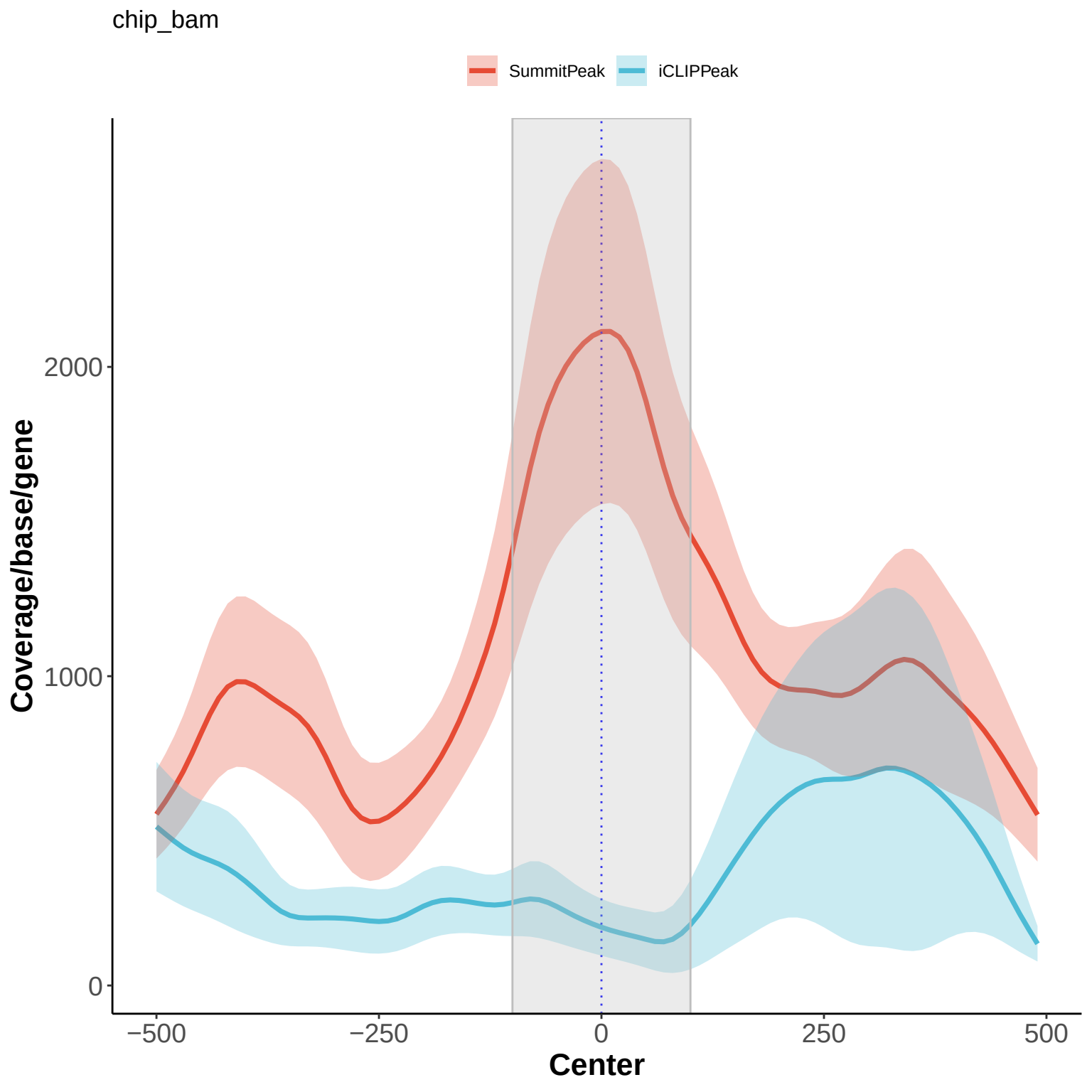
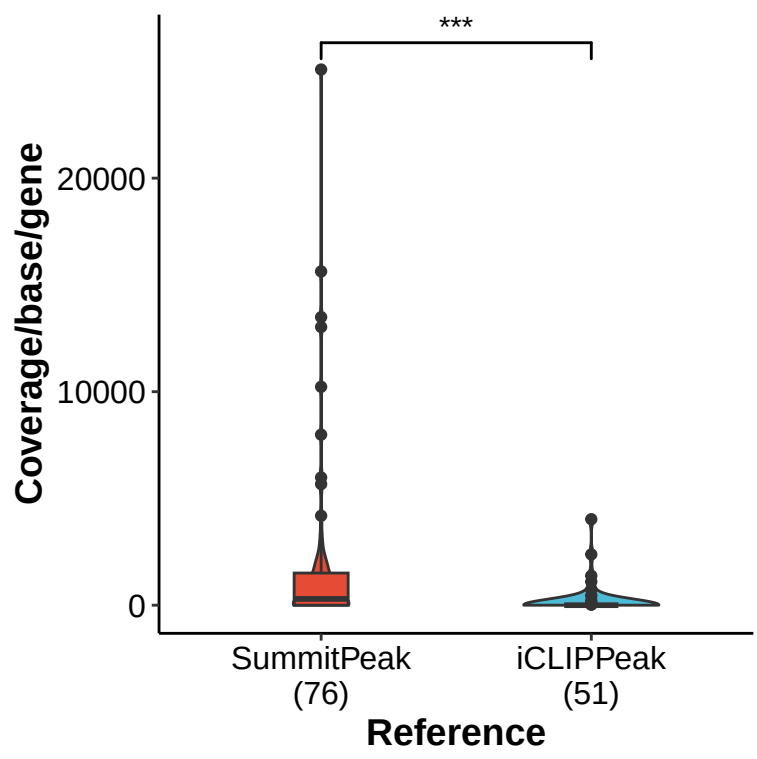
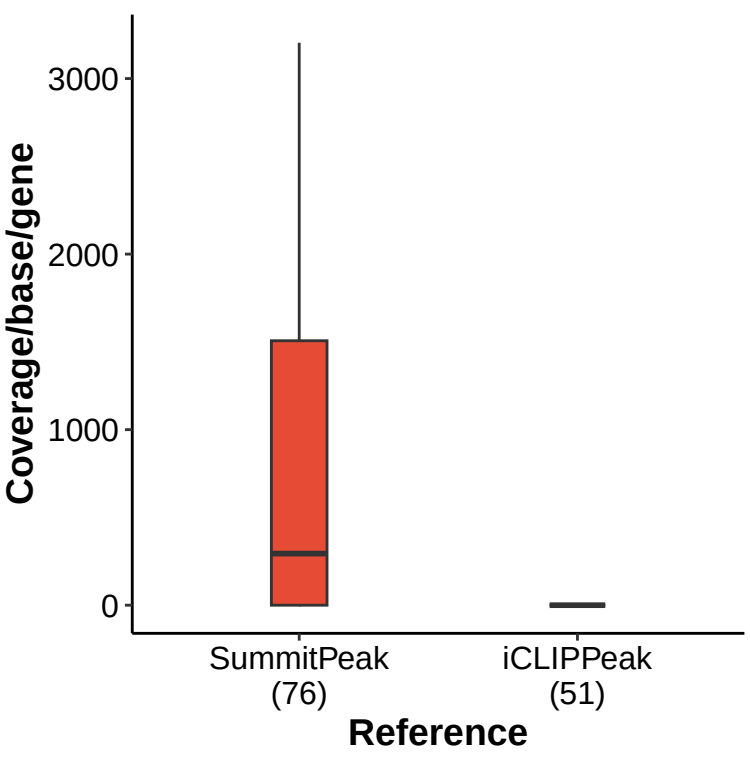
