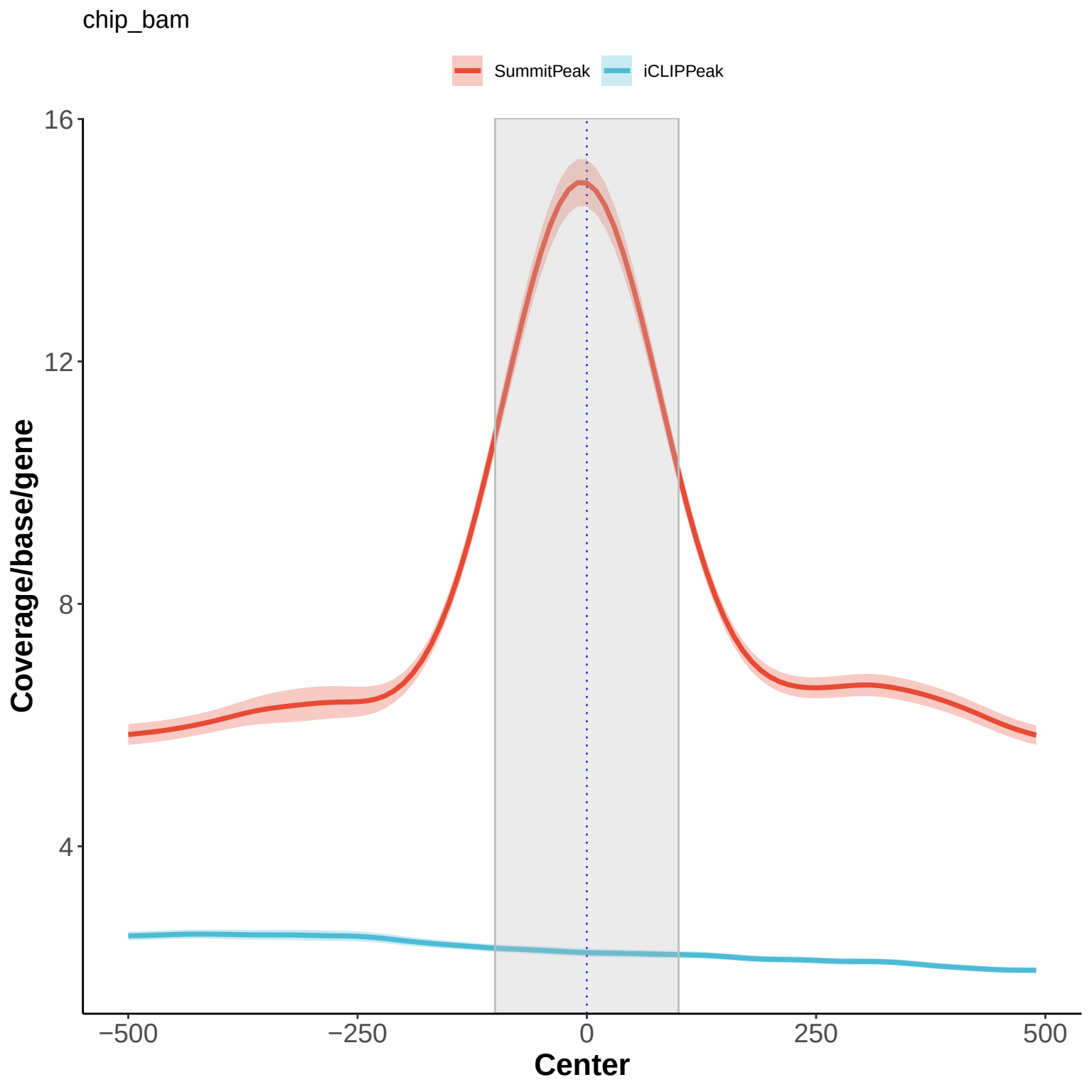
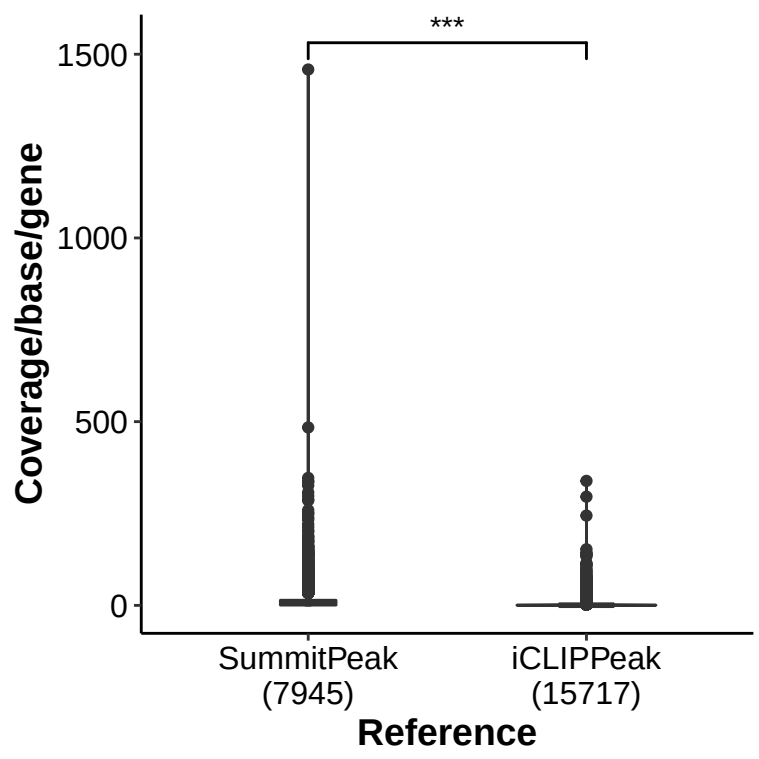
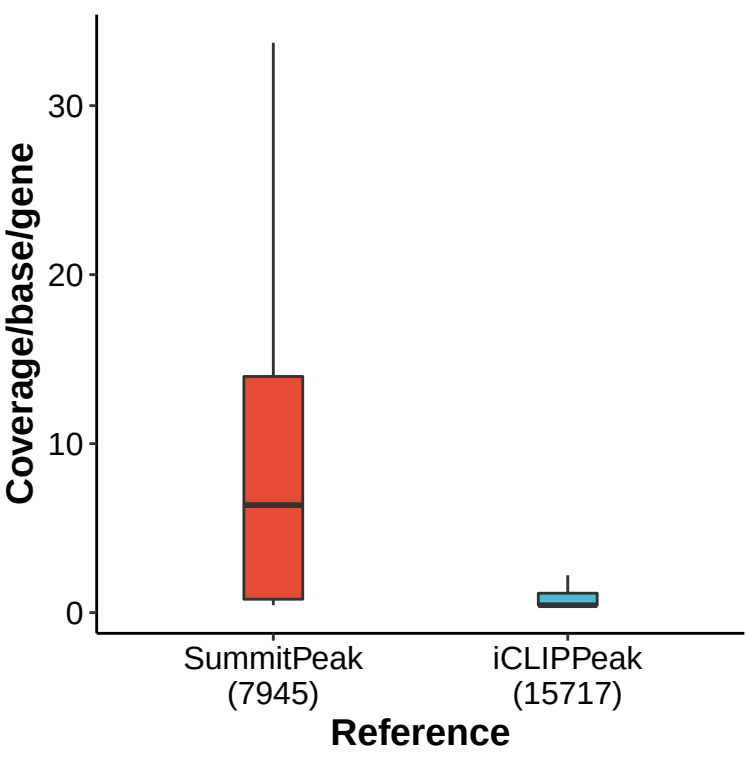
