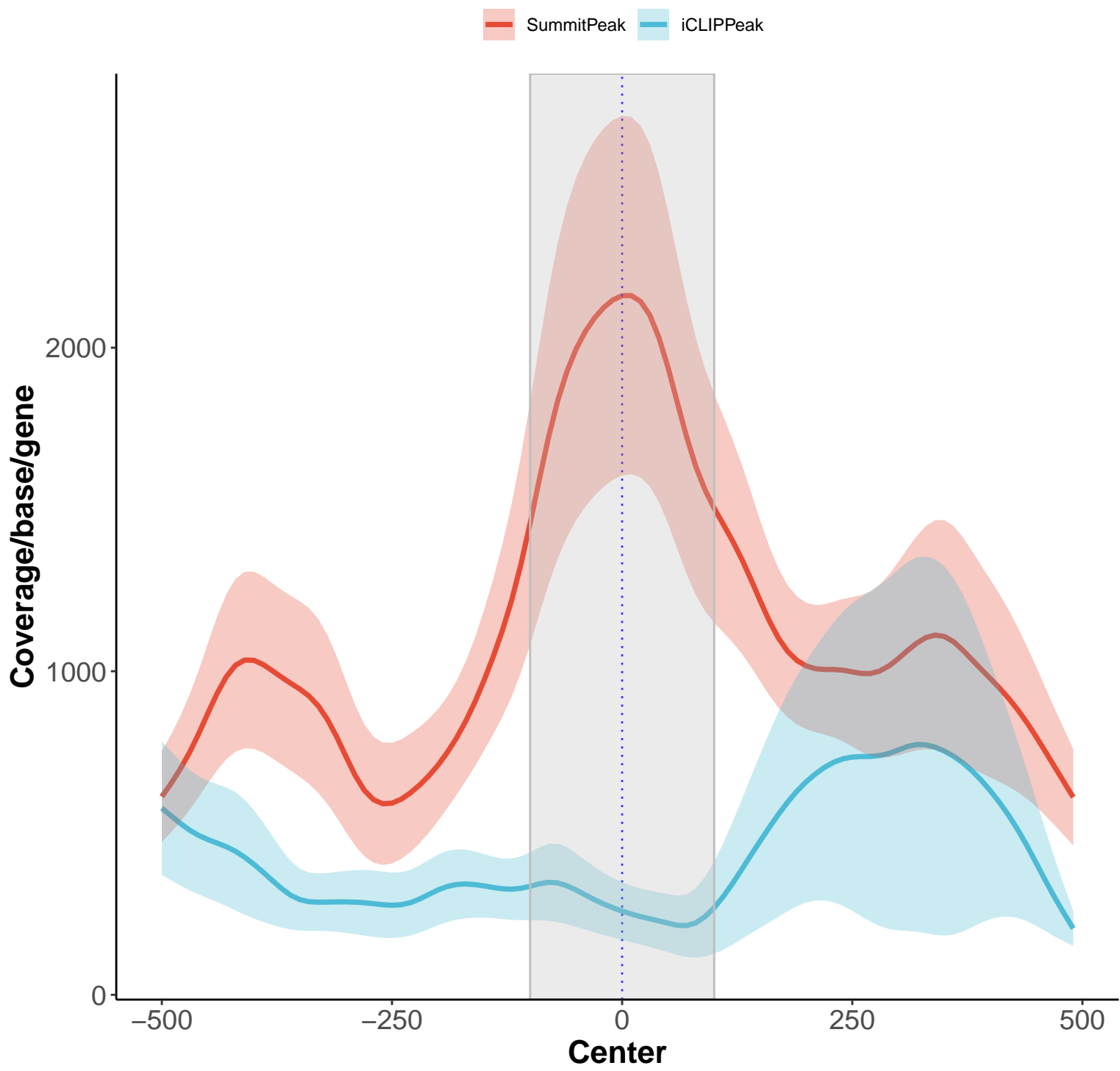
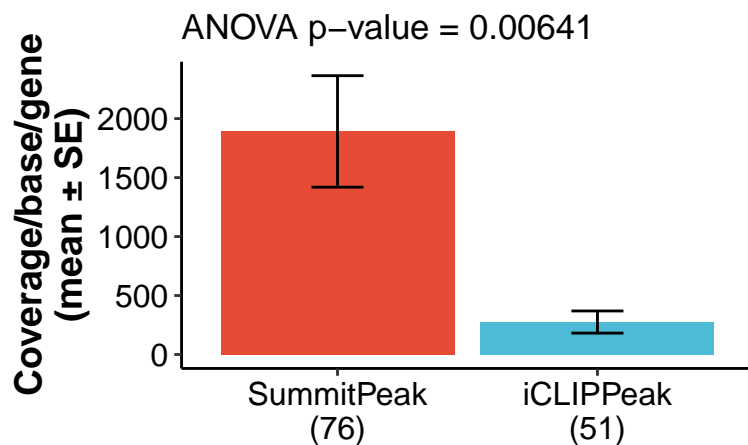
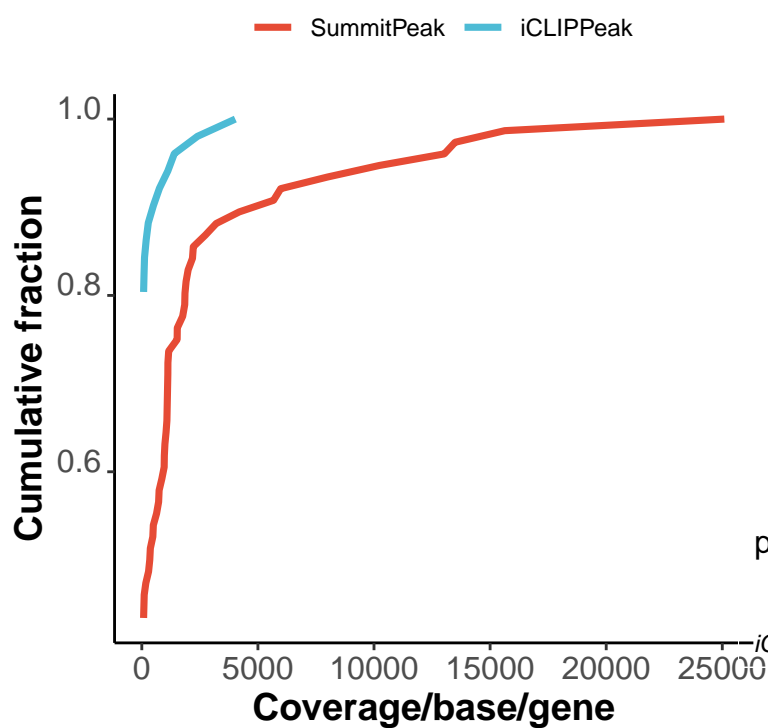
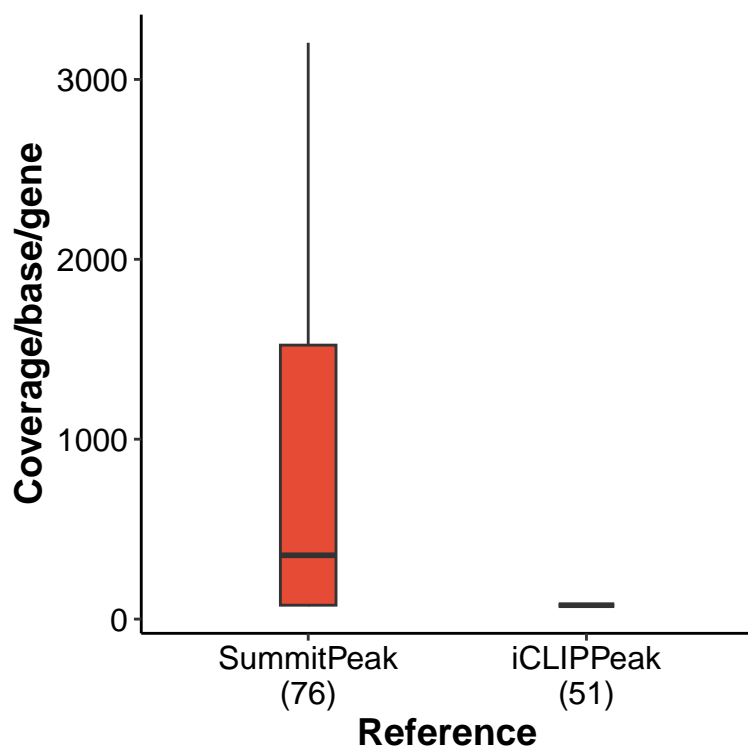
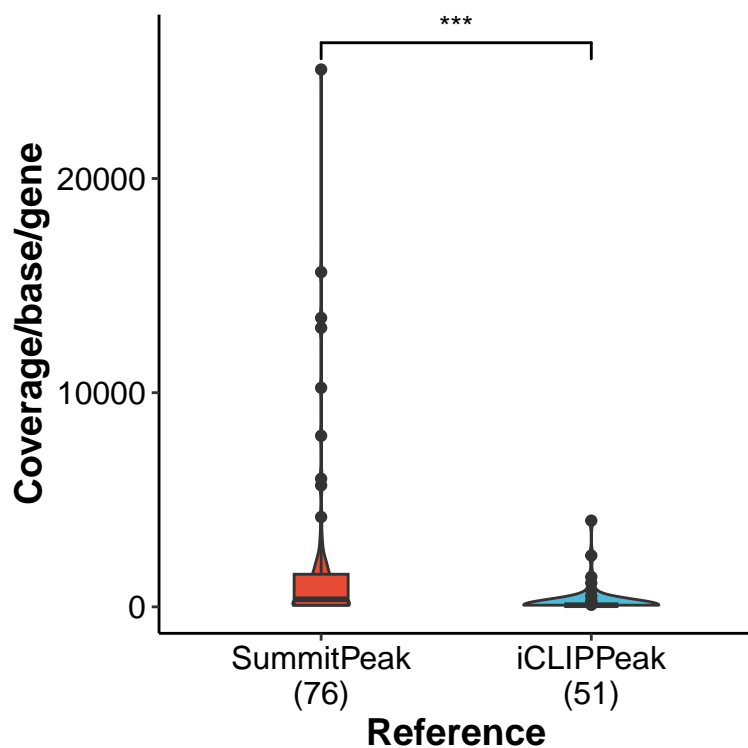


