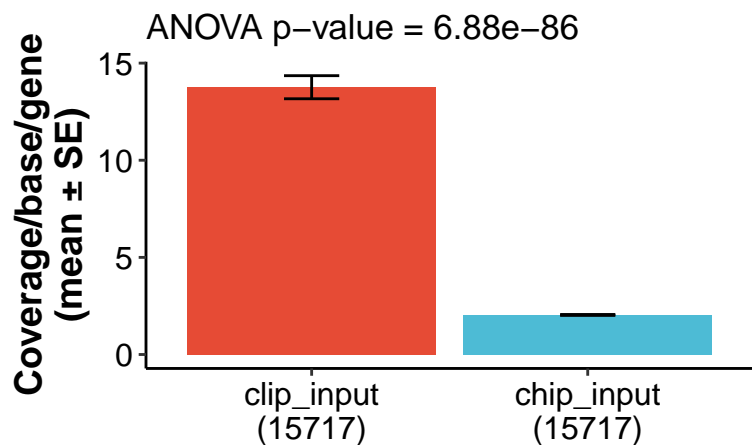
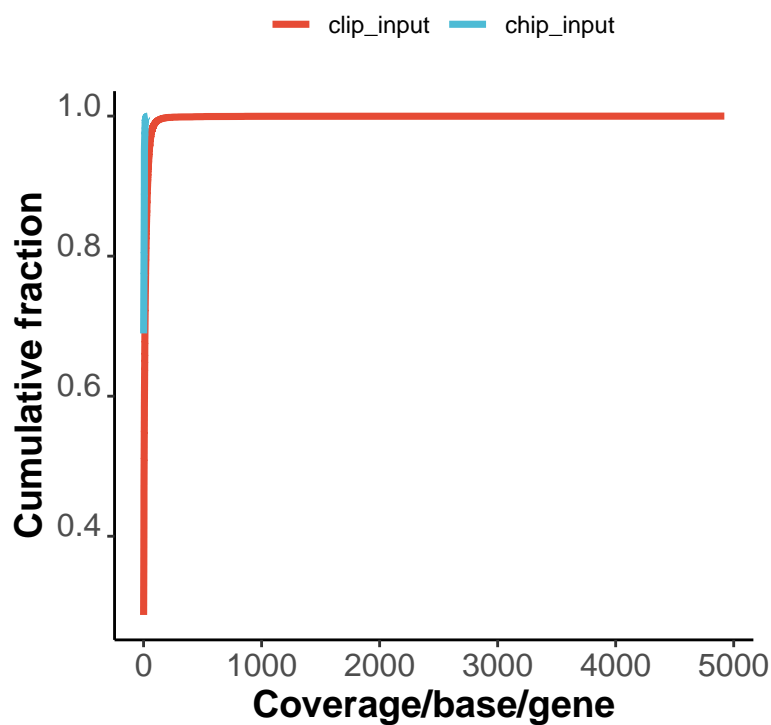
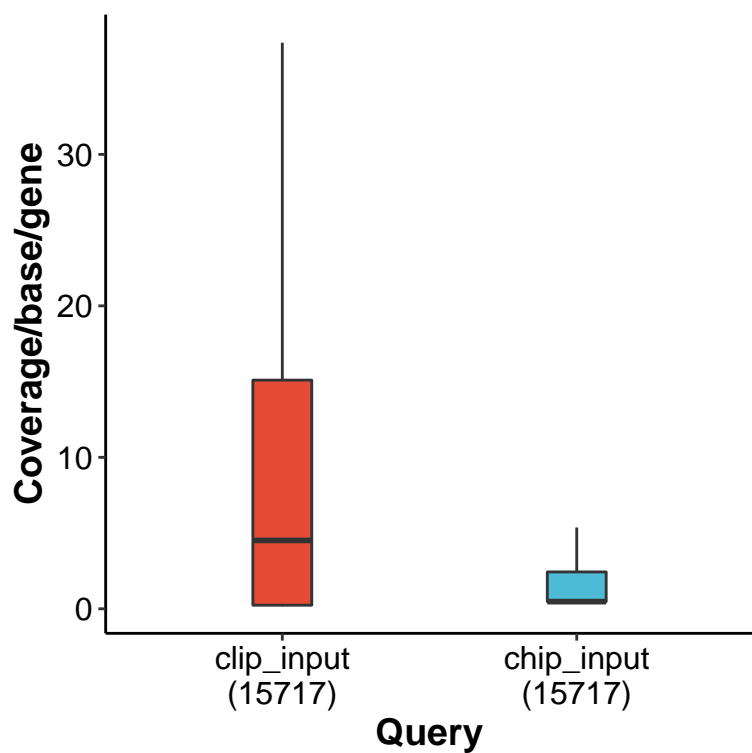
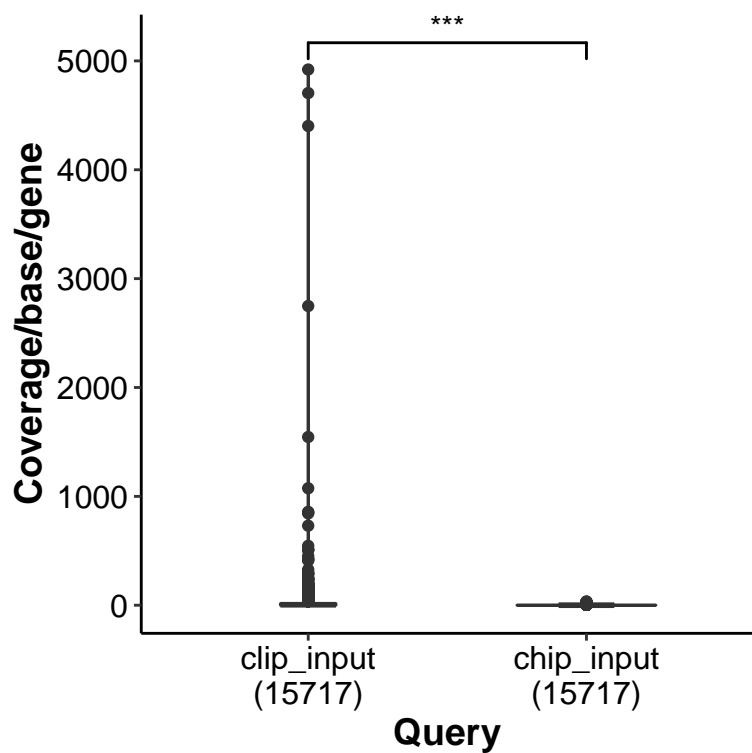




