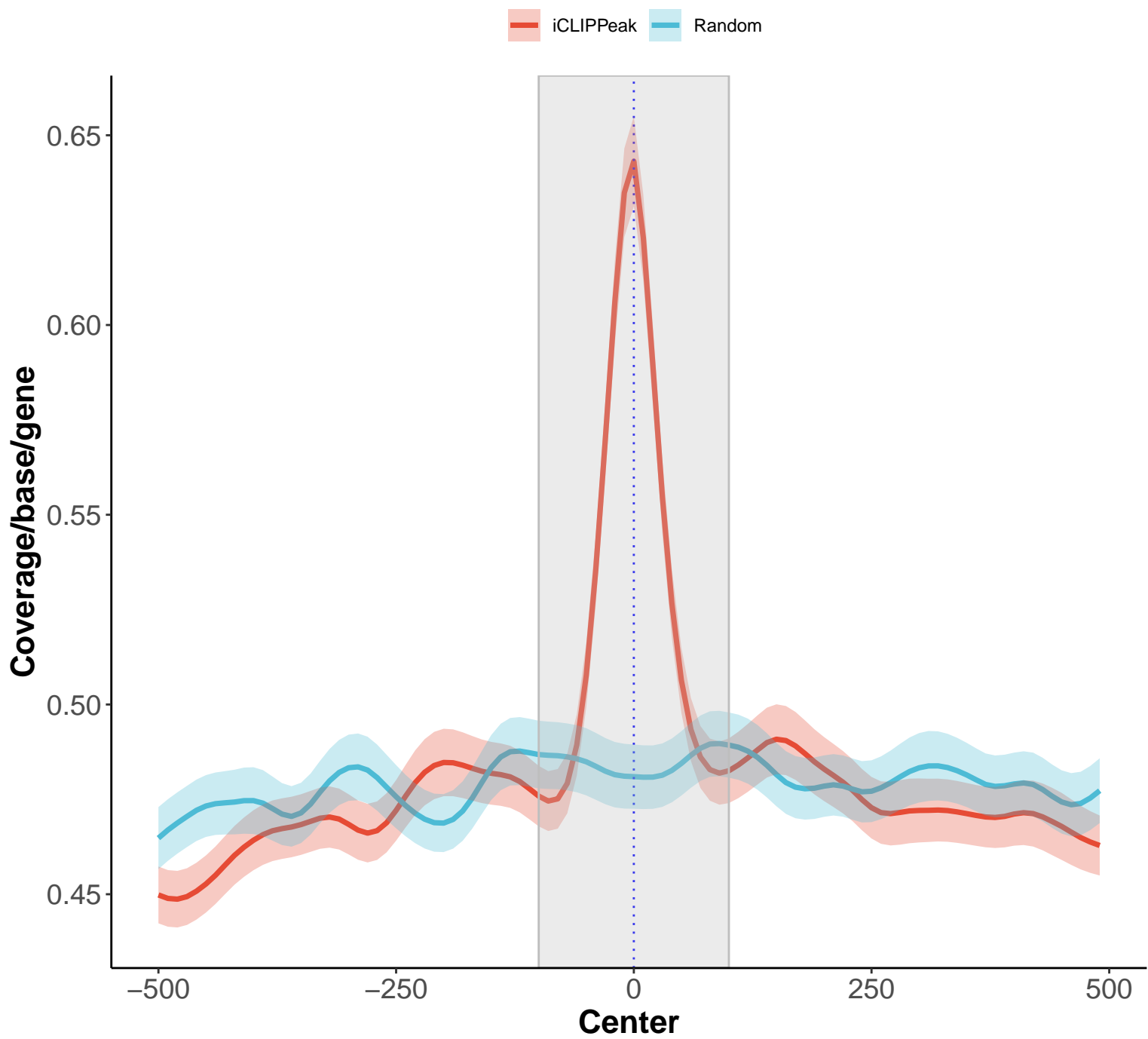
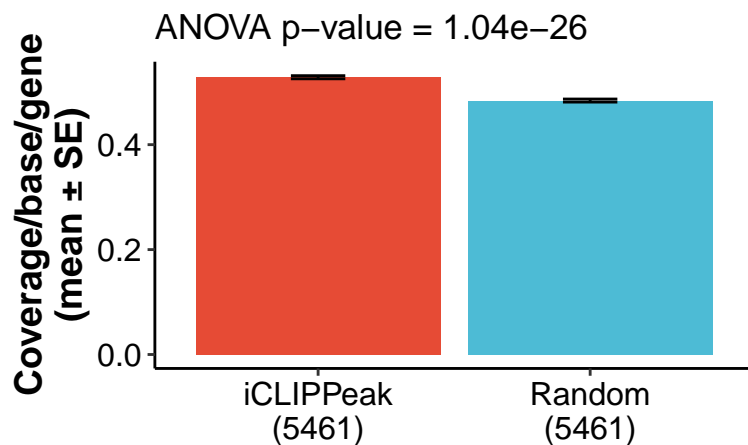
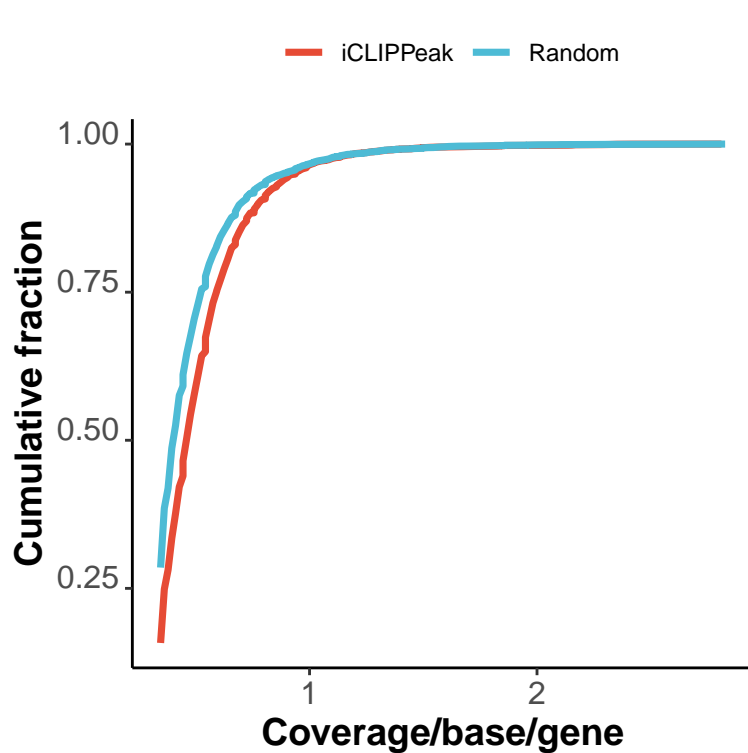
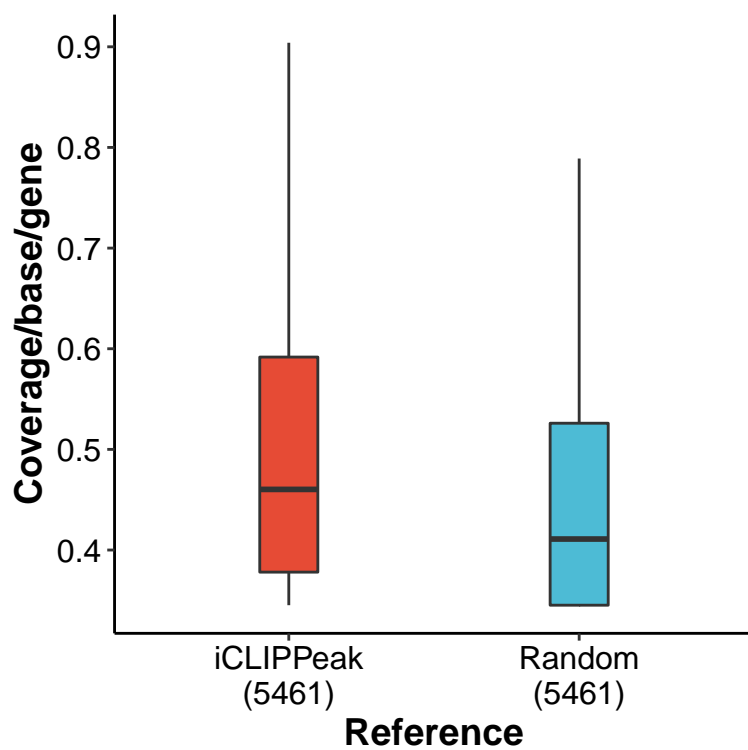
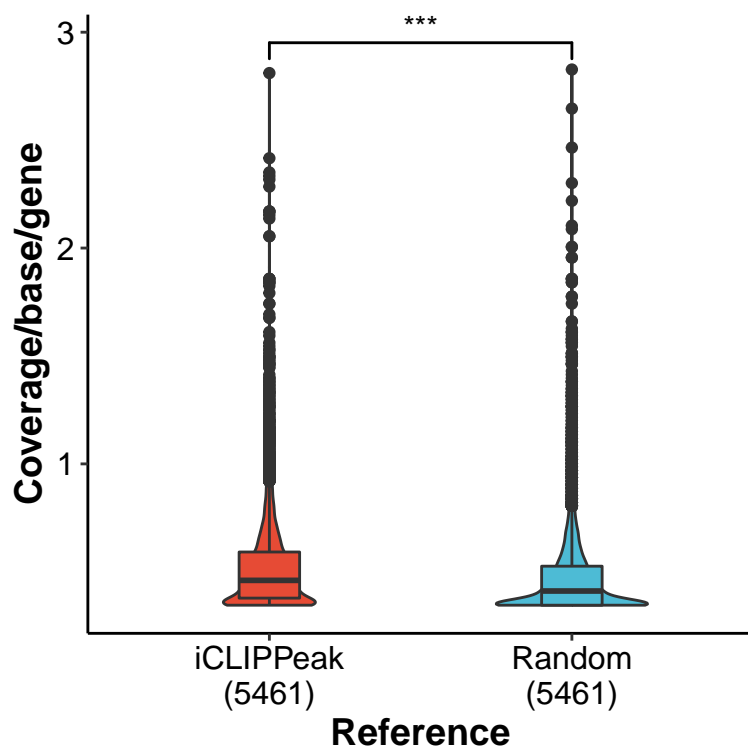


Feature: Transcript
Reference size: 5461
Sample name: clip_bam



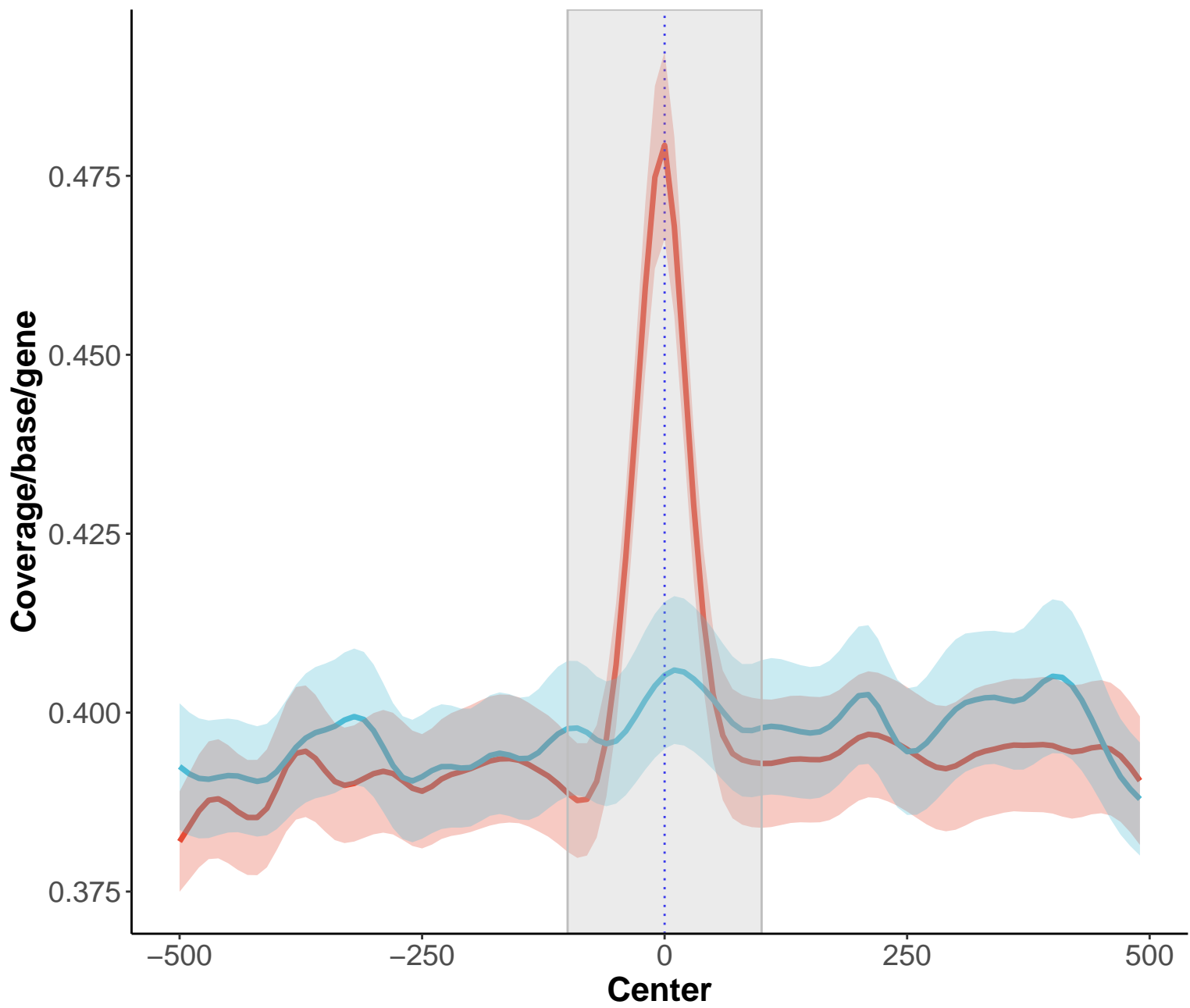


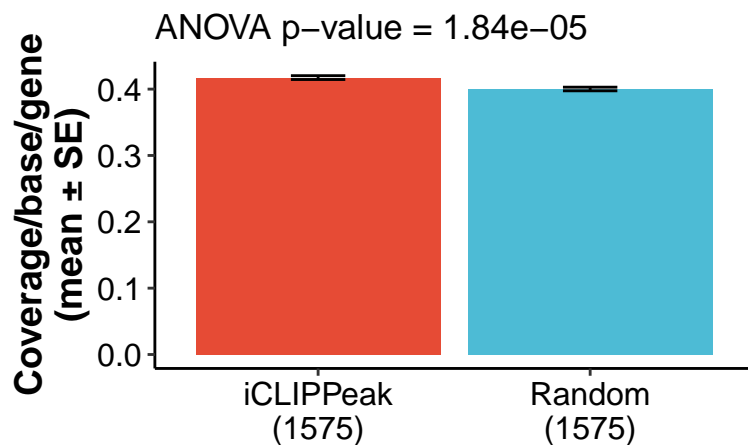
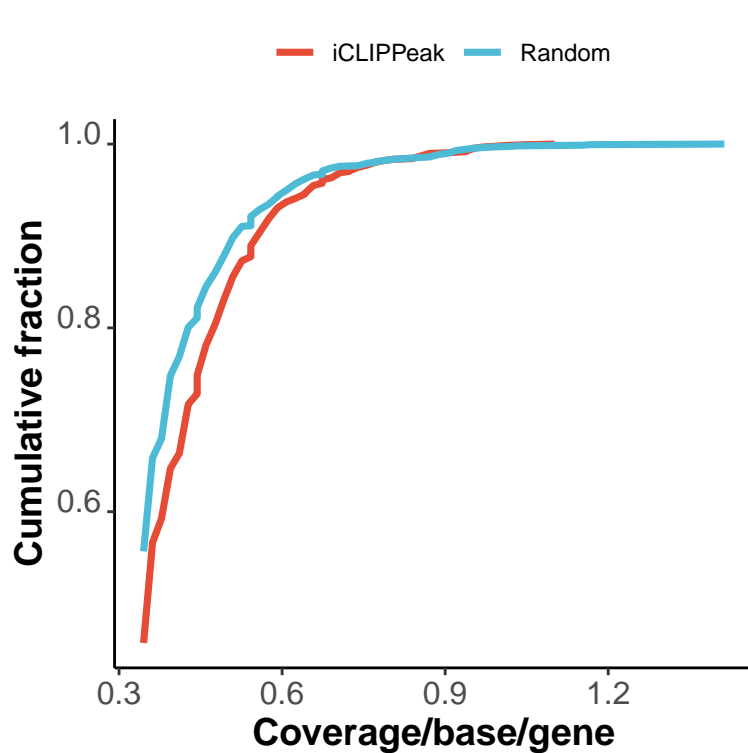
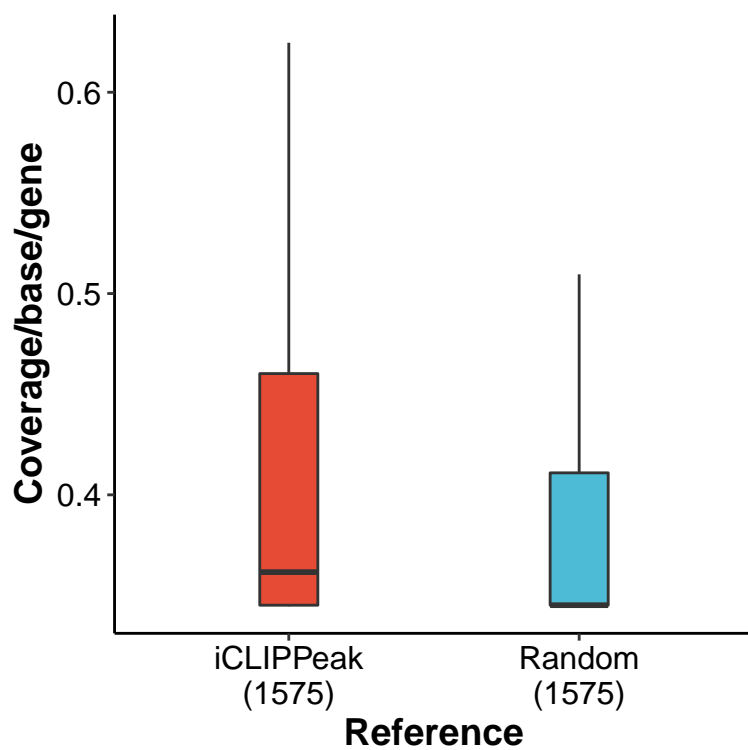
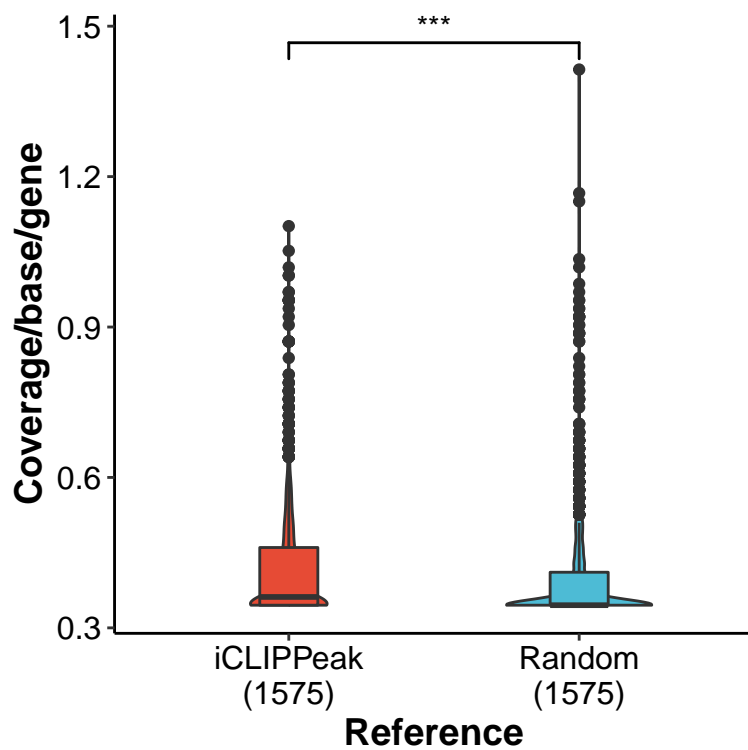
post hoc TukeyHSD test

