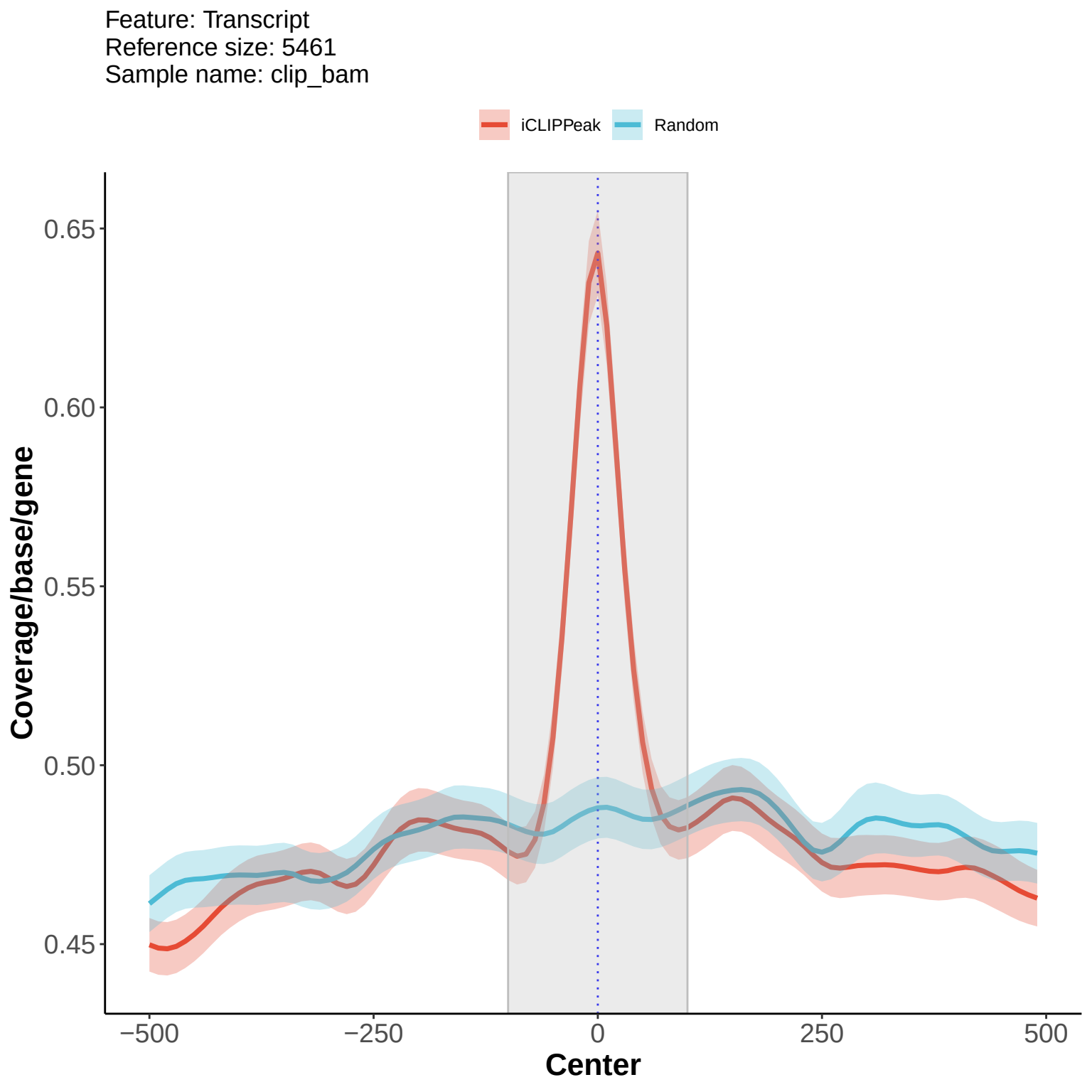
Feature: Transcript
Reference size: 5461
Sample name: clip_bam
iCLIPPeak
Random
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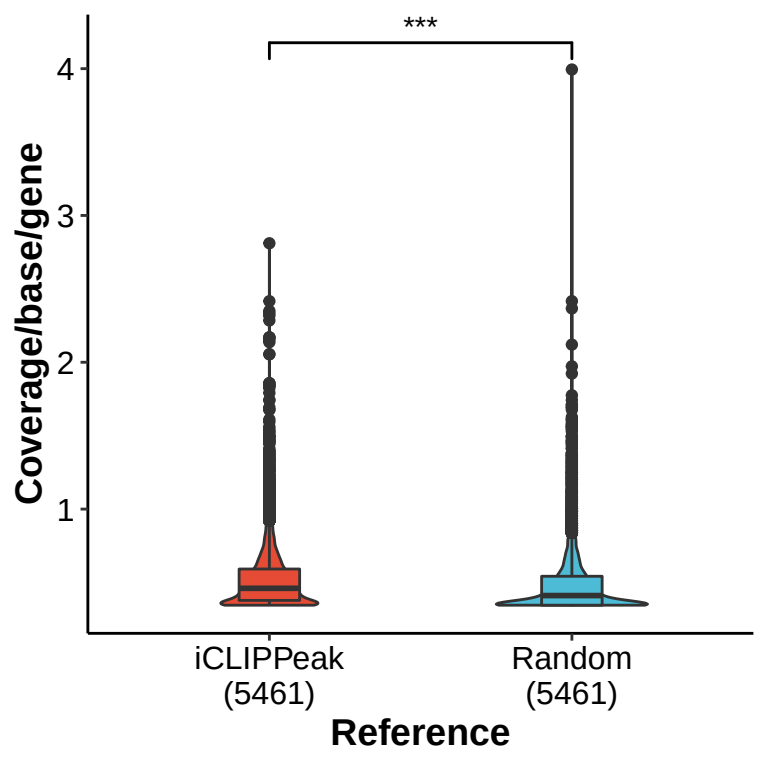