chip_bam



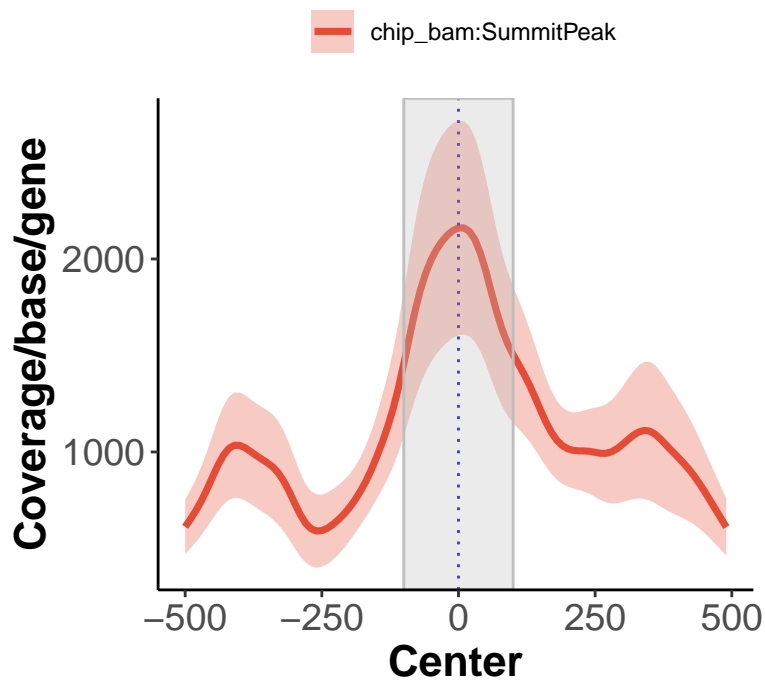


post hoc TukeyHSD test

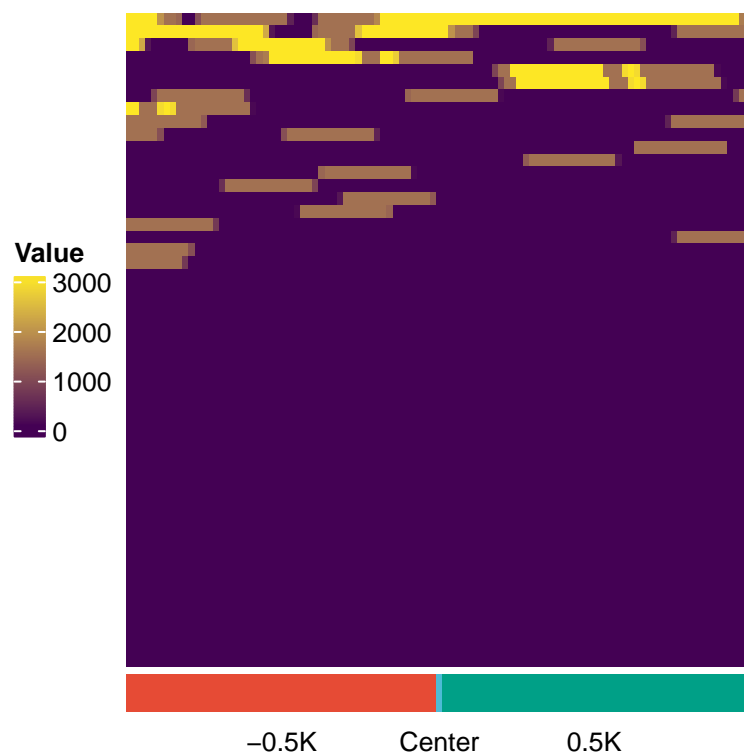
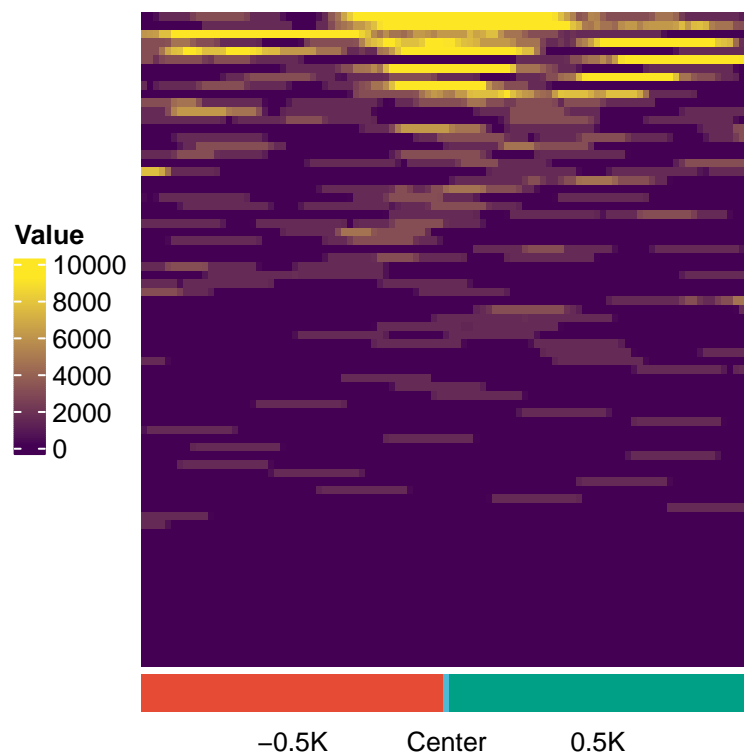
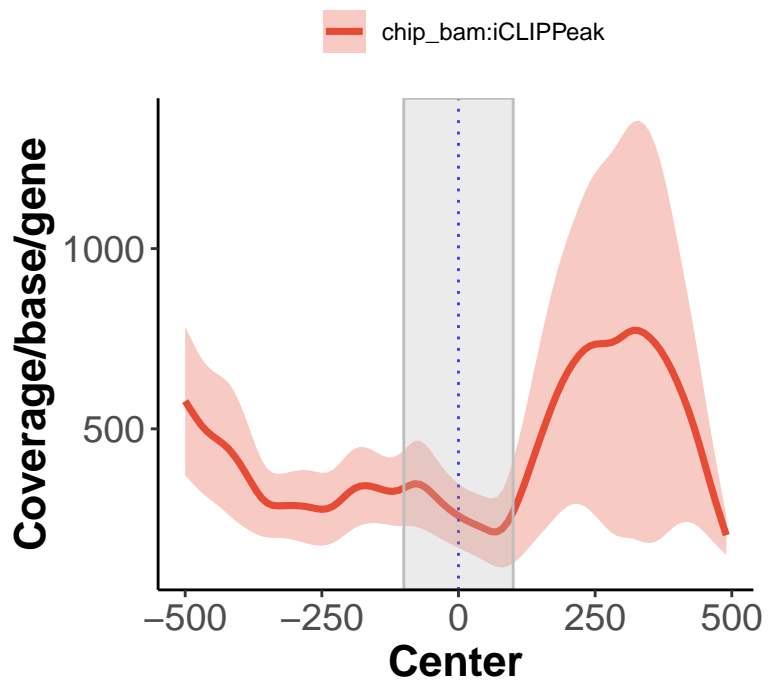
diff	lwr	upr	p adj
-1616.018	-2769.494	-462.543	0.0064