	diff	lwr	upr	p adj
<i>Random-iCLIPPeak</i>	-0.044	-0.053	-0.036	0

Feature: 5'UTR
Reference size: 1575
Sample name: clip_bam

iCLIPPeak Random

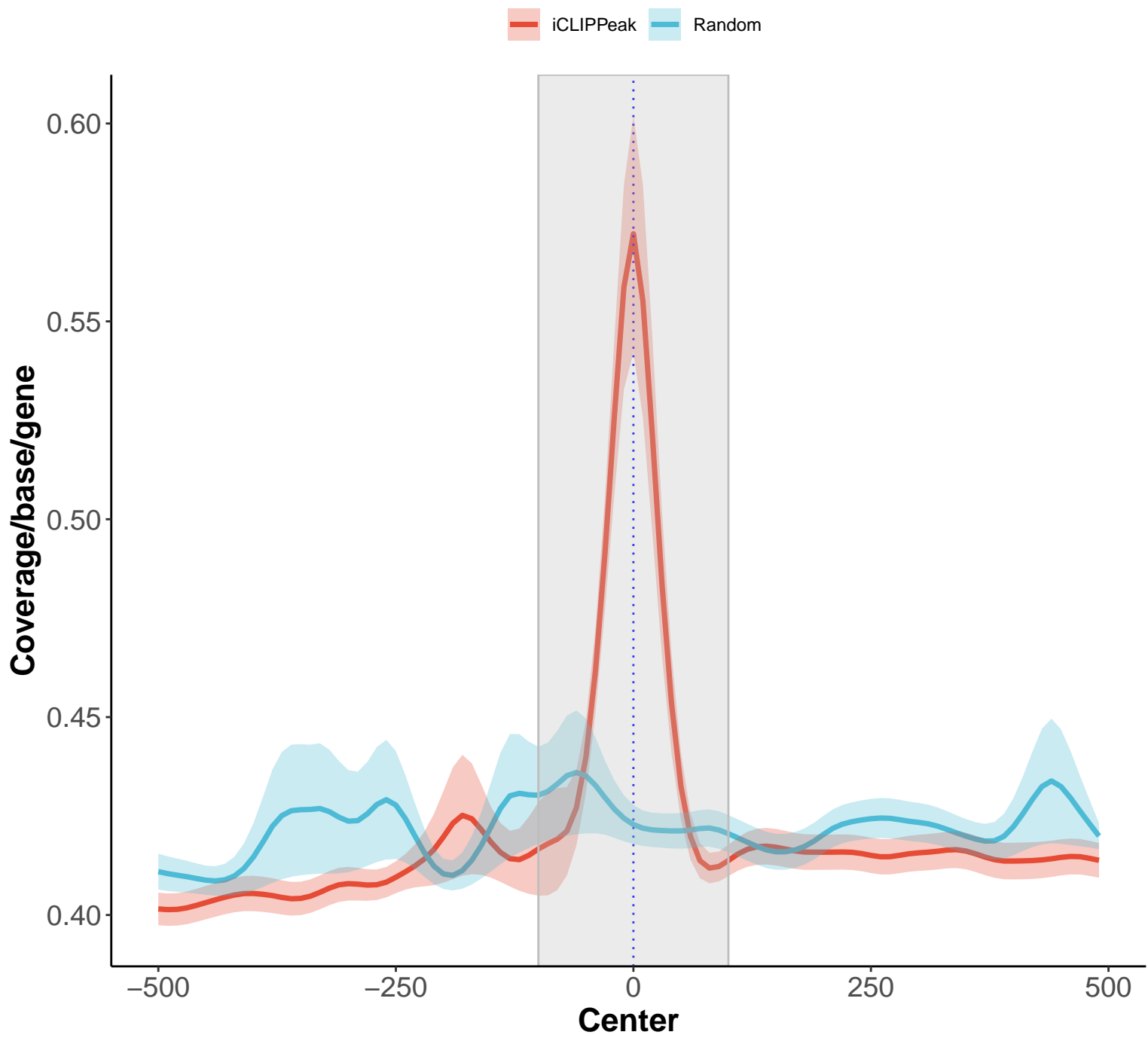


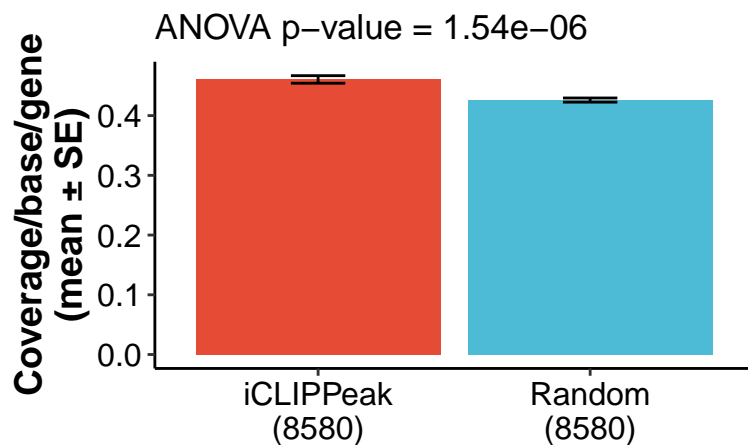
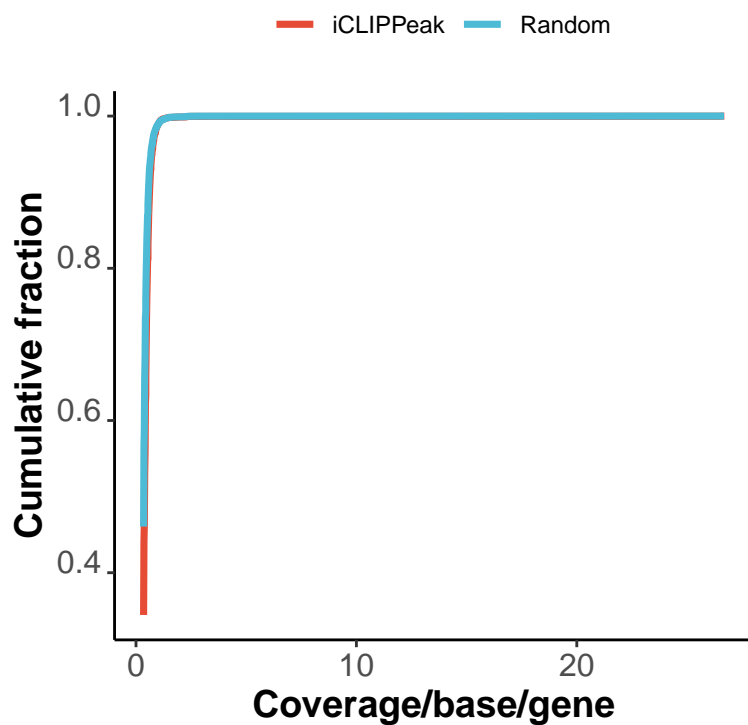
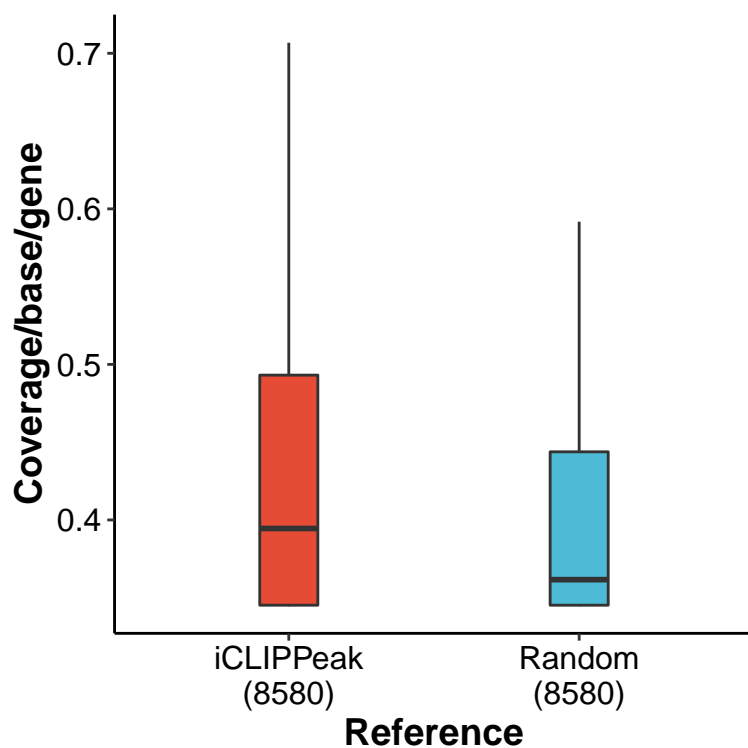
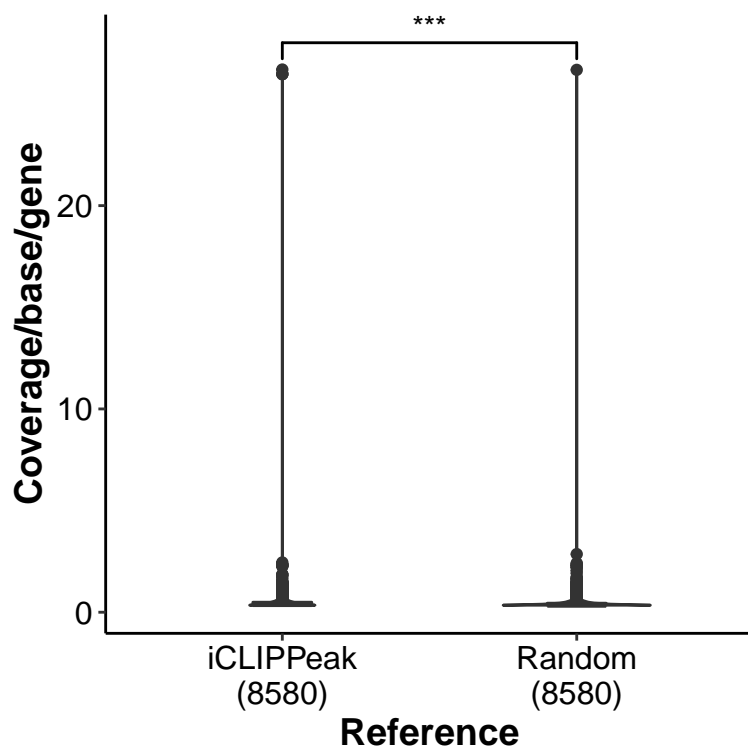


post hoc TukeyHSD test

	diff	lwr	upr	p adj
<i>Random-iCLIPPeak</i>	-0.017	-0.025	-0.009	1.84×10^{-5}

Feature: CDS
Reference size: 8580
Sample name: clip_bam

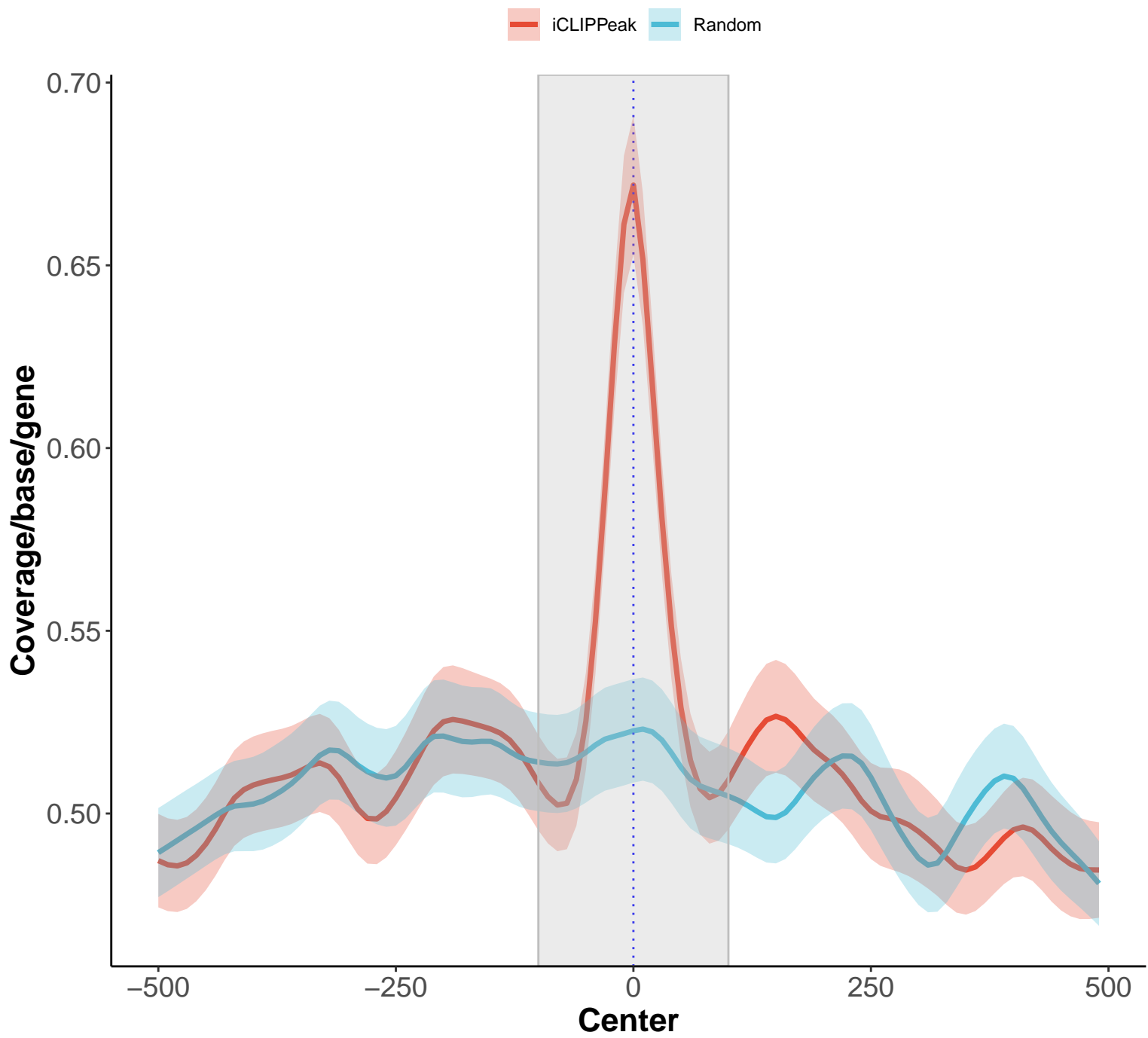


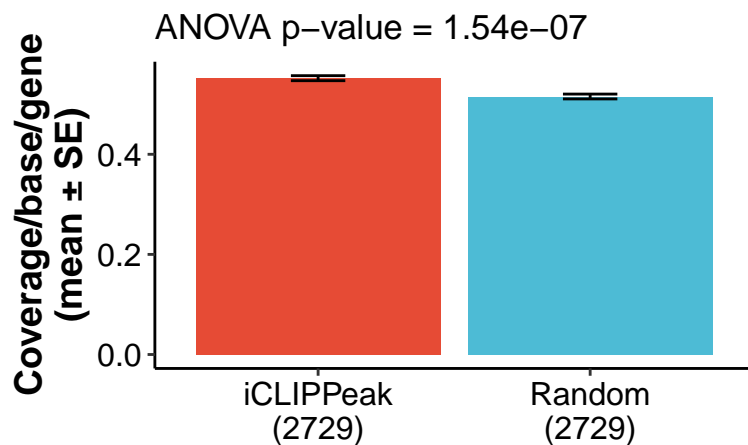
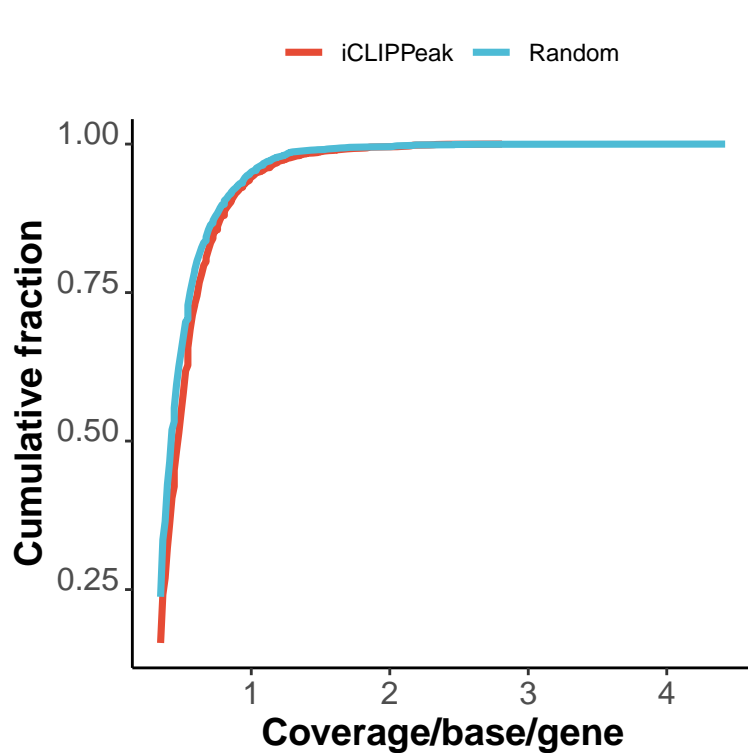
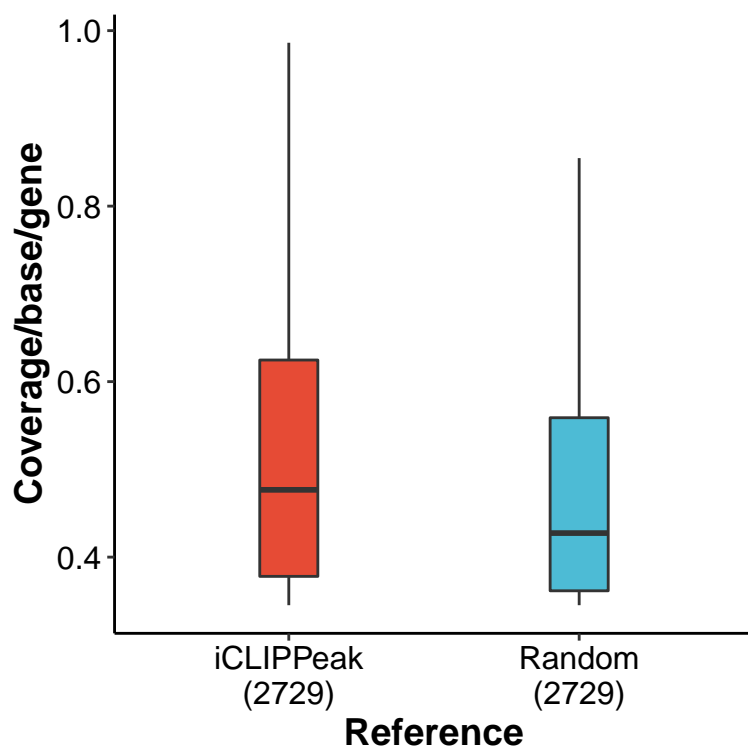
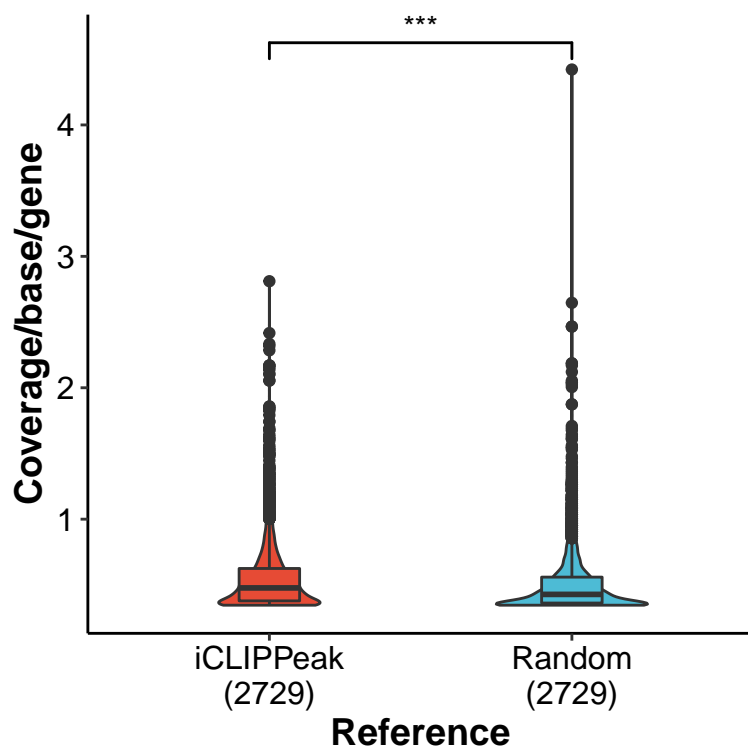


