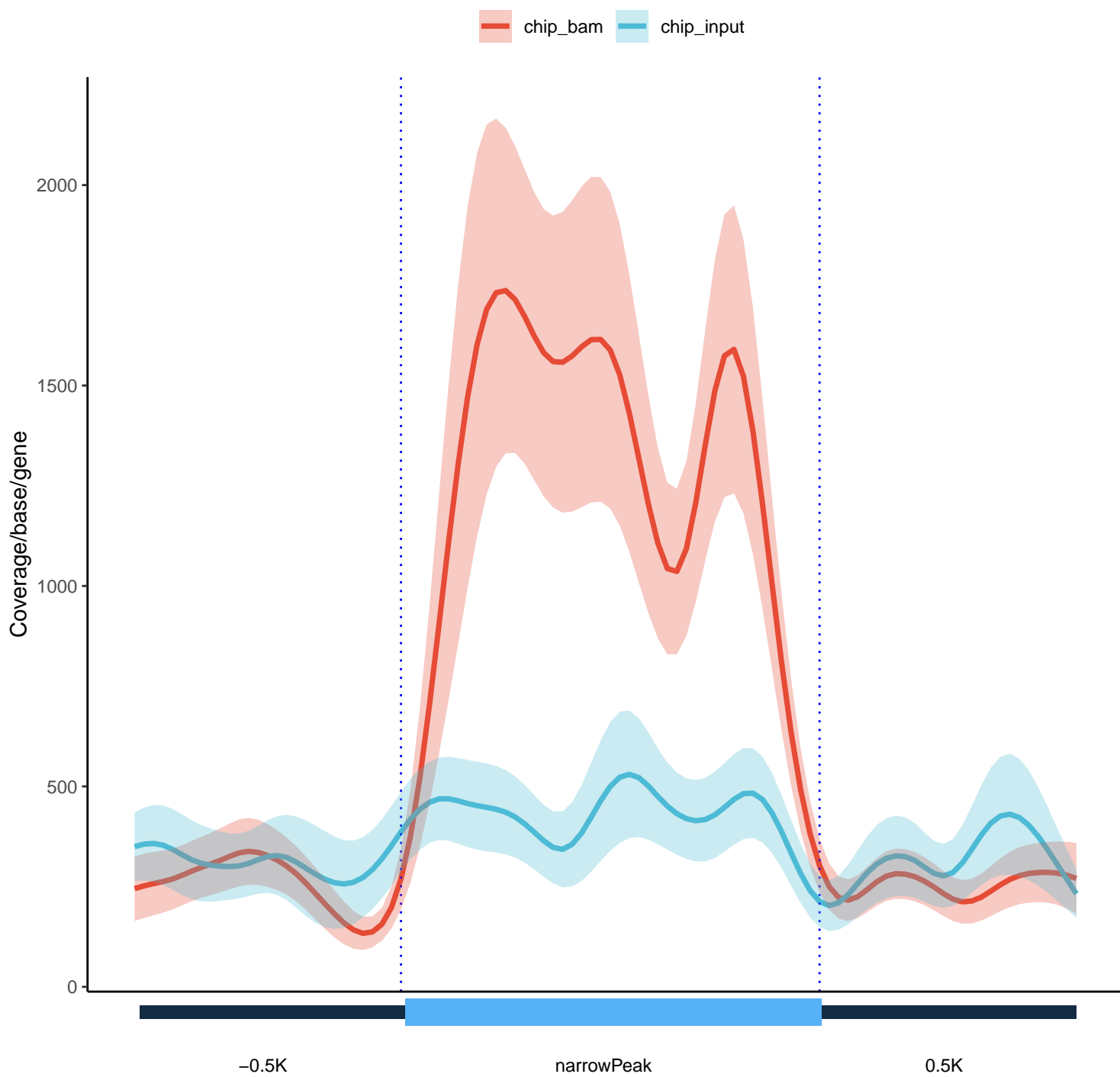
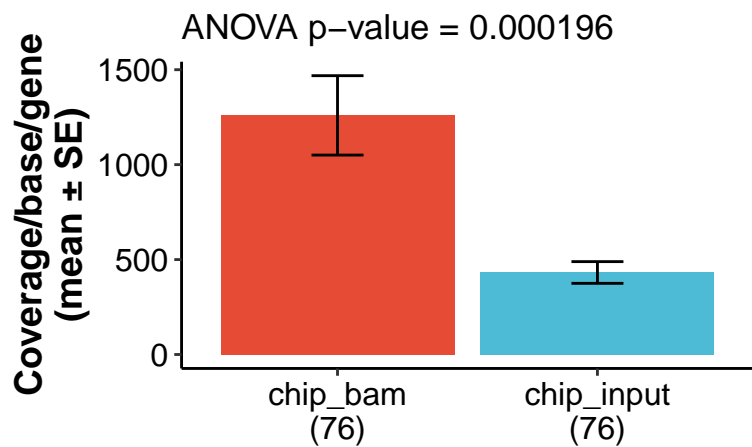
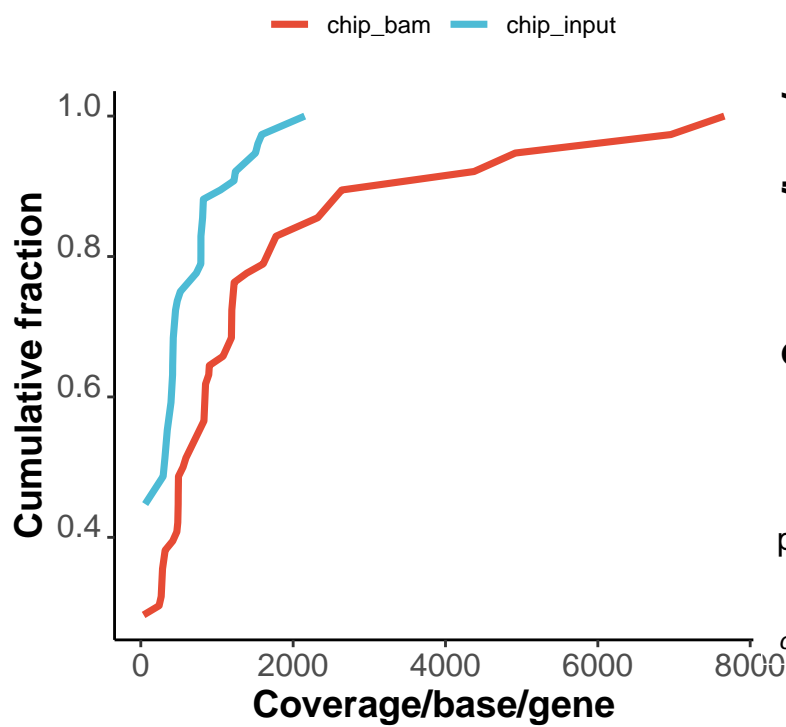
