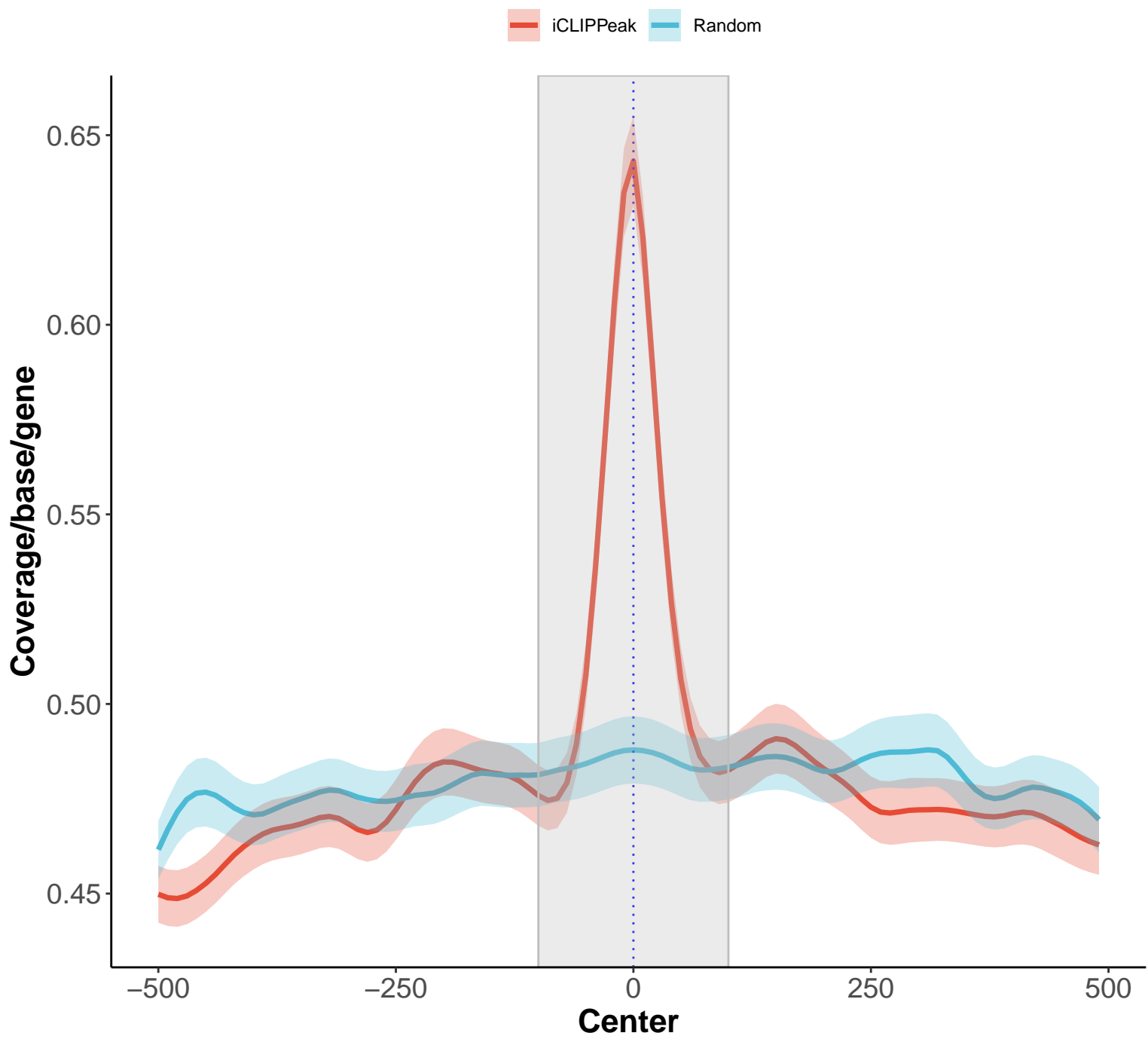
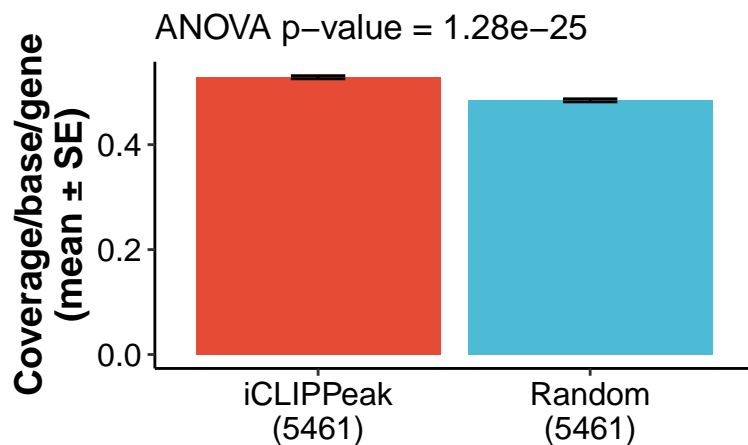
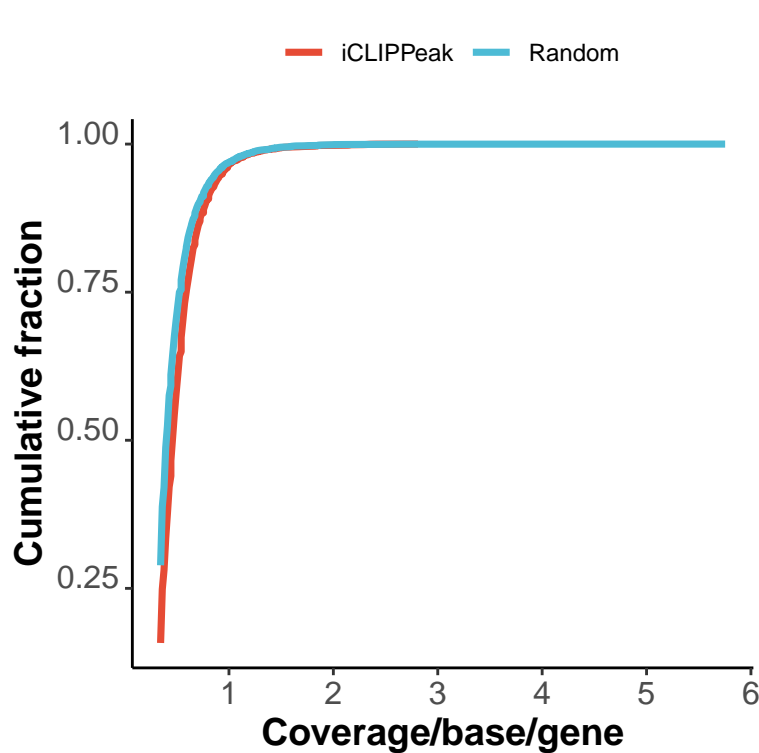
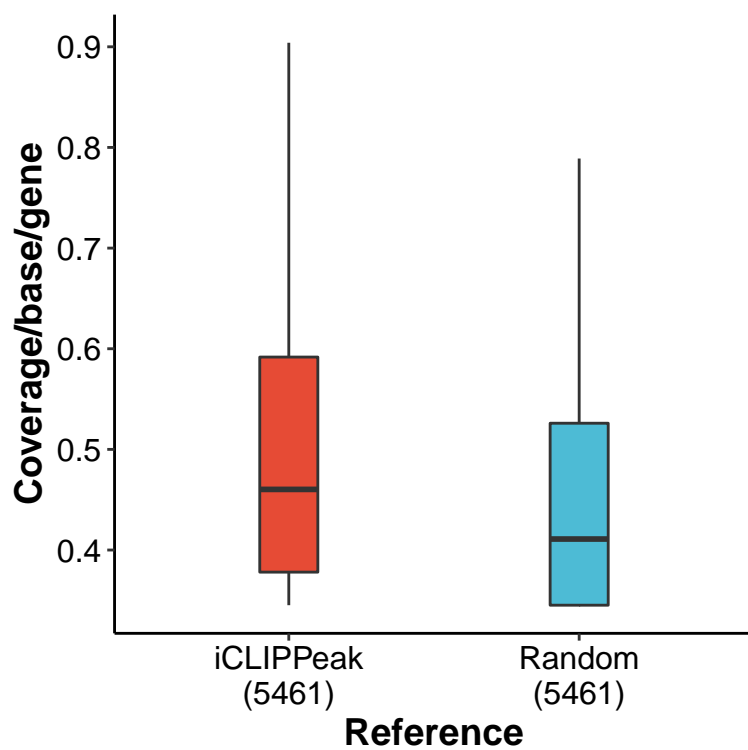
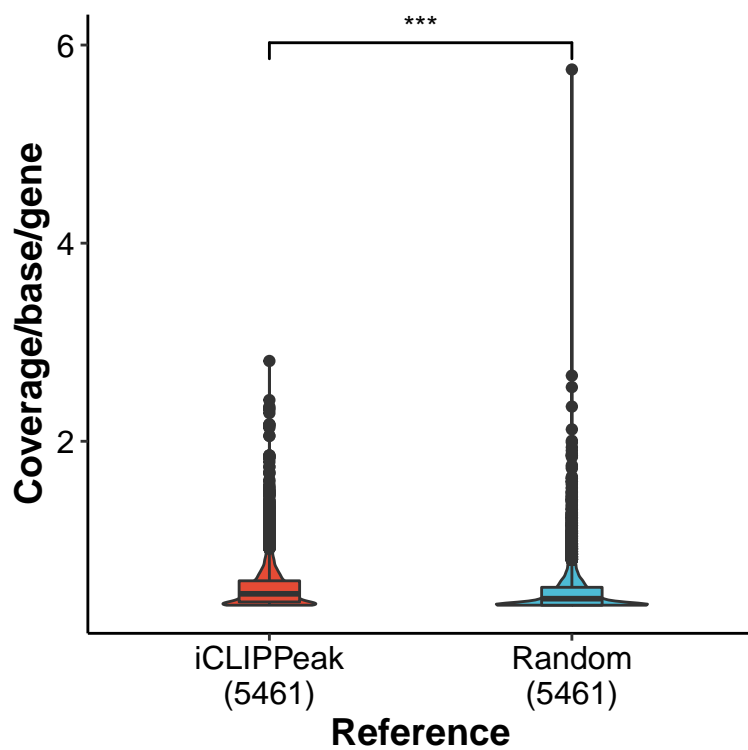


Feature: Transcript
Reference size: 5461
Sample name: clip_bam



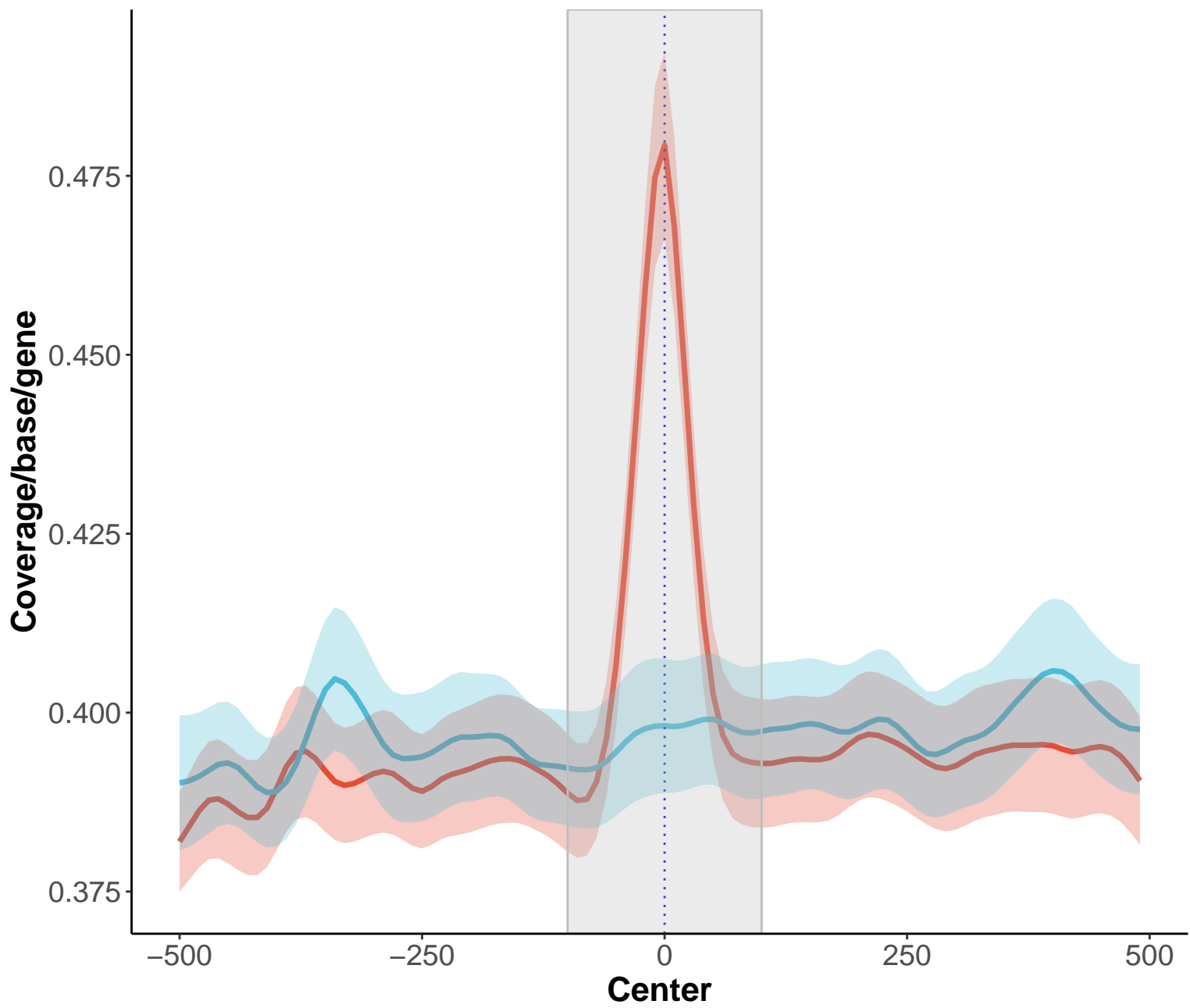


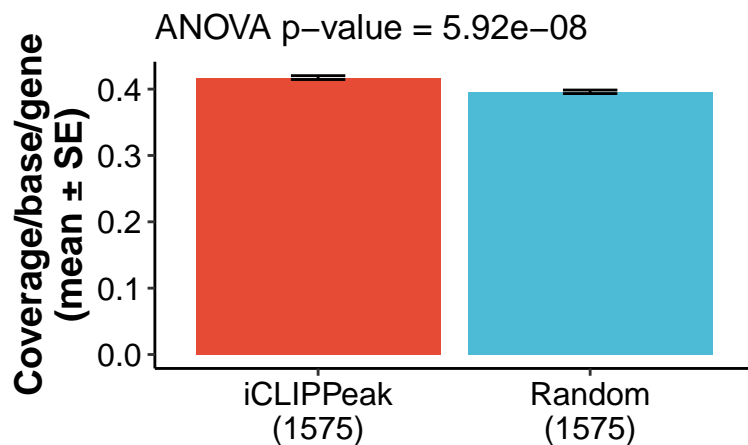
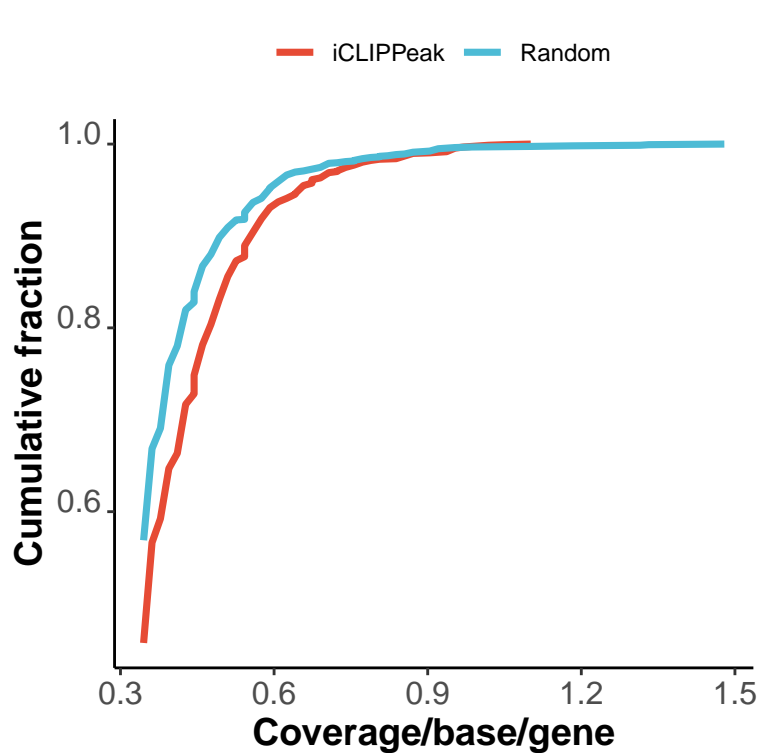
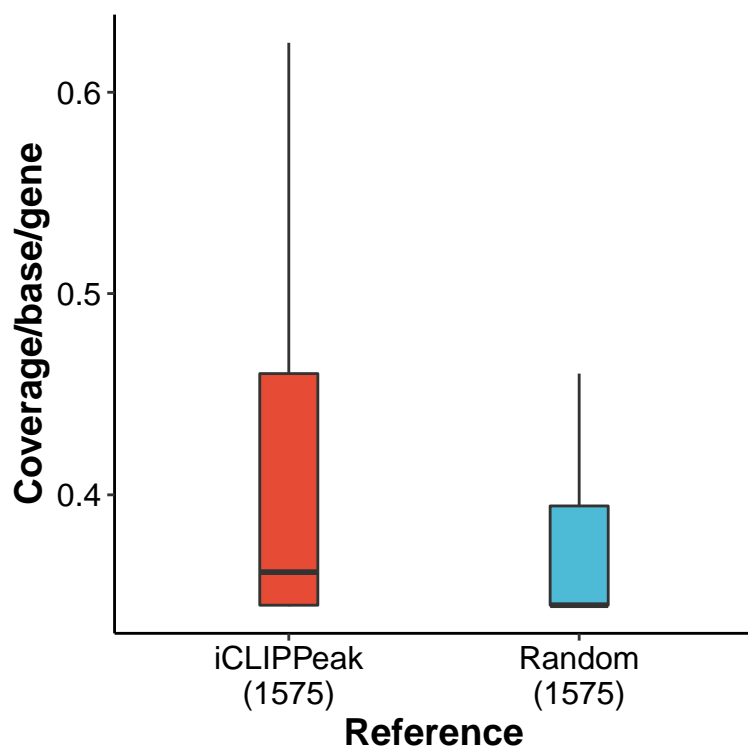
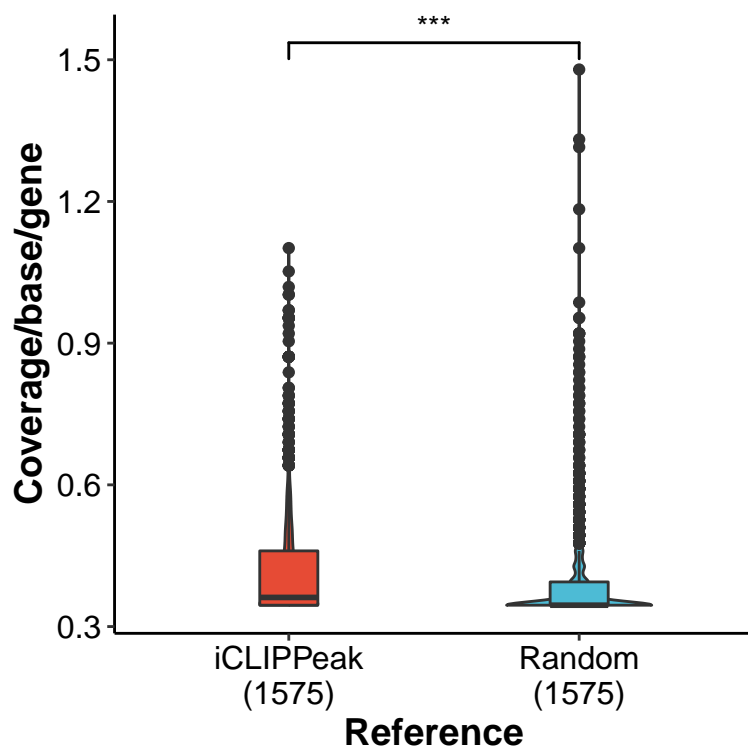
post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.044	-0.052	-0.036	0