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.035	-0.049	-0.02	1.57e-06

Feature: 3'UTR
Reference size: 2729
Sample name: clip_bam

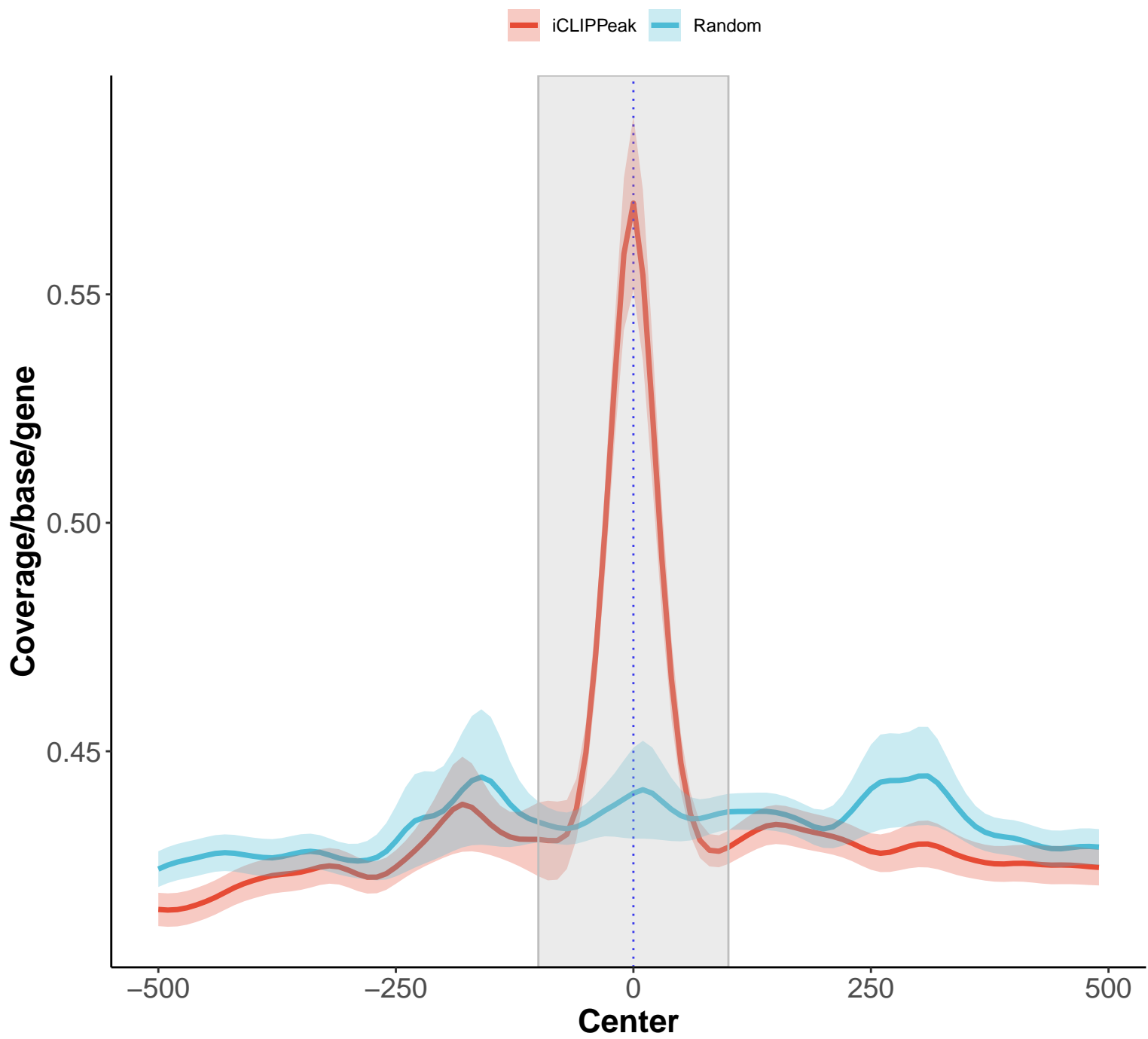


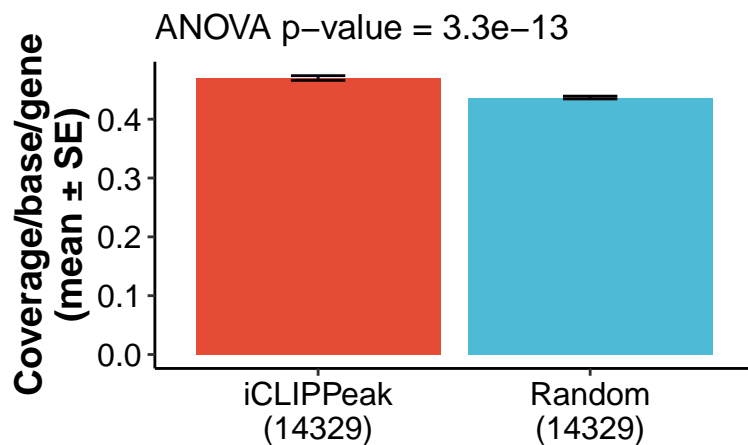
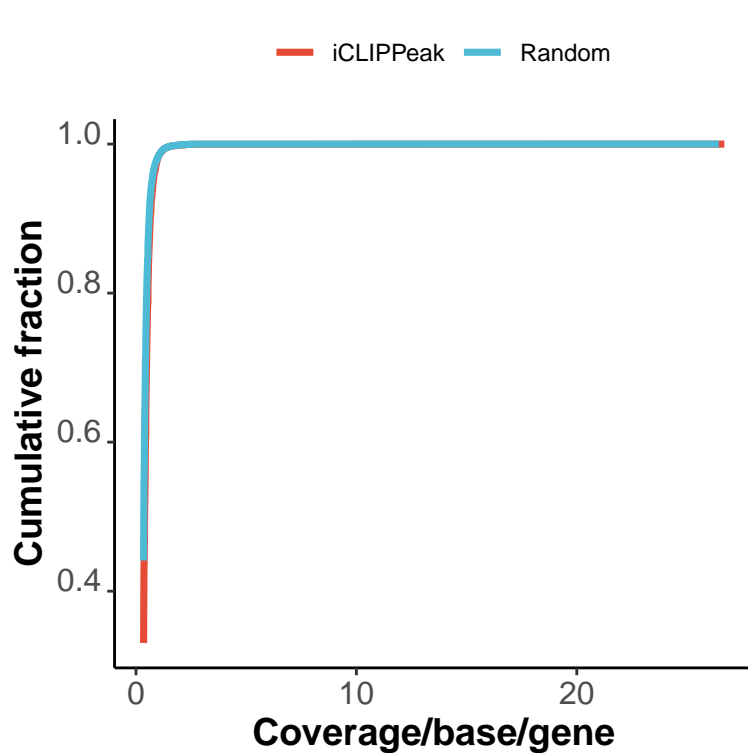
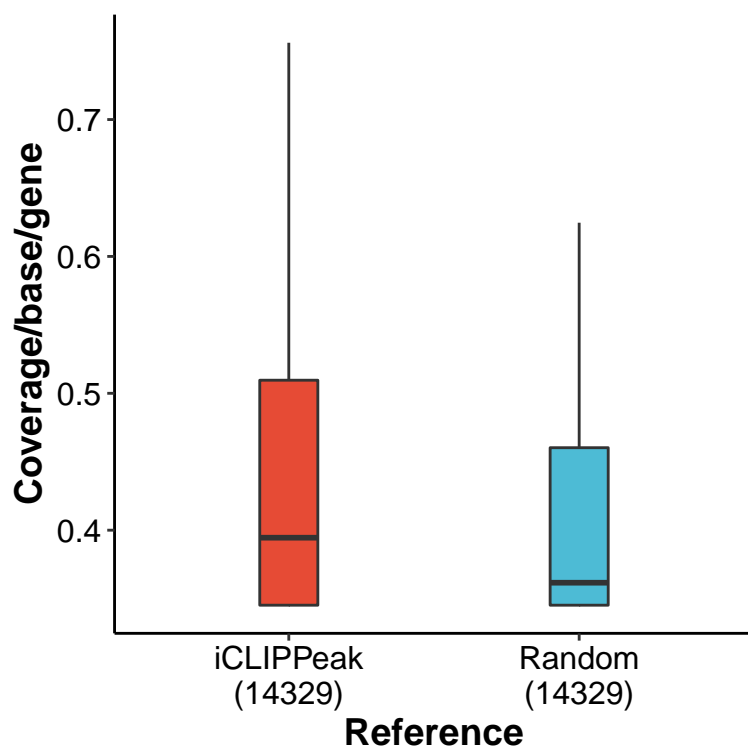
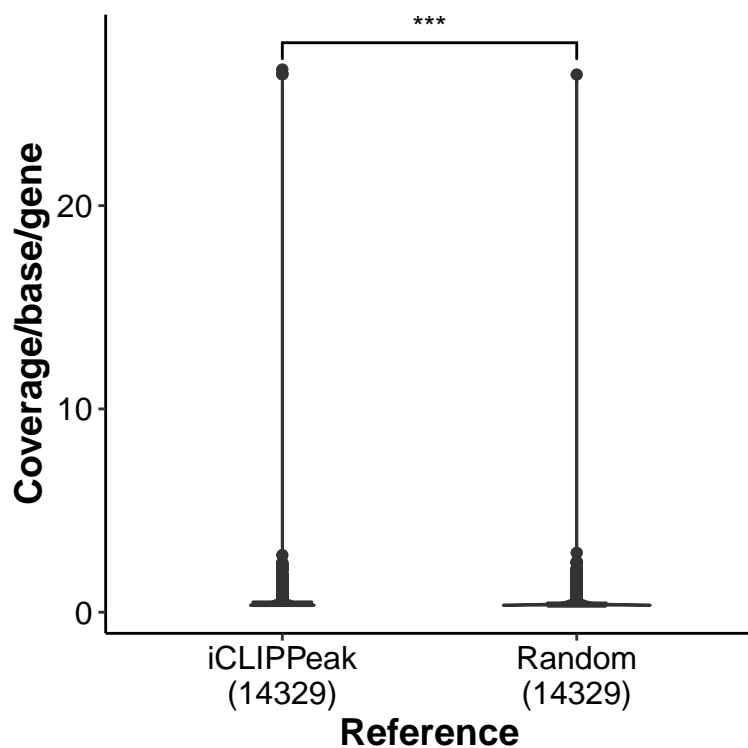


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.037	-0.05	-0.023	1.54e-07

Feature: Gene
Reference size: 14329
Sample name: clip_bam



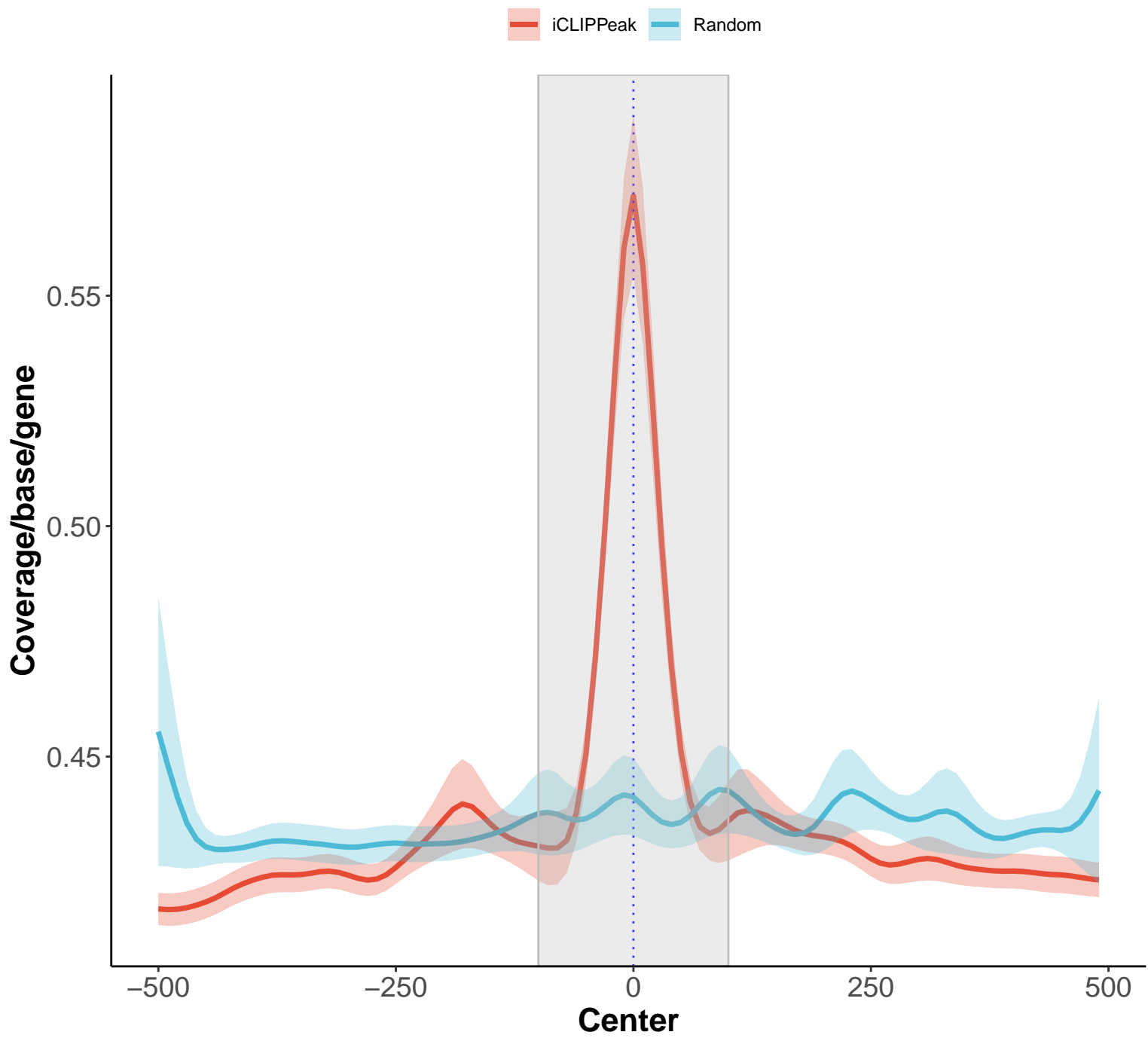


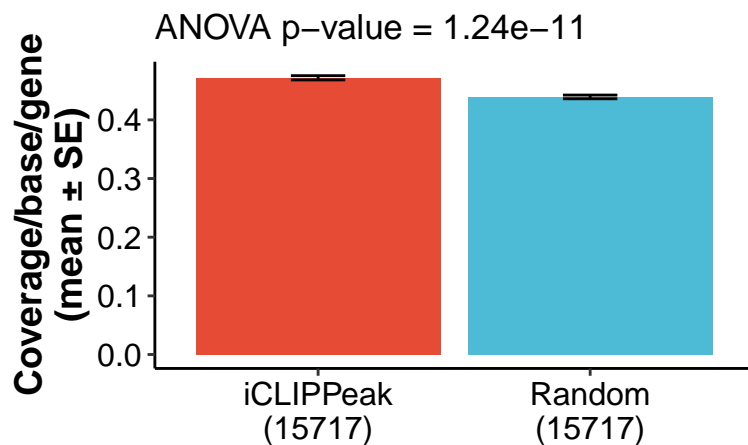
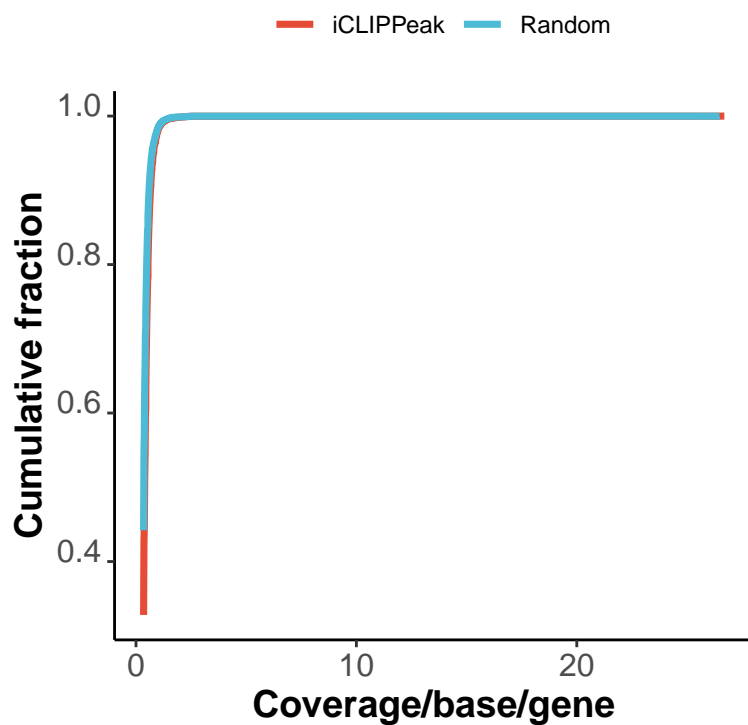
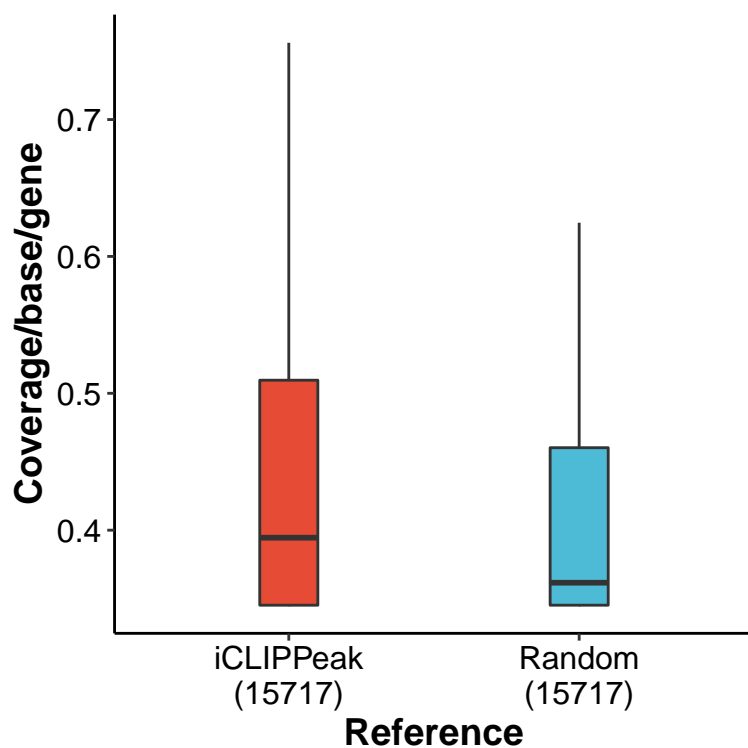
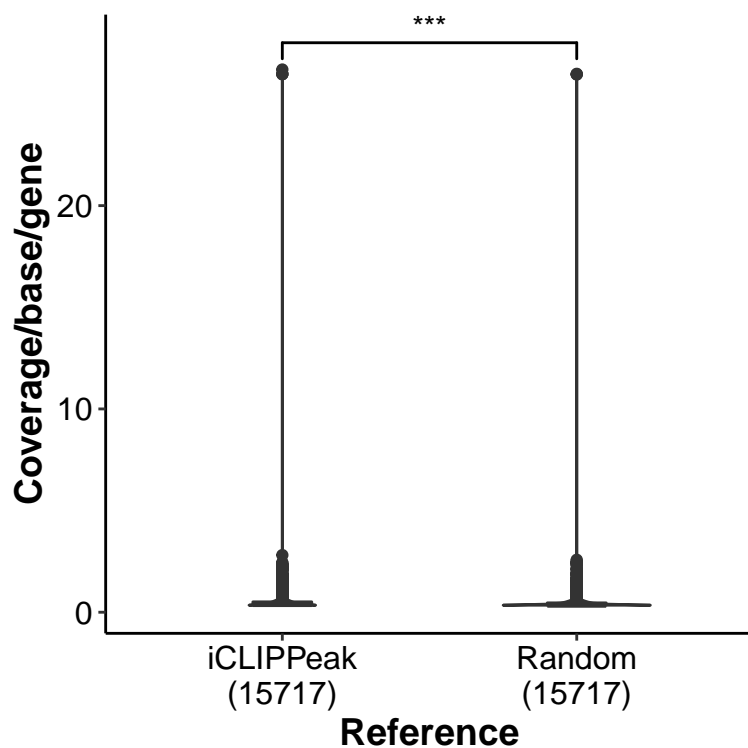
ANOVA p-value = $3.3e-13$

post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.033	-0.042	-0.024	$3.36e-13$

Feature: unrestricted
Reference size: 15717
Sample name: clip_bam

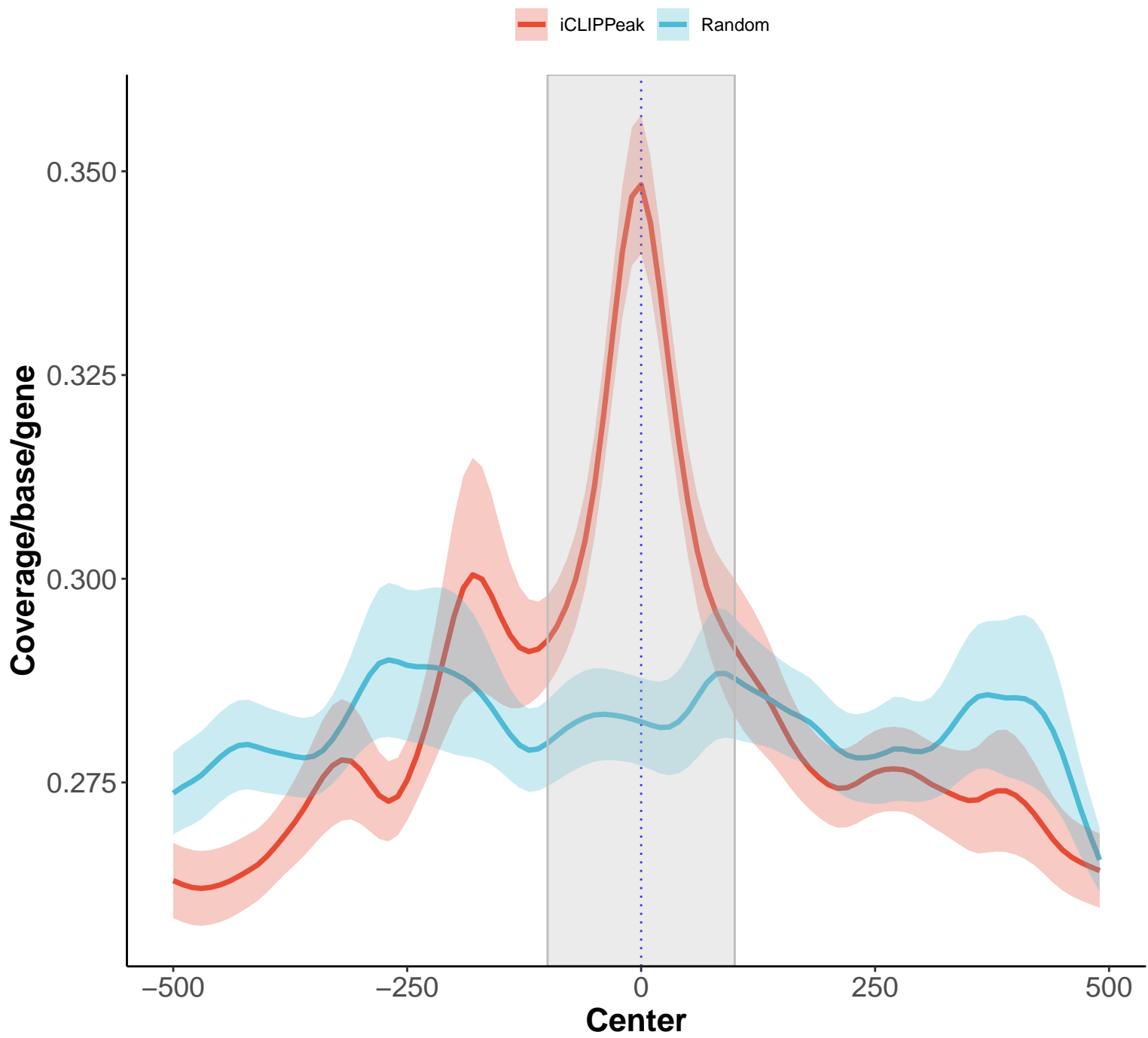


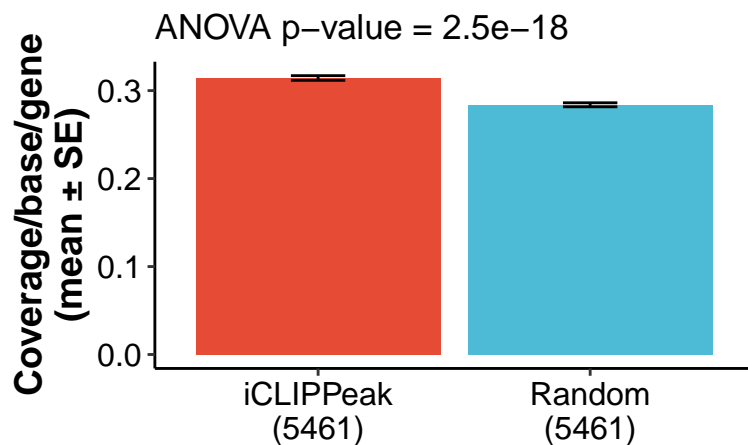
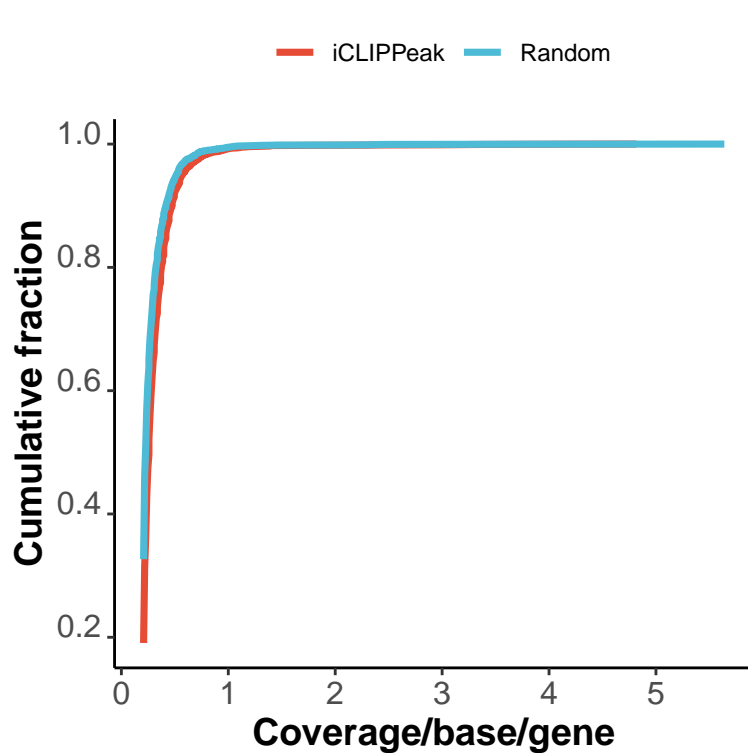
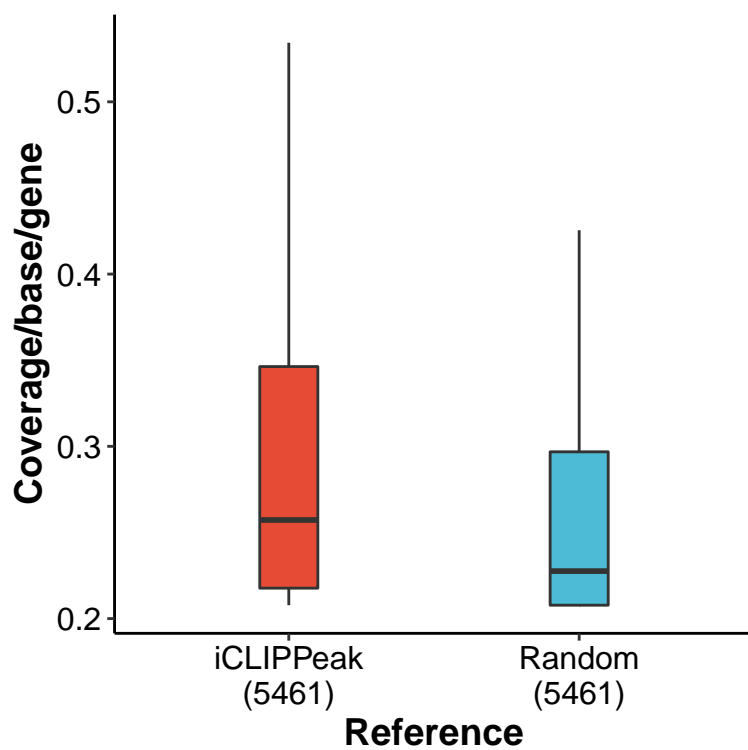
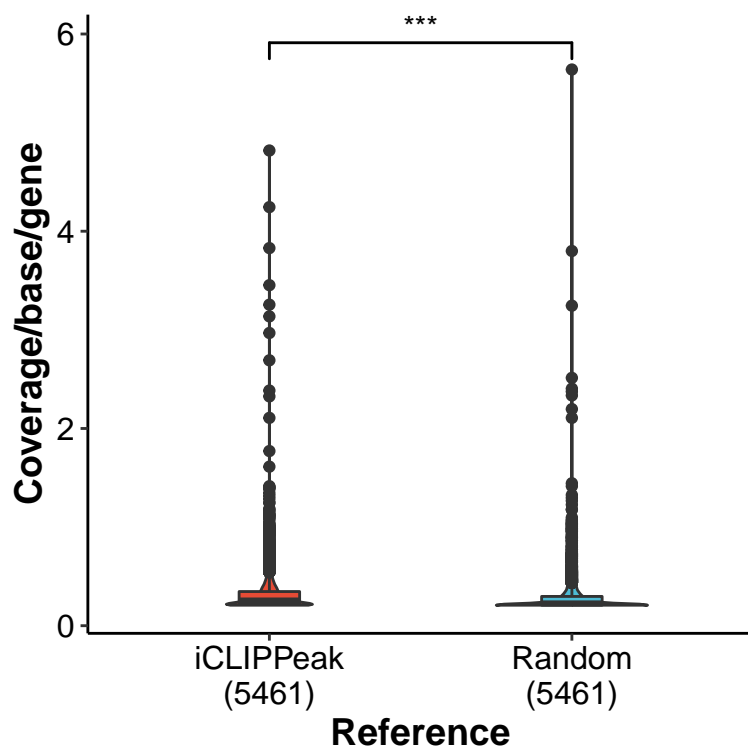