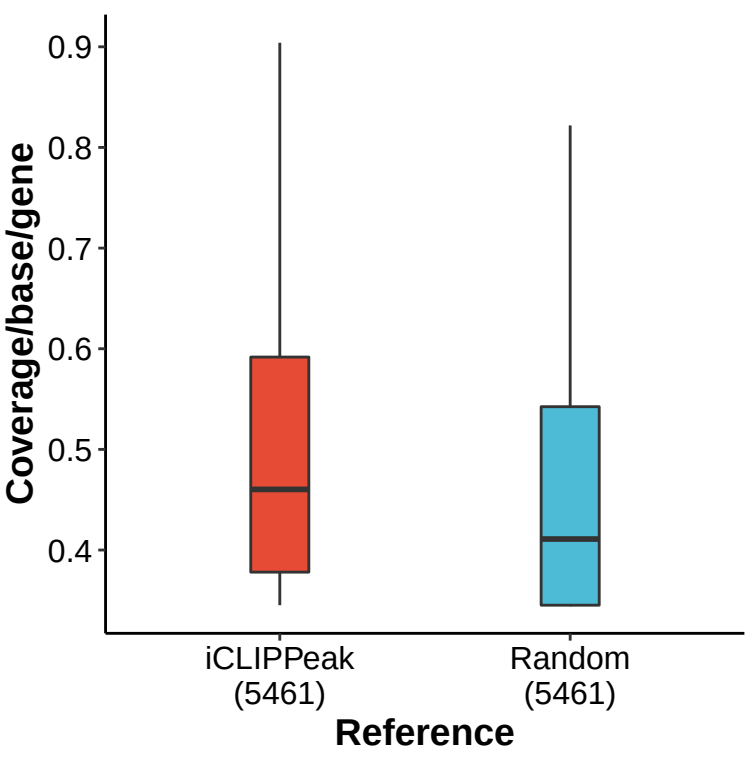
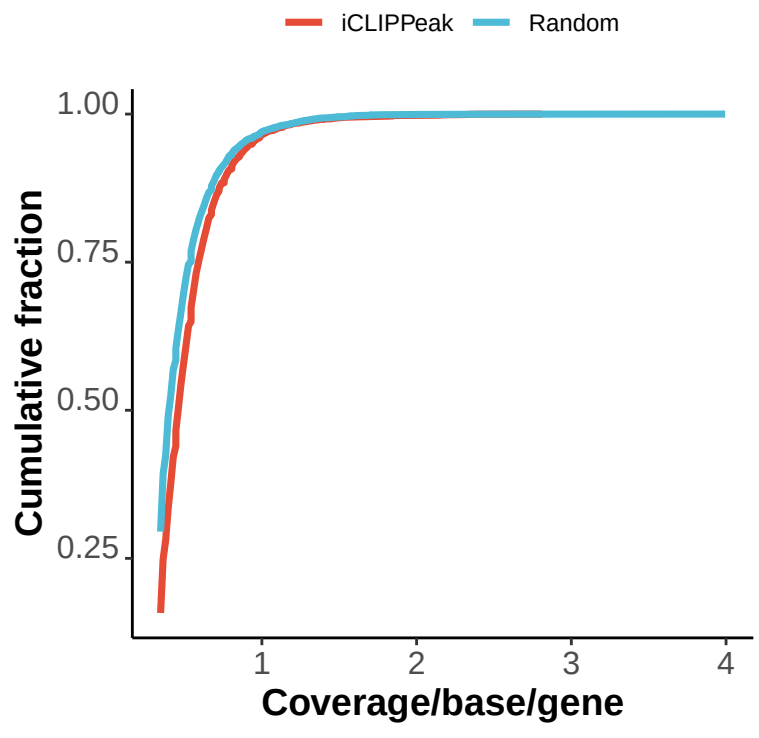
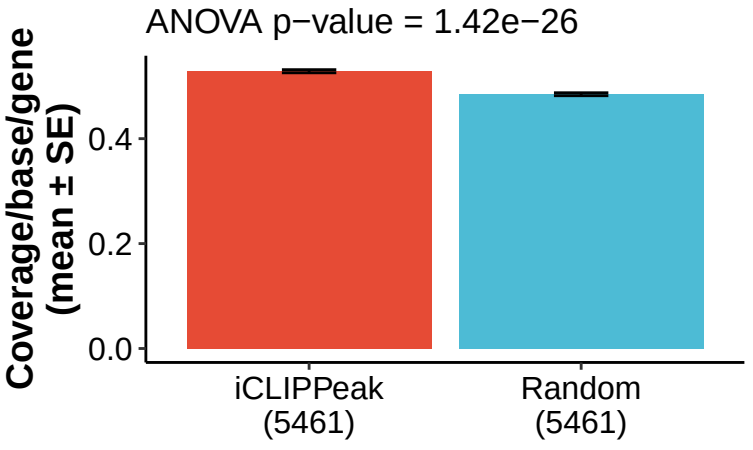
0.60
0.55
0.50
0.45
Coverage/base/gene
−500
−250
0
250
500