iCLIPPeak-SummitPeak

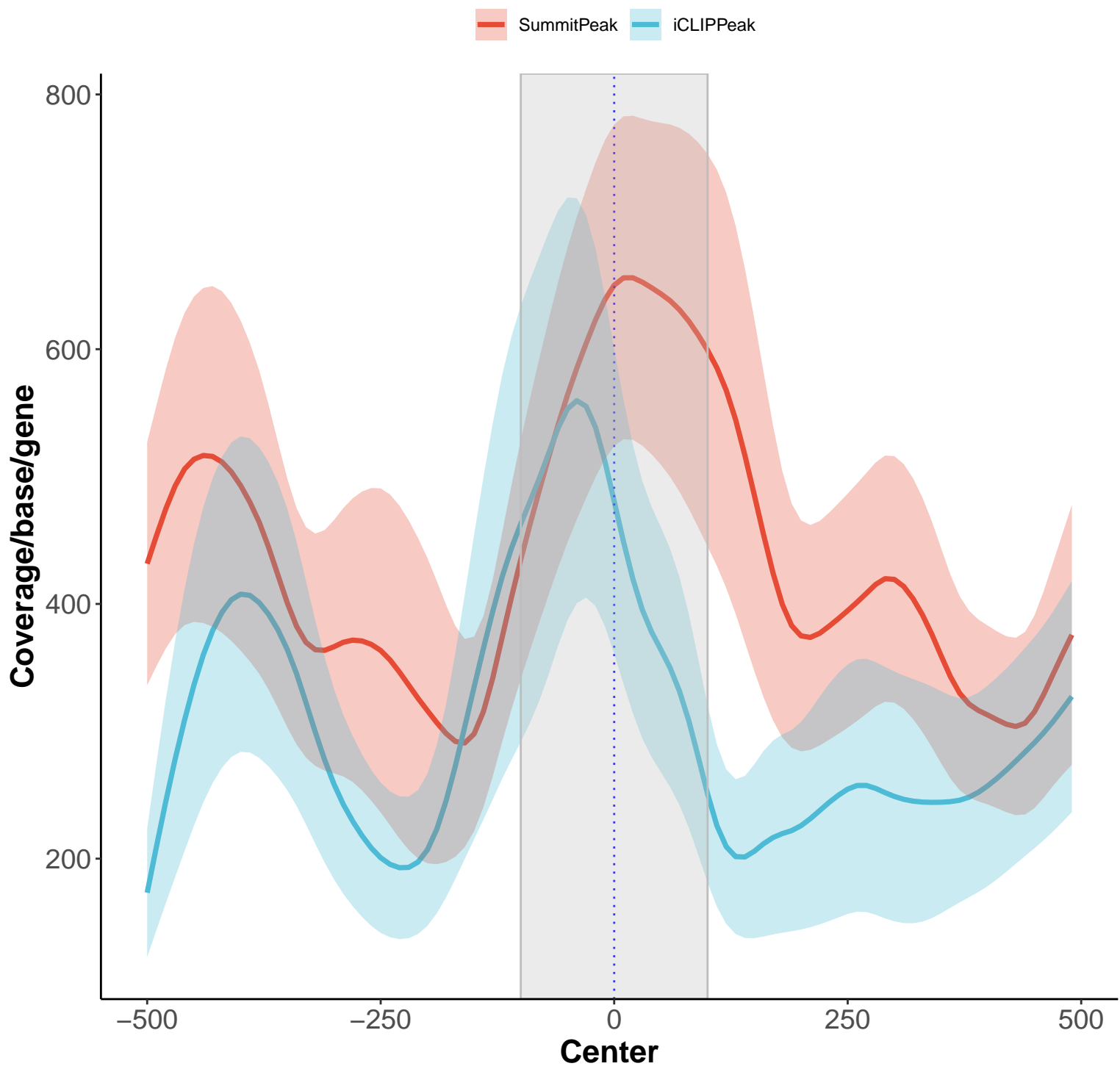
chip_bam:SummitPeak

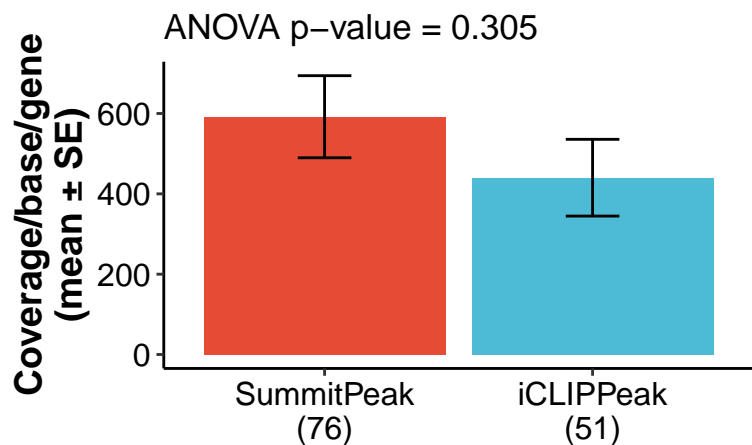