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

iCLIPPeak Random

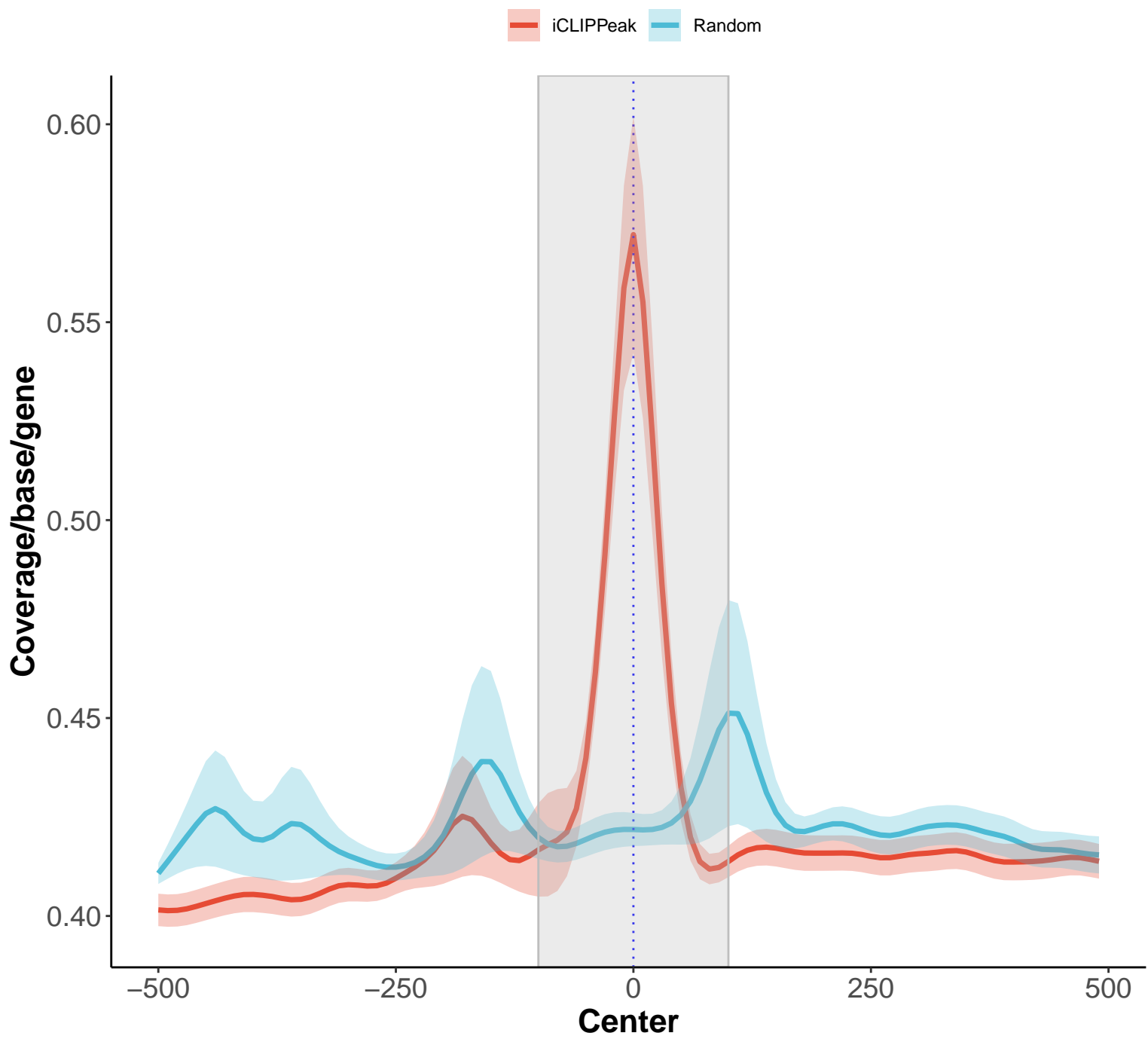


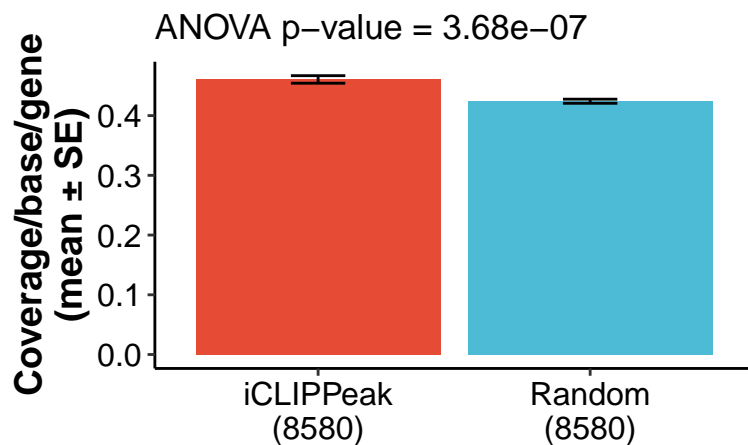
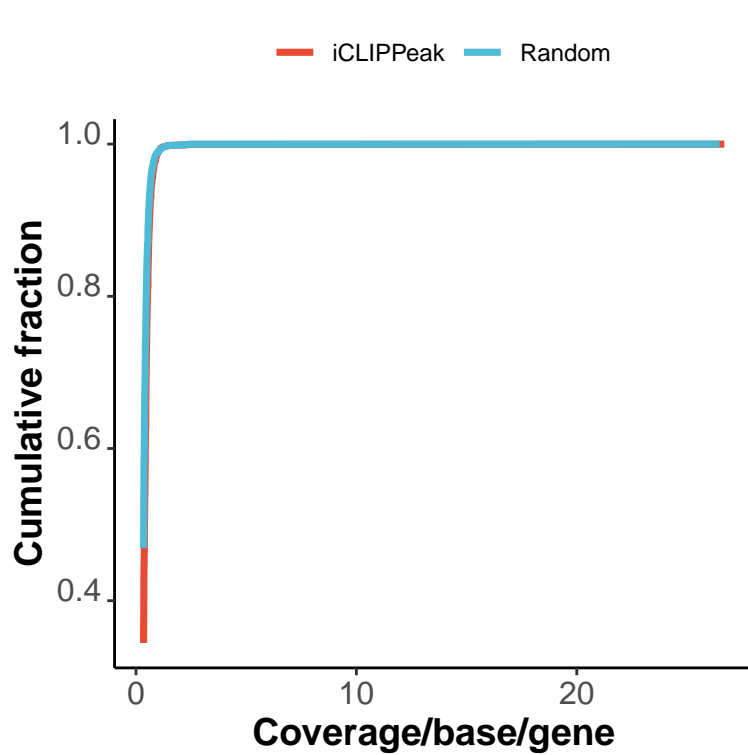
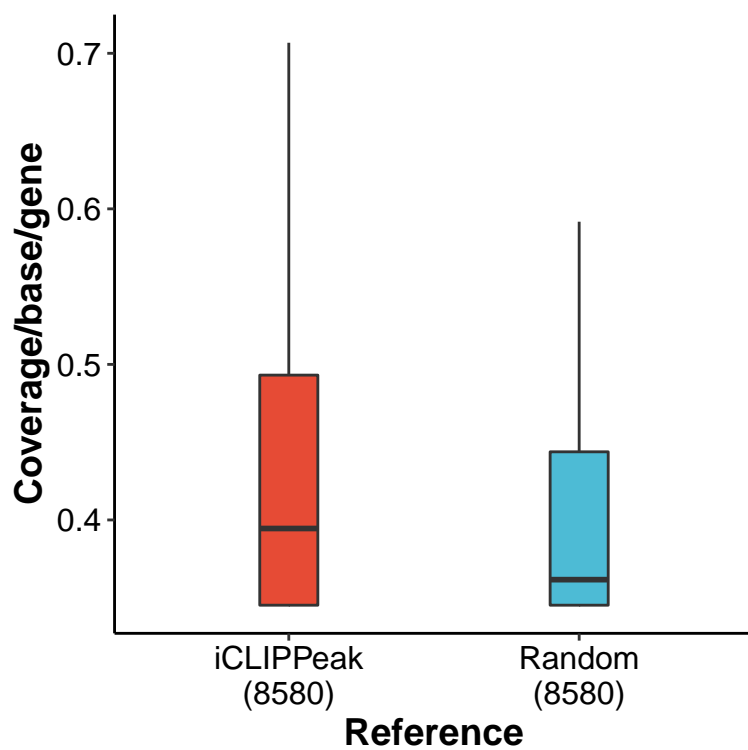
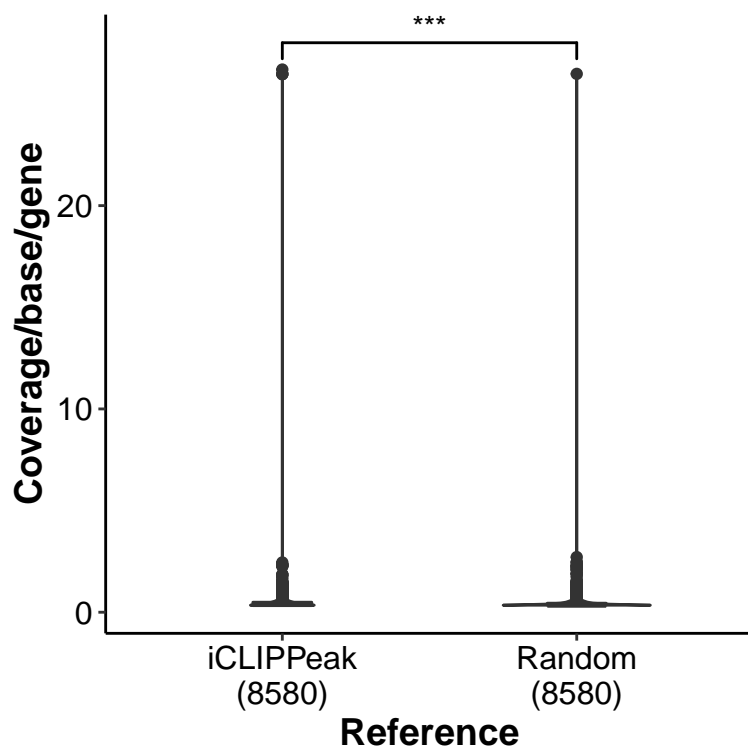


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.021	-0.029	-0.014	5.72e-08

Feature: CDS
Reference size: 8580
Sample name: clip_bam

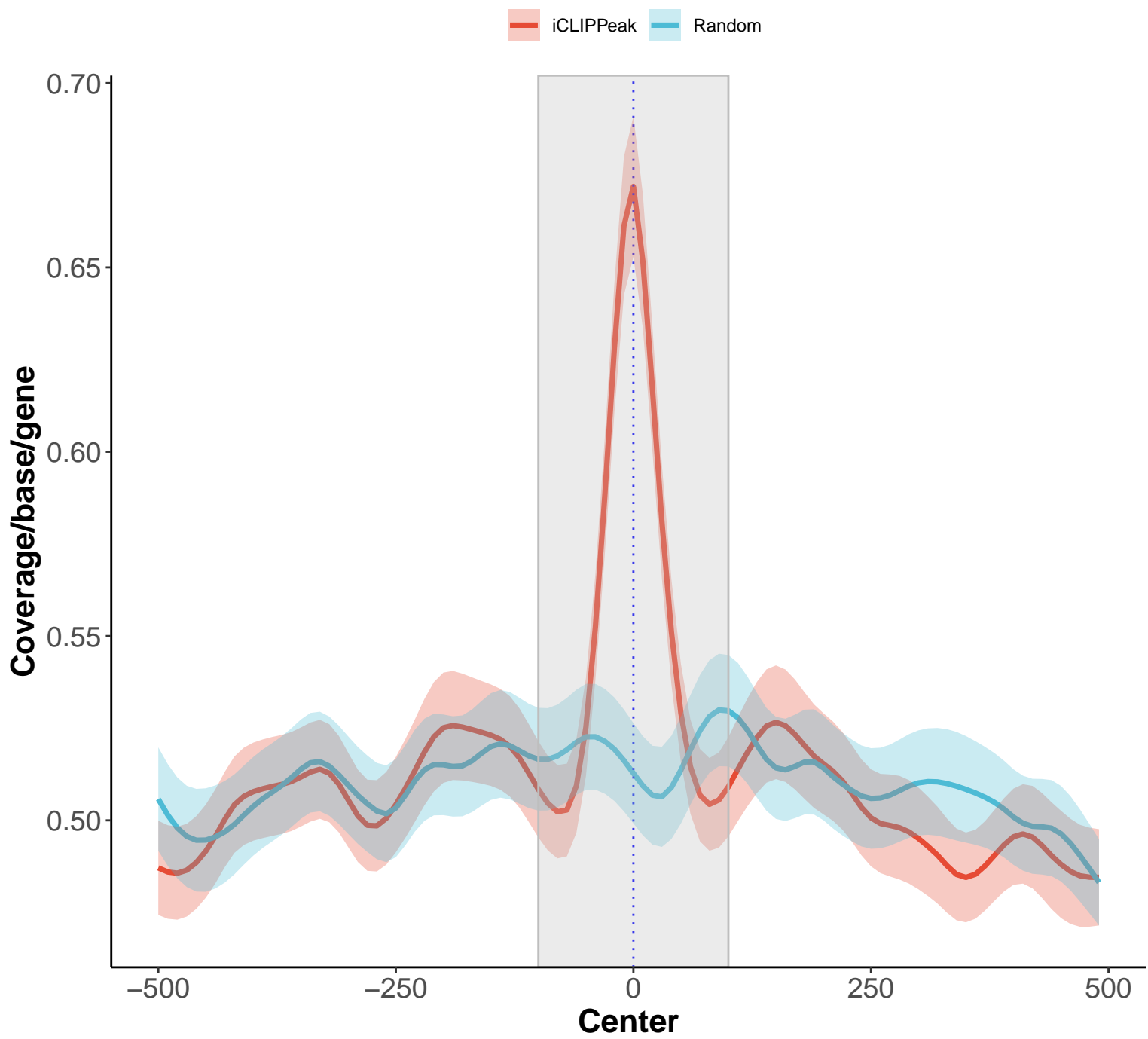


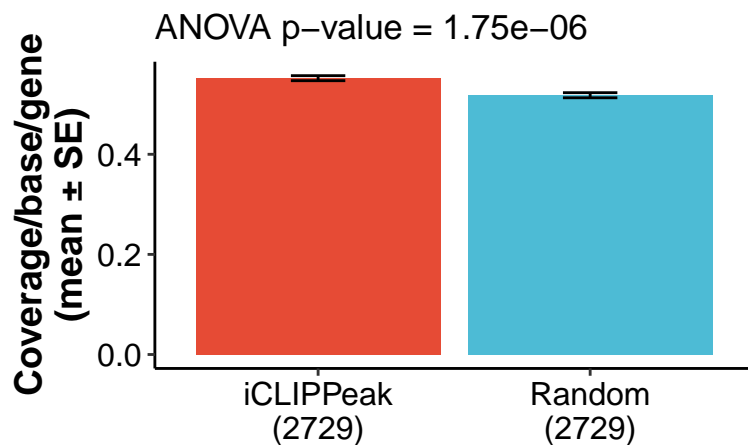
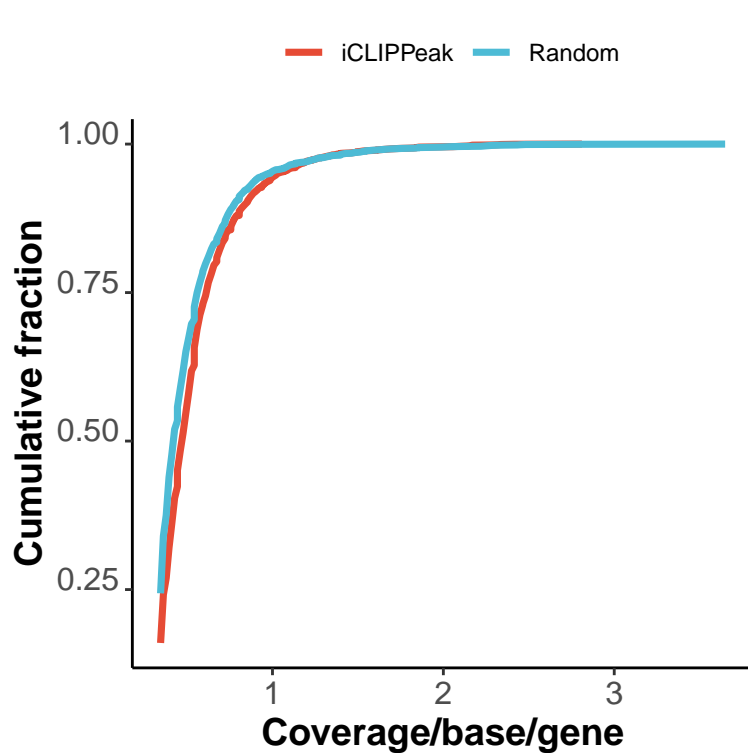
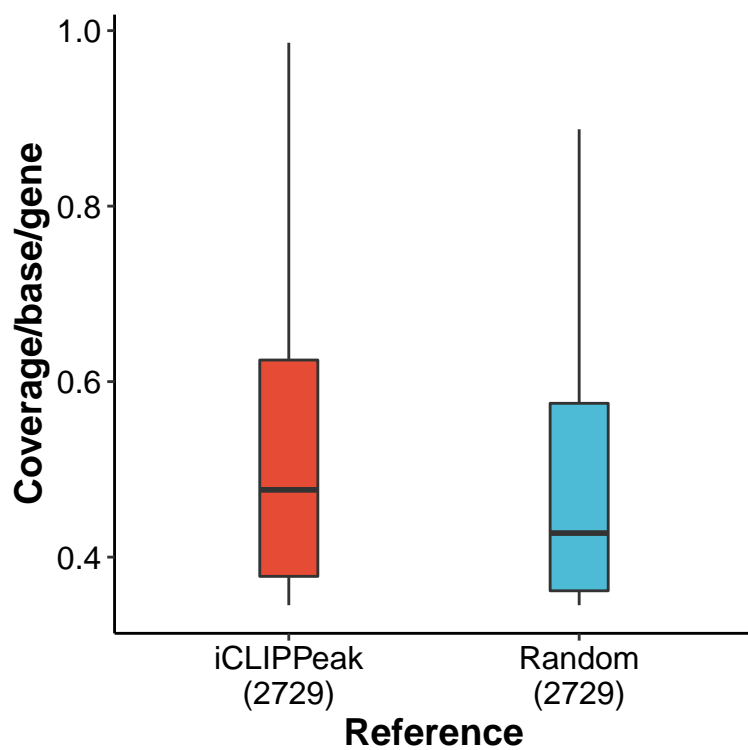
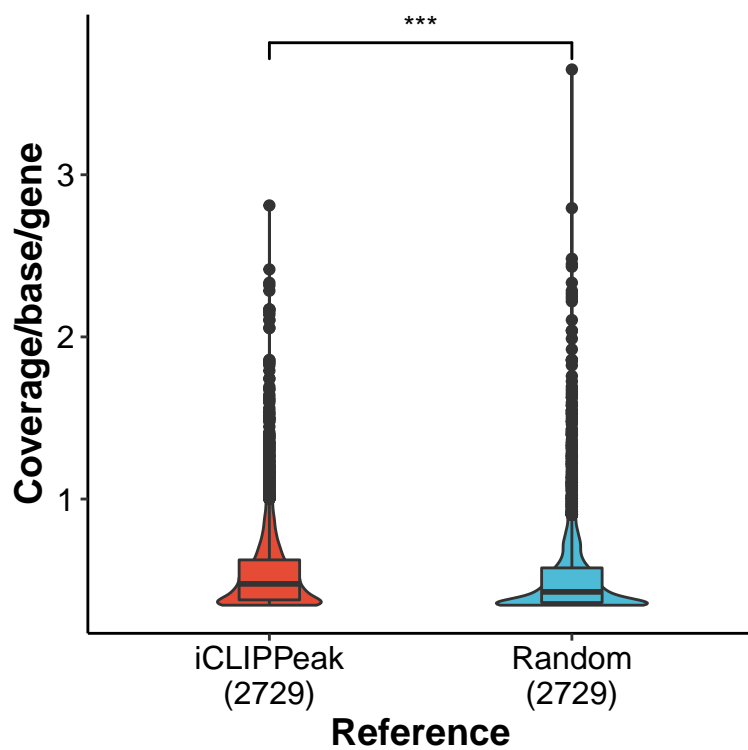


