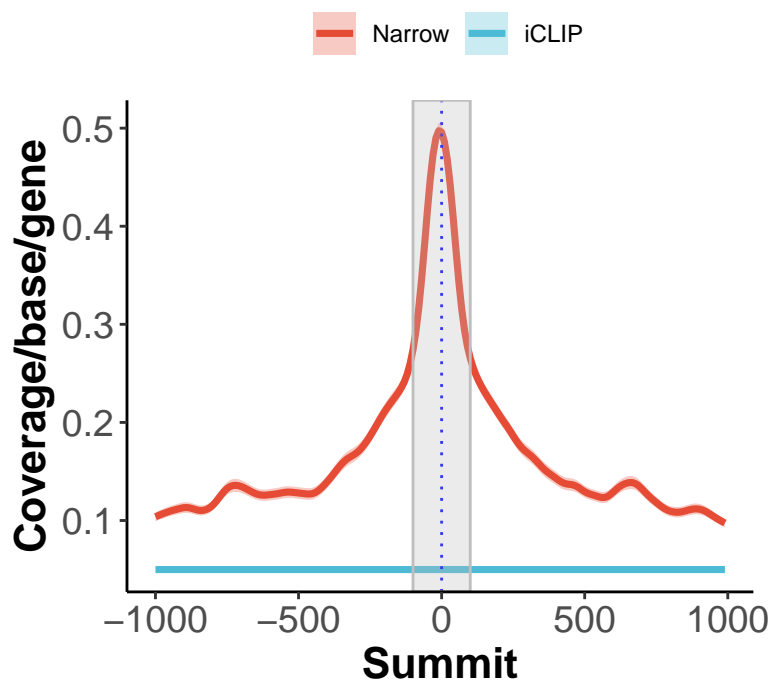
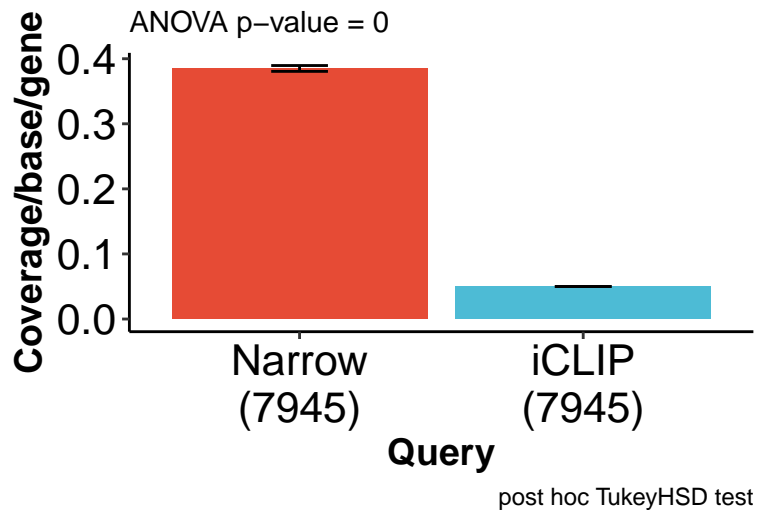


Summit



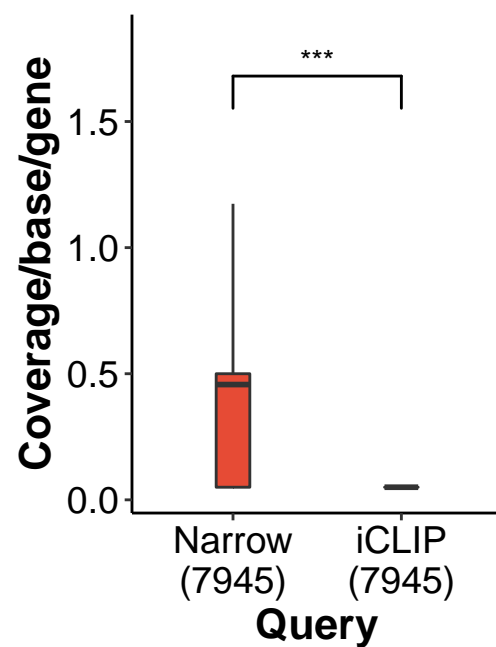
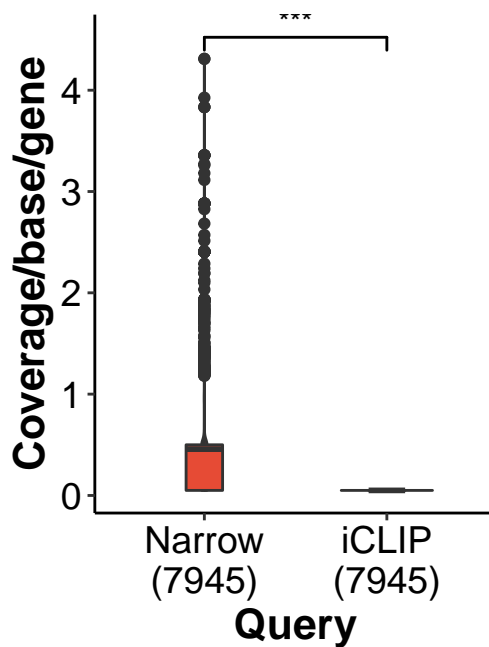
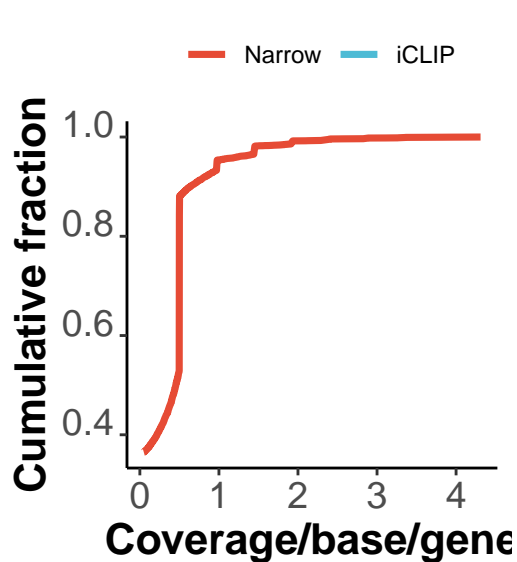

