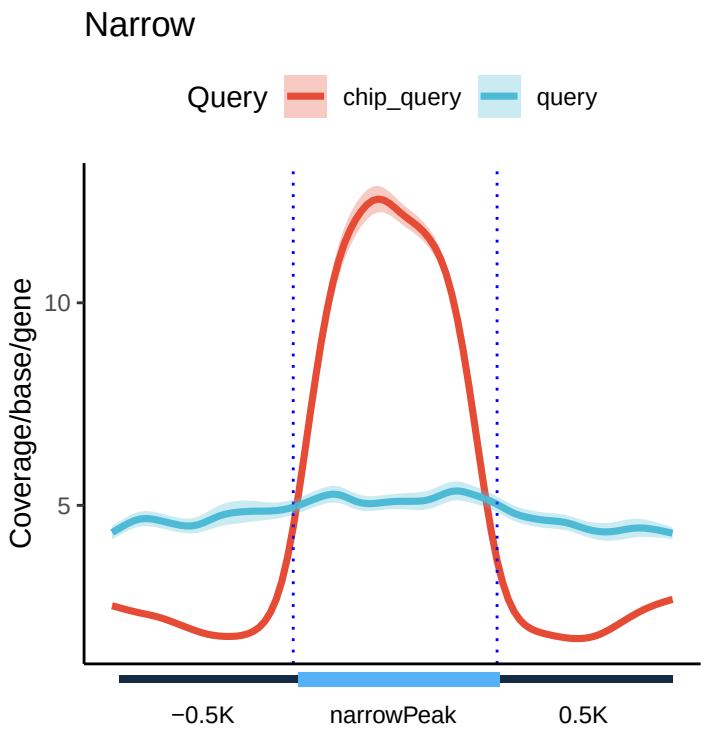
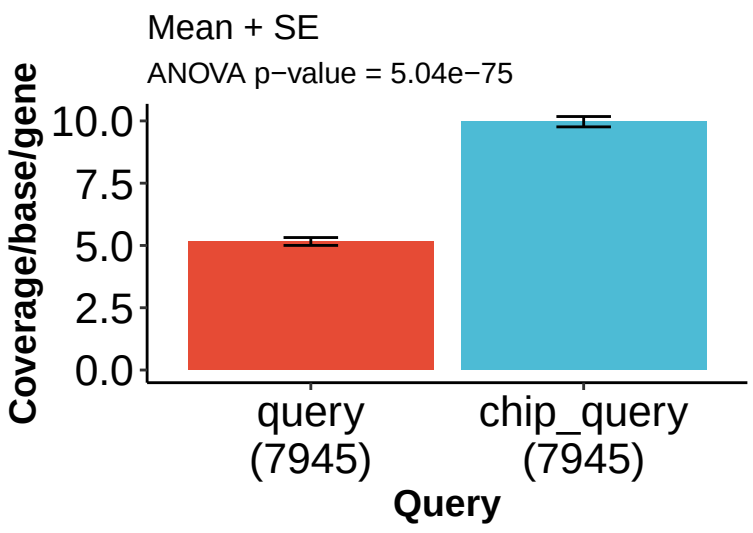
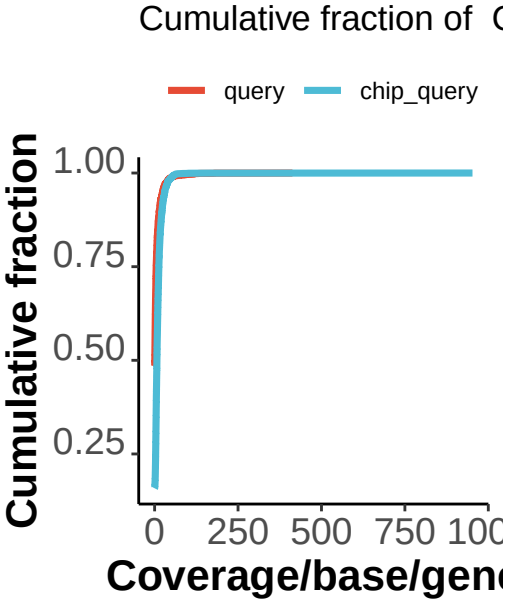
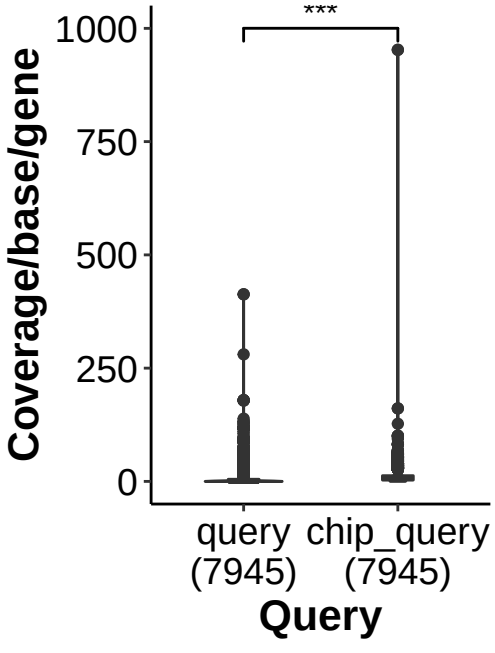


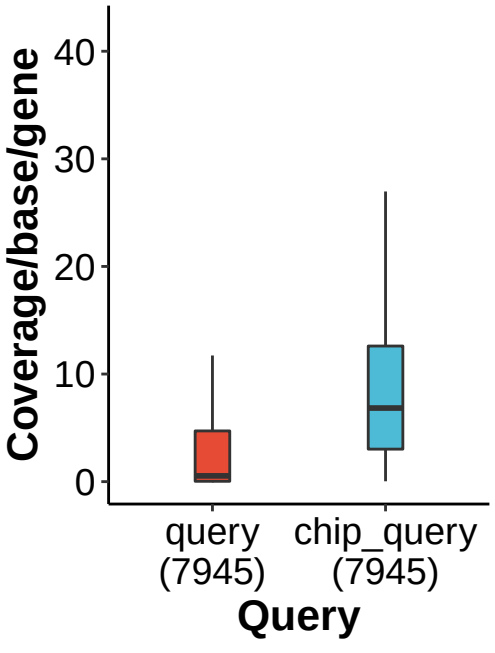


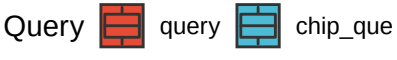
post hoc TukeyHSD test

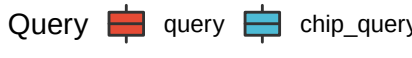
	diff	lwr	upr	p adj
chip_query−query	4.808	4.296	5.319	2.04e−08

