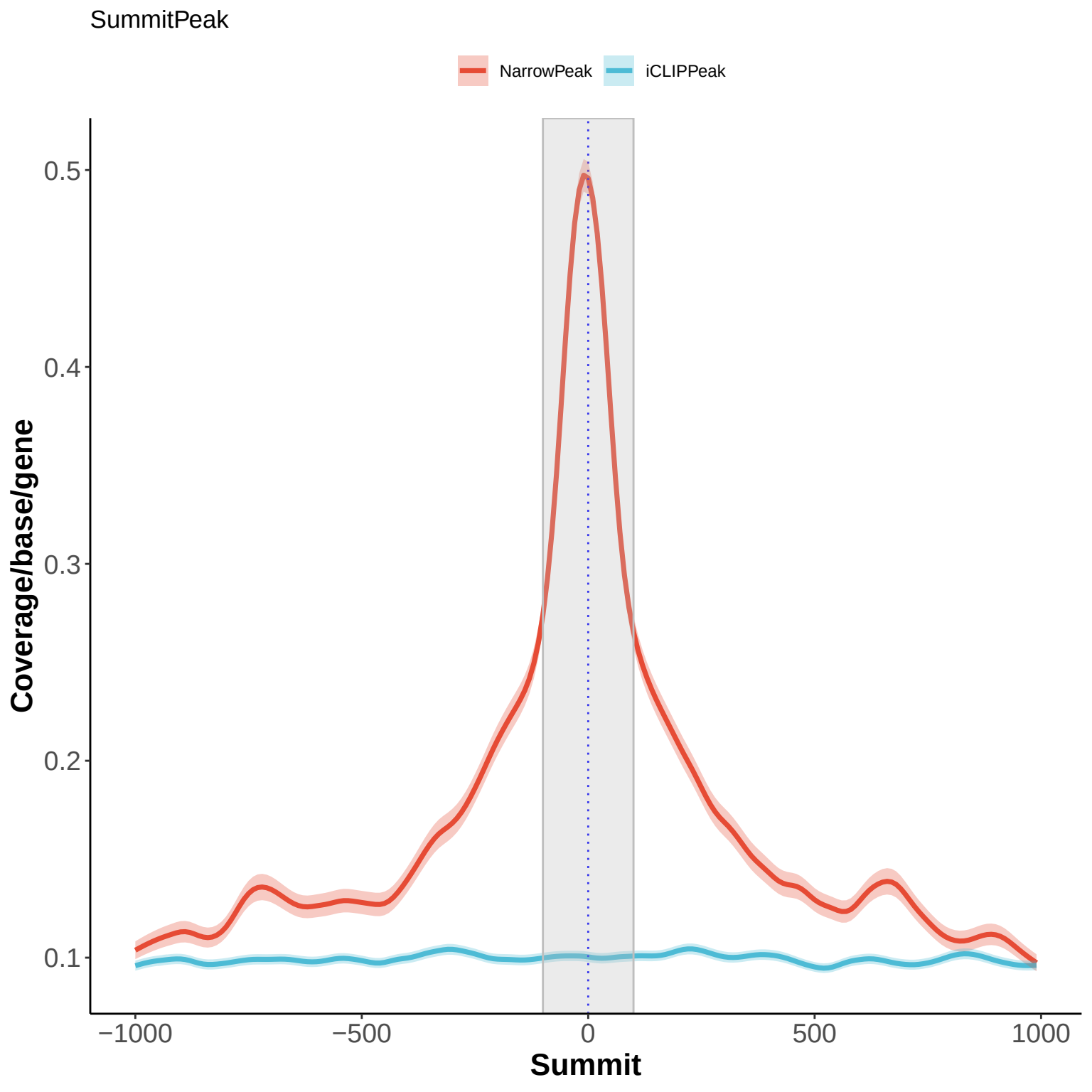
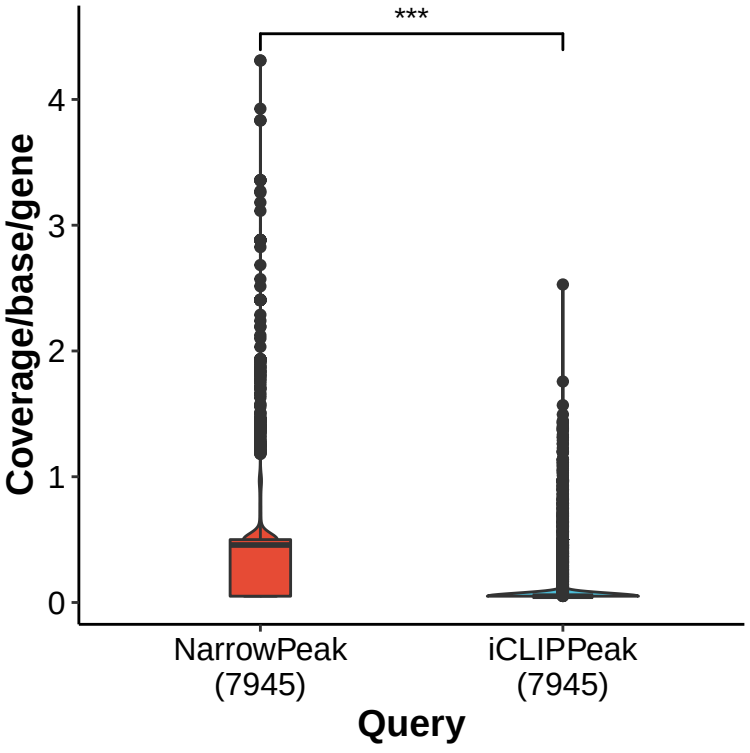