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.036	-0.051	-0.022	4e-07

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

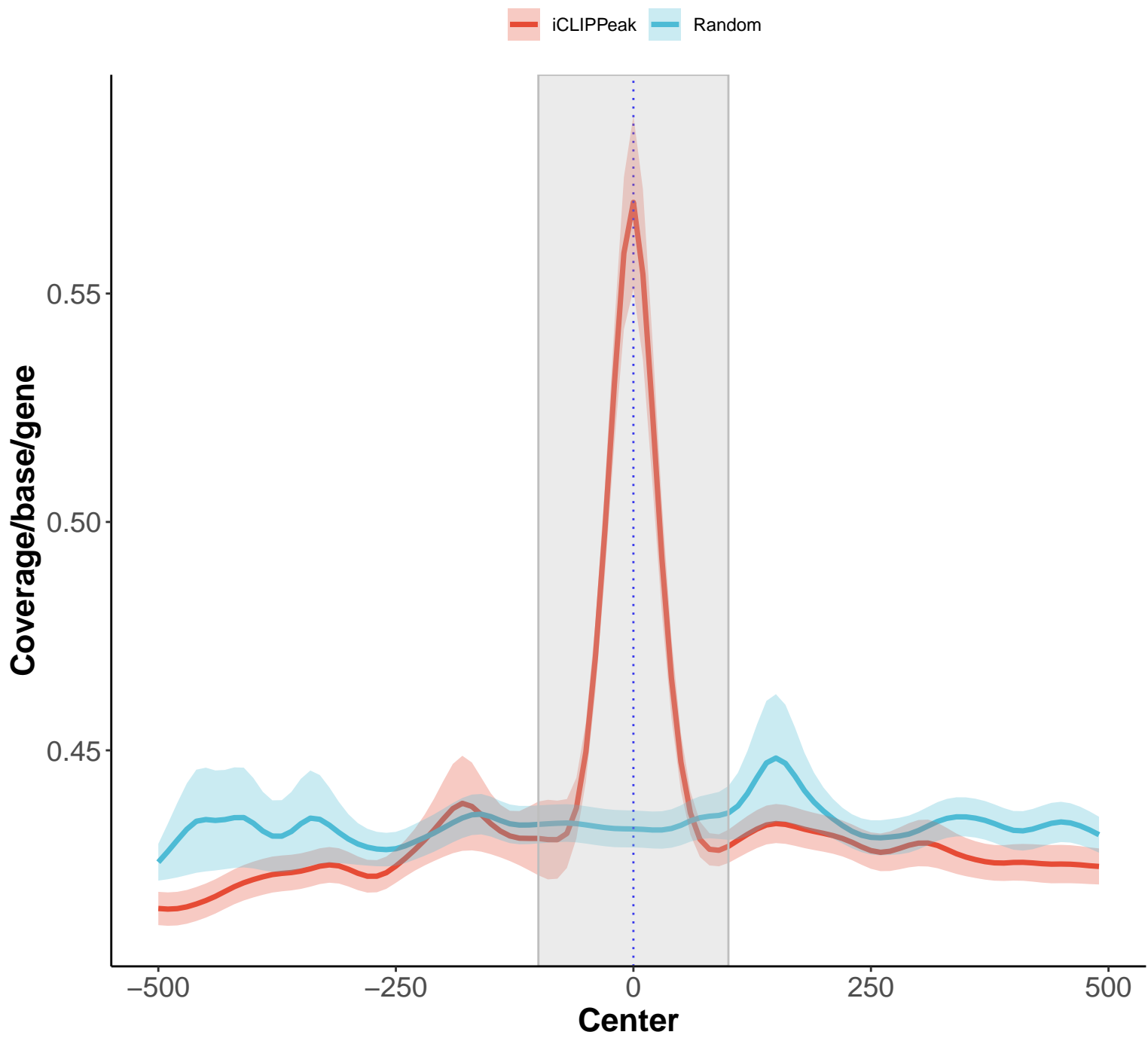


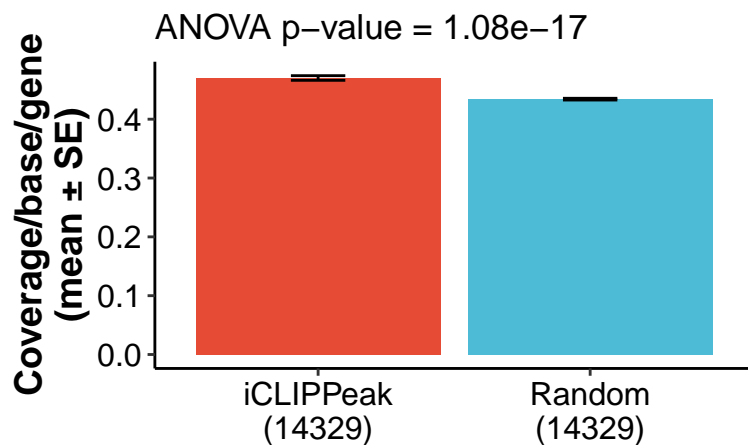
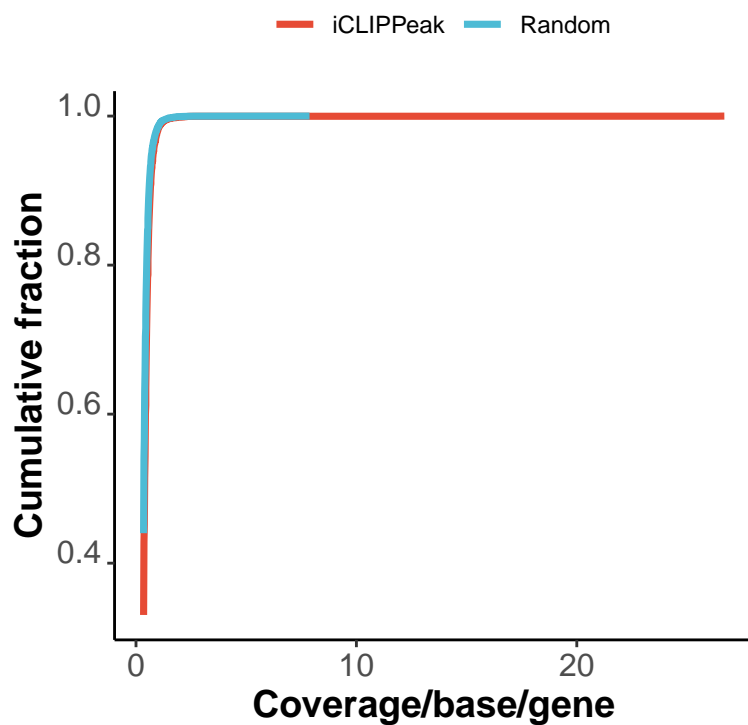
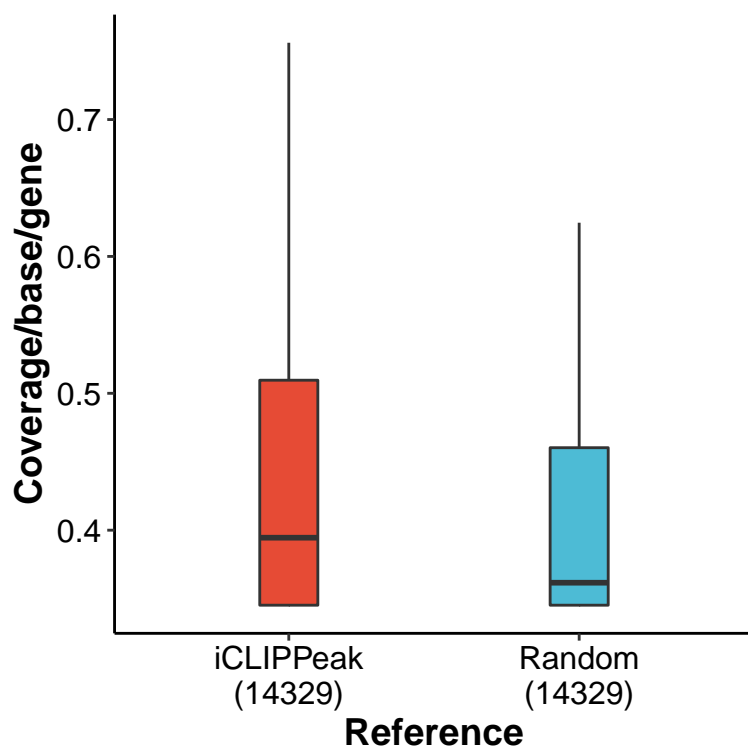
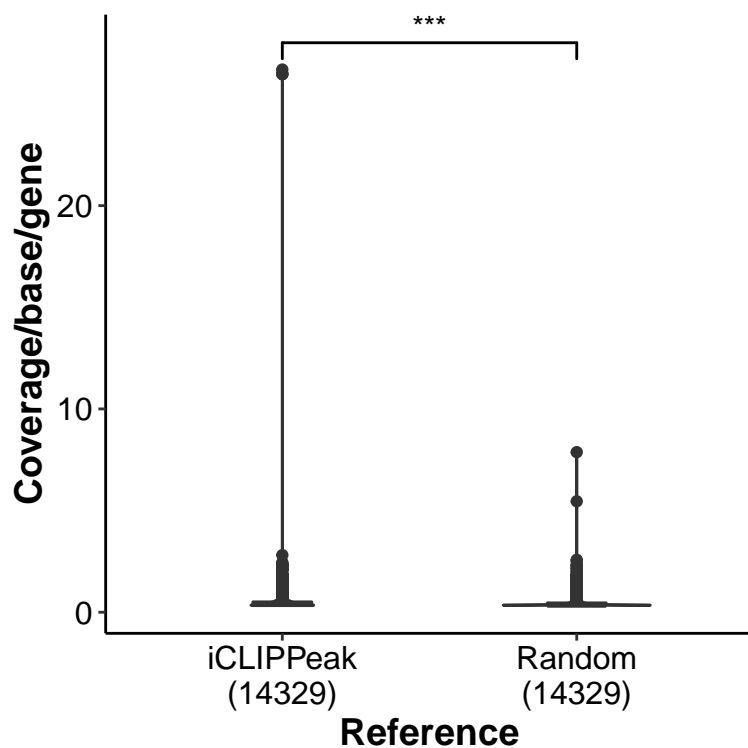


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.034	-0.048	-0.02	$1.75e-06$

Feature: Gene
Reference size: 14329
Sample name: clip_bam

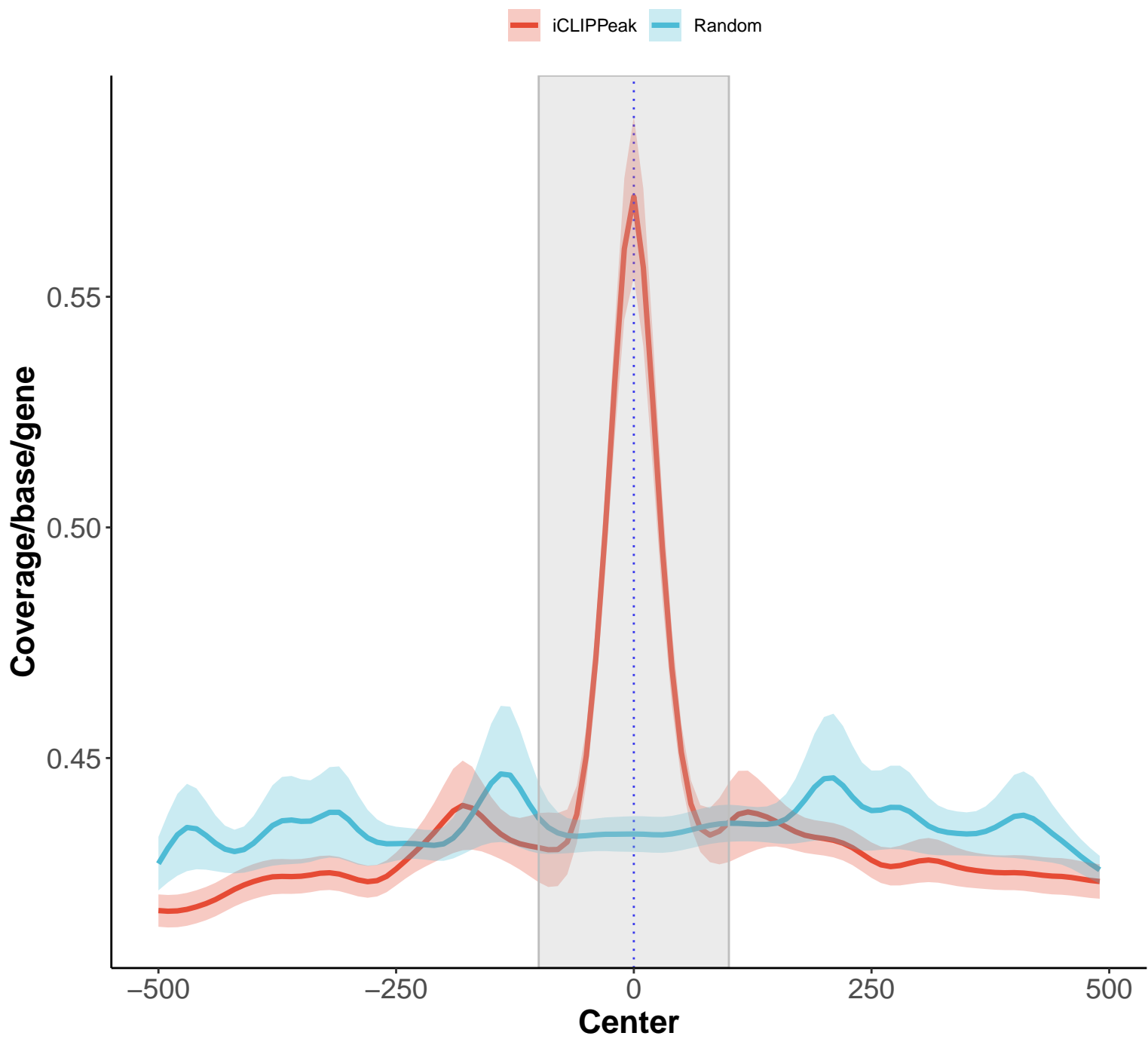


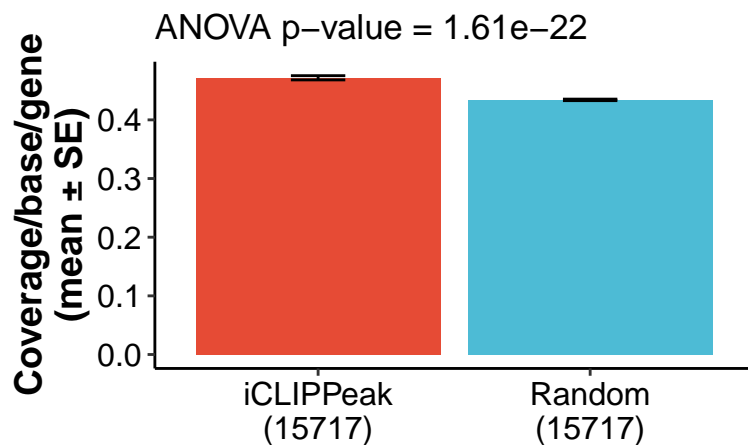
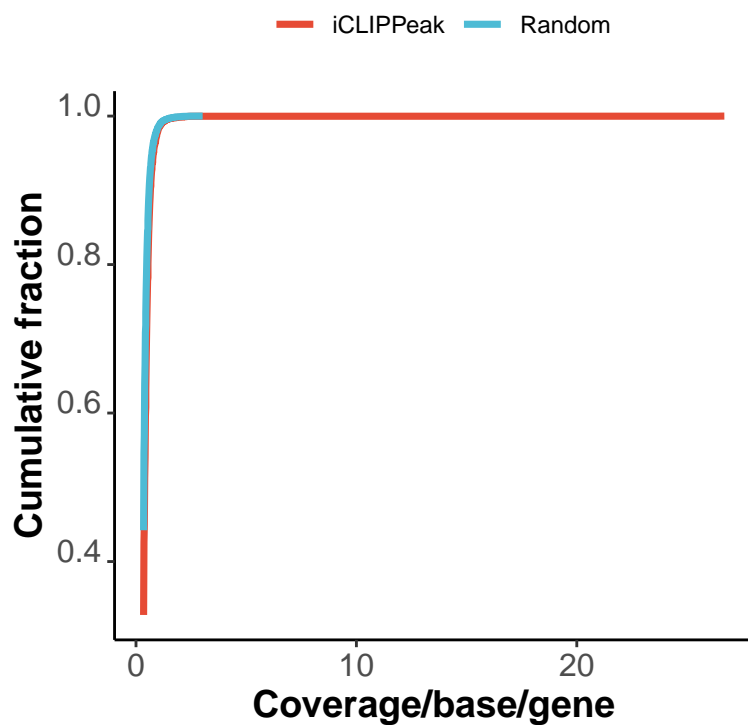
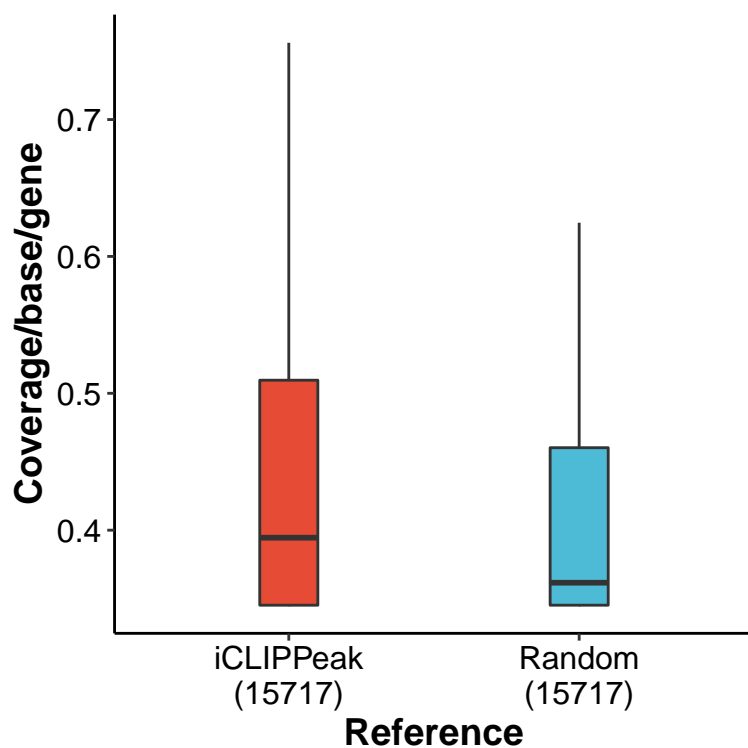
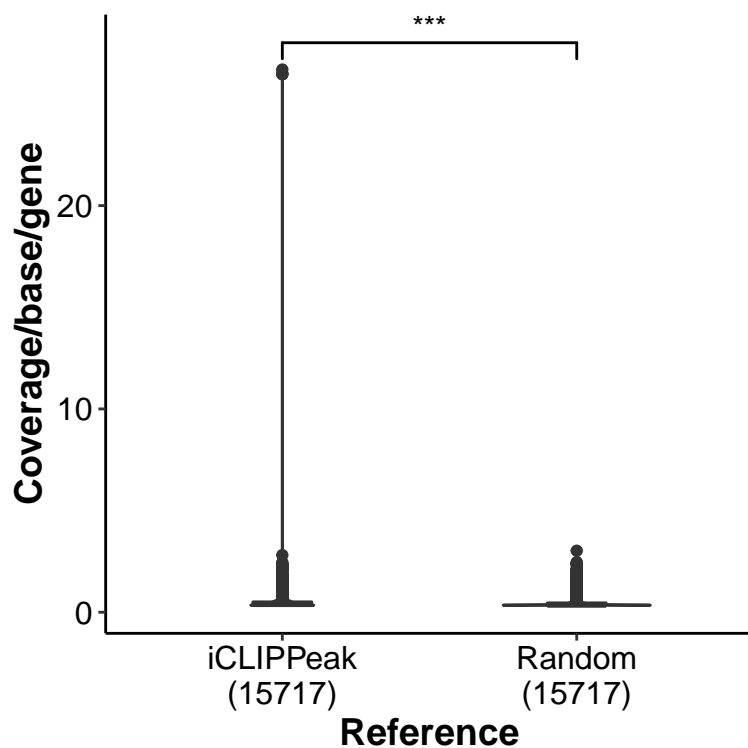


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.036	-0.044	-0.028	1.82e-14

Feature: unrestricted
Reference size: 15717
Sample name: clip_bam

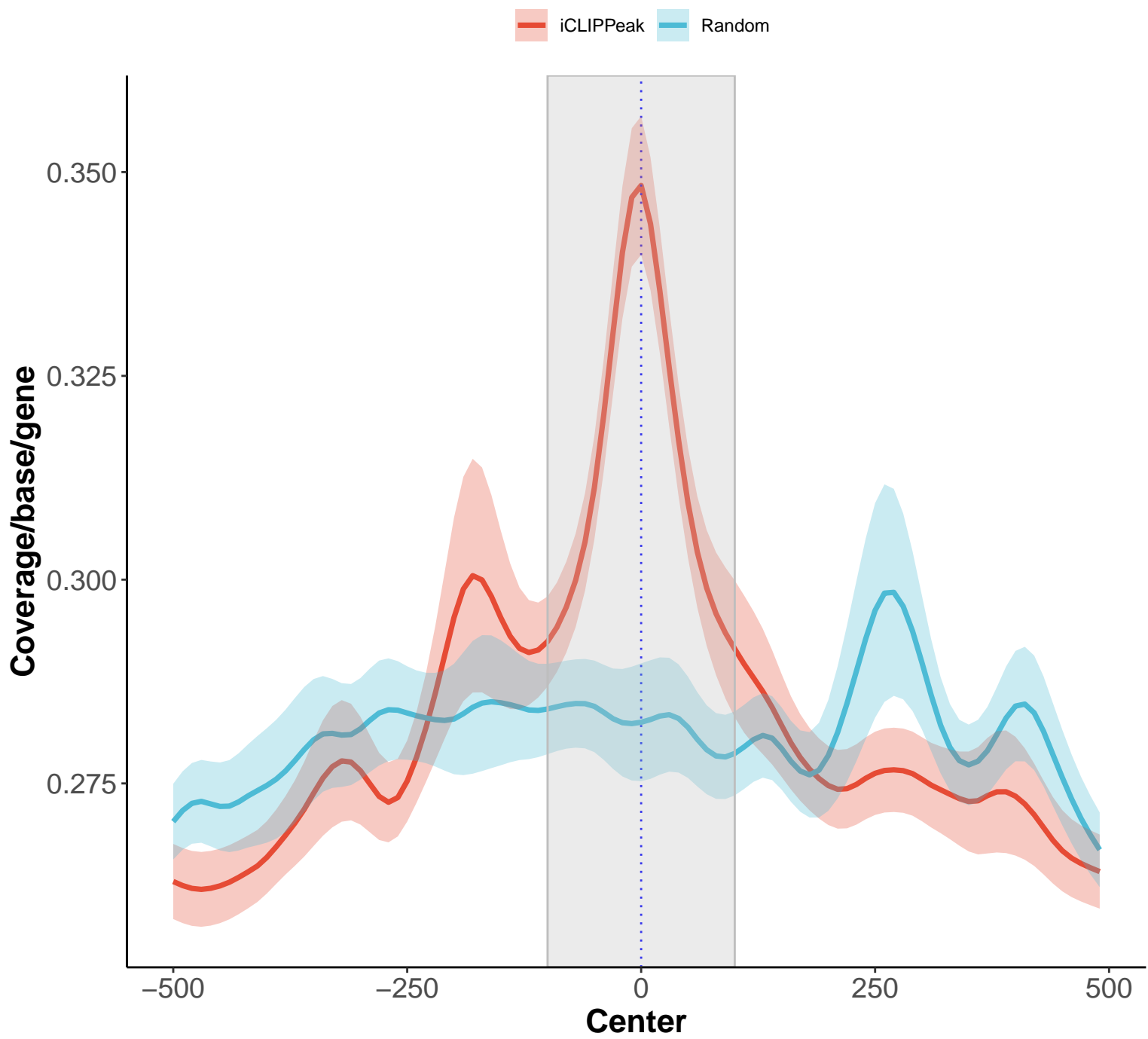


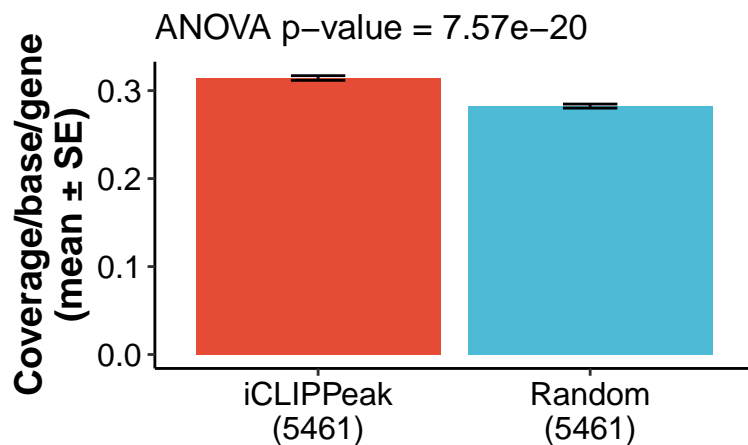
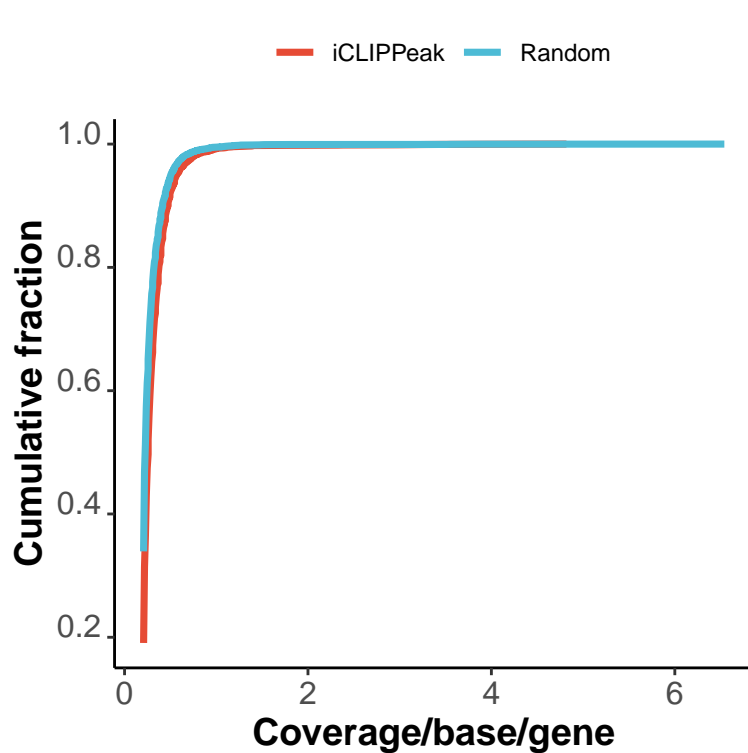
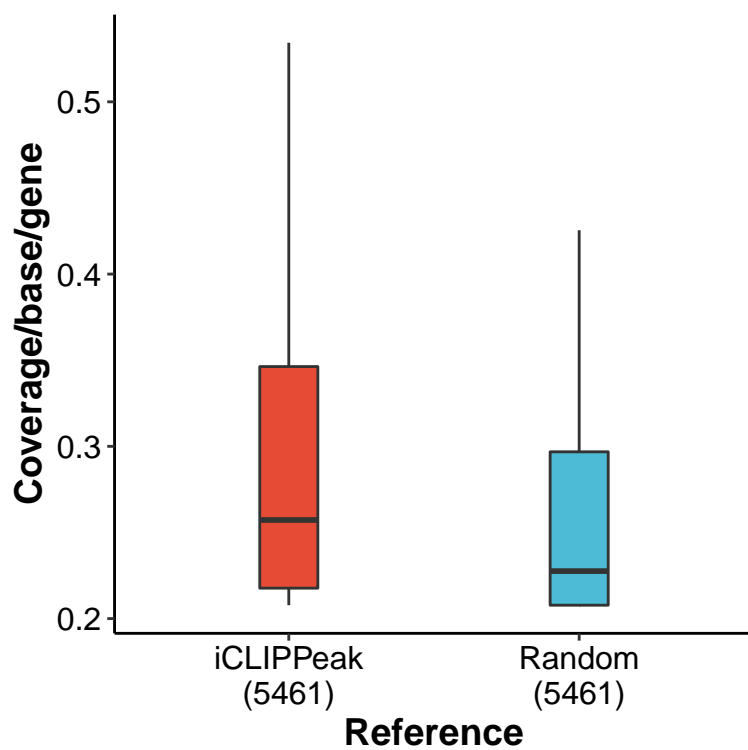
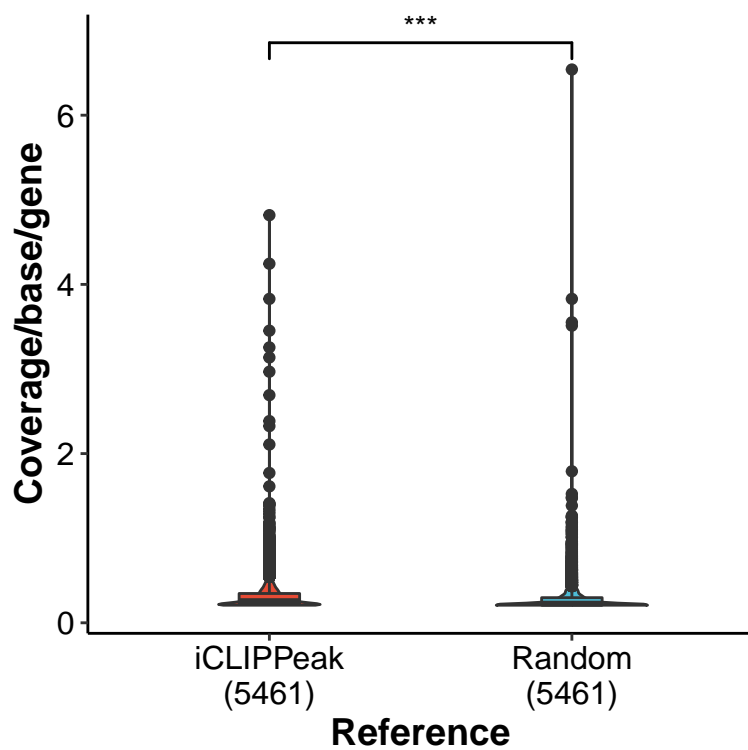