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.033	-0.042	-0.023	1.22e-11

Feature: Transcript
Reference size: 5461
Sample name: clip_input

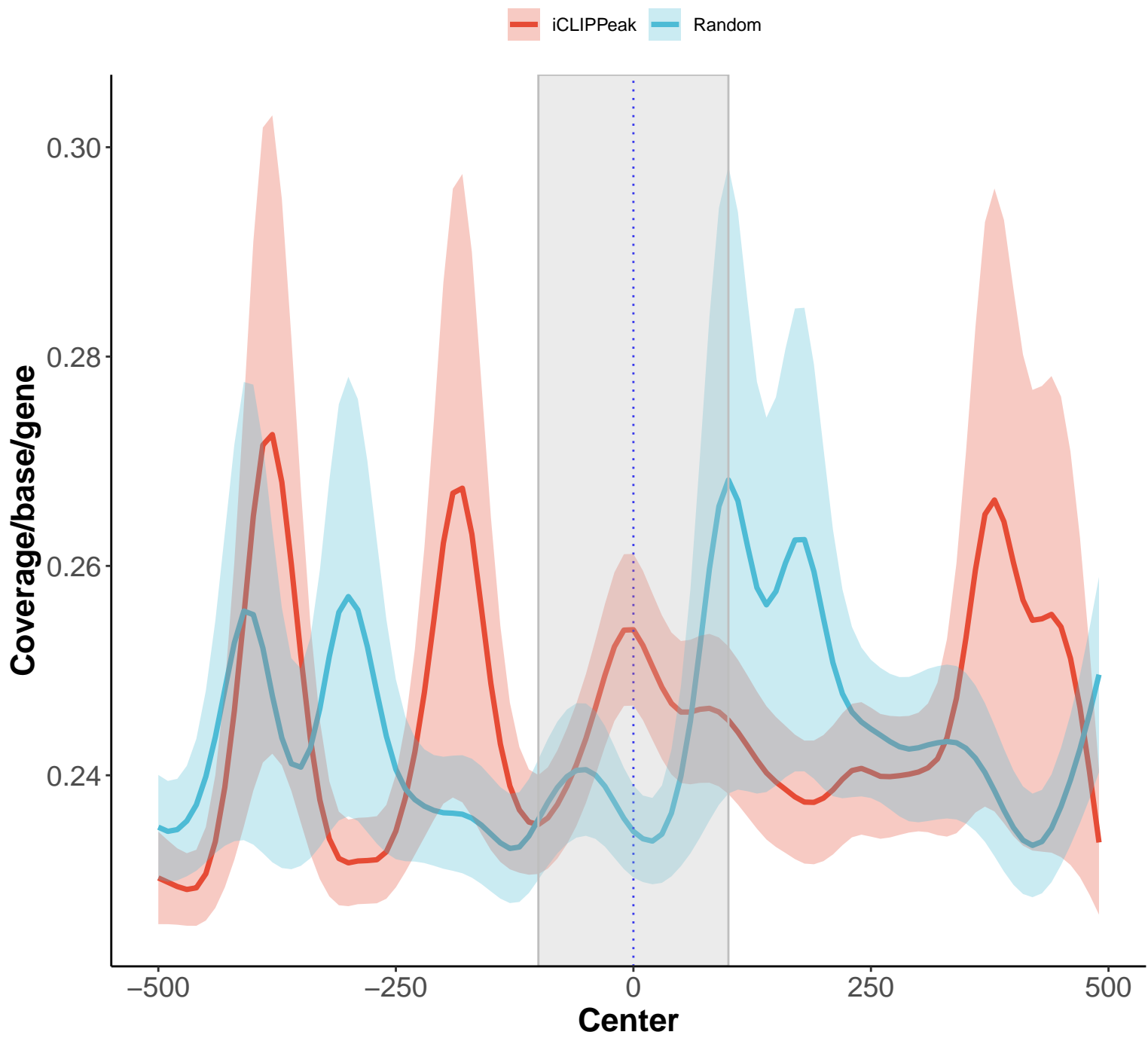


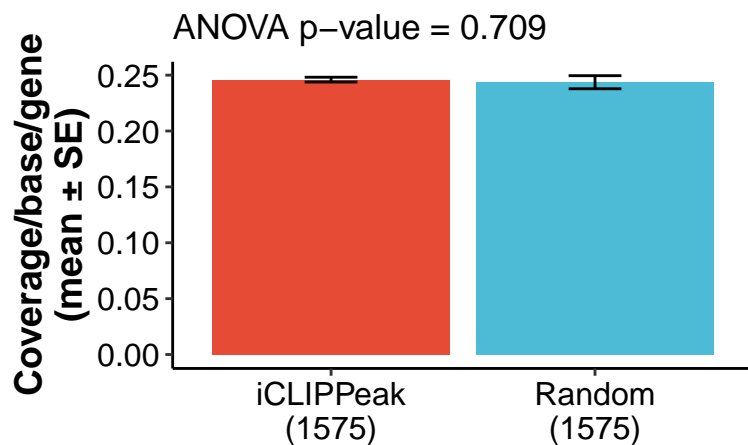
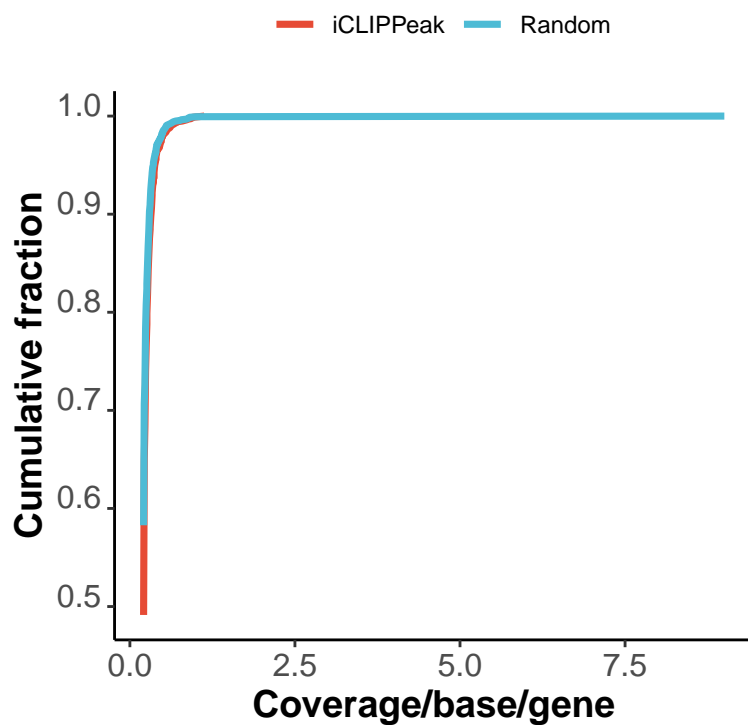
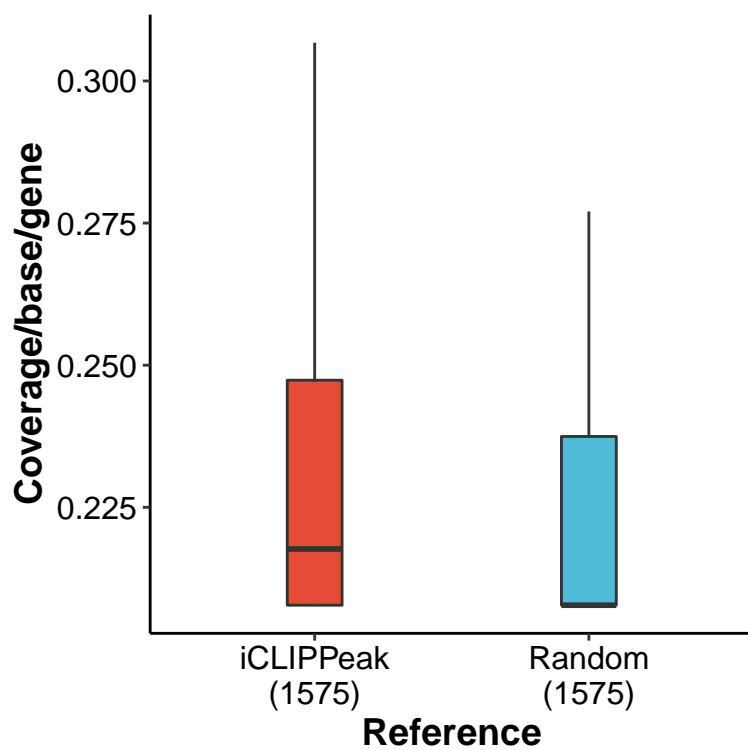
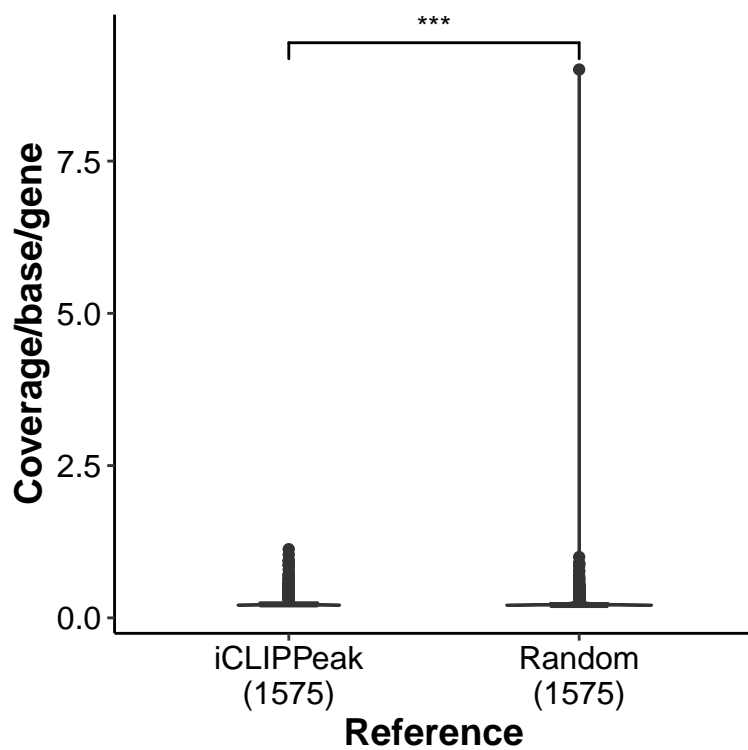


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.03	-0.037	-0.024	0

Feature: 5'UTR
Reference size: 1575
Sample name: clip_input

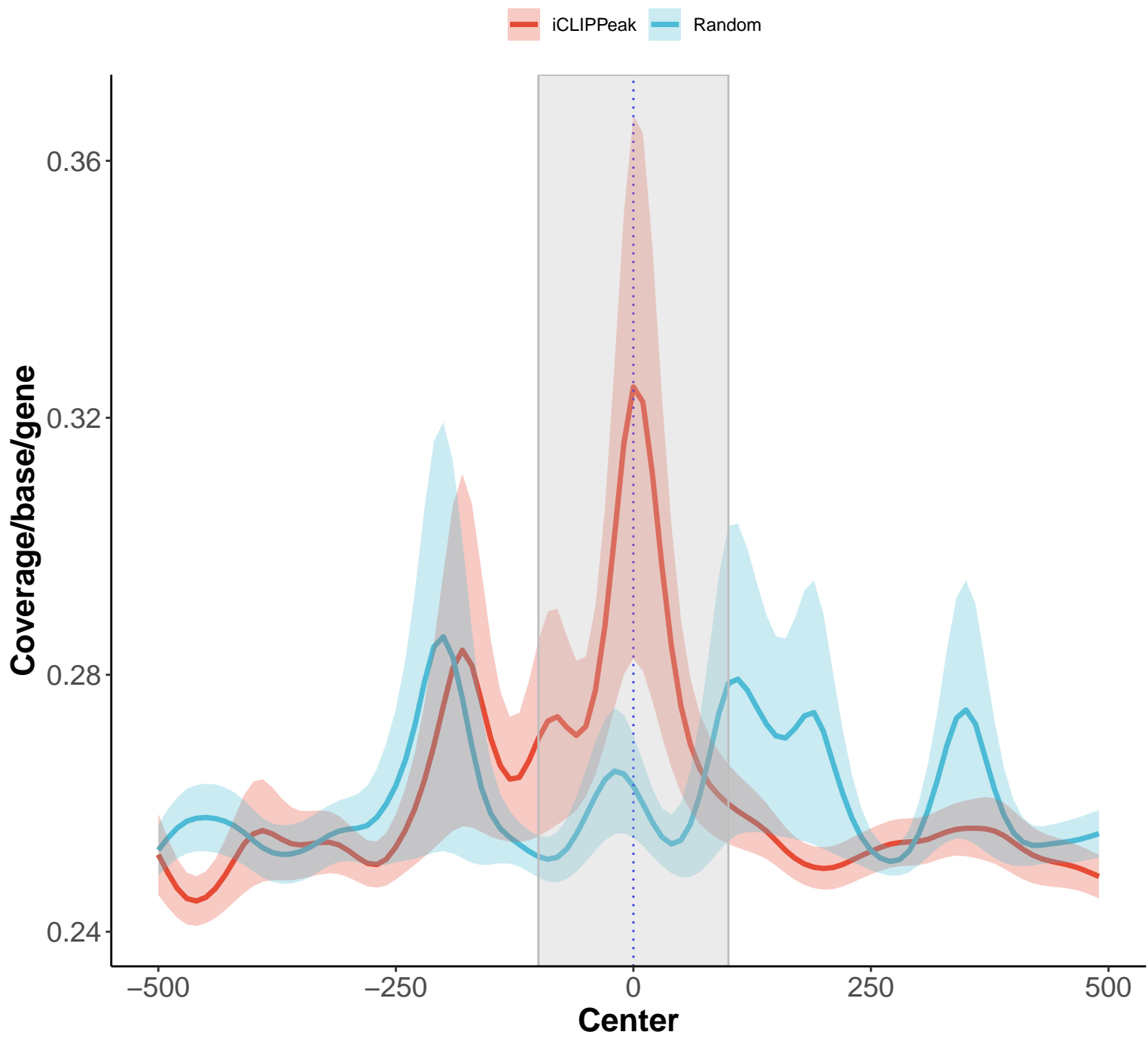


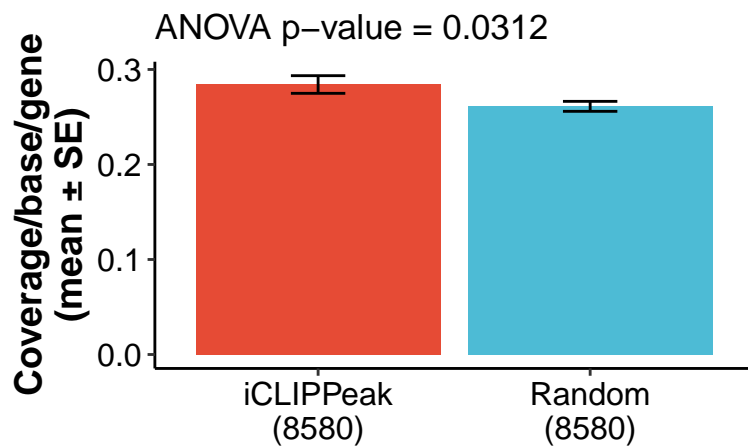
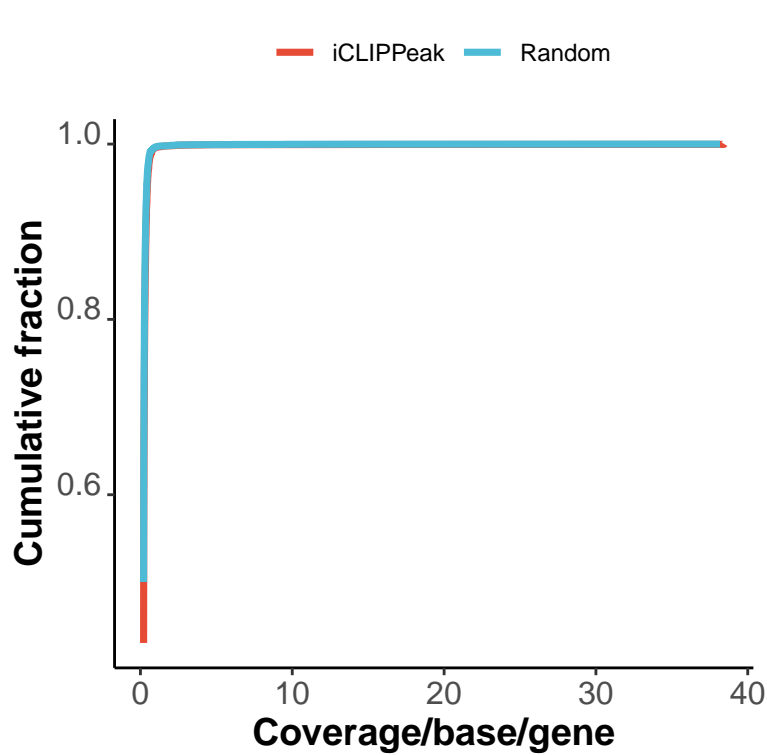
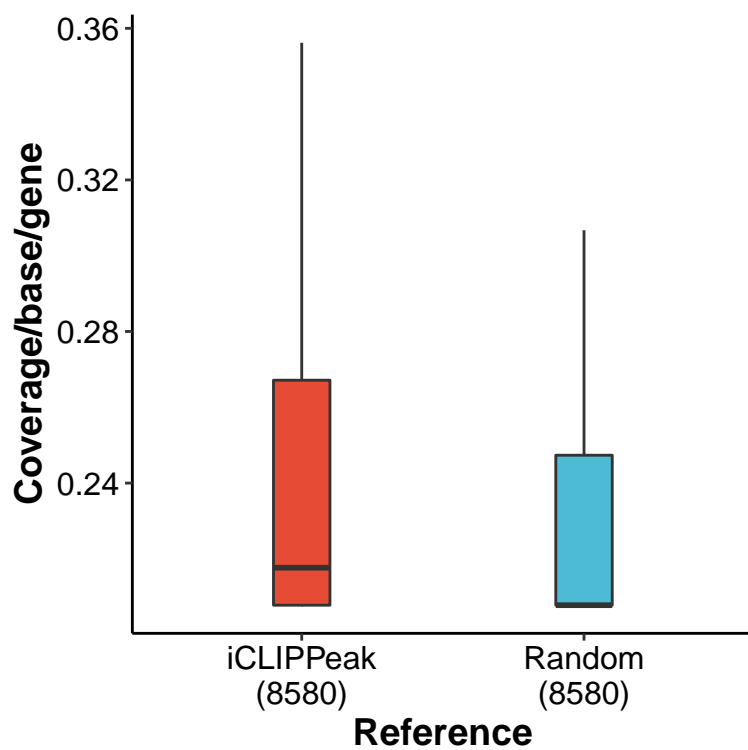
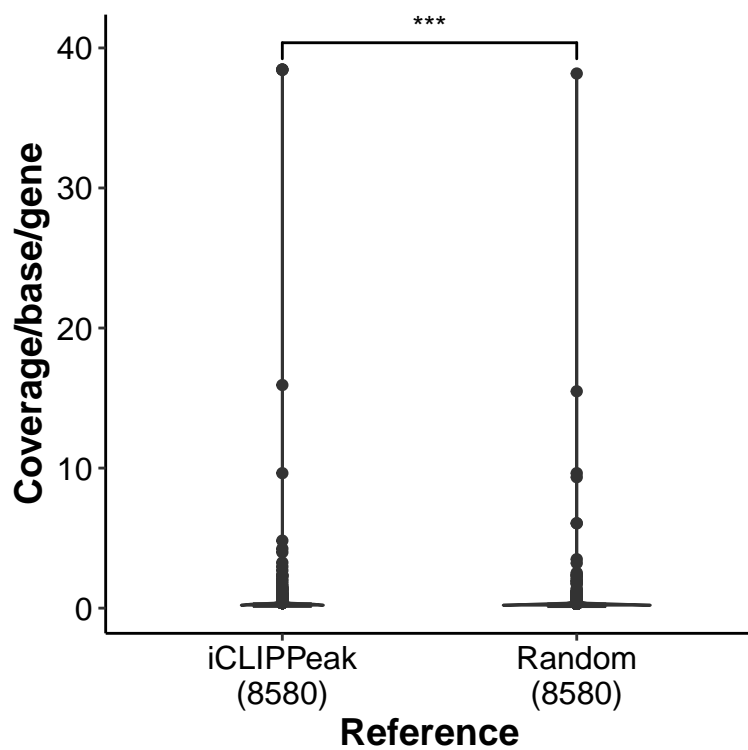