Center



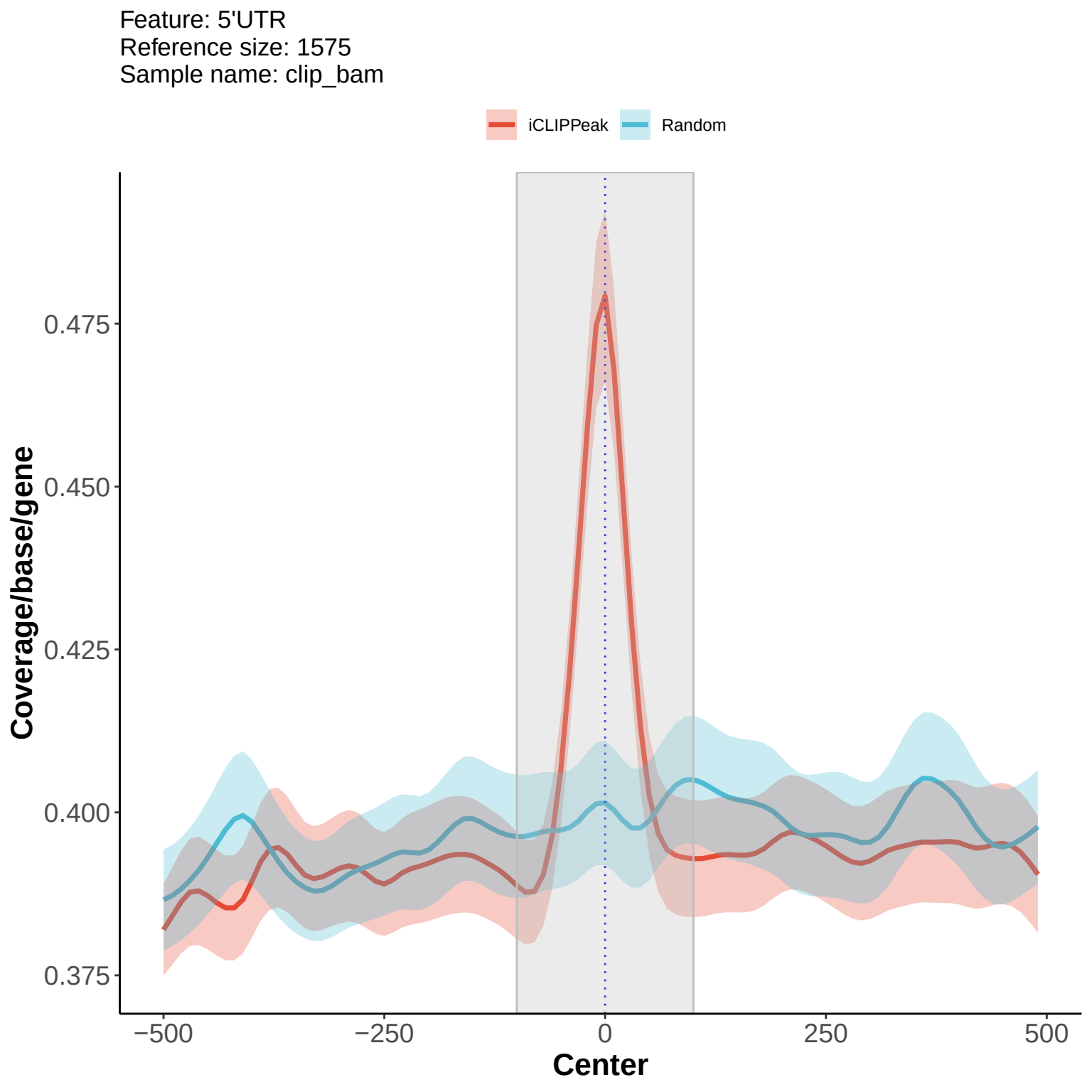






post hoc TukeyHSD test

	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
Coverage/base/gene
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0.425