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.038	-0.045	-0.03	2.19e-14

Feature: Transcript
Reference size: 5461
Sample name: clip_input

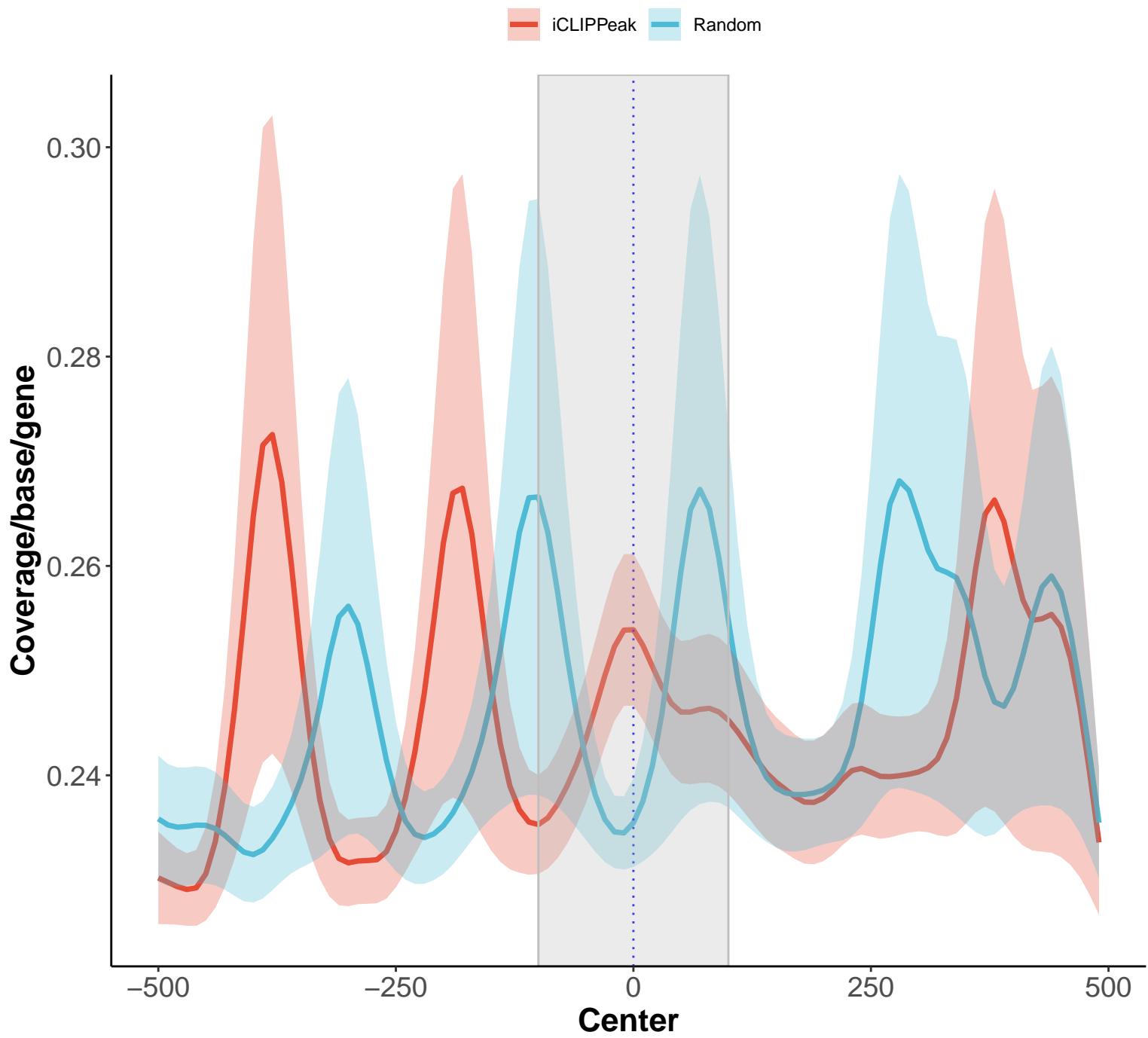


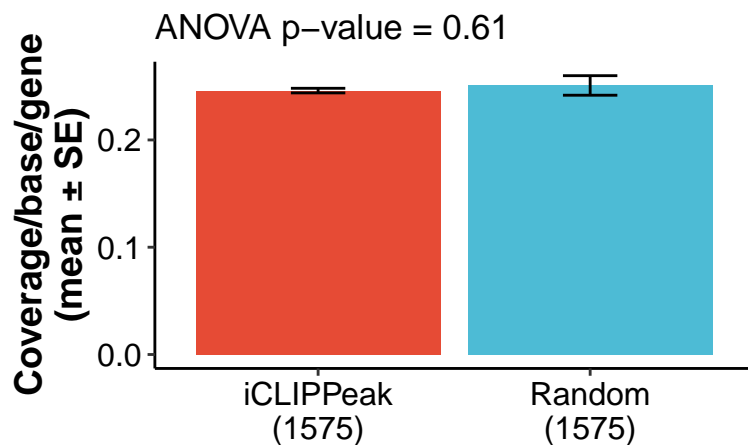
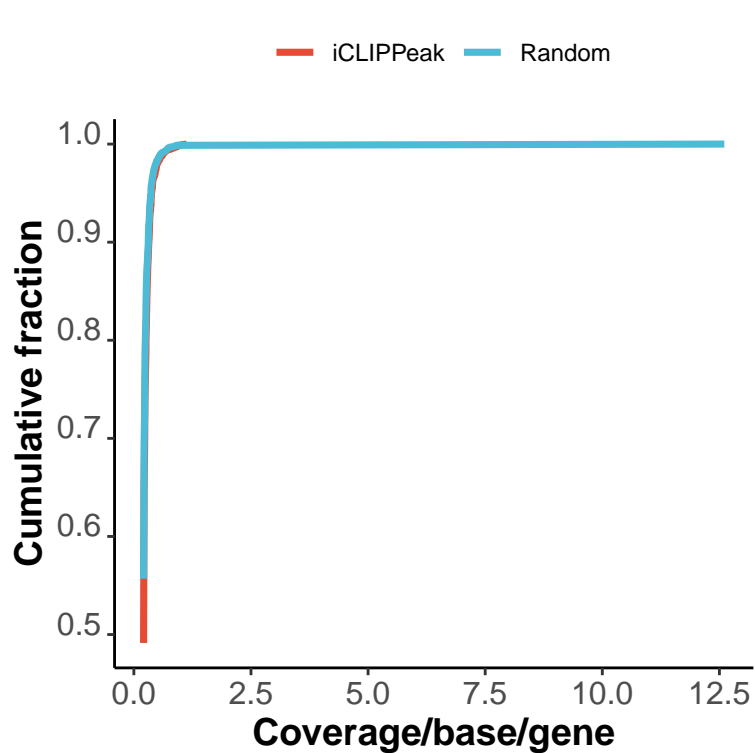
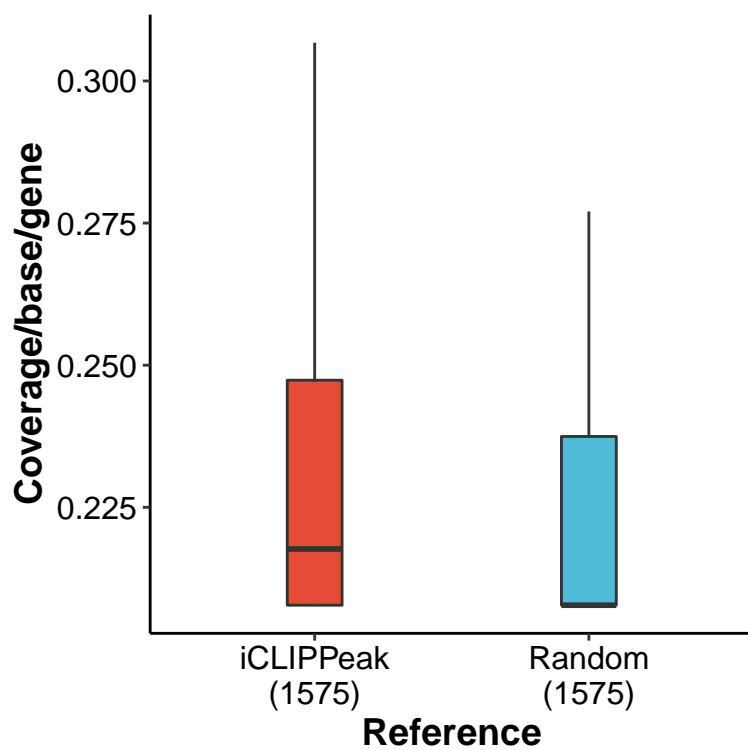
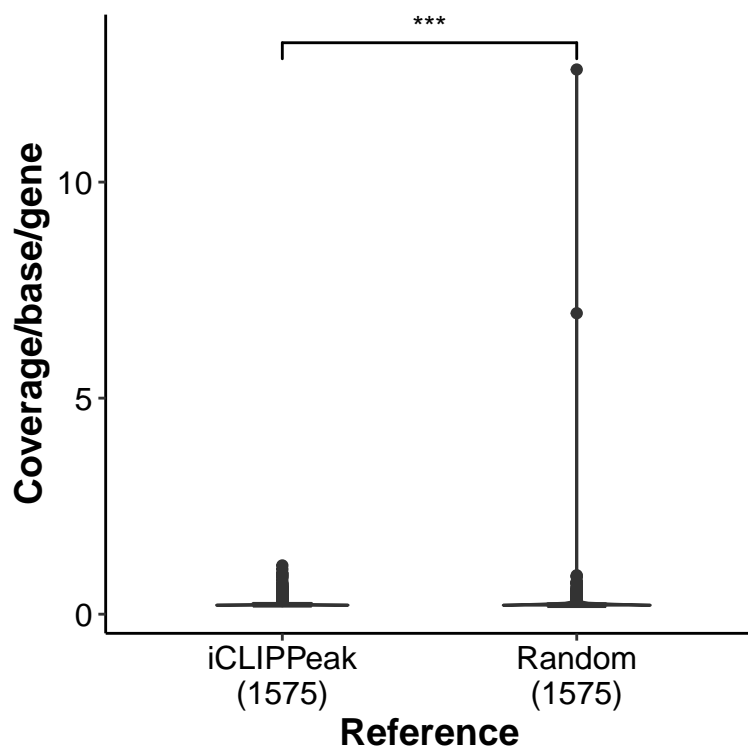


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.032	-0.039	-0.025	0

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

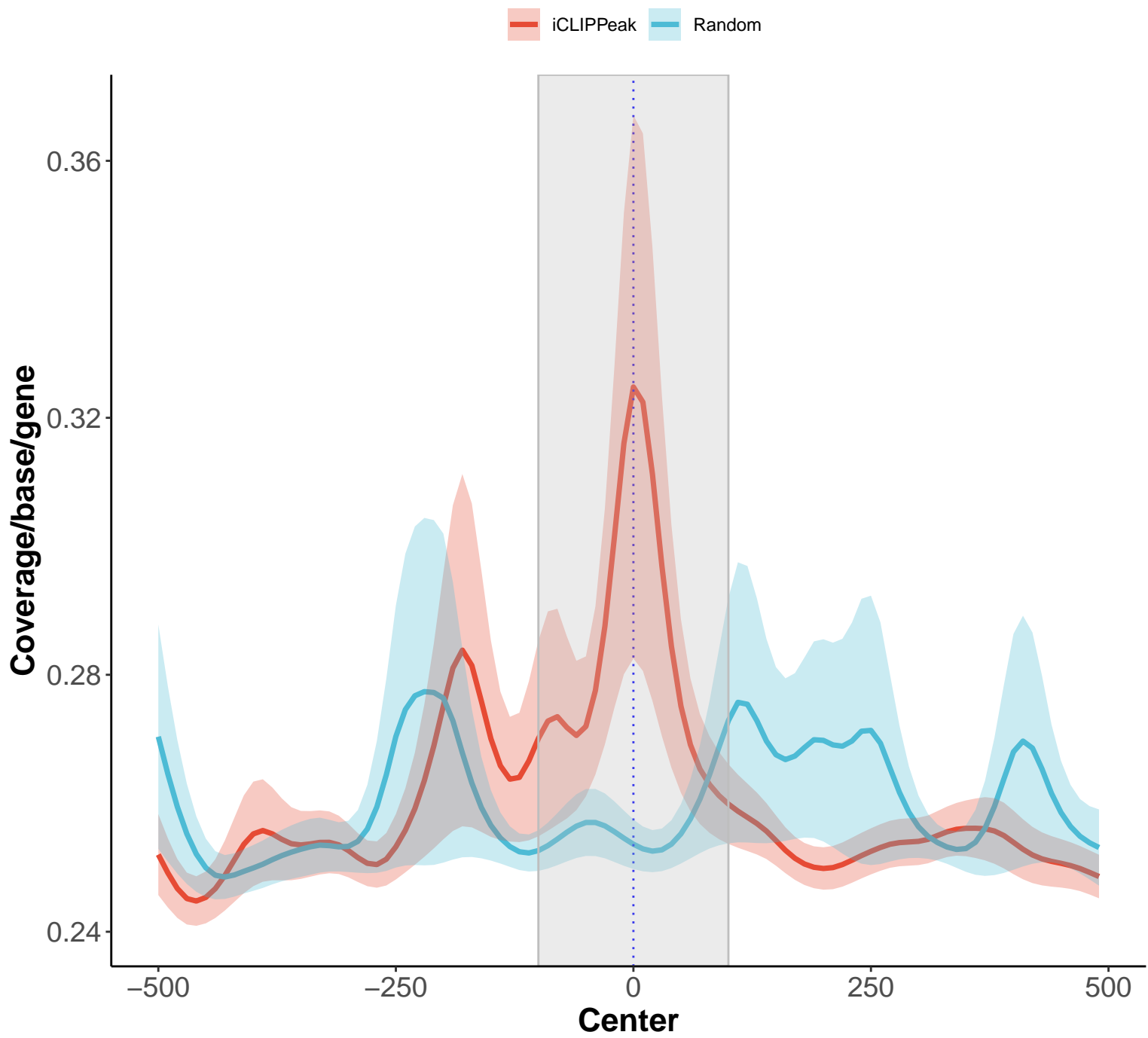


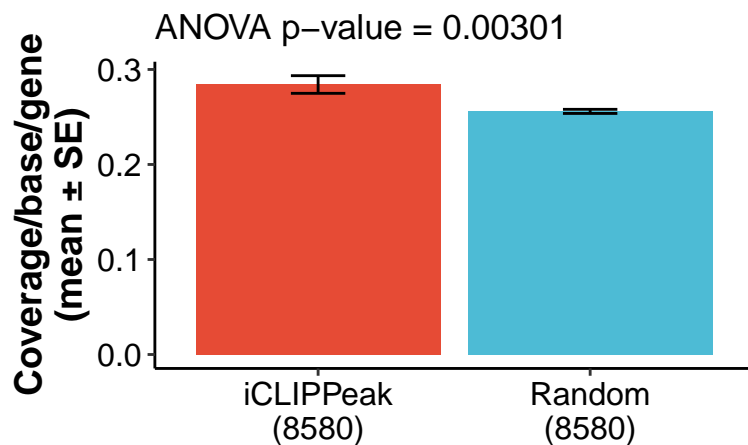
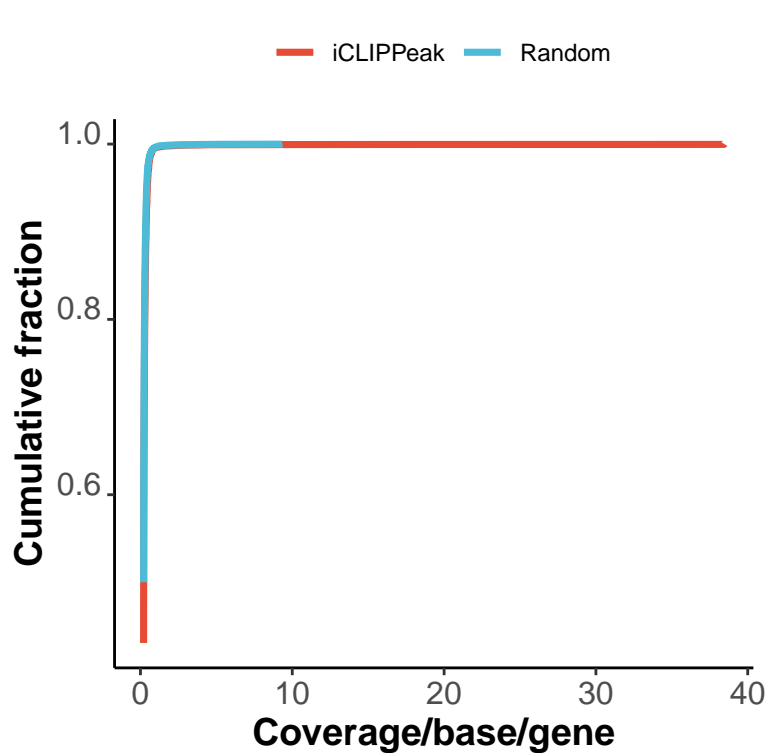
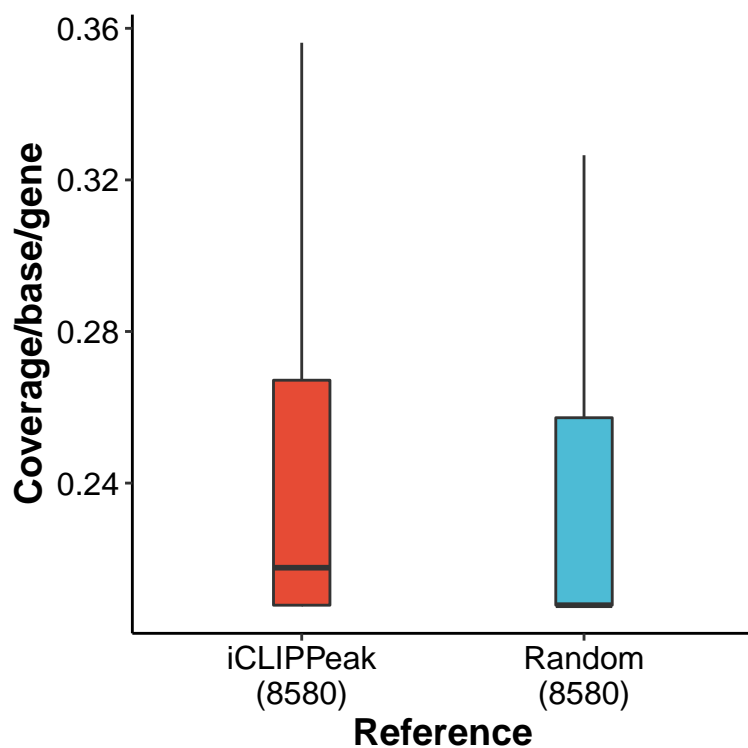
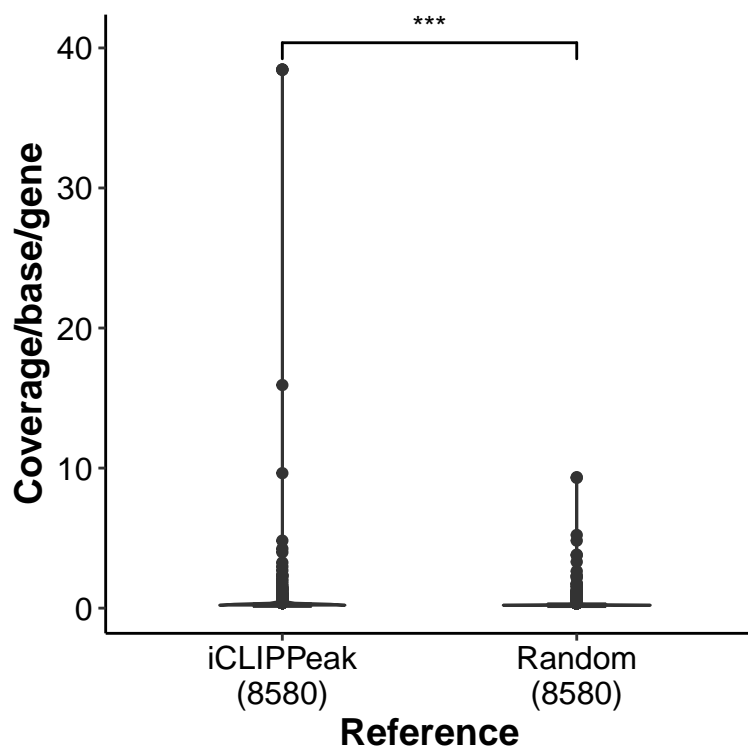