post hoc TukeyHSD test

	diff	lwr	upr	p adj
chip_input-clip_input	-0.584	-1.35	0.181	0.135

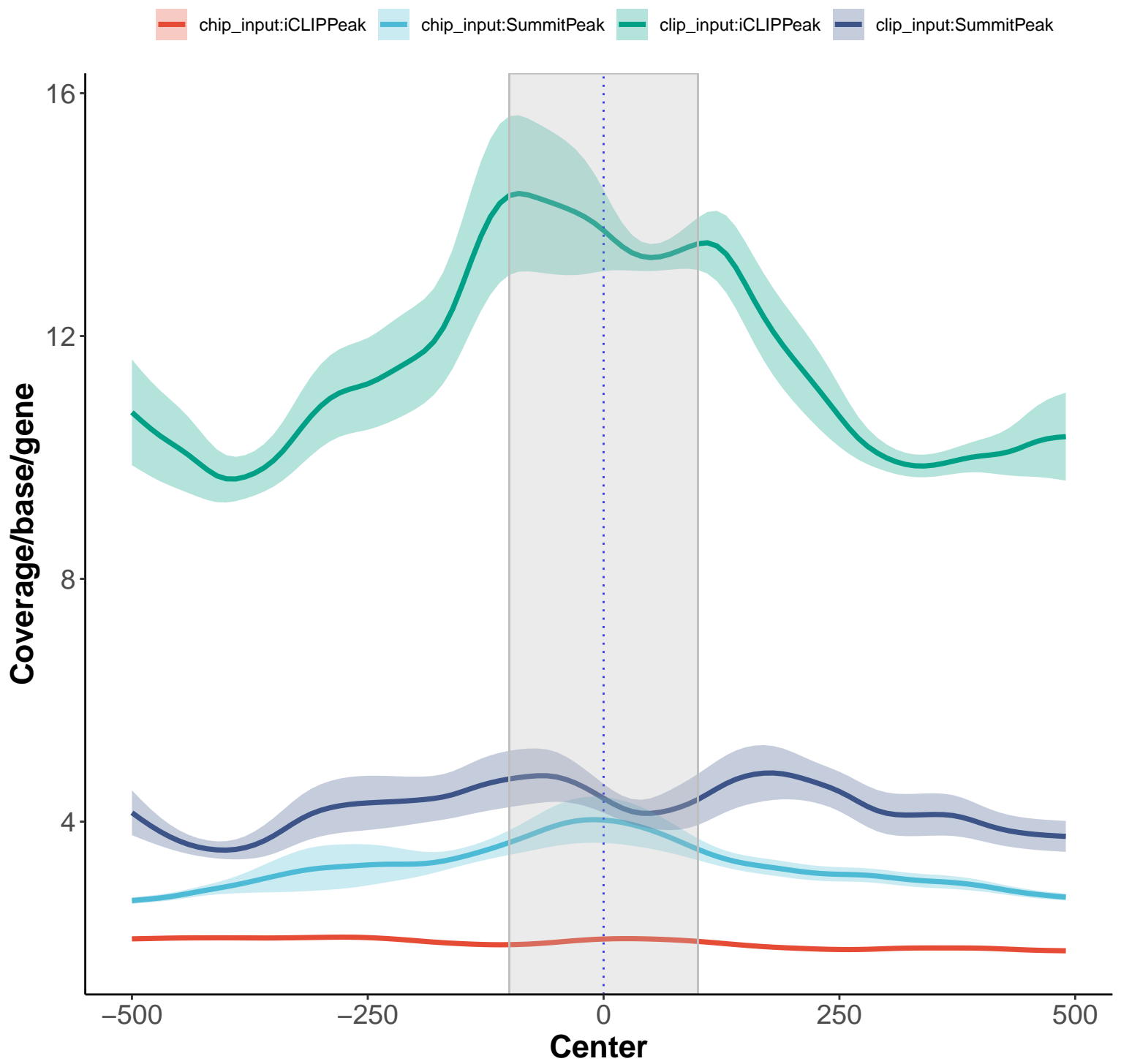




post hoc TukeyHSD test

	diff	lwr	upr	p adj
chip_input-clip_input	-11.722	-12.888	-10.556	0

clip_input:SummitPeak, clip_input:iCLIPPeak, chip_input:SummitPeak, chip_input:iCLIPPeak



clip_input:Summ

clip_input:iCLIPPea

chip_input:Summ

chip_input:iCLIPPea

clip_input:SummitPe

clip_input:iCLIPPea

chip_input:SummitPe

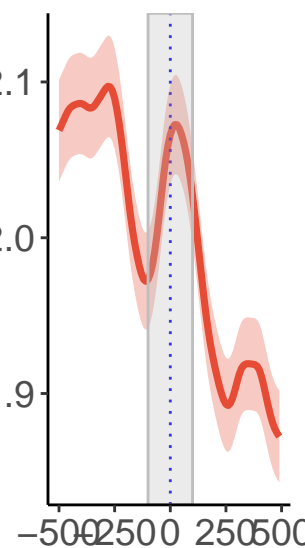
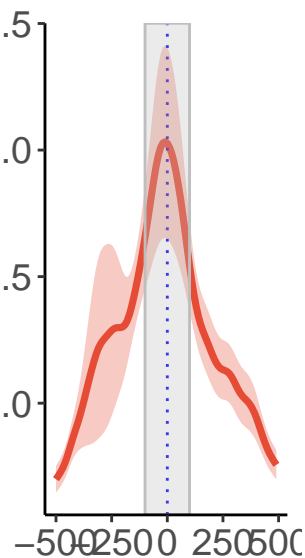
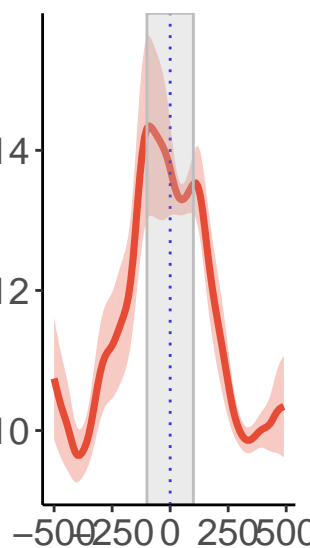
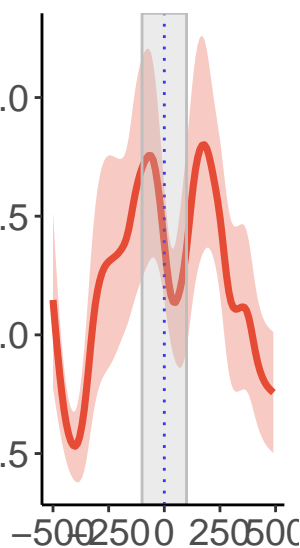
chip_input:iCLIPPea

Coverage/base/gene

Coverage/base/gene

Coverage/base/gene

Coverage/base/gene

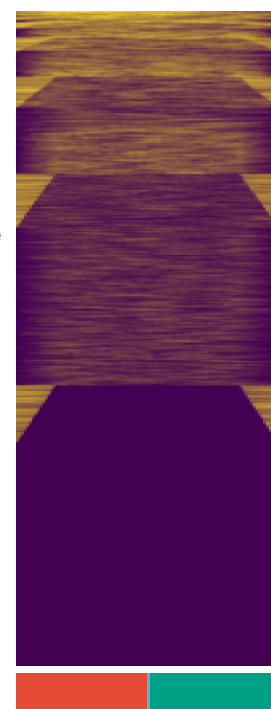
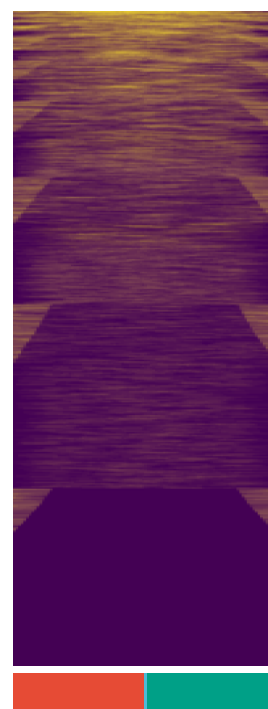
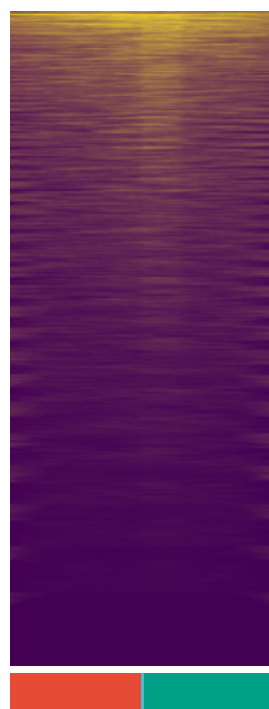
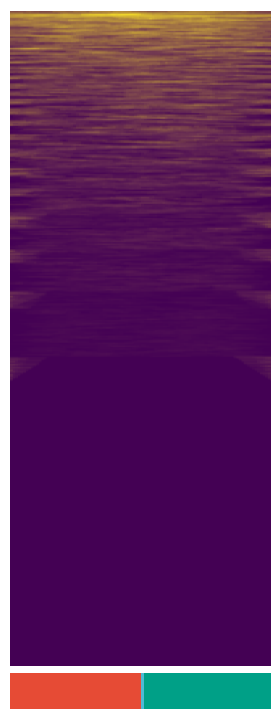