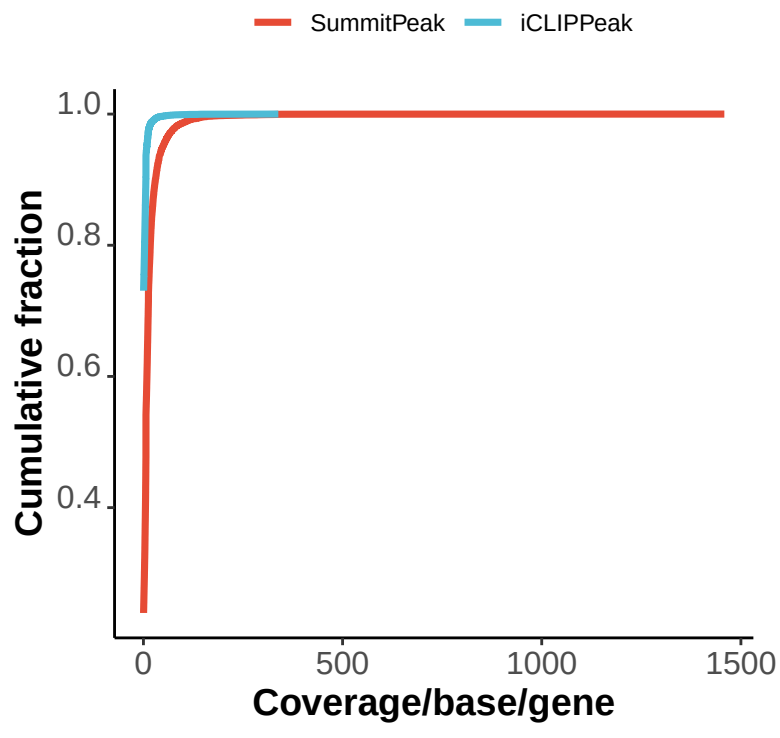
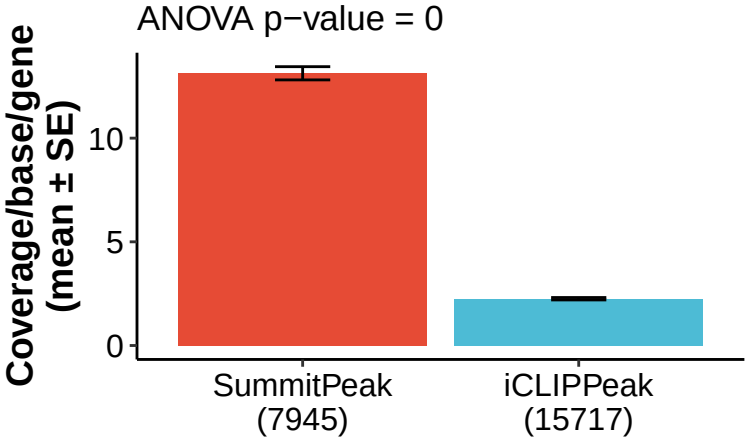