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.002	-0.015	0.01	0.709

Feature: CDS
Reference size: 8580
Sample name: clip_input

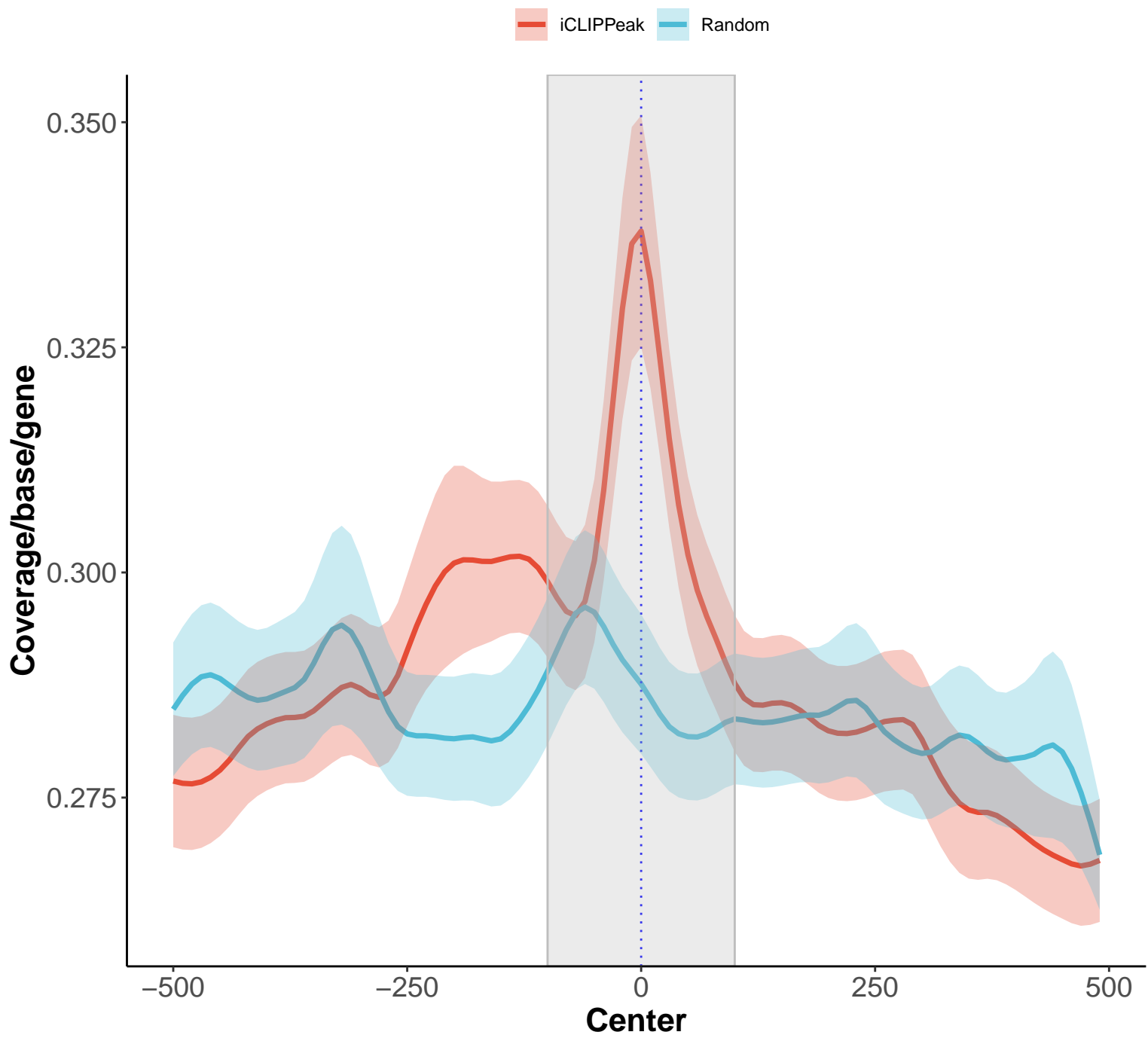


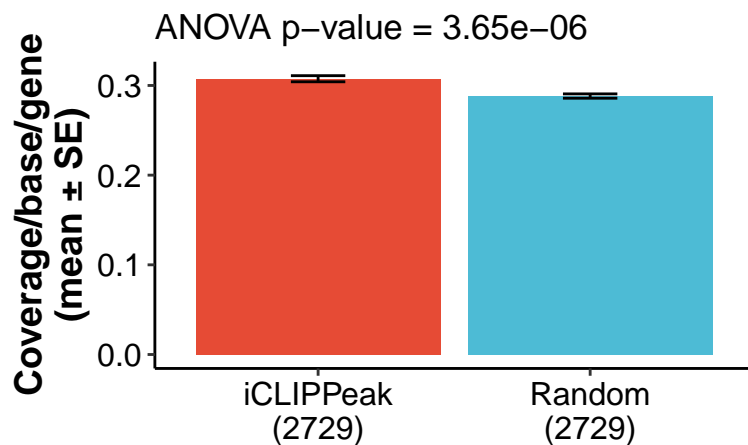
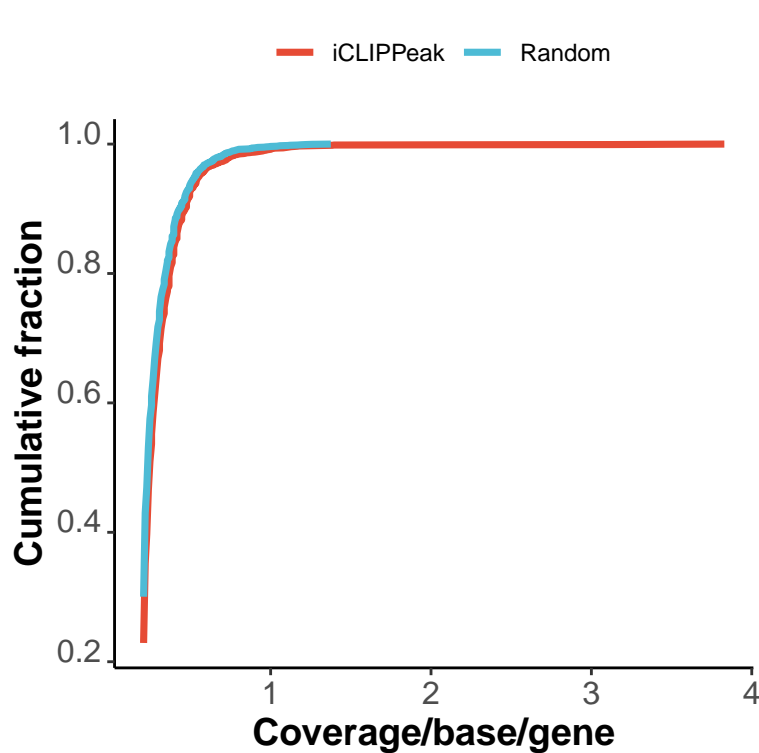
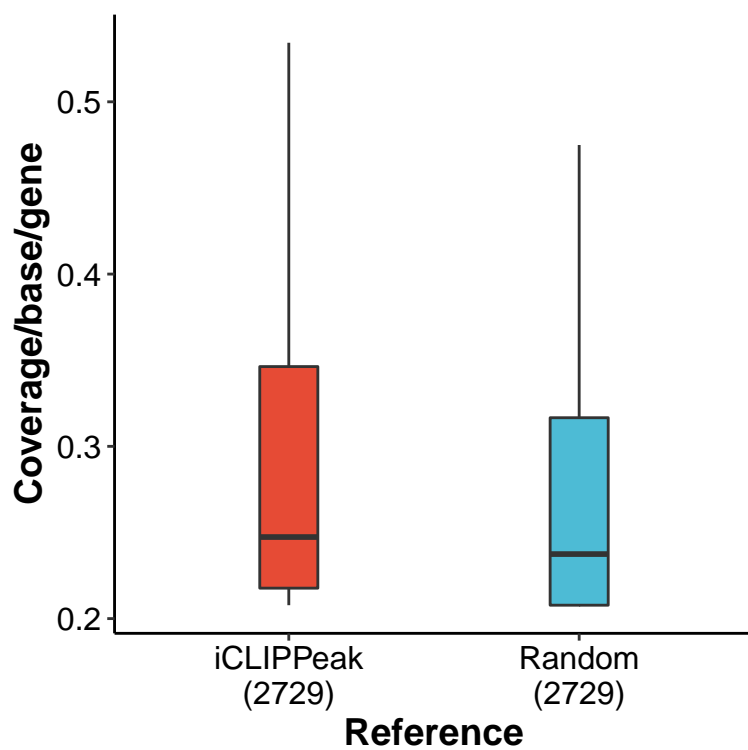
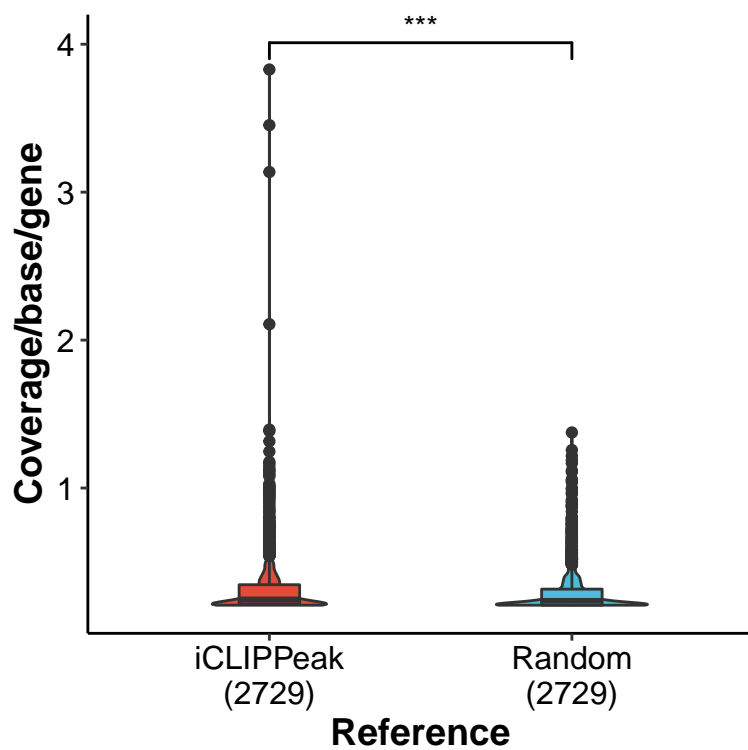


post hoc TukeyHSD test

	diff	lwr	upr	p adj
<i>Random-iCLIPPeak</i>	-0.023	-0.044	-0.002	0.0312

Feature: 3'UTR
Reference size: 2729
Sample name: clip_input

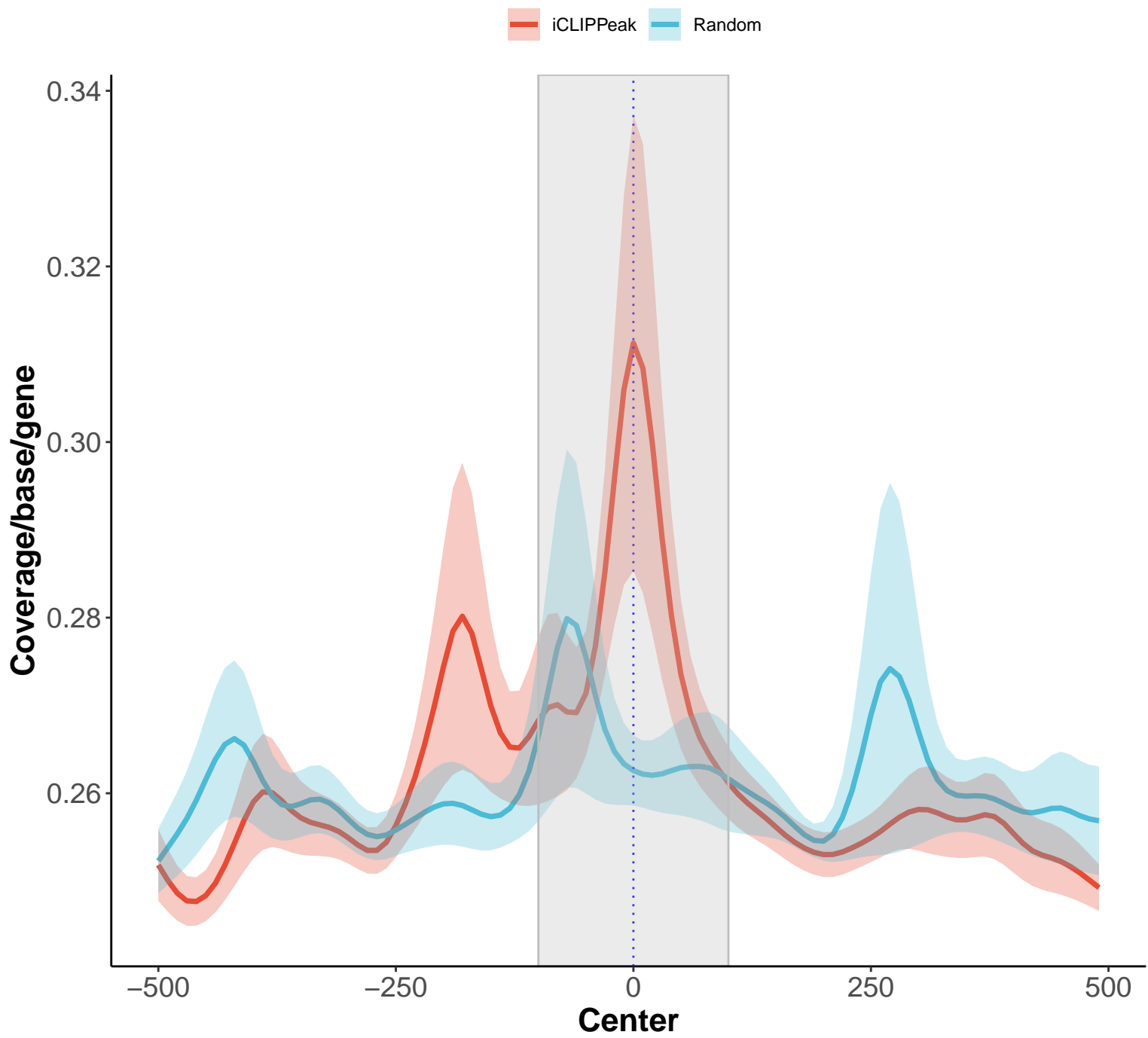


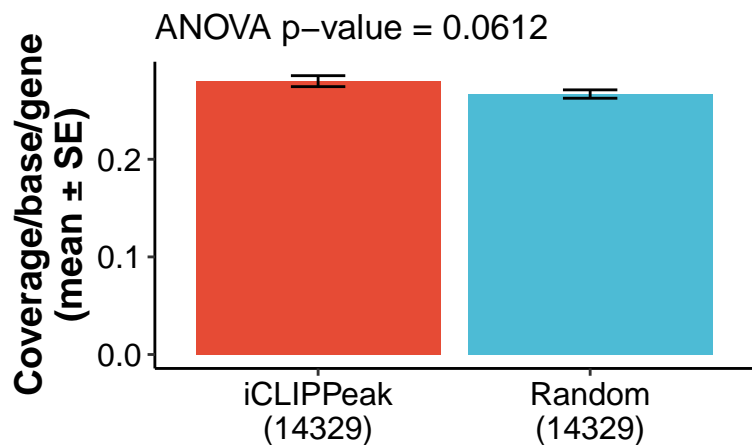
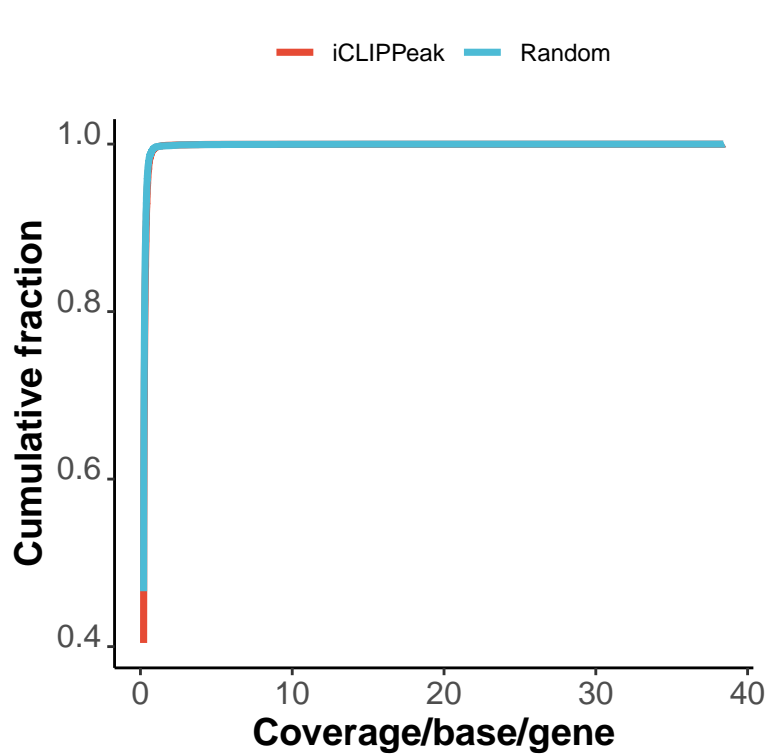
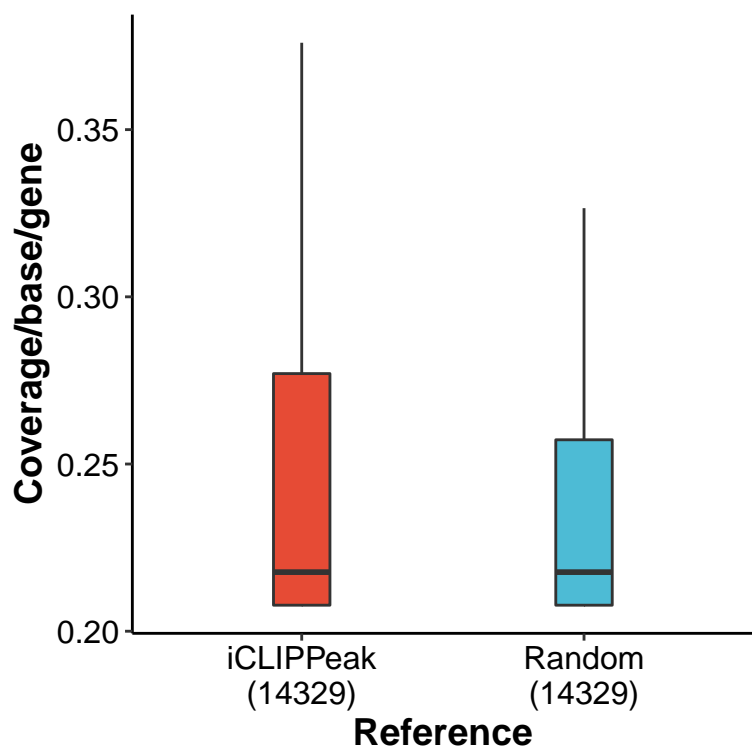
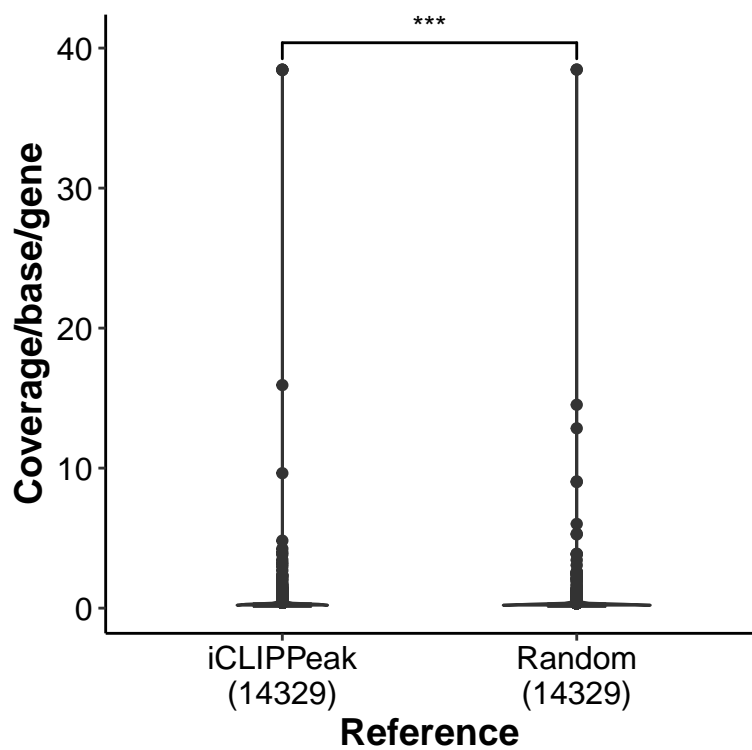


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.019	-0.027	-0.011	3.65×10^{-6}