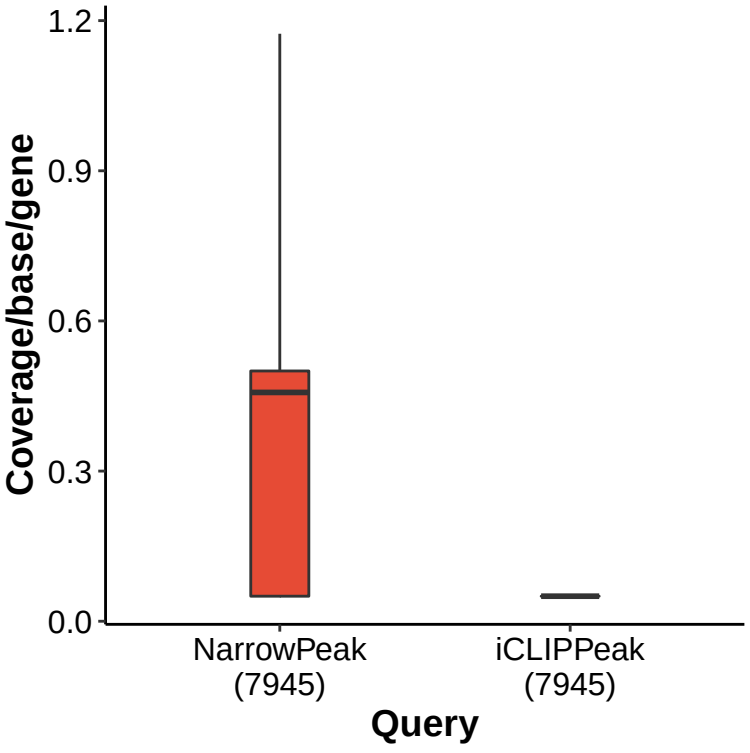
