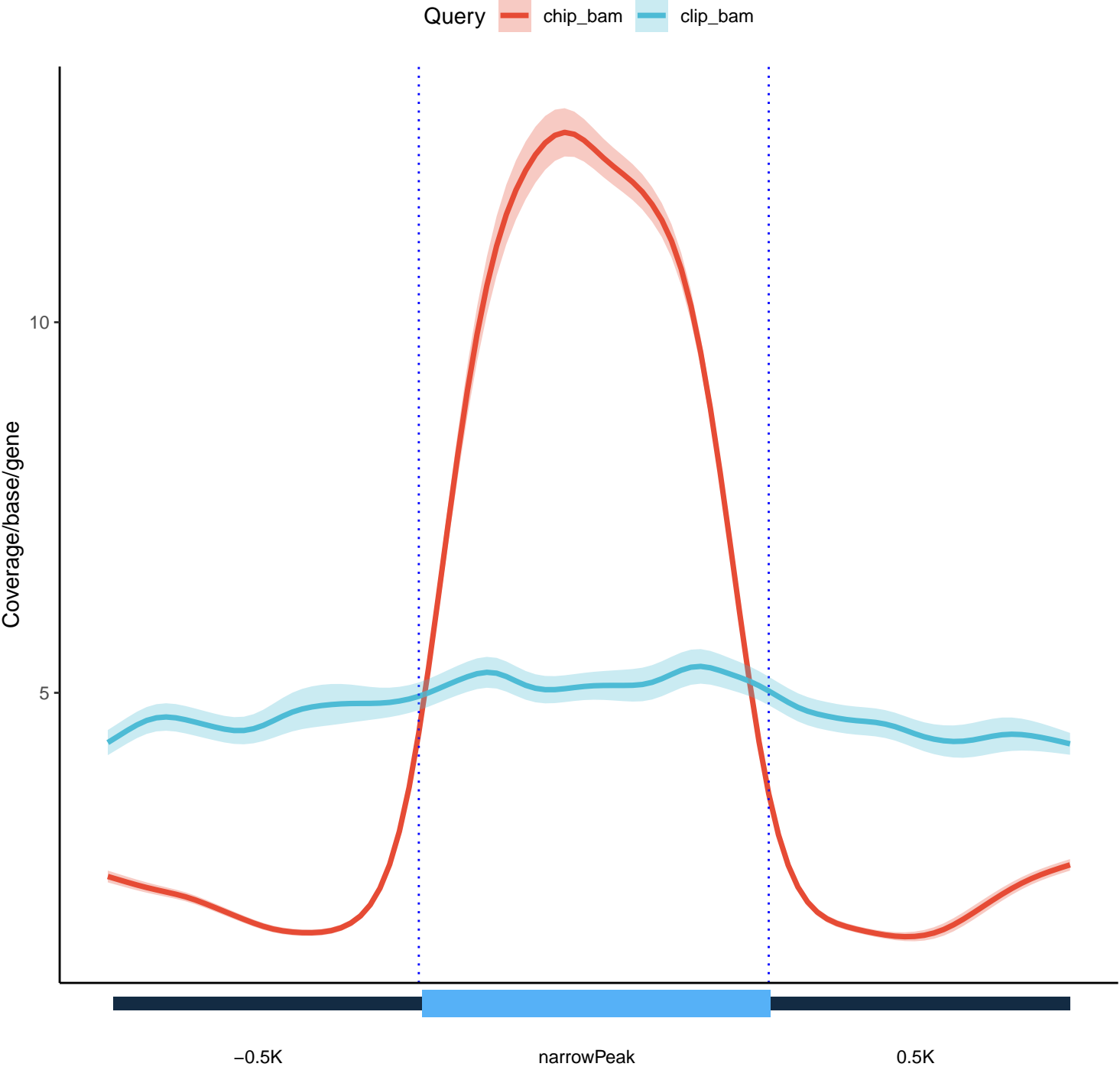
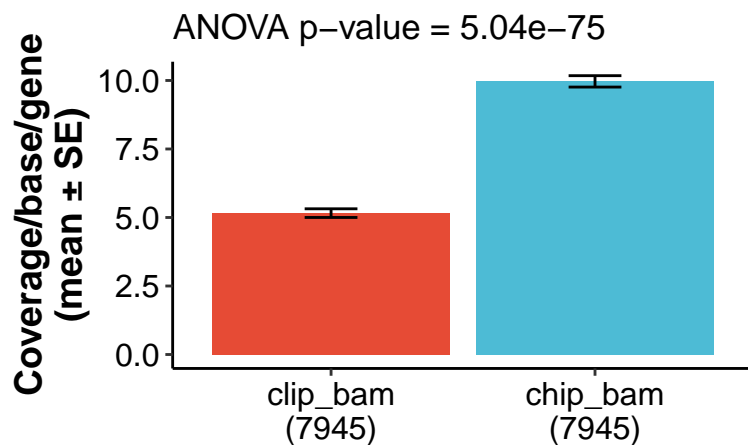
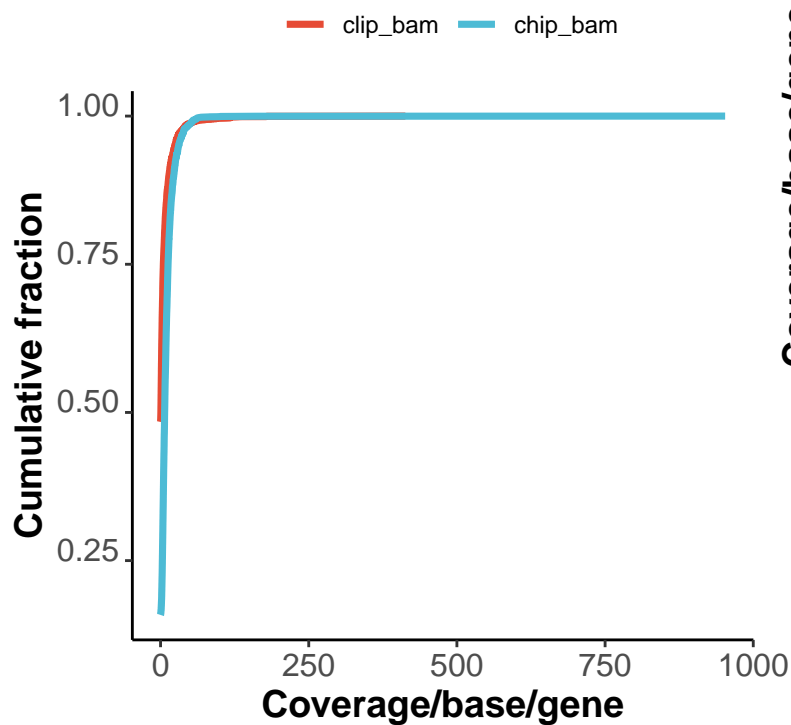
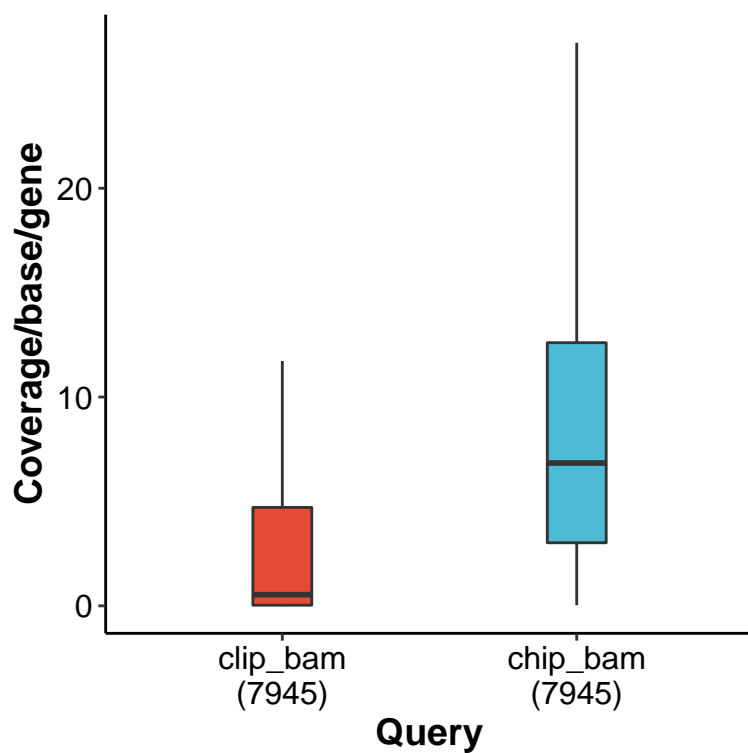
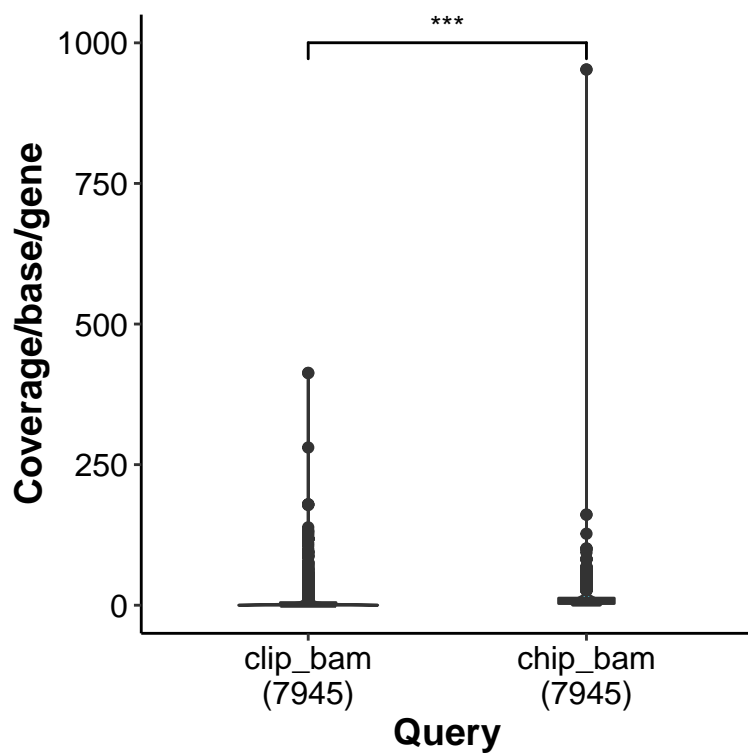