Center

Center

Center

Center

Value
40
30
20
10
0Value
80
60
40
20
0Value
20
15
10
5
0Value
10
8
6
4
2
0

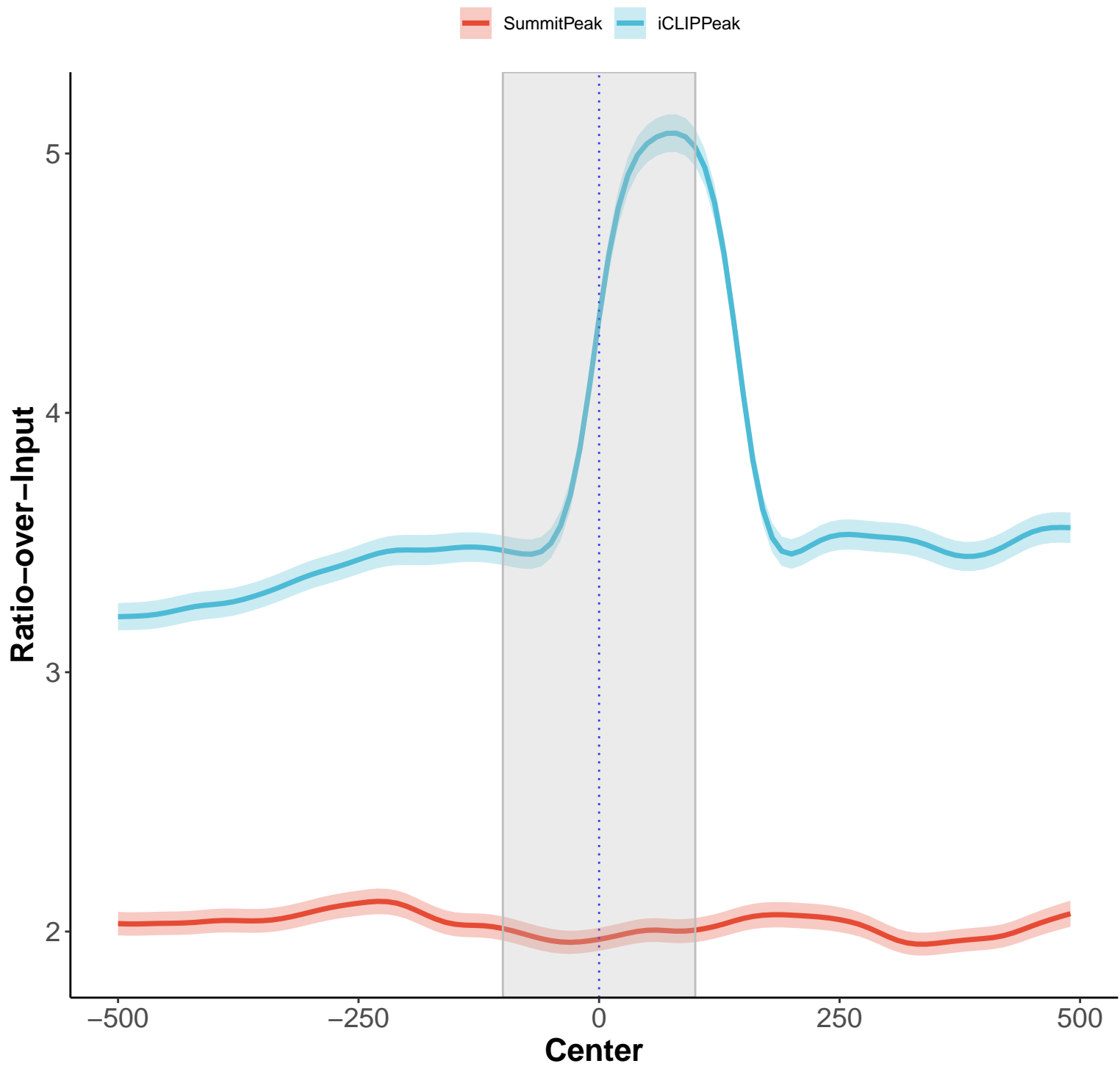
-0.5KCenter0.5K

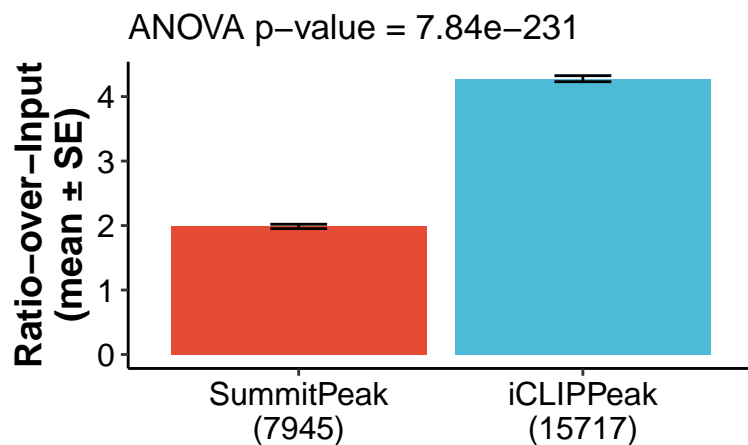
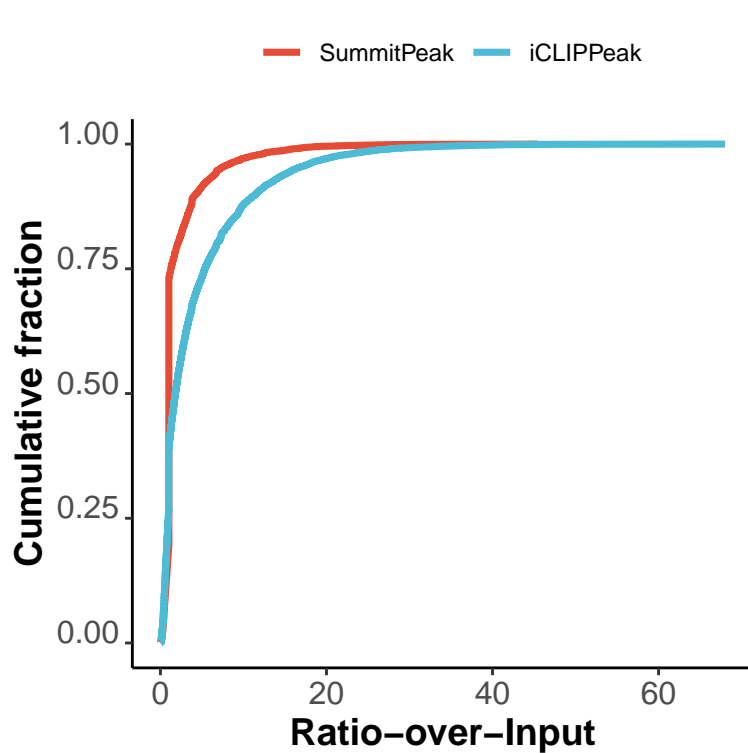
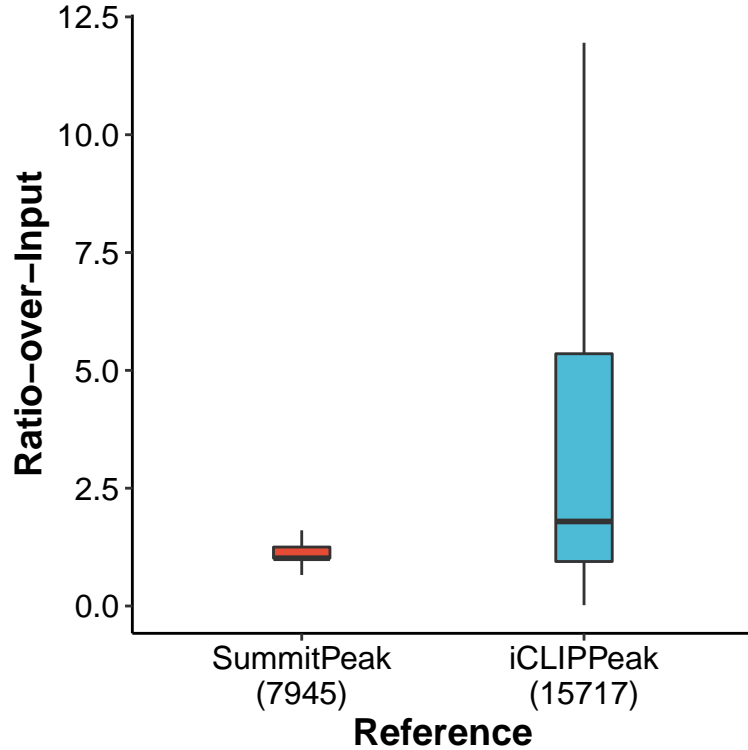
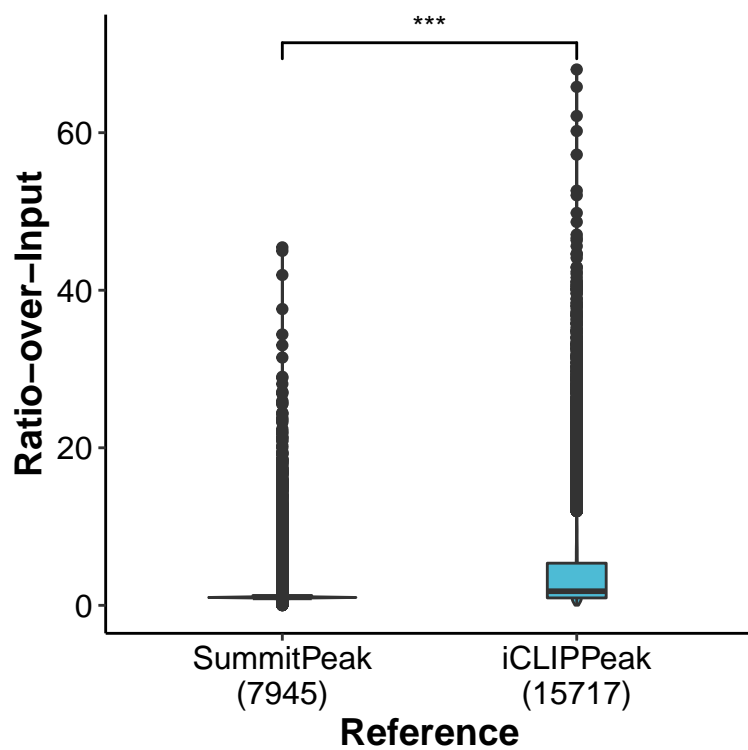
-0.5KCenter0.5K