Mean + SE



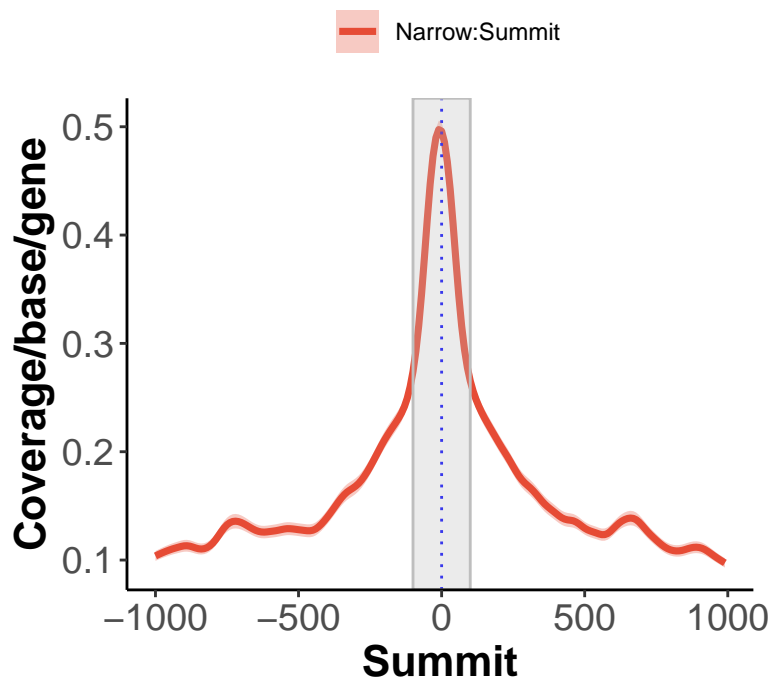
diff	lwr	upr	p adj
-0.335	-0.344	-0.326	2.04e-08