chip_bam
SummitPeak
iCLIPPeak
16
12
8
4
Coverage/base/gene
−500
−250
0
250
500
Center



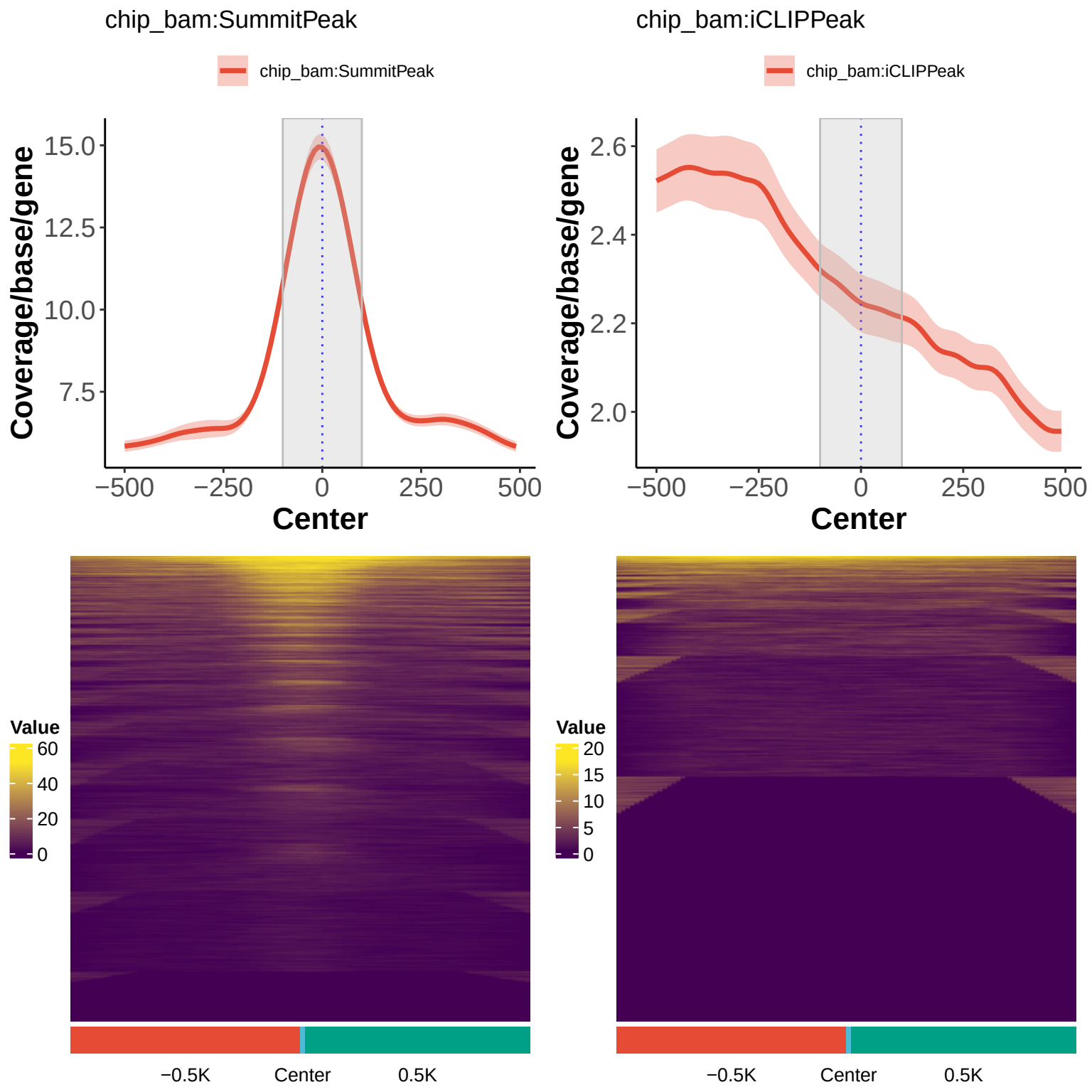



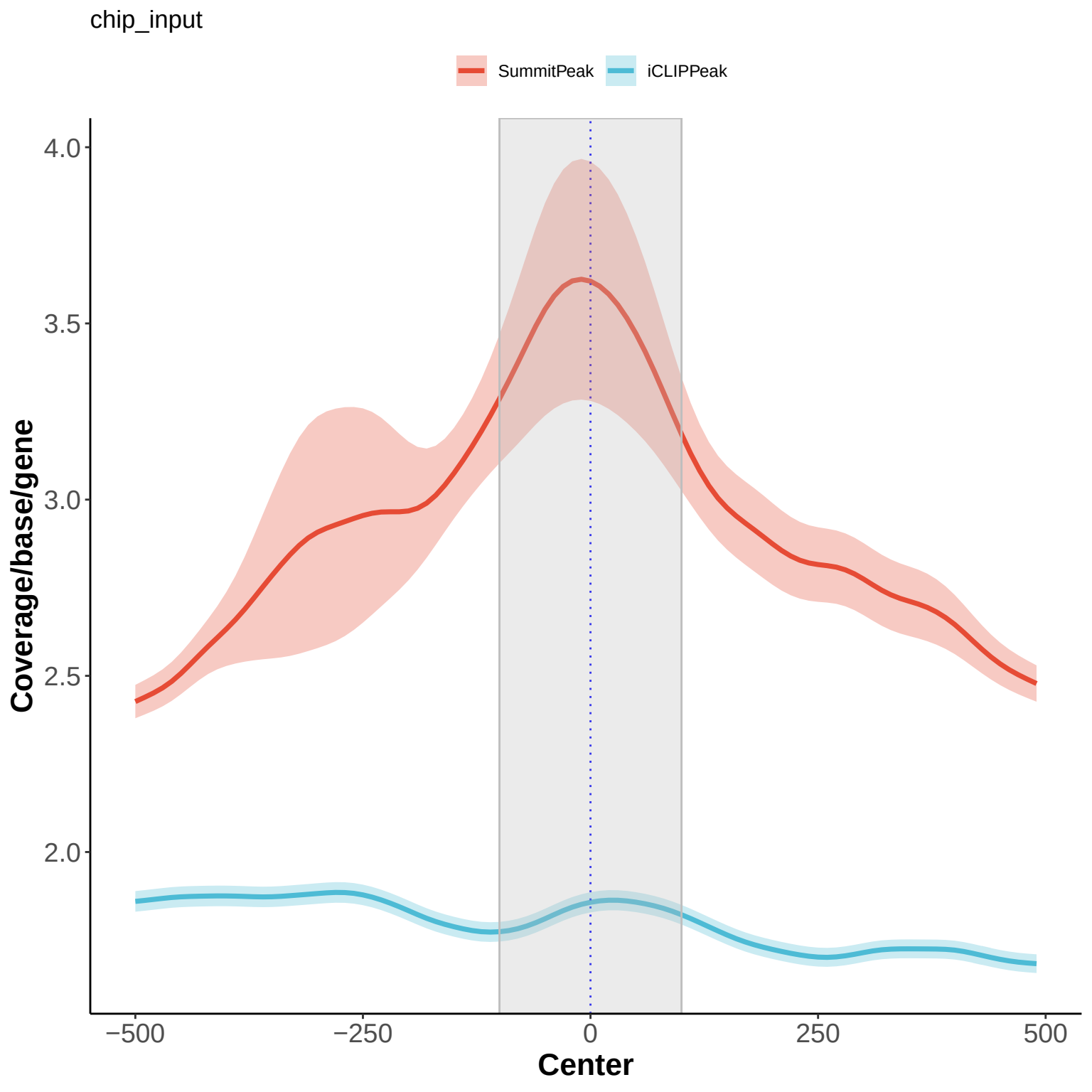



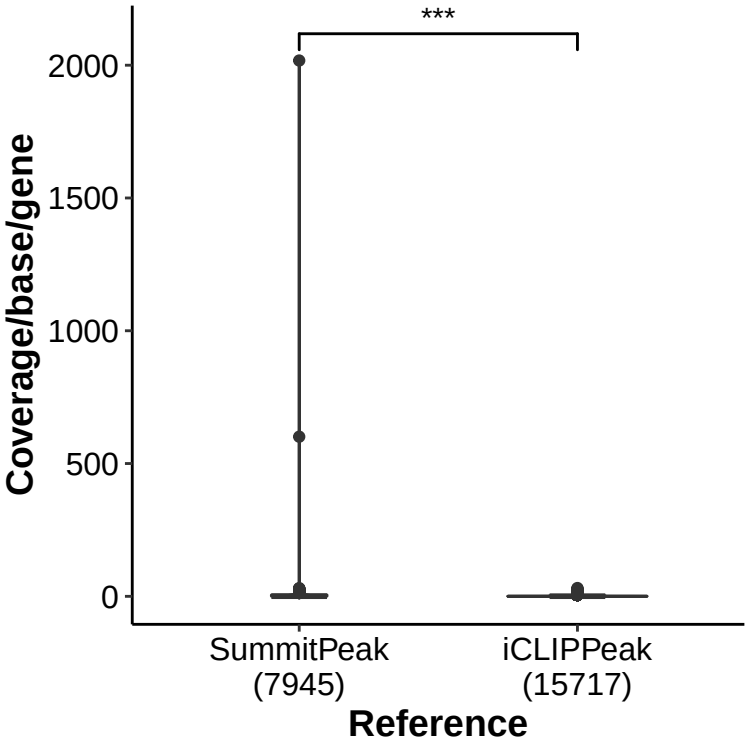



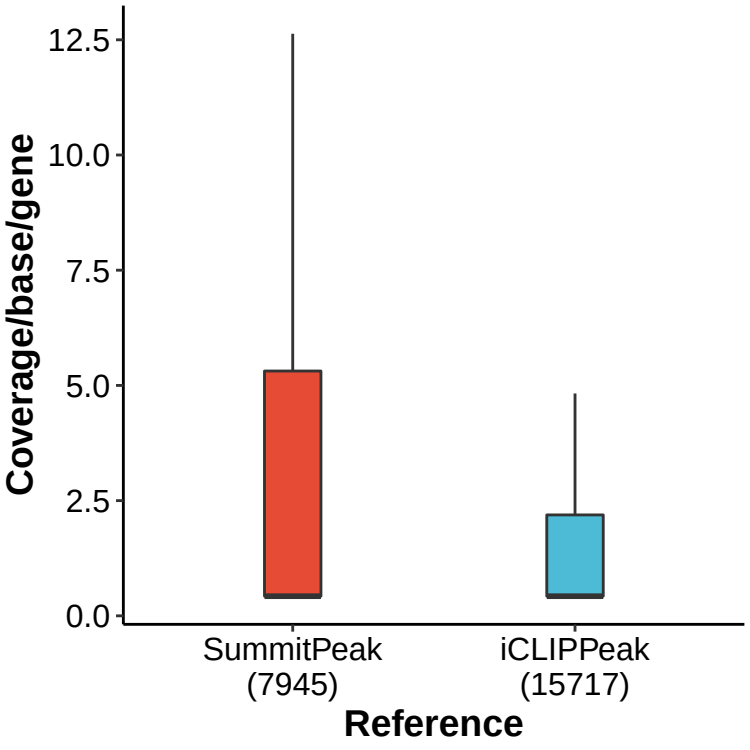

post hoc TukeyHSD test