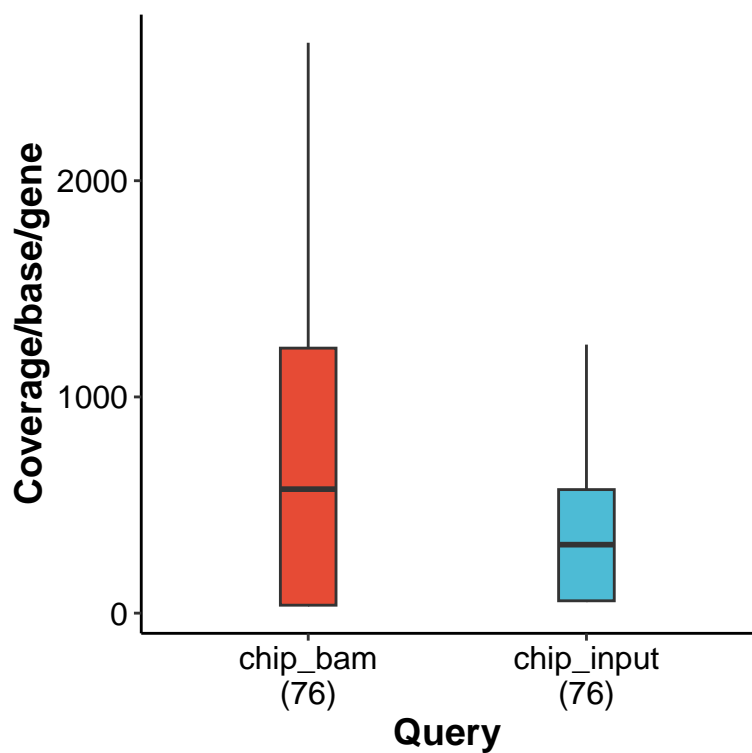
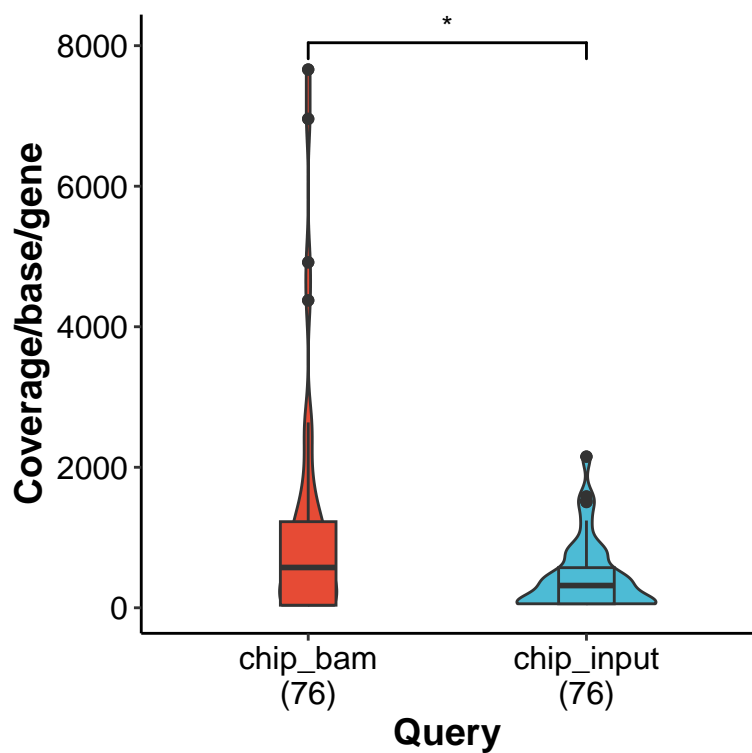


