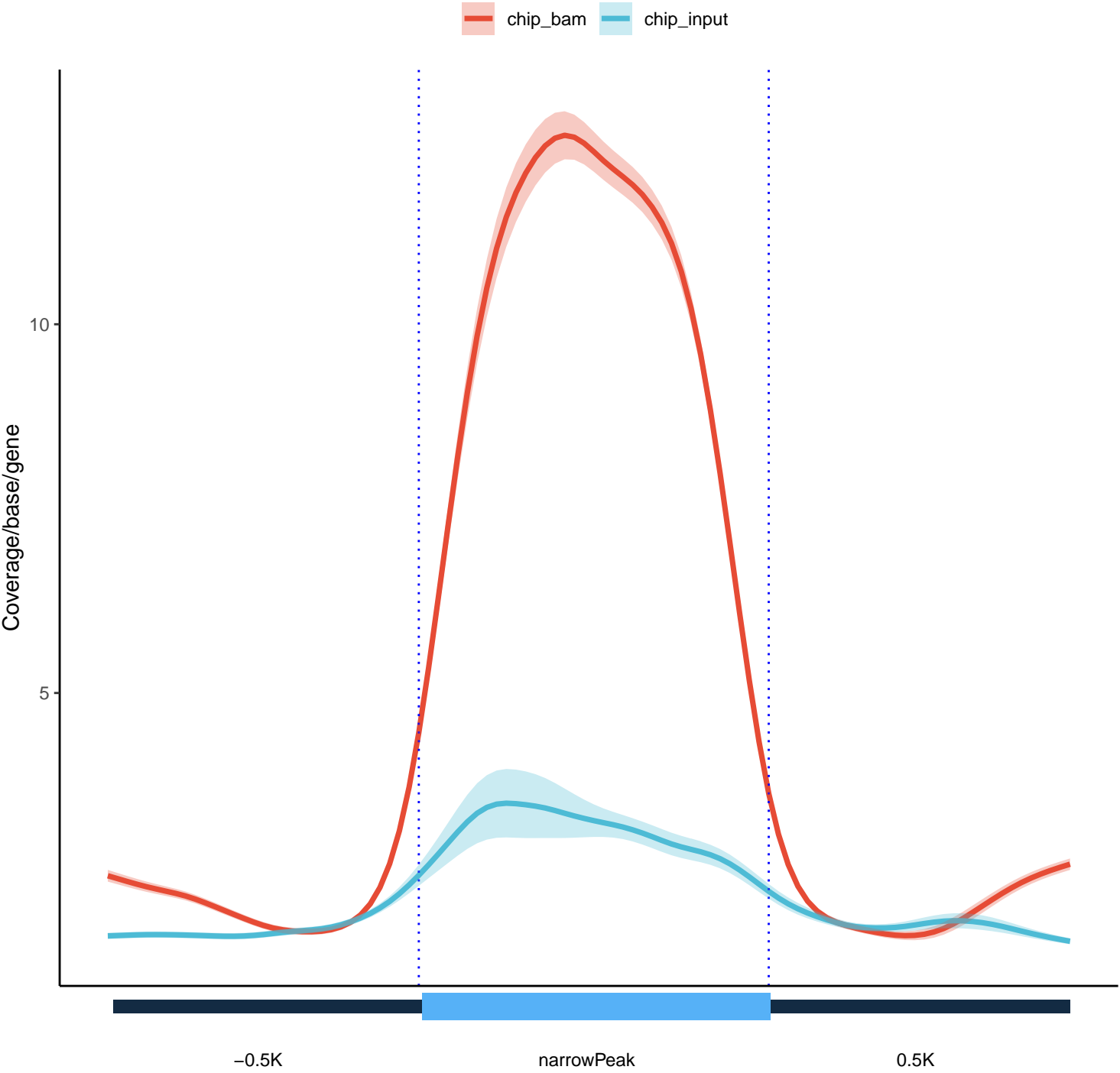
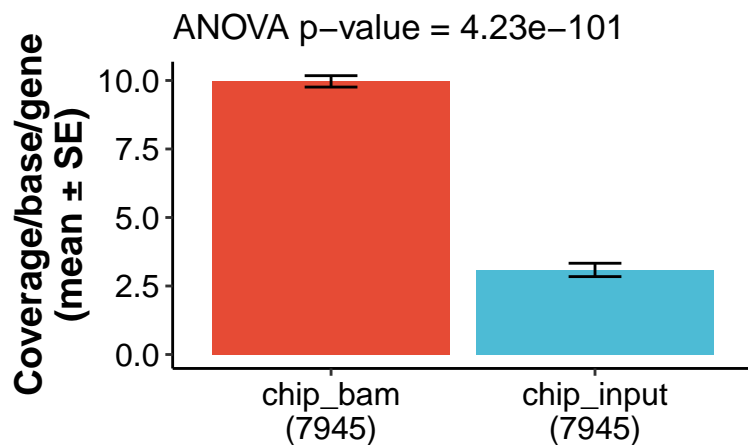
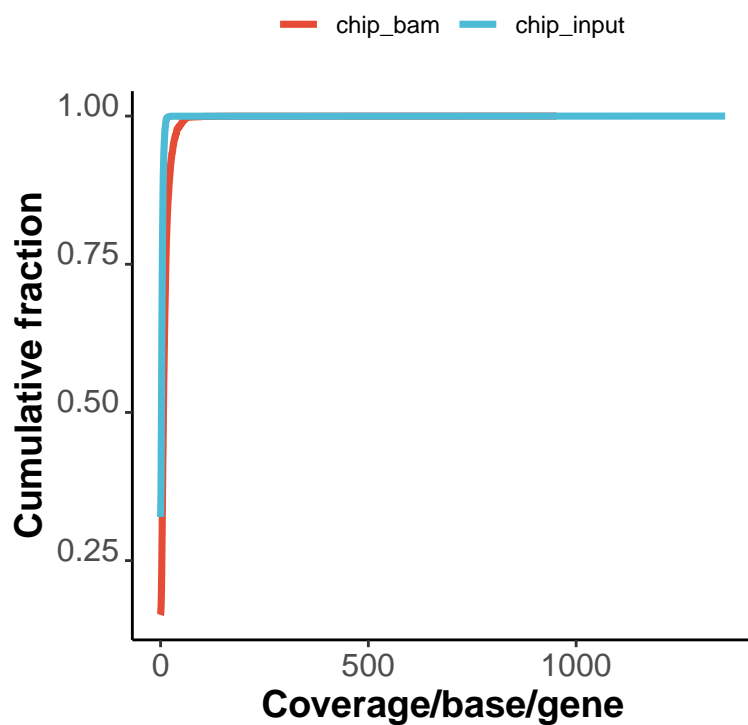