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0.375
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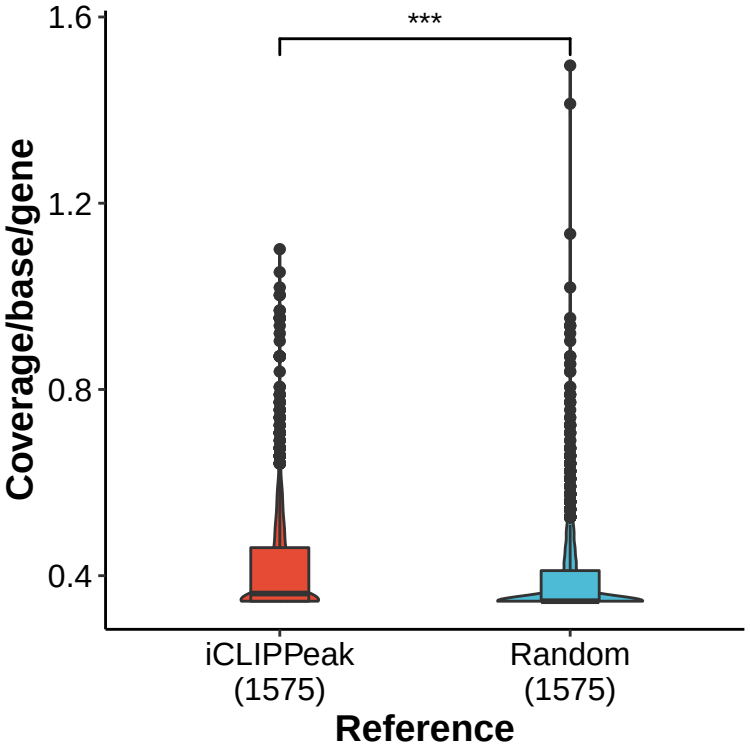
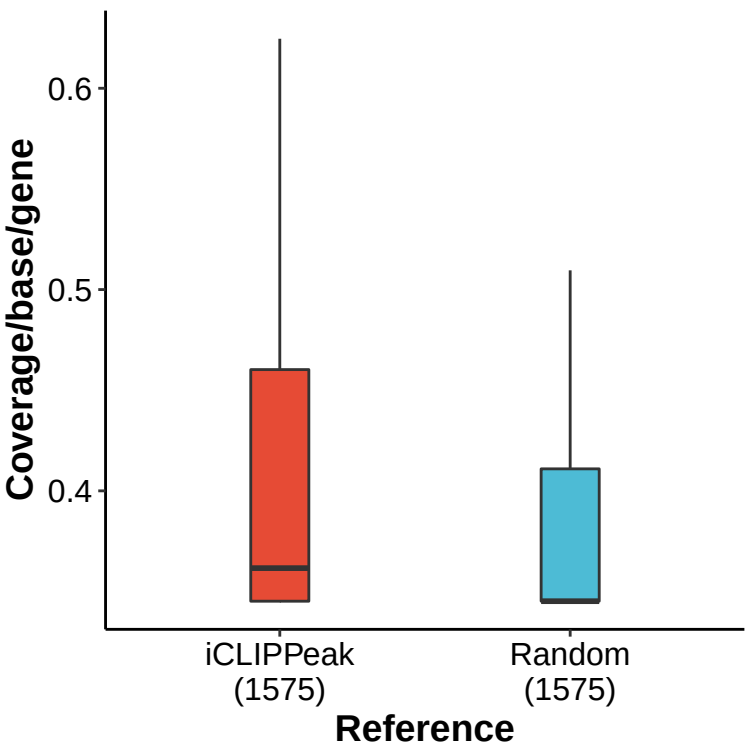