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	0.005	-0.014	0.023	0.61

Feature: CDS
Reference size: 8580
Sample name: clip_input

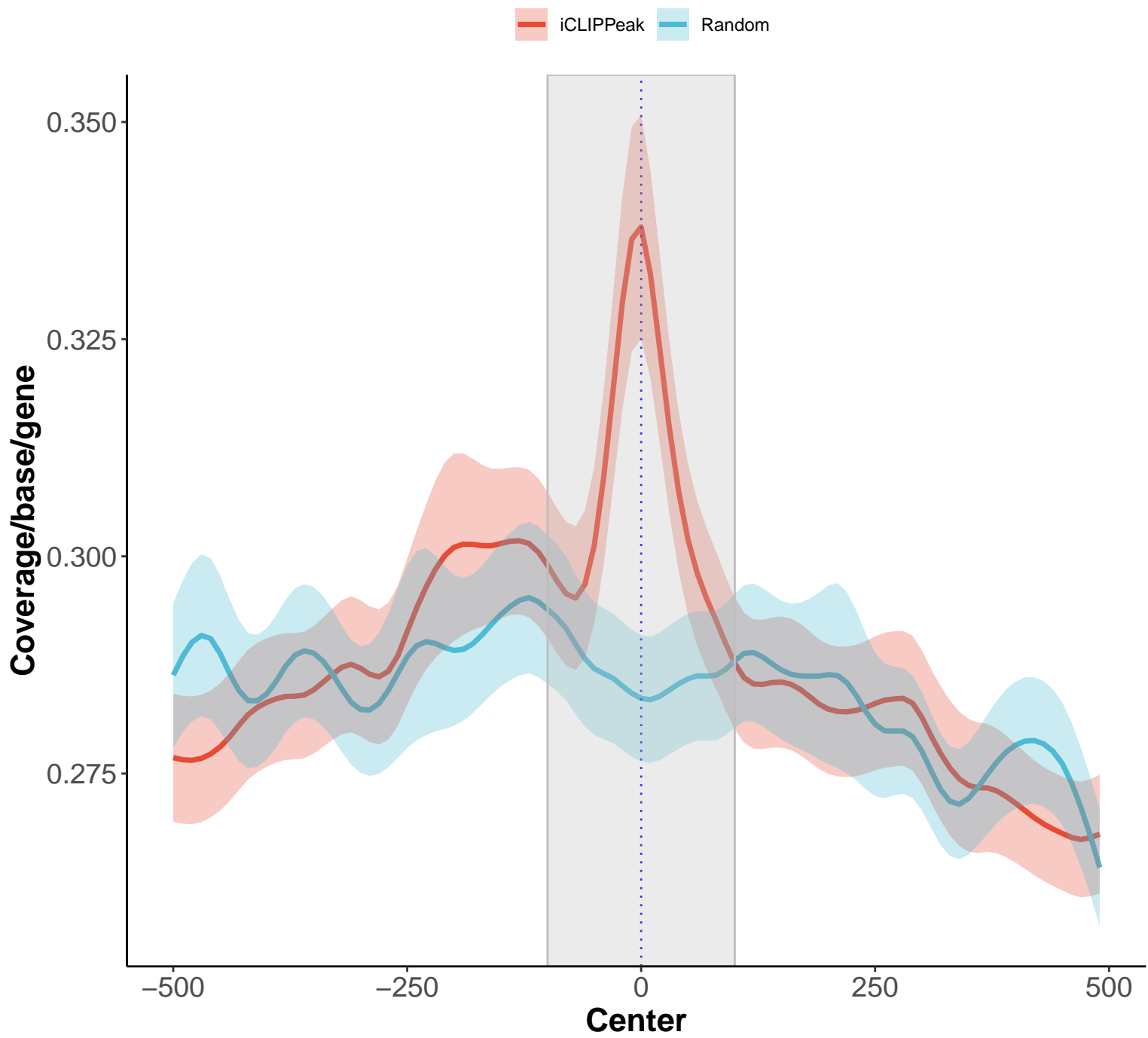


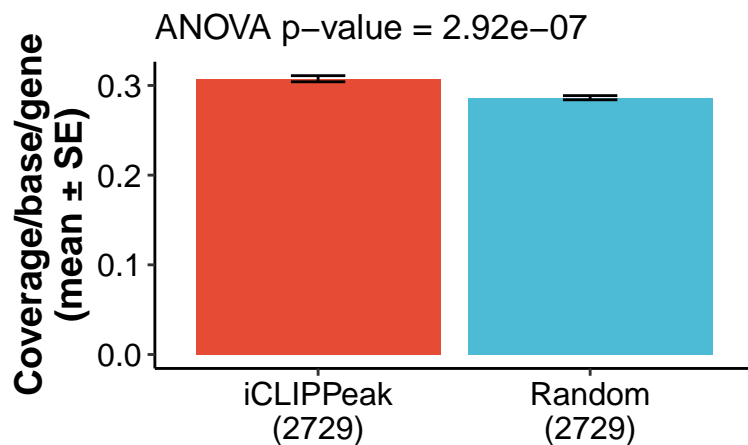
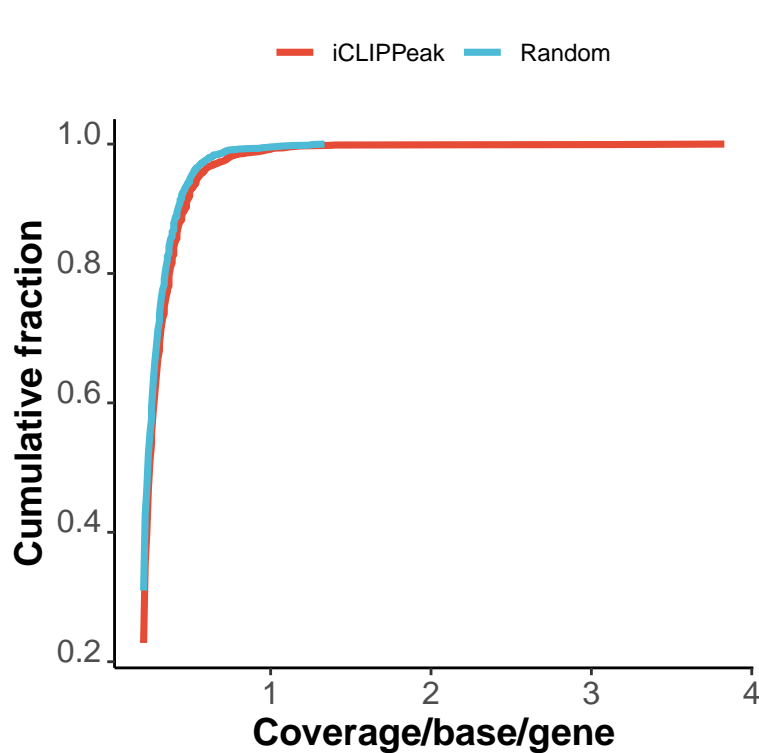
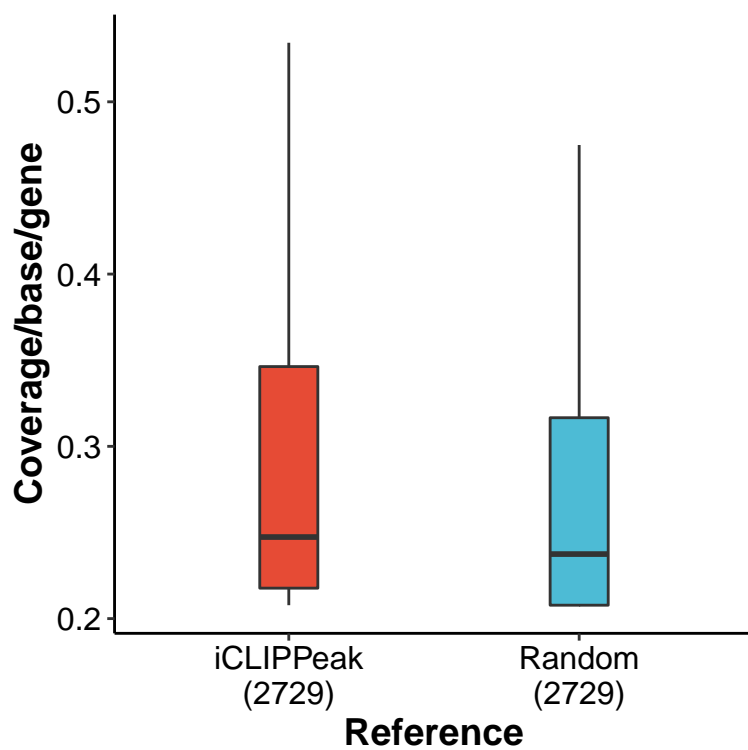
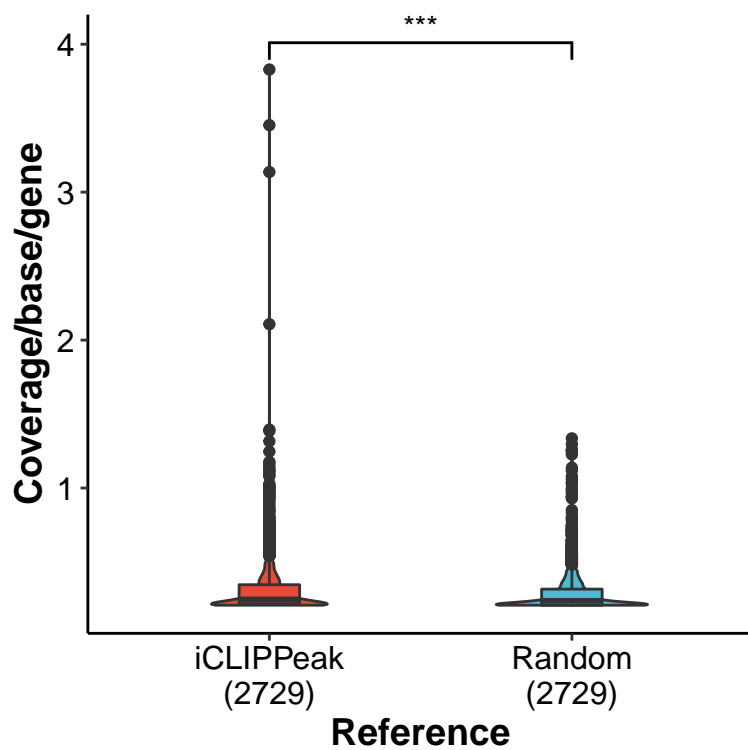


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.028	-0.047	-0.01	0.00301

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

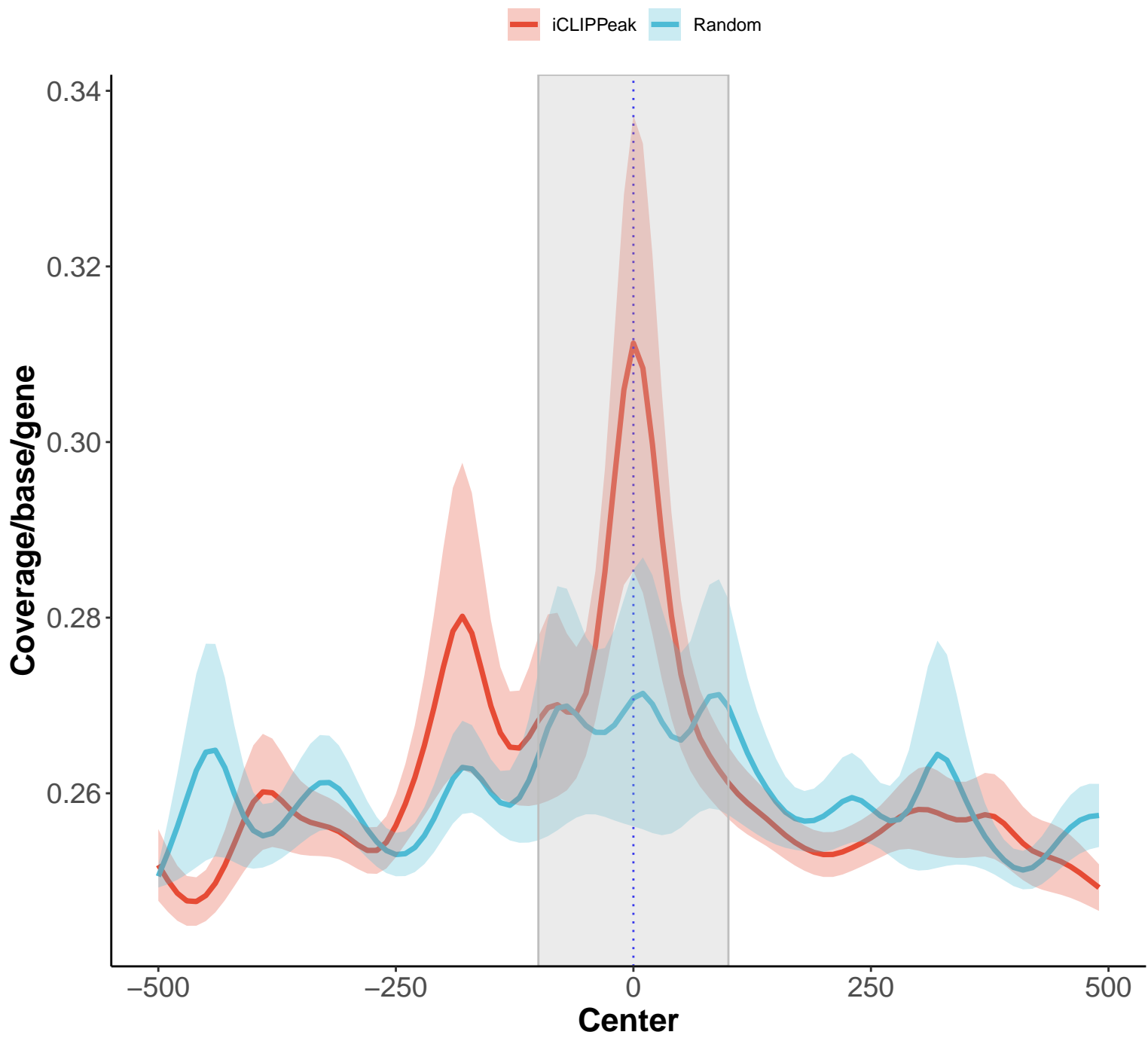


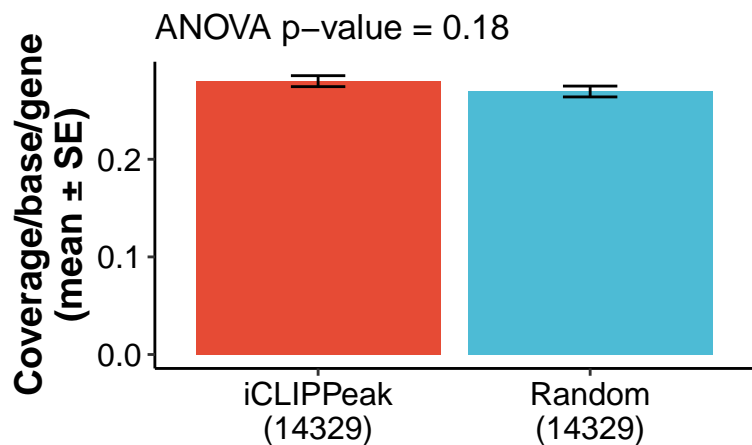
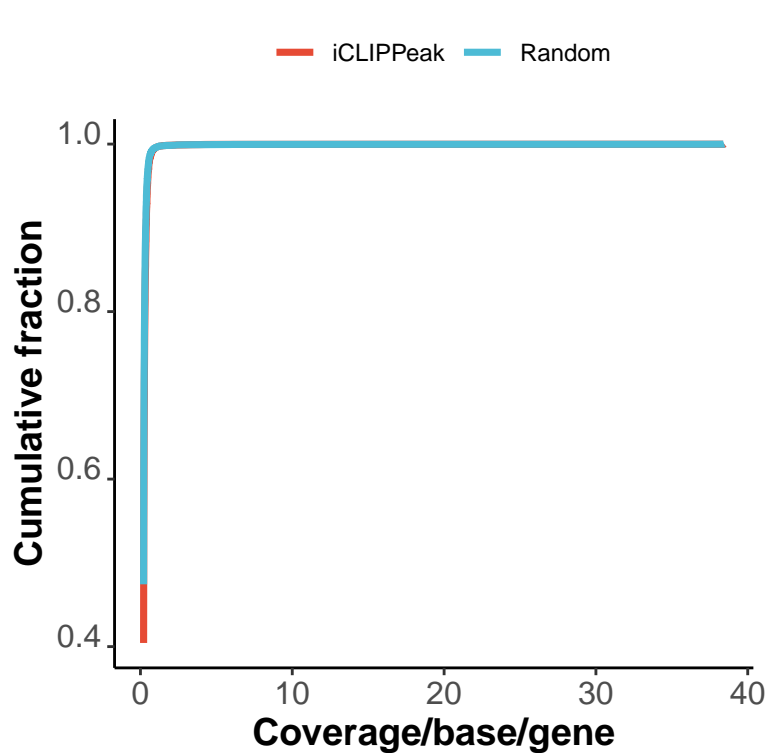
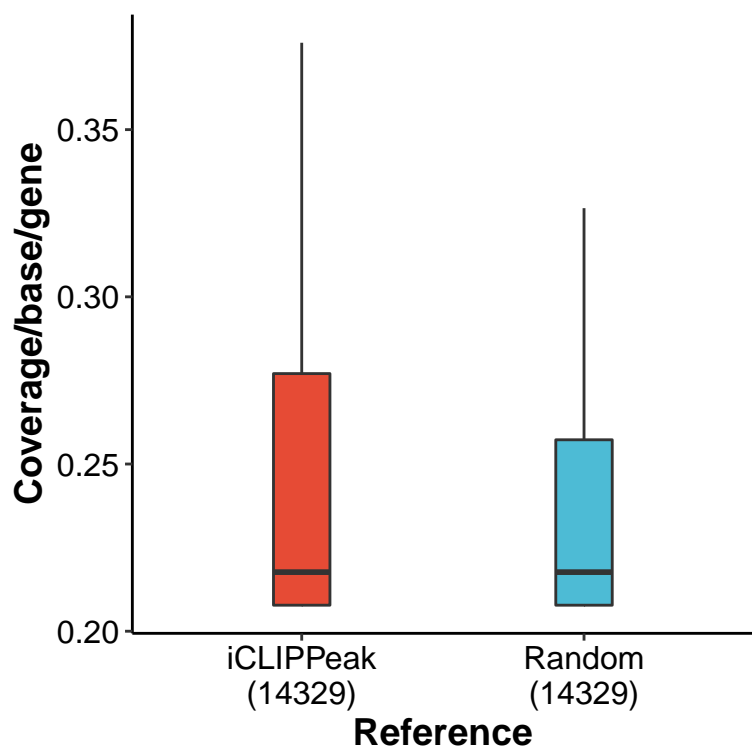
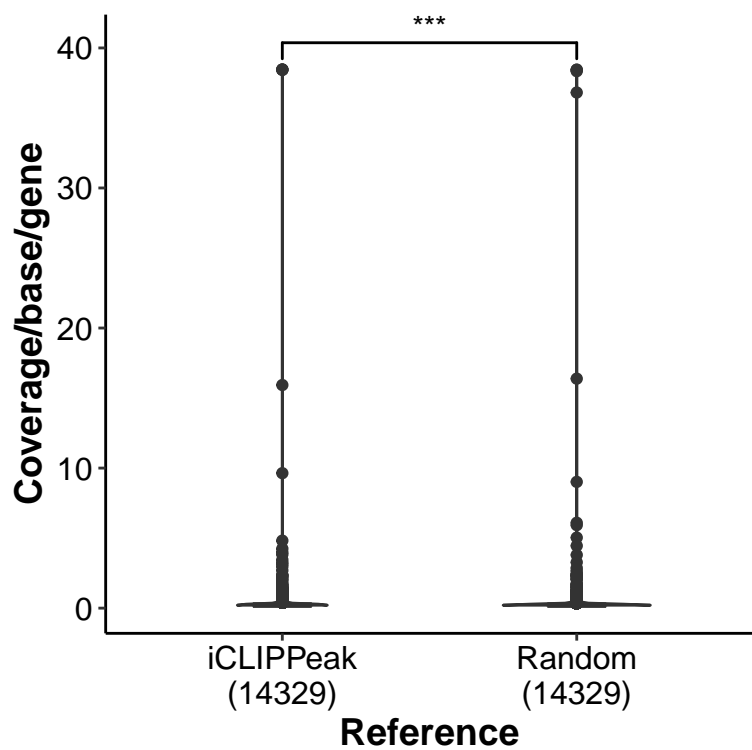