NarrowPeak

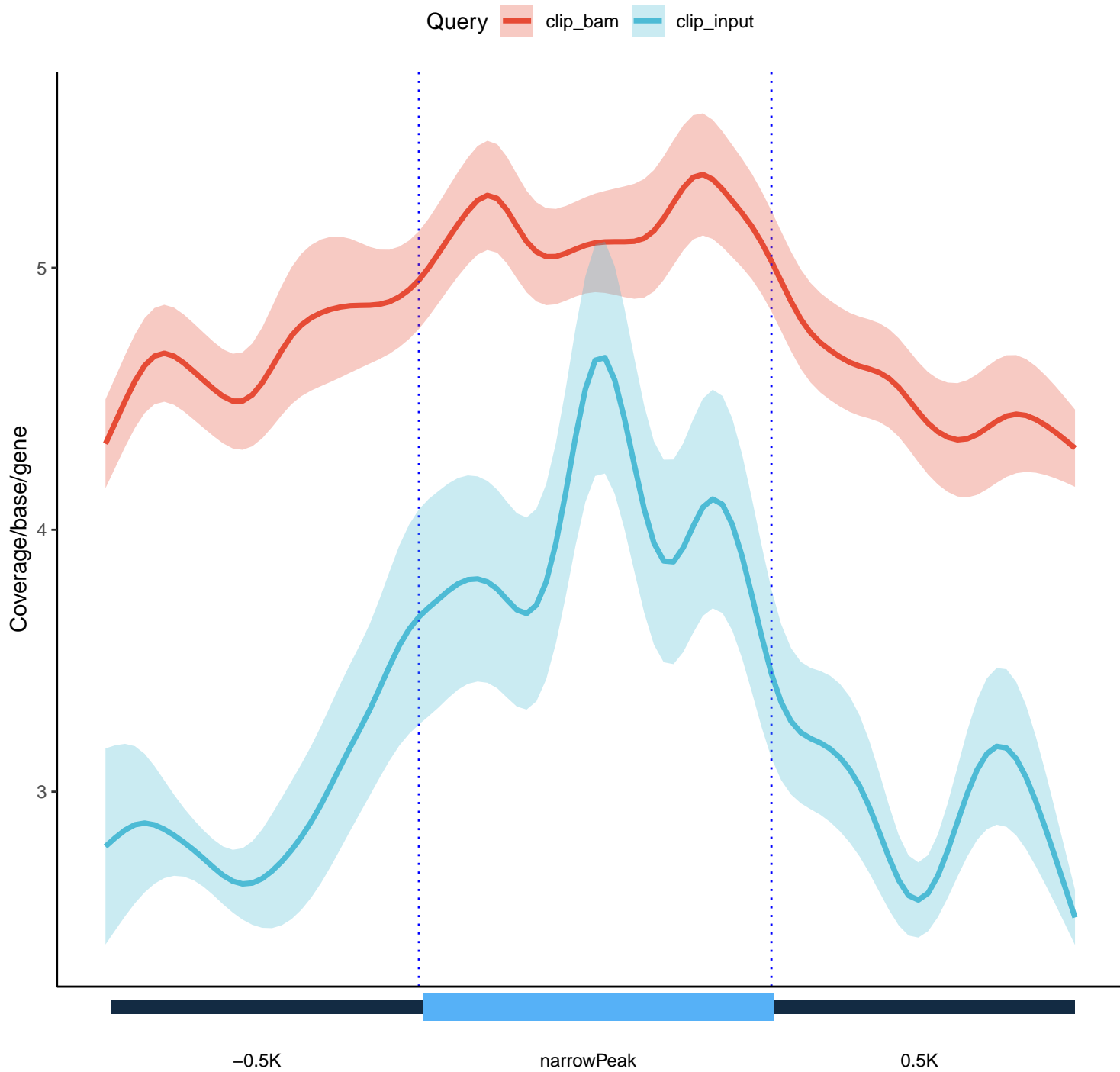


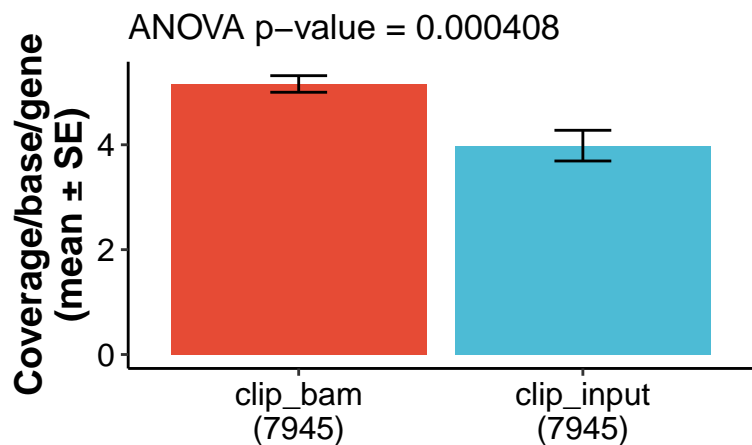
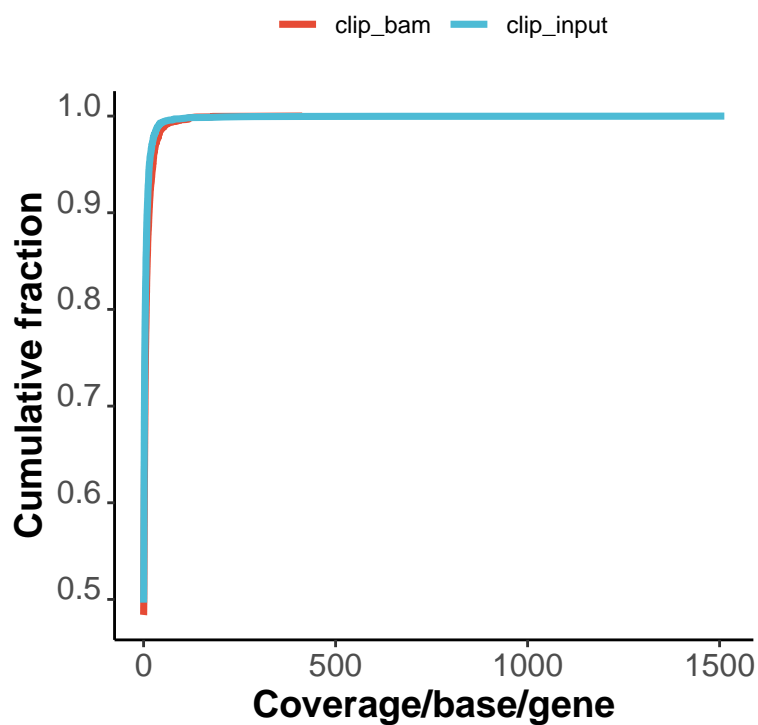
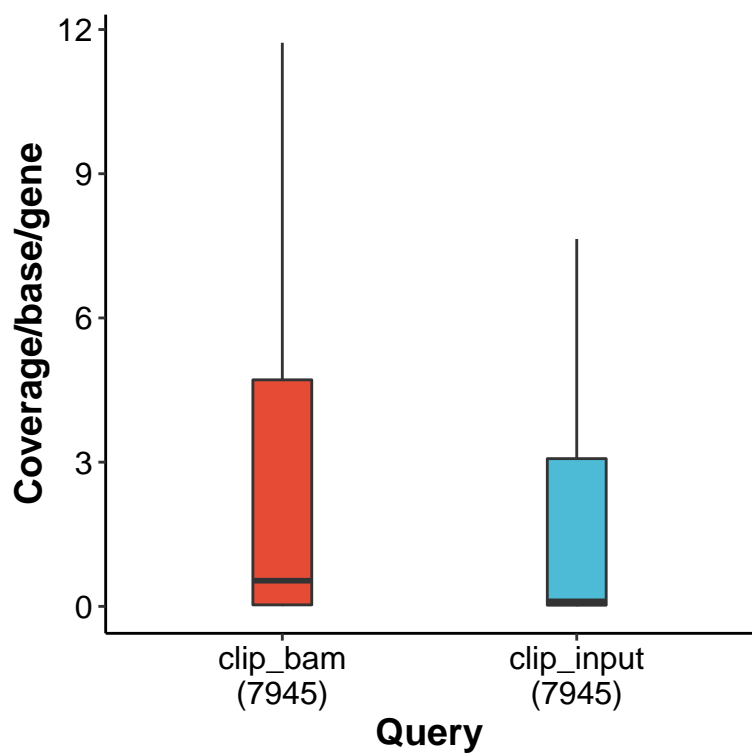
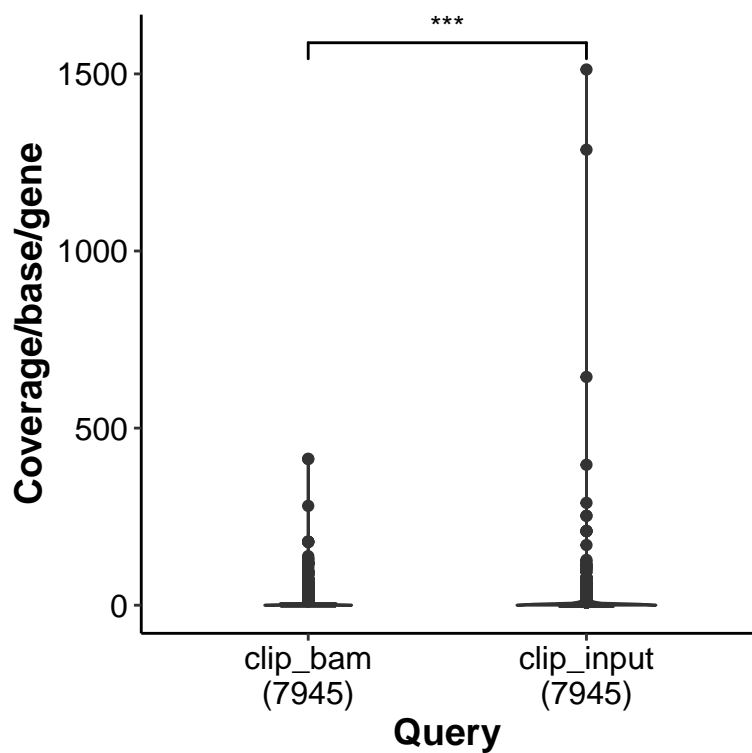


post hoc TukeyHSD test

	diff	lwr	upr	p adj
chip_bam-clip_bam	4.808	4.296	5.319	2.04e-08

# NarrowPeak

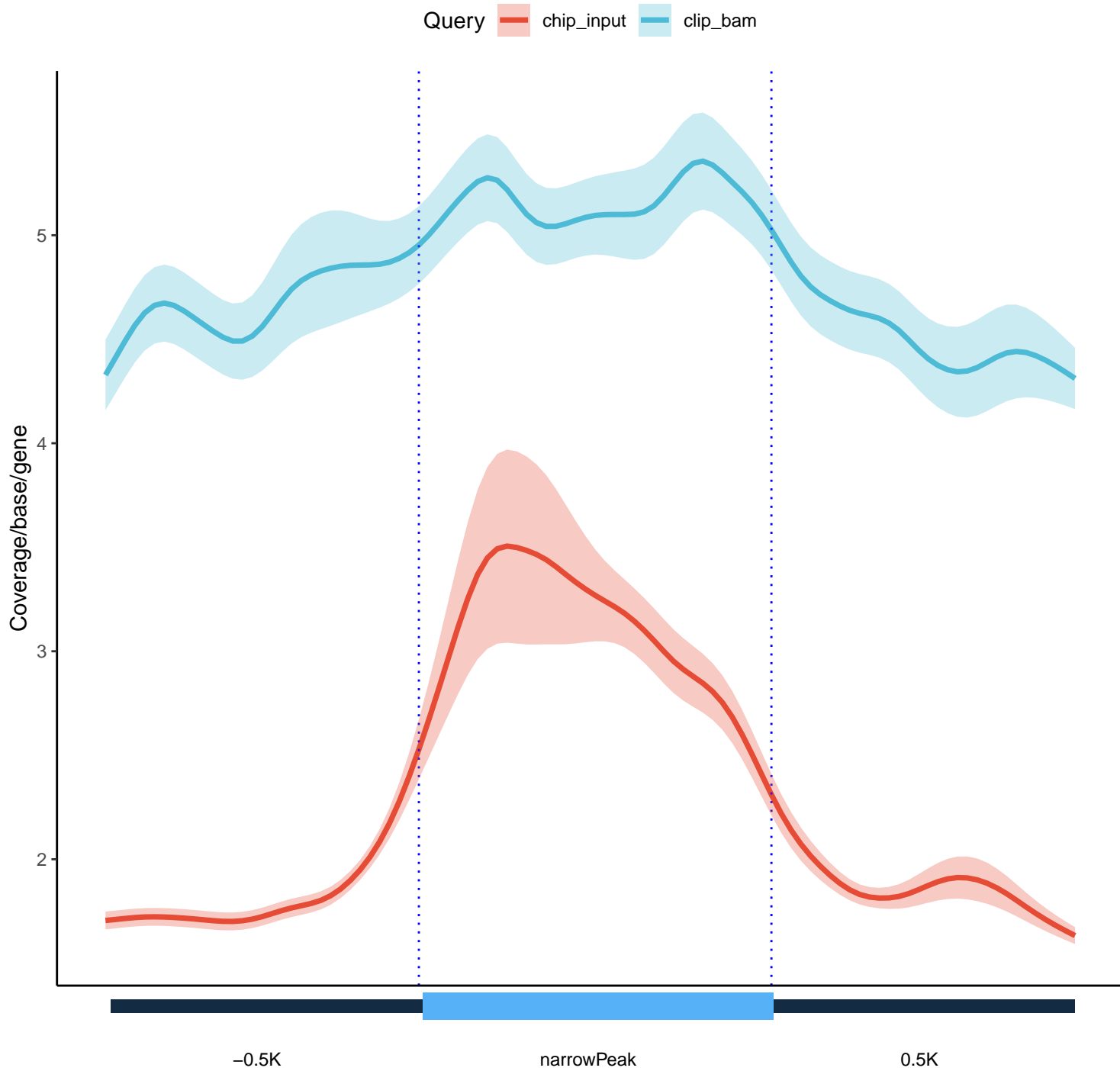


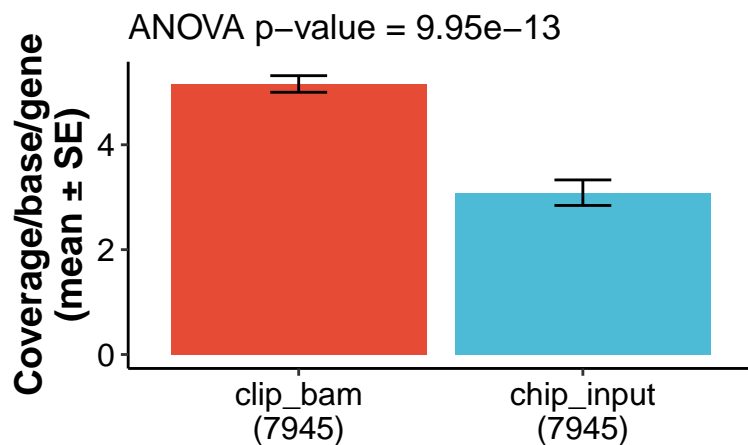
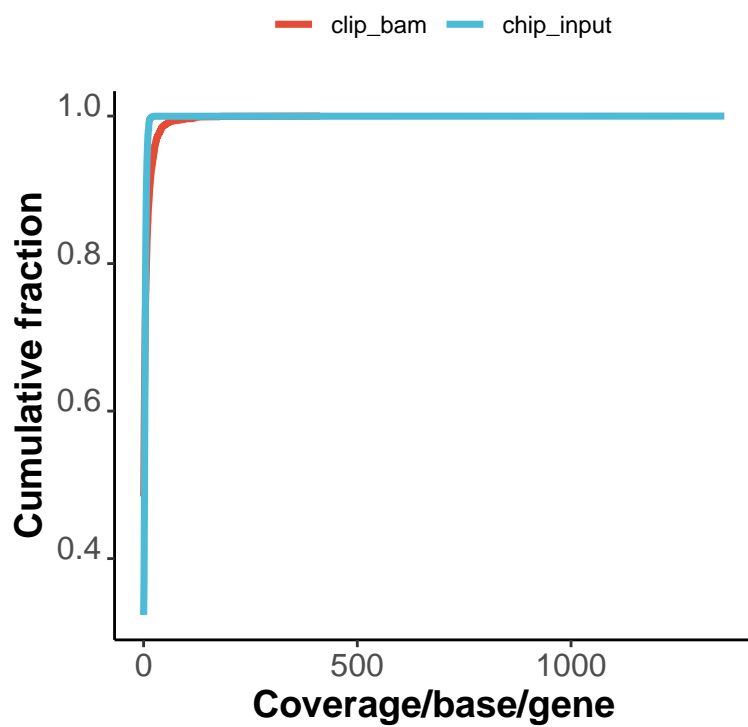
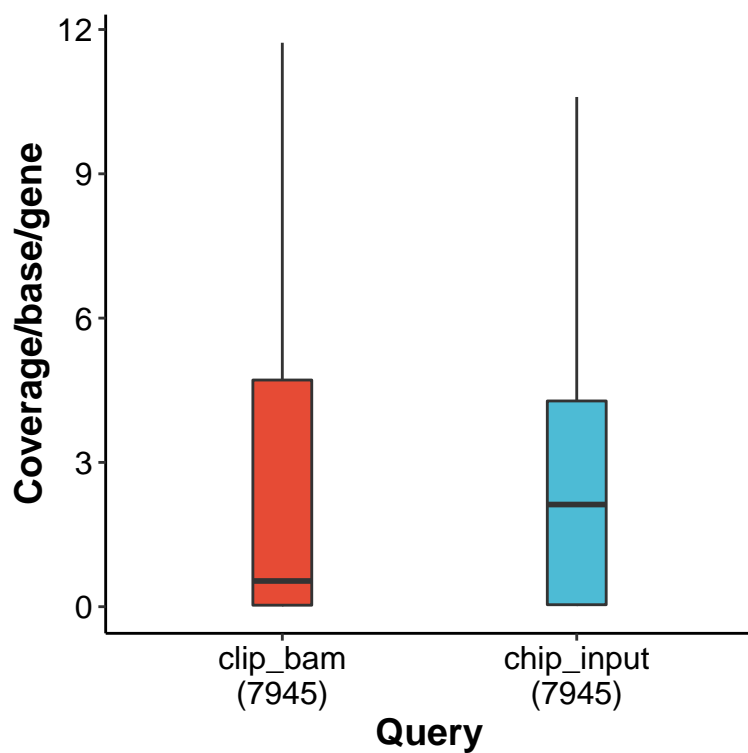
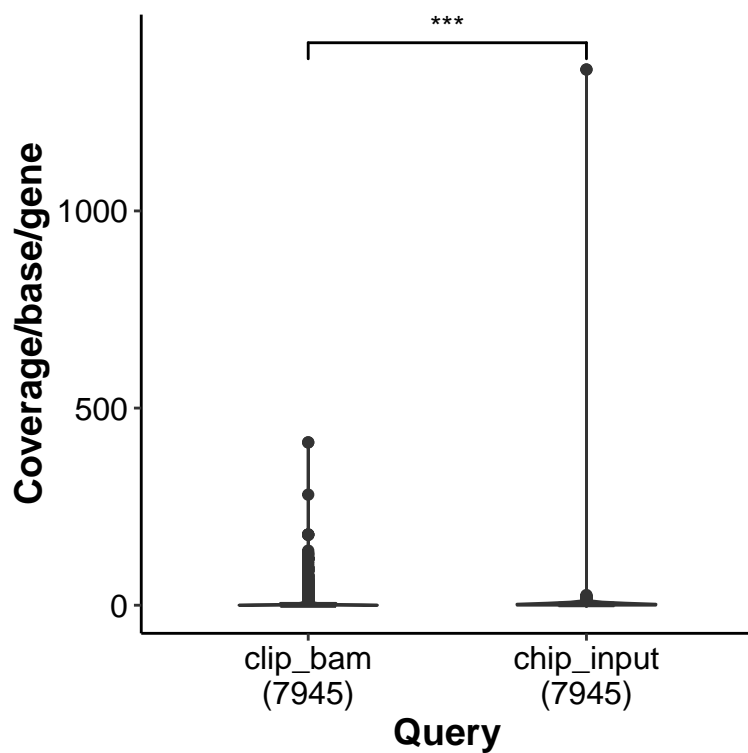