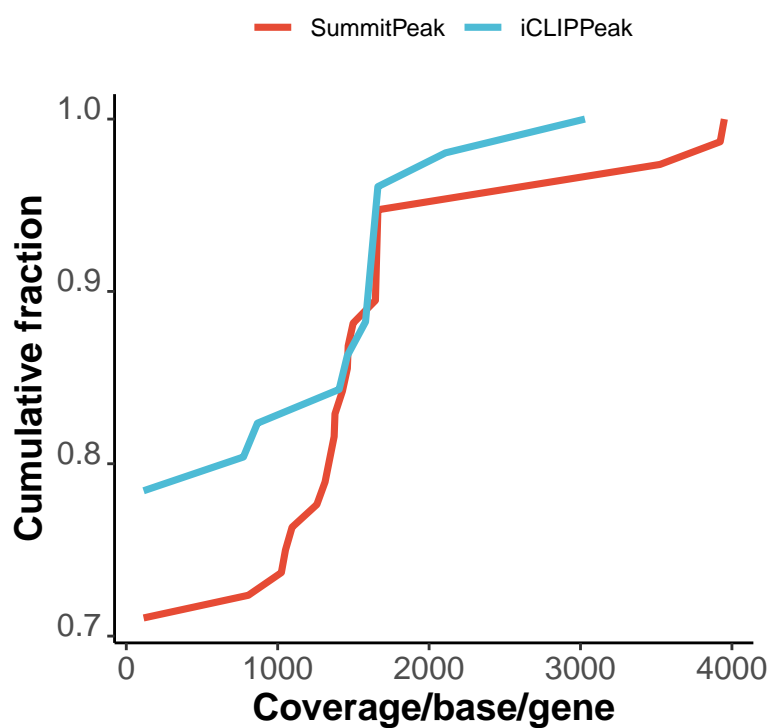
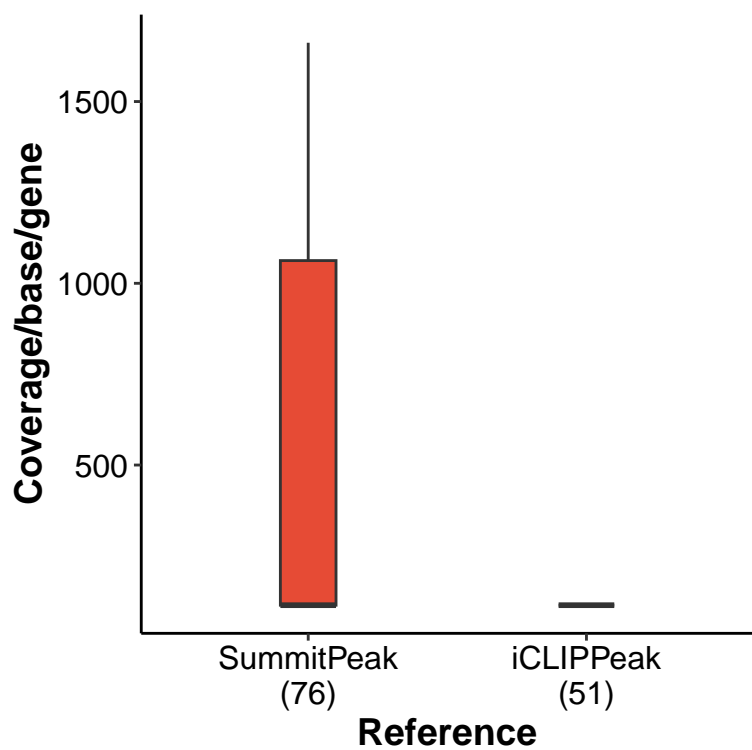
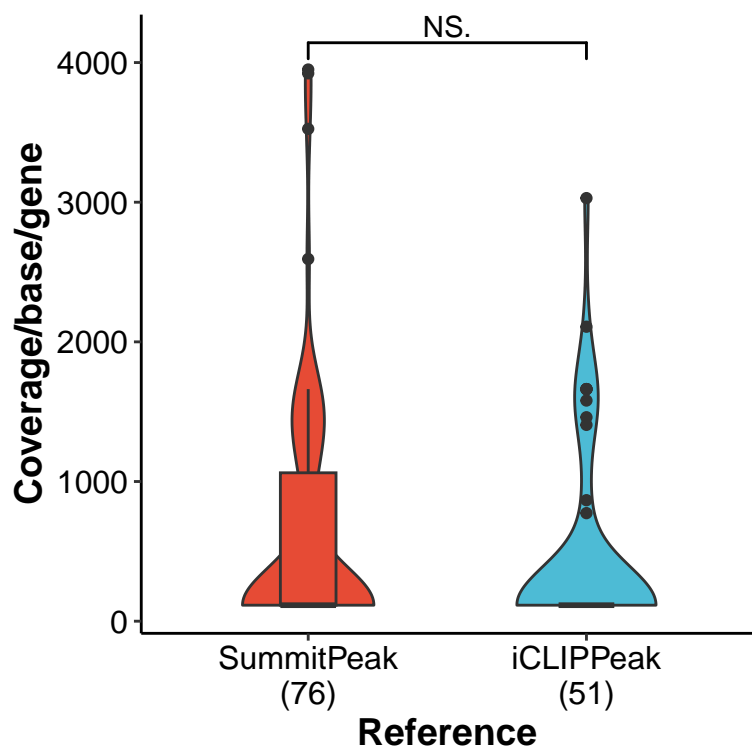