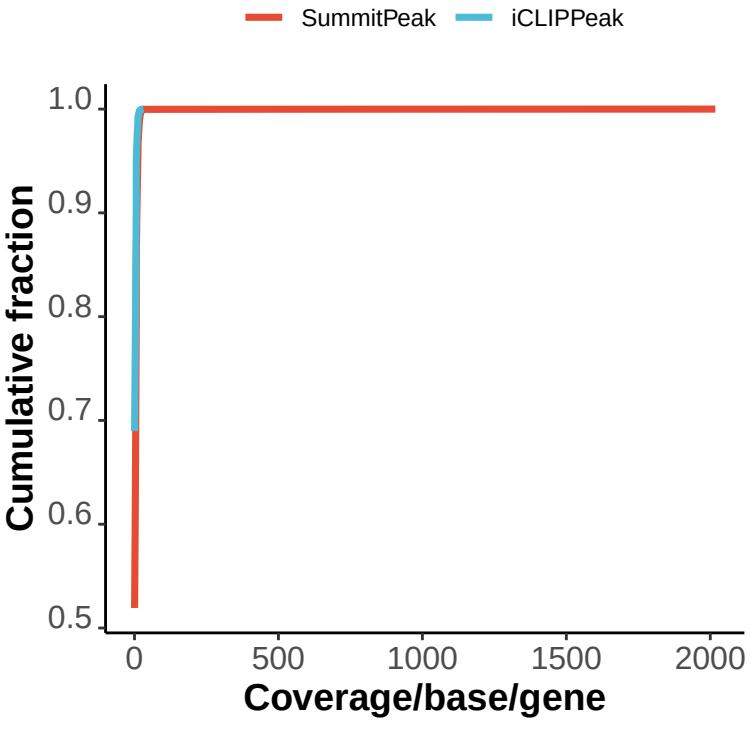
| | diff | lwr | upr | p adj |
|---|---|---|---|---|
| *iCLIPPeak−SummitPeak* | −10.872 | −11.344 | −10.4 | 0 |

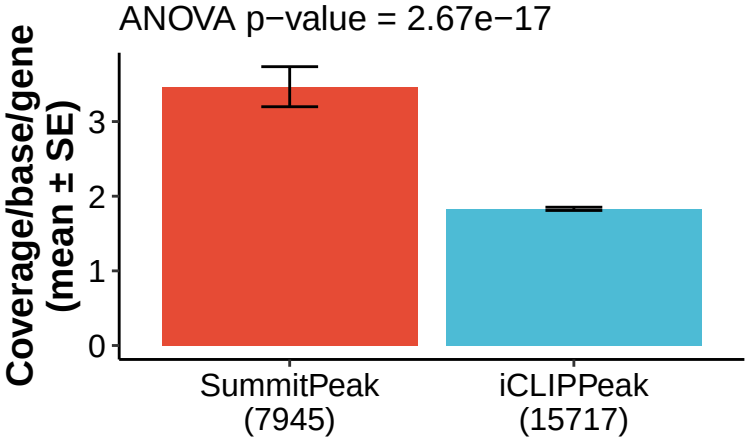

chip_bam:SummitPeak
chip_bam:SummitPeak
Coverage/base/gene
15.0
12.5
10.0
7.5
−500
−250
0
250
500
Center
chip_bam:iCLIPPeak
chip_bam:iCLIPPeak
Coverage/base/gene
2.6
2.4
2.2
2.0
−500
−250
0
250
500
Center
Value
60
40
20
0
−0.5K
Center
0.5K
Value
20
15
10
5
0
−0.5K
Center
0.5K


chip_input
SummitPeak
iCLIPPeak
4.0
3.5
3.0
2.5
2.0
Coverage/base/gene
−500
−250
0
250
500
Center