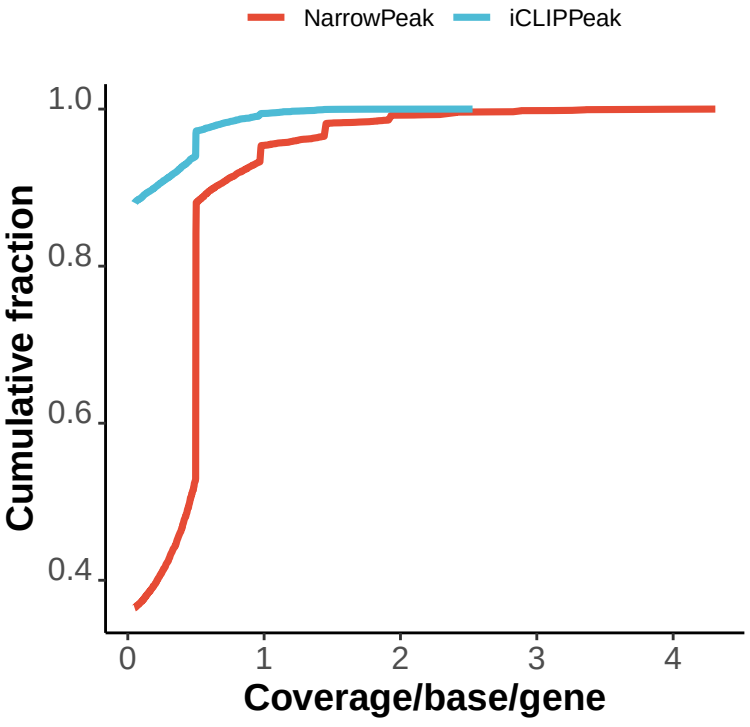
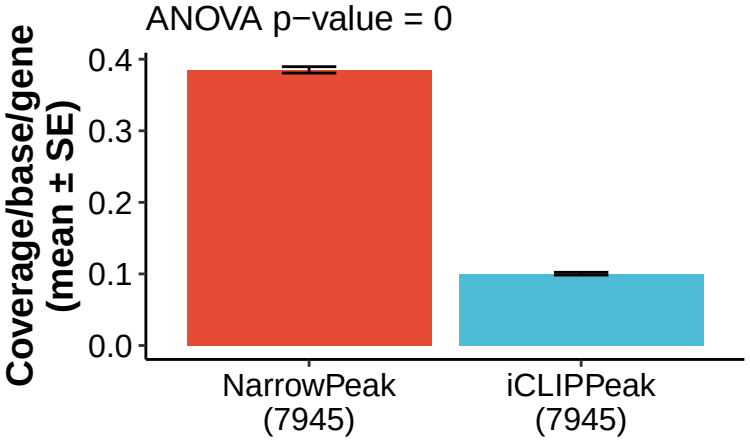