post hoc TukeyHSD test

	diff	lwr	upr	p adj
clip_input-clip_bam	-1.176	-1.828	-0.524	0.000408

# NarrowPeak

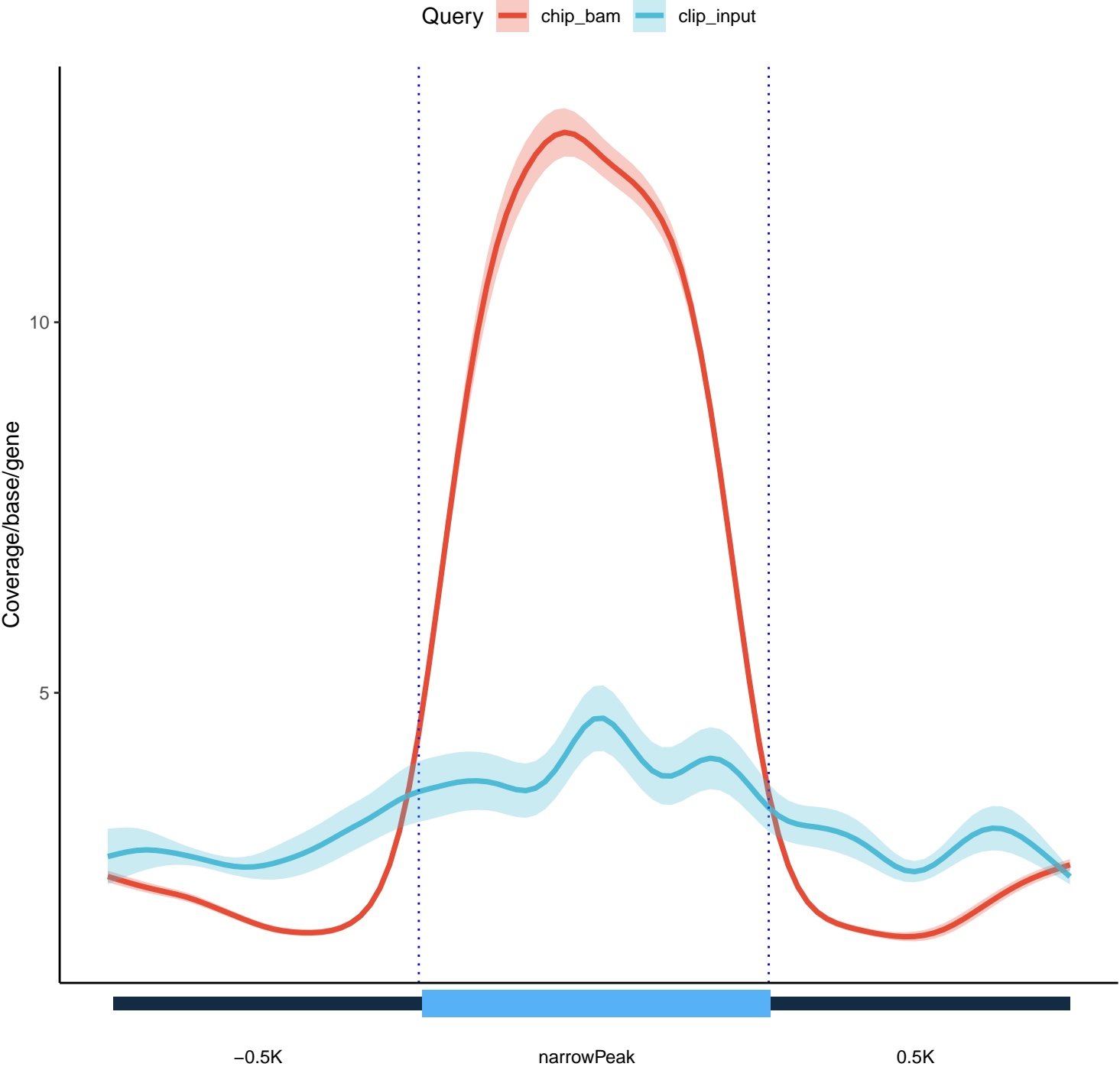


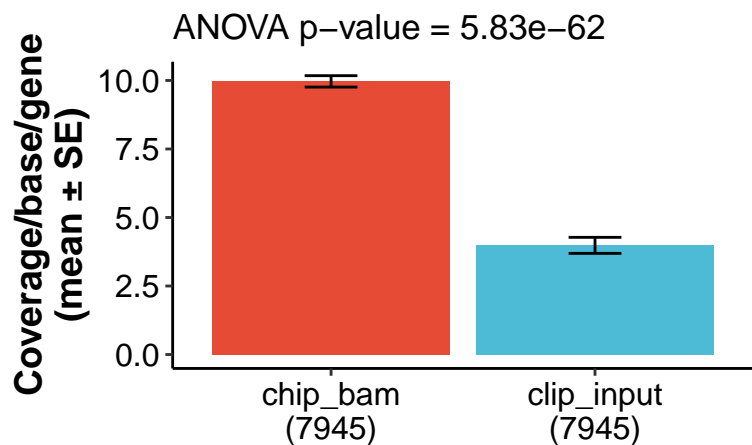
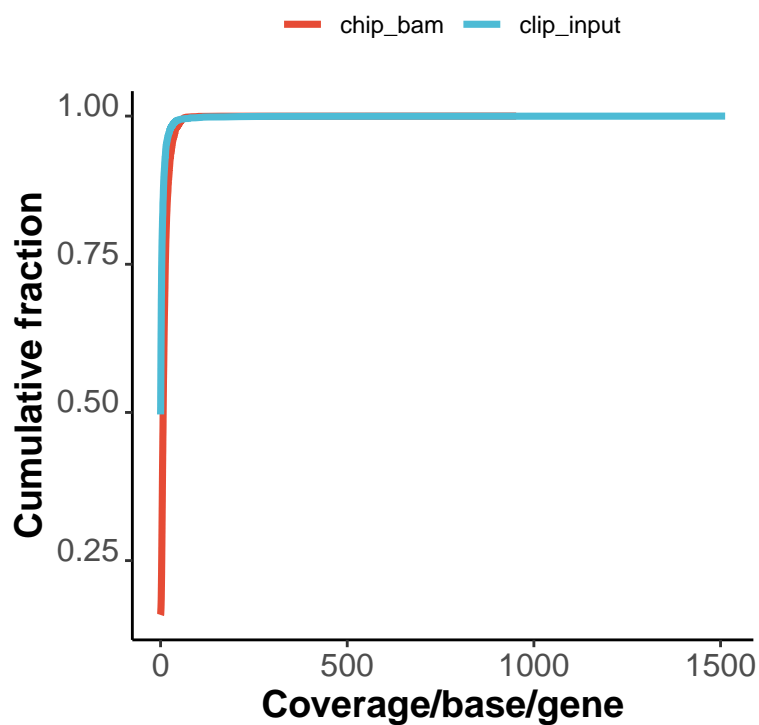
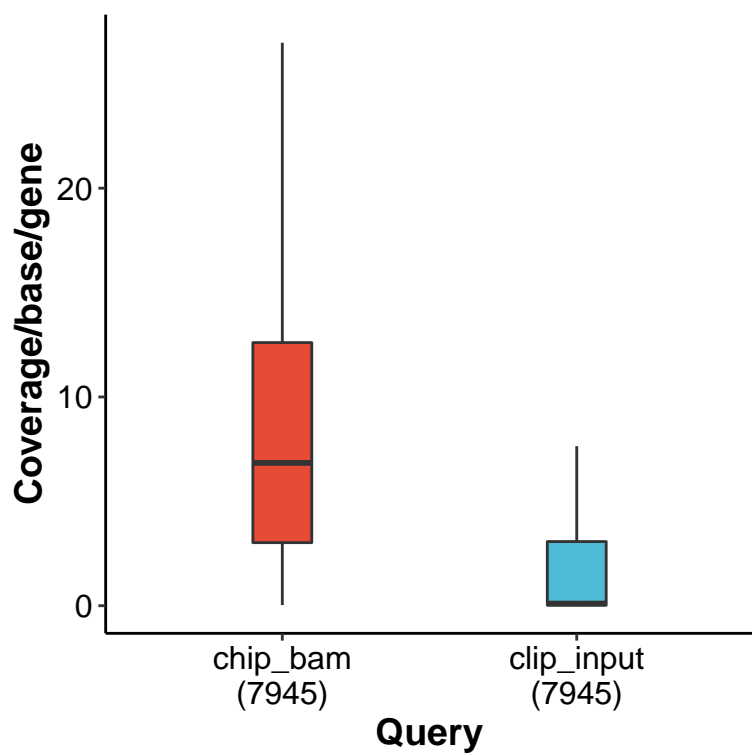
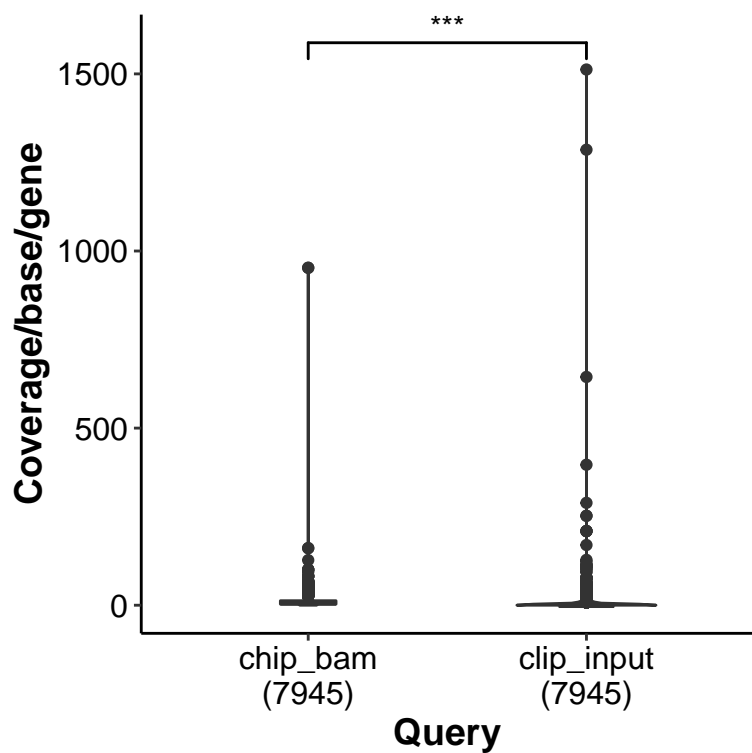


post hoc TukeyHSD test

	diff	lwr	upr	p adj
chip_input-clip_bam	-2.073	-2.643	-1.504	$2.04 \times 10^{-8}$

NarrowPeak



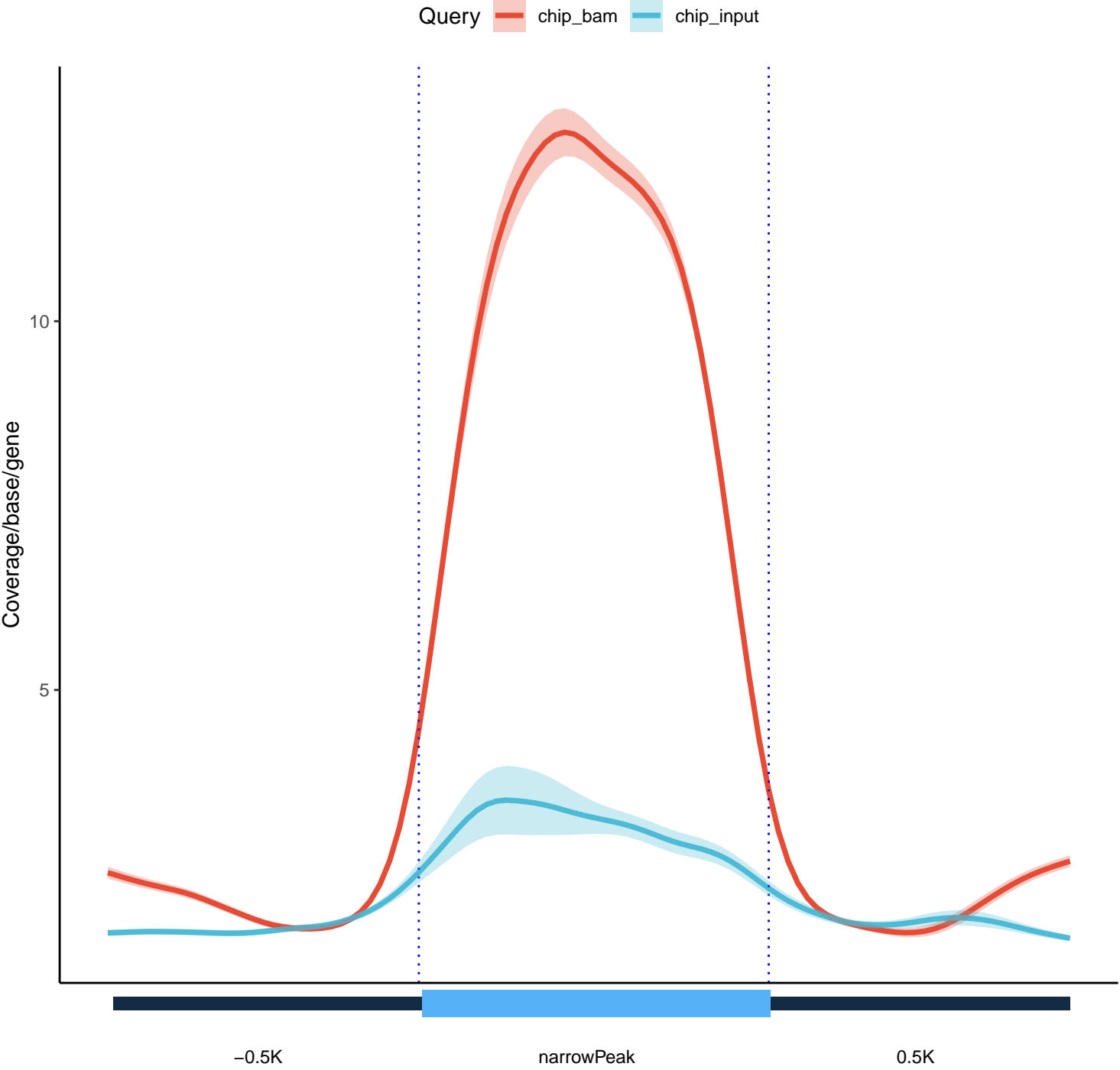


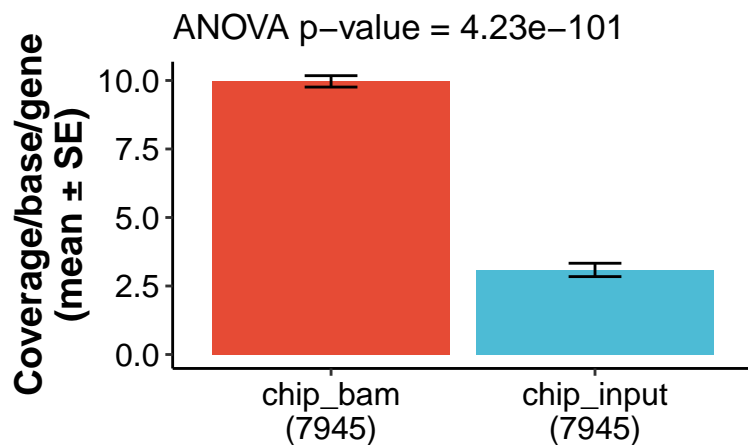
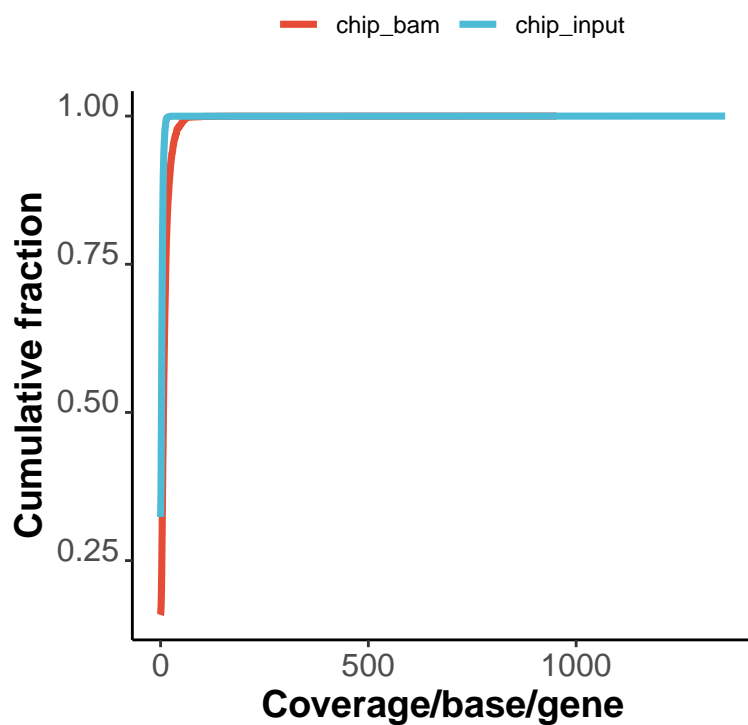
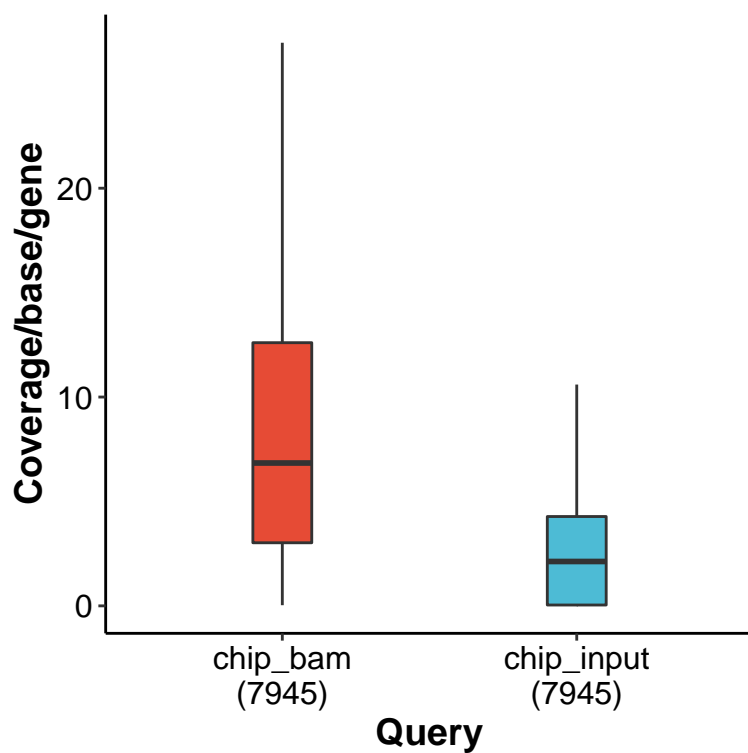
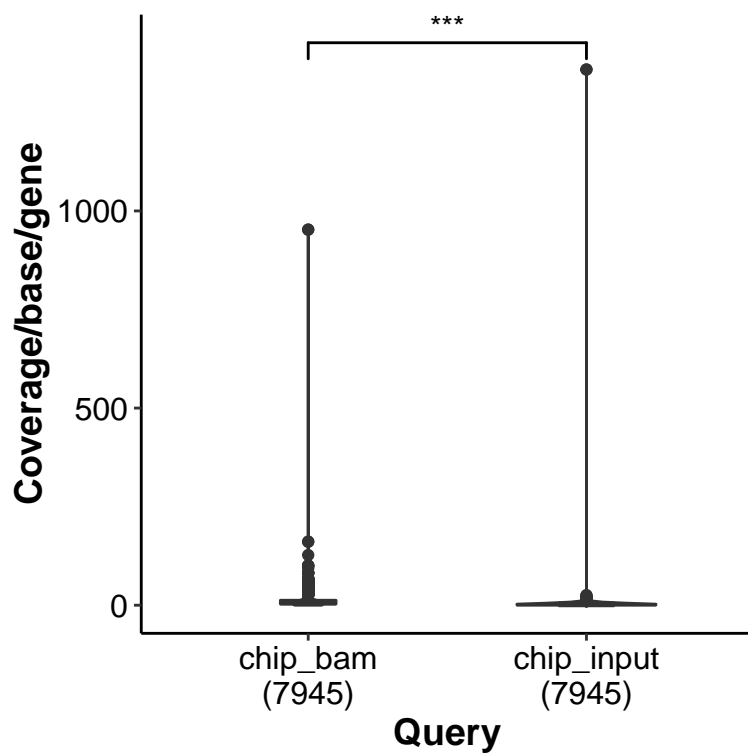
post hoc TukeyHSD test