-0.5KCenter0.5K

-0.5KCenter0.5K

clip_bam

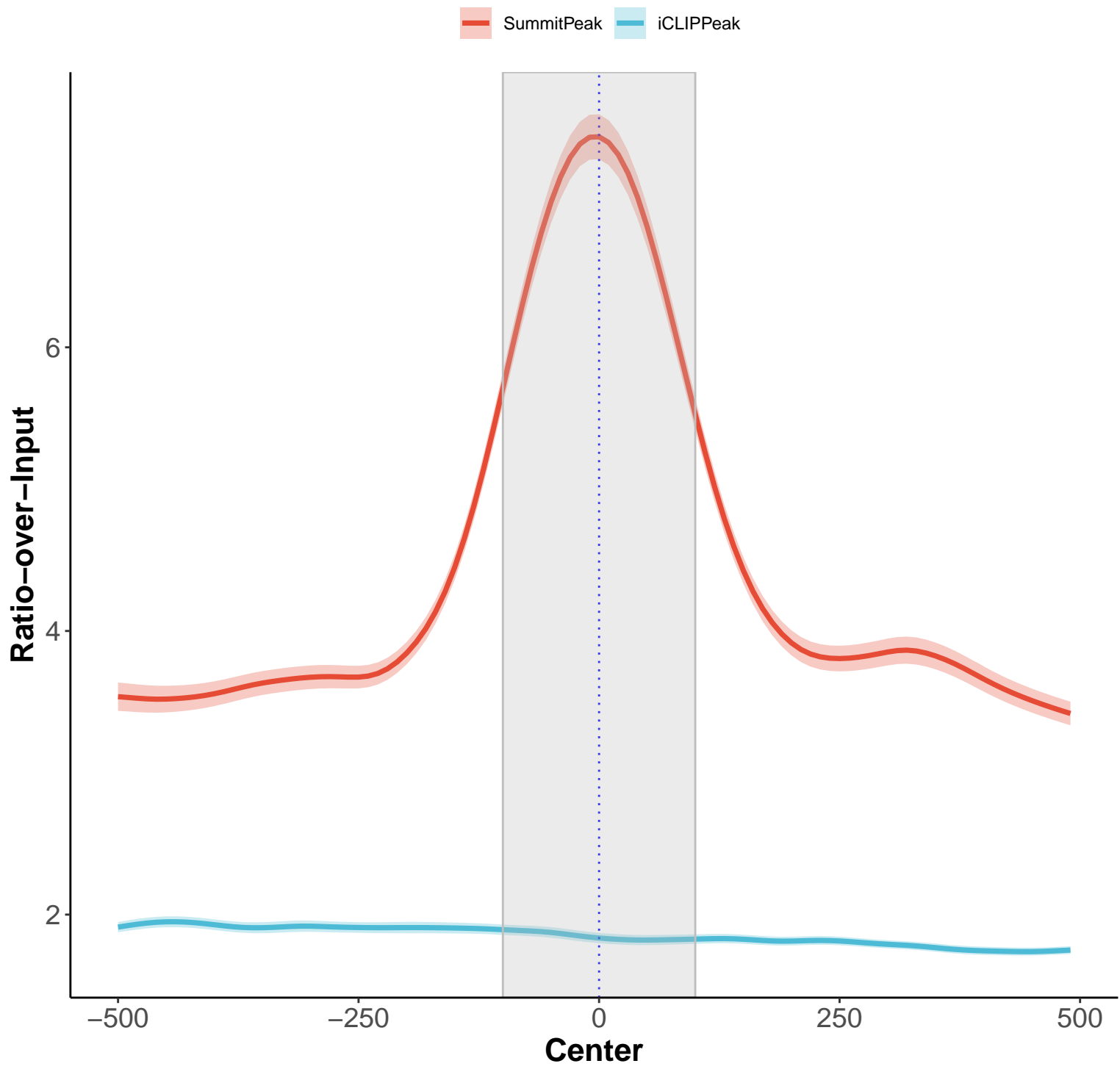


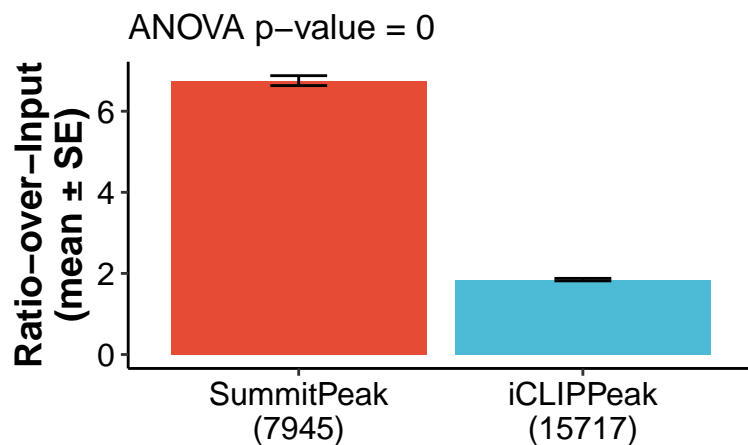
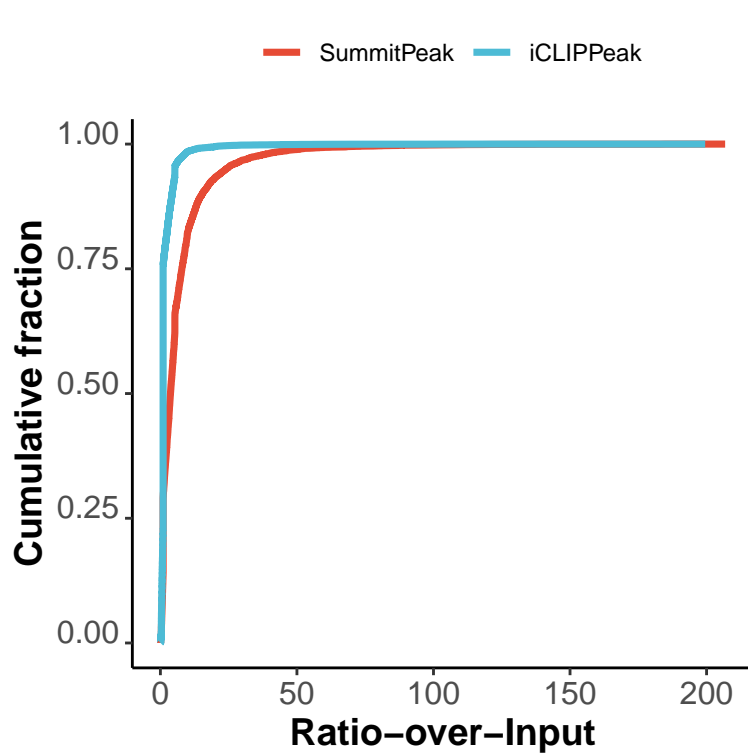
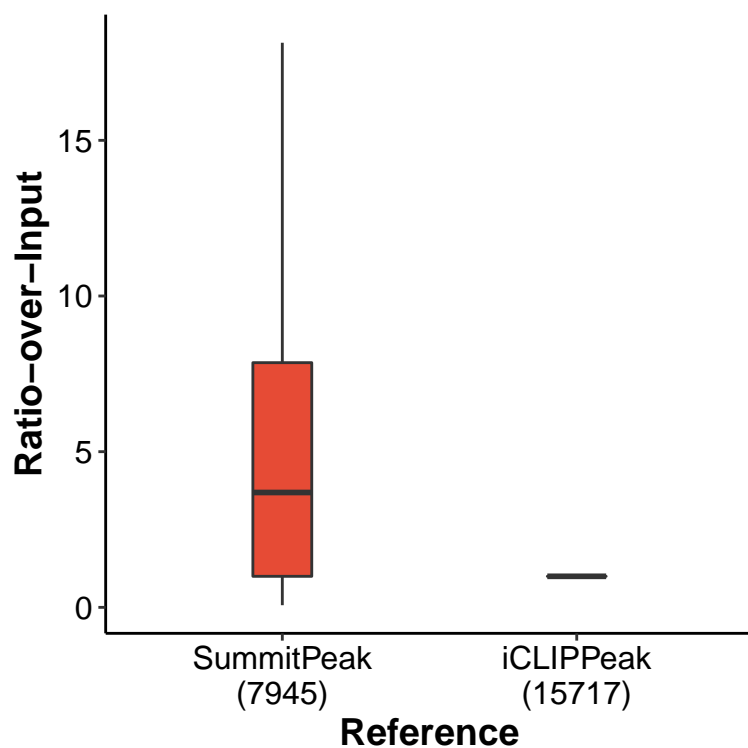
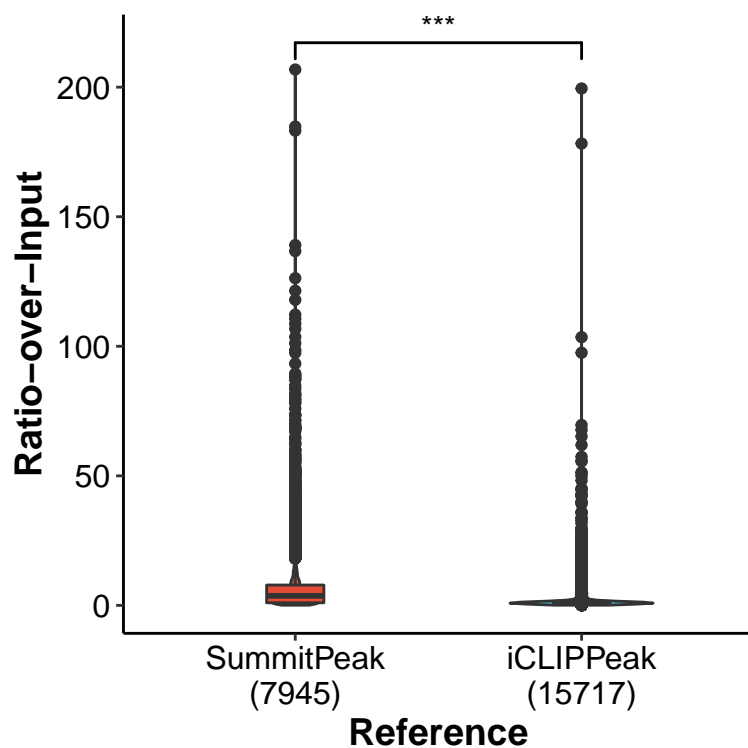