Feature: Gene
Reference size: 14329
Sample name: clip_input

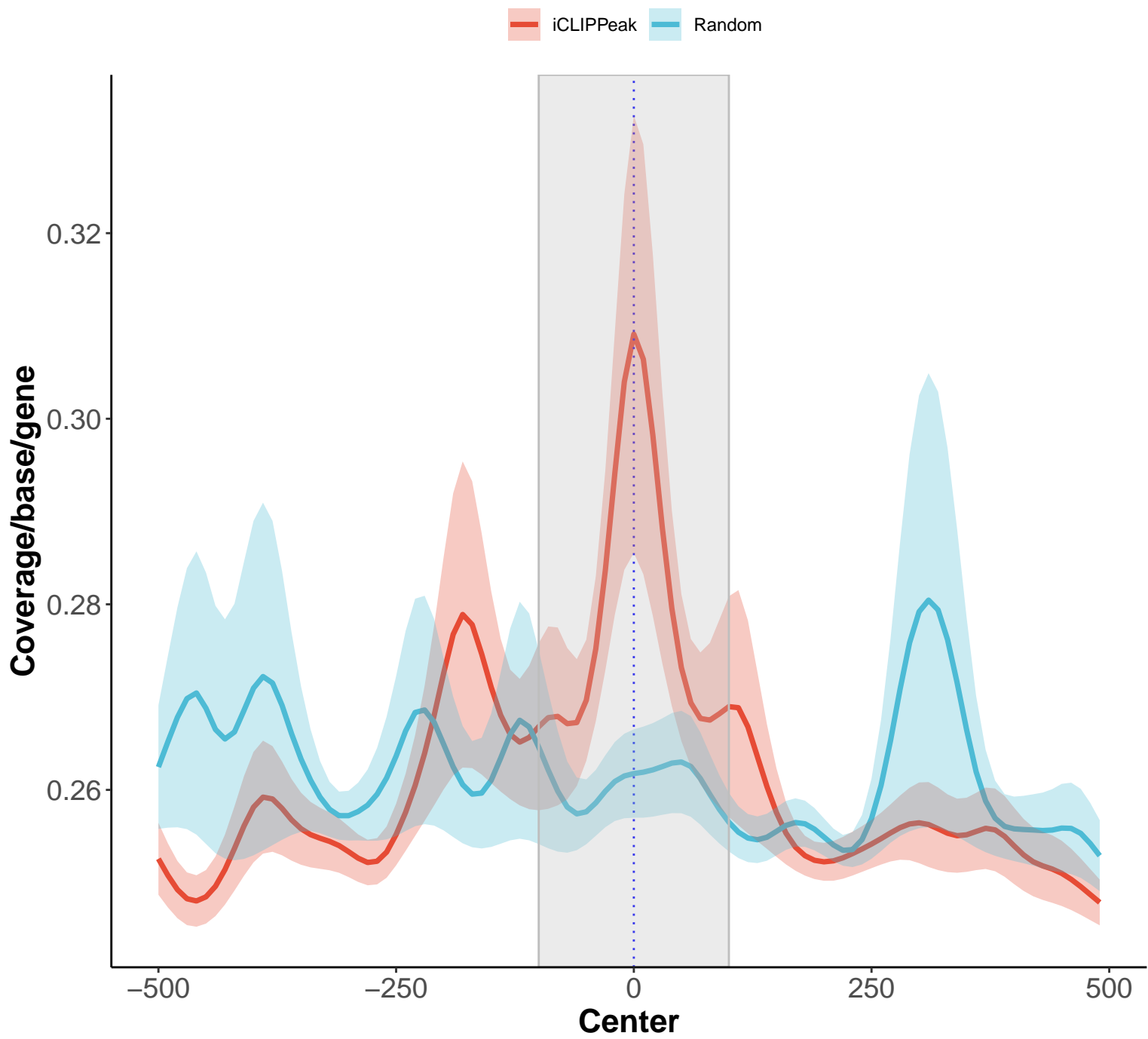


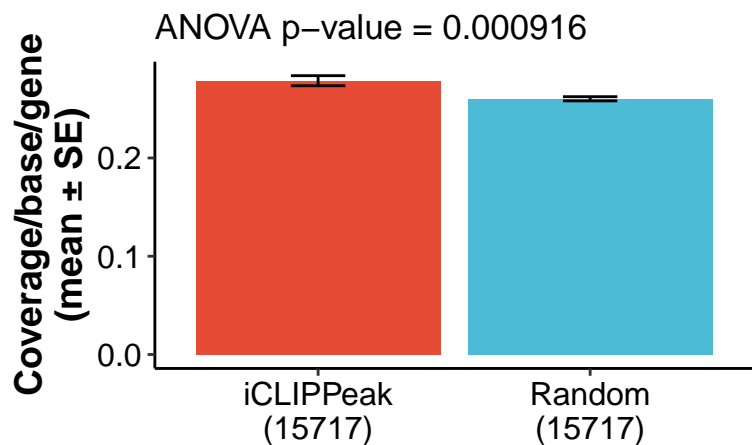
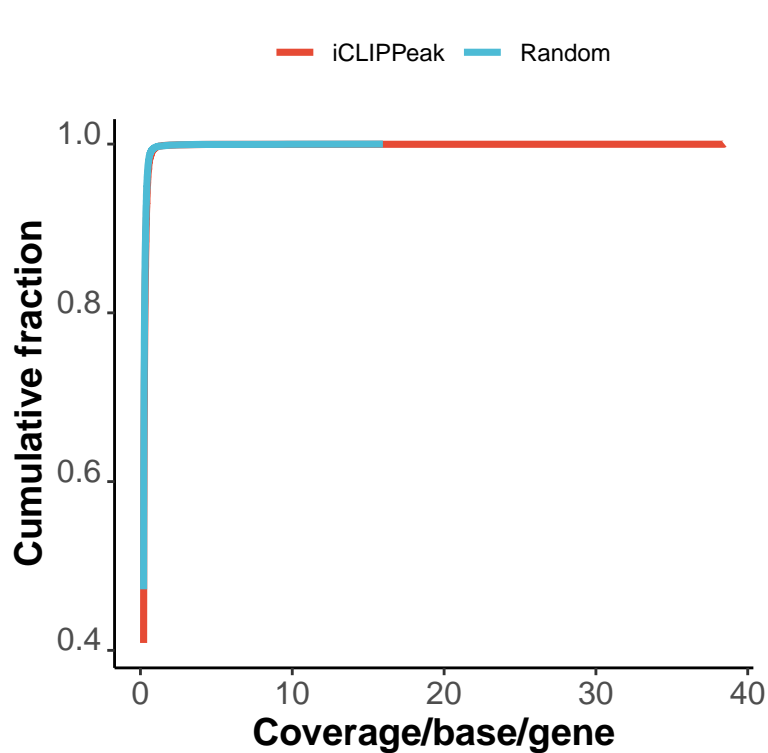
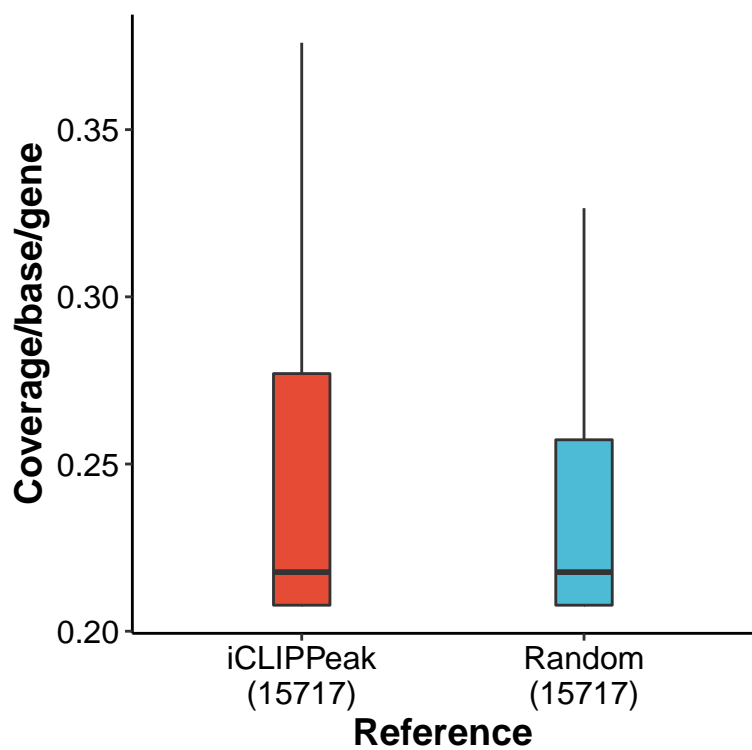
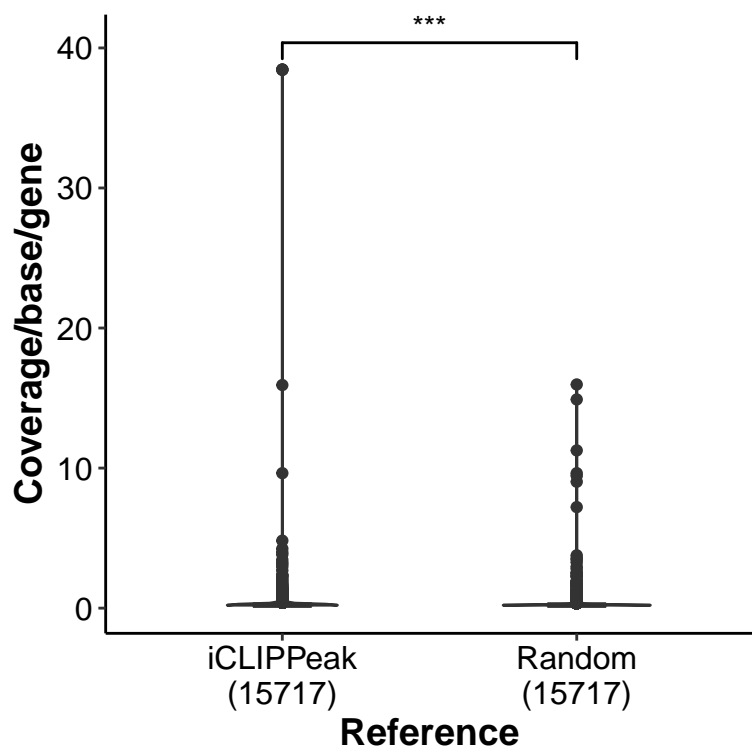


post hoc TukeyHSD test

	diff	lwr	upr	p adj
<i>Random-iCLIPPeak</i>	-0.013	-0.027	0.001	0.0612

Feature: unrestricted
Reference size: 15717
Sample name: clip_input

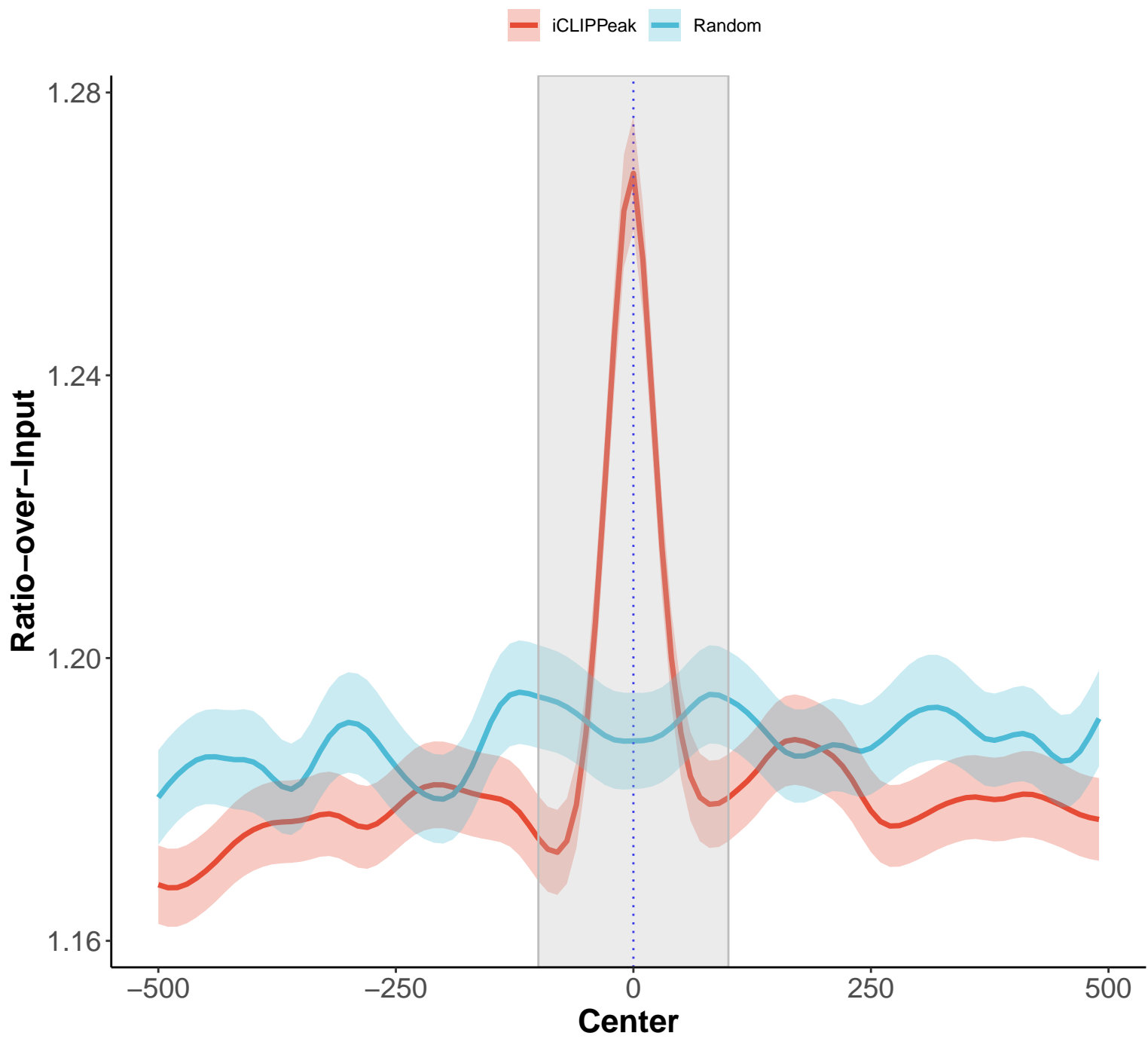


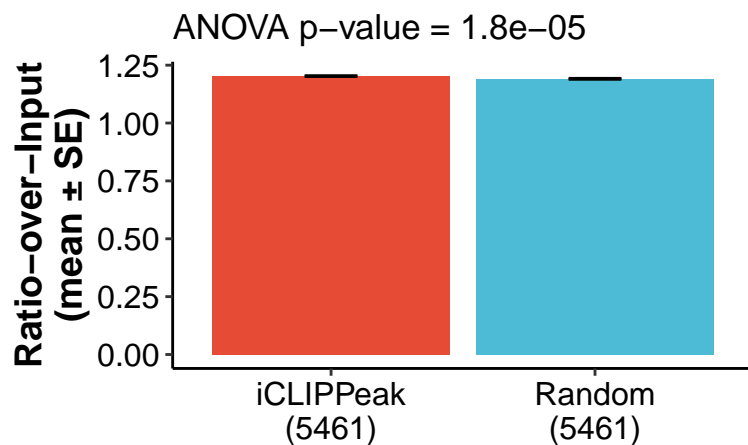
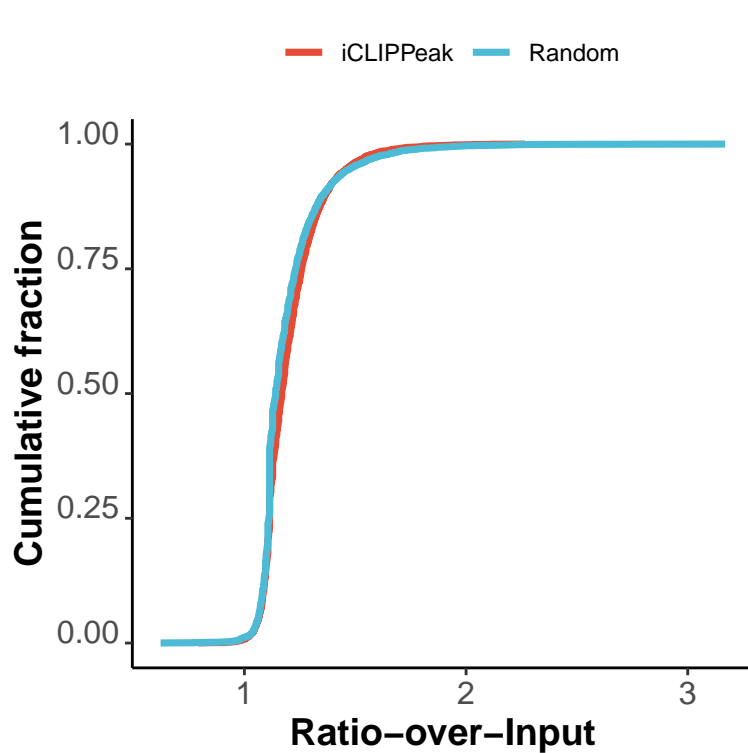
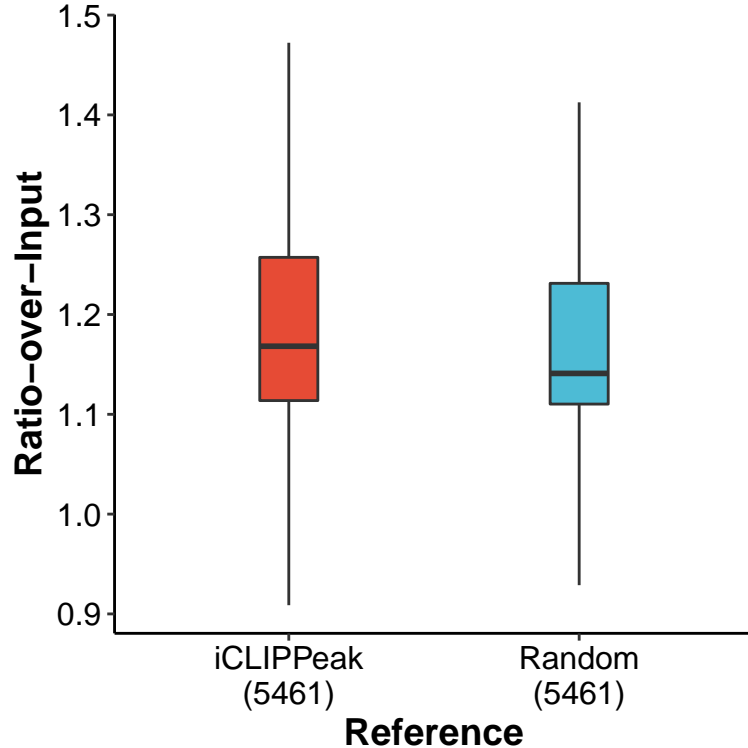
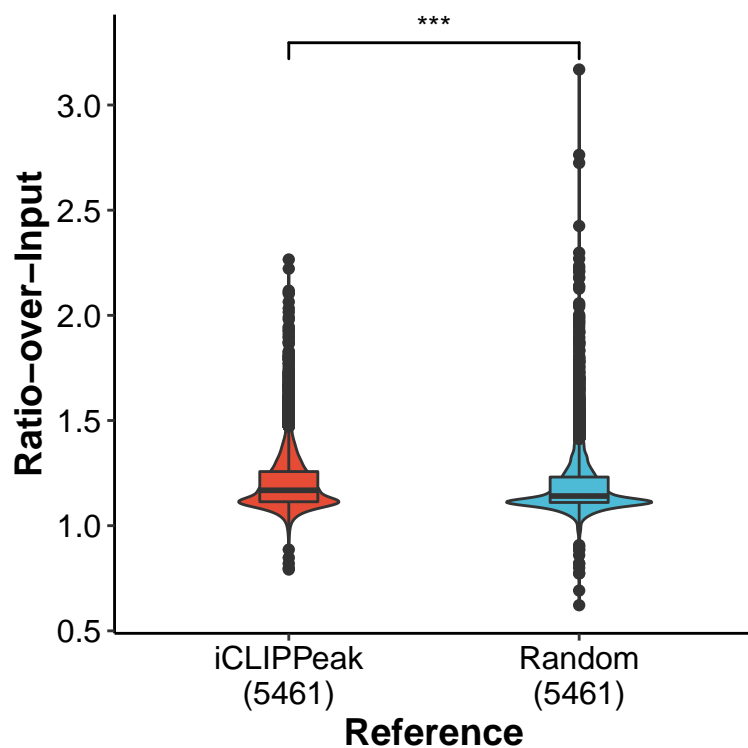