SummitPeak
NarrowPeak
iCLIPPeak
0.5
0.4
0.3
0.2
0.1
Coverage/base/gene
−1000
−500
0
500
1000
Summit



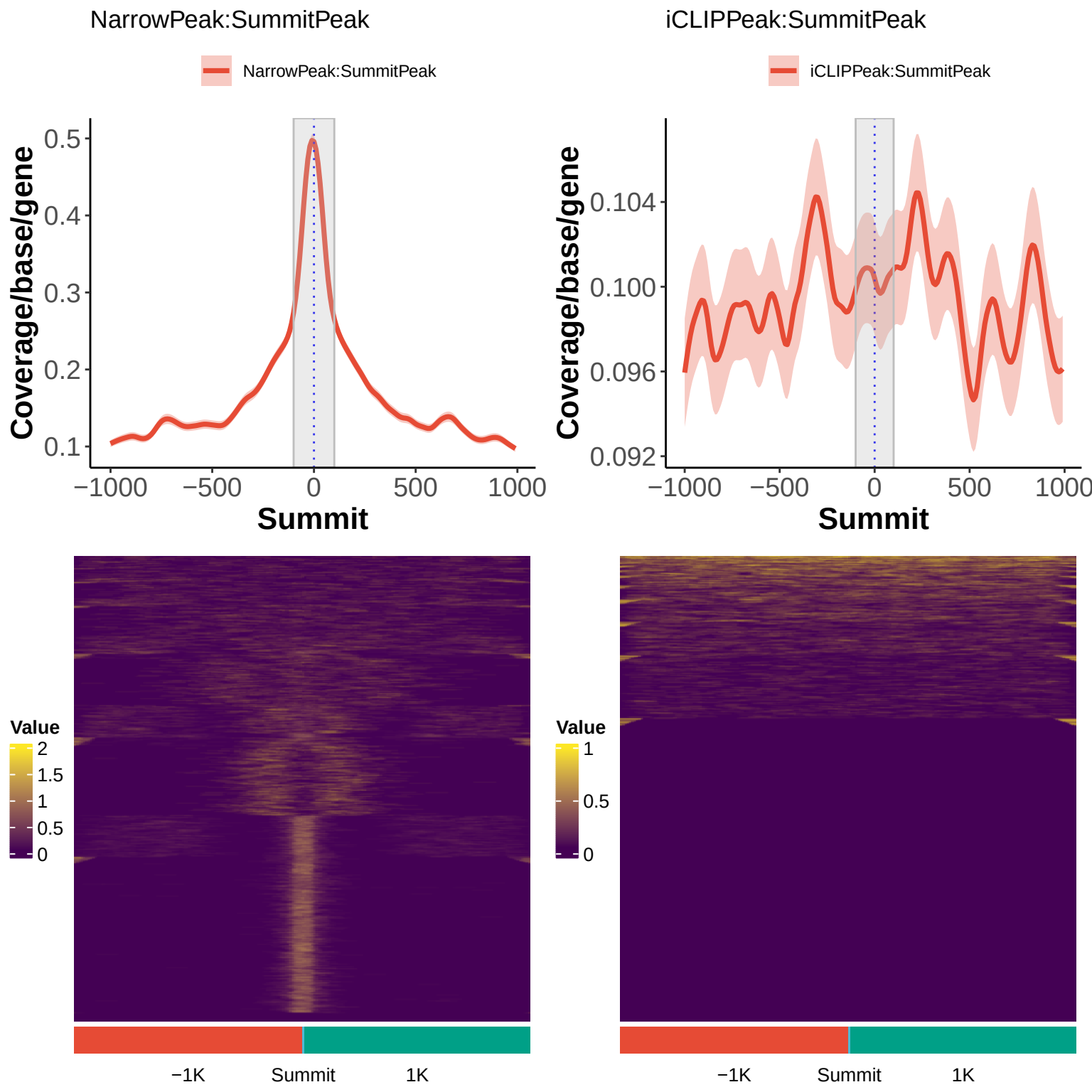






post hoc TukeyHSD test

	diff	lwr	upr	p adj
iCLIPPeak−NarrowPeak	−0.285	−0.294	−0.275	2.04e−08


NarrowPeak:SummitPeak
NarrowPeak:SummitPeak
Coverage/base/gene
0.5
0.4
0.3
0.2
0.1
−1000
−500
0
500
1000
Summit
iCLIPPeak:SummitPeak
iCLIPPeak:SummitPeak
Coverage/base/gene
0.104
0.100
0.096
0.092
−1000
−500
0
500
1000
Summit
Value
2
1.5
1
0.5
0
−1K
Summit
1K
Value
1
0.5
0
−1K
Summit
1K

Plotting parameters:

functionName: "plot_locus"
queryFiles: c(NarrowPeak =
C:/Users/greenblatt/AppData/Local/Programs/R/R−4.2.1/library/GenomicPlot/extdata/test_chip_peak_chr19.narrowPeak
iCLIPPeak =
"C:/Users/greenblatt/AppData/Local/Programs/R/R−4.2.1/library/GenomicPlot/extdata/test_clip_peak_chr19.bed")
centerFiles: c(SummitPeak =
"C:/Users/greenblatt/AppData/Local/Programs/R/R−4.2.1/library/GenomicPlot/extdata/test_chip_peak_chr19.bed")
txdb: NULL
ext: c(−1000, 1000)
hl: c(−100, 100)
shade: TRUE
smooth: TRUE
importParams: list(offset = 0, fix_width = 100, fix_point = "center", norm = FALSE, useScore
= FALSE, outRle = TRUE, useSizeFactor = FALSE, genome = "hg19")
verbose: FALSE
binSize: 10
refPoint: "center"
Xlab: "Summit"
Ylab: "Coverage/base/gene"
inputFiles: NULL
stranded: TRUE
heatmap: TRUE
scale: FALSE
outPrefix: "test_plot_locus1"
rmOutlier: 0
transform: NA
statsMethod: "wilcox.test"
heatRange: NULL
hw: c(8, 8)
nc: 2