post hoc TukeyHSD test

	diff	lwr	upr	p adj
iCLIPPeak-SummitPeak	2.291	2.155	2.428	0

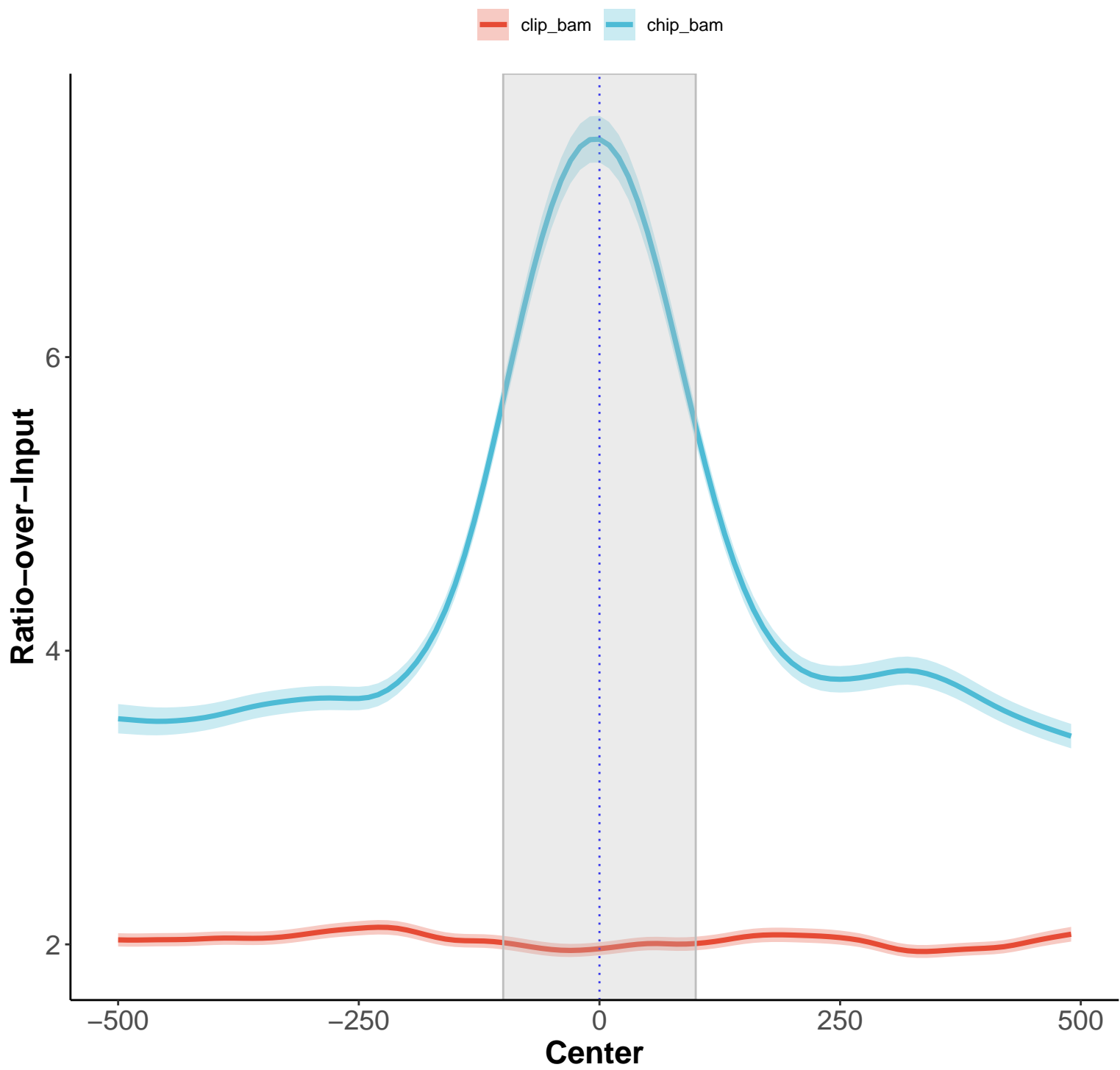
chip_bam

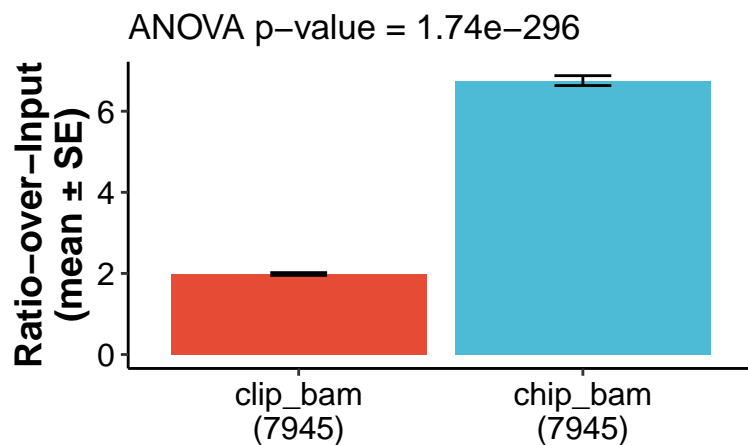
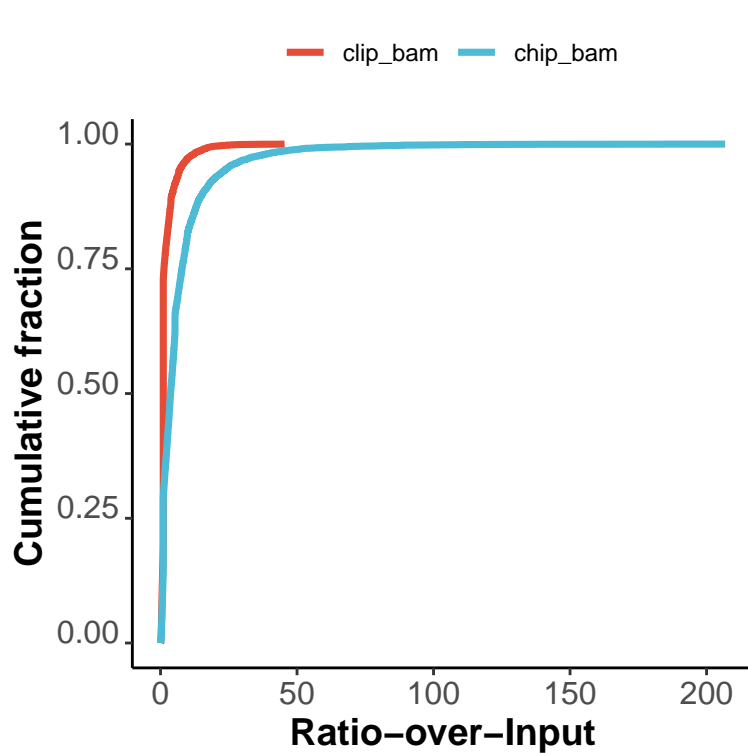
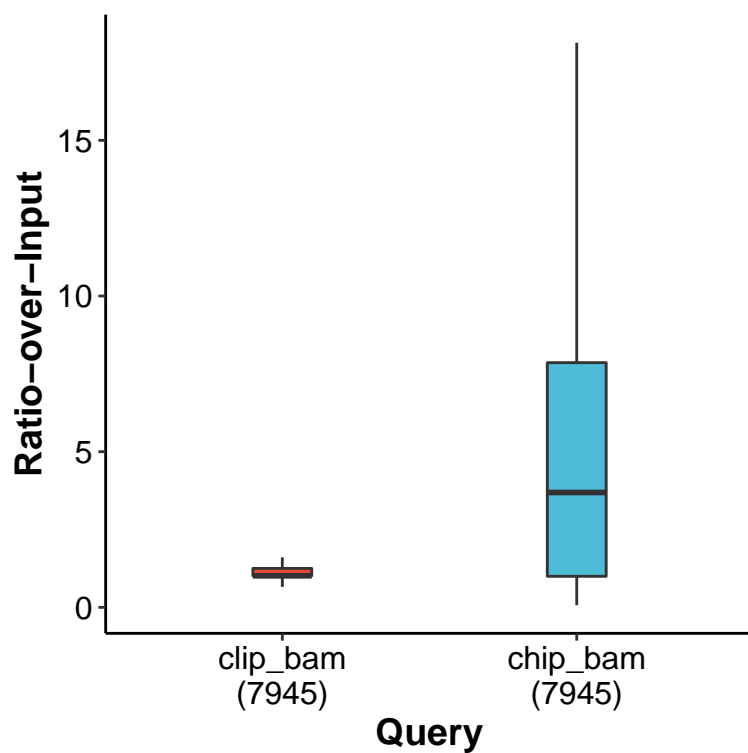
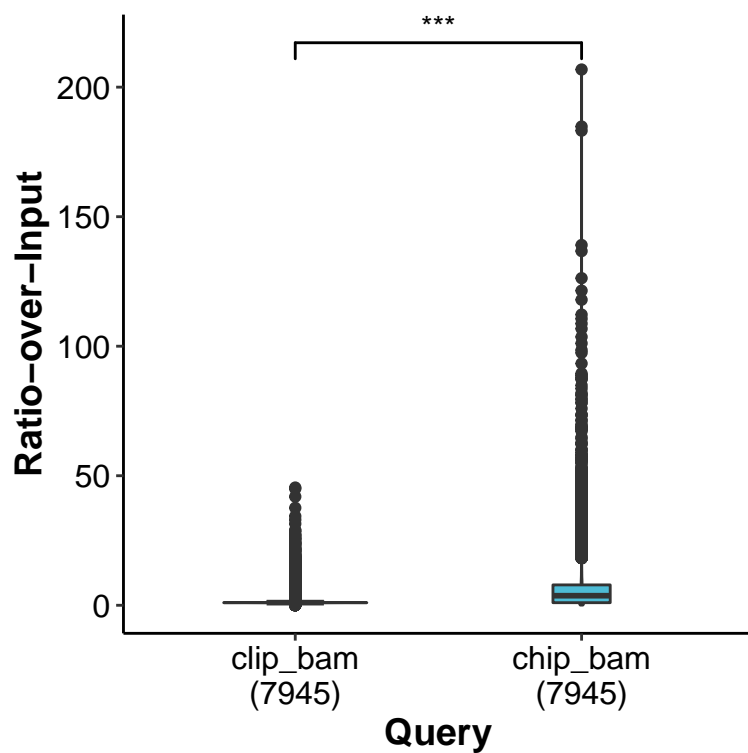