post hoc TukeyHSD test

	diff	lwr	upr	p adj
<i>Random-iCLIPPeak</i>	-0.021	-0.029	-0.013	2.92×10^{-7}

Feature: Gene
Reference size: 14329
Sample name: clip_input

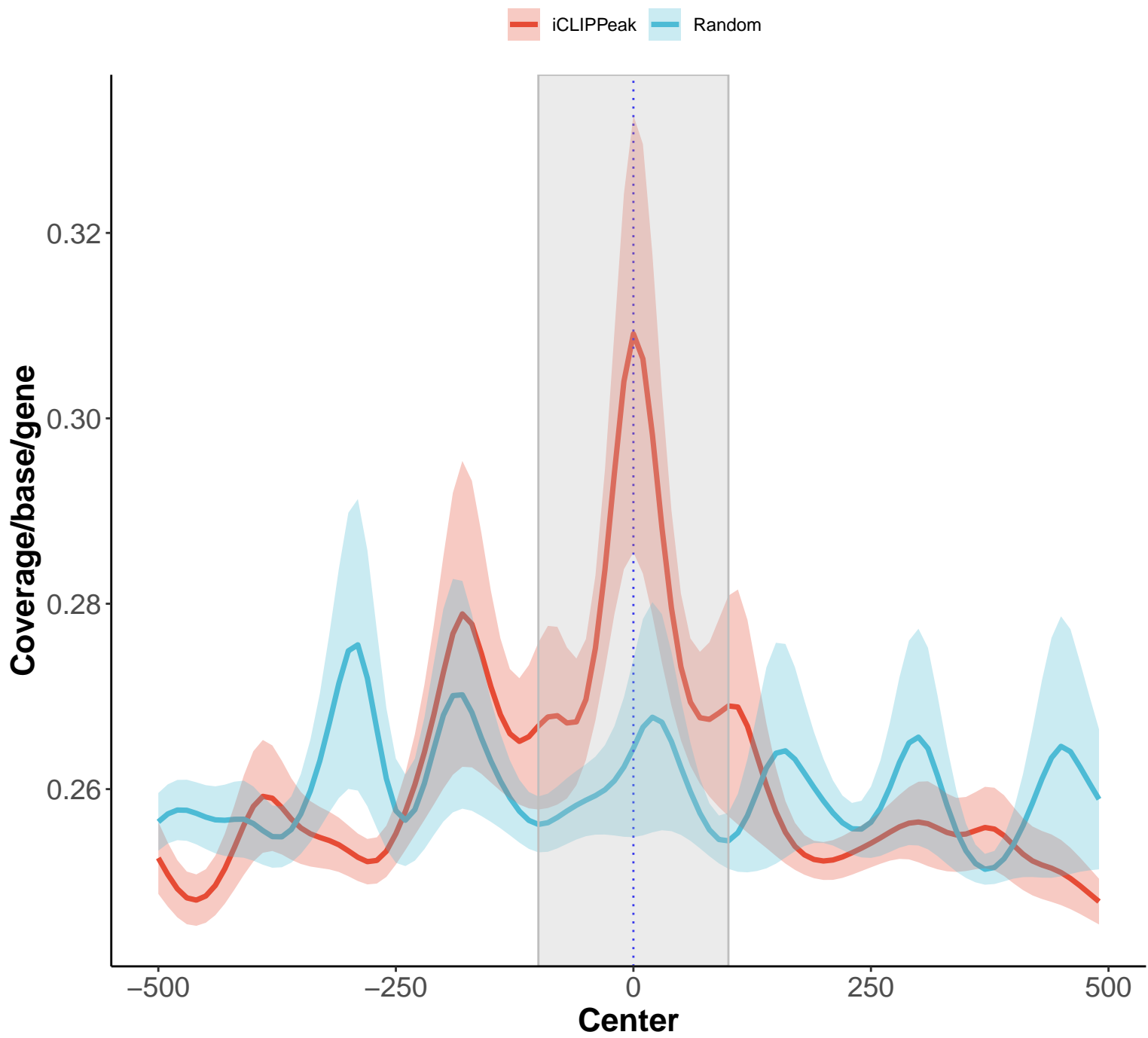


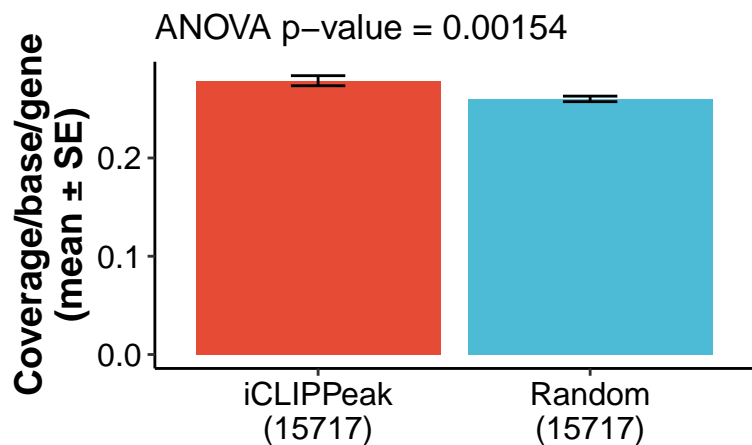
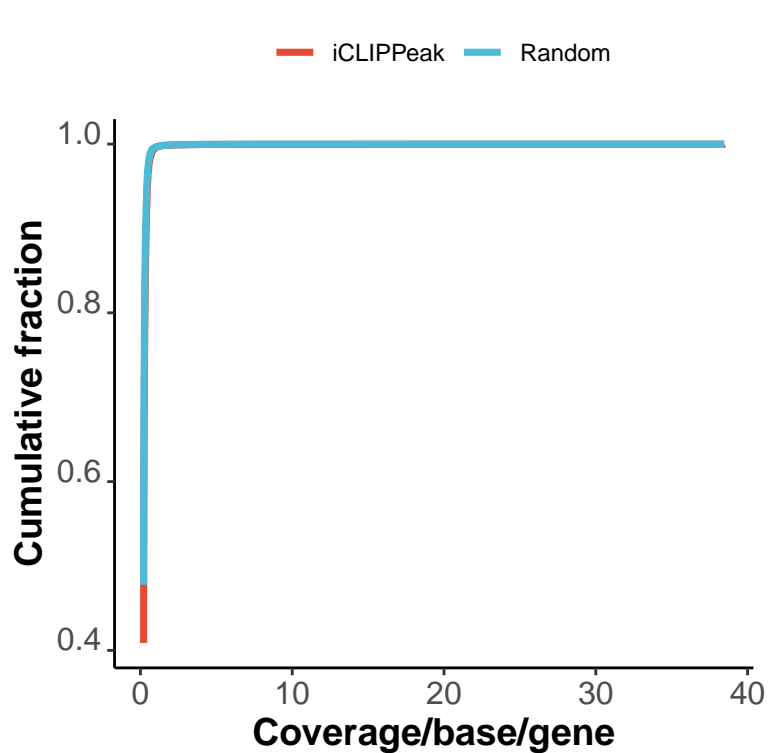
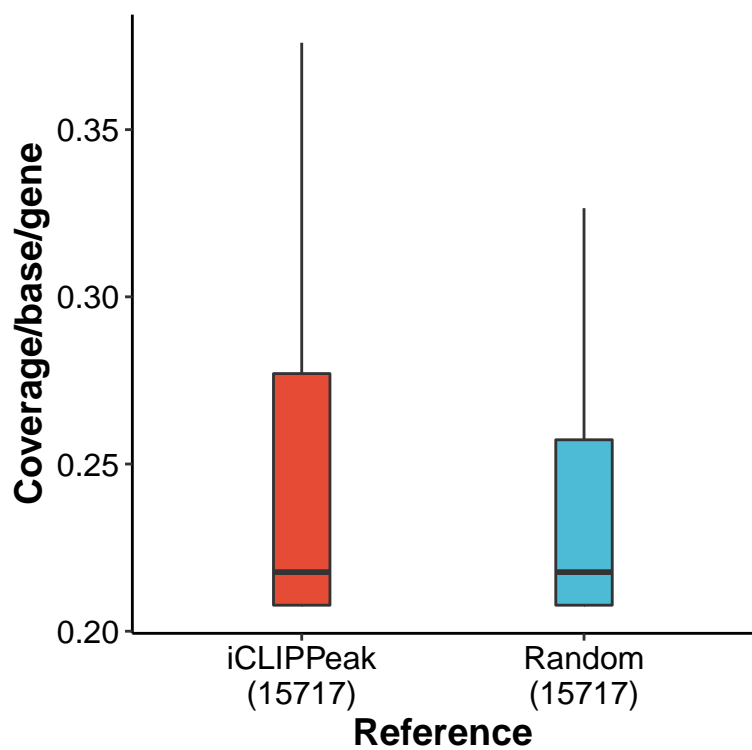
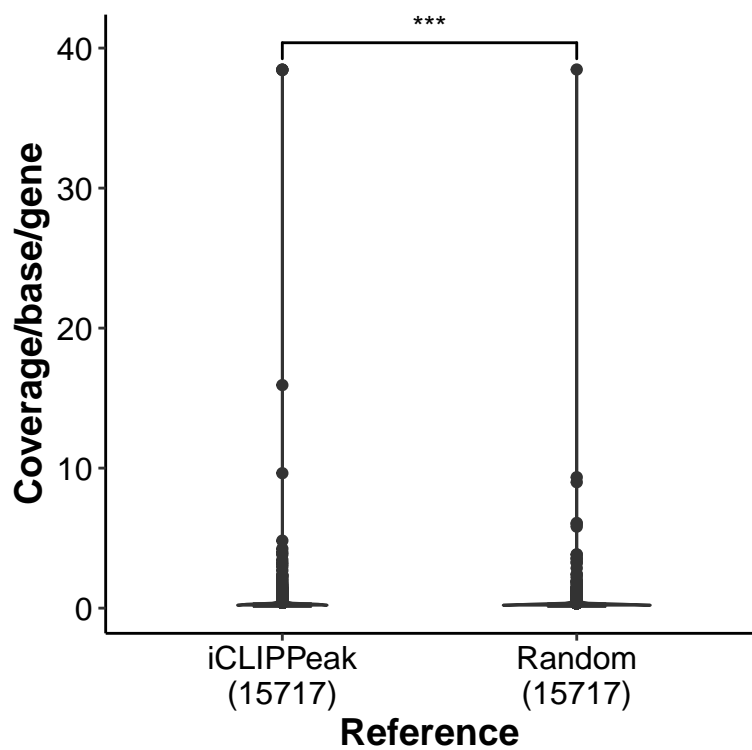


post hoc TukeyHSD test

	diff	lwr	upr	p adj
<i>Random-iCLIPPeak</i>	-0.011	-0.026	0.005	0.18

Feature: unrestricted
Reference size: 15717
Sample name: clip_input

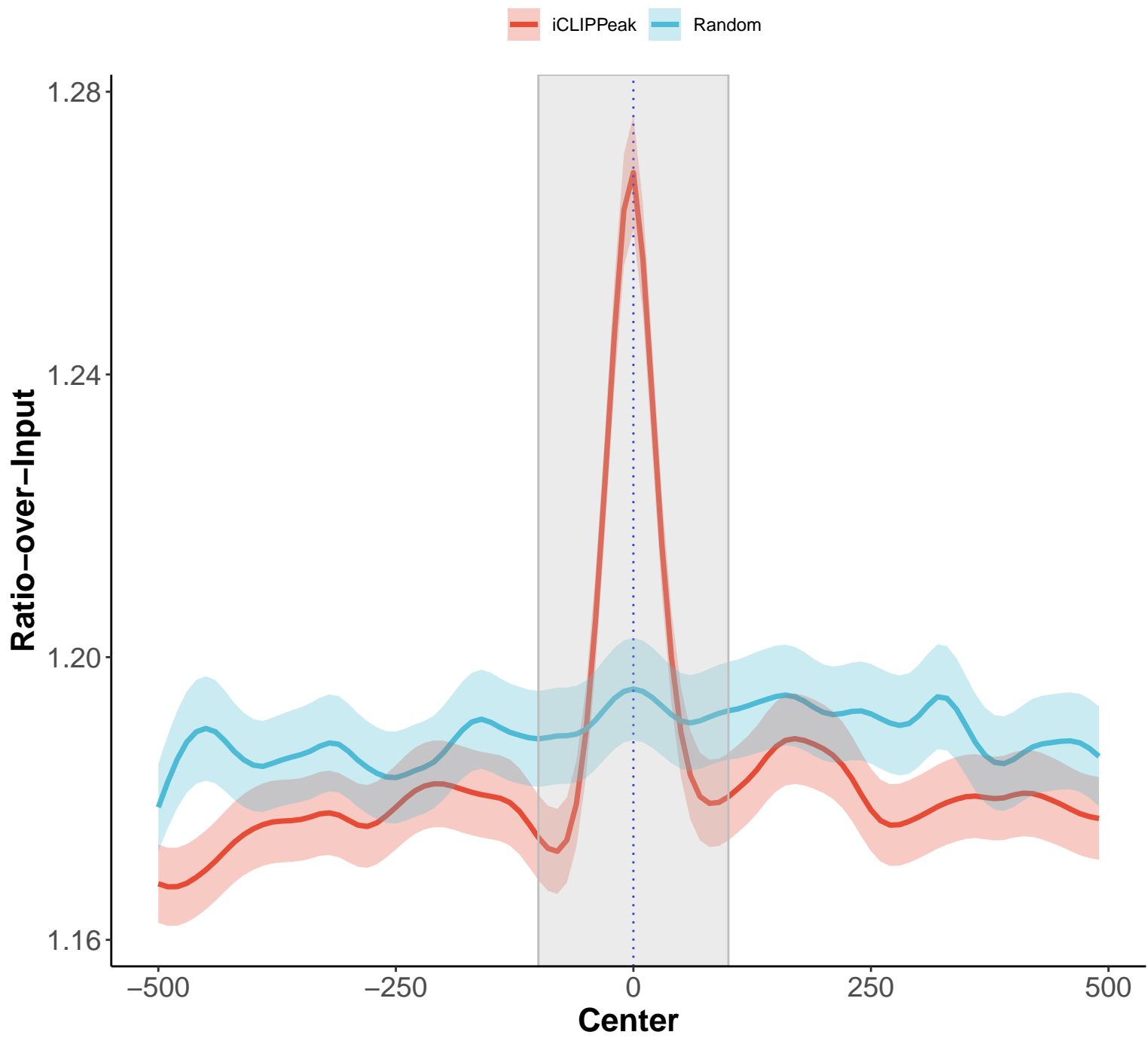


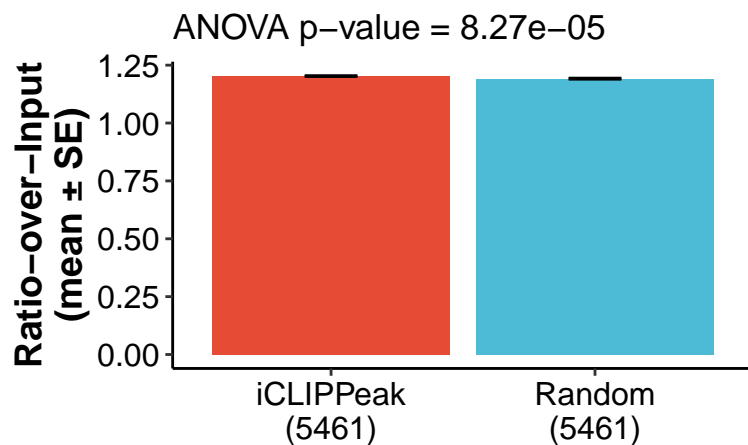
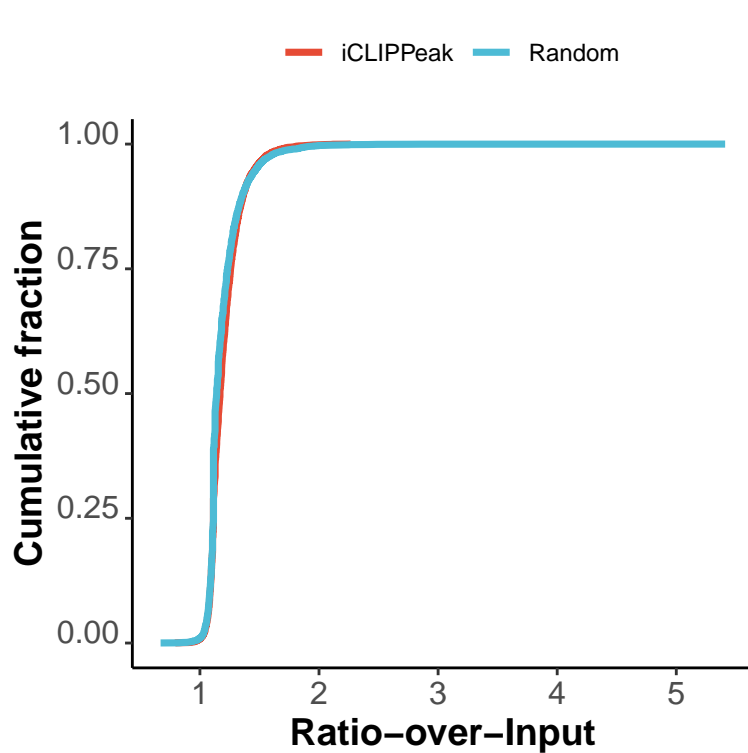
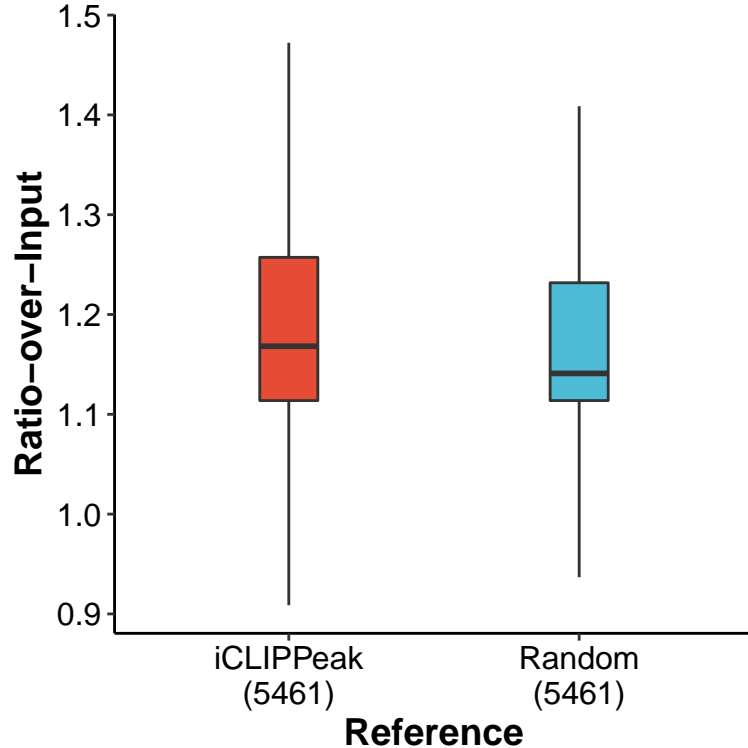
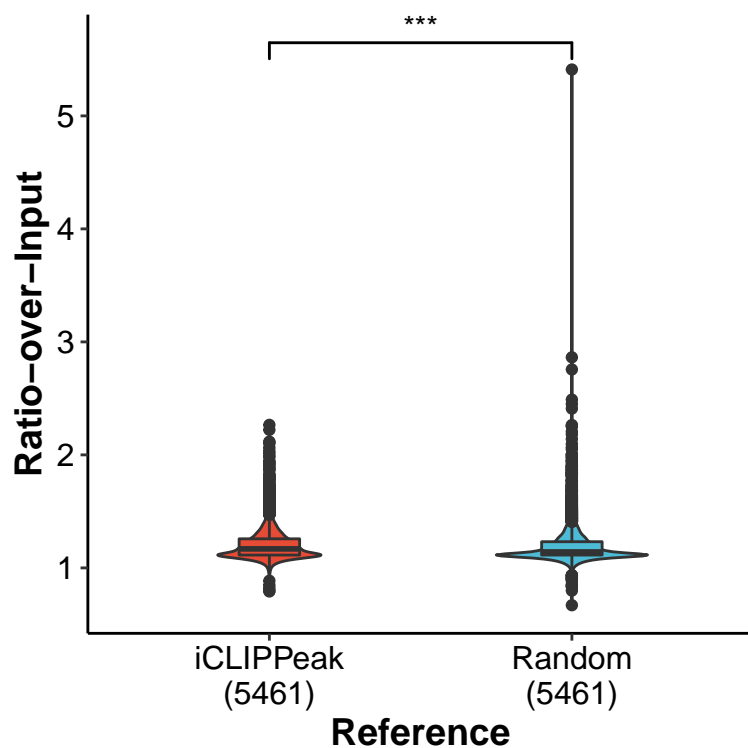