chip_bam:iCLIPPeak



chip_input

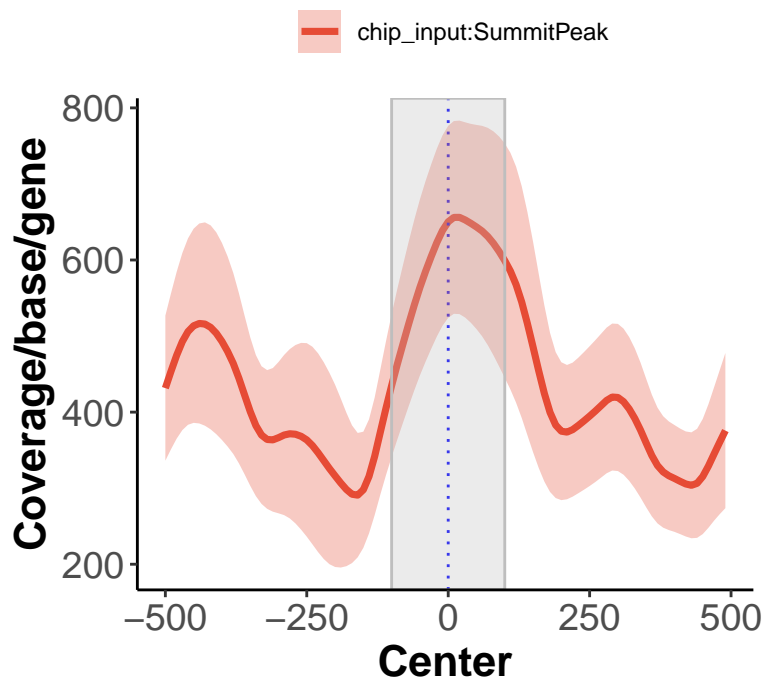




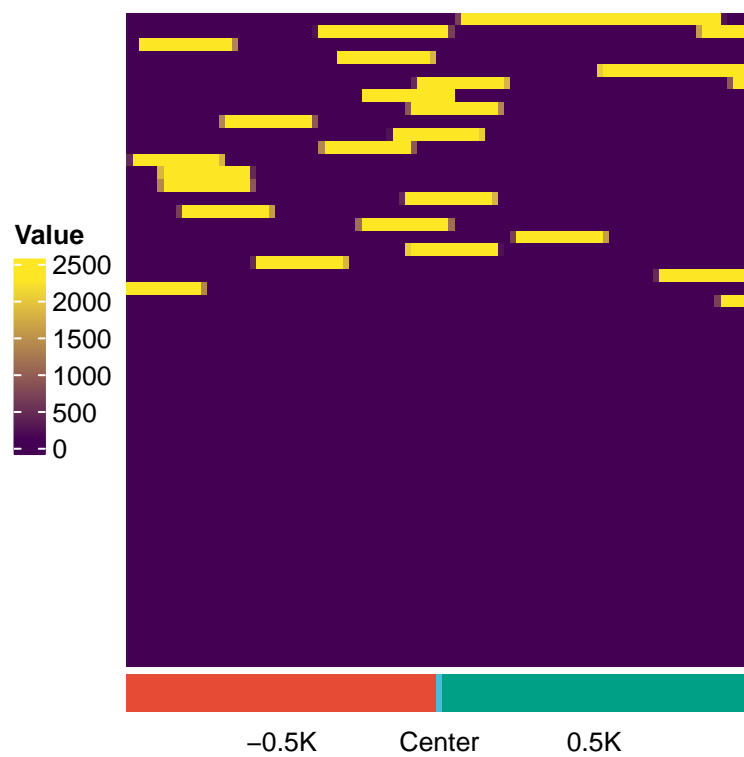
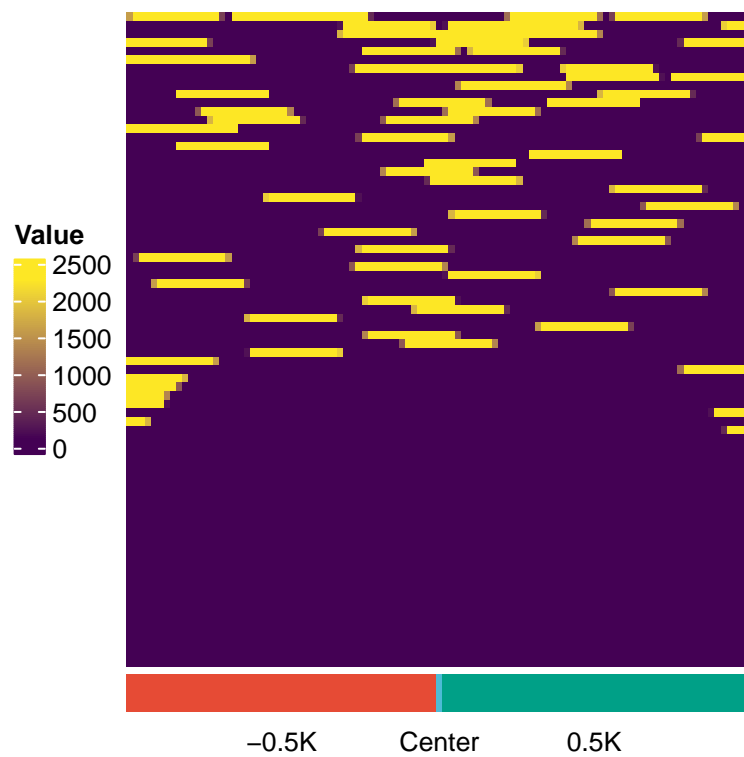
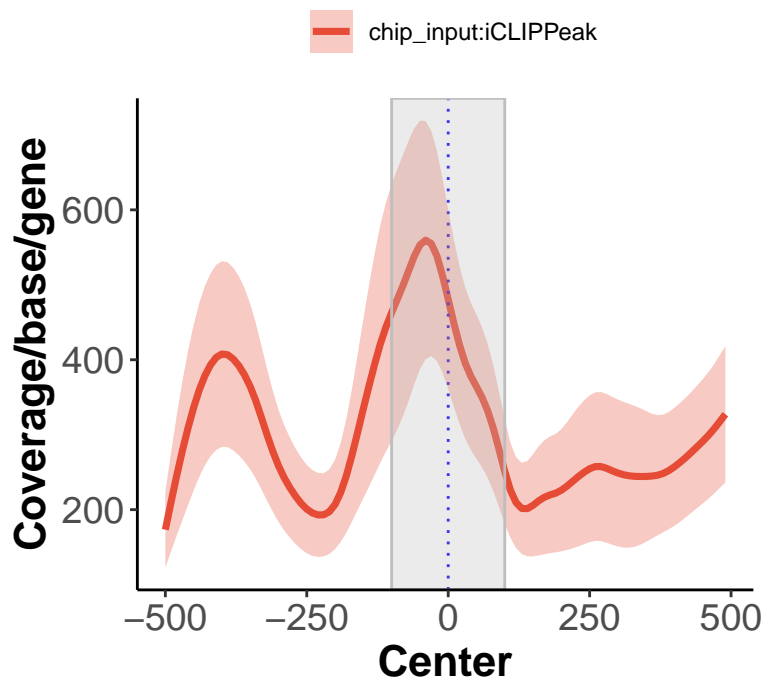
post hoc TukeyHSD test