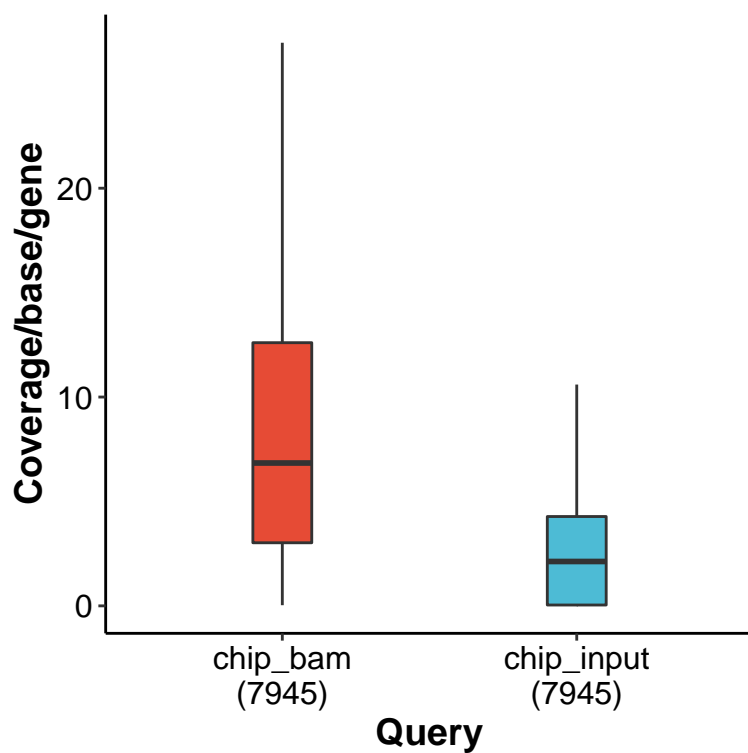
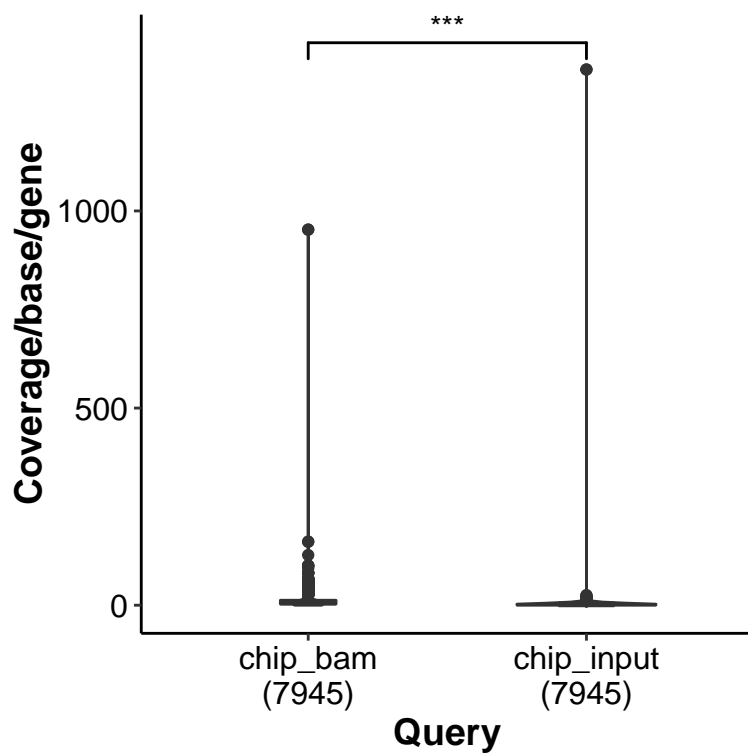