	diff	lwr	upr	p adj
clip_input-chip_bam	-5.984	-6.687	-5.281	2.04e-08



NarrowPeak

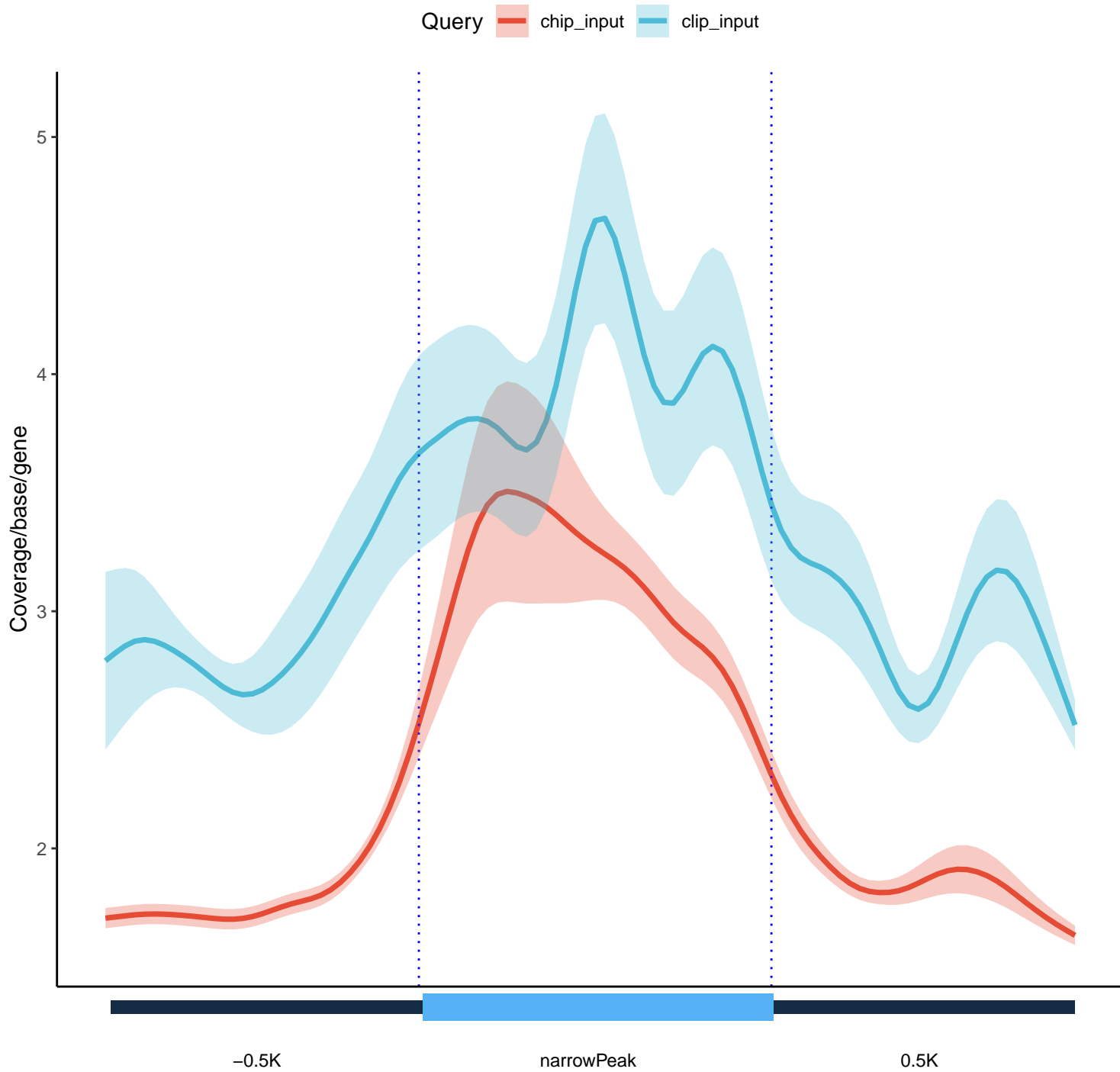


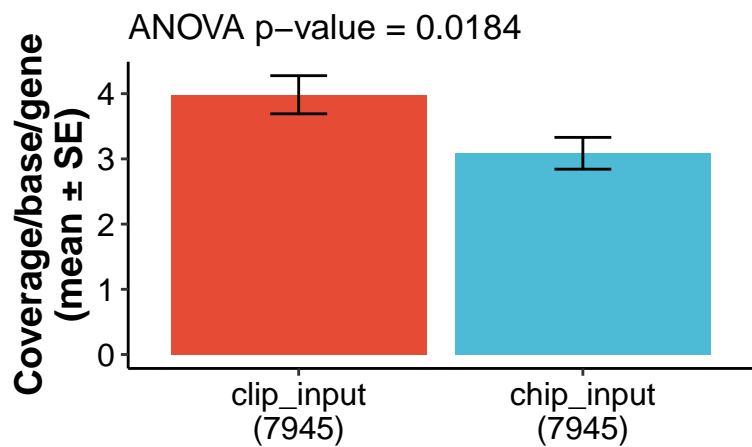
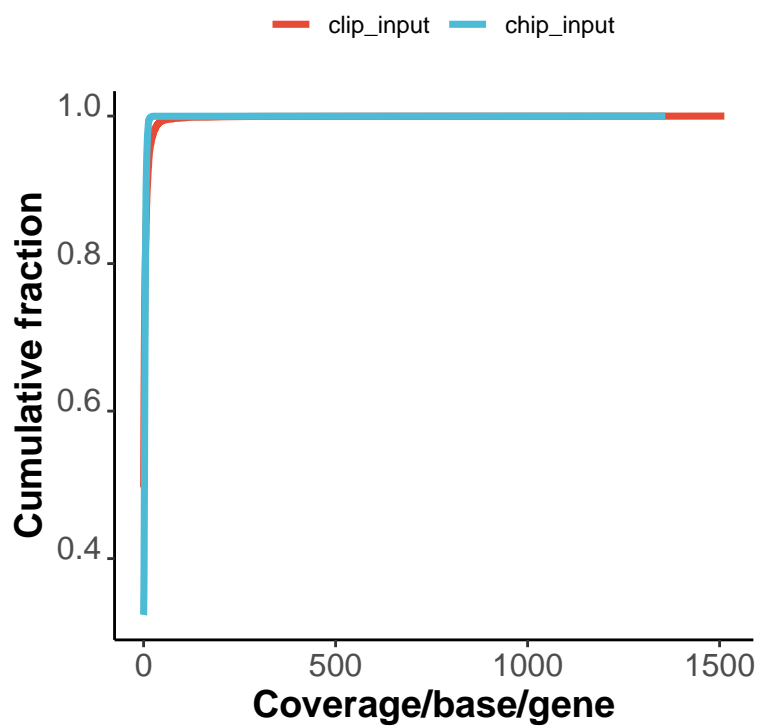
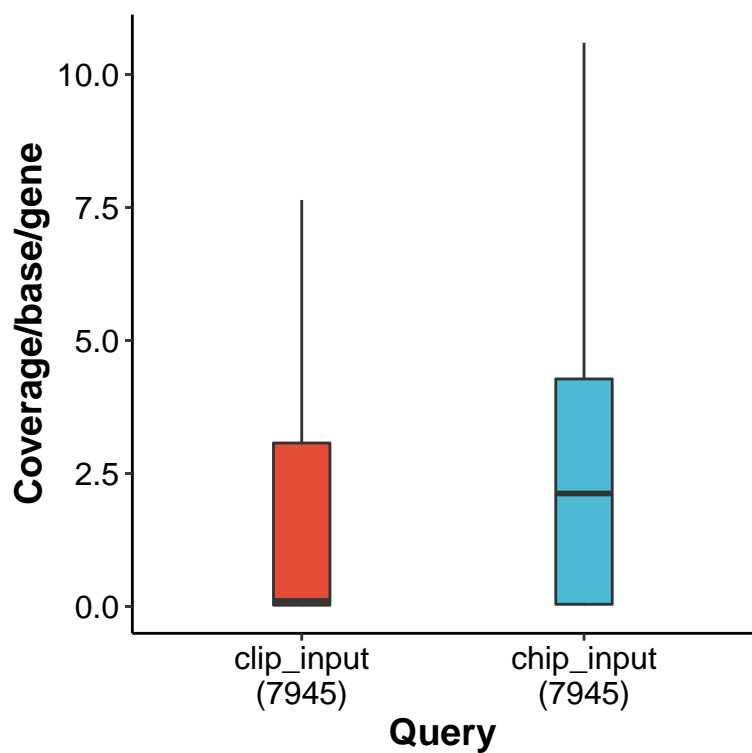
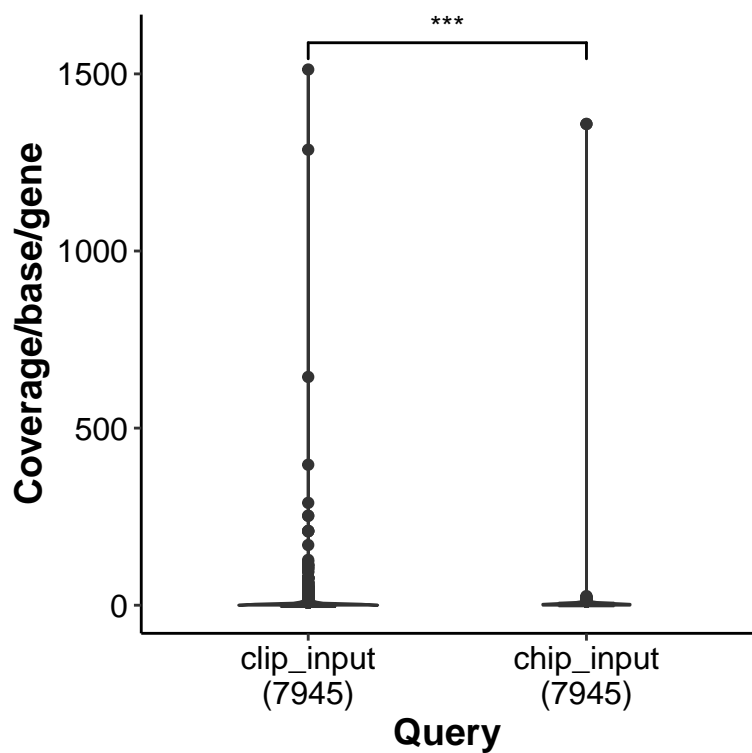


post hoc TukeyHSD test

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

# NarrowPeak



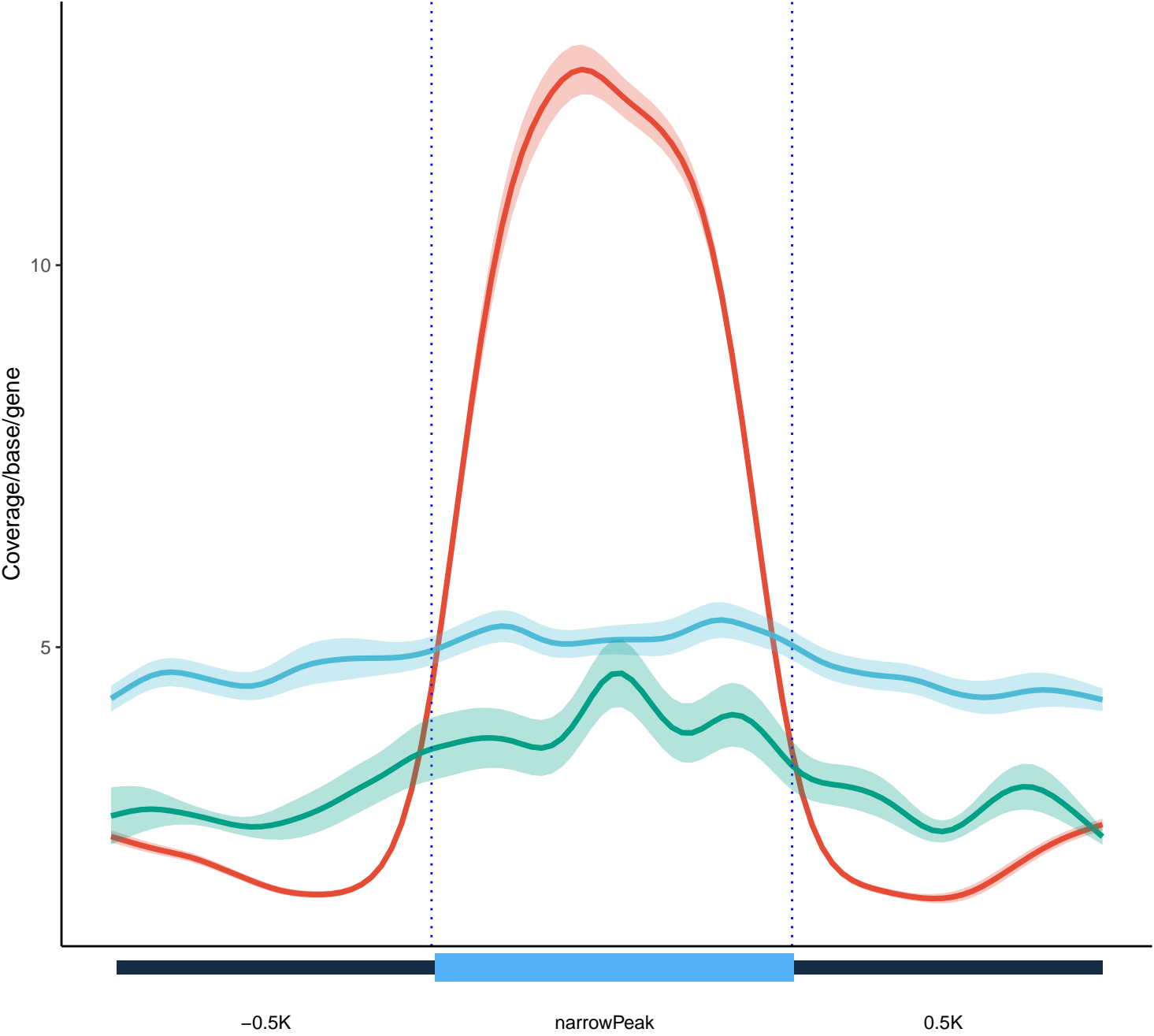


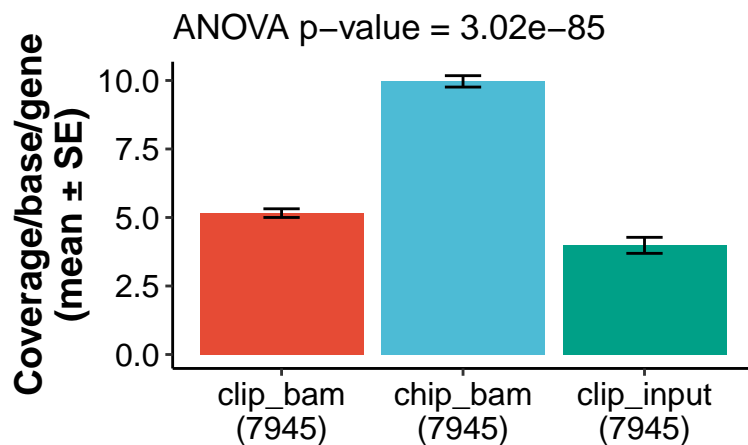
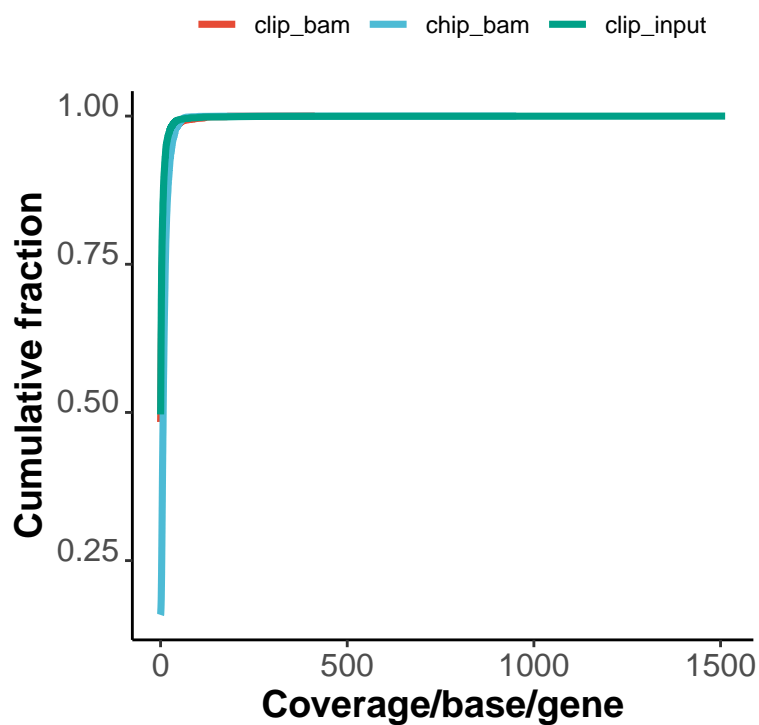
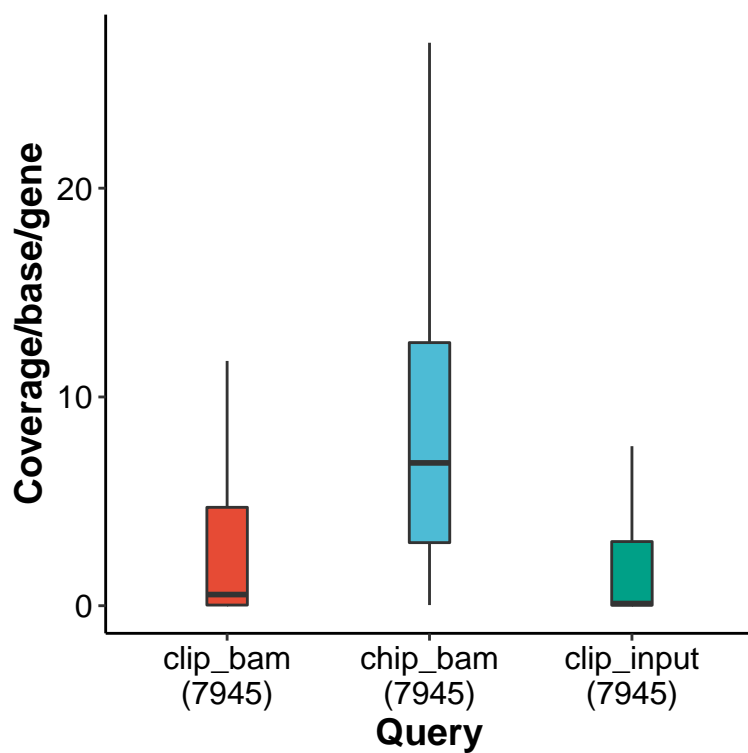
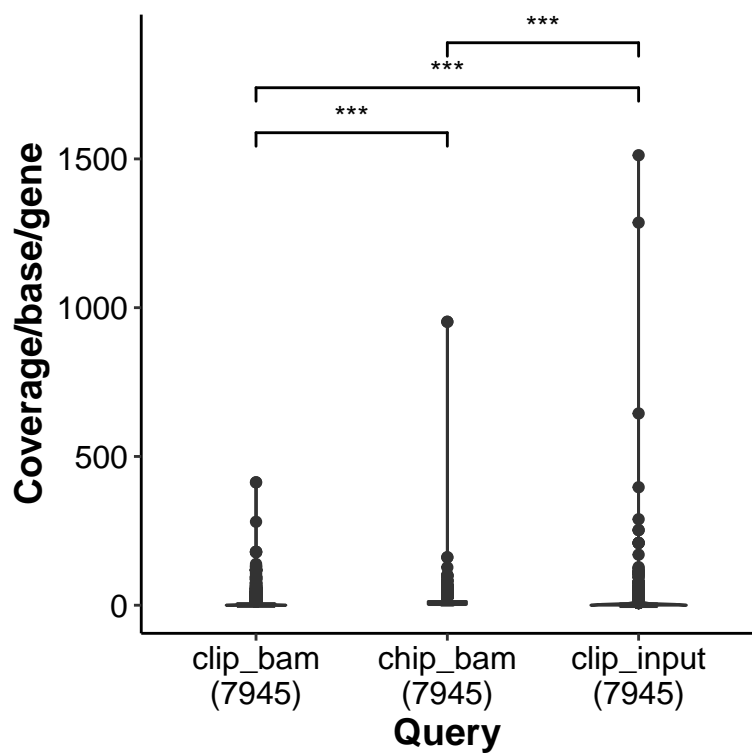
ANOVA p-value = 0.0184