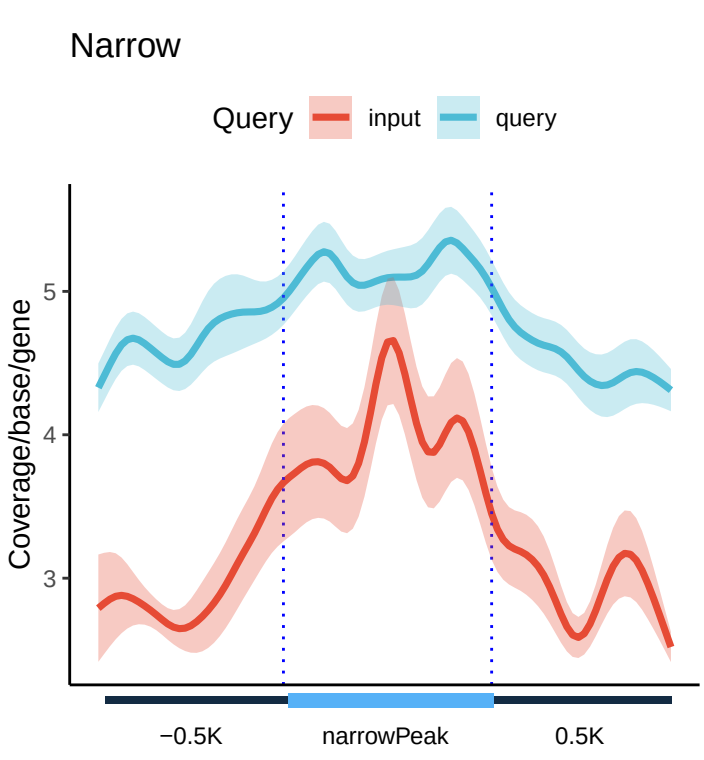


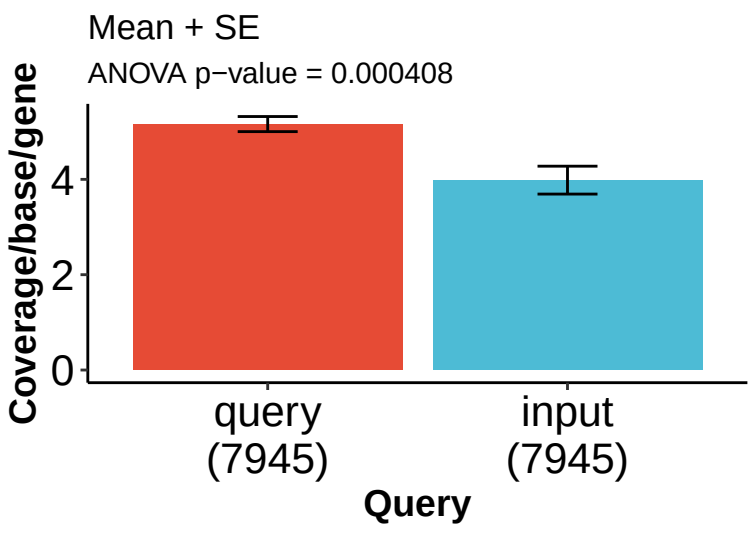






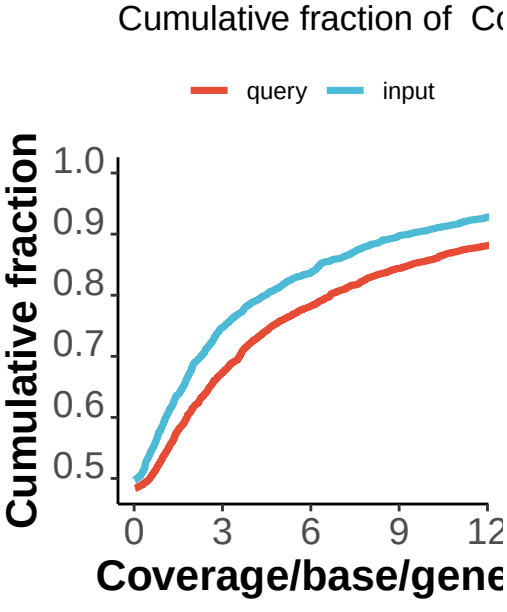


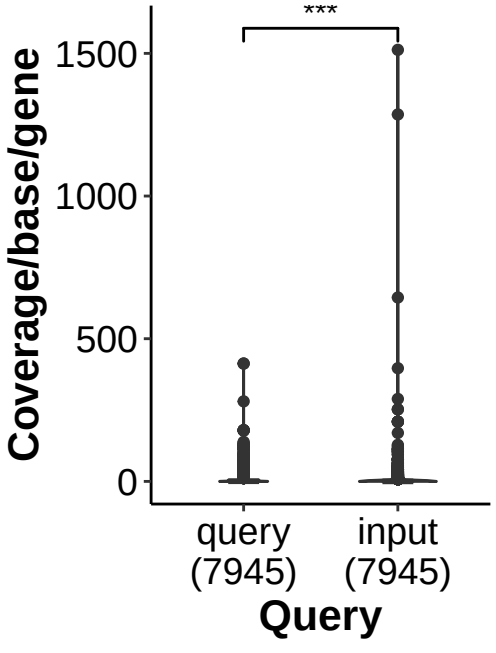


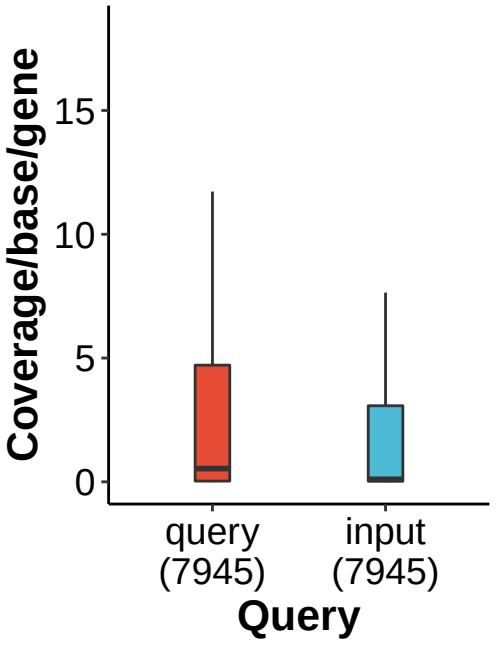


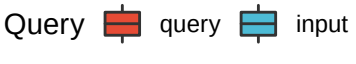
post hoc TukeyHSD test

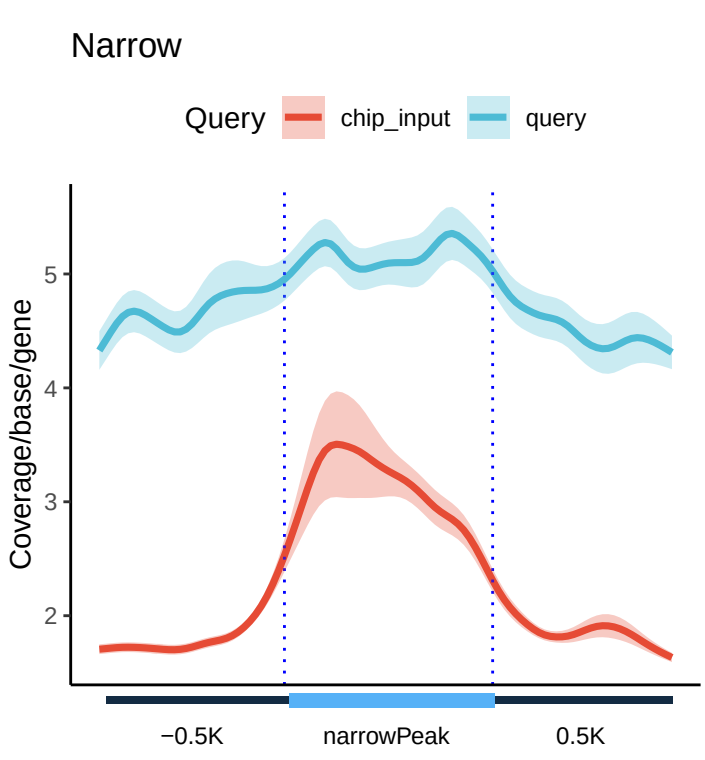
	diff	lwr	upr	p adj
input−query	−1.176	−1.828	−0.524	0.000408

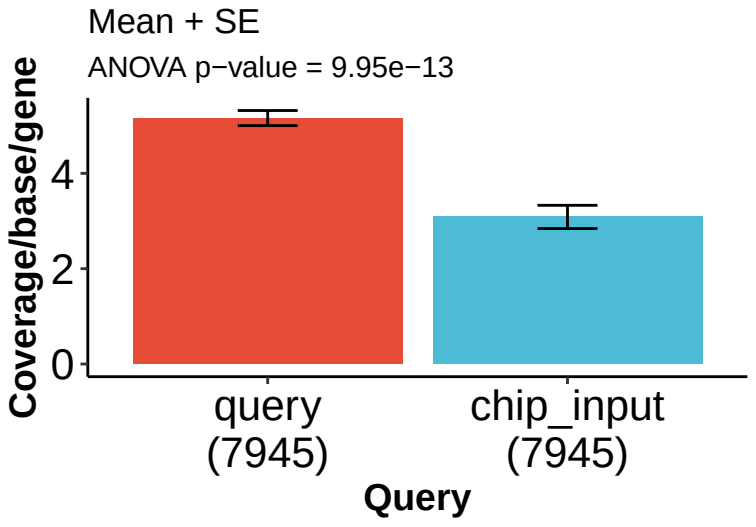






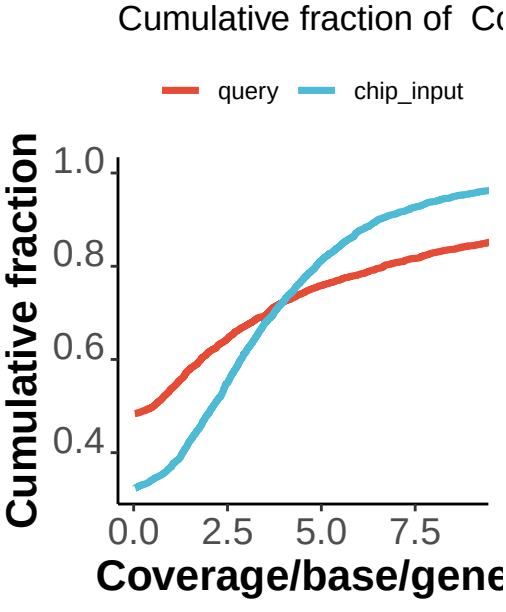


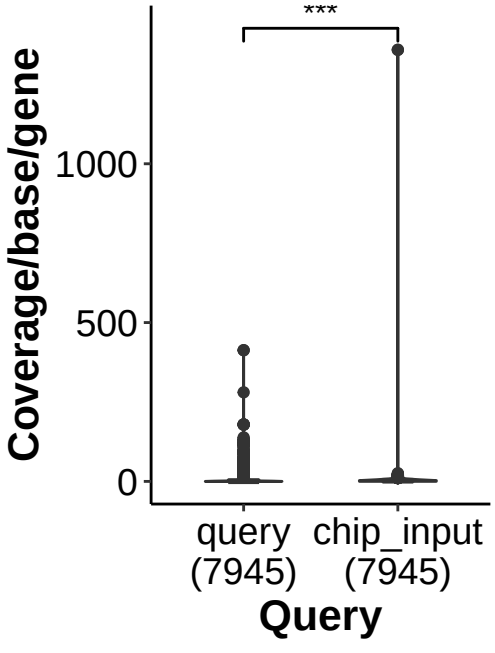


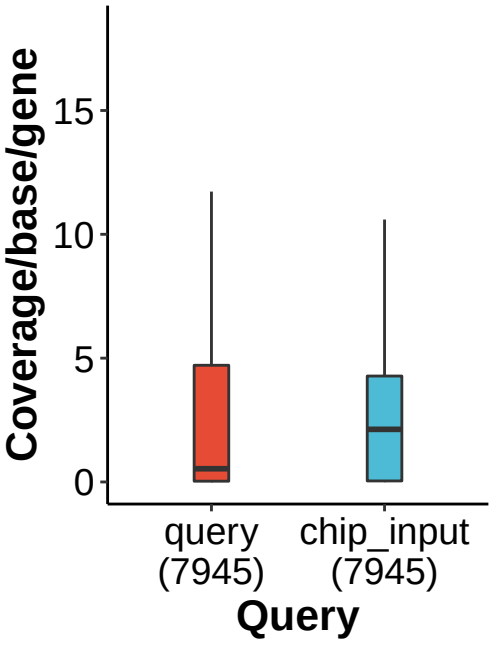


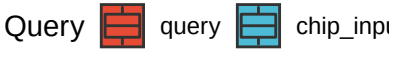
post hoc TukeyHSD test

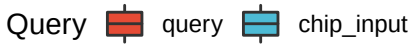
	diff	lwr	upr	p adj
chip_input−query	−2.073	−2.643	−1.504	2.04e−08

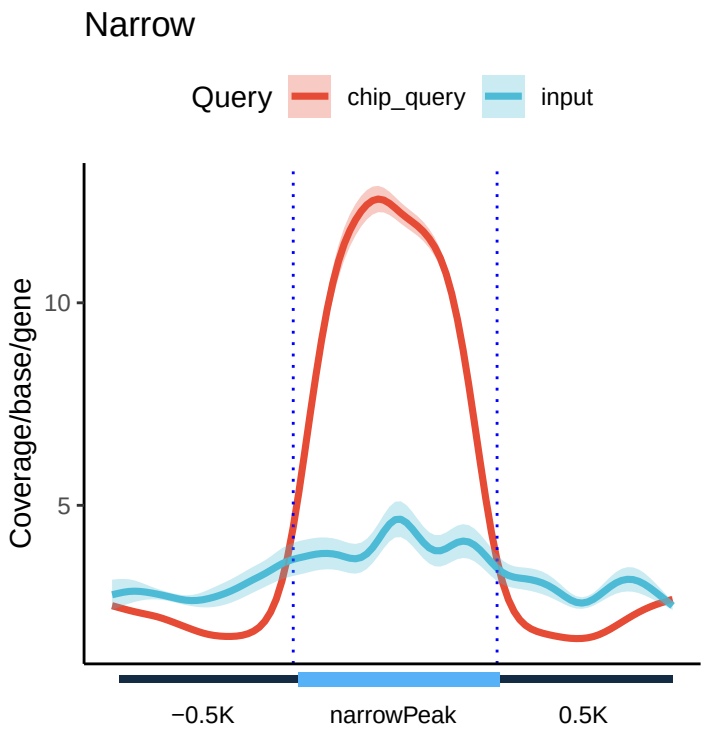


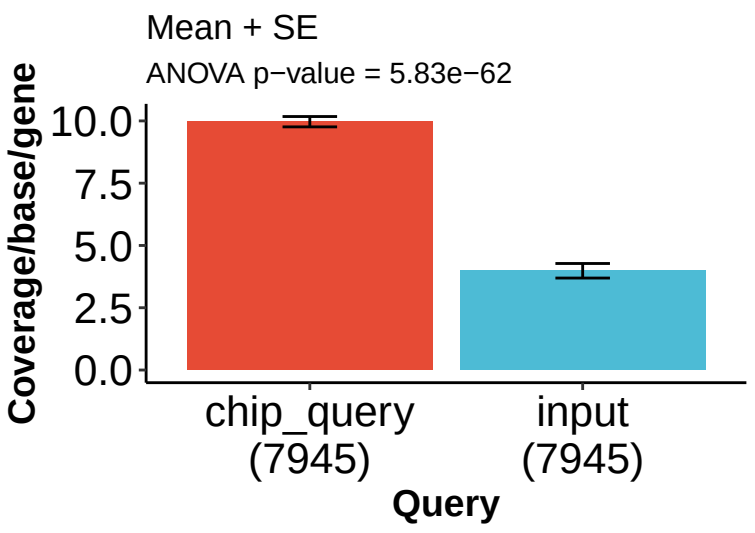






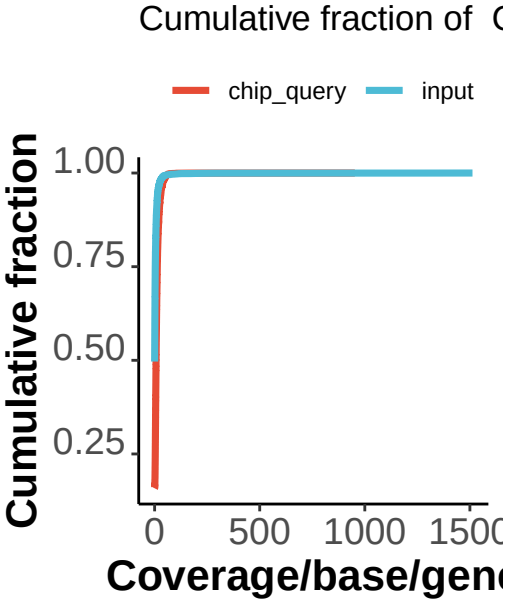


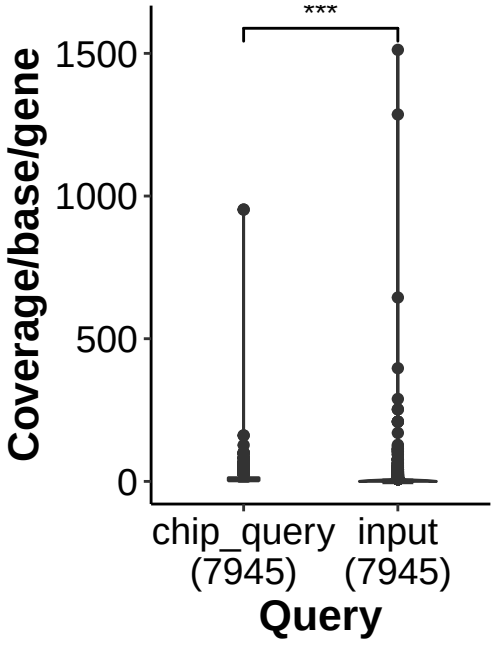


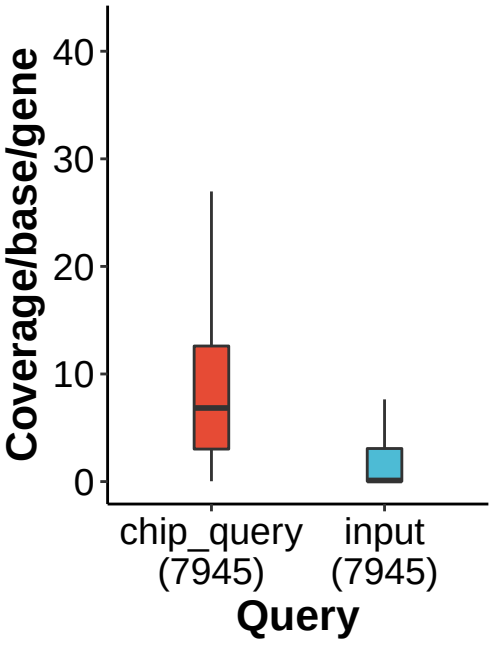


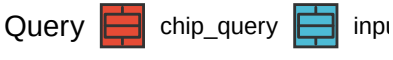
post hoc TukeyHSD test

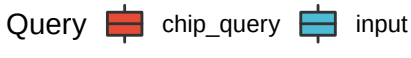
	diff	lwr	upr	p adj
input−chip_query	−5.984	−6.687	−5.281	2.04e−08