NarrowPeak



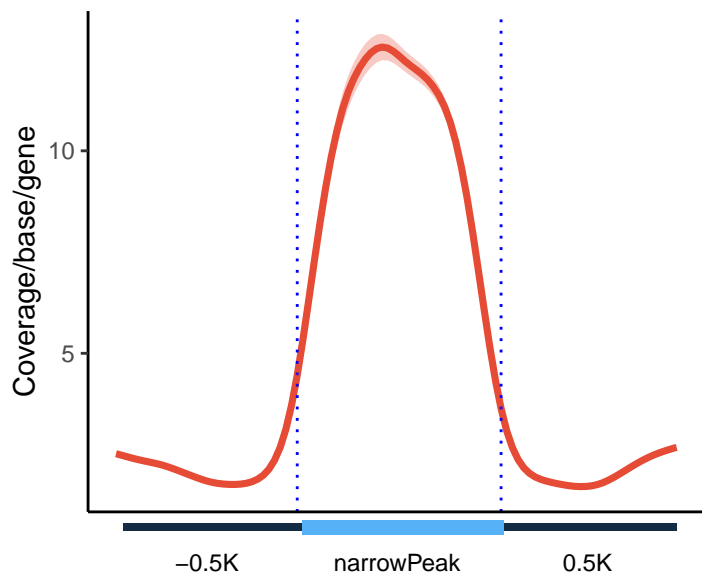


post hoc TukeyHSD test

	diff	lwr	upr	p adj
chip_input-chip_bam	-6.881	-7.509	-6.254	$2.04e-08$