	diff	lwr	upr	p adj
chip_input-clip_input	-0.897	-1.644	-0.151	0.0184

NarrowPeak

Query chip\_bam clip\_bam clip\_input

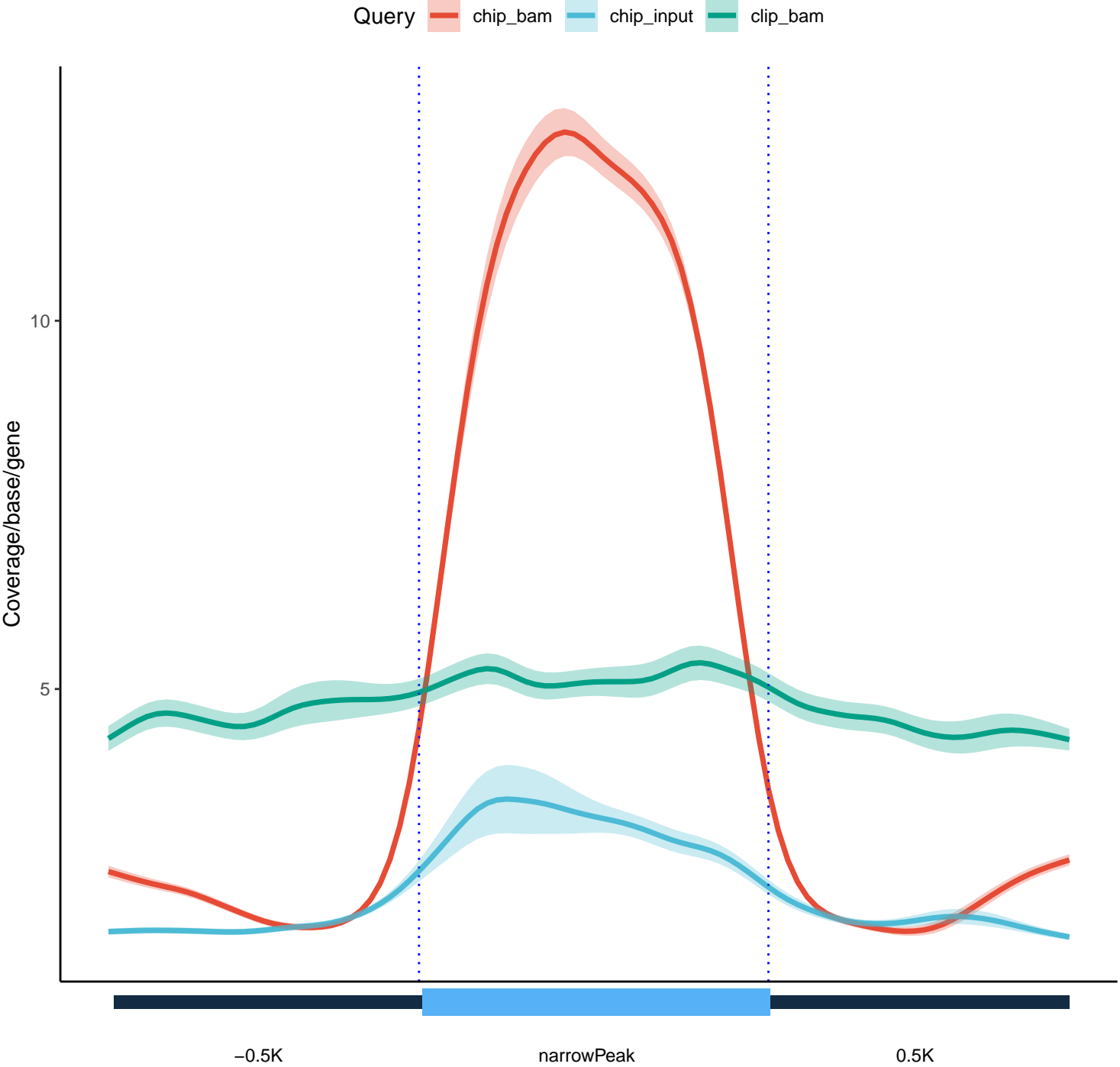


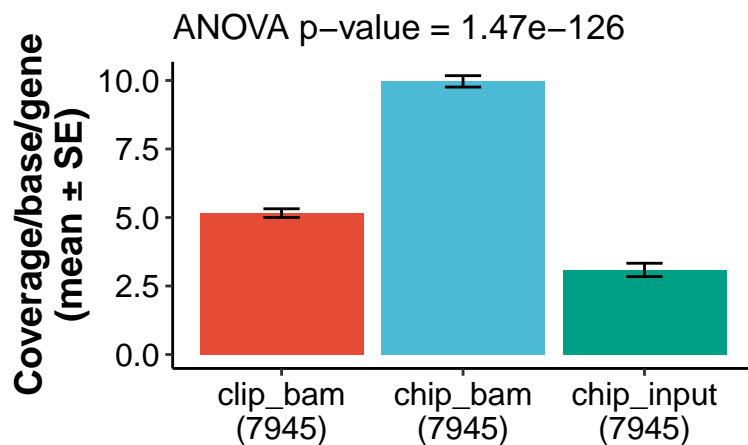
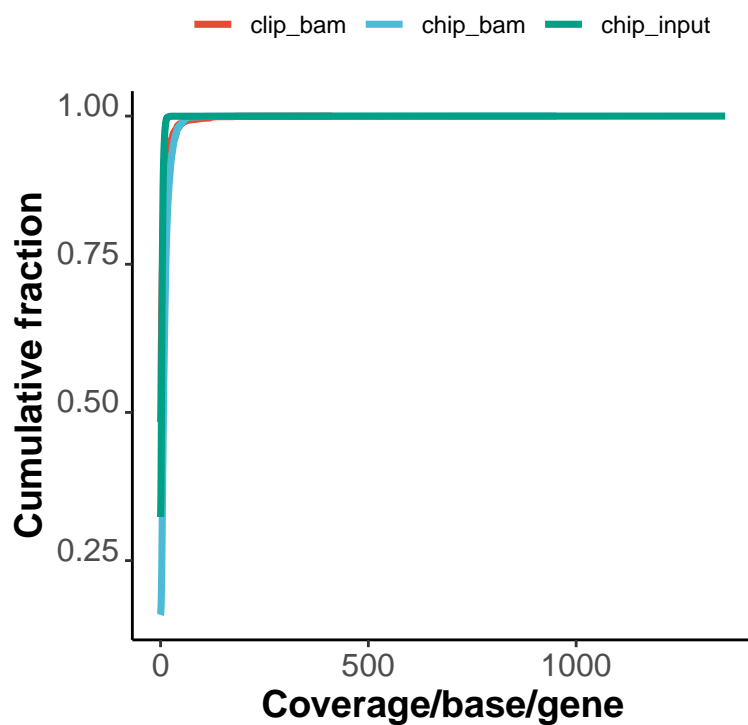
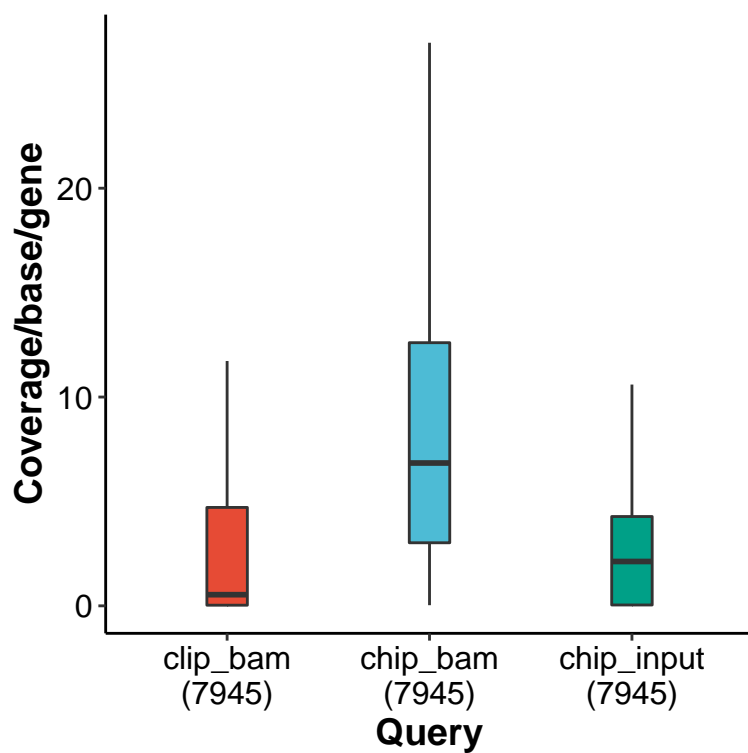
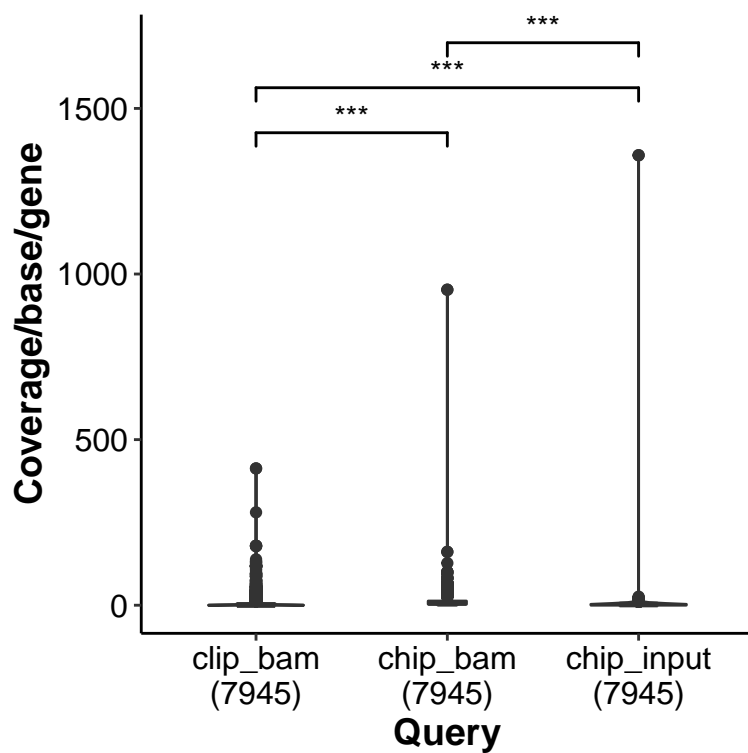


post hoc TukeyHSD test

	diff	lwr	upr	p adj
<i>chip_bam-clip_bam</i>	4.808	4.058	5.558	0e+00
<i>clip_input-clip_bam</i>	-1.176	-1.926	-0.426	7e-04
<i>clip_input-chip_bam</i>	-5.984	-6.734	-5.234	0e+00