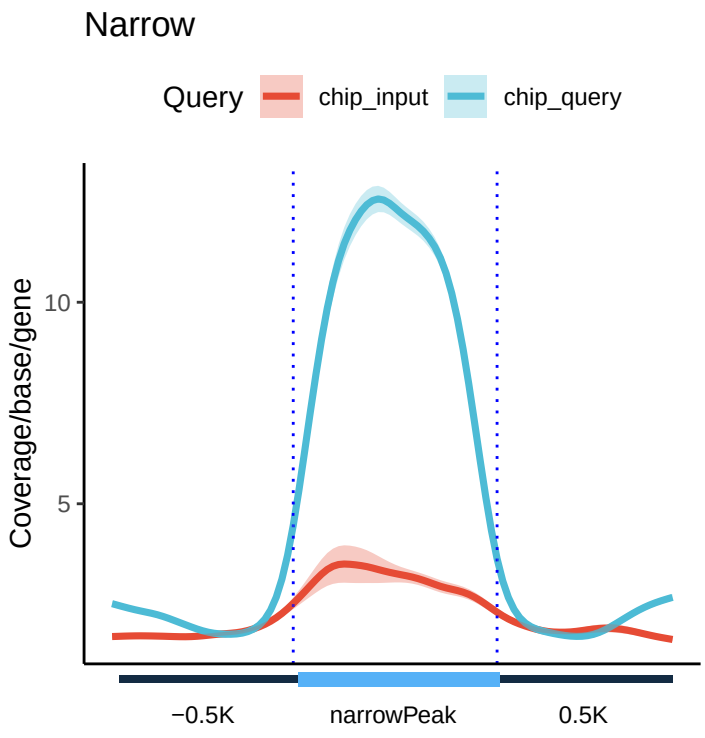


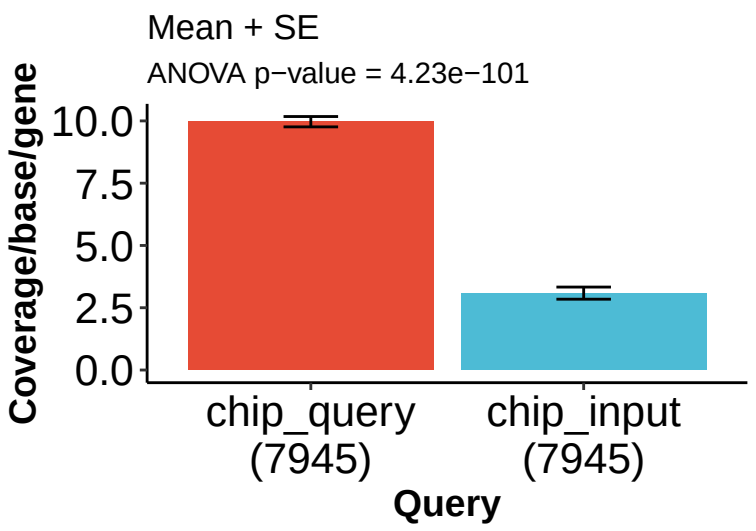






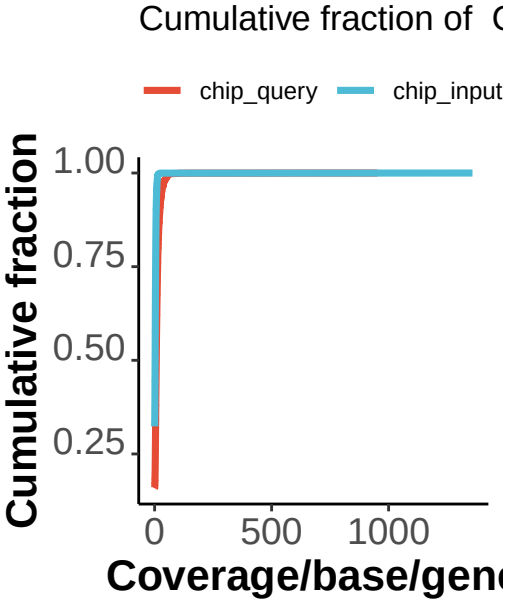


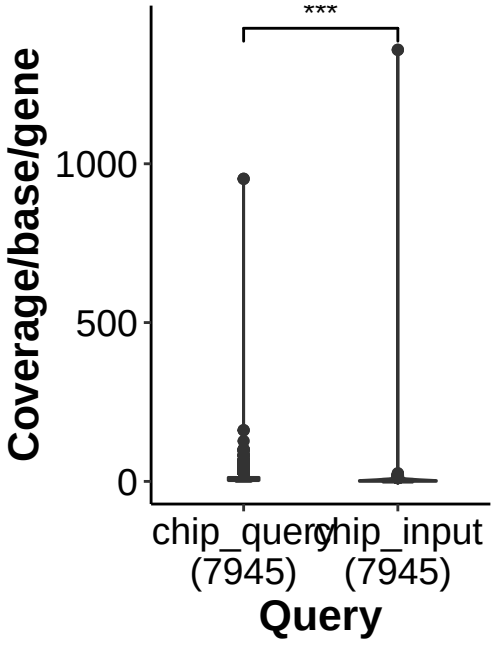


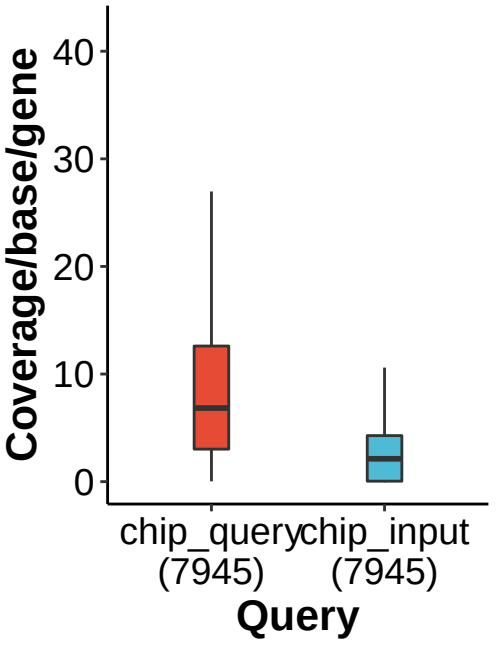


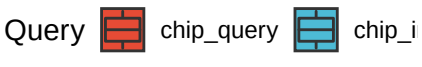
post hoc TukeyHSD test

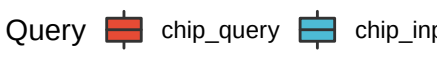
	diff	lwr	upr	p adj
chip_input−chip_query	−6.881	−7.509	−6.254	2.04e−0