# NarrowPeak



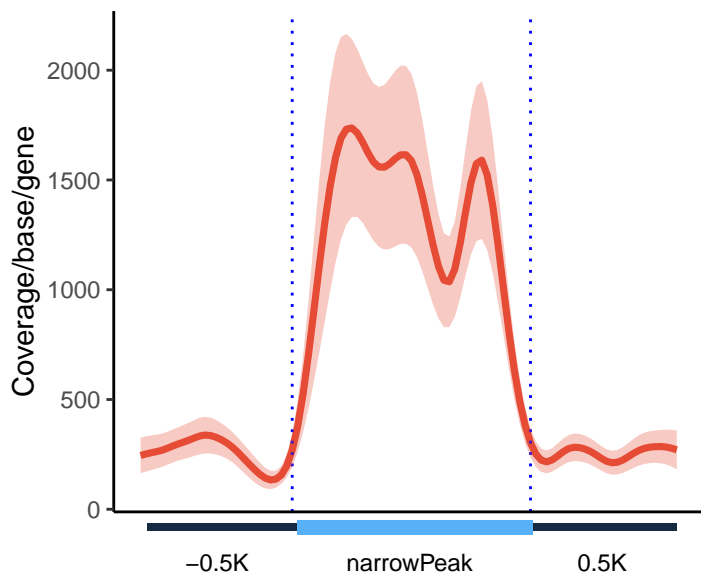


post hoc TukeyHSD test

	diff	lwr	upr	p adj
chip_input-chip_bam	-827.431	-1255.61	-399.251	0.000196