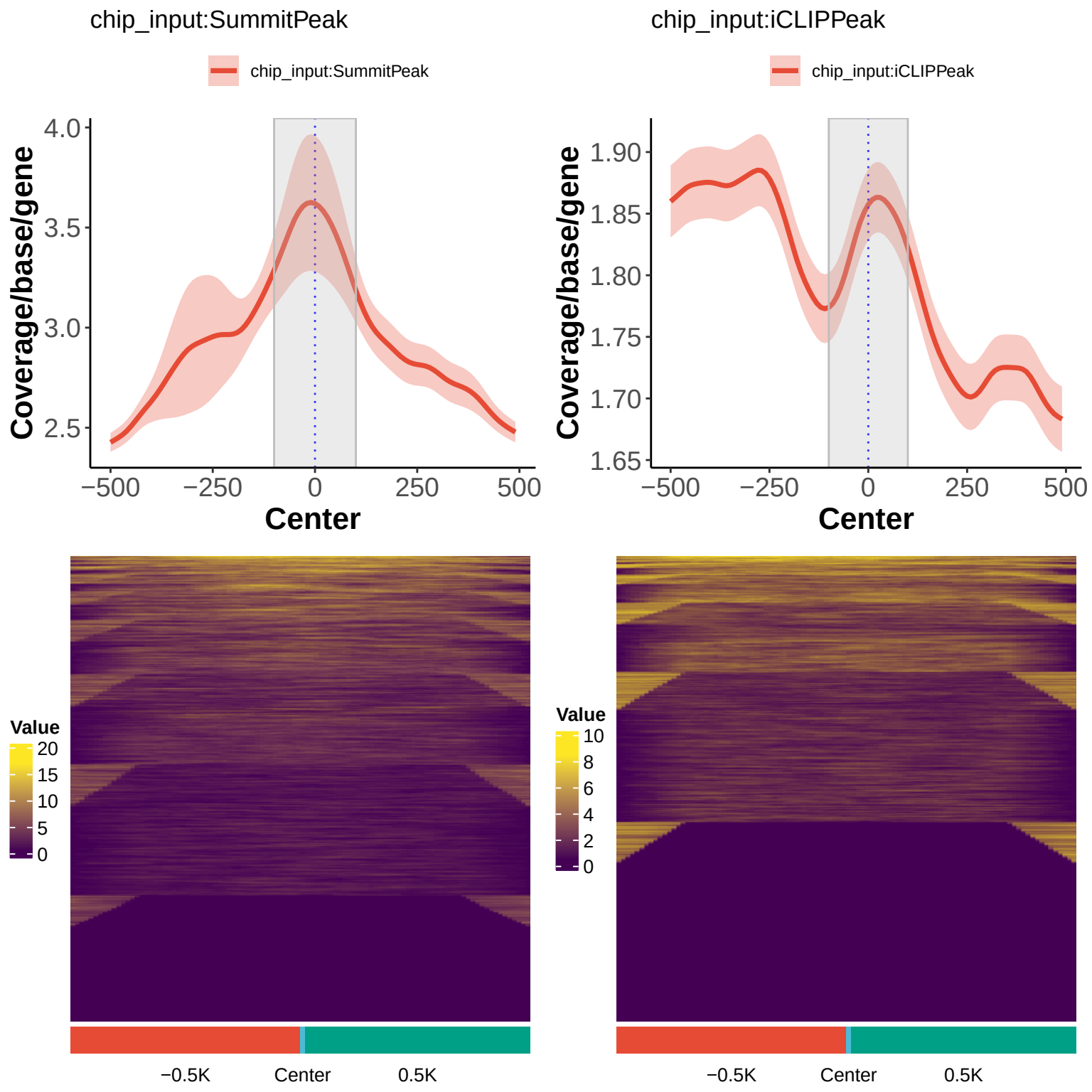



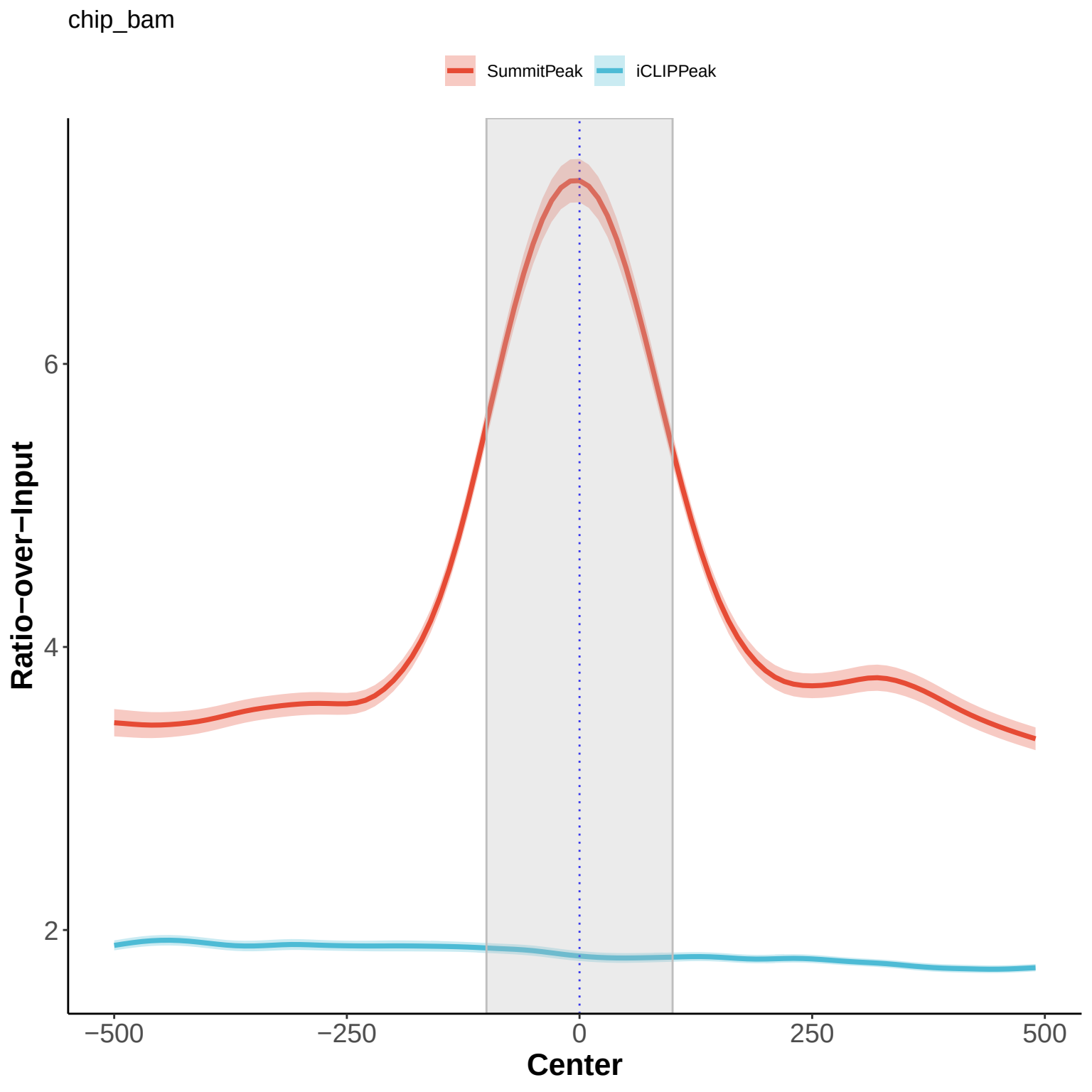



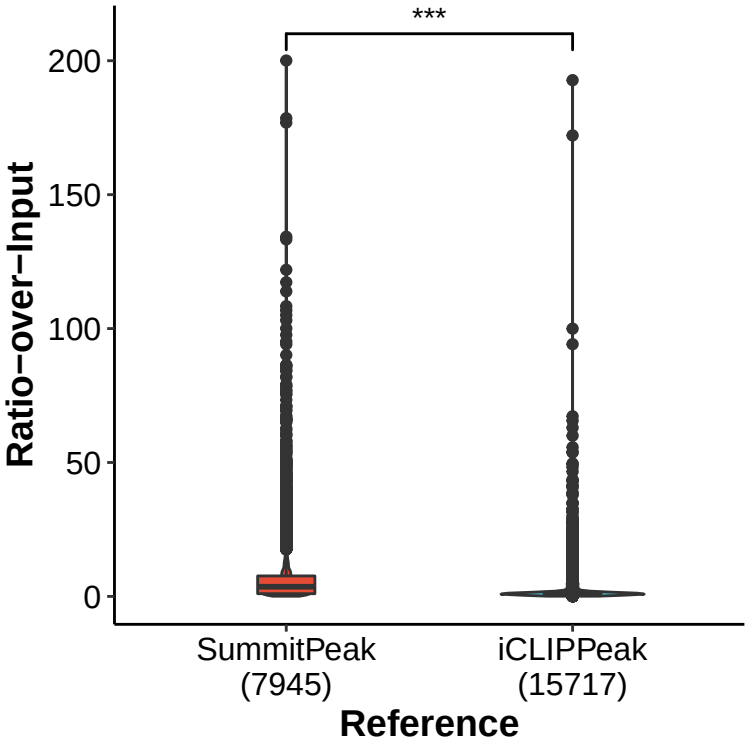



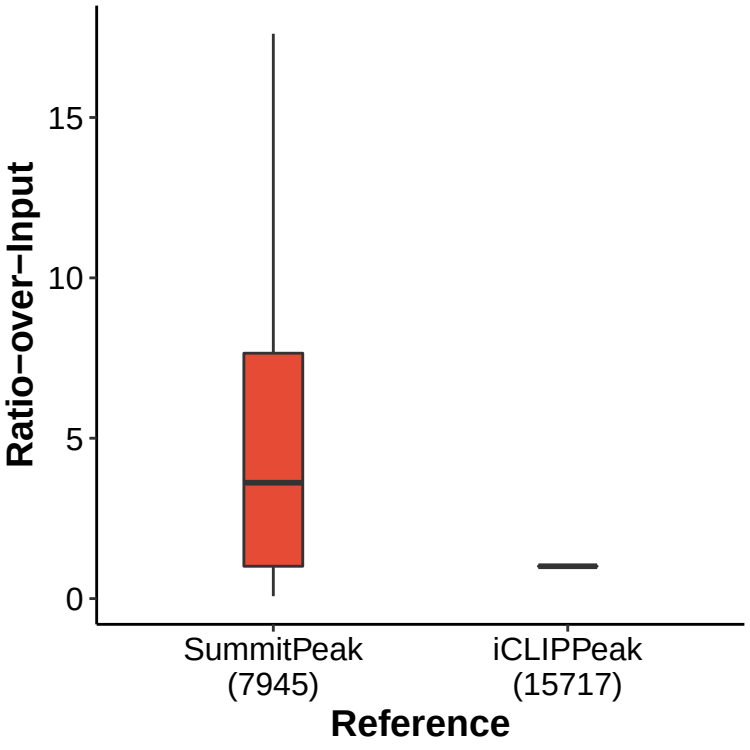