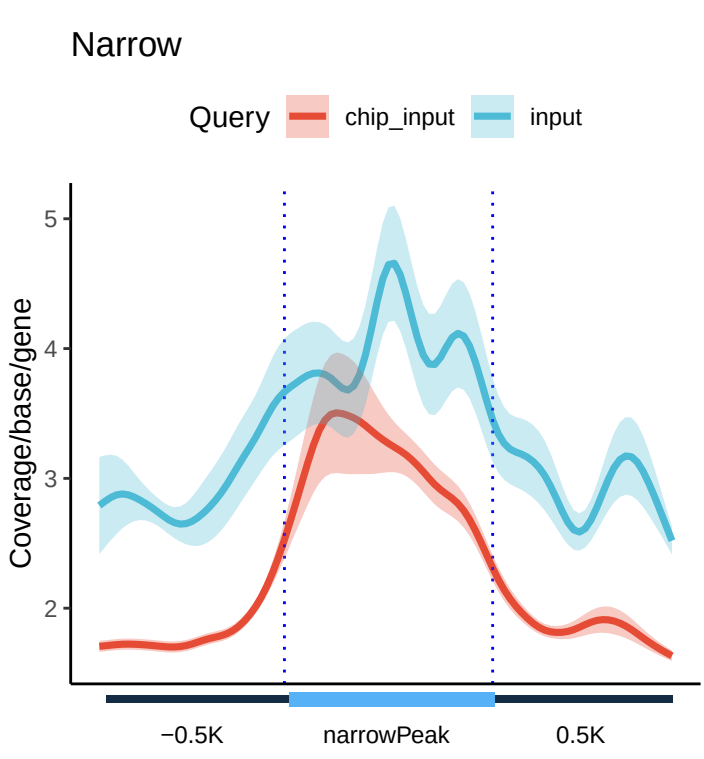


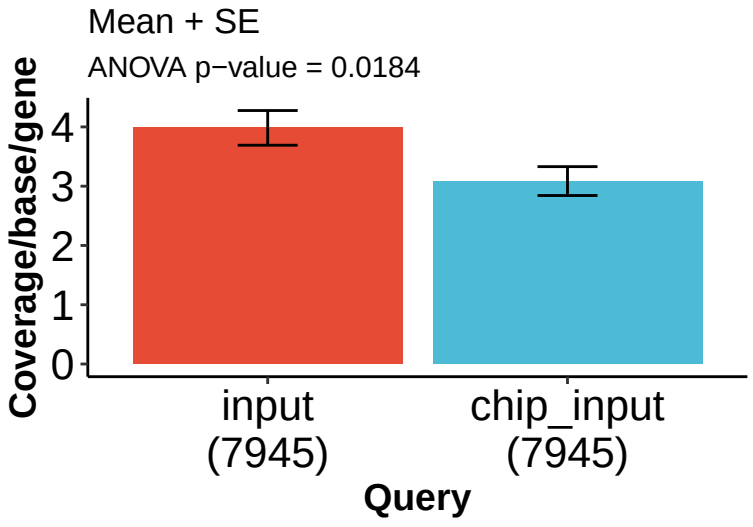






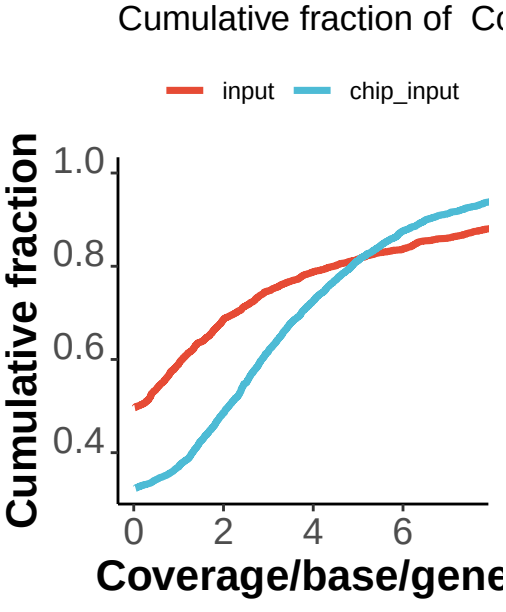


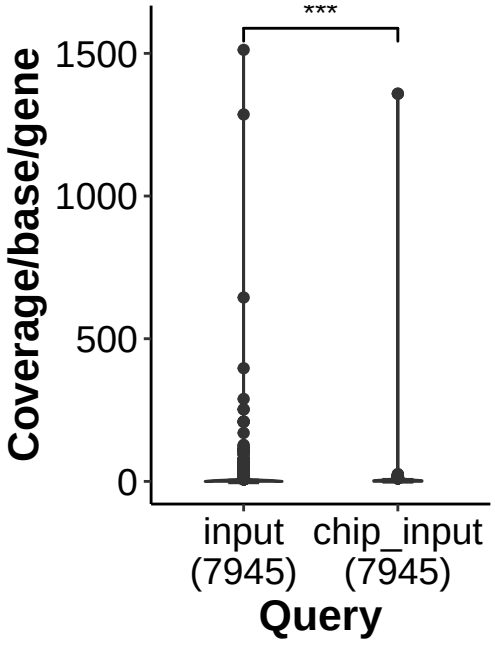


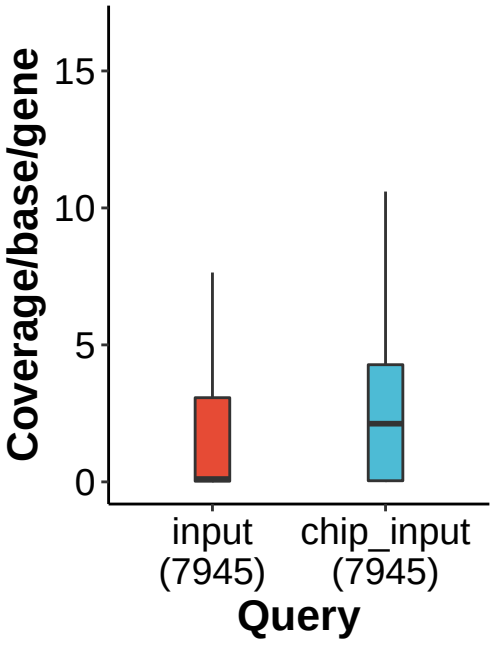


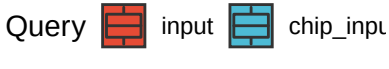
post hoc TukeyHSD test

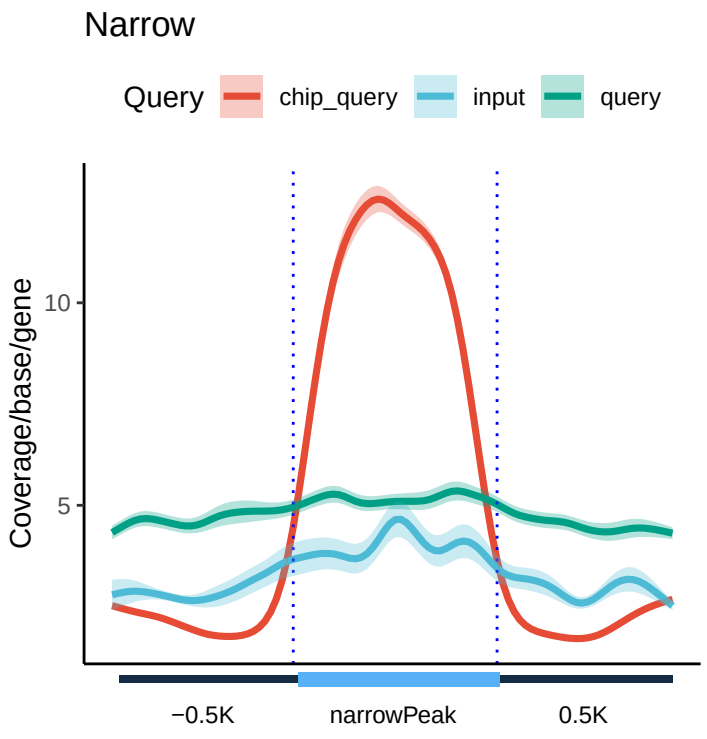
	diff	lwr	upr	p adj
chip_input−input	−0.897	−1.644	−0.151	0.0184

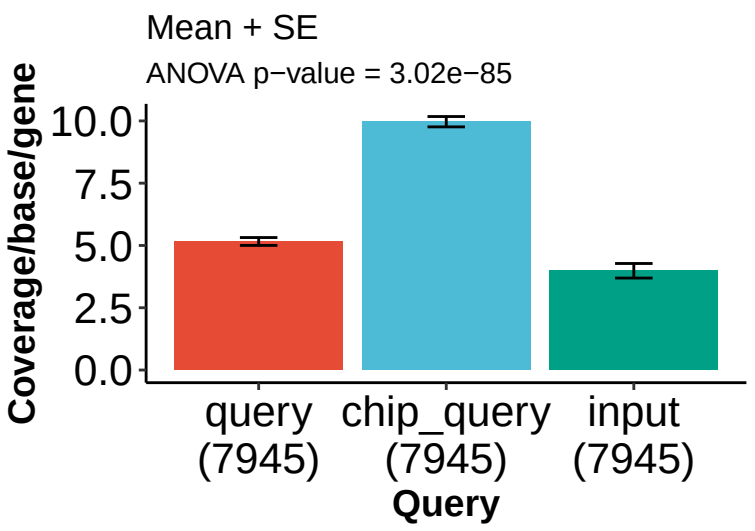






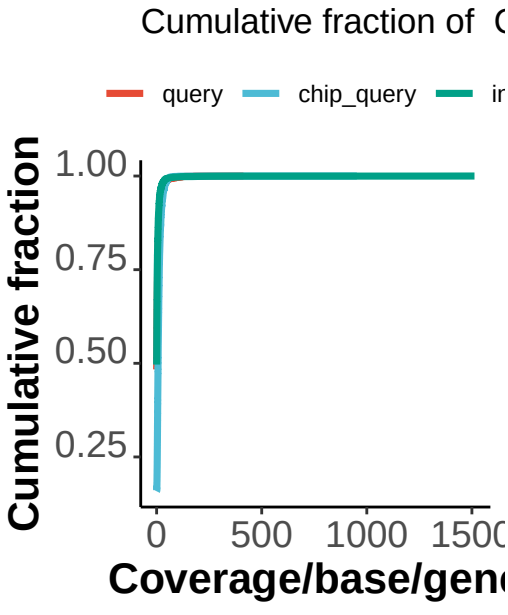


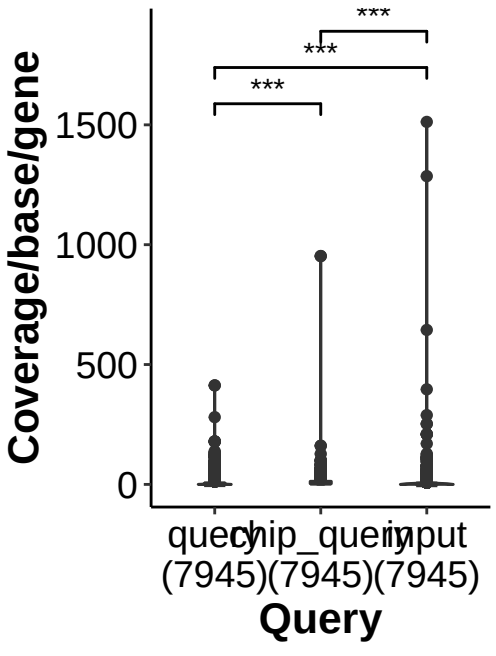


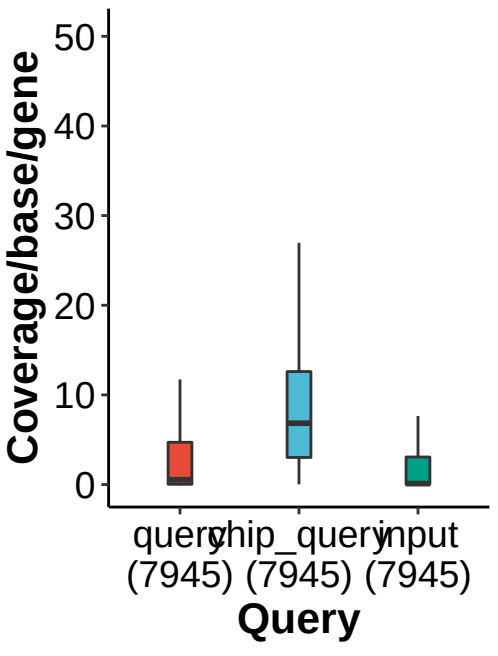


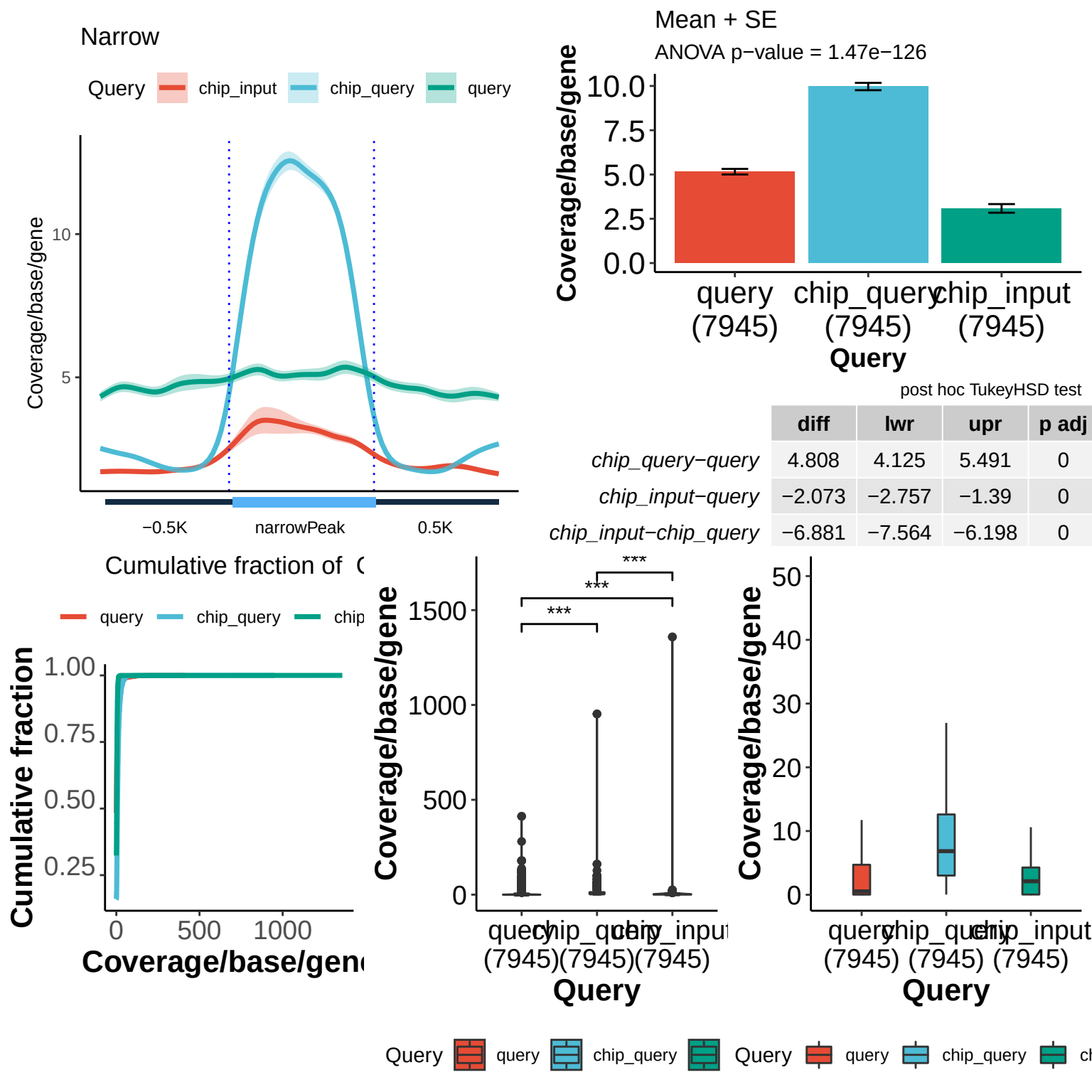
post hoc TukeyHSD test

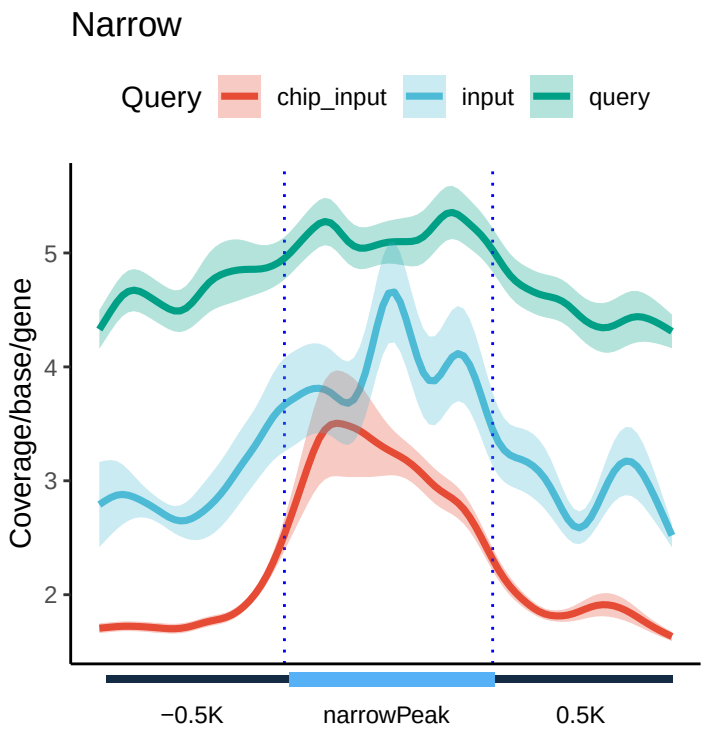
	diff	lwr	upr	p adj
chip_query−query	4.808	4.058	5.558	0e+00
input−query	−1.176	−1.926	−0.426	7e−04
input−chip_query	−5.984	−6.734	−5.234	0e+00