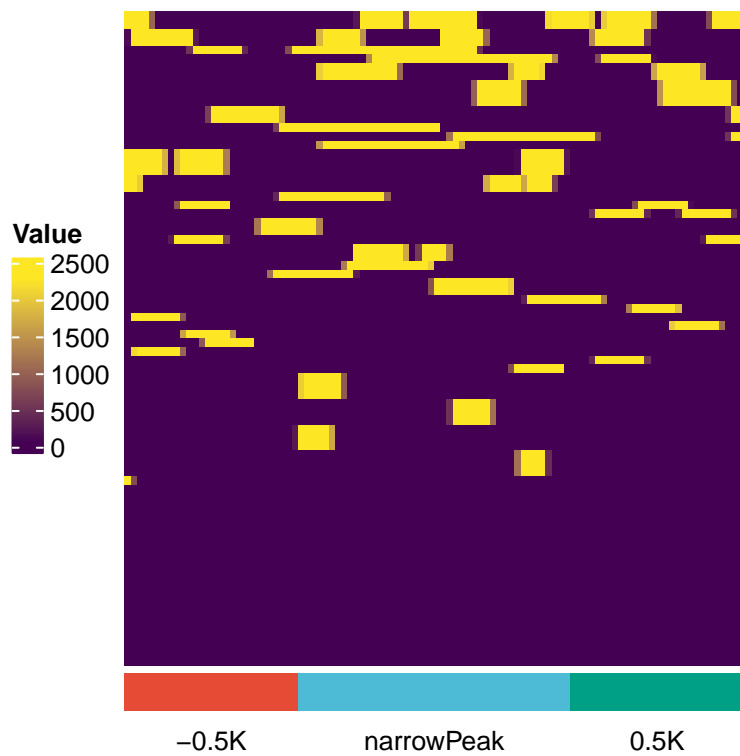
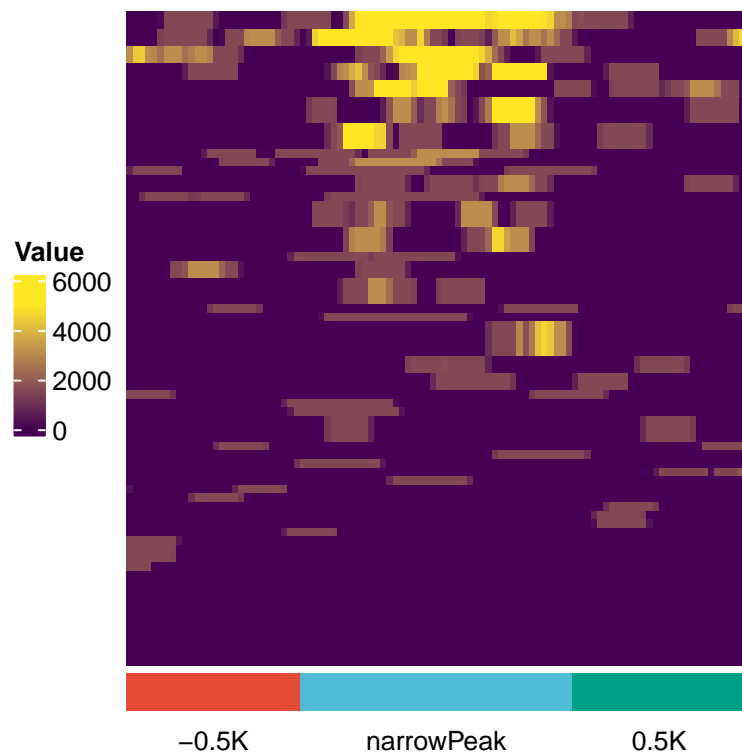
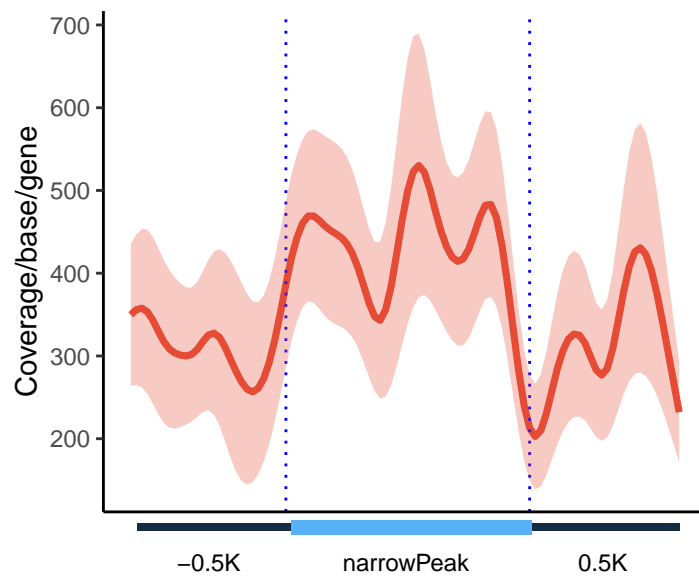
NarrowPeak