	diff	lwr	upr	p adj
iCLIPPeak-SummitPeak	-151.795	-443.34	139.751	0.305

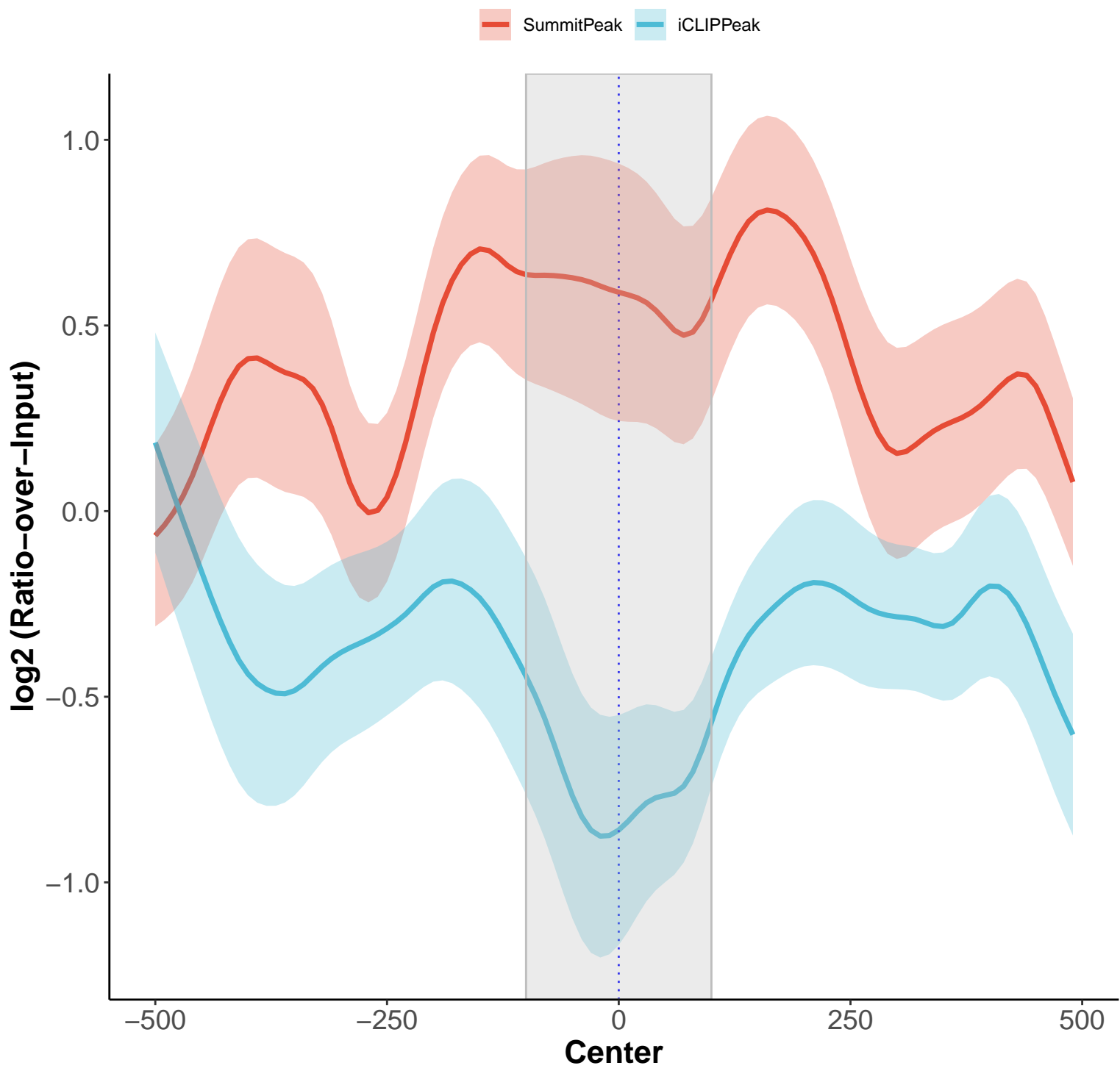
chip_input:SummitPeak