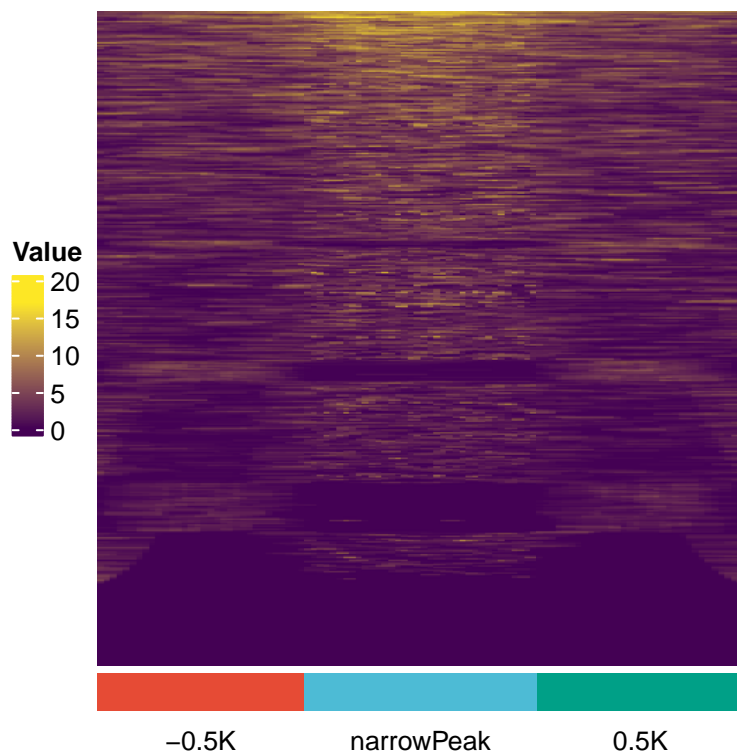
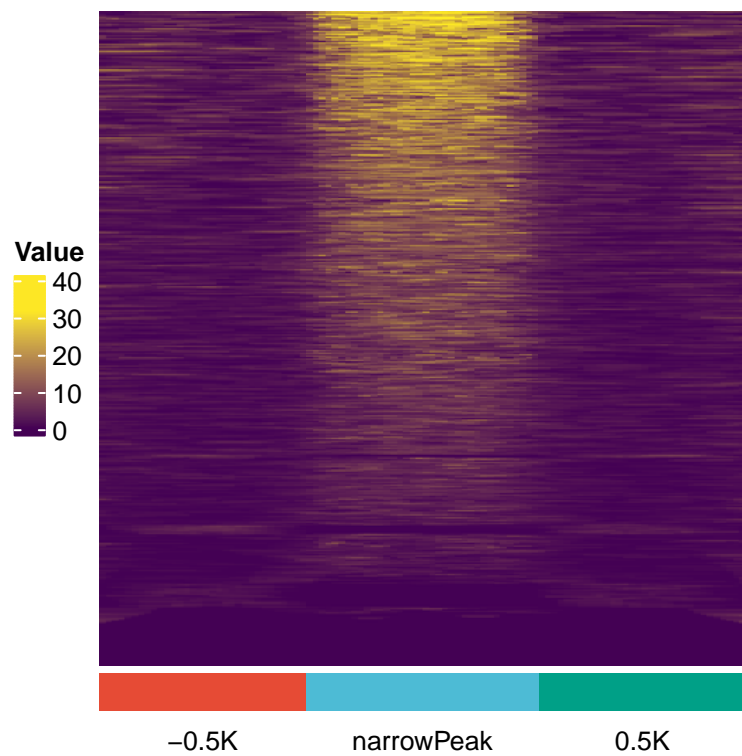
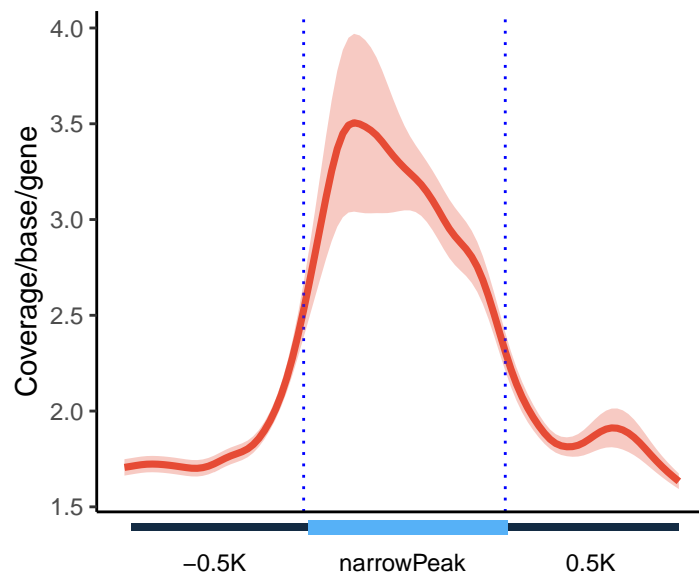
NarrowPeak