post hoc TukeyHSD test

	diff	lwr	upr	p adj
iCLIPPeak-SummitPeak	-4.908	-5.098	-4.717	0

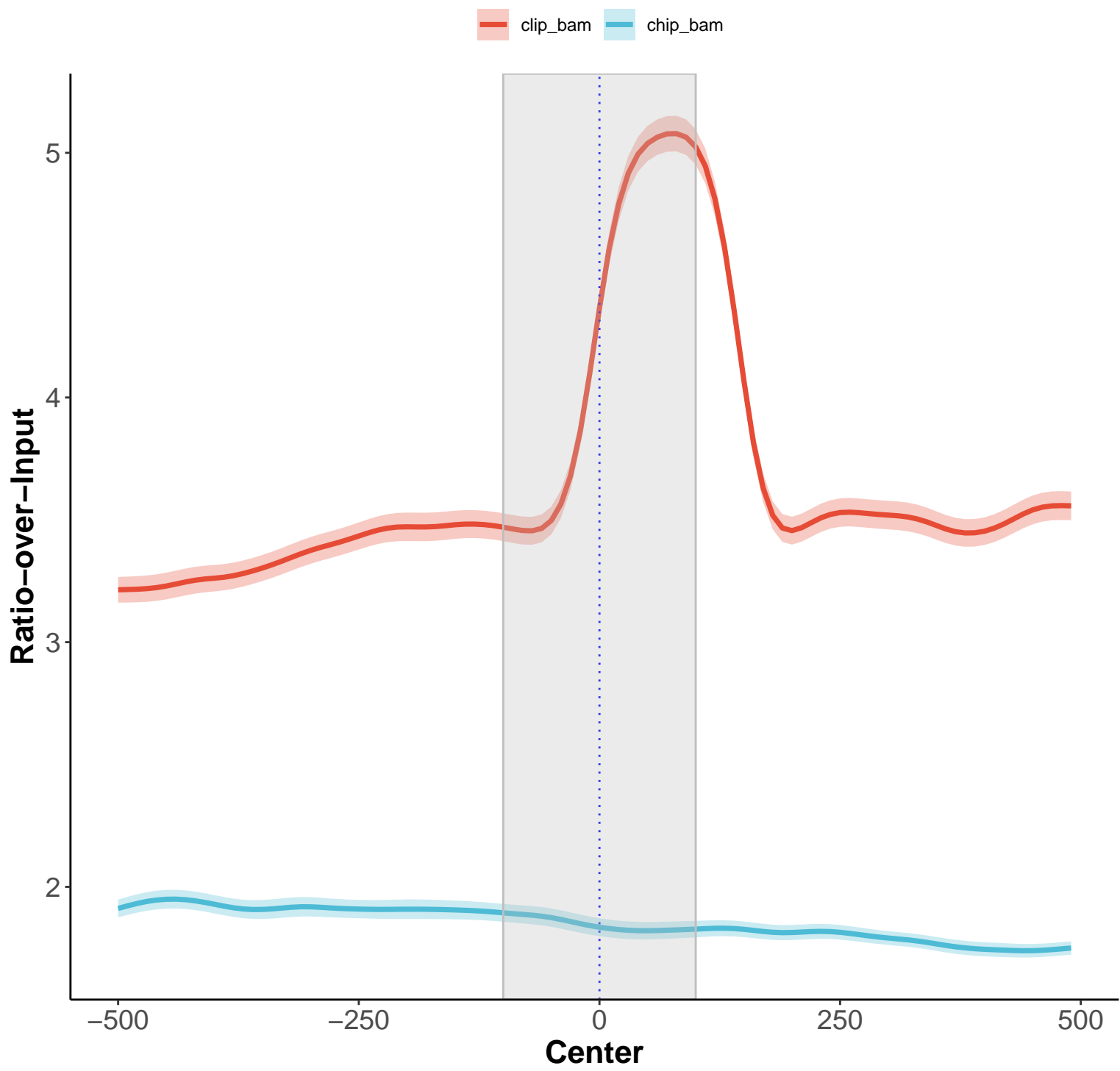


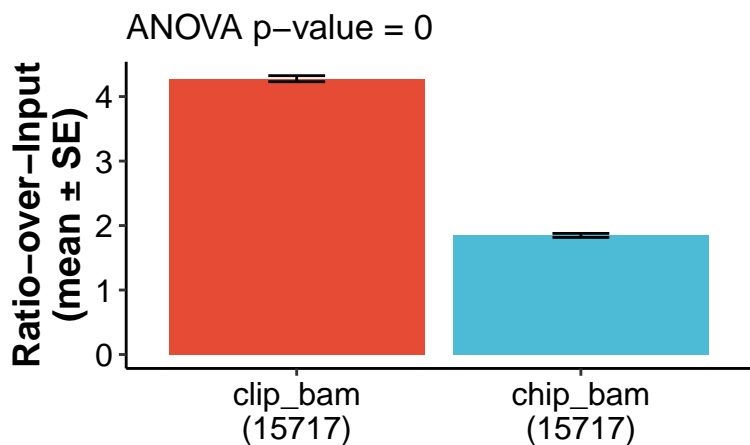
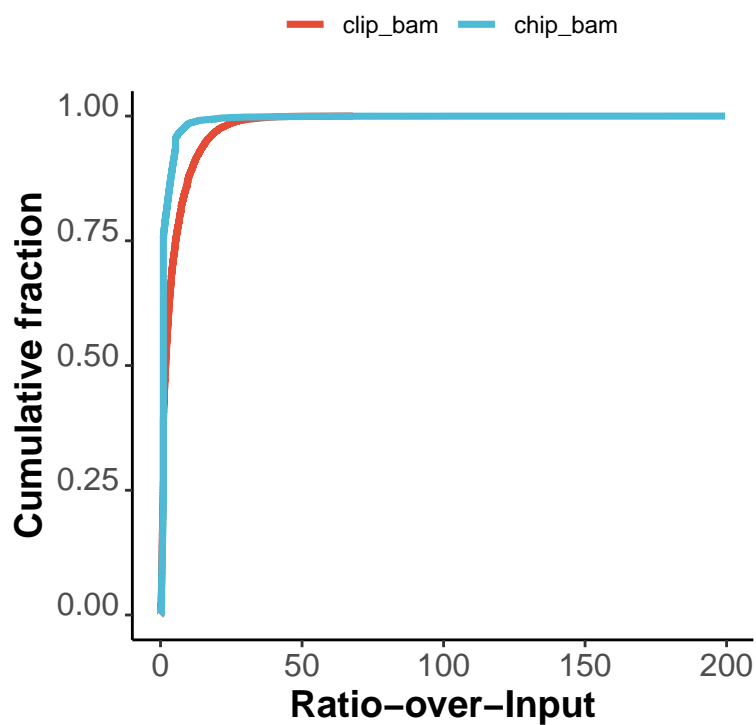
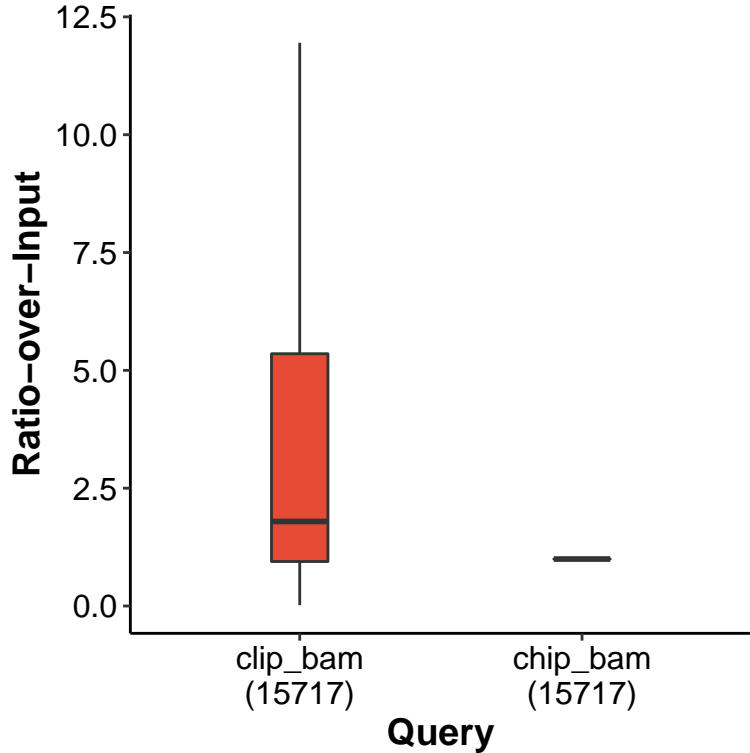
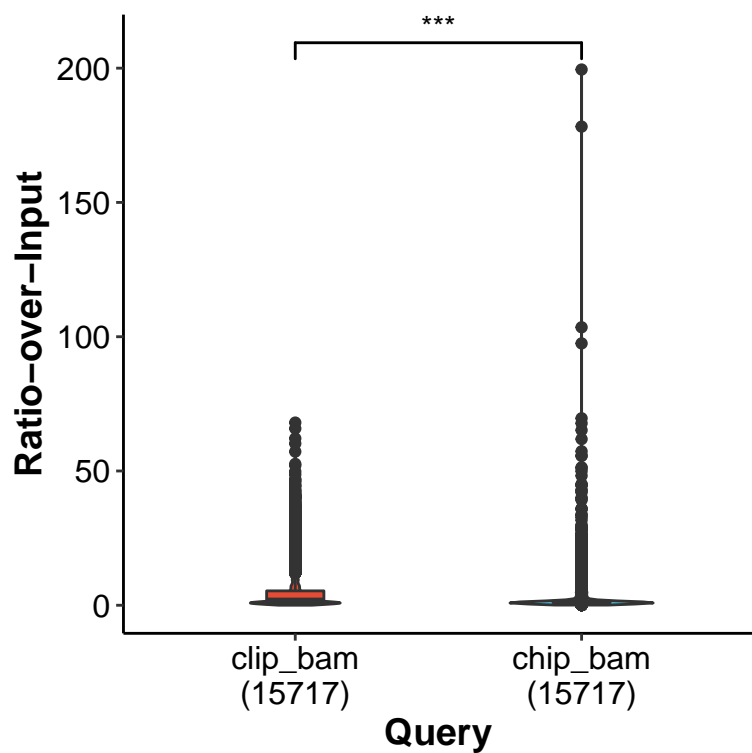