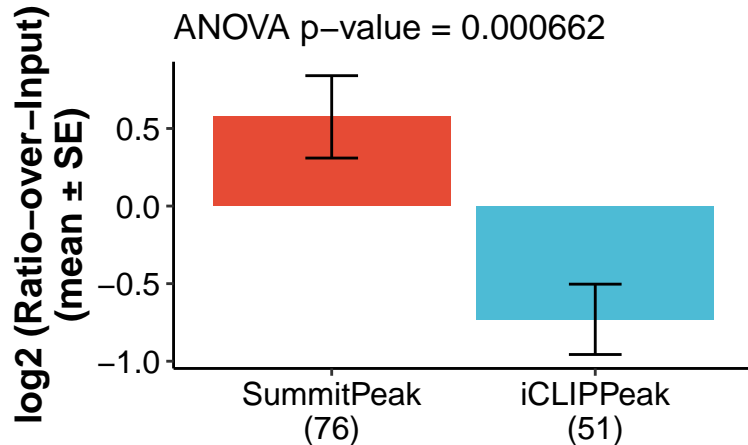
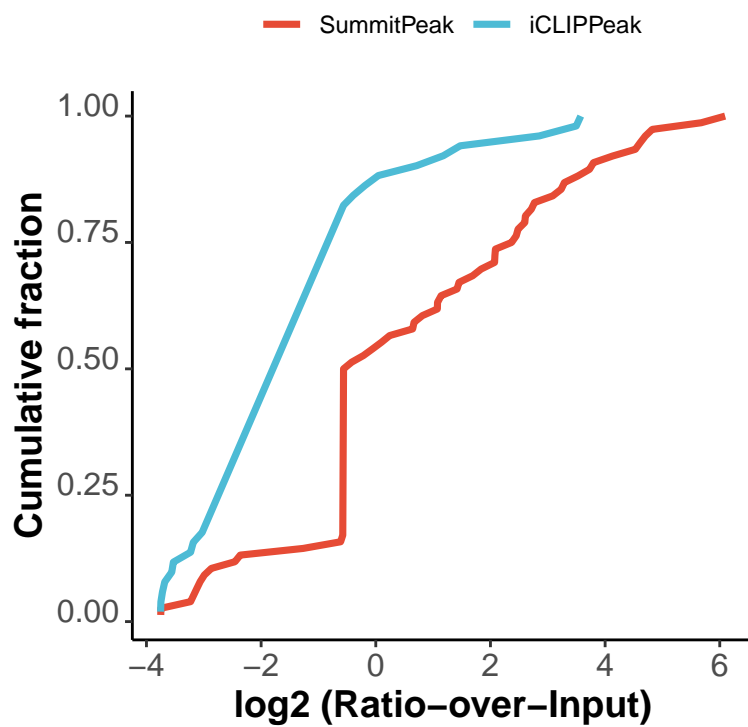
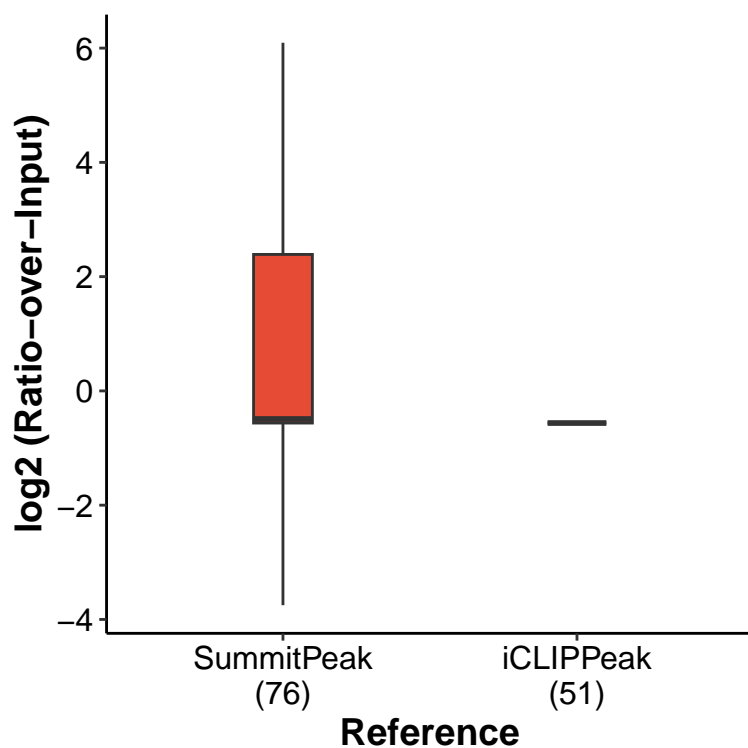
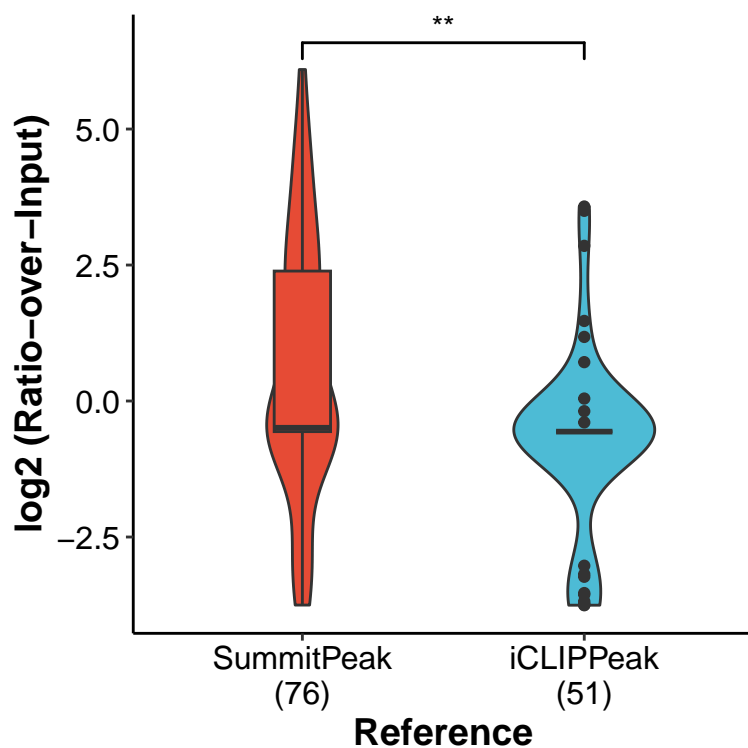