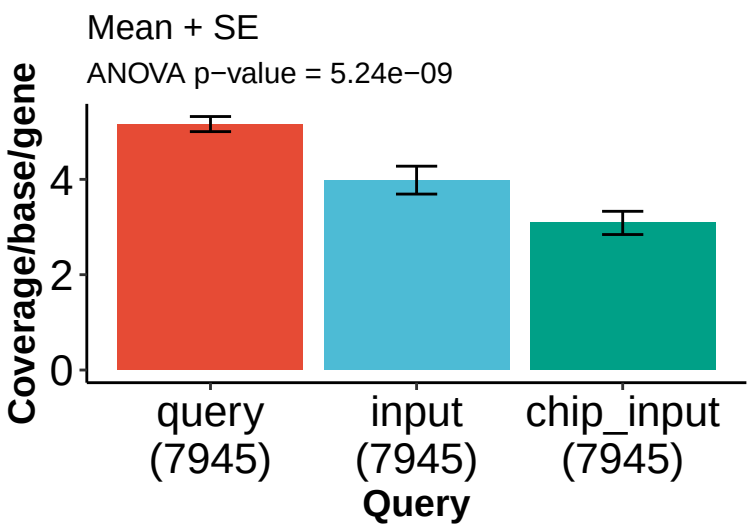






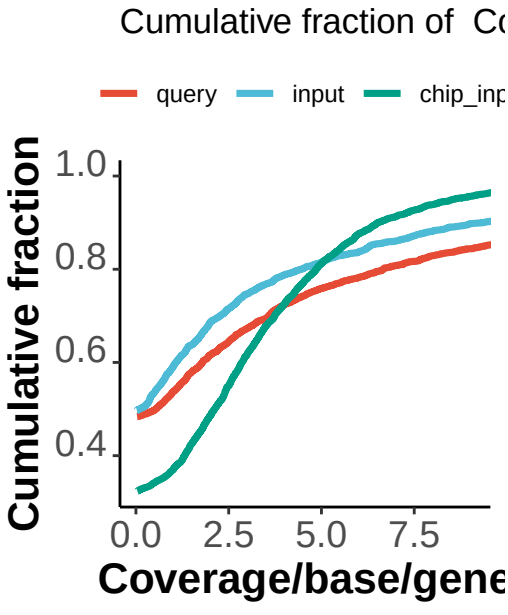

Narrow
Query
chip_input
chip_query
query
Coverage/base/gene
10
5
−0.5K
narrowPeak
0.5K
Mean + SE
ANOVA p−value = 1.47e−126
Coverage/base/gene
10.0
7.5
5.0
2.5
0.0
query (7945)
chip_query (7945)
chip_input (7945)
Query
post hoc TukeyHSD test
diff
lwr
upr
p adj
chip_query−query 4.808 4.125 5.491 0
chip_input−query −2.073 −2.757 −1.39 0
chip_input−chip_query −6.881 −7.564 −6.198 0
Cumulative fraction of (
query
chip_query
chip
Cumulative fraction
1.00
0.75
0.50
0.25
0
500
1000
Coverage/base/gen
***
***
***
Coverage/base/gene
1500
1000
500
0
query (7945)
chip_query (7945)
chip_input (7945)
Query
Coverage/base/gene
50
40
30
20
10
0
query (7945)
chip_query (7945)
chip_input (7945)
Query
Query
query
chip_query
Query
query
chip_query

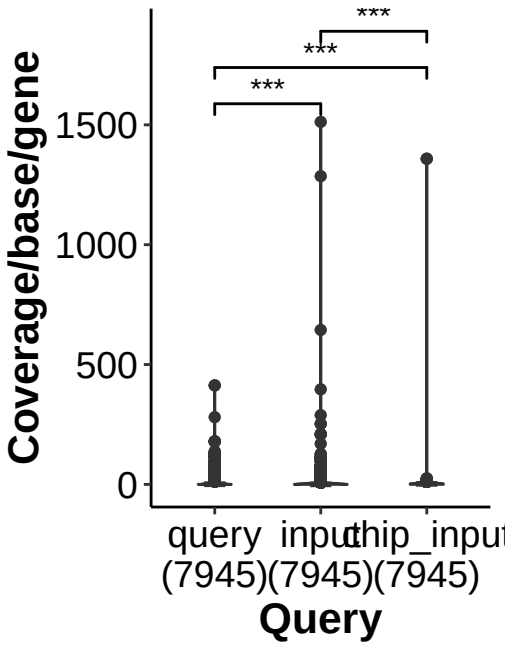


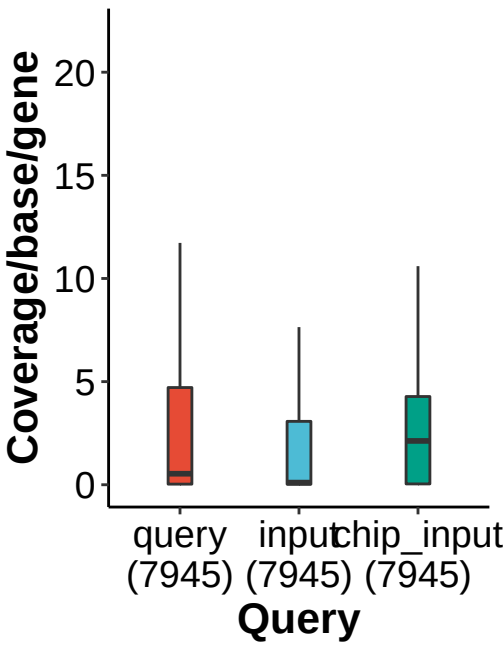


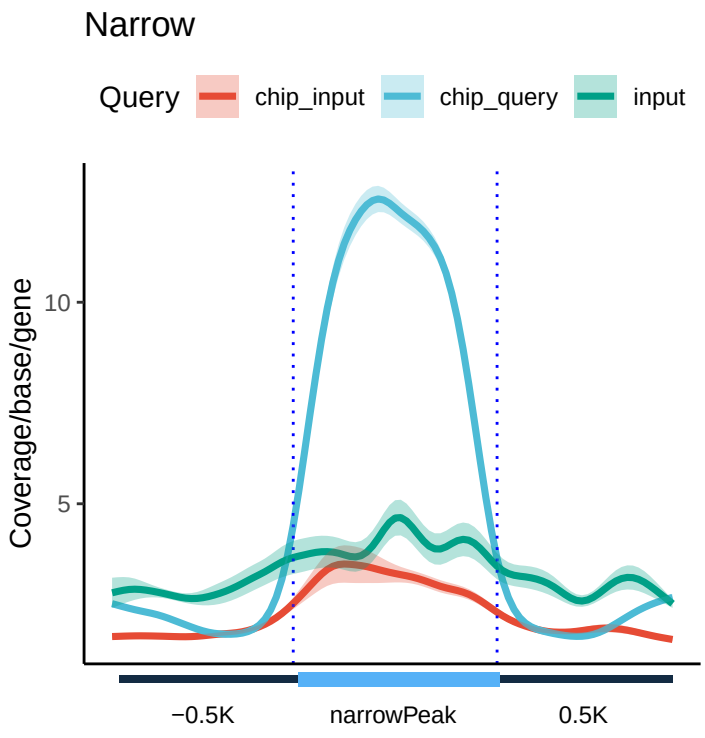
post hoc TukeyHSD test

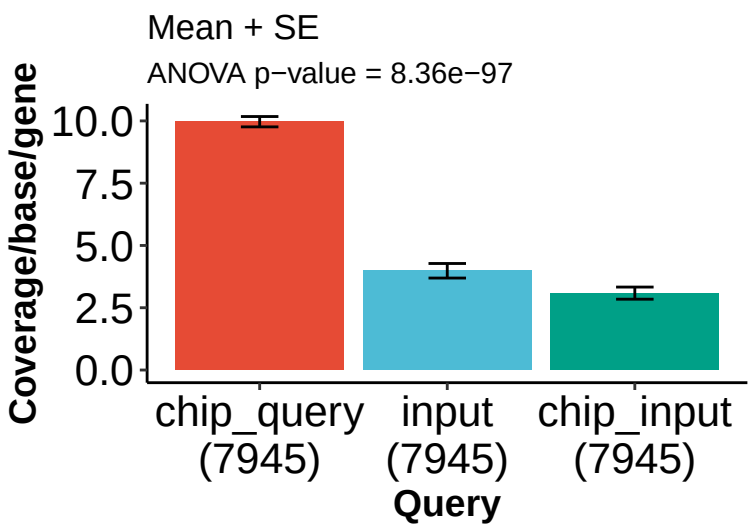
	diff	lwr	upr	p adj
input−query	−1.176	−1.965	−0.387	0.00139
chip_input−query	−2.073	−2.862	−1.284	0.00000
chip_input−input	−0.897	−1.686	−0.108	0.02098