ANOVA p-value = $1.74\text{e-}296$

post hoc TukeyHSD test

	diff	lwr	upr	p adj
chip_bam-clip_bam	4.769	4.52	5.017	$2.04\text{e-}08$



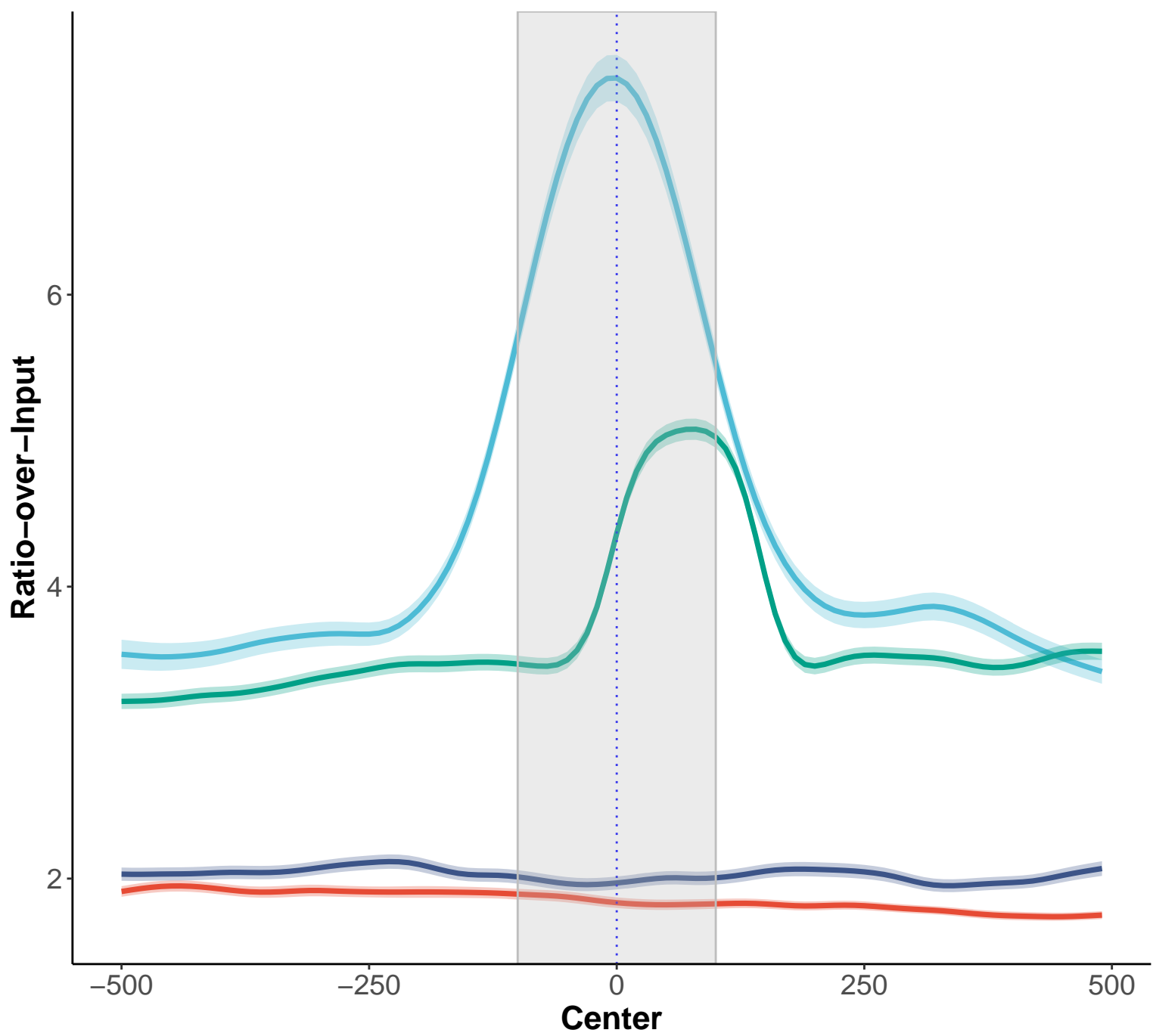


post hoc TukeyHSD test

	diff	lwr	upr	p adj
chip_bam-clip_bam	-2.43	-2.54	-2.321	0

clip_bam:SummitPeak, clip_bam:iCLIPPeak, chip_bam:SummitPeak, chip_bam:iCLIPPeak

chip_bam:iCLIPPeak chip_bam:SummitPeak clip_bam:iCLIPPeak clip_bam:SummitPeak



clip_bam:Summit

clip_bam:iCLIP

chip_bam:Summit

chip_bam:iCLIP

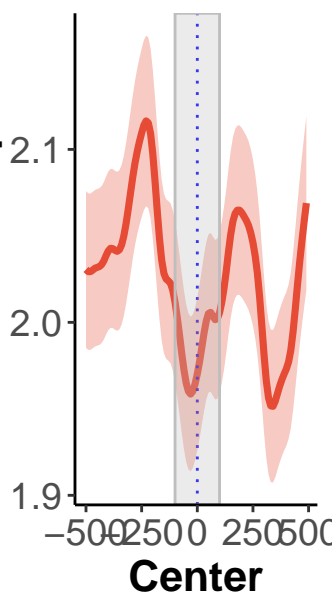
clip_bam:SummitPe

clip_bam:iCLIPPe

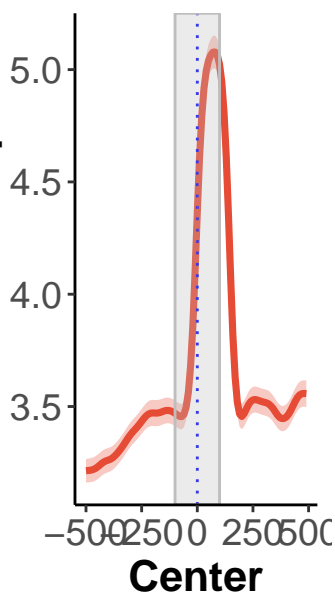
chip_bam:SummitPe

chip_bam:iCLIPPe

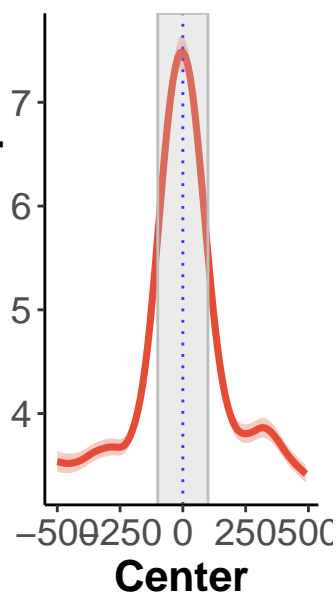
Ratio-over-Input



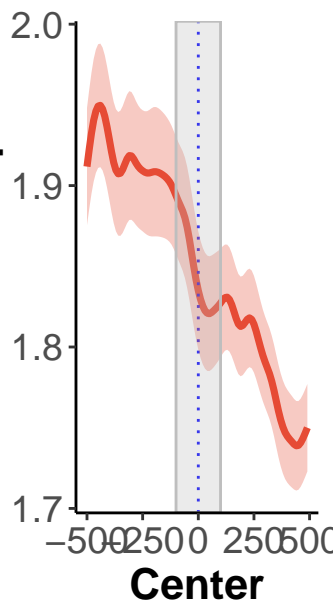
Ratio-over-Input



Ratio-over-Input



Ratio-over-Input

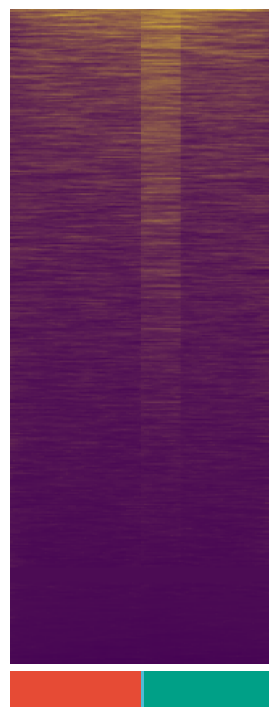


Value



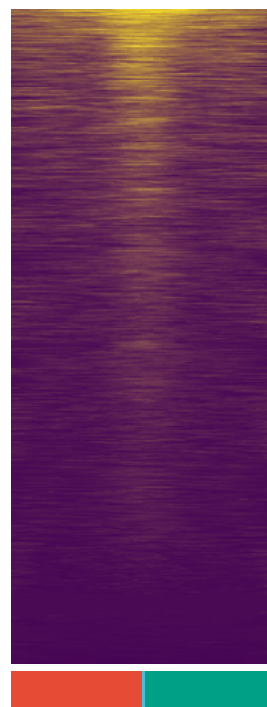
-0.5KCenter0.5K

Value



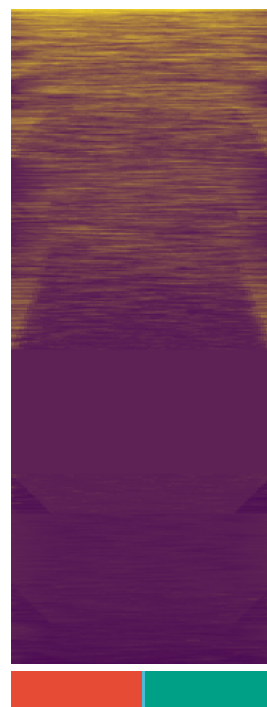
-0.5KCenter0.5K

Value



-0.5KCenter0.5K

Value



-0.5KCenter0.5K

Plotting parameters:

```
functionName: "plot_locus"  
  queryFiles: c(clip_bam =  
"C:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/GenomicPlot/extdata/treat_chr19.bam",  