chip_input:iCLIPPeak



chip_bam

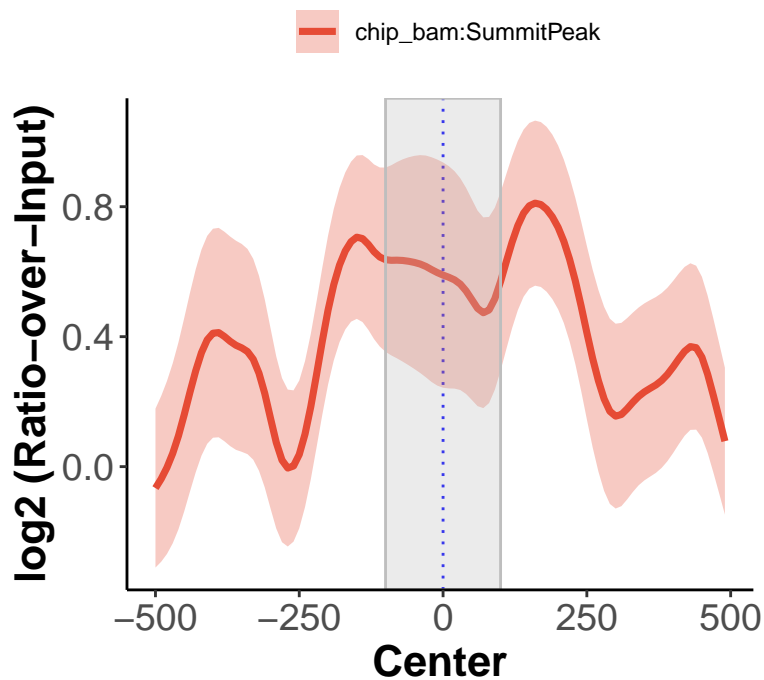




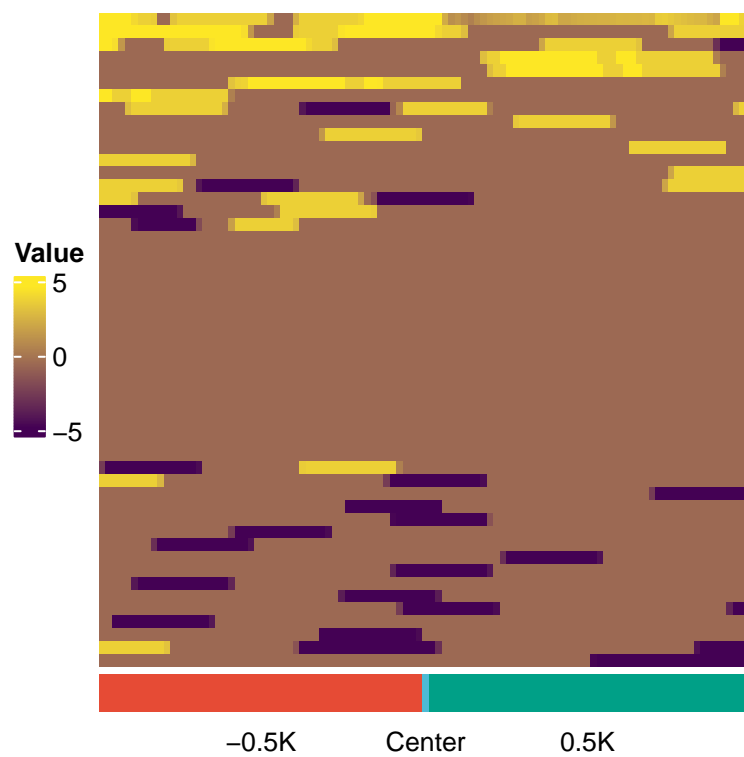
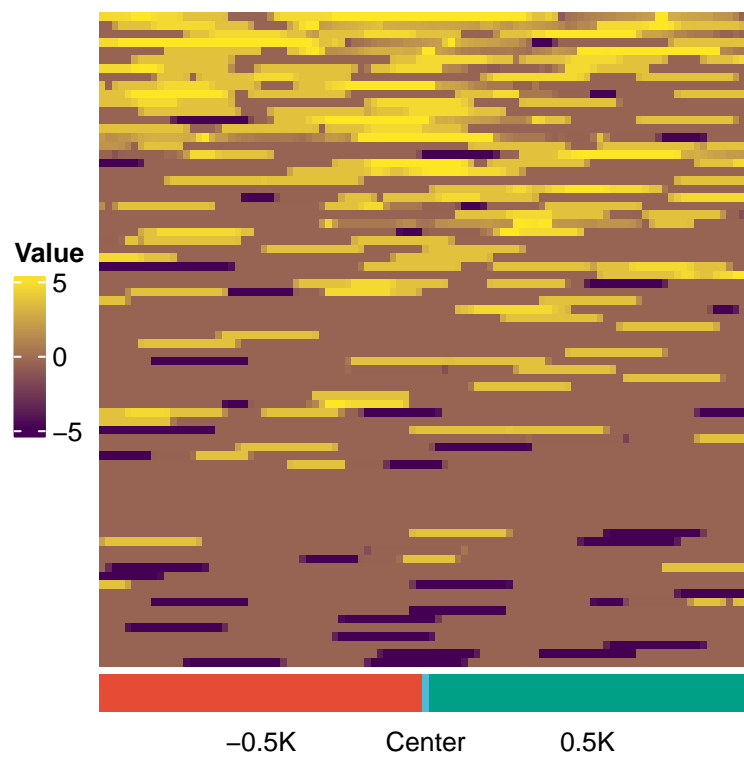
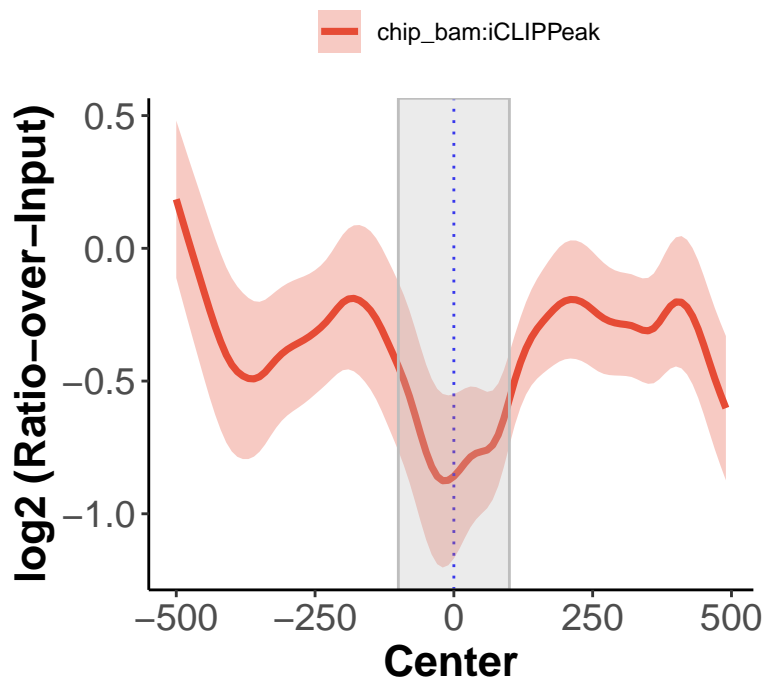
post hoc TukeyHSD test

	diff	lwr	upr	p adj
iCLIPPeak-SummitPeak	-1.305	-2.044	-0.566	0.000662

chip_bam:SummitPeak



chip_bam:iCLIPPeak



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, 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
```