post hoc TukeyHSD test

	diff	lwr	upr	p adj
<i>Random-iCLIPPeak</i>	-0.019	-0.03	-0.007	0.00154

Feature: Transcript
Reference size: 5461
Sample name: clip_bam

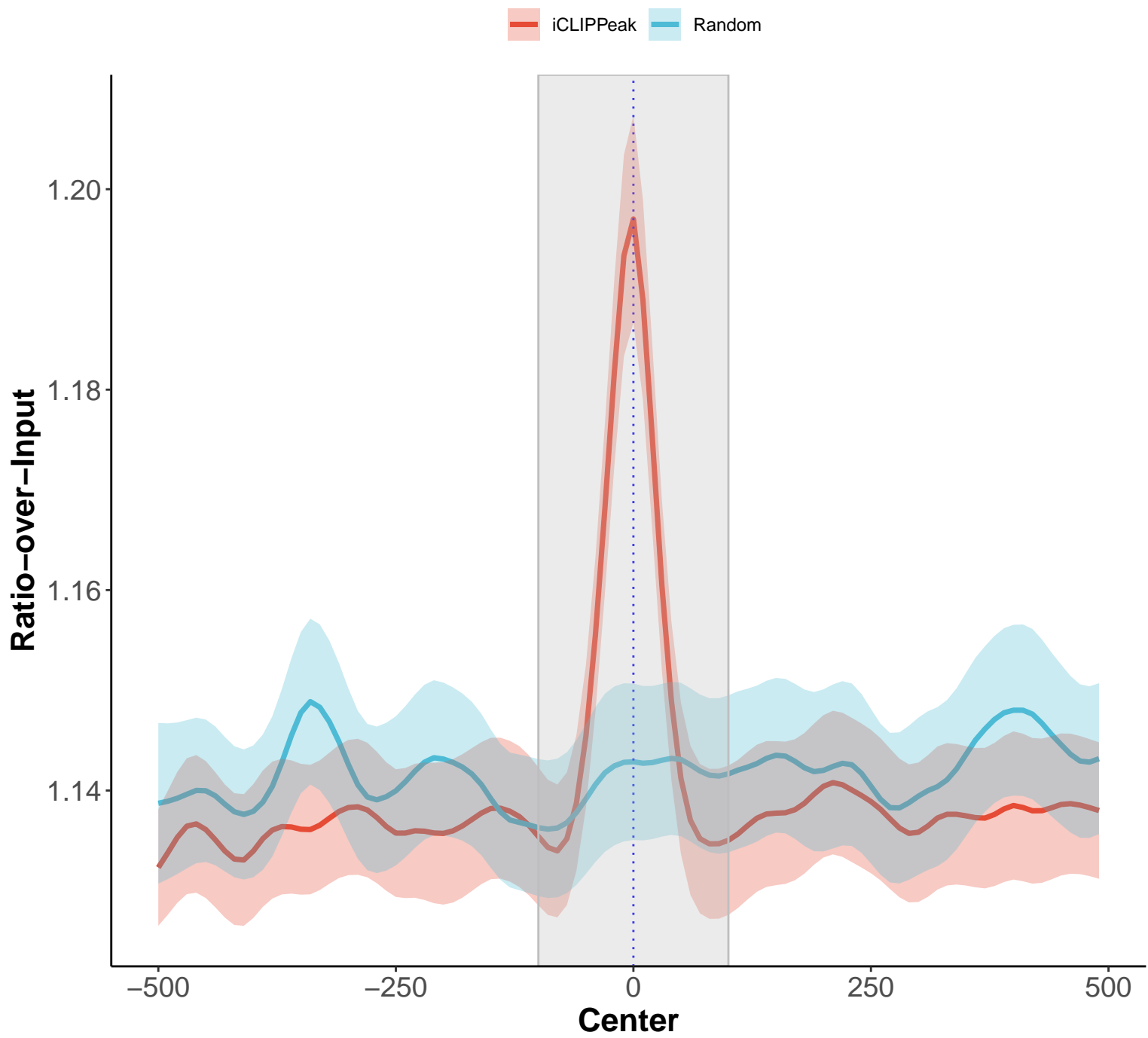


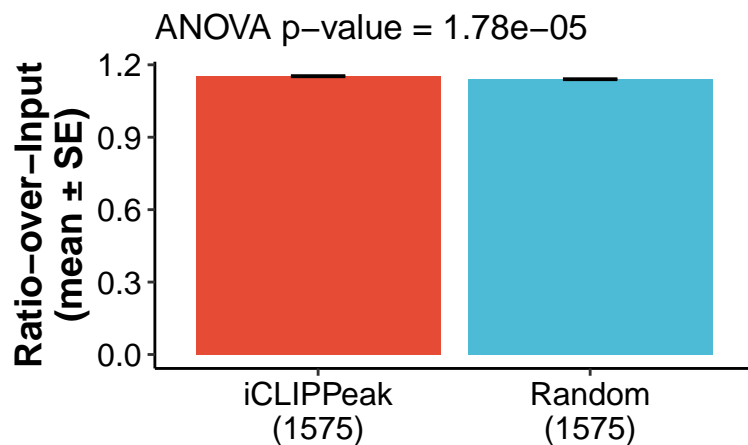
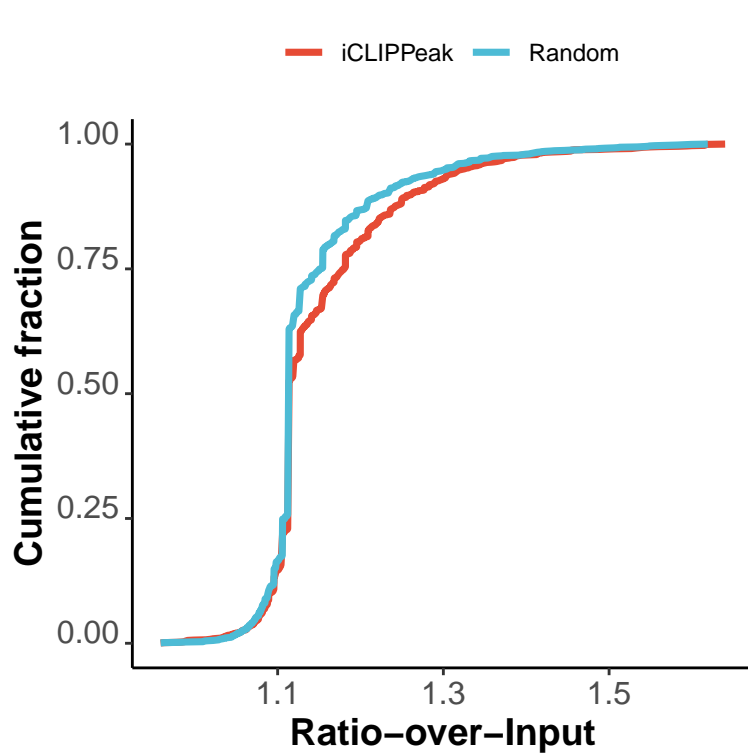
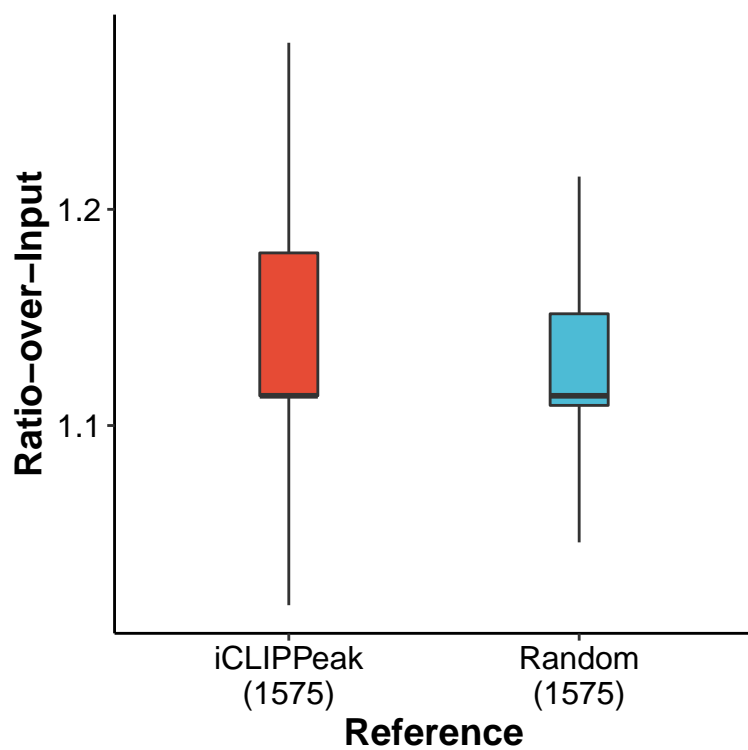
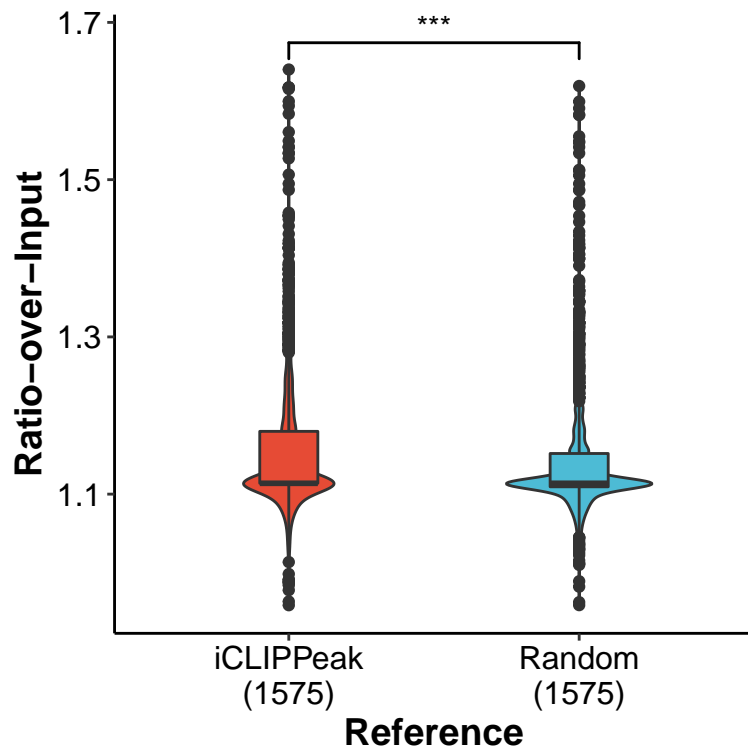


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.011	-0.017	-0.006	8.27e-05

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



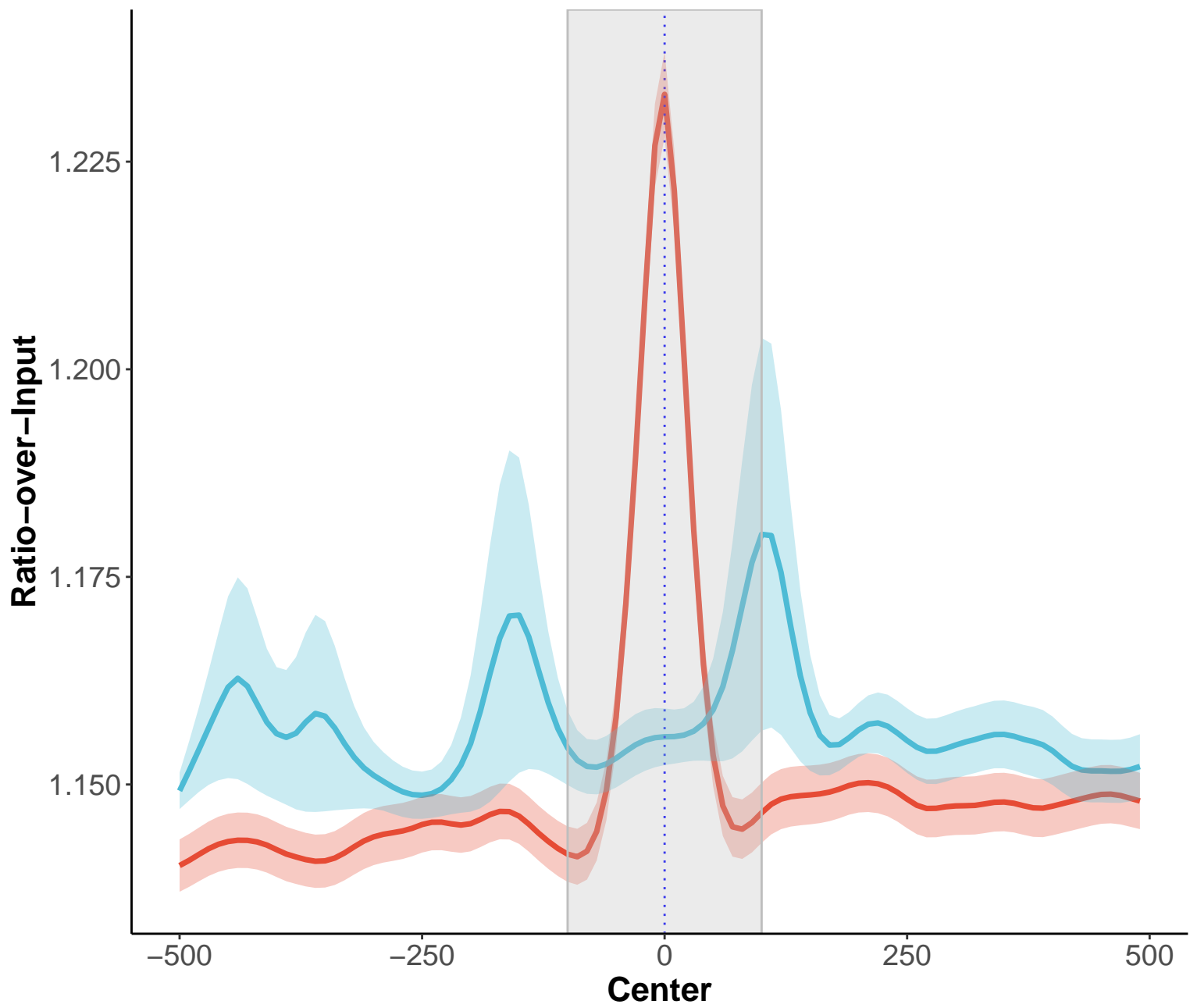


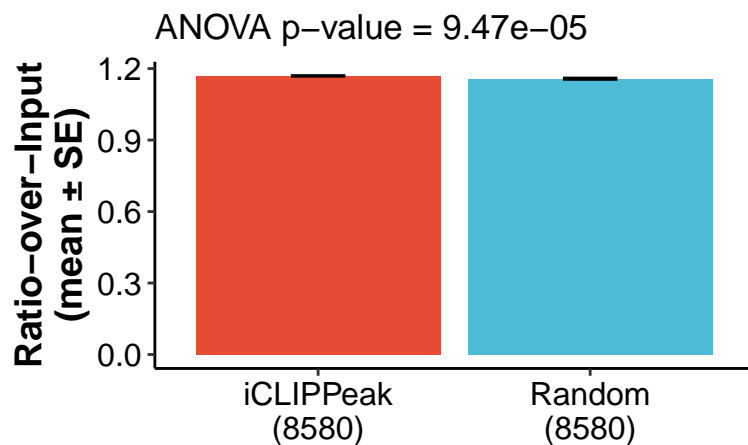
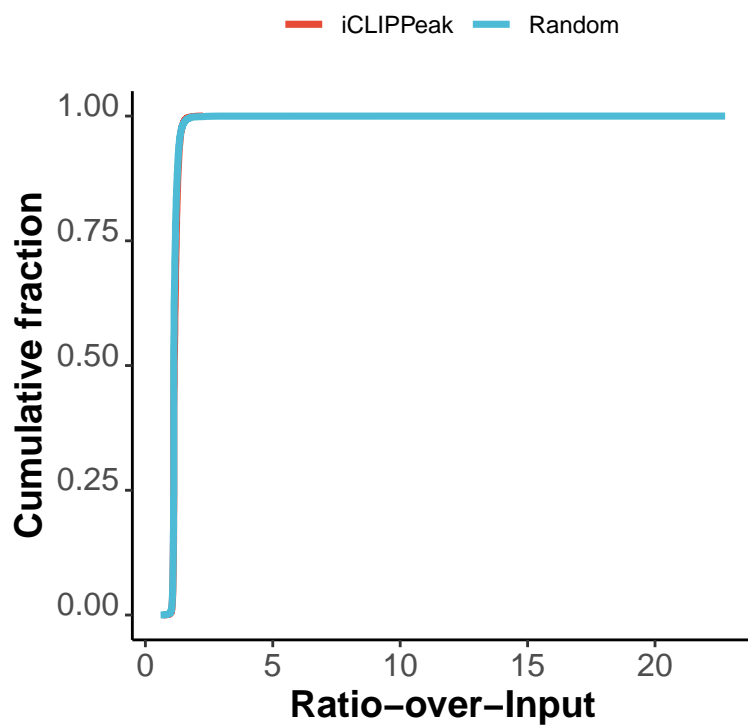
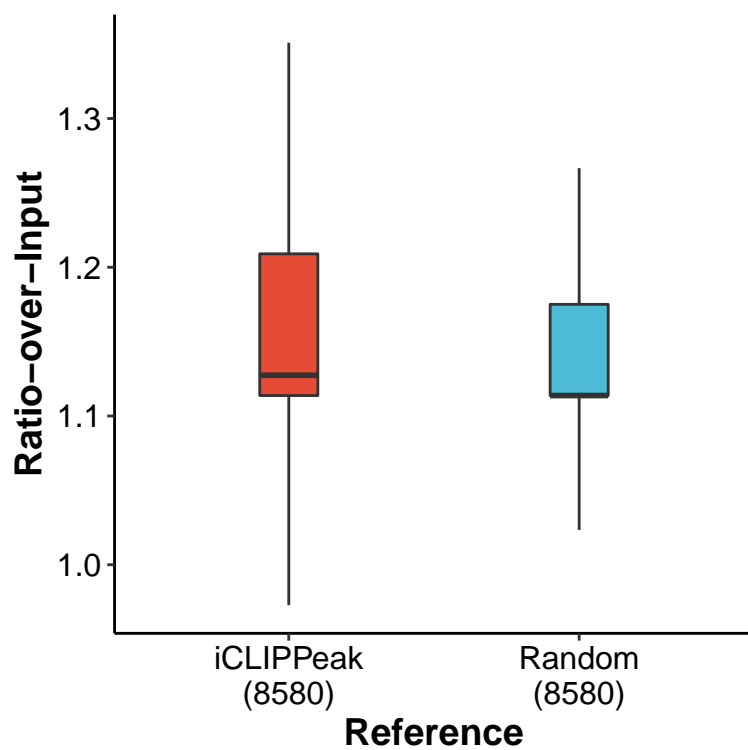
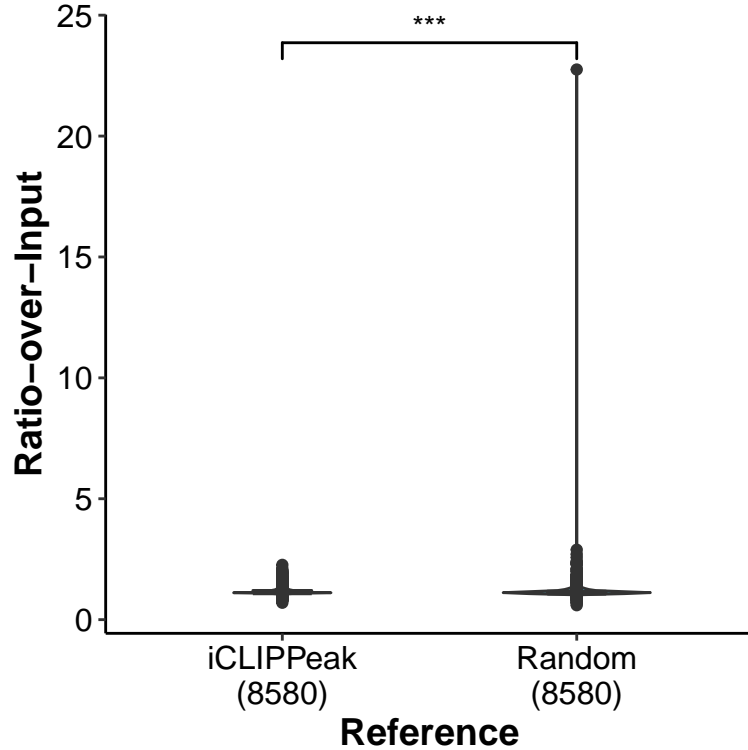
post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.012	-0.018	-0.007	1.78×10^{-5}

Feature: CDS
Reference size: 8580
Sample name: clip_bam

iCLIPPeak Random

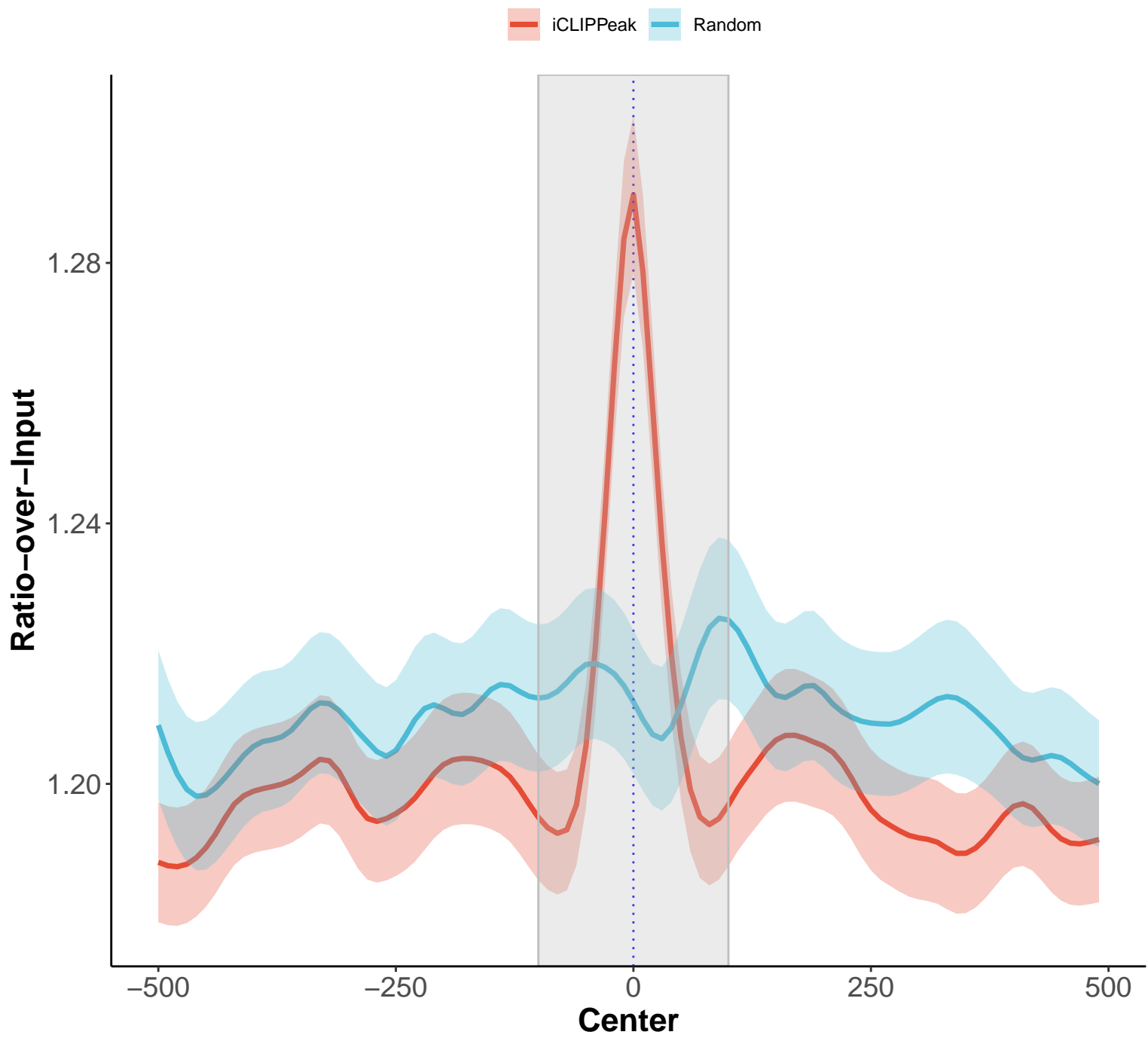


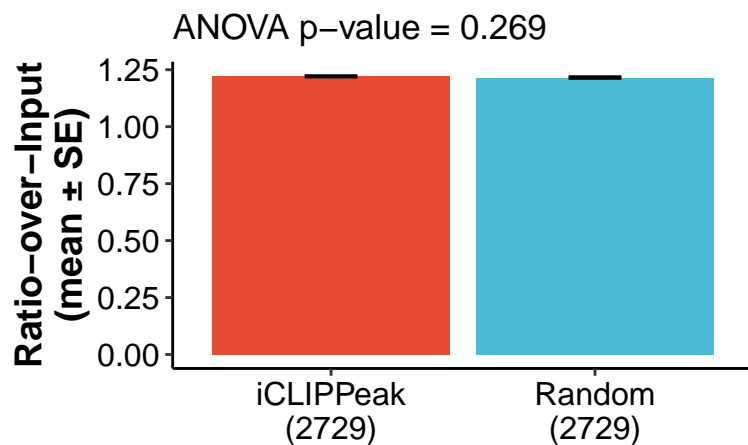
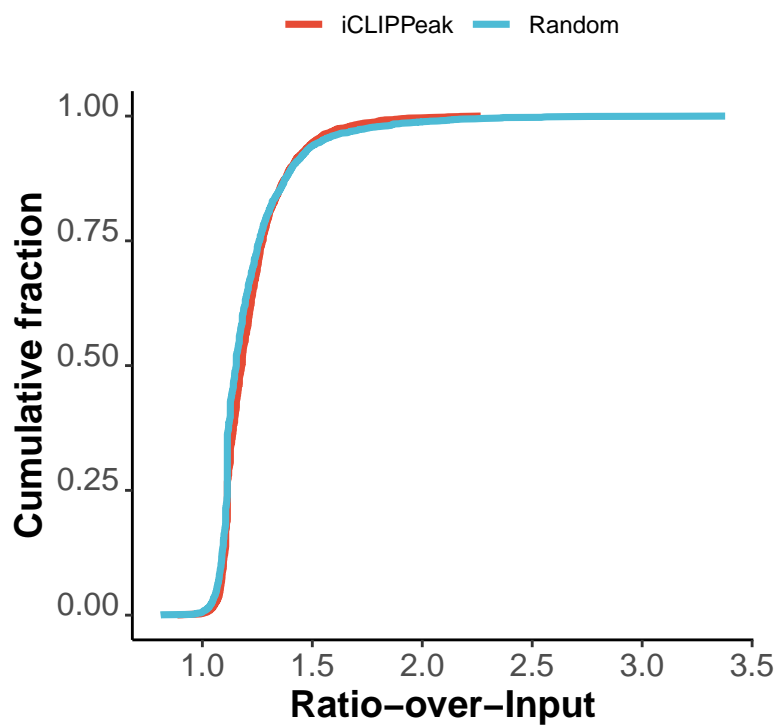
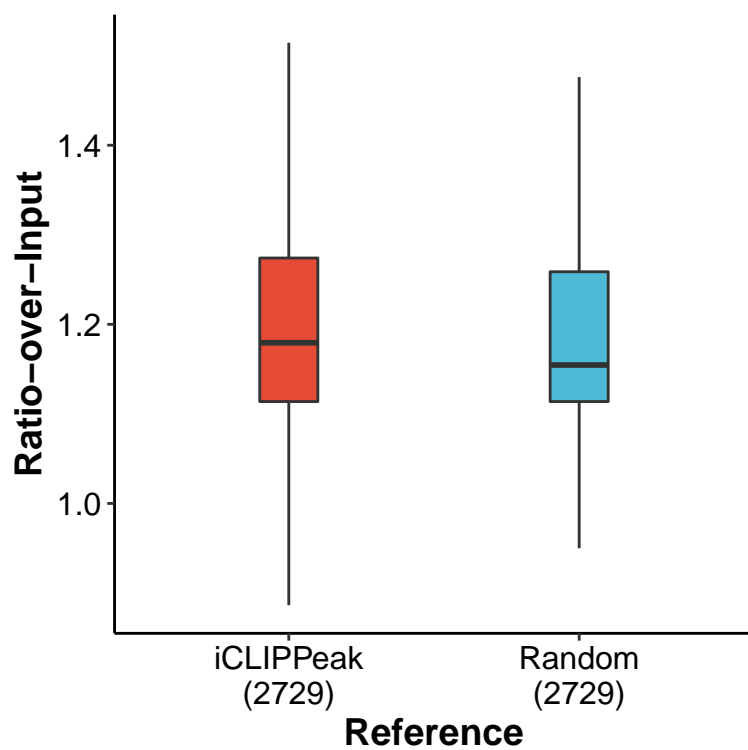
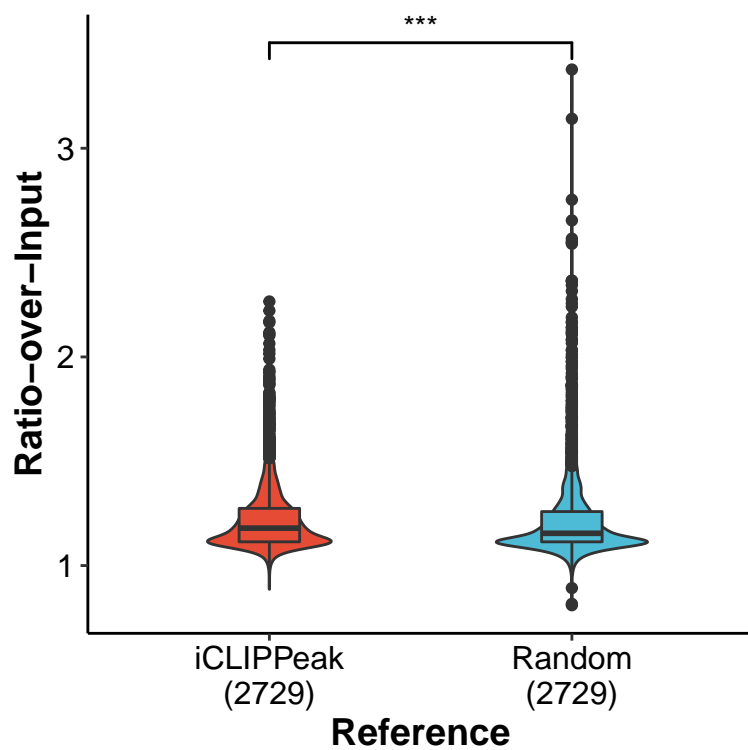