post hoc TukeyHSD test

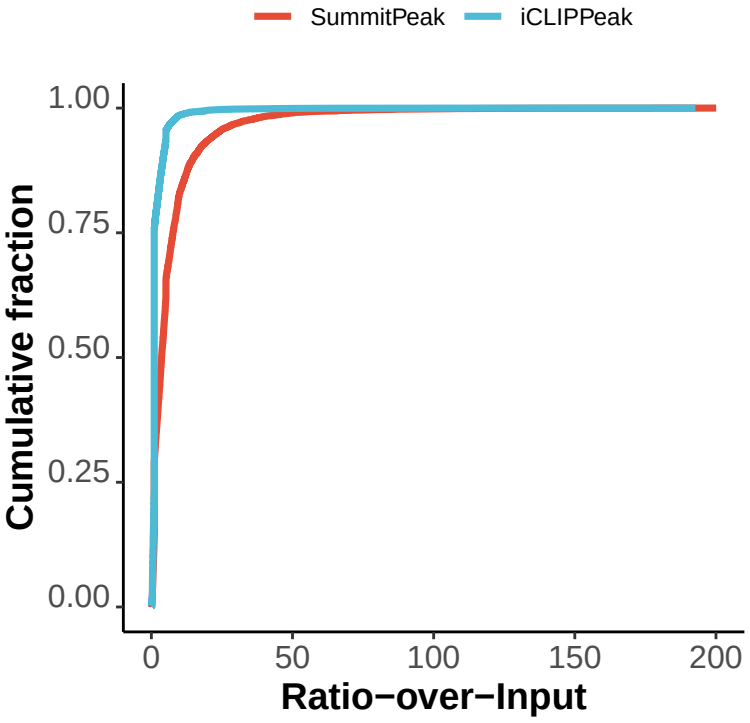
| | diff | lwr | upr | p adj |
|---|---|---|---|---|
| *iCLIPPeak−SummitPeak* | −1.636 | −2.015 | −1.257 | 0 |