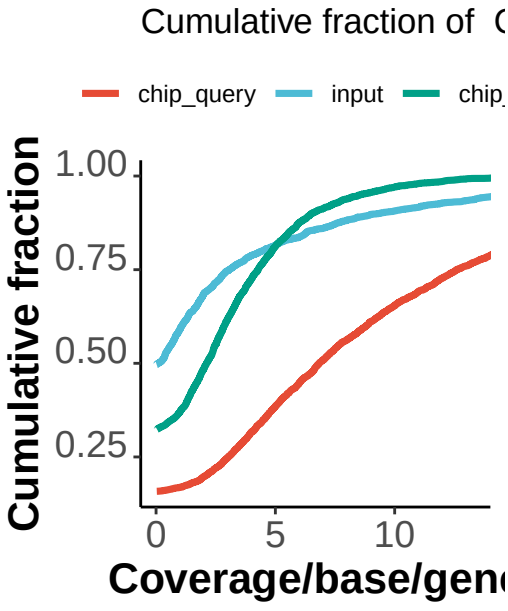


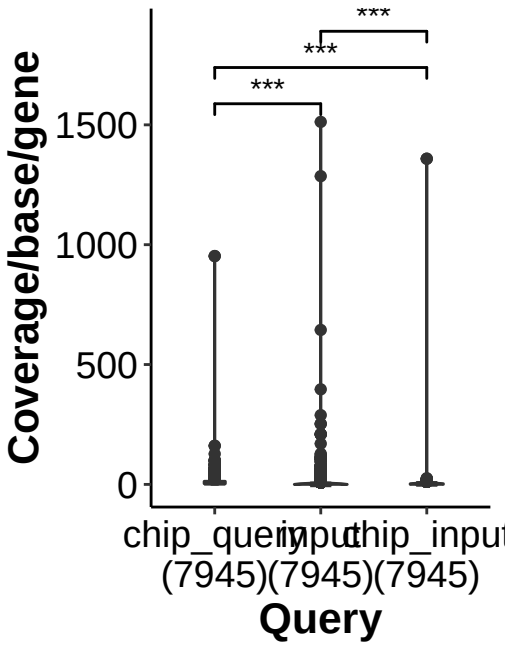


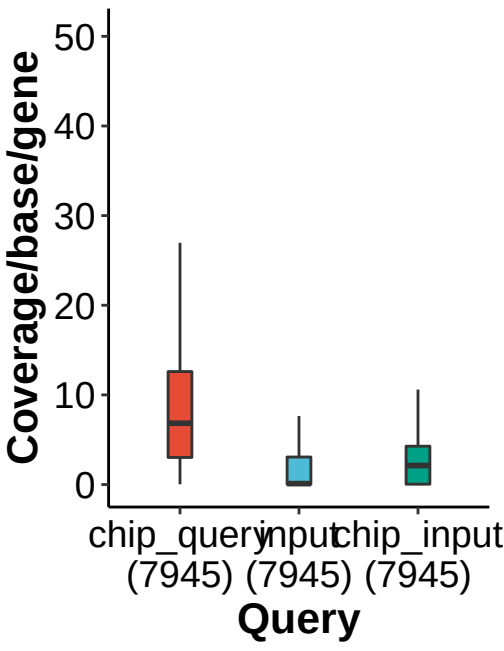


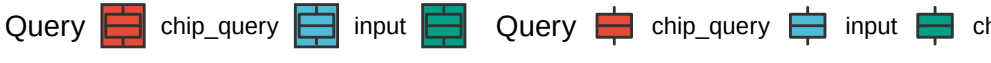
post hoc TukeyHSD test

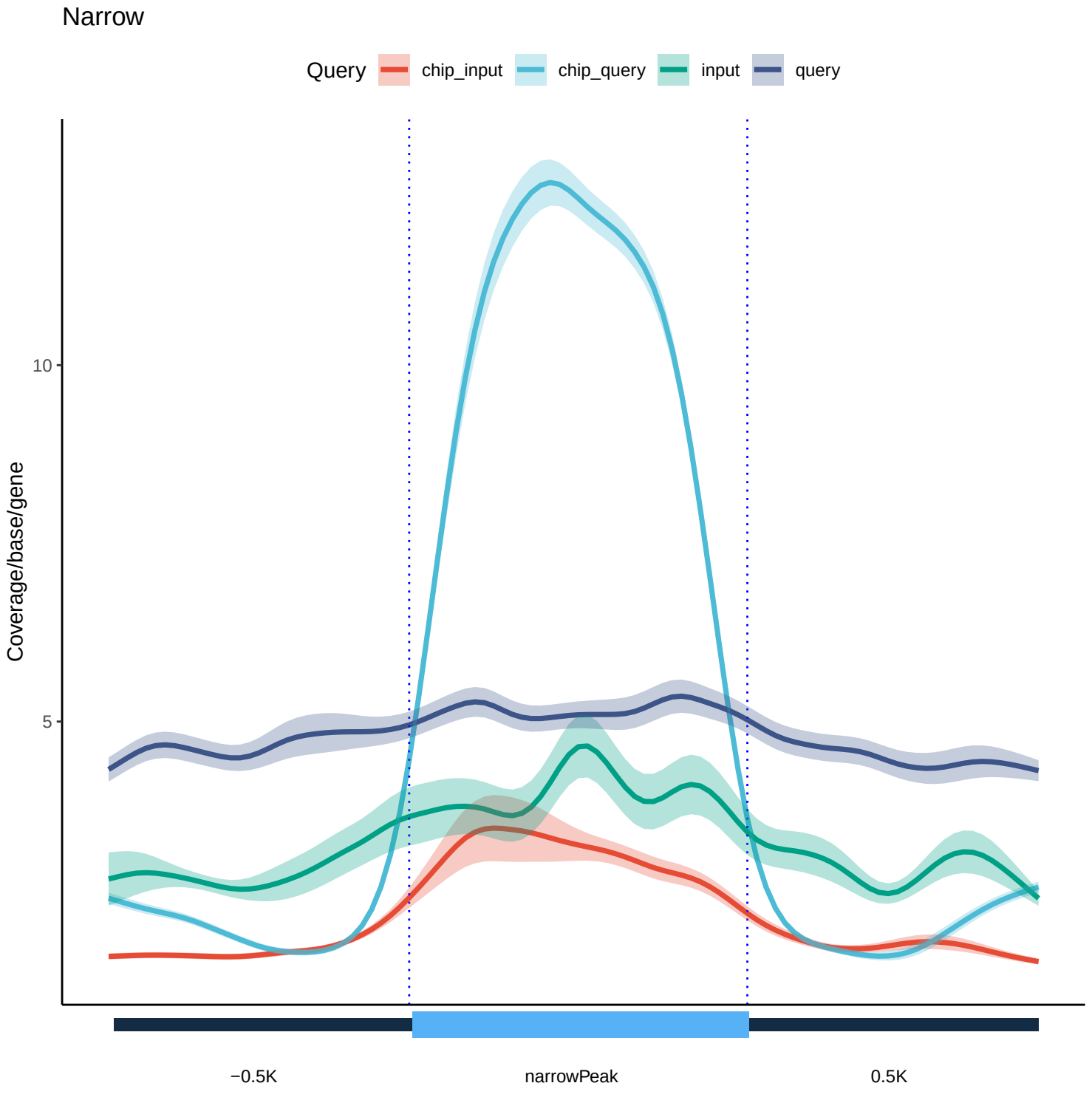
	diff	lwr	upr	p adj
input−chip_query	−5.984	−6.814	−5.154	0.0000
chip_input−chip_query	−6.881	−7.711	−6.051	0.0000
chip_input−input	−0.897	−1.727	−0.068	0.0303