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.018	-0.029	-0.008	0.000915

Feature: Transcript
Reference size: 5461
Sample name: clip_bam

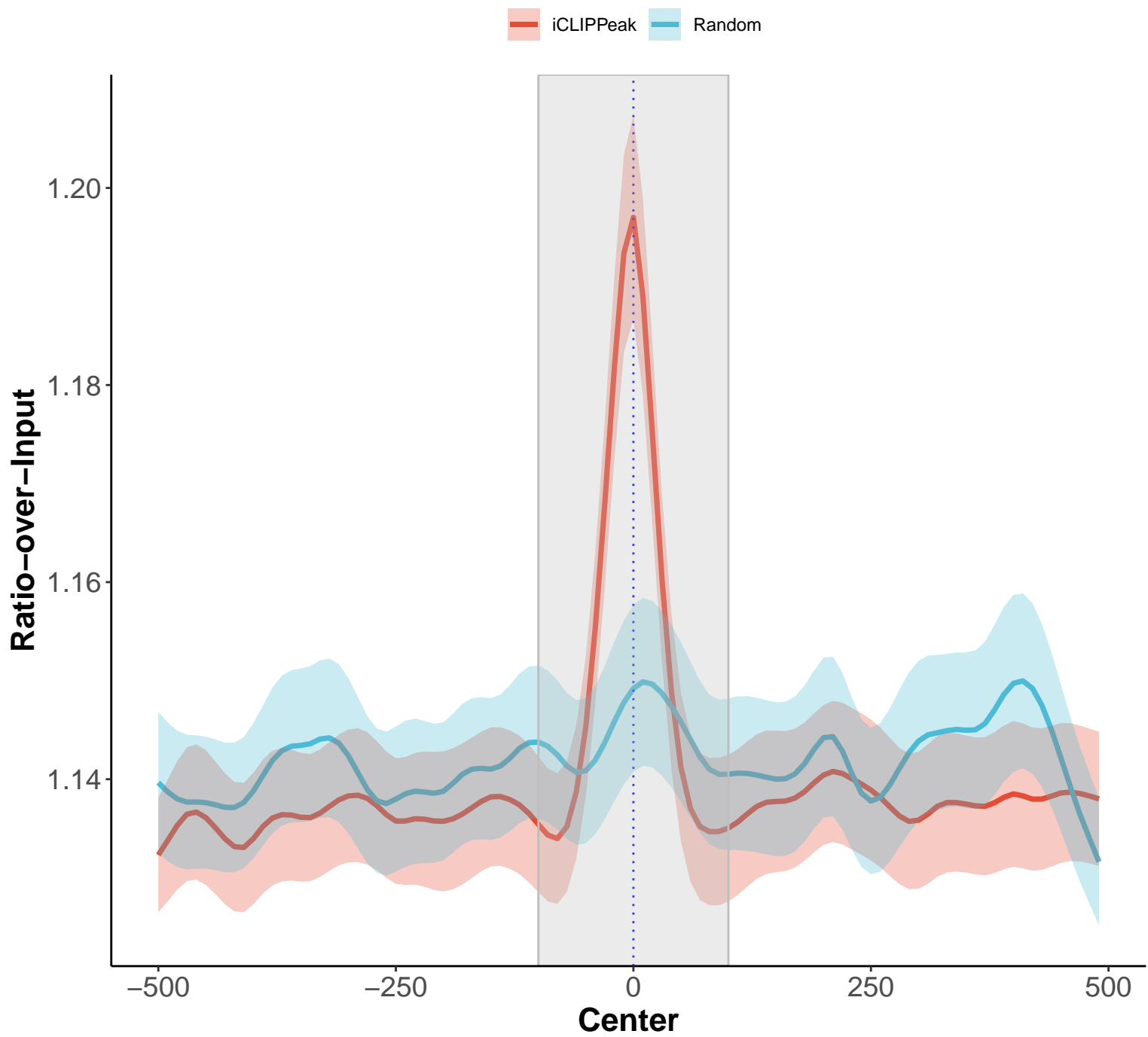


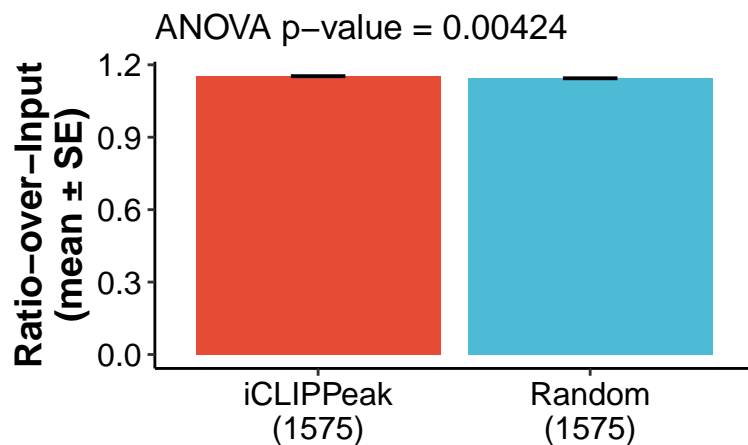
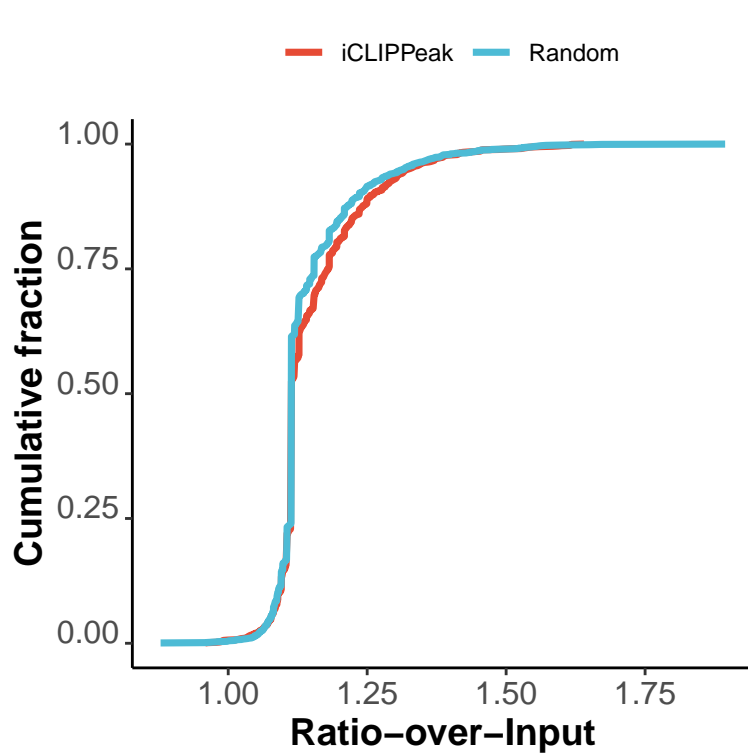
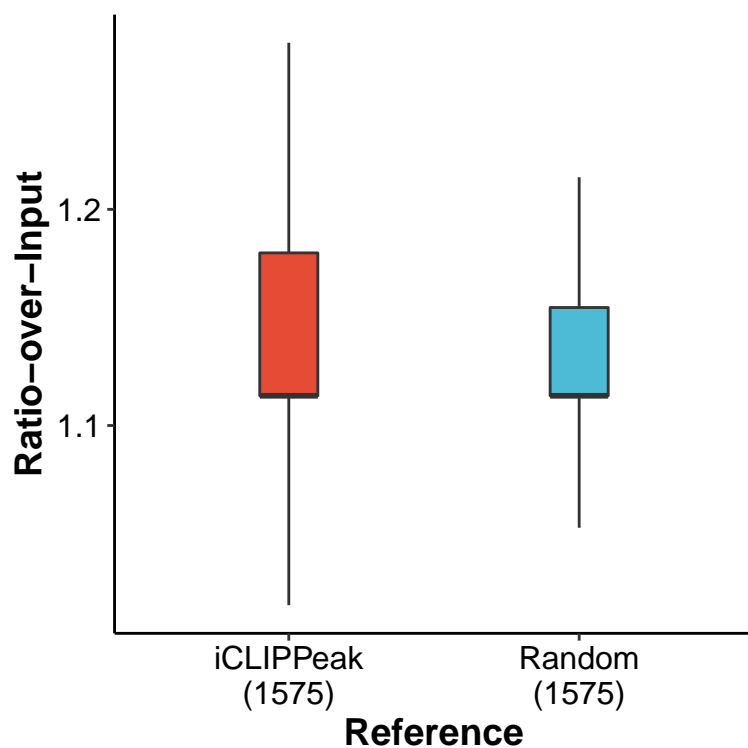
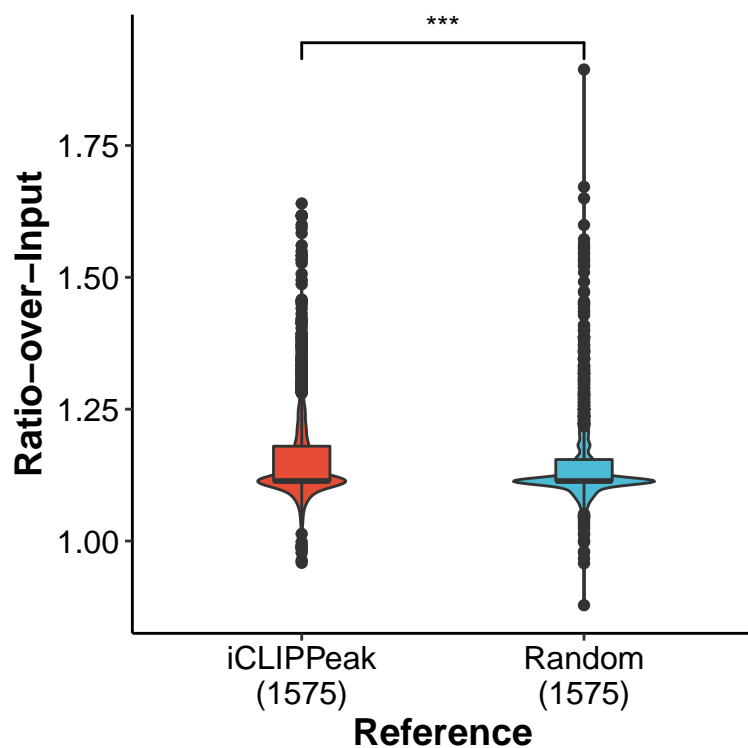


post hoc TukeyHSD test

	diff	lwr	upr	p adj
<i>Random-iCLIPPeak</i>	-0.012	-0.017	-0.006	$1.8e-05$

Feature: 5'UTR
Reference size: 1575
Sample name: clip_bam



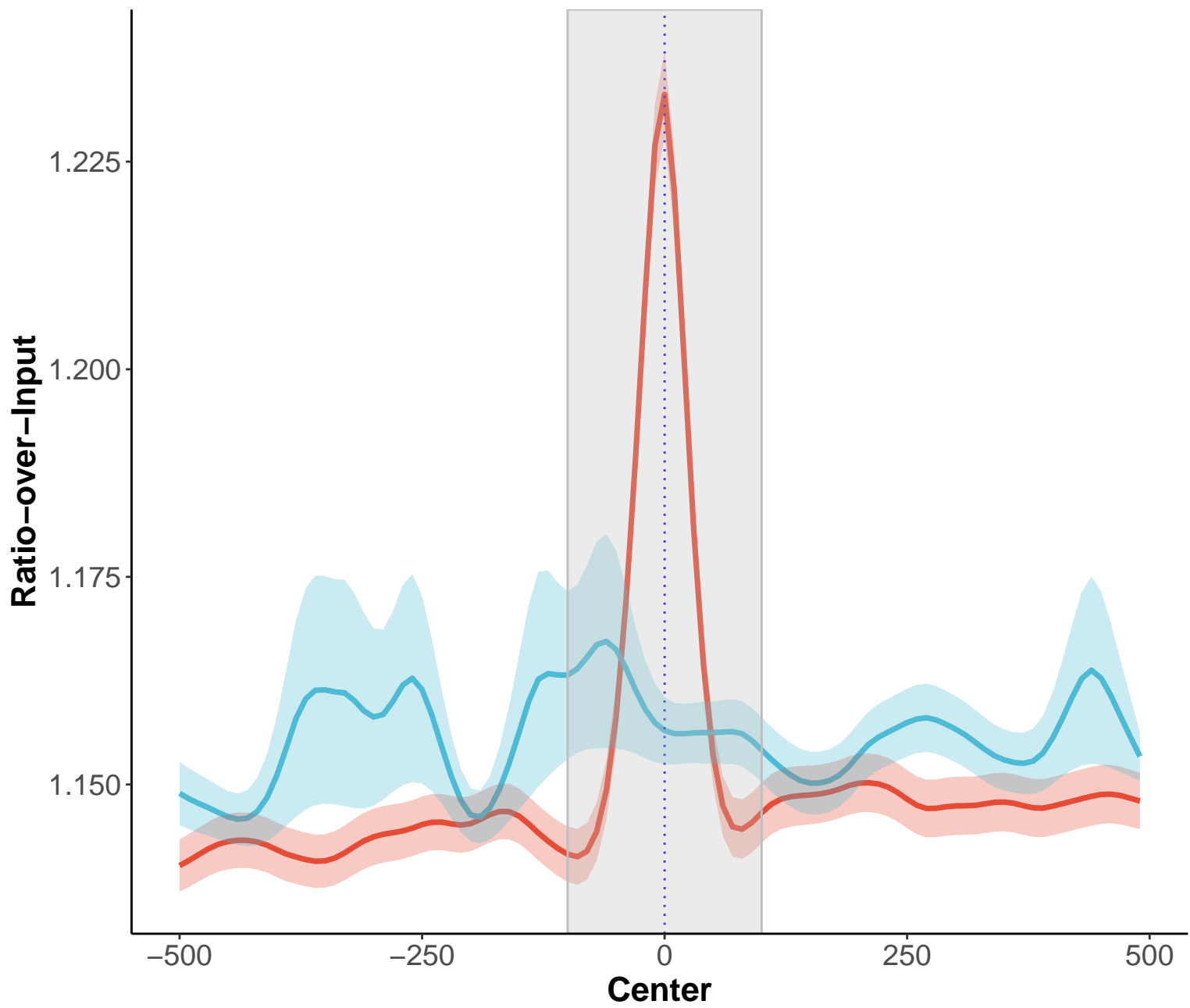


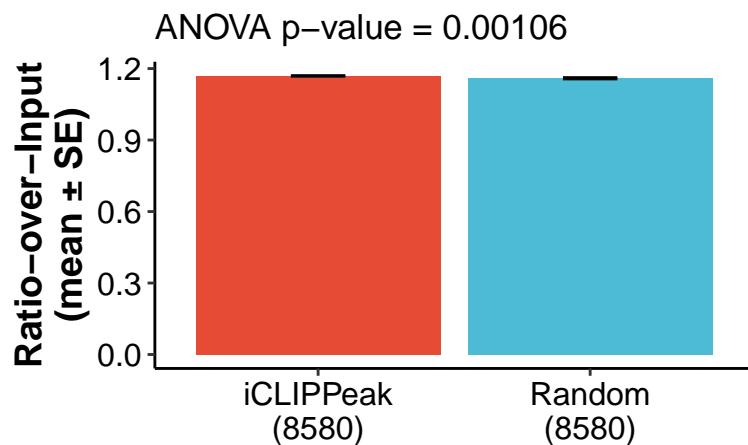
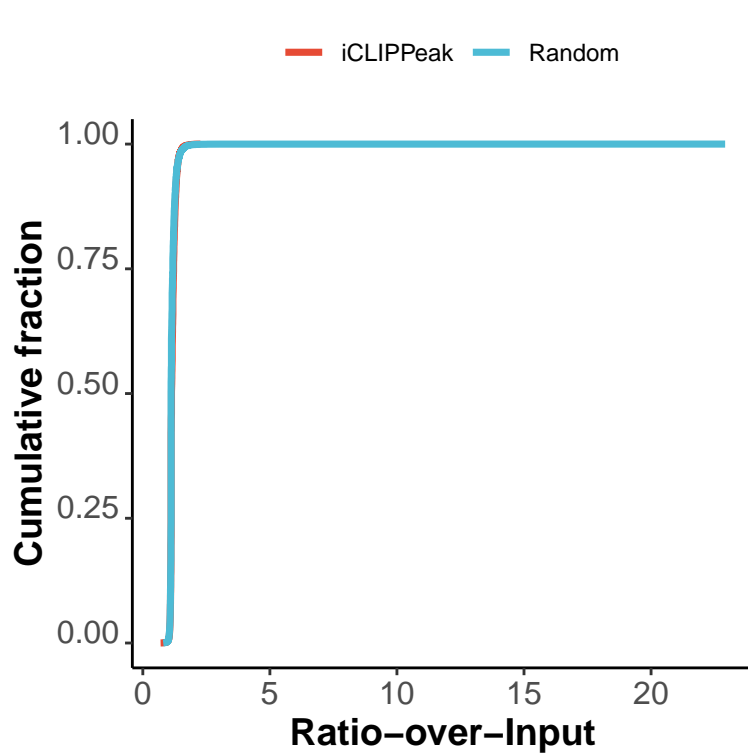
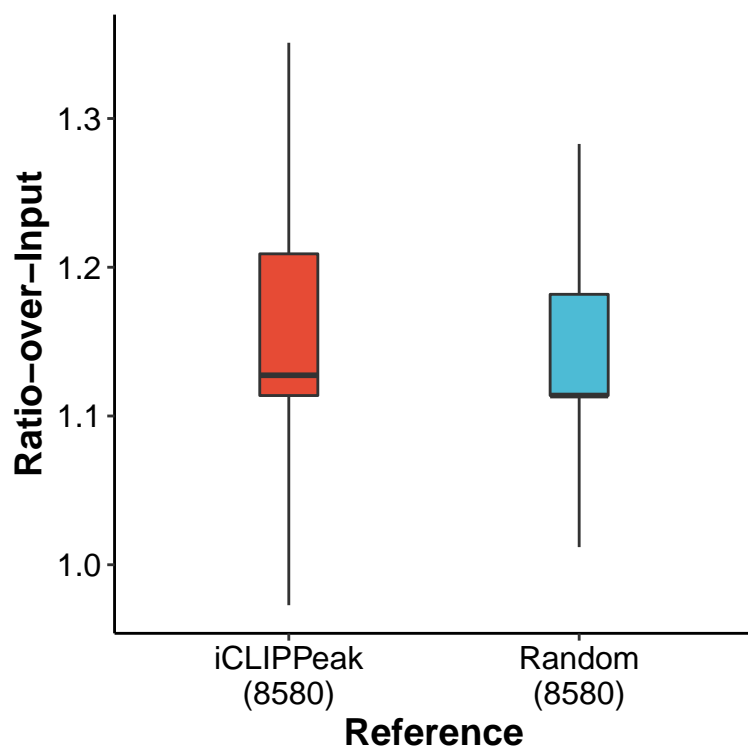
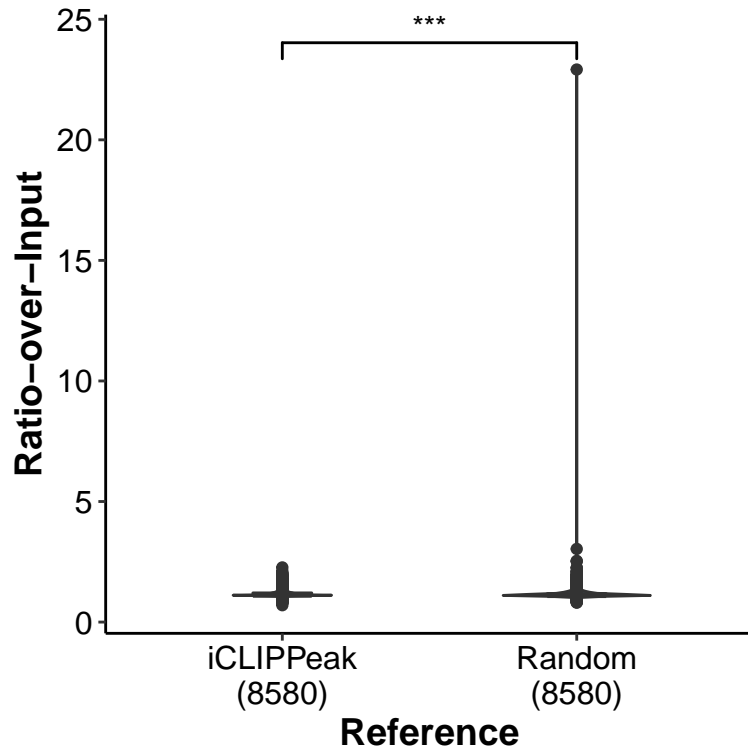
post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.009	-0.014	-0.003	0.00424

Feature: CDS
Reference size: 8580
Sample name: clip_bam

iCLIPPeak Random

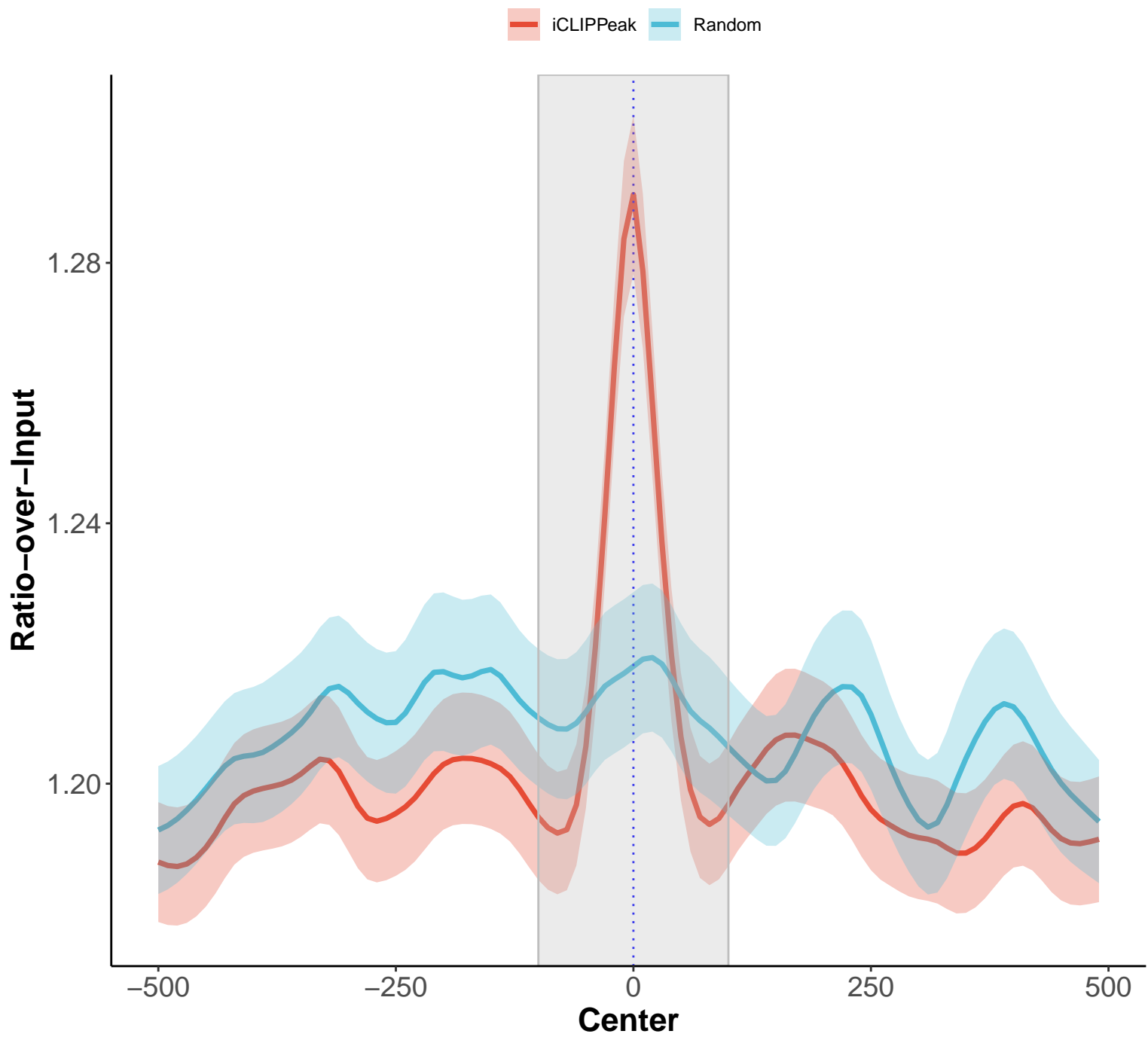


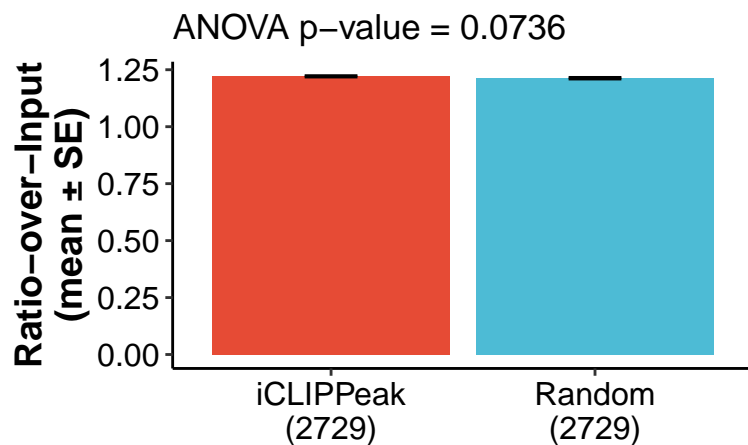
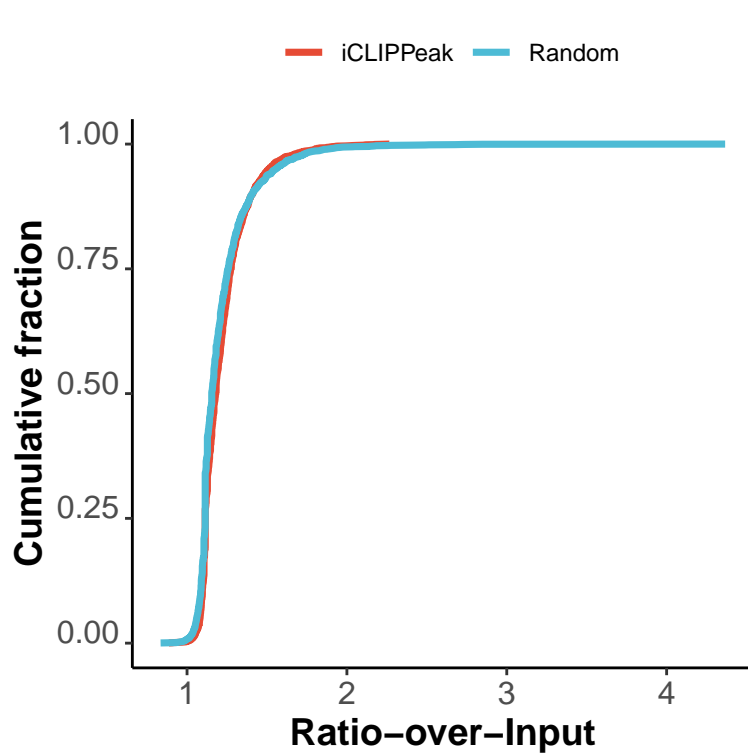
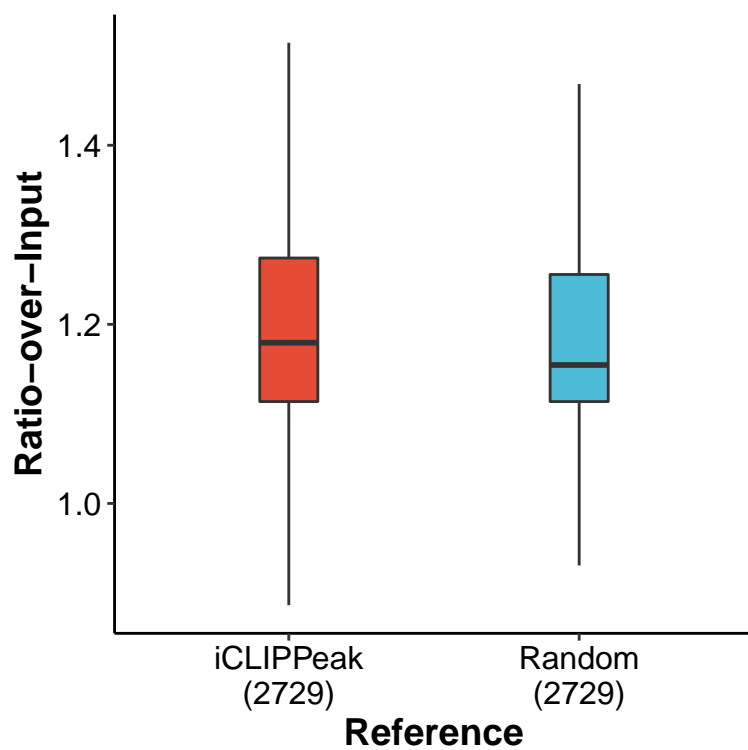
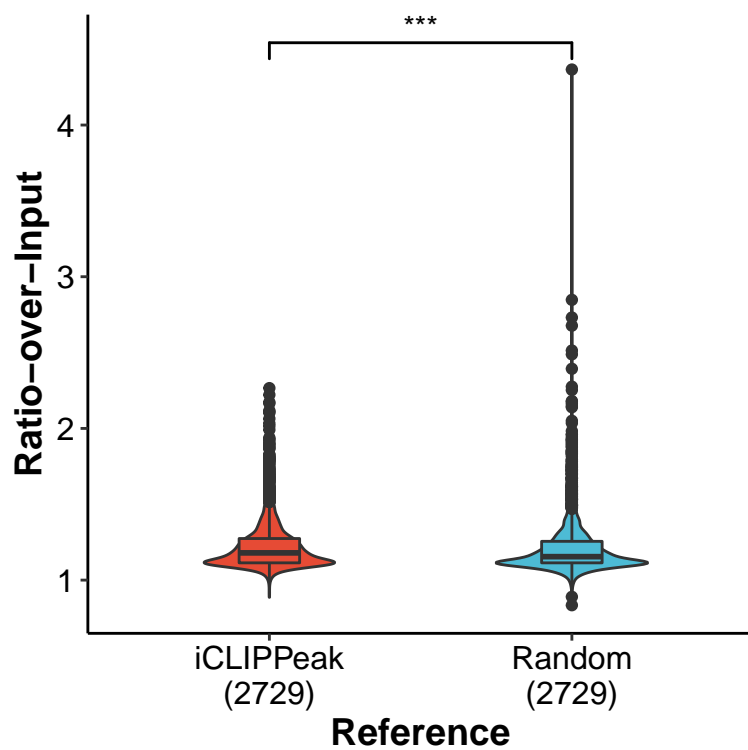


