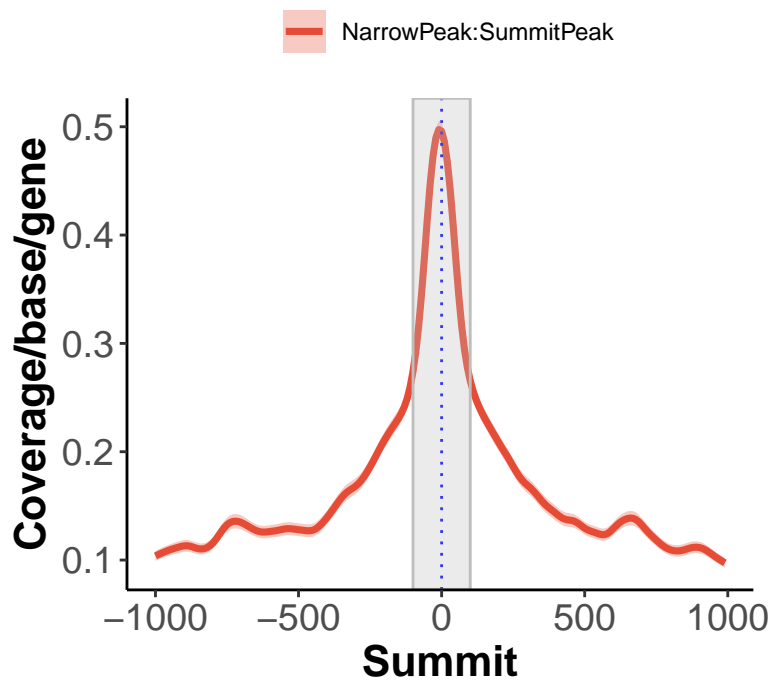


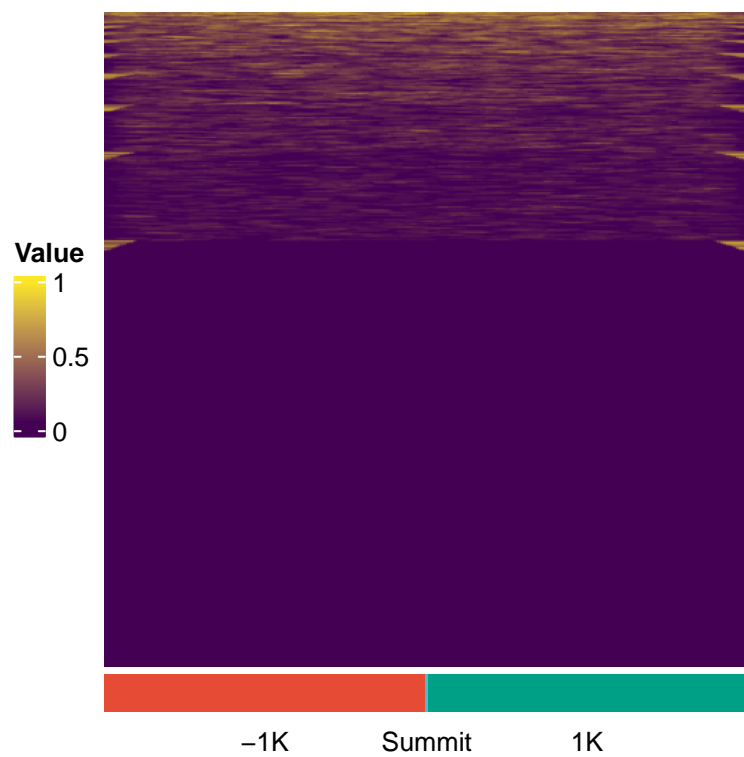
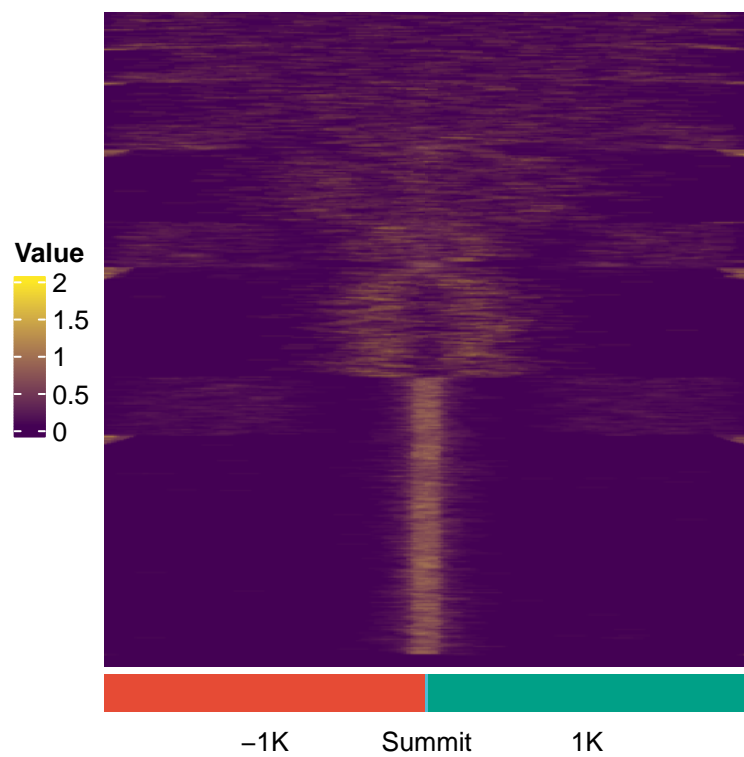
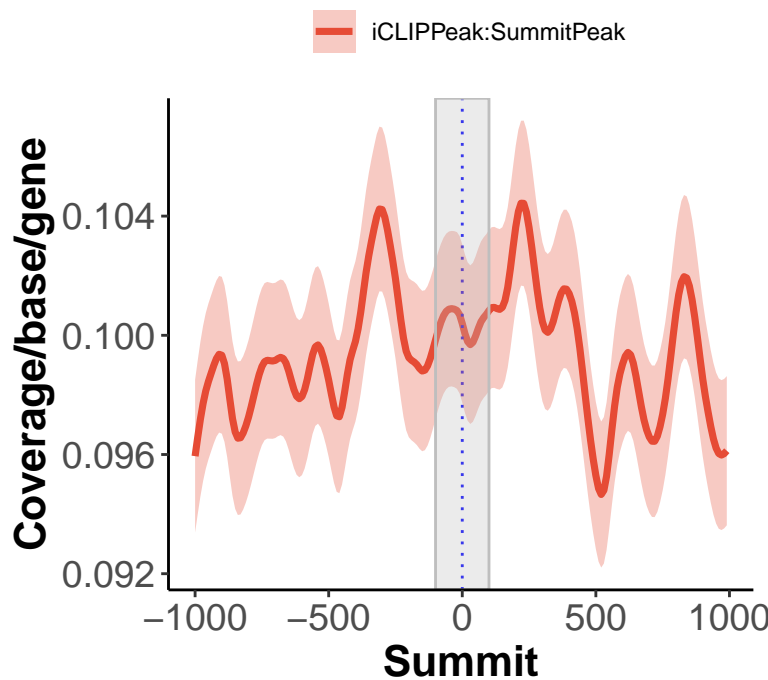
post hoc TukeyHSD test

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

NarrowPeak:SummitPeak



iCLIPPeak:SummitPeak



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
```