    chip_bam =  
"C:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/GenomicPlot/extdata/chip_treat_chr19.bam")  
    centerFiles: c(SummitPeak =  
"C:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/GenomicPlot/extdata/test_chip_peak_chr19.bed",  
      iCLIPPeak =  
"C:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/GenomicPlot/extdata/test_clip_peak_chr19.bed")  
      txdb: NULL  
      ext: c(-500, 500)  
      hl: c(-100, 100)  
      shade: TRUE  
      smooth: TRUE  
importParams: list(offset = 0, fix_width = 150, fix_point = "start", norm = TRUE, useScore =  
  FALSE, outRle = TRUE, useSizeFactor = TRUE, genome = "hg19")  
  verbose: FALSE  
  binSize: 10  
  refPoint: "center"  
  Xlab: "Center"  
  Ylab: "Coverage/base/gene"  
  inputFiles: c(clip_input =  
"C:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/GenomicPlot/extdata/input_chr19.bam",  
    chip_input =  
"C:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/GenomicPlot/extdata/chip_input_chr19.bam")  
    stranded: TRUE  
    heatmap: TRUE  
    scale: FALSE  
outPrefix: "test_plot_locus2"  
  rmOutlier: 0  
  transform: NA  
  statsMethod: "wilcox.test"  
  heatRange: NULL  
  hw: c(8, 8)  
  nc: 2
```