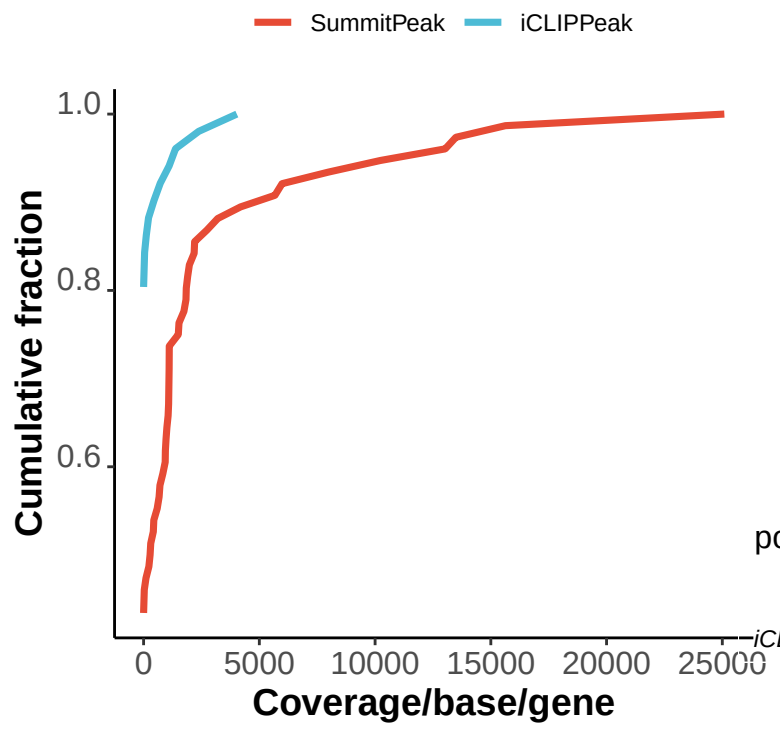
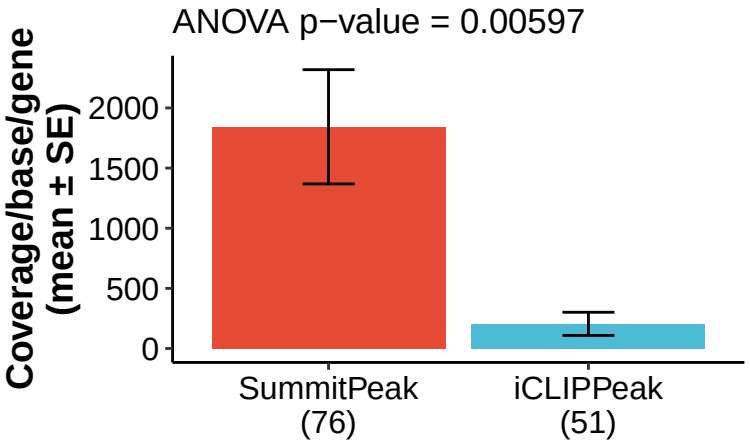