iCLIP-Narrow

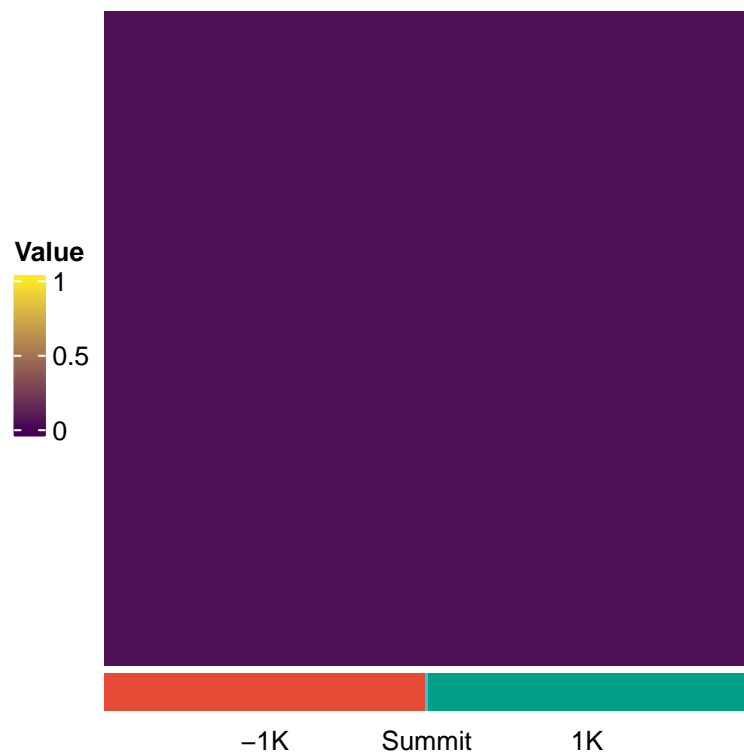
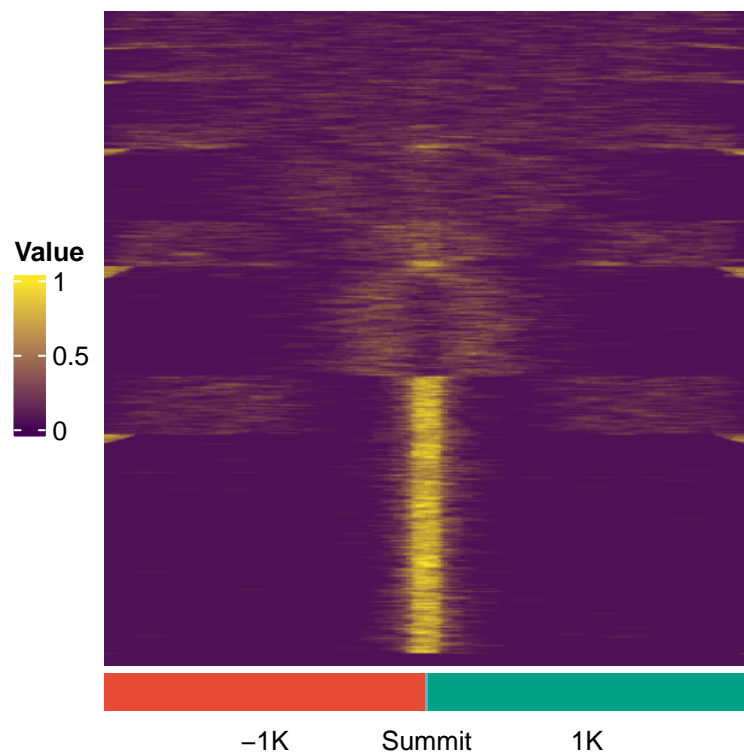
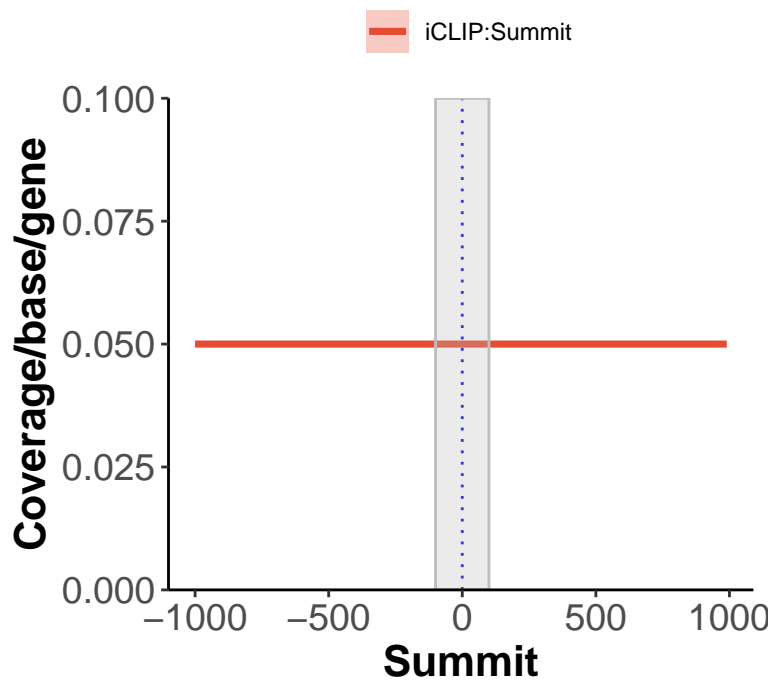
Cumulative fraction of C

Query  Narrow  iCLIPQuery  Narrow  iCLIP

Narrow:Summit



iCLIP:Summit



Plotting parameters:

```
functionName: "plot_locus"  
queryFiles: c(Narrow =  
"C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/test_chip_peak_chr19.narrowPeak",  
iCLIP =  
"C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/test_clip_peak_chr19.bed")  
centerFiles: c(Summit =  
"C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/test_chip_peak_chr19.bed")  
txdb: NULL  
ext: c(-1000, 1000)  
hl: c(-100, 100)  
shade: TRUE  
smooth: TRUE  
handleInputParams: 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: TRUE  
transform: NA  
statsMethod: "wilcox.test"  
heatRange: c(0, 1)  
hw: c(8, 8)  
nc: 2
```