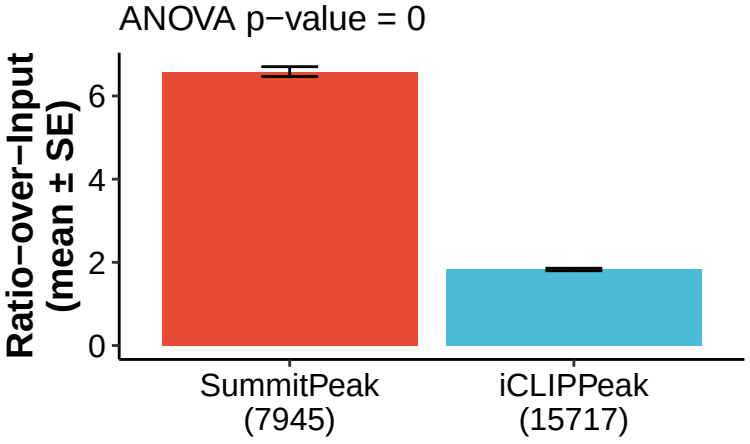

chip_input:SummitPeak
chip_input:SummitPeak
Coverage/base/gene
4.0
3.5
3.0
2.5
−500
−250
0
250
500
Center
chip_input:iCLIPPeak
chip_input:iCLIPPeak
Coverage/base/gene
1.90
1.85
1.80
1.75
1.70
1.65
−500
−250
0
250
500
Center
Value
20
15
10
5
0
−0.5K
Center
0.5K
Value
10
8
6
4
2
0
−0.5K
Center
0.5K


chip_bam
SummitPeak
iCLIPPeak
Ratio−over−Input
6
4
2
−500
−250
0
250
500
Center



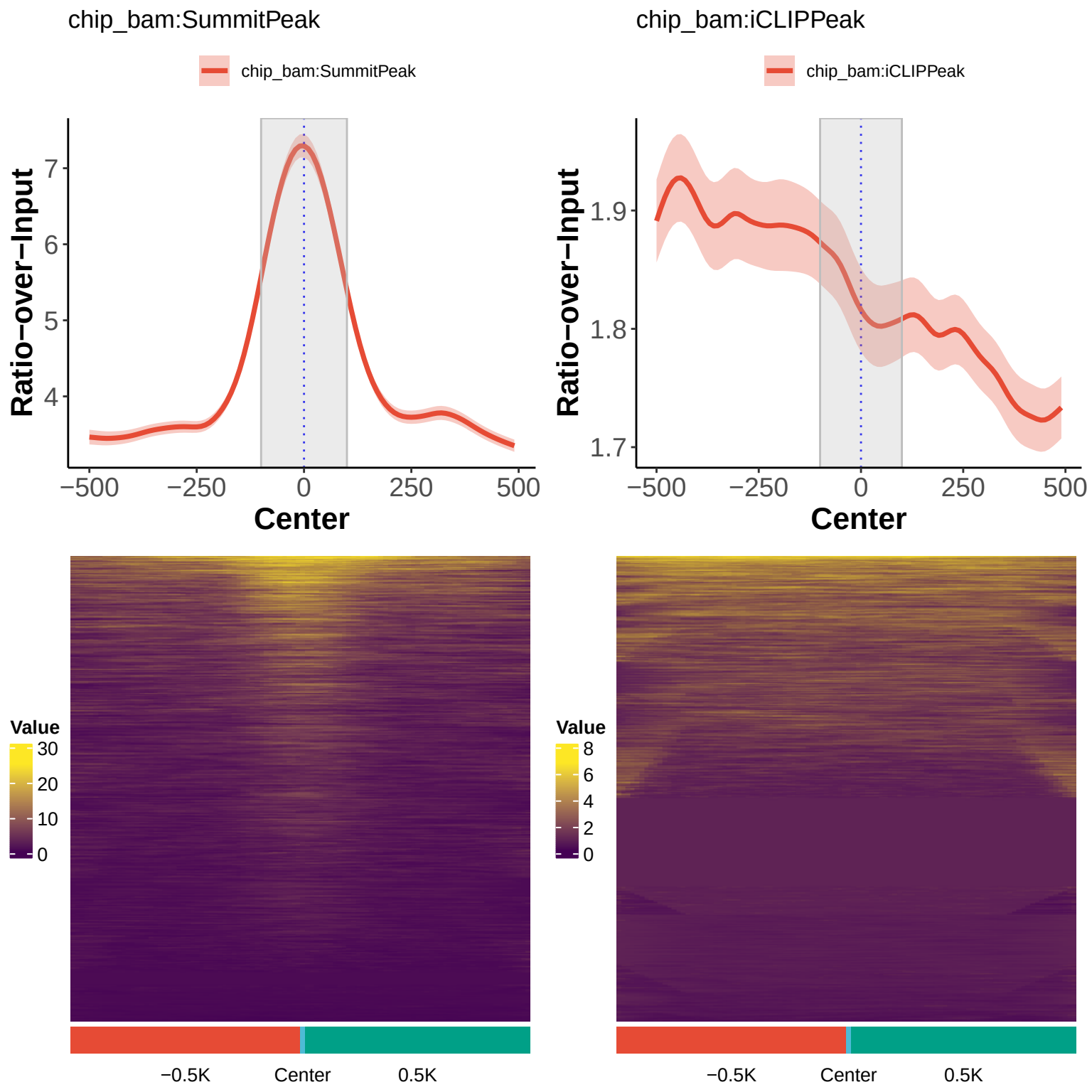




post hoc TukeyHSD test

| | diff | lwr | upr | p adj |
|---|---|---|---|---|
| *iCLIPPeak−SummitPeak* | −4.758 | −4.942 | −4.574 | 0 |


chip_bam:SummitPeak
chip_bam:SummitPeak
Ratio−over−Input
7
6
5
4
−500
−250
0
250
500
Center
chip_bam:iCLIPPeak
chip_bam:iCLIPPeak
Ratio−over−Input
1.9
1.8
1.7
−500
−250
0
250
500
Center
Value
30
20
10
0
−0.5K
Center
0.5K
Value
8
6
4
2
0
−0.5K
Center
0.5K

Plotting parameters:

functionName: "plot_locus"
queryFiles: c(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 = FALSE, genome = "hg19")
verbose: FALSE
binSize: 10
refPoint: "center"
Xlab: "Center"
Ylab: "Coverage/base/gene"
inputFiles: c(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