chip_bam
SummitPeak
iCLIPPeak
Coverage/base/gene
2000
1000
0
−500
−250
0
250
500
Center



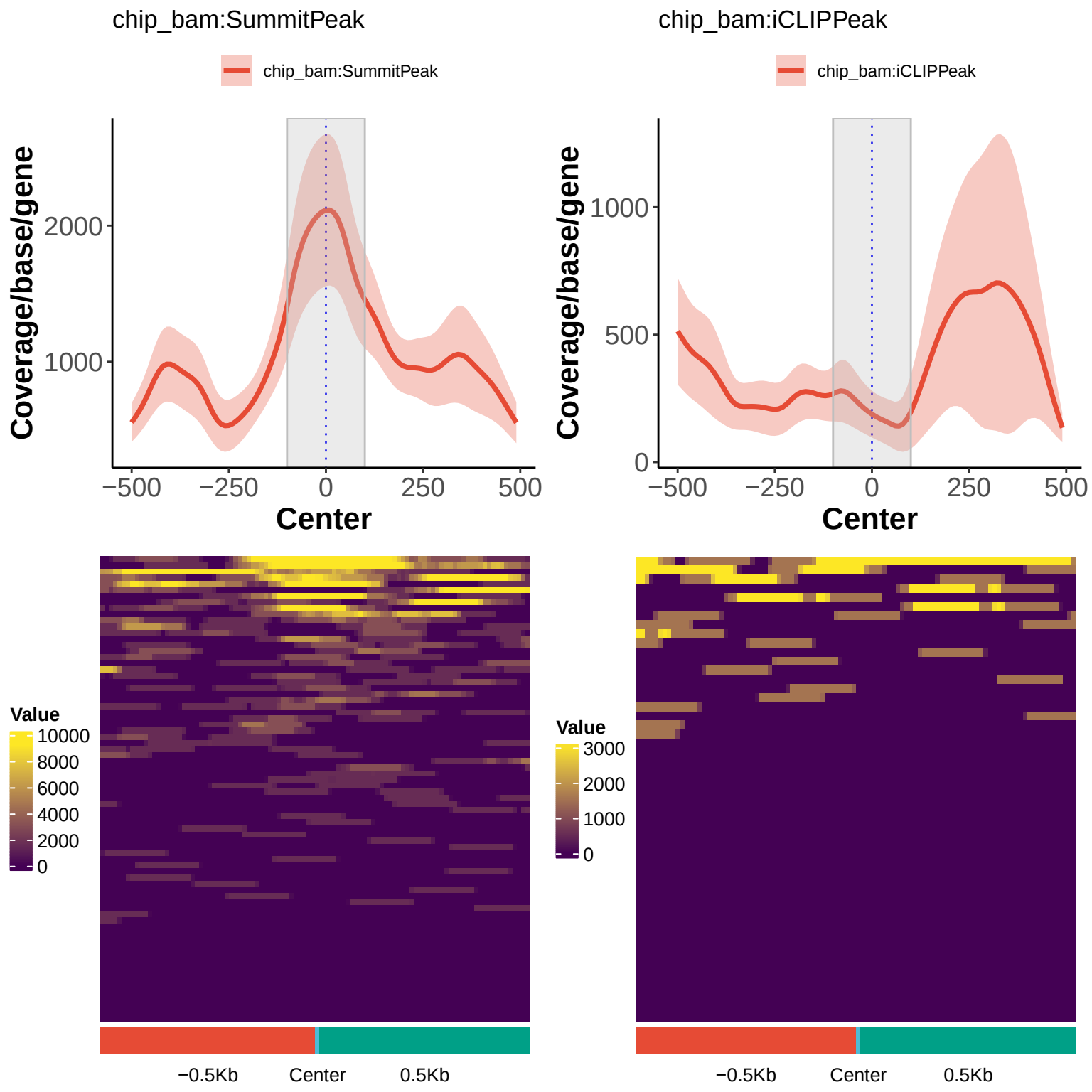


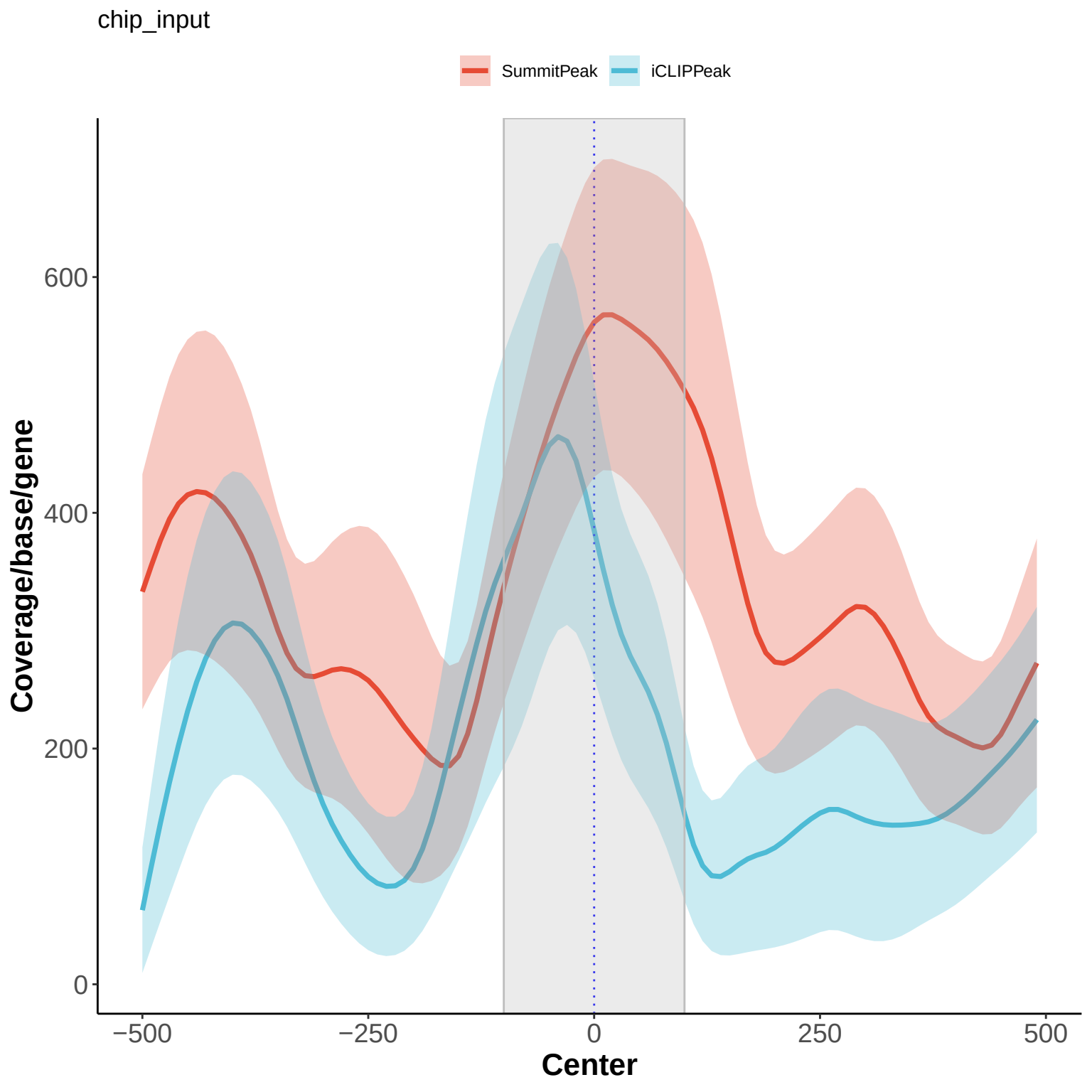


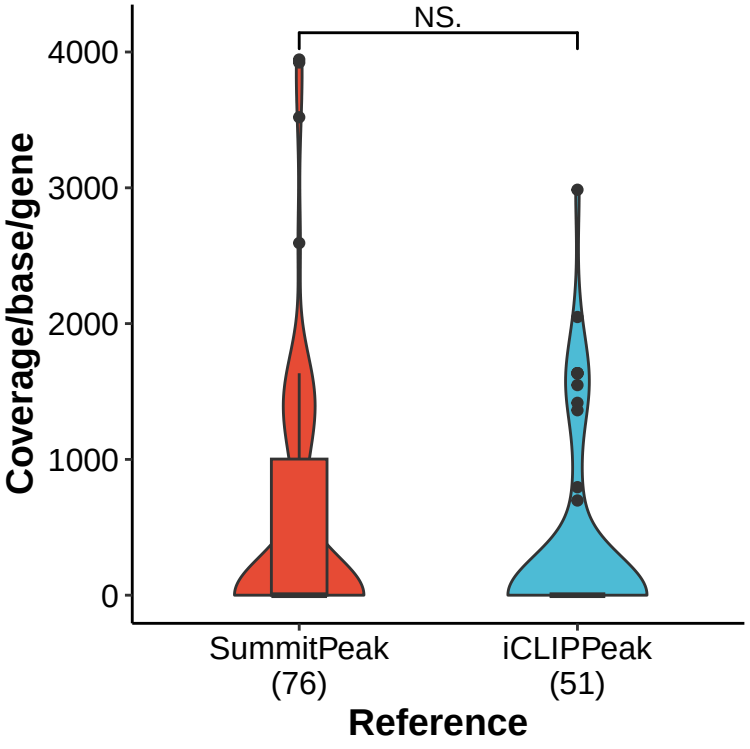