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.01	-0.016	-0.004	0.00106

Feature: 3'UTR
Reference size: 2729
Sample name: clip_bam

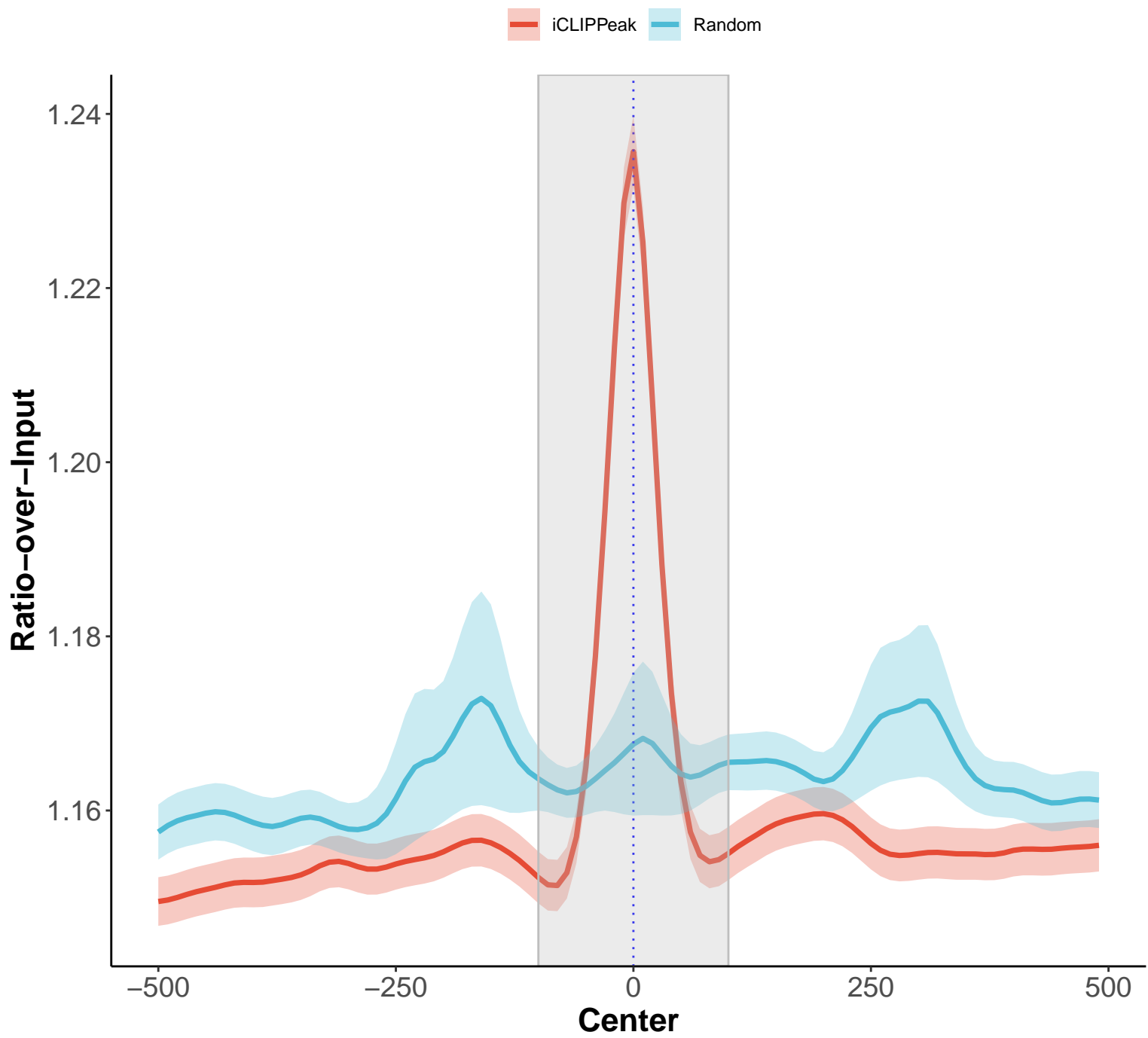


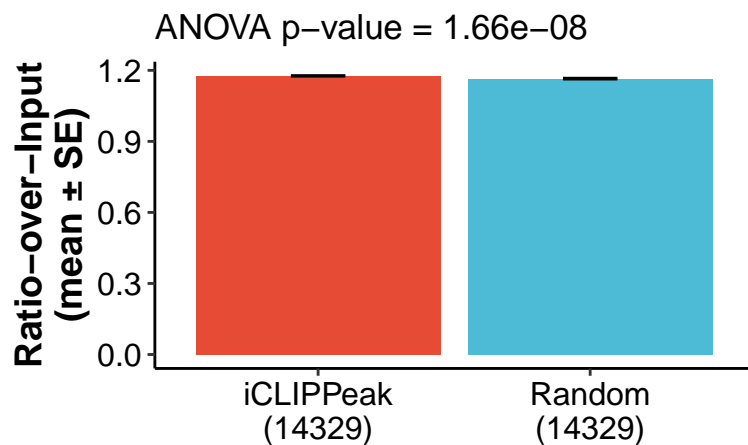
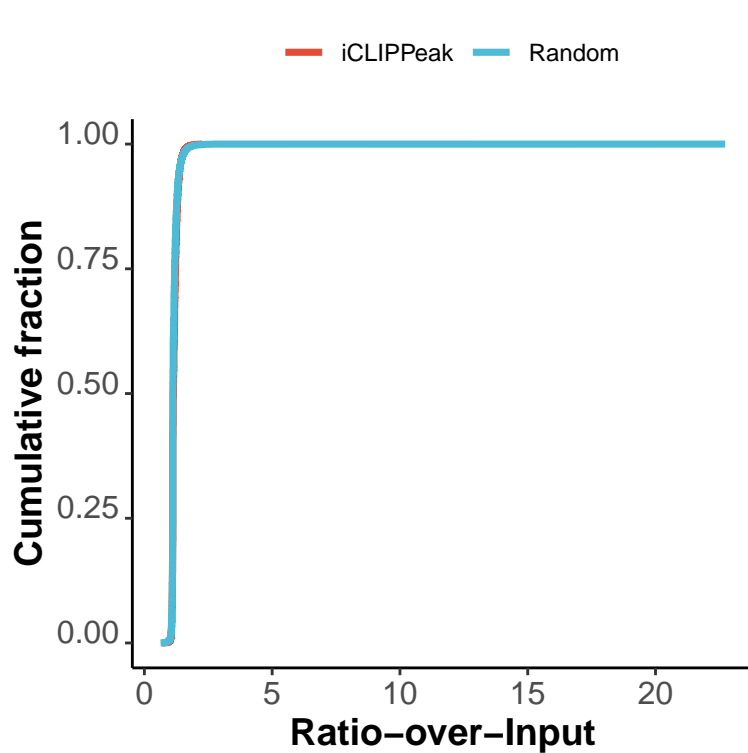
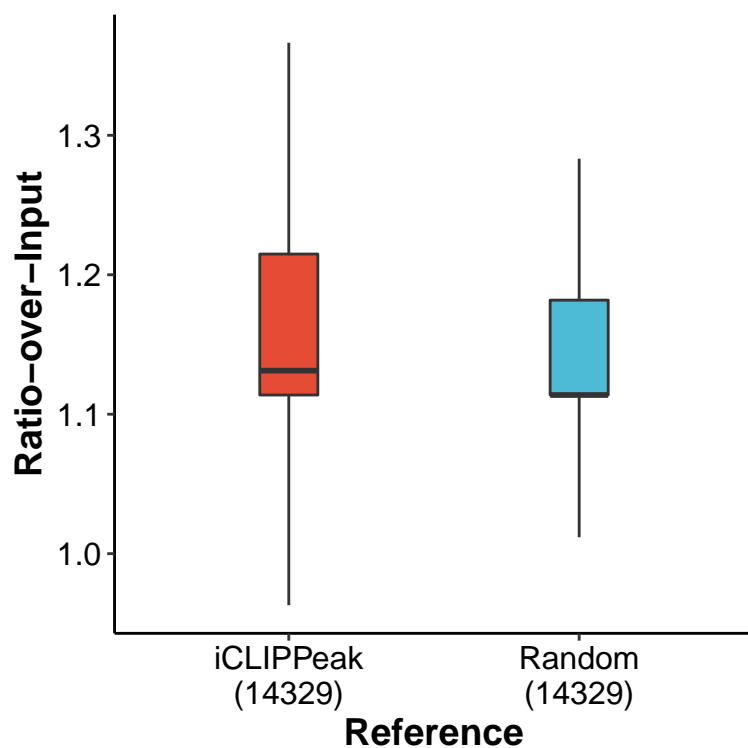
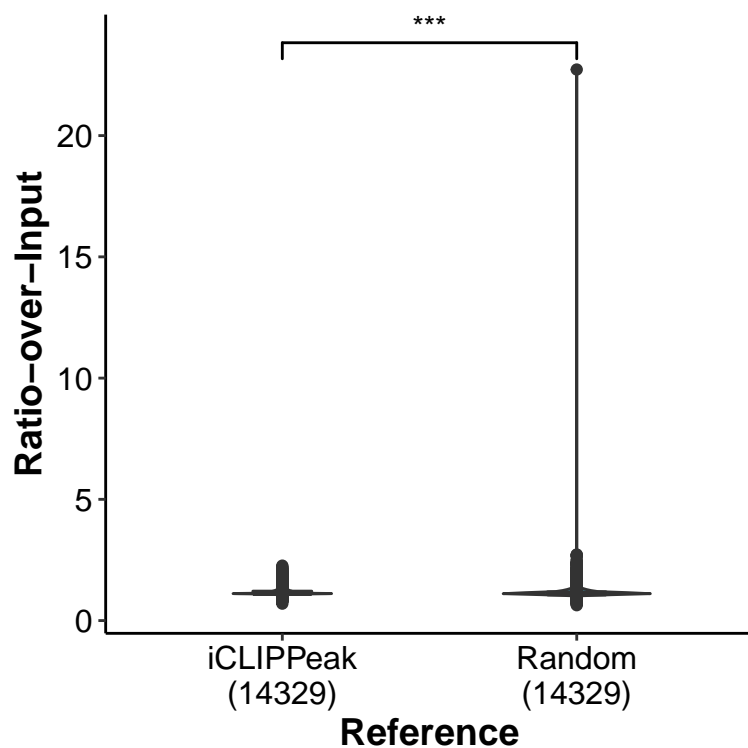


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.008	-0.017	0.001	0.0736

Feature: Gene
Reference size: 14329
Sample name: clip_bam

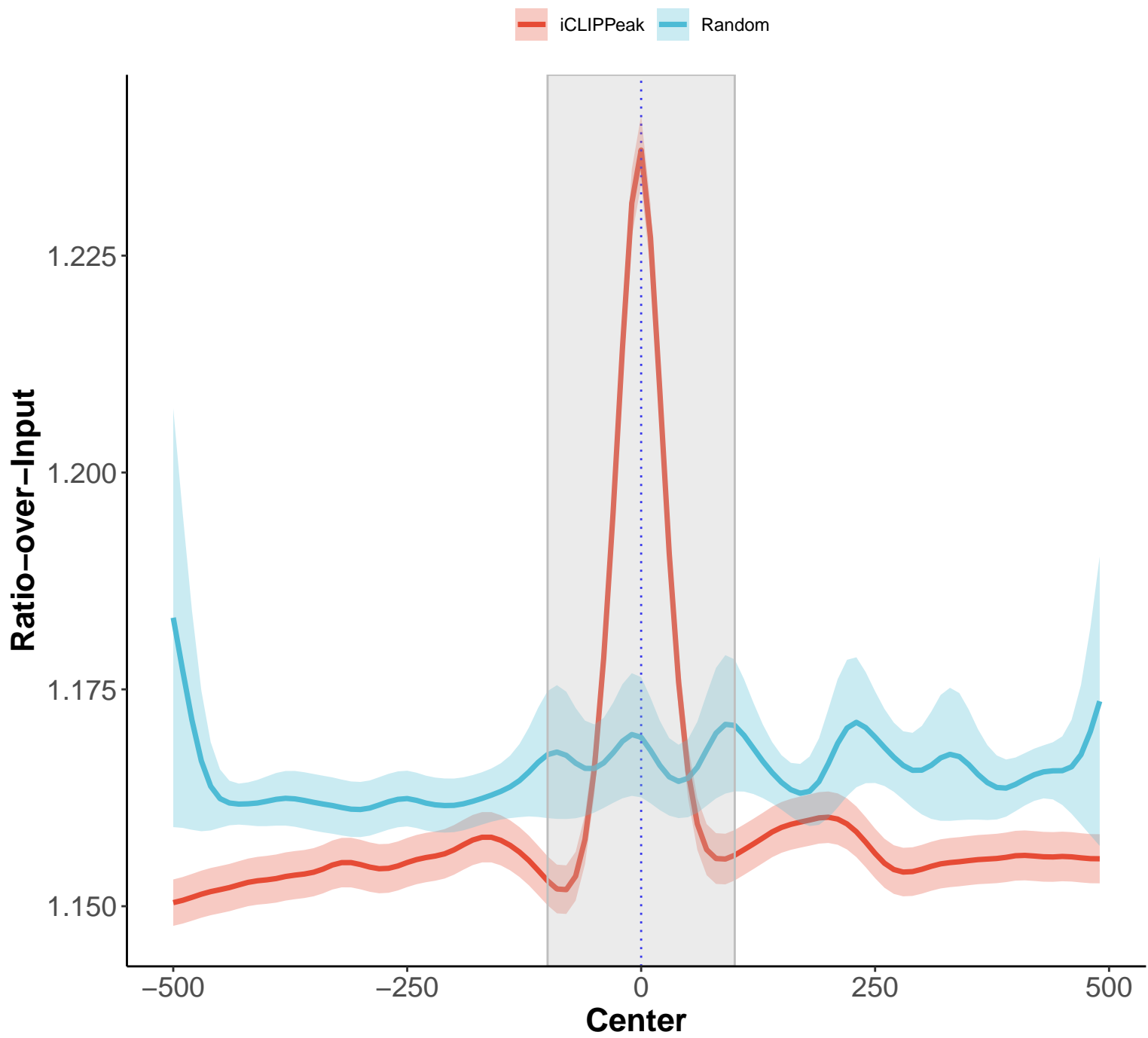


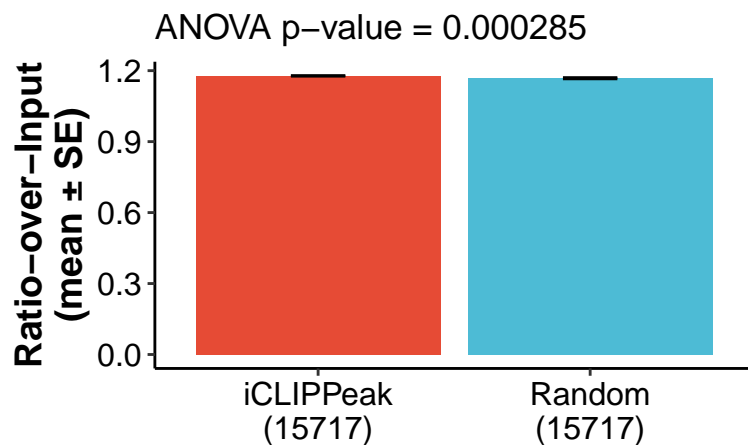
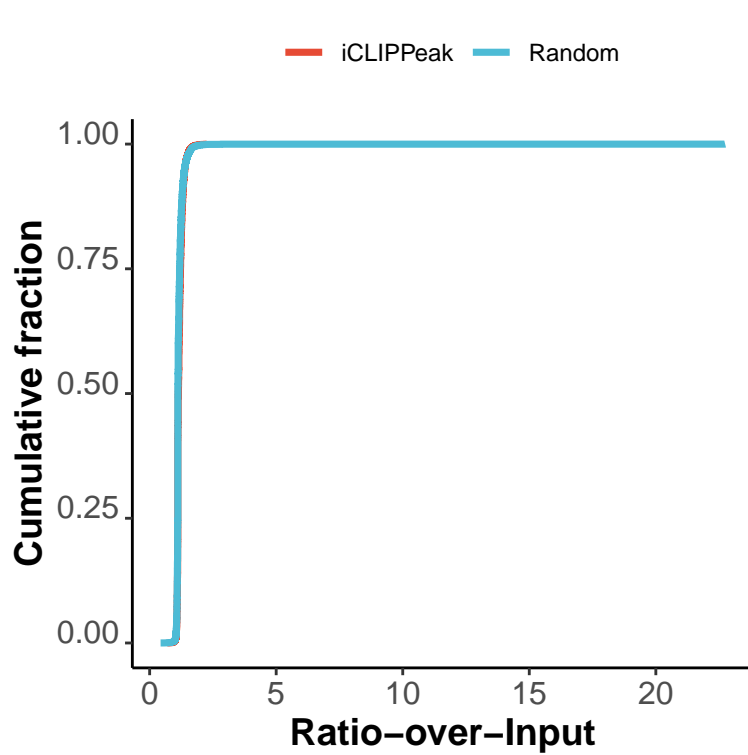
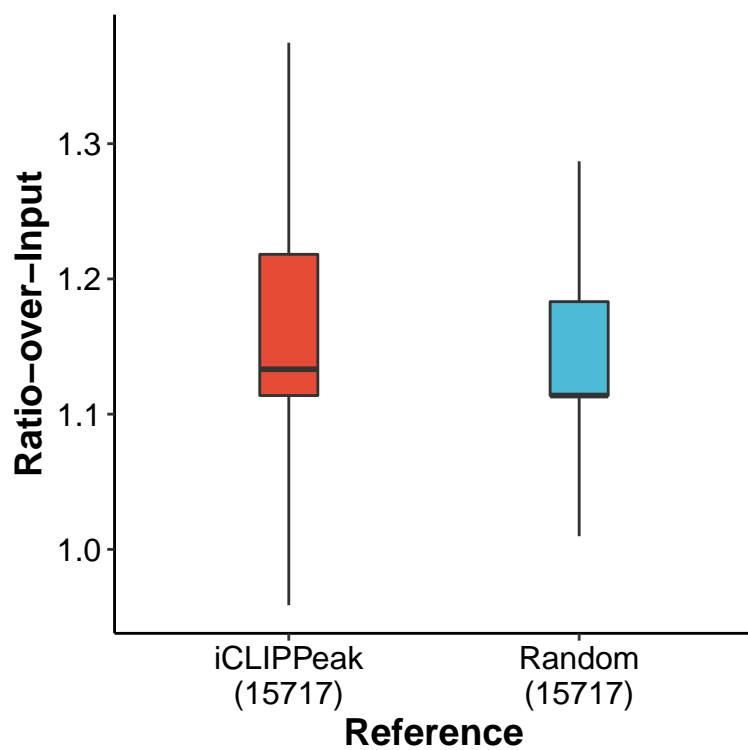
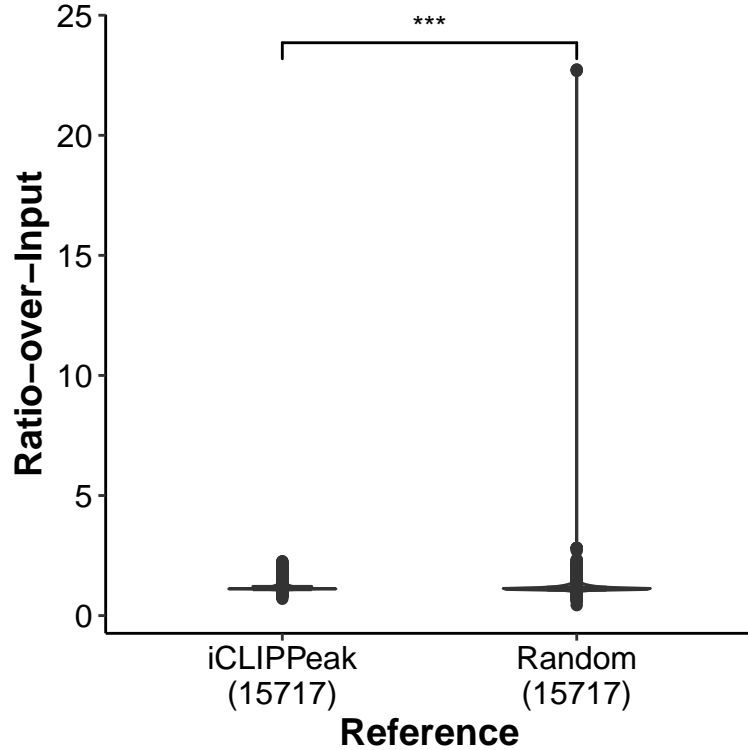


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.012	-0.016	-0.008	1.65e-08

Feature: unrestricted
Reference size: 15717
Sample name: clip_bam





post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.01	-0.015	-0.005	0.000285

Plotting parameters:

```
functionName: "plot_locus_with_random"
queryFiles: c(clip_bam =
"C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/treat_chr19.bam")
centerFiles: c(iCLIPPeak =
"C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/test_clip_peak_chr19.bed")
txdb: new("TxDb", .xData = <environment>)
ext: c(-500, 500)
hl: c(-100, 100)
shade: TRUE
importParams: list(offset = -1, fix_width = 0, fix_point = "start", norm = TRUE, useScore =
FALSE, outRle = TRUE, useSizeFactor = FALSE, genome = "hg19")
verbose: FALSE
smooth: TRUE
transform: NA
binSize: 10
refPoint: "center"
Xlab: "Center"
Ylab: "Coverage/base/gene"
inputFiles: c(clip_input =
"C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/input_chr19.bam")
stranded: TRUE
scale: FALSE
outPrefix: "test_plot_locus_with_random"
rmOutlier: 0
n_random: 1
hw: c(8, 8)
statsMethod: "wilcox.test"
nc: 2
```