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.012	-0.017	-0.006	9.48e-05

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

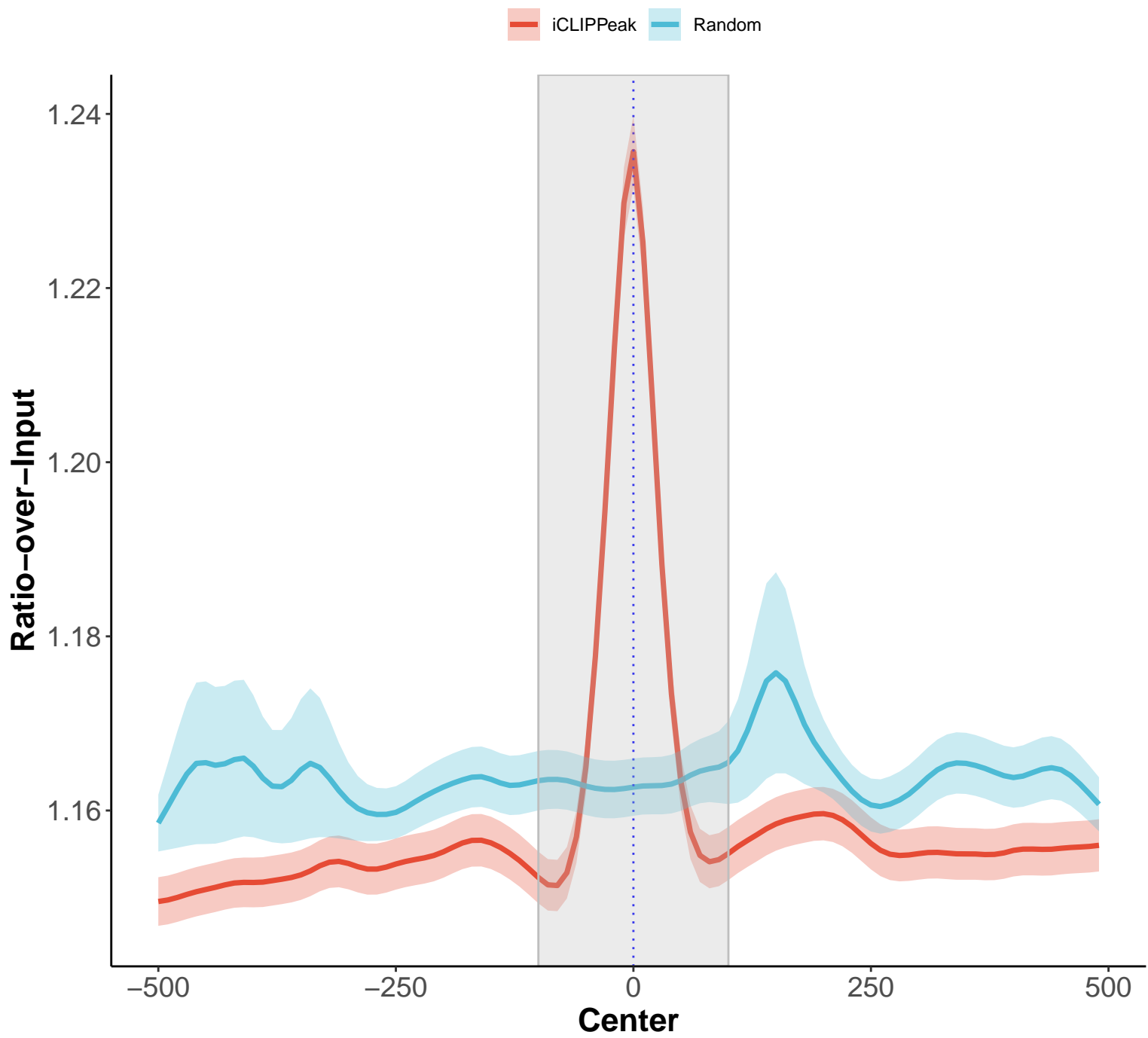


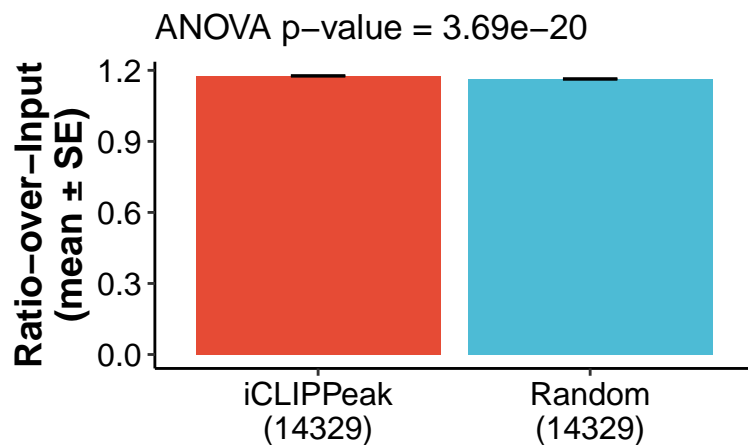
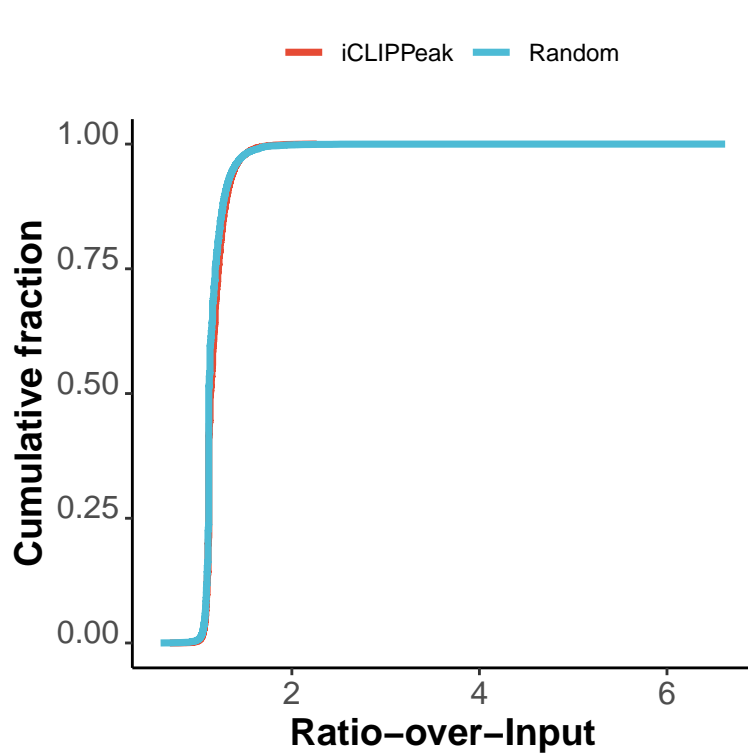
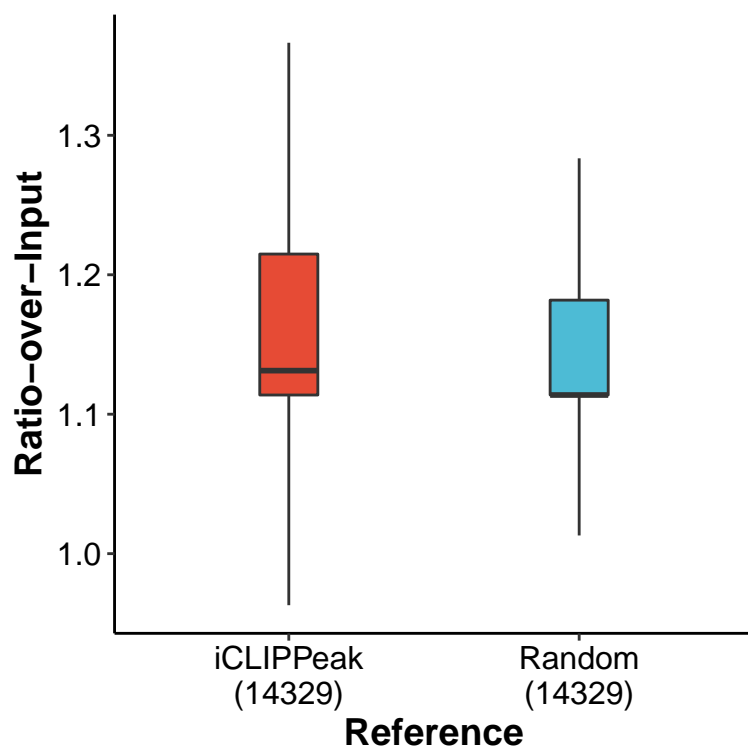
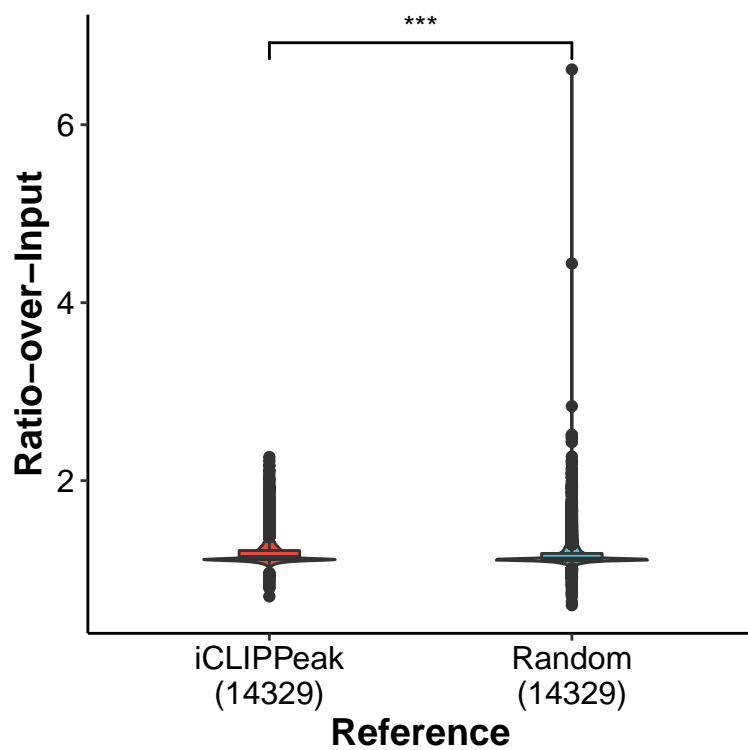


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.005	-0.014	0.004	0.269

Feature: Gene
Reference size: 14329
Sample name: clip_bam

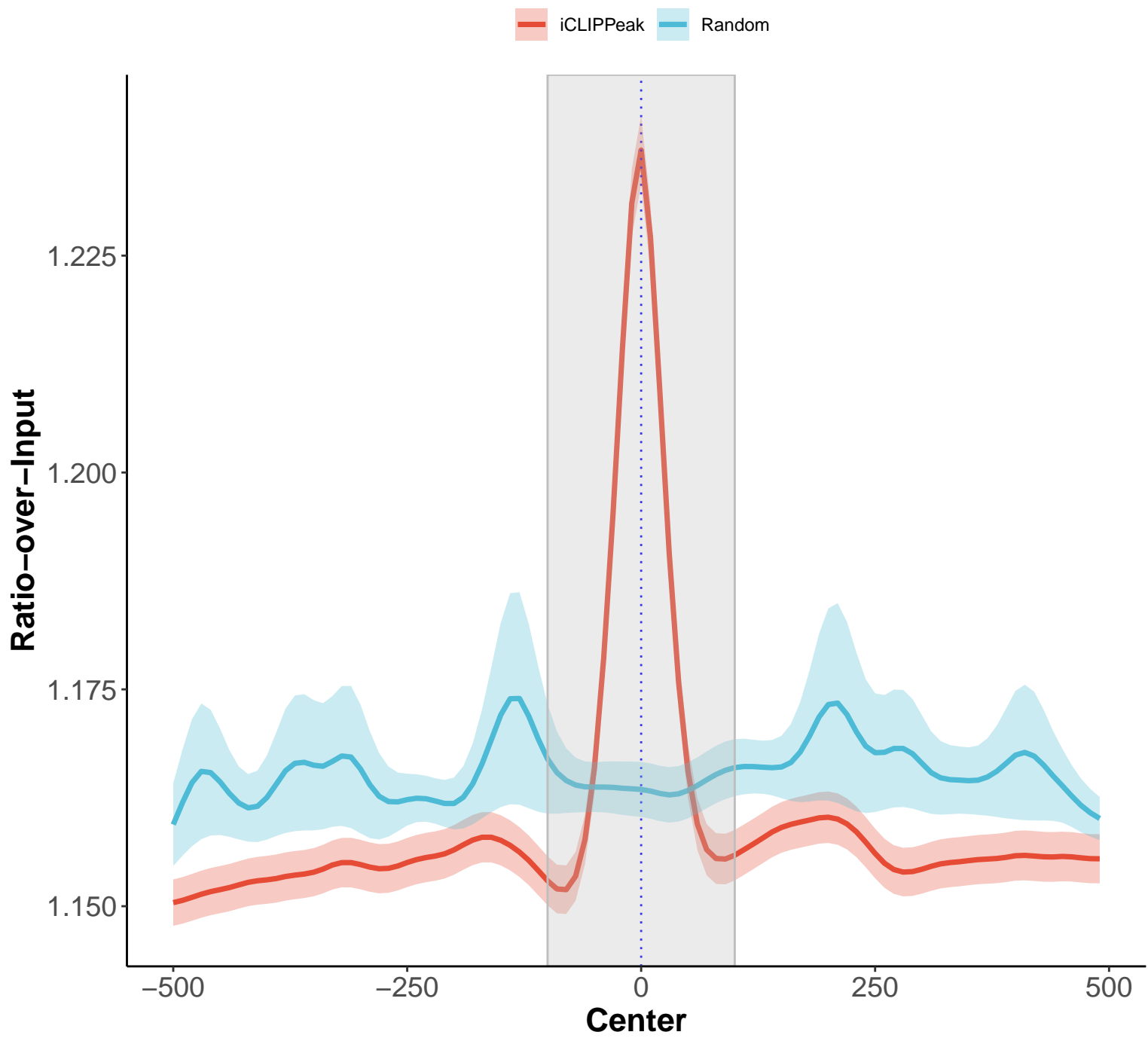


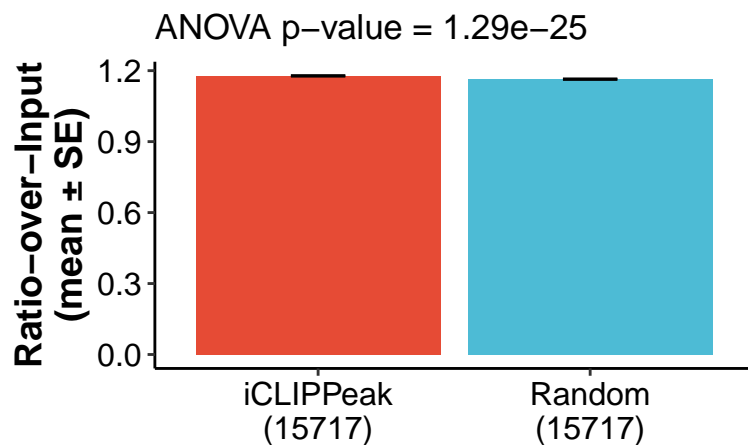
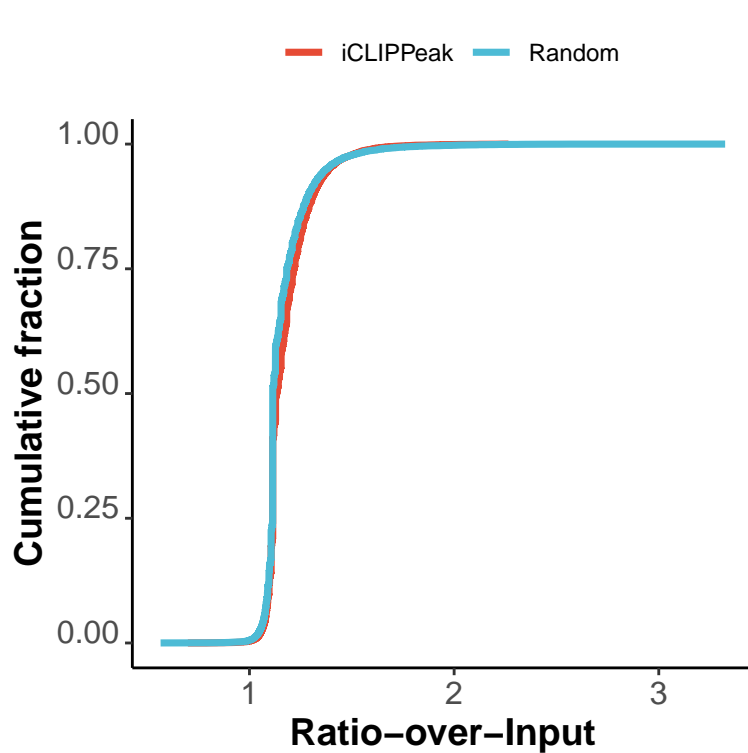
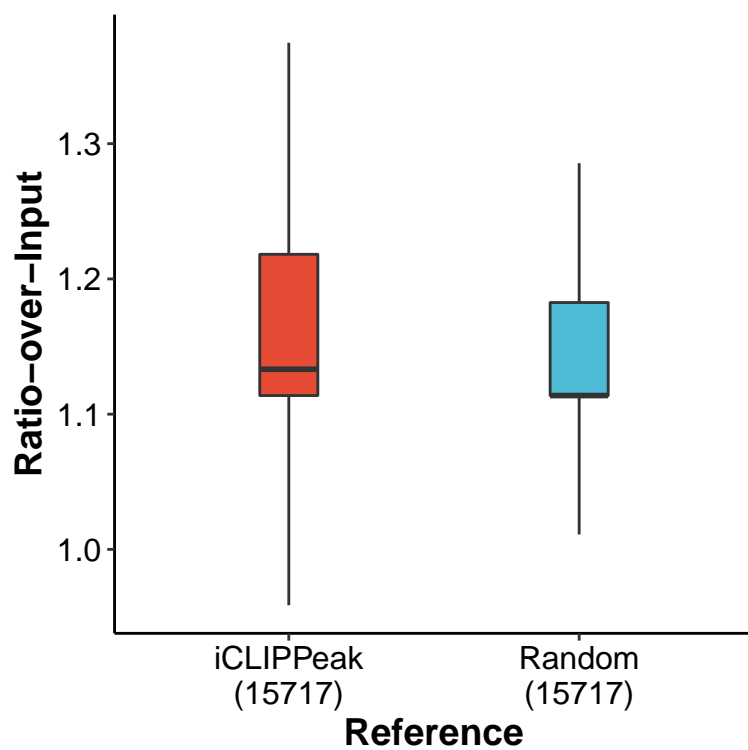
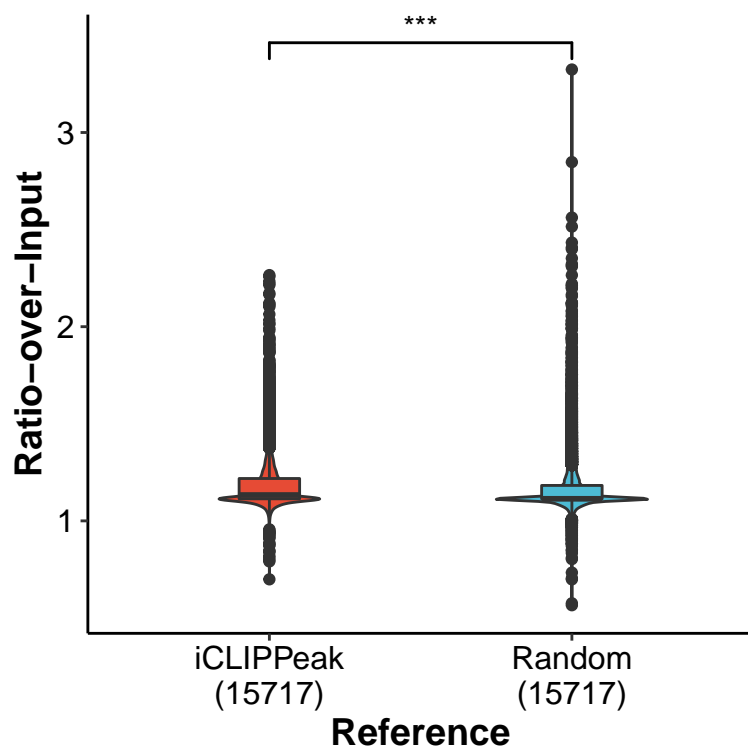


post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random-iCLIPPeak	-0.013	-0.016	-0.01	2.28×10^{-14}

Feature: unrestricted
Reference size: 15717
Sample name: clip_bam





post hoc TukeyHSD test

	diff	lwr	upr	p adj
<i>Random-iCLIPPeak</i>	-0.014	-0.016	-0.011	1.87×10^{-14}

Plotting parameters:

```
functionName: "plot_locus_with_random"
queryFiles: c(clip_bam =
"C:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/GenomicPlot/extdata/treat_chr19.bam")
centerFiles: c(iCLIPPeak =
"C:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/GenomicPlot/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:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/GenomicPlot/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
```