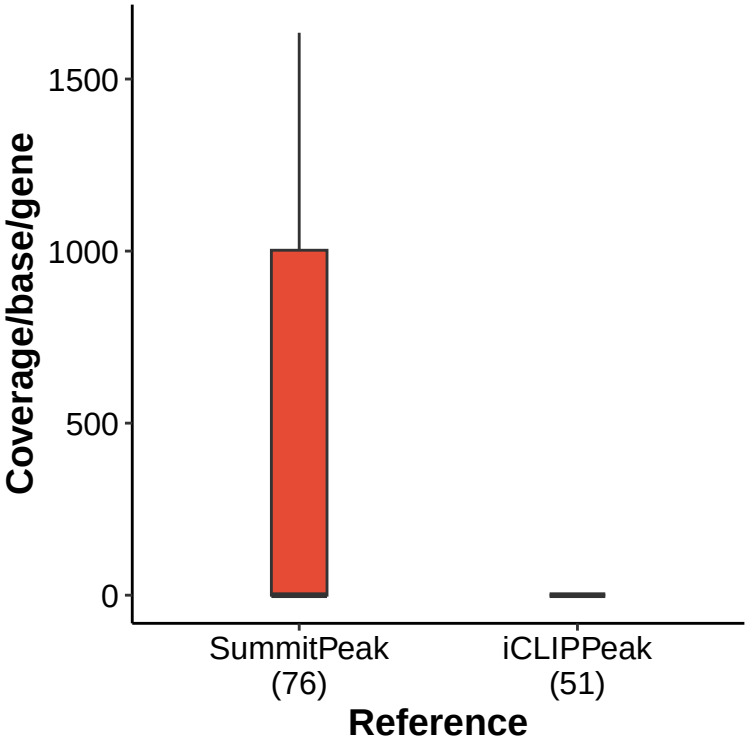
post hoc TukeyHSD test

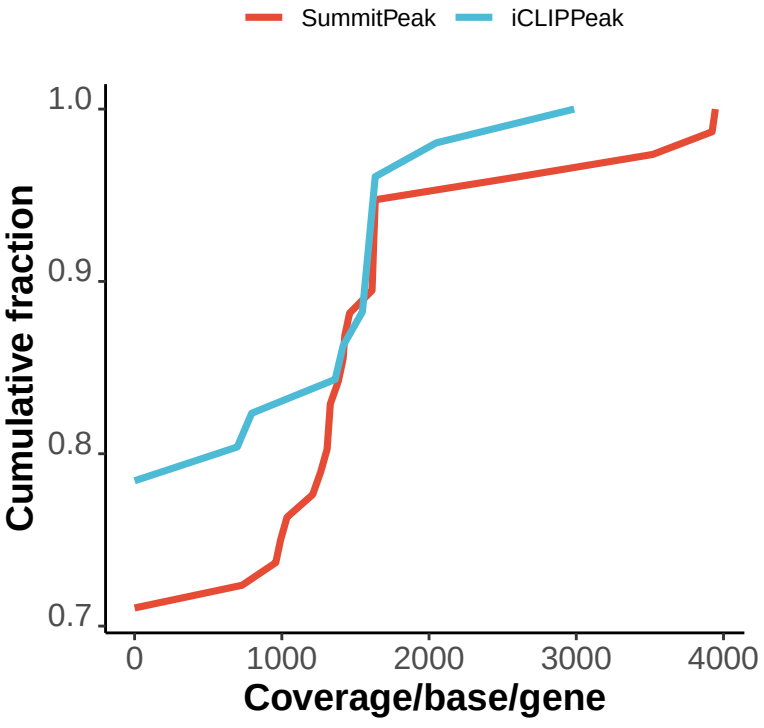
	diff	lwr	upr	p adj
iCLIPPeak−SummitPeak	−1638.302	−2797.535	−479.069	0.0059