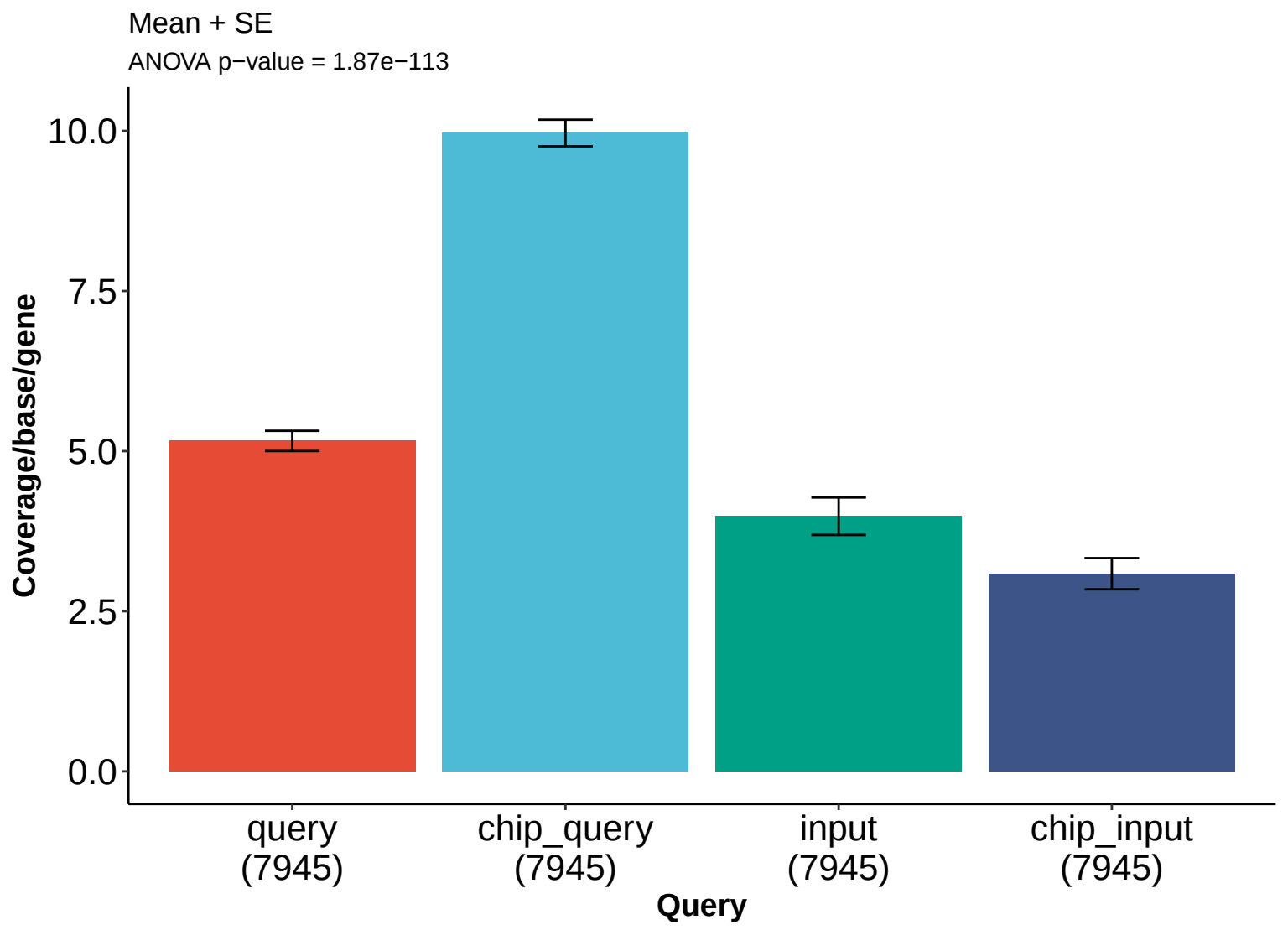






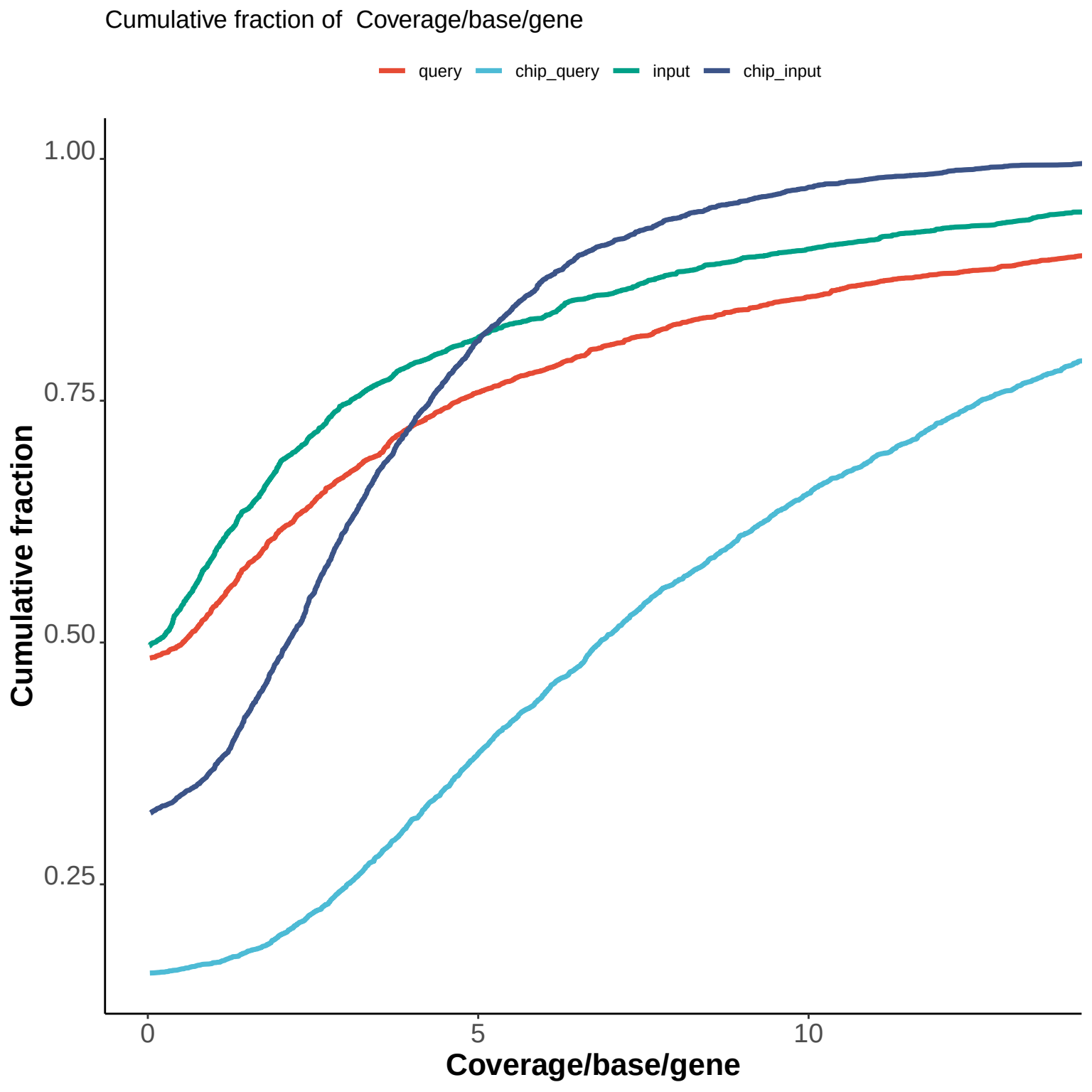


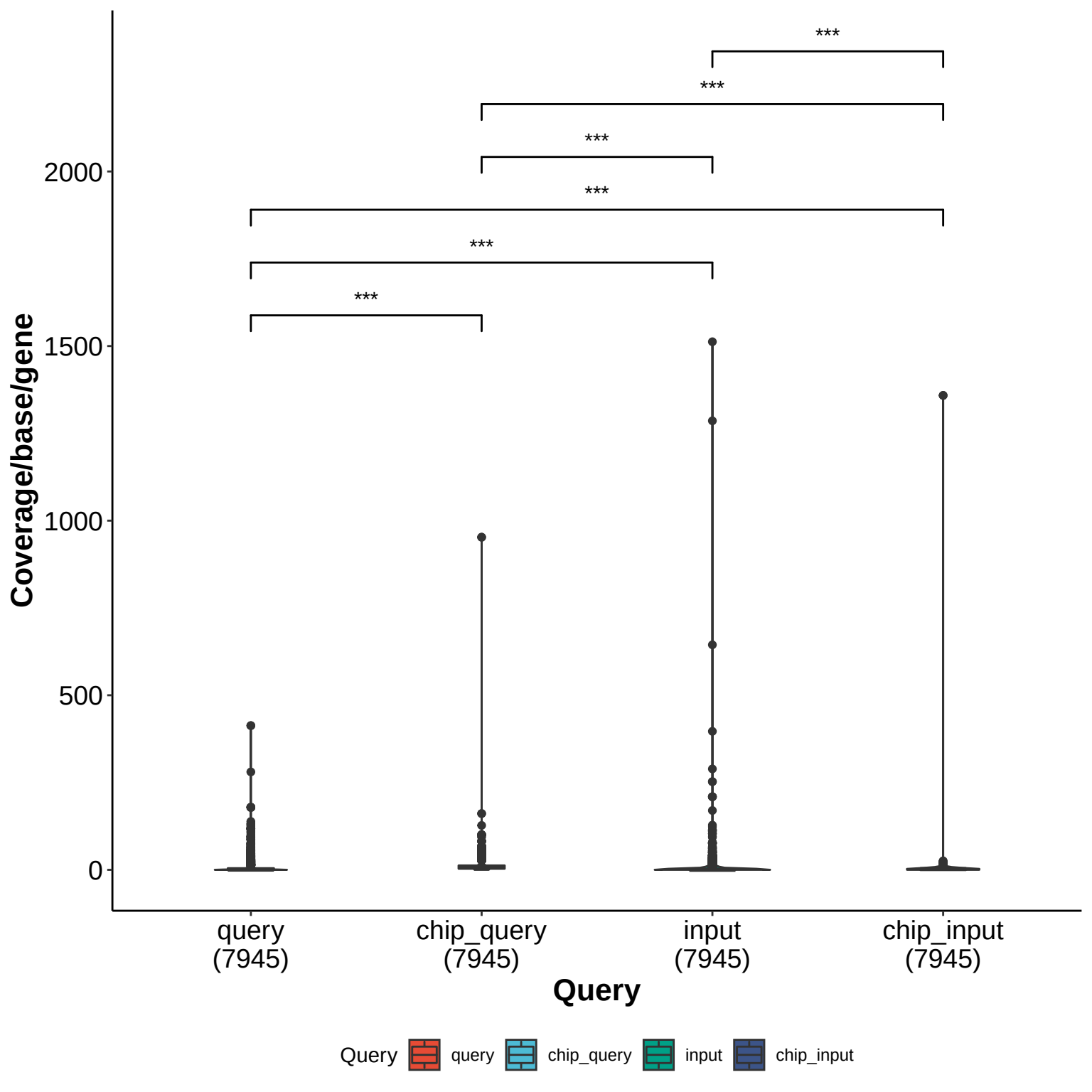

Narrow
Query
chip_input
chip_query
input
query
Coverage/base/gene
10
5
−0.5K
narrowPeak
0.5K

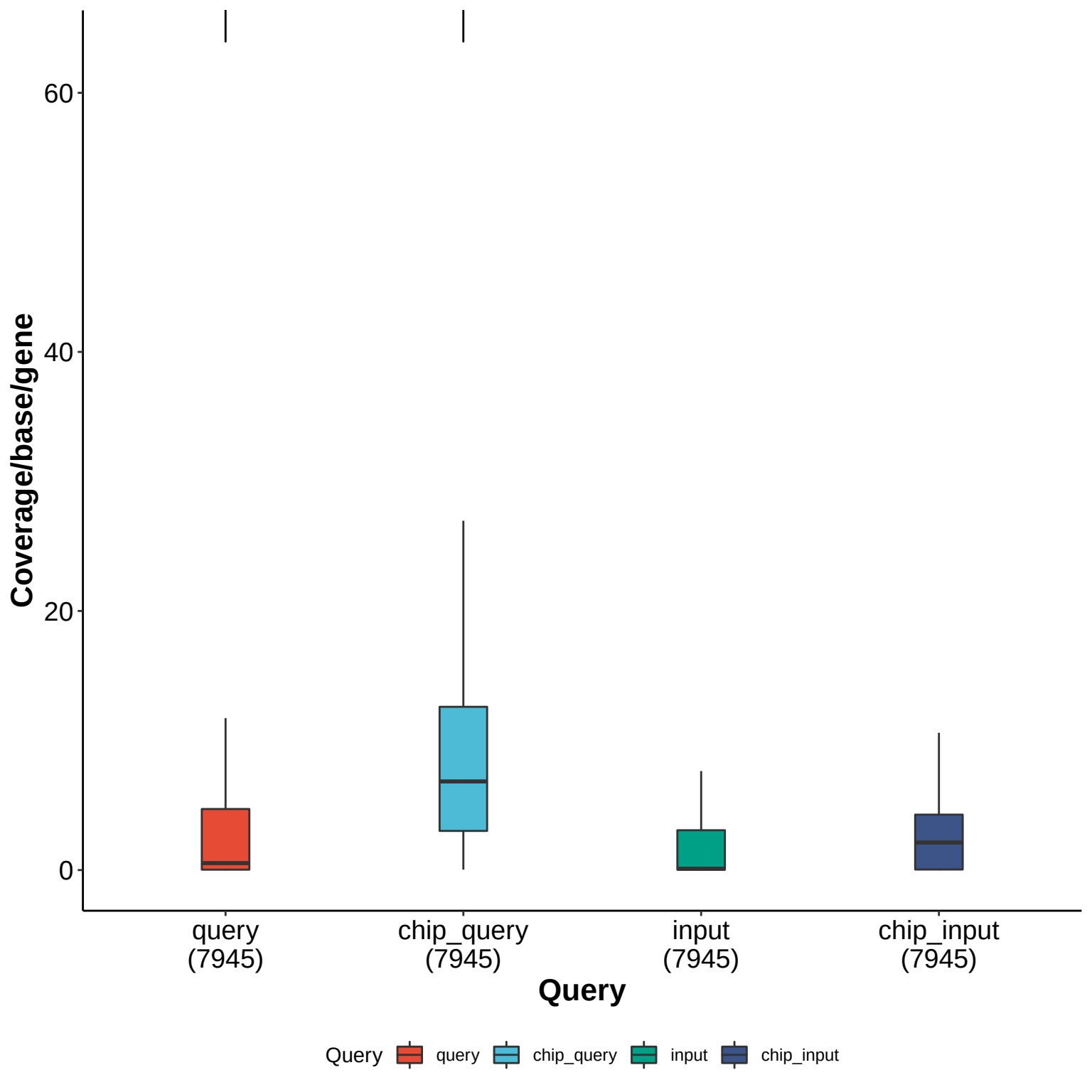


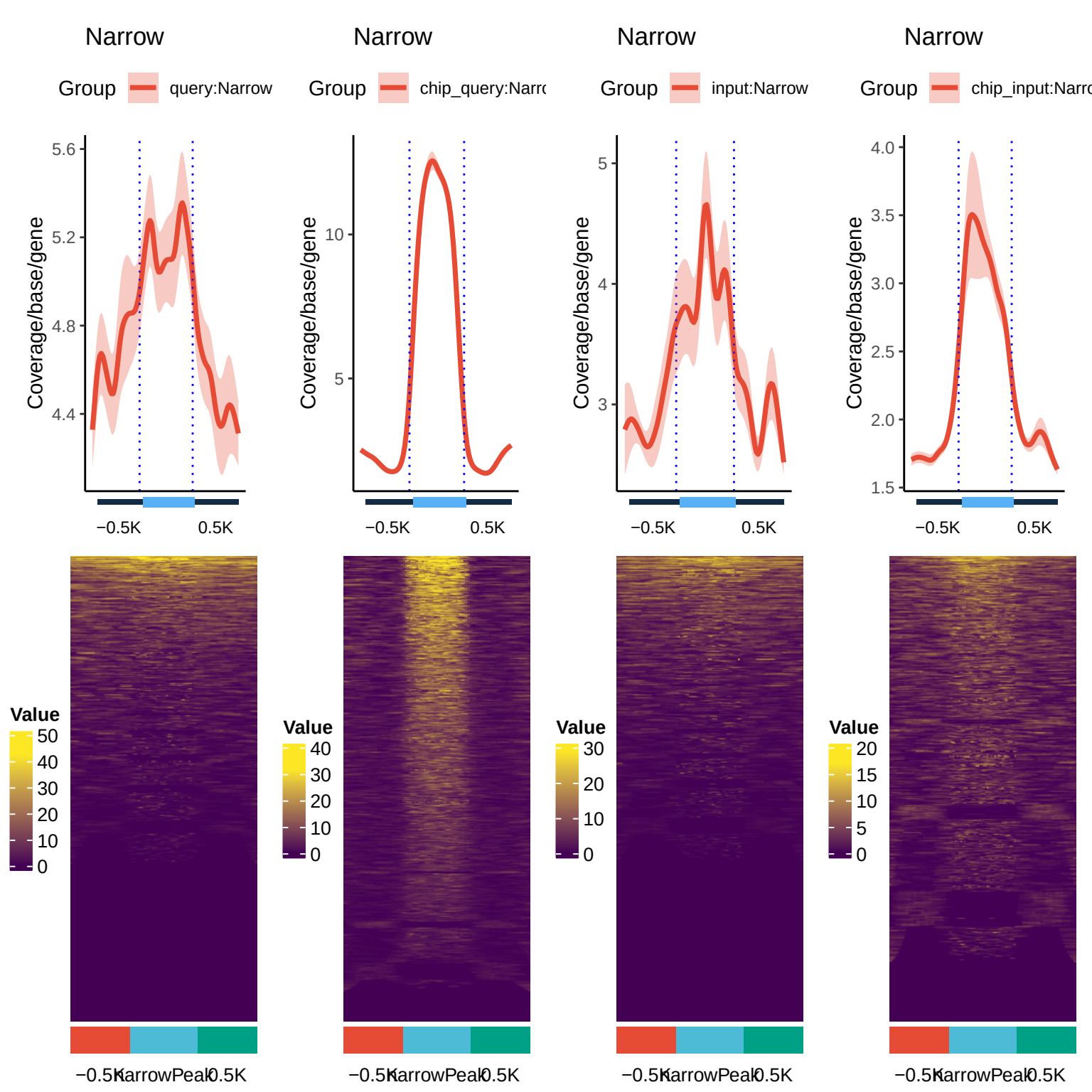
post hoc TukeyHSD test

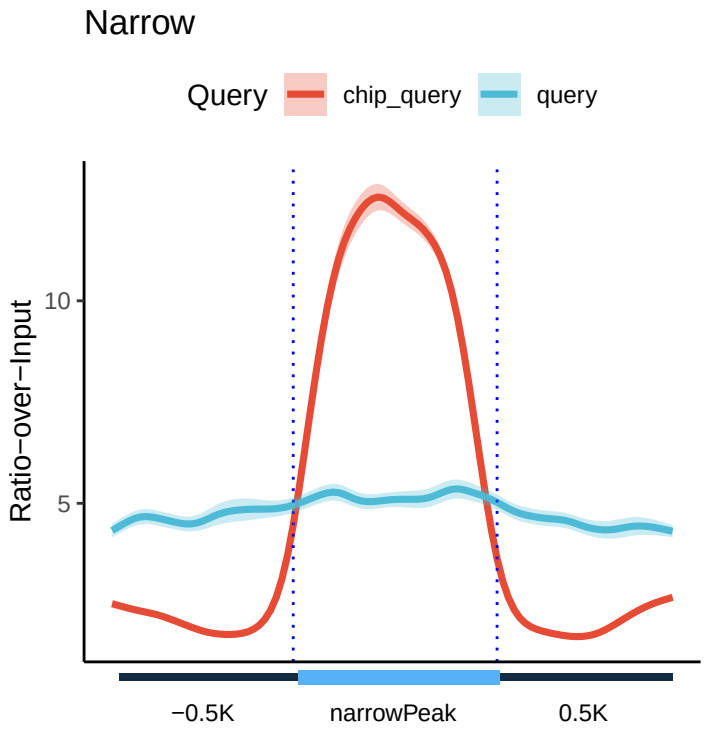
	diff	lwr	upr	p adj
chip_query−query	4.808	3.969	5.646	0.00e+00
input−query	−1.176	−2.014	−0.337	1.79e−03
chip_input−query	−2.073	−2.912	−1.235	1.27e−09
input−chip_query	−5.984	−6.822	−5.145	0.00e+00
chip_input−chip_query	−6.881	−7.72	−6.043	0.00e+00
chip_input−input	−0.897	−1.736	−0.059	3.04e−02