NarrowPeak



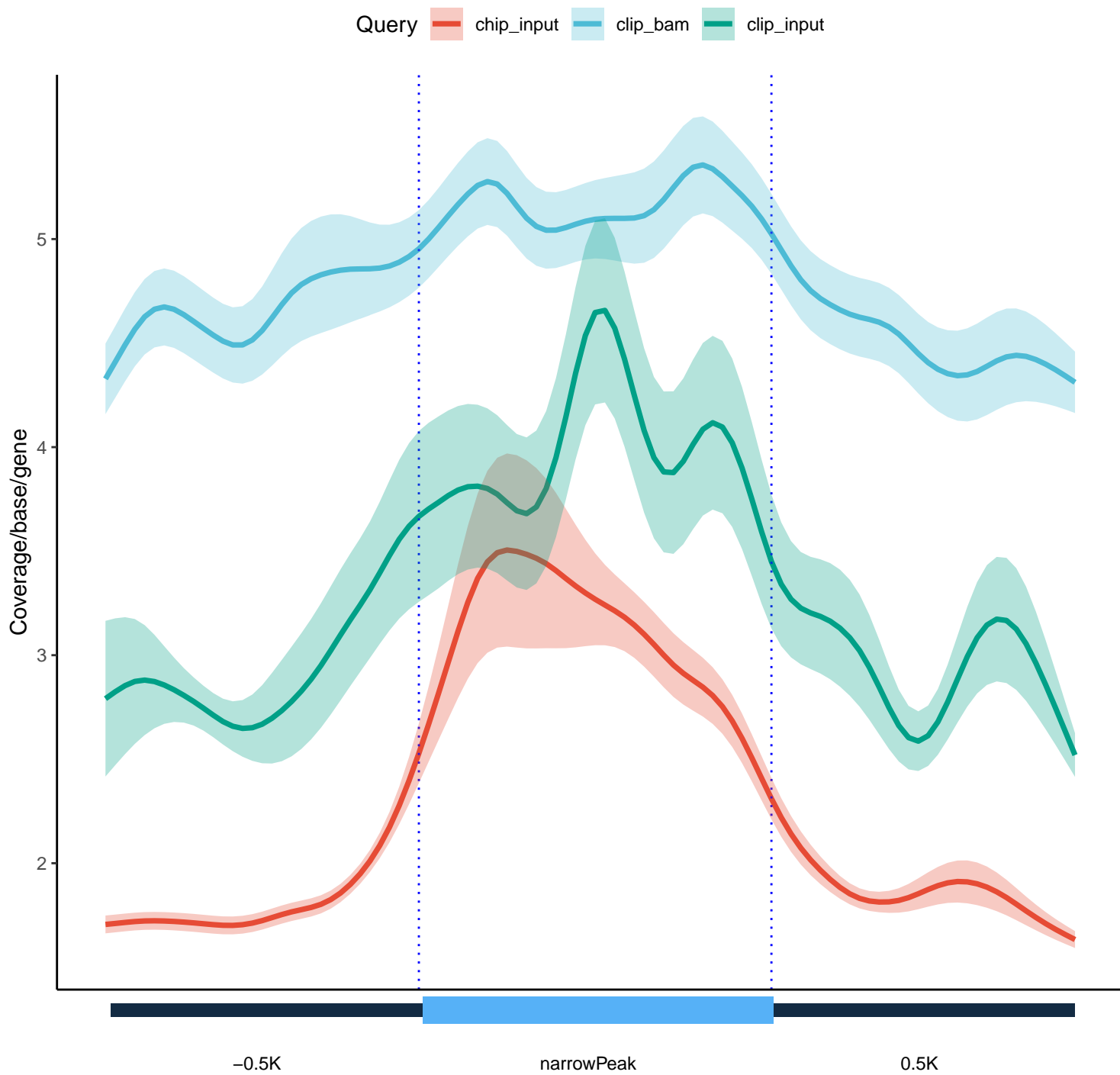


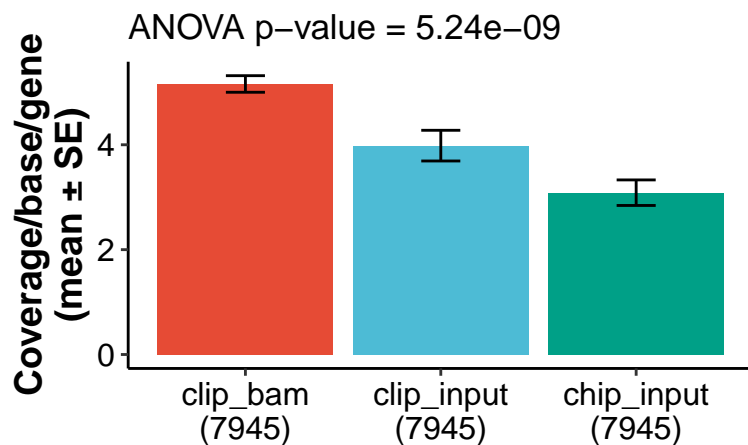
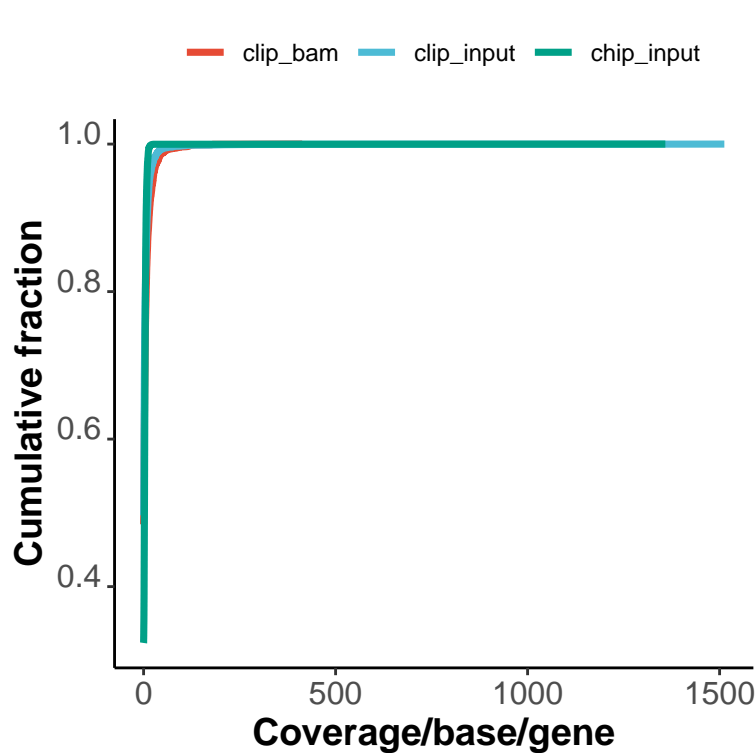
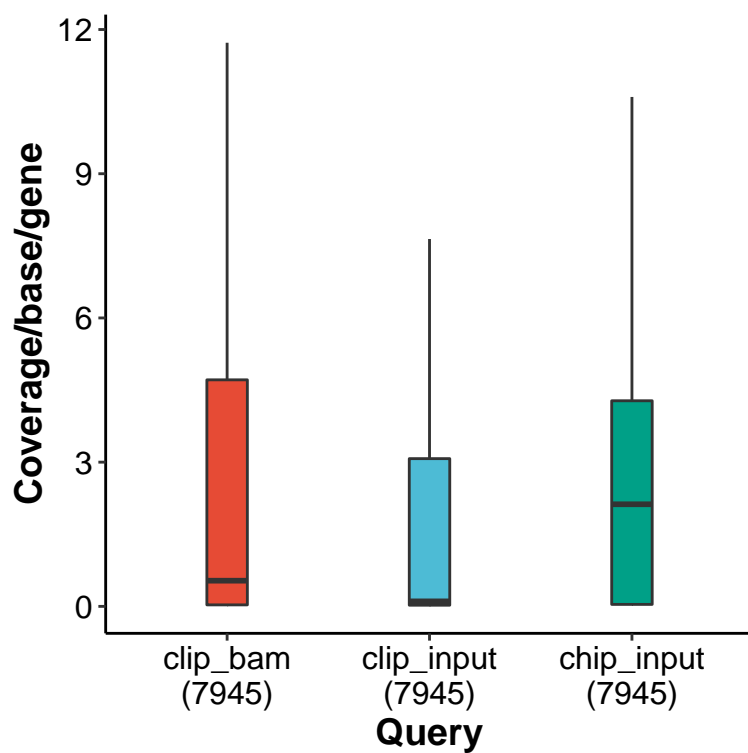
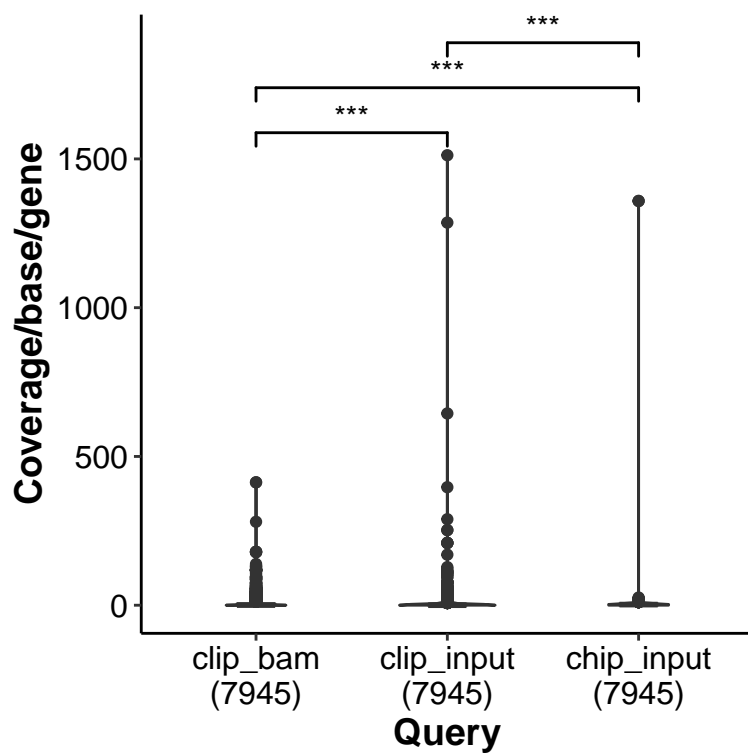
post hoc TukeyHSD test

	diff	lwr	upr	p adj
chip_bam-clip_bam	4.808	4.125	5.491	0
chip_input-clip_bam	-2.073	-2.757	-1.39	0
chip_input-chip_bam	-6.881	-7.564	-6.198	0



# NarrowPeak

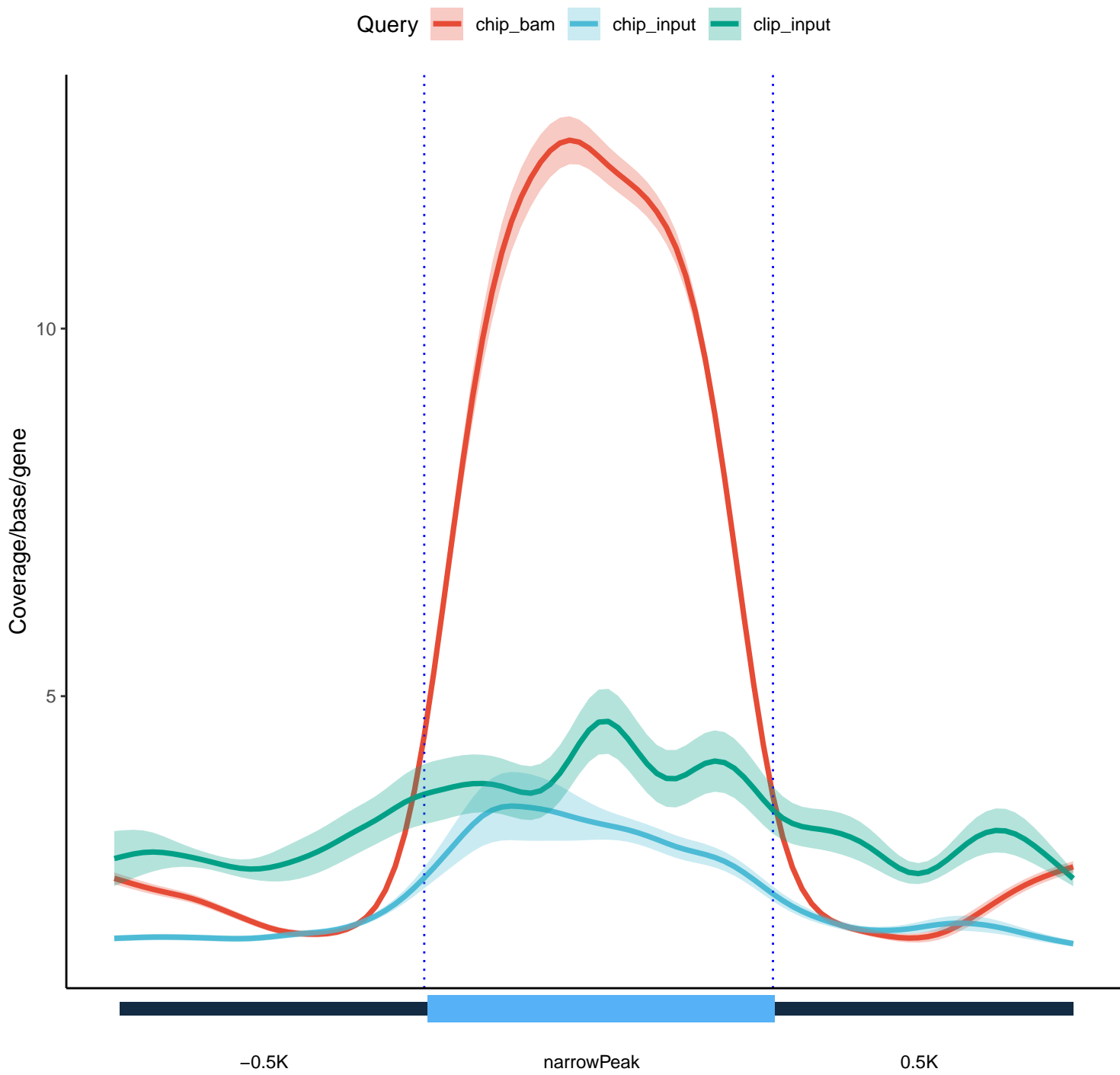


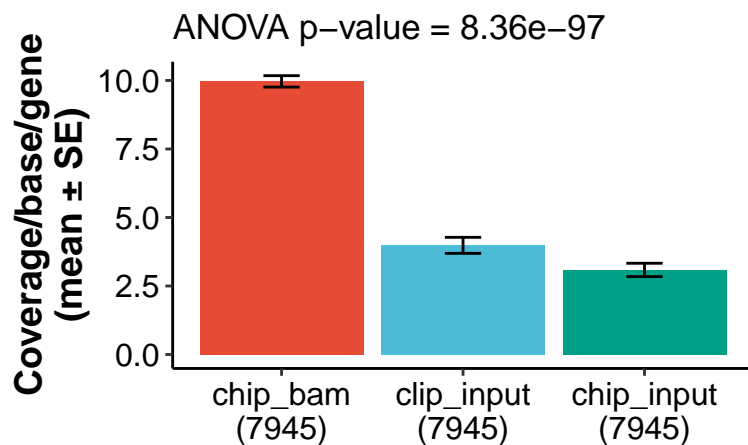
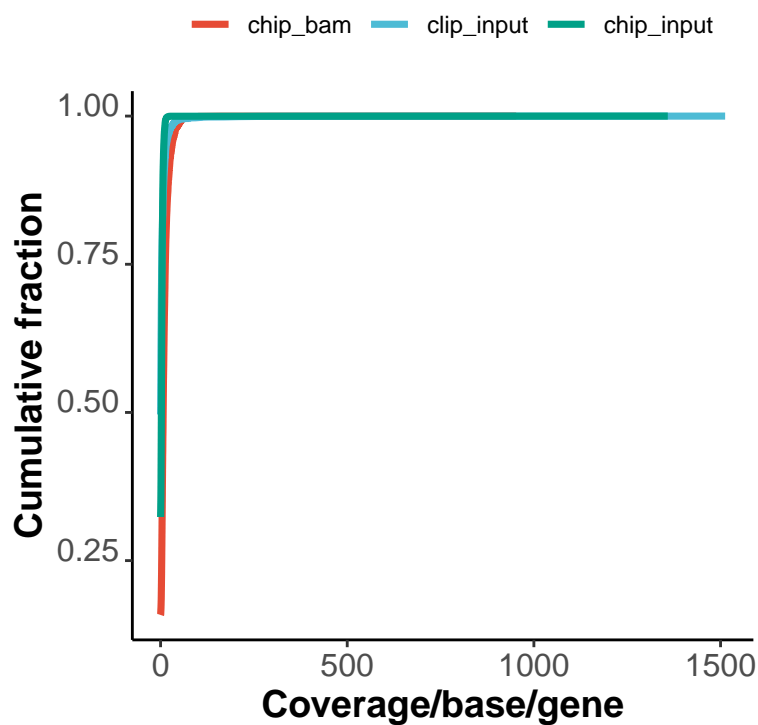
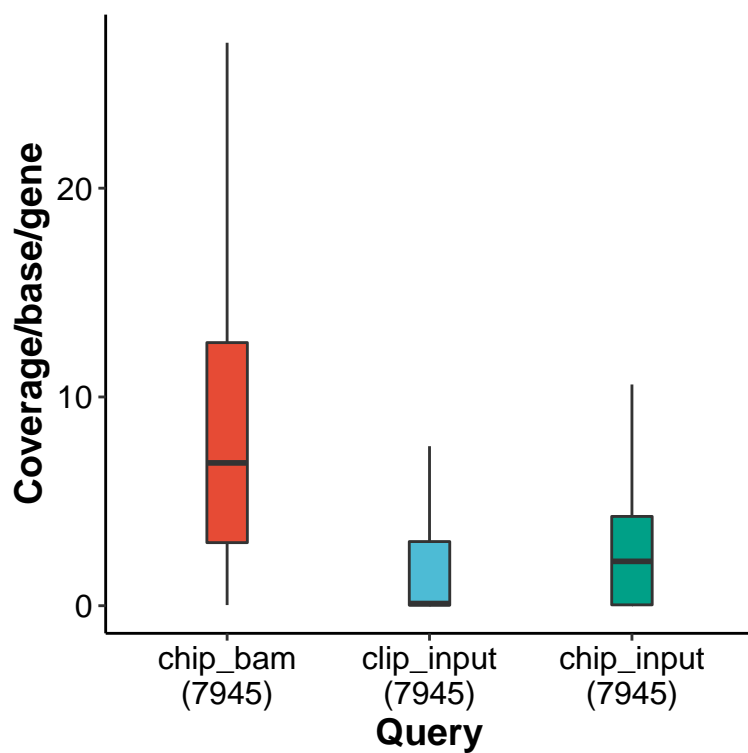
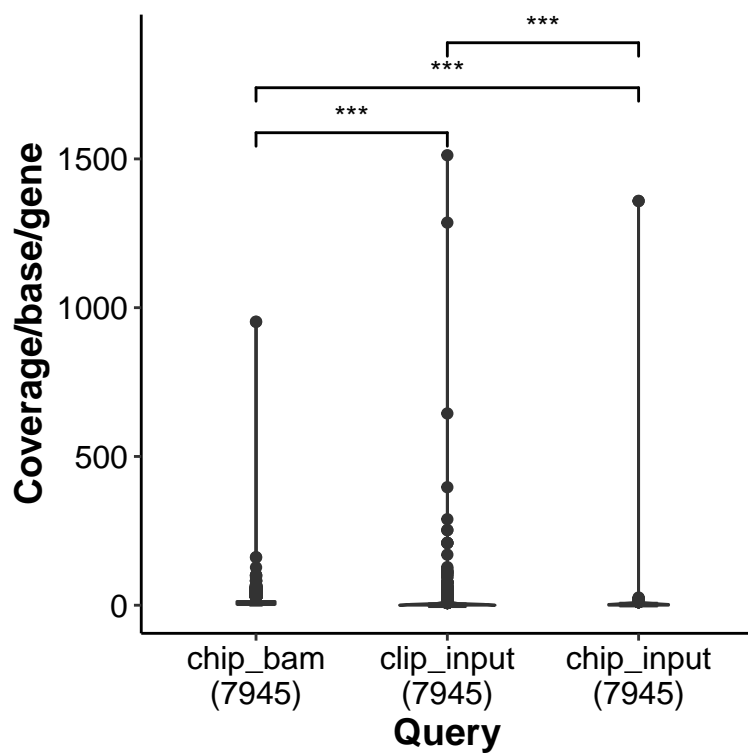


post hoc TukeyHSD test

	diff	lwr	upr	p adj
<i>clip_input-clip_bam</i>	-1.176	-1.965	-0.387	0.00139
<i>chip_input-clip_bam</i>	-2.073	-2.862	-1.284	0.00000
<i>chip_input-clip_input</i>	-0.897	-1.686	-0.108	0.02098