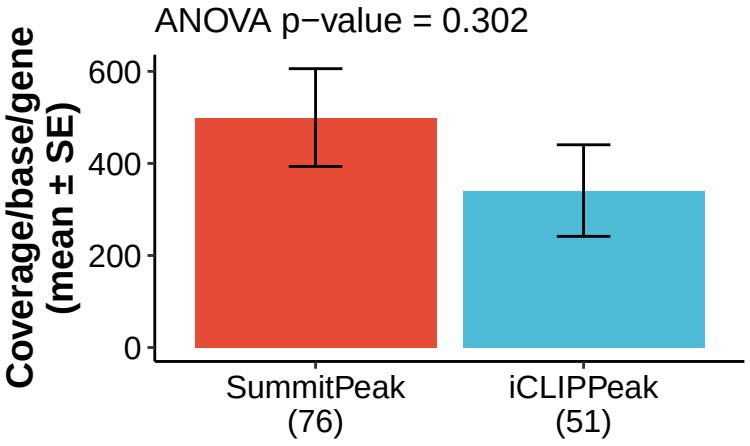

chip_bam:SummitPeak
chip_bam:SummitPeak
Coverage/base/gene
2000
1000
−500
−250
0
250
500
Center
chip_bam:iCLIPPeak
chip_bam:iCLIPPeak
Coverage/base/gene
1000
500
0
−500
−250
0
250
500
Center
Value
10000
8000
6000
4000
2000
0
−0.5Kb
Center
0.5Kb
Value
3000
2000
1000
0
−0.5Kb
Center
0.5Kb


chip_input
SummitPeak
iCLIPPeak
600
400
200
0
Coverage/base/gene
−500
−250
0
250
500
Center