chip\_bam:NarrowPeak

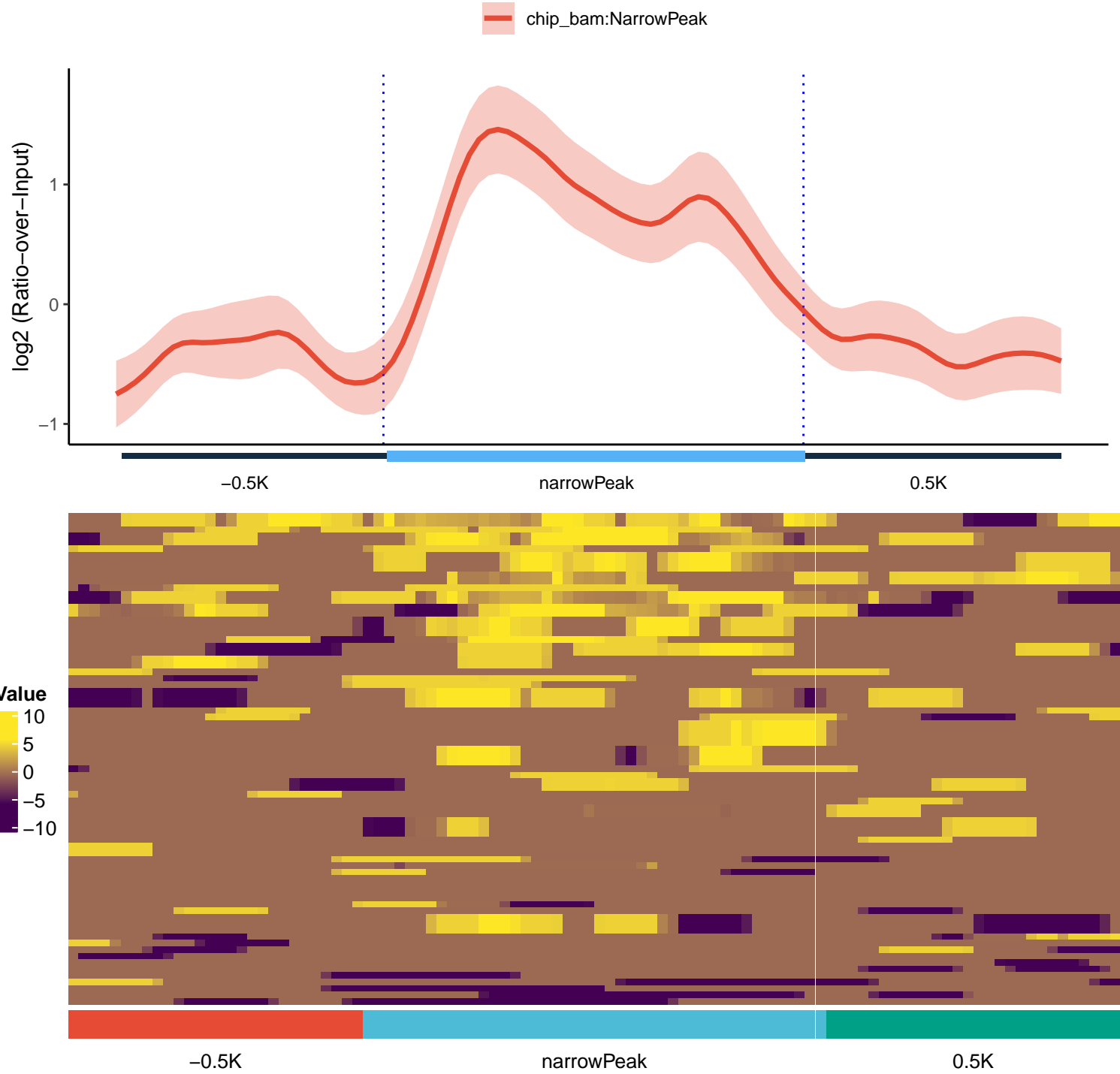


NarrowPeak

chip\_input:NarrowPeak



NarrowPeak



Plotting parameters:

```
functionName: "plot_region"
queryFiles: c(chip_bam =
"C:/Users/greenblatt/AppData/Local/R/win-library/4.3/GenomicPlot/extdata/chip_treat_chr19.bam")
centerFiles: c(NarrowPeak =
"C:/Users/greenblatt/AppData/Local/R/win-library/4.3/GenomicPlot/extdata/test_chip_peak_chr19.narrowPeak")
txdb: NULL
regionName: "narrowPeak"
inputFiles: c(chip_input =
"C:/Users/greenblatt/AppData/Local/R/win-library/4.3/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: "log2"
outPrefix: "test_plot_region"
rmOutlier: 0
heatRange: NULL
Ylab: "Coverage/base/gene"
statsMethod: "wilcox.test"
hw: c(8, 8)
nc: 2
```