NarrowPeak



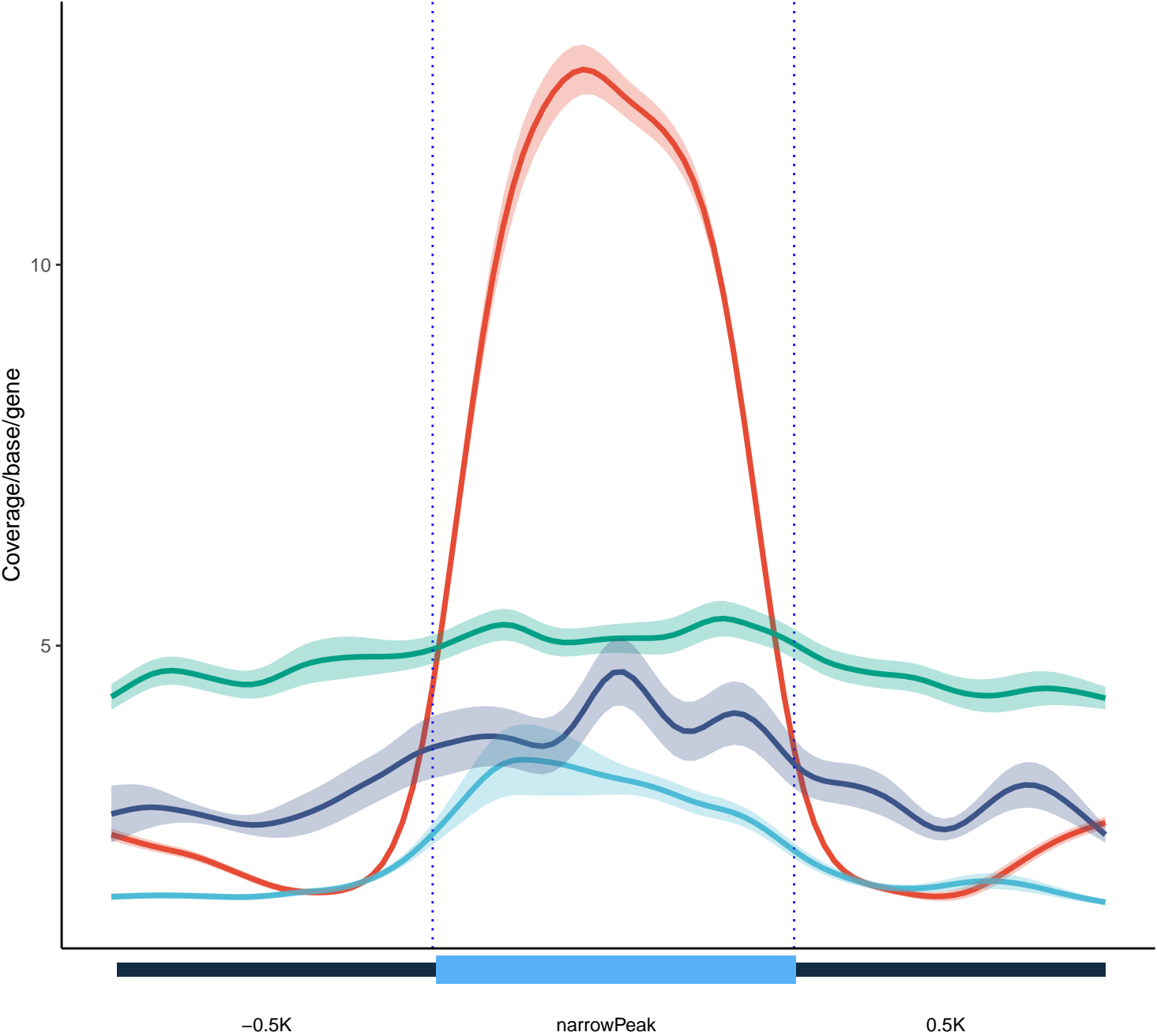


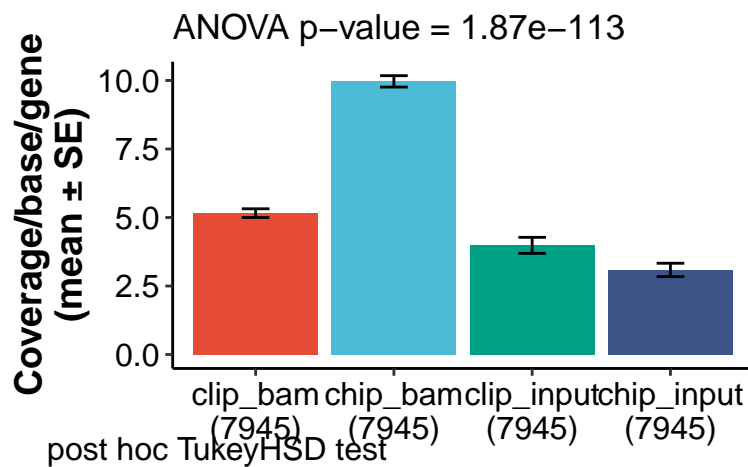
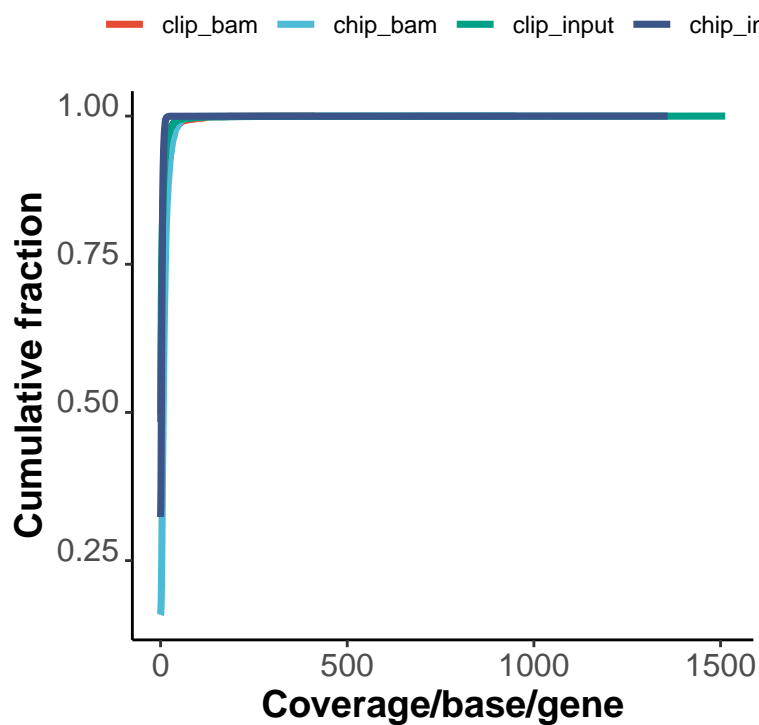
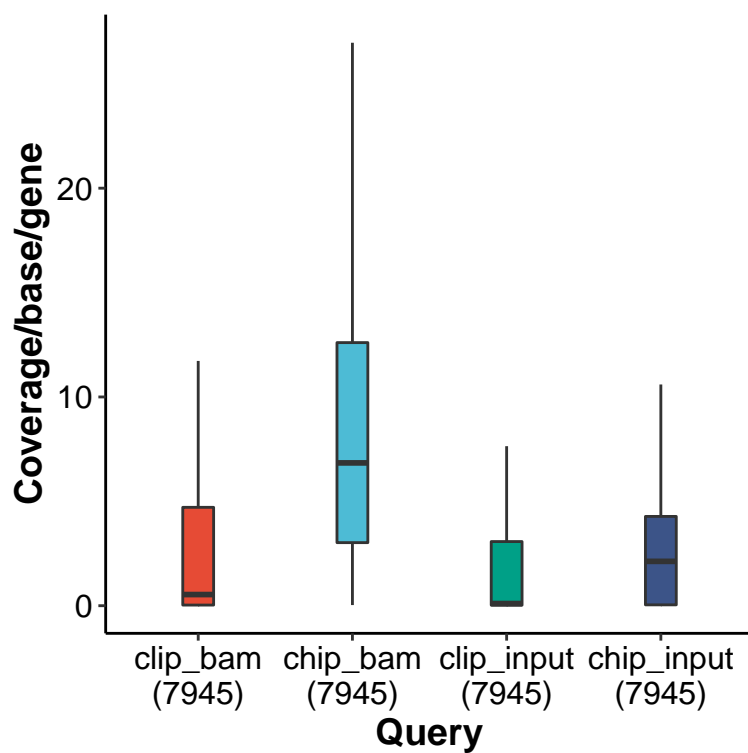
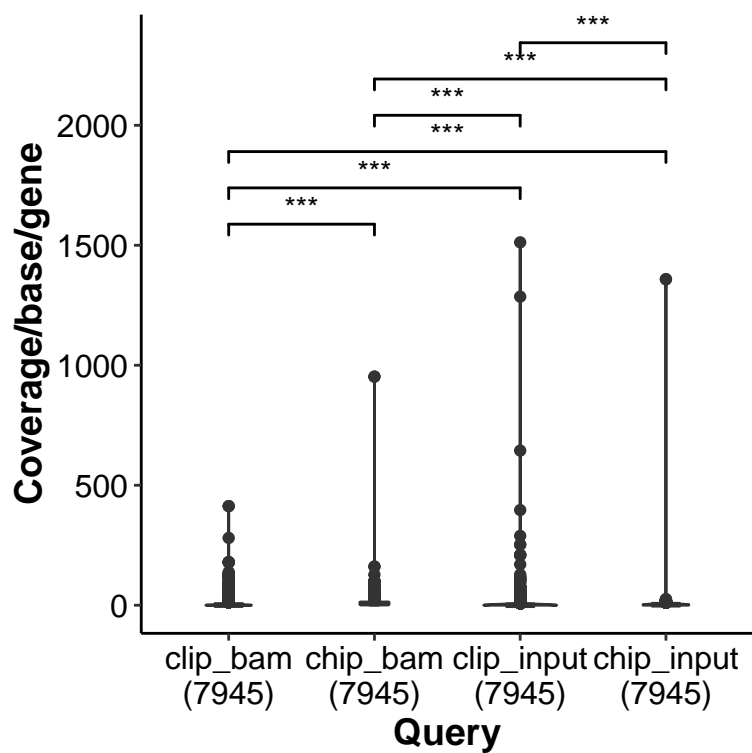
post hoc TukeyHSD test

	diff	lwr	upr	p adj
<i>clip_input-chip_bam</i>	-5.984	-6.814	-5.154	0.0000
<i>chip_input-chip_bam</i>	-6.881	-7.711	-6.051	0.0000
<i>chip_input-clip_input</i>	-0.897	-1.727	-0.068	0.0303

NarrowPeak

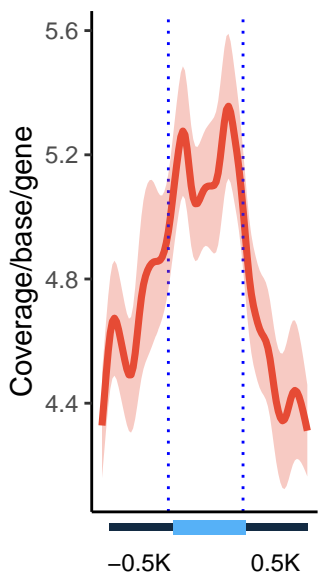
Query chip\_bam chip\_input clip\_bam clip\_input




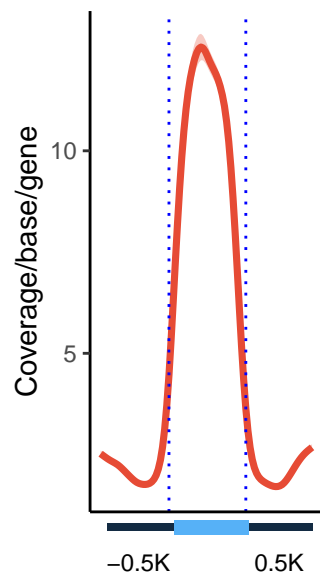


	diff	lwr	upr	p adj
chip_bam-clip_bam	4.808	3.969	5.646	0.00e+00
clip_input-clip_bam	-1.176	-2.014	-0.337	1.79e-03
chip_input-clip_bam	-2.073	-2.912	-1.235	1.27e-09
clip_input-chip_bam	-5.984	-6.822	-5.145	0.00e+00
chip_input-chip_bam	-6.881	-7.72	-6.043	0.00e+00


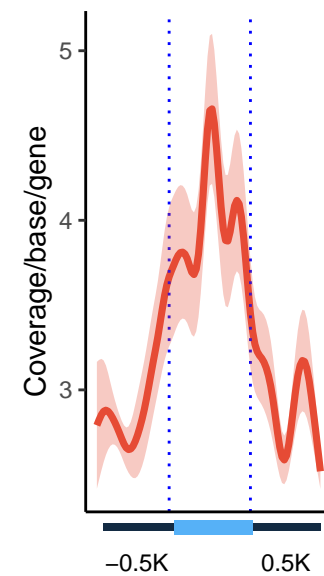
NarrowPeak

Group  clip\_bam:NarrowF

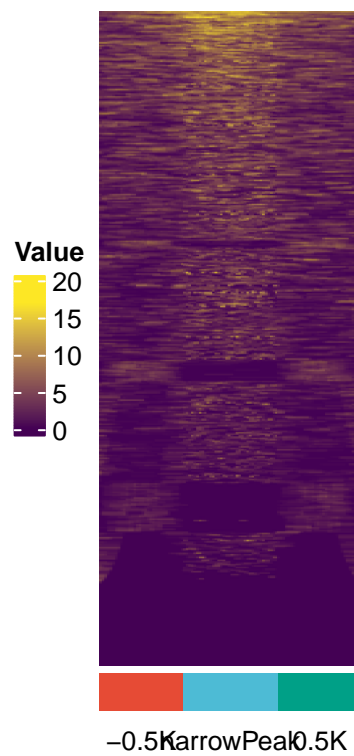
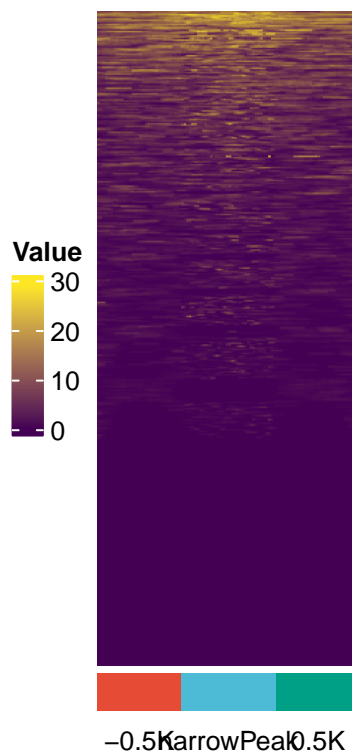
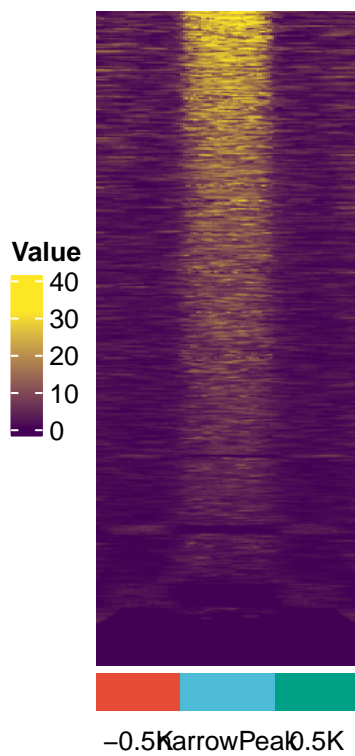
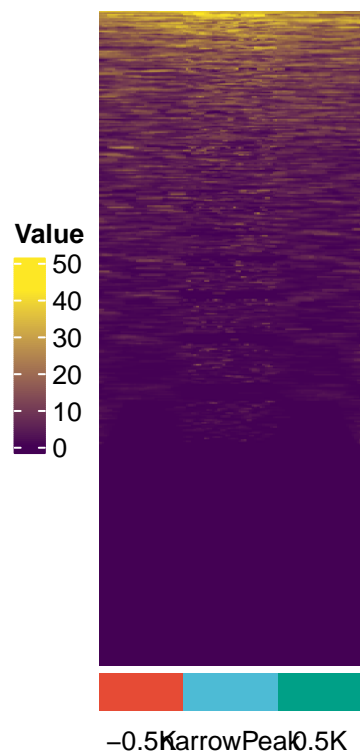
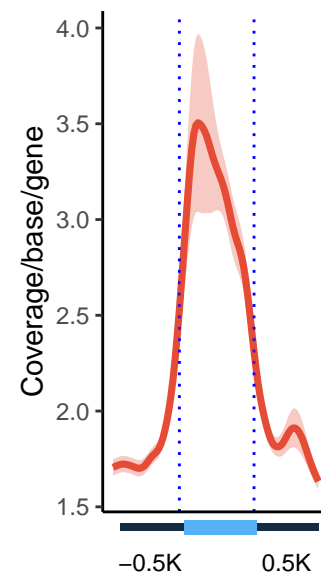
NarrowPeak