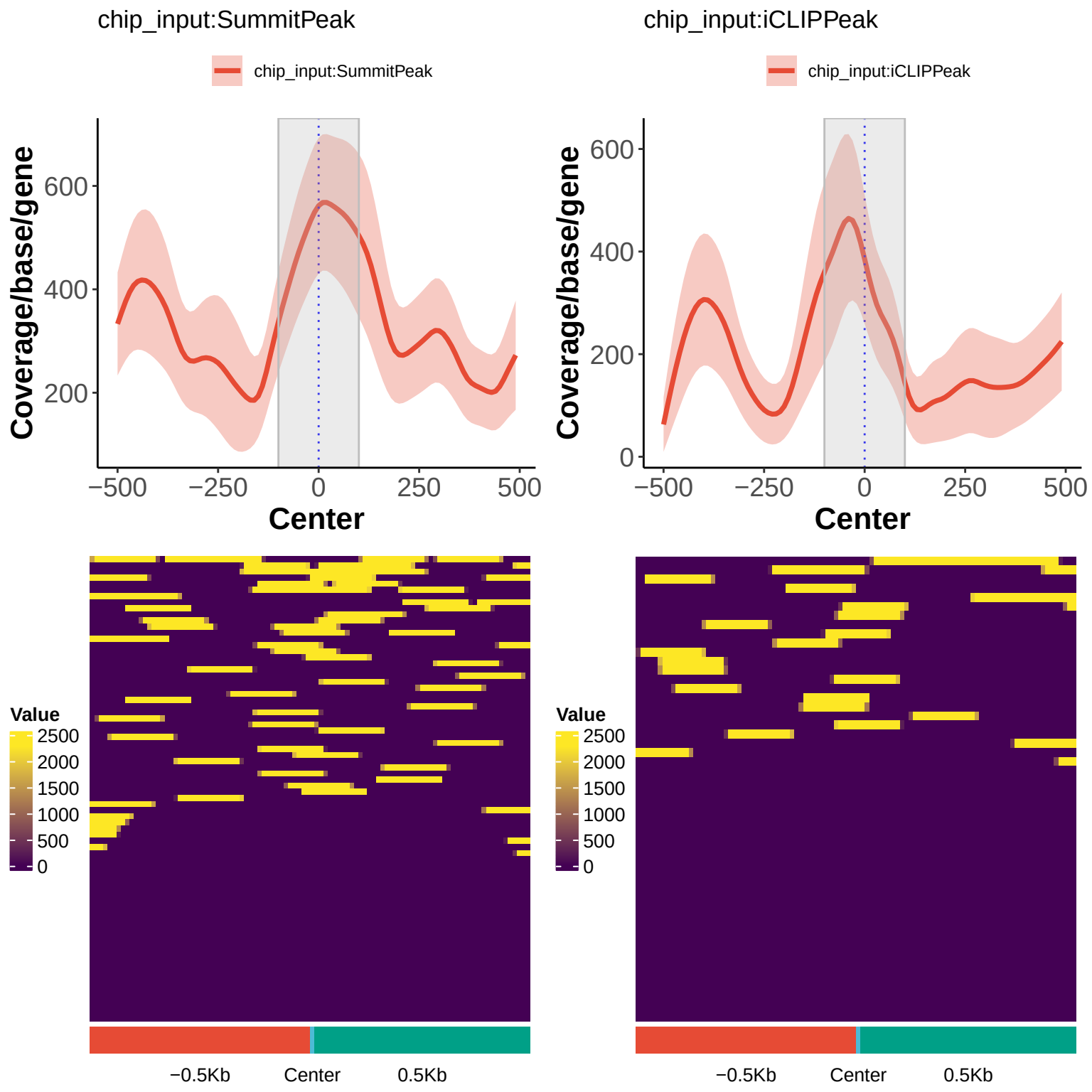


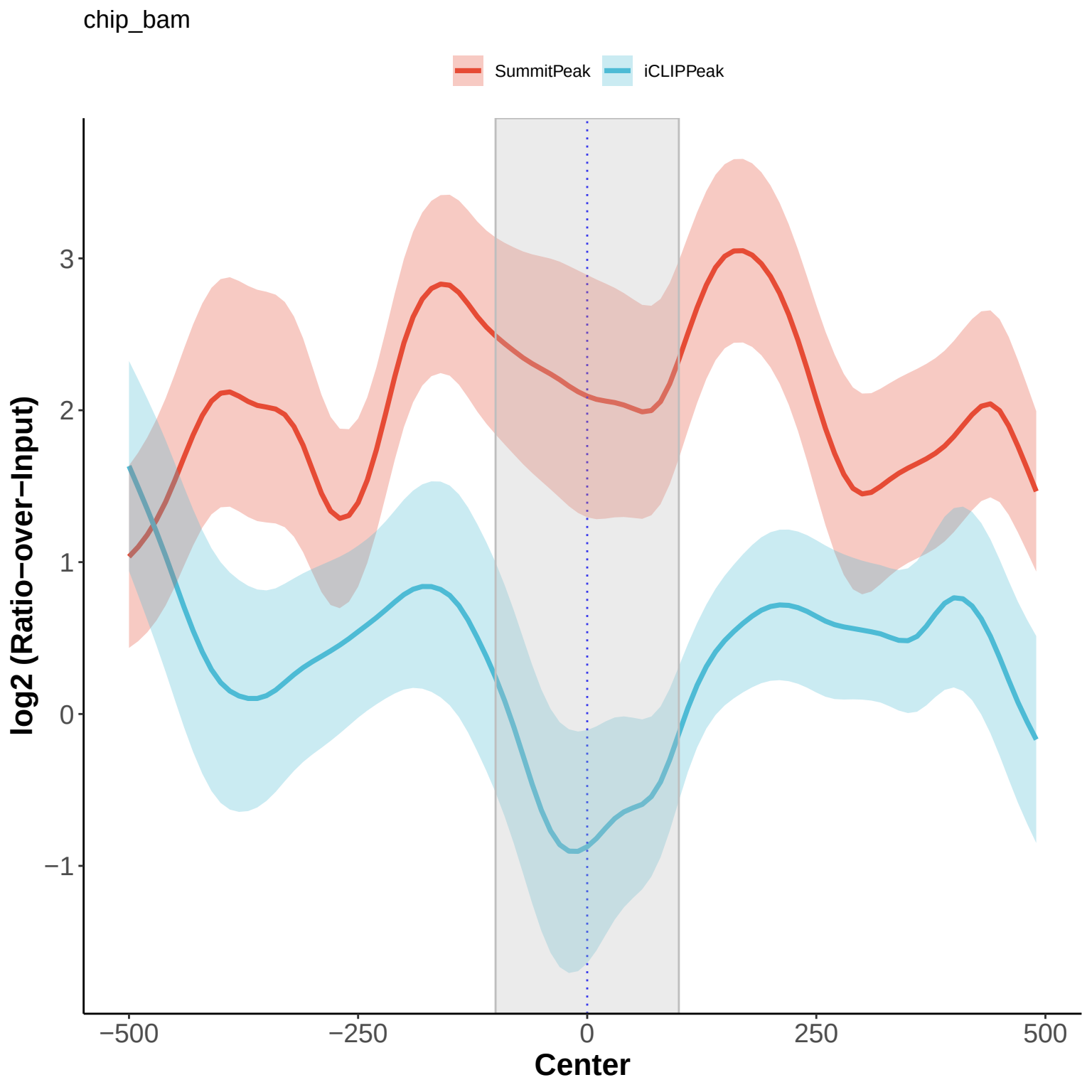


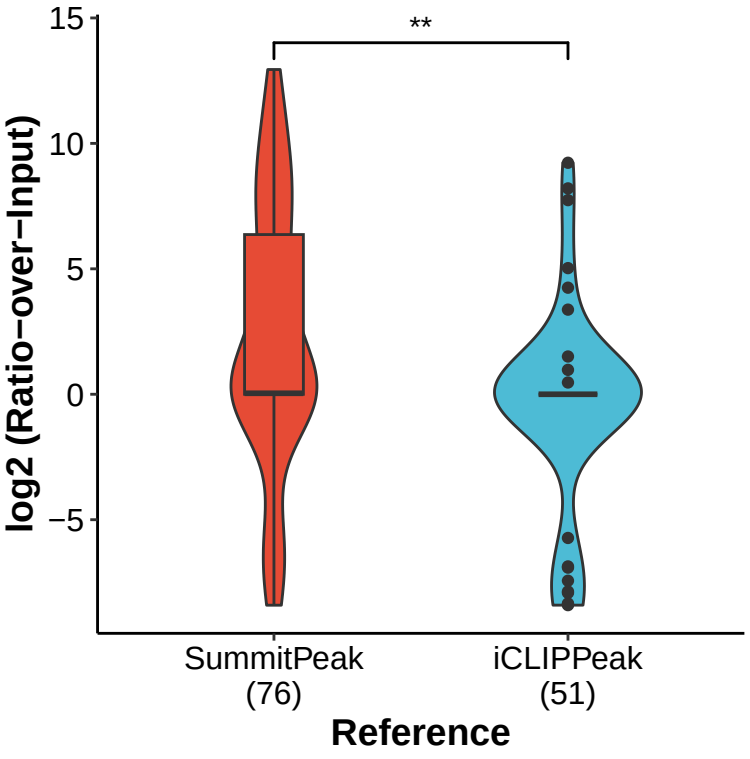


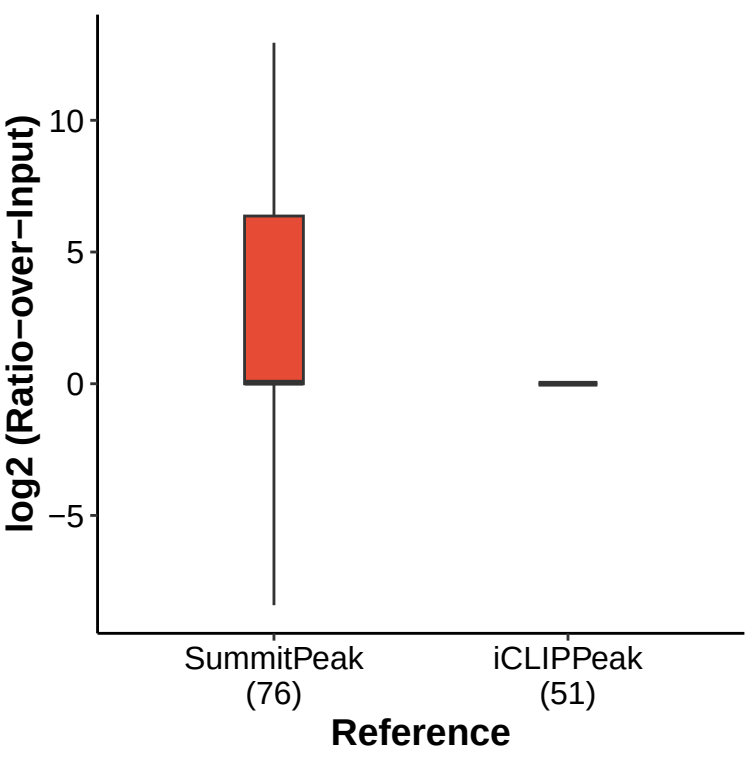
post hoc TukeyHSD test

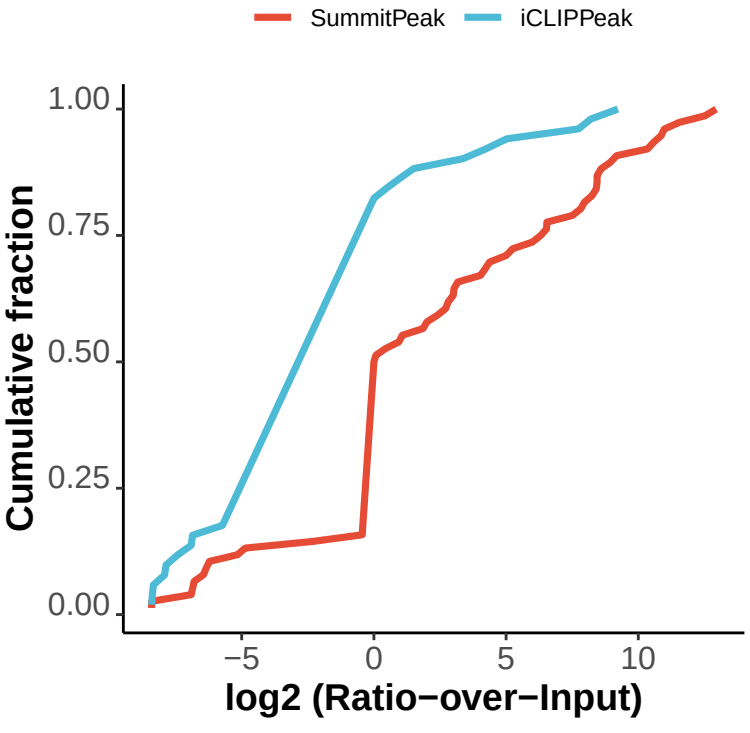
	diff	lwr	upr	p adj
iCLIPPeak−SummitPeak	−158.67	−461.845	144.505	0.302

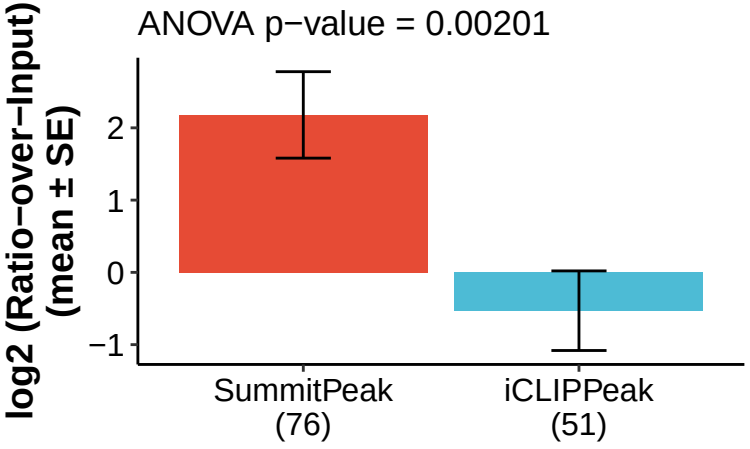

chip_input:SummitPeak
chip_input:SummitPeak
Coverage/base/gene
600
400
200
−500
−250
0
250
500
Center
chip_input:iCLIPPeak
chip_input:iCLIPPeak
Coverage/base/gene
600
400
200
0
−500
−250
0
250
500
Center
Value
2500
2000
1500
1000
500
0
−0.5Kb
Center
0.5Kb
Value
2500
2000
1500
1000
500
0
−0.5Kb
Center
0.5Kb


chip_bam
SummitPeak
iCLIPPeak
log2 (Ratio−over−Input)
3
2
1
0
−1
−500
−250
0
250
500
Center