chip\_bam:NarrowPeak

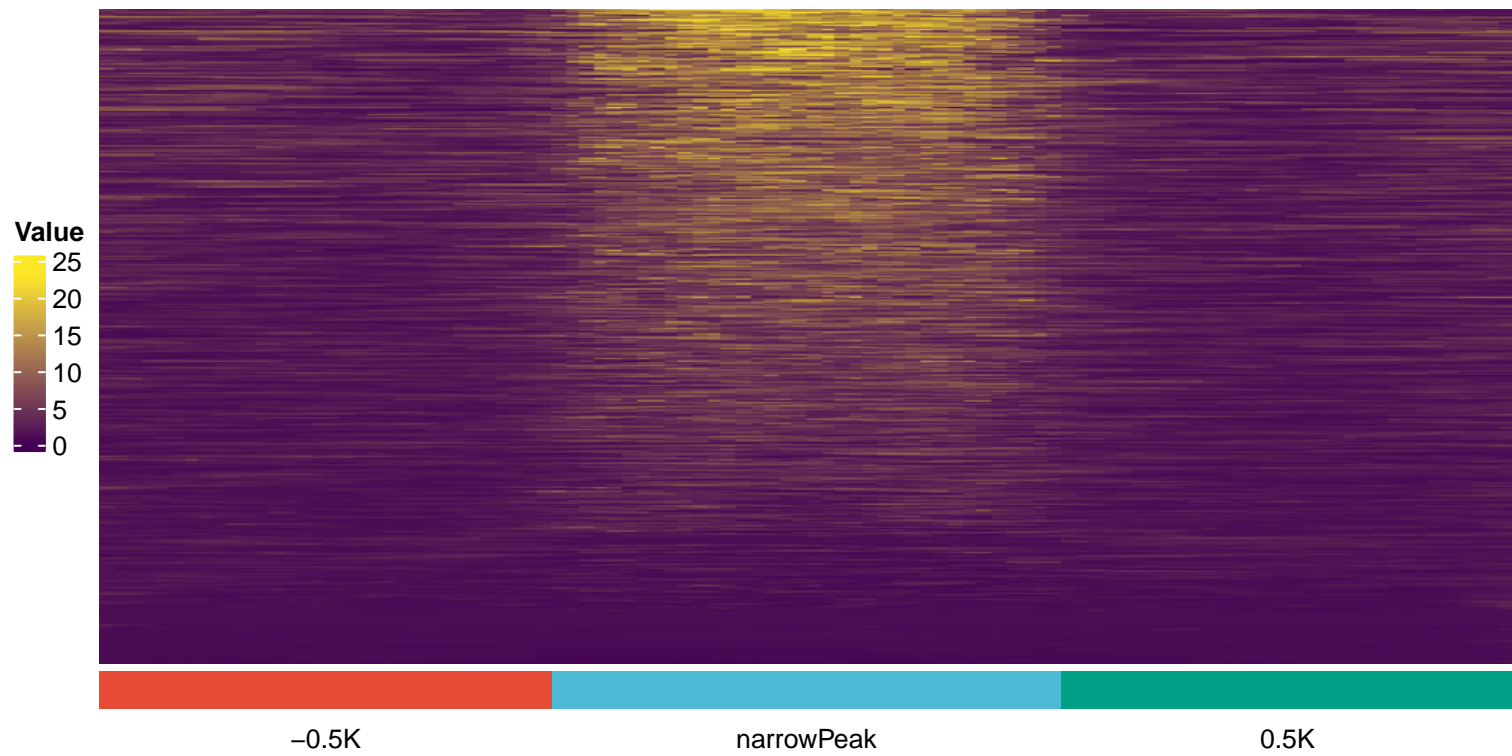
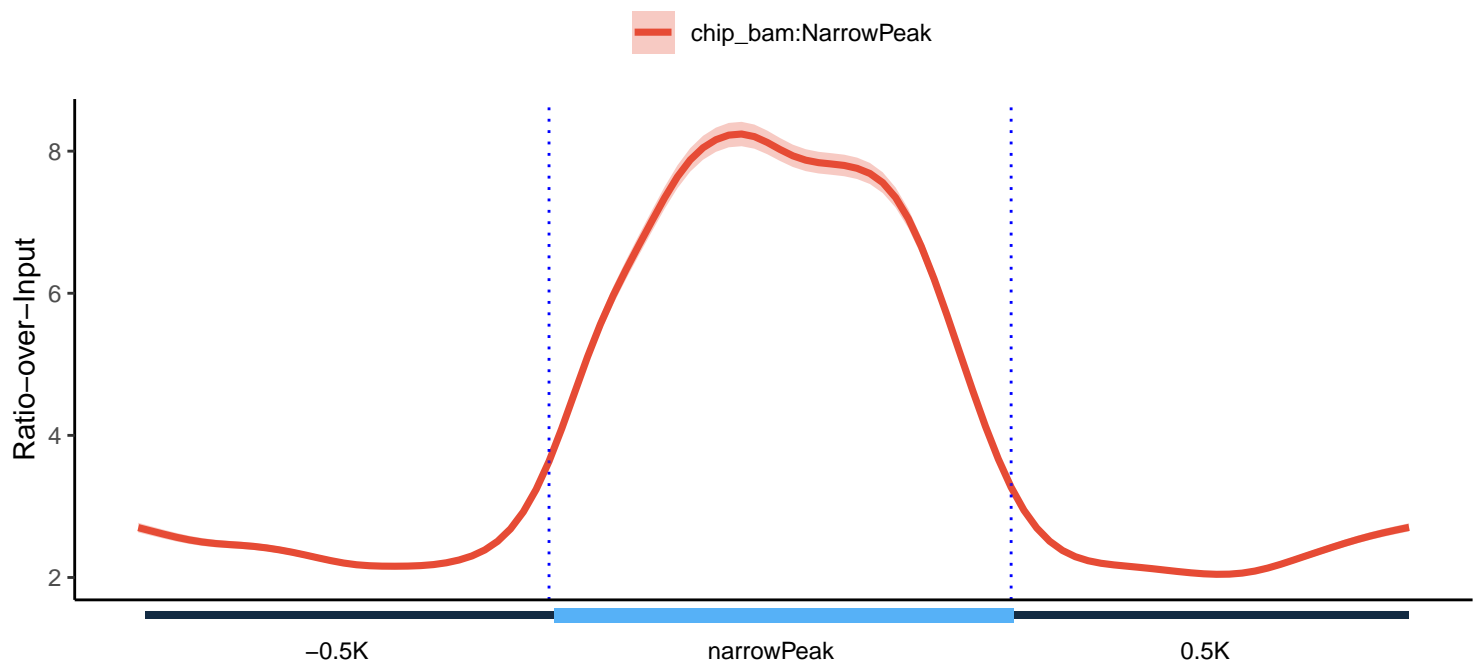


NarrowPeak

chip\_input:NarrowPeak



# NarrowPeak



Plotting parameters:

```
functionName: "plot_region"
queryFiles: c(chip_bam =
"C:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/GenomicPlot/extdata/chip_treat_chr19.bam")
centerFiles: c(NarrowPeak =
C:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/GenomicPlot/extdata/test_chip_peak_chr19.narrowPeak
txdb: NULL
regionName: "narrowPeak"
inputFiles: c(chip_input =
"C:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/GenomicPlot/extdata/chip_input_chr19.bam")
nbins: 100
importParams: list(offset = 0, fix_width = 150, fix_point = "start", norm = TRUE, useScore =
FALSE, outRle = TRUE, useSizeFactor = FALSE, genome = "hg19")
verbose: FALSE
scale: FALSE
heatmap: TRUE
fiveP: -500
threeP: 500
smooth: TRUE
stranded: TRUE
transform: NA
outPrefix: "test_plot_region"
rmOutlier: 0
heatRange: NULL
Ylab: "Coverage/base/gene"
statsMethod: "wilcox.test"
hw: c(8, 8)
nc: 2
```