Group  chip\_bam:NarrowF

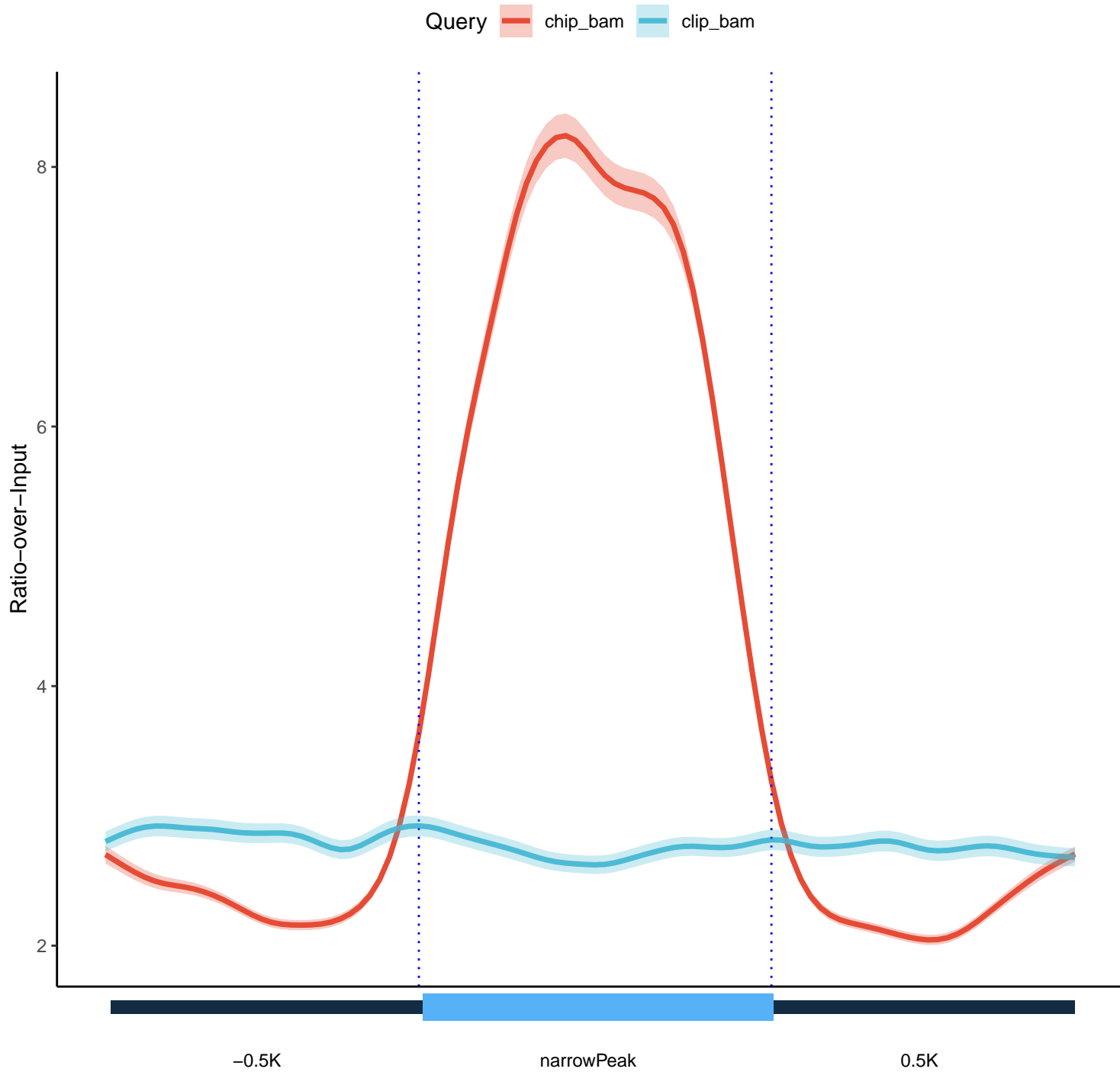
NarrowPeak

Group  clip\_input:NarrowPi

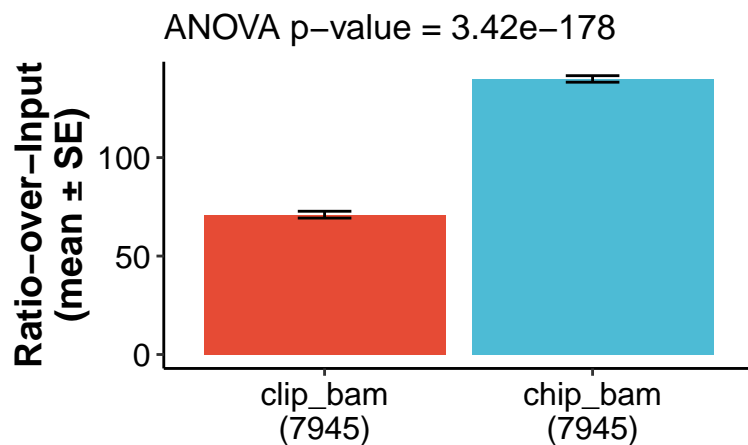
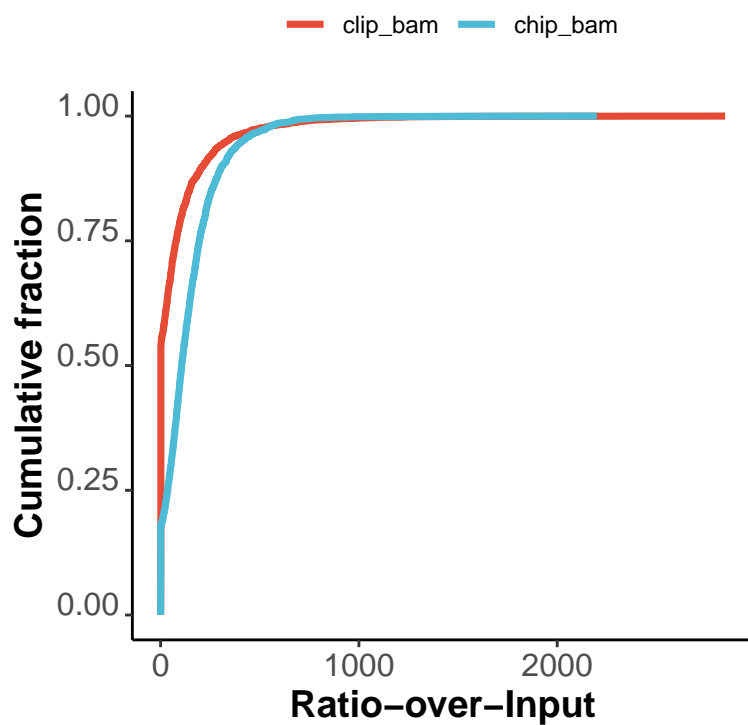
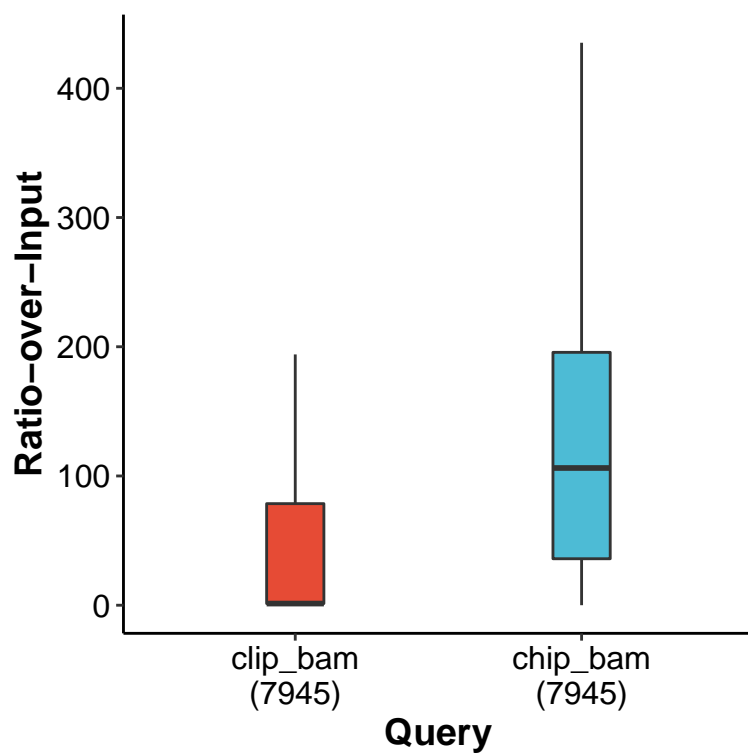
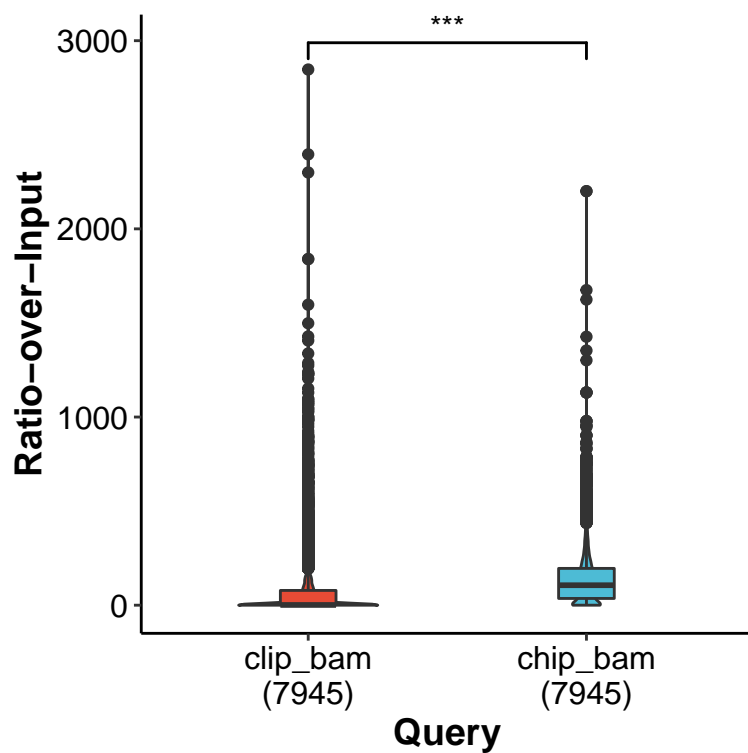
NarrowPeak

Group  chip\_input:Narroww

# NarrowPeak





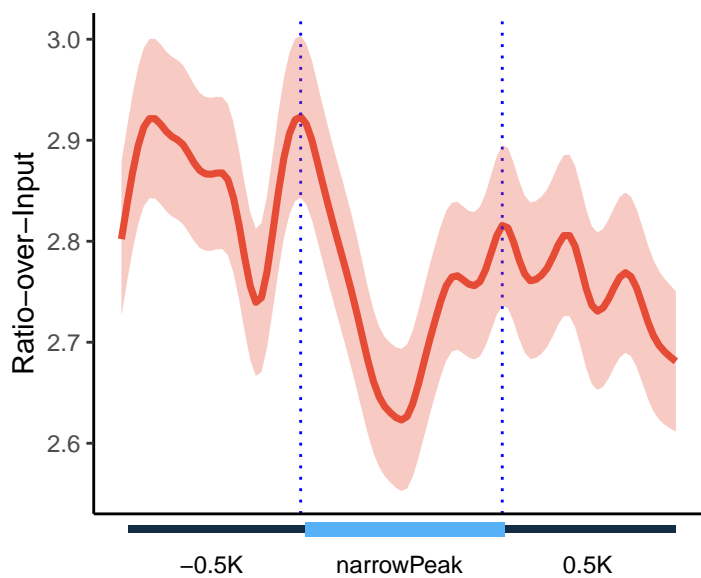


post hoc TukeyHSD test

	diff	lwr	upr	p adj
chip_bam-clip_bam	68.926	64.24	73.612	2.04e-08

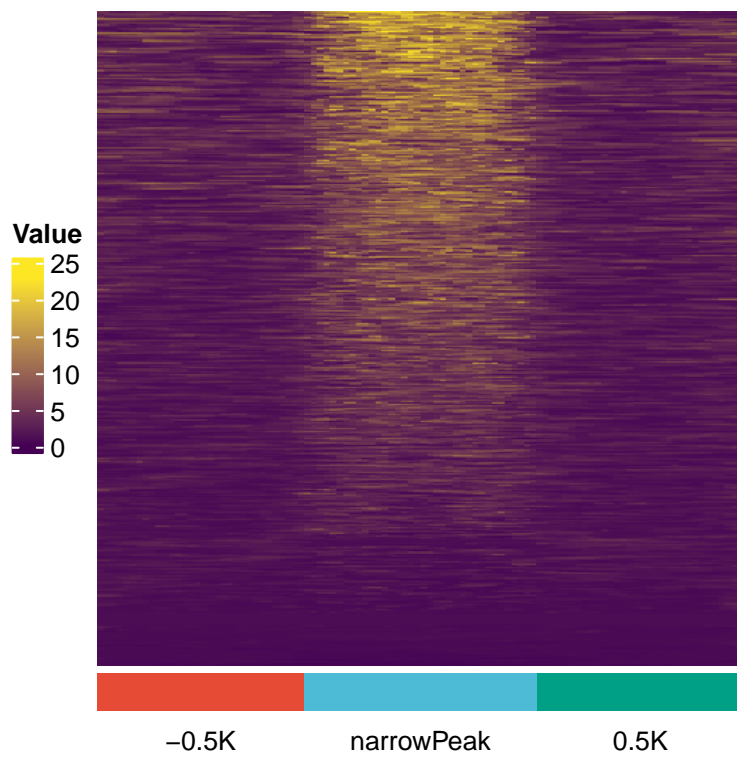
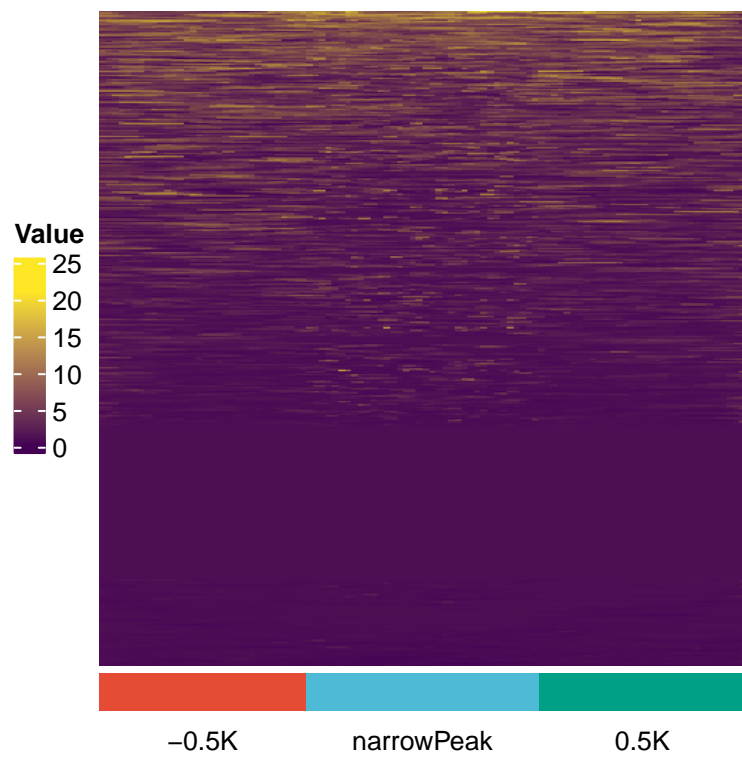
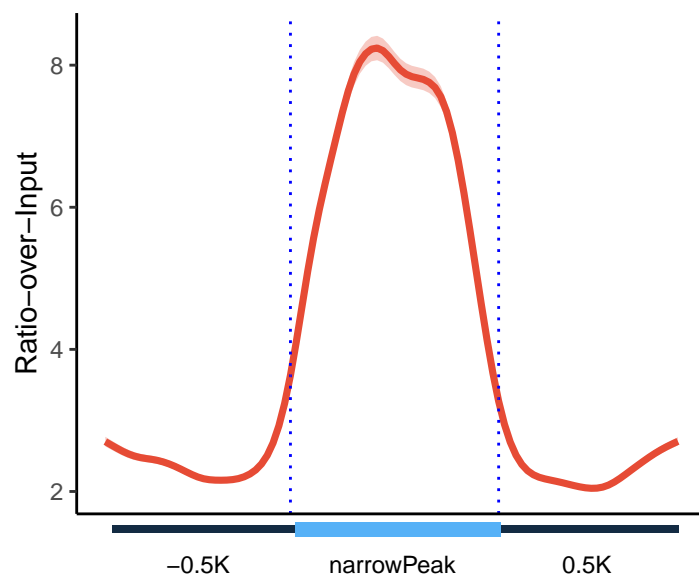
NarrowPeak

Group clip\_bam:NarrowPeak



NarrowPeak

Group chip\_bam:NarrowPeak



Plotting parameters:

```
functionName: "plot_region"
queryFiles: c(clip_bam =
"C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/treat_chr19.bam", clip_bam
= "C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/chip_treat_chr19.bam")
centerFiles: c(NarrowPeak =
"C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/test_chip_peak_chr19.narrowPeak")
txdb: NULL
regionName: "narrowPeak"
inputFiles: c(clip_input =
"C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/input_chr19.bam",
chip_input =
"C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/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
```