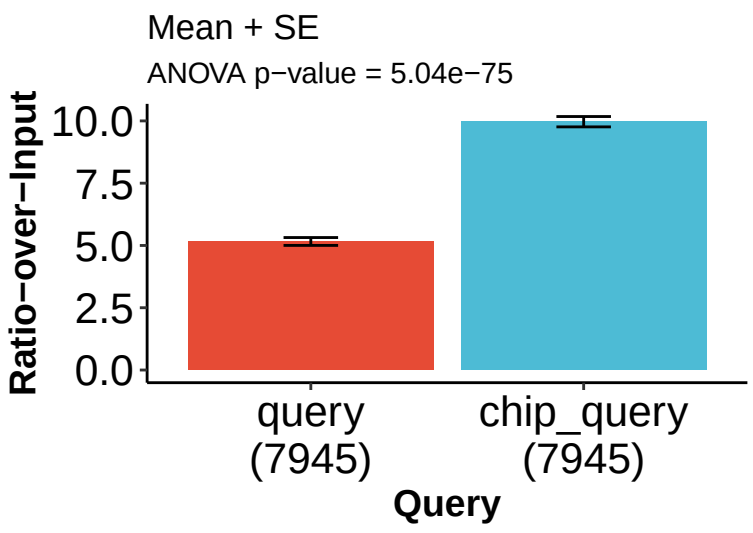

Cumulative fraction of Coverage/base/gene
query
chip_query
input
chip_input
1.00
0.75
0.50
0.25
Cumulative fraction
0
5
10
Coverage/base/gene


***
***
***
***
***
***
2000
1500
1000
500
0
Coverage/base/gene
query
(7945)
chip_query
(7945)
input
(7945)
chip_input
(7945)
Query
Query
query
chip_query
input
chip_input


60
40
20
0
Coverage/base/gene
query
(7945)
chip_query
(7945)
input
(7945)
chip_input
(7945)
Query
Query
query
chip_query
input
chip_input

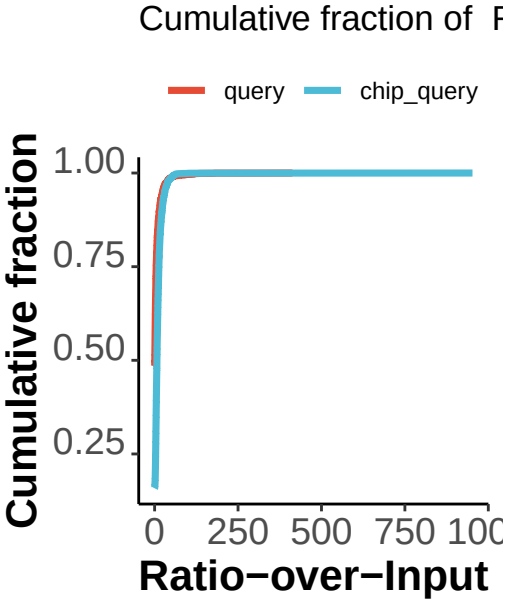

Narrow
Group
query:Narrow
Coverage/base/gene
5.6
5.2
4.8
4.4
−0.5K
0.5K
Value
50
40
30
20
10
0
−0.5K
NarrowPeak
0.5K
Narrow
Group
chip_query:Narrc
Coverage/base/gene
10
5
−0.5K
0.5K
Value
40
30
20
10
0
−0.5K
NarrowPeak
0.5K
Narrow
Group
input:Narrow
Coverage/base/gene
5
4
3
−0.5K
0.5K
Value
30
20
10
0
−0.5K
NarrowPeak
0.5K
Narrow
Group
chip_input:Narrc
Coverage/base/gene
4.0
3.5
3.0
2.5
2.0
1.5
−0.5K
0.5K
Value
20
15
10
5
0
−0.5K
NarrowPeak
0.5K

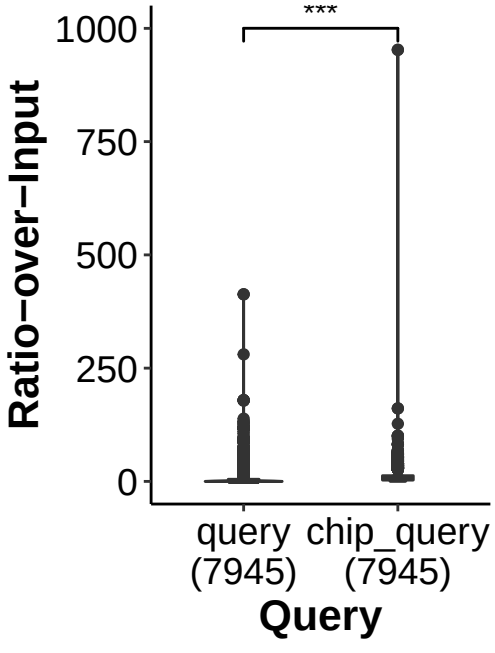


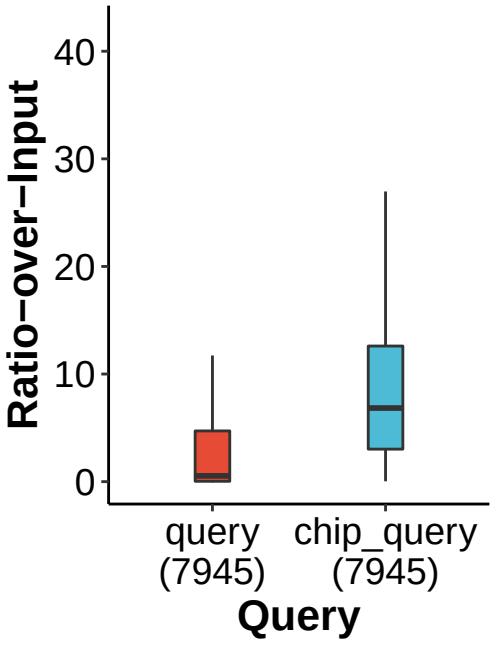


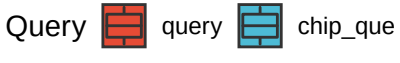
post hoc TukeyHSD test

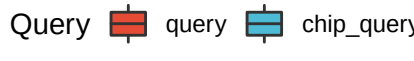
	diff	lwr	upr	p adj
chip_query−query	4.808	4.296	5.319	2.04e−08

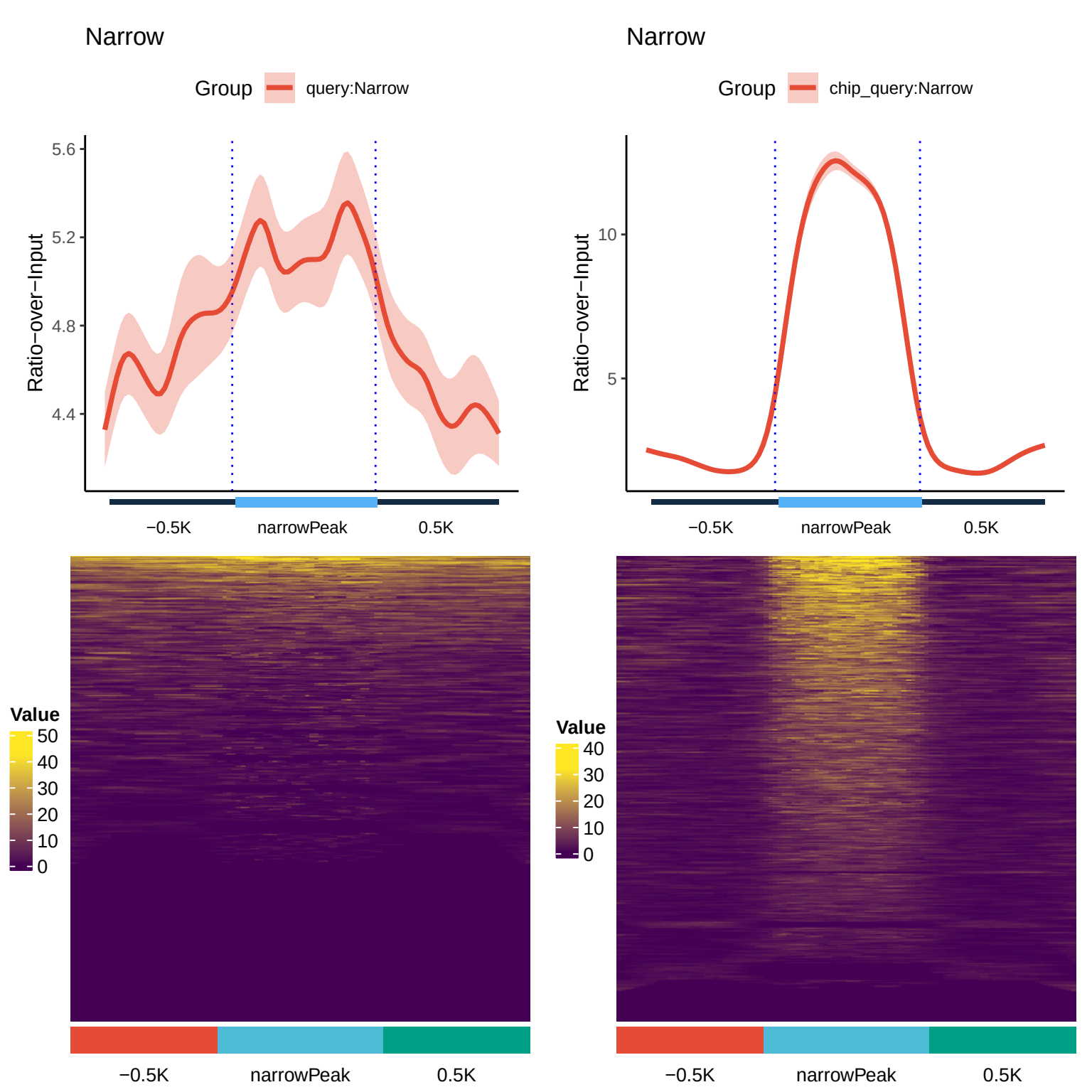











Narrow
Group
query:Narrow
Ratio−over−Input
5.6
5.2
4.8
4.4
−0.5K
narrowPeak
0.5K
Value
50
40
30
20
10
0
−0.5K
narrowPeak
0.5K
Narrow
Group
chip_query:Narrow
Ratio−over−Input
10
5
−0.5K
narrowPeak
0.5K
Value
40
30
20
10
0
−0.5K
narrowPeak
0.5K

Plotting parameters:

functionName: "plot_region"
queryFiles: c(query = "C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/treat_chr19.bam",
chip_query =
"C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/chip_treat_chr19.bam")
centerFiles: c(Narrow =
"C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/test_chip_peak_chr19.narrowPeak")
txdb: NULL
regionName: "narrowPeak"
inputFiles: c(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
handleInputParams: 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: FALSE
heatRange: NULL
Ylab: "Coverage/base/gene"
statsMethod: "wilcox.test"
hw: c(8, 8)
nc: 2