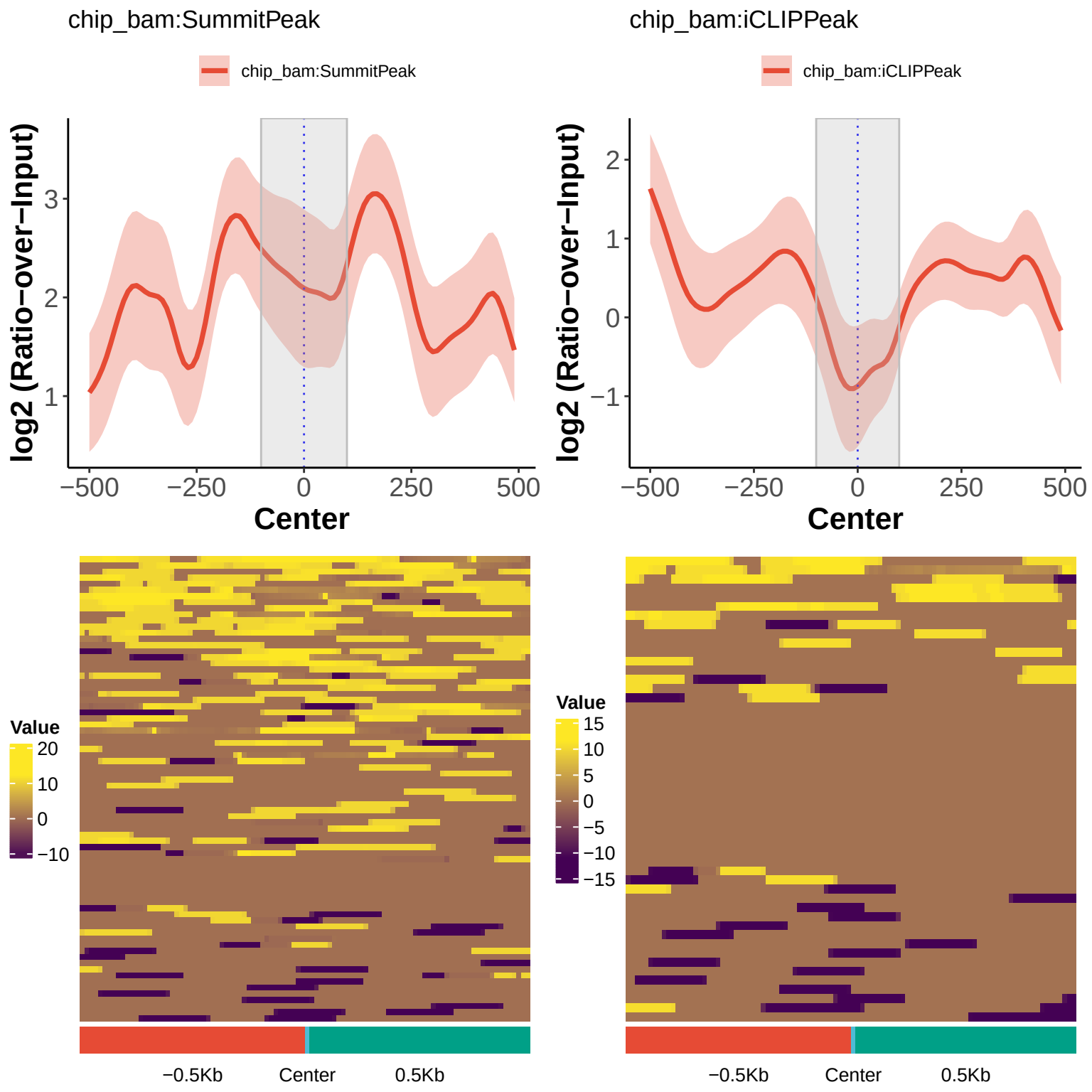






post hoc TukeyHSD test

	diff	lwr	upr	p adj
iCLIPPeak−SummitPeak	−2.709	−4.409	−1.01	0.00201


chip_bam:SummitPeak
chip_bam:SummitPeak
log2 (Ratio−over−Input)
3
2
1
−500
−250
0
250
500
Center
chip_bam:iCLIPPeak
chip_bam:iCLIPPeak
log2 (Ratio−over−Input)
2
1
0
−1
−500
−250
0
250
500
Center
Value
20
10
0
−10
−0.5Kb
Center
0.5Kb
Value
15
10
5
0
−5
−10
−15
−0.5Kb
Center
0.5Kb

Plotting parameters:

functionName: "plot_locus"
queryFiles: c(chip_bam =
"C:/Users/greenblatt/AppData/Local/R/win−library/4.3/GenomicPlot/extdata/chip_treat_chr19.bam")
centerFiles: c(SummitPeak =
"C:/Users/greenblatt/AppData/Local/R/win−library/4.3/GenomicPlot/extdata/test_chip_peak_chr19.bed",
iCLIPPeak =
"C:/Users/greenblatt/AppData/Local/R/win−library/4.3/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 = FALSE, saveRds = FALSE, genome = "hg19")
verbose: FALSE
binSize: 10
refPoint: "center"
Xlab: "Center"
Ylab: "Coverage/base/gene"
inputFiles: c(chip_input =
"C:/Users/greenblatt/AppData/Local/R/win−library/4.3/GenomicPlot/extdata/chip_input_chr19.bam")
stranded: TRUE
heatmap: TRUE
scale: FALSE
outPrefix: "test_plot_locus2"
rmOutlier: 0
transform: "log2"
statsMethod: "wilcox.test"
heatRange: NULL
hw: c(8, 8)
nc: 2