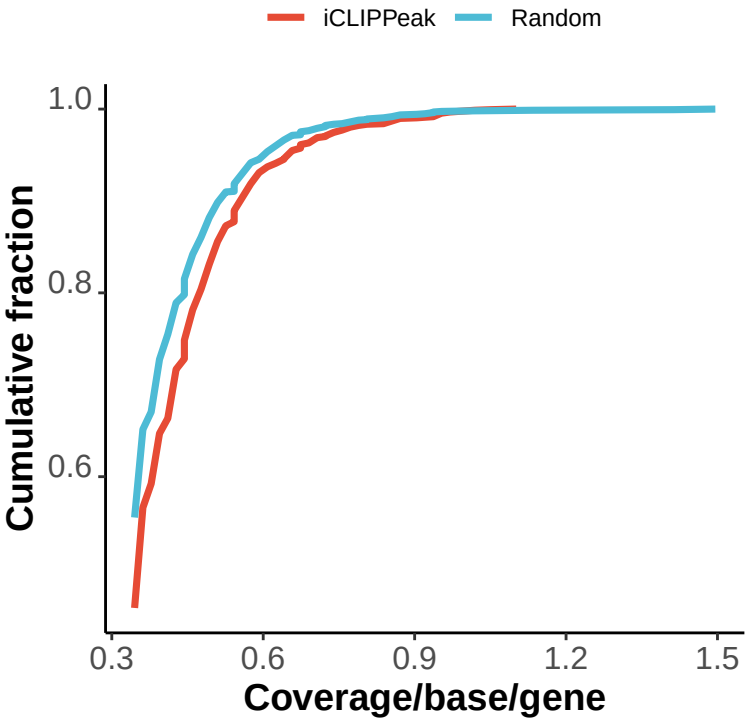
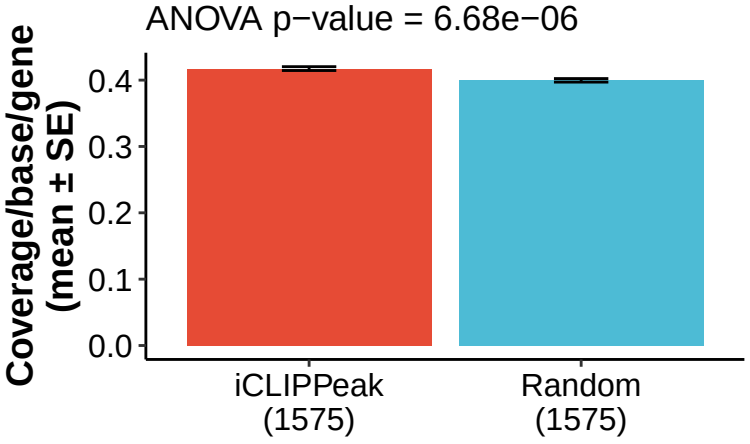
−250
0
250
500
Center



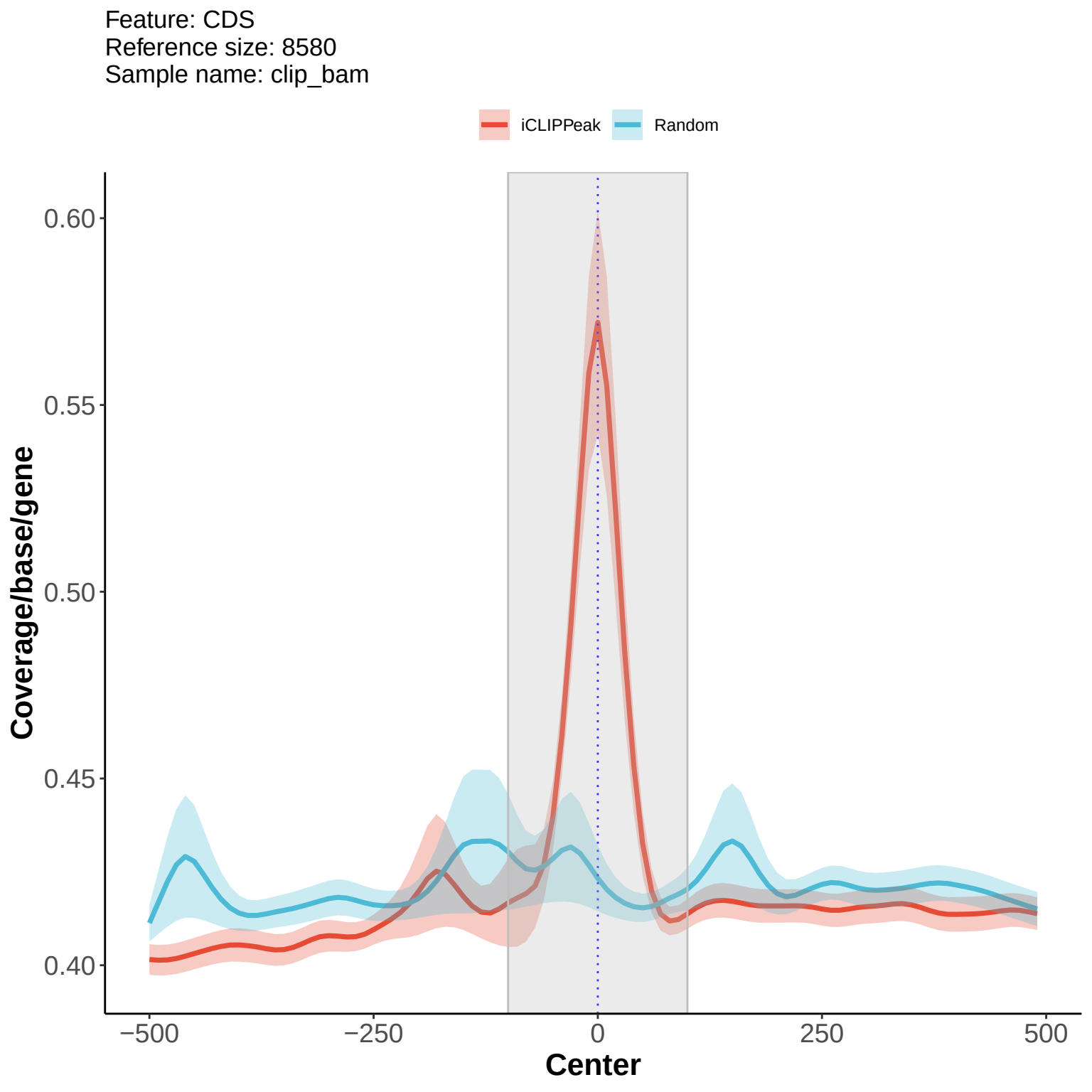






post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random−iCLIPPeak	−0.018	−0.025	−0.01	6.68e−06


Feature: CDS
Reference size: 8580
Sample name: clip_bam
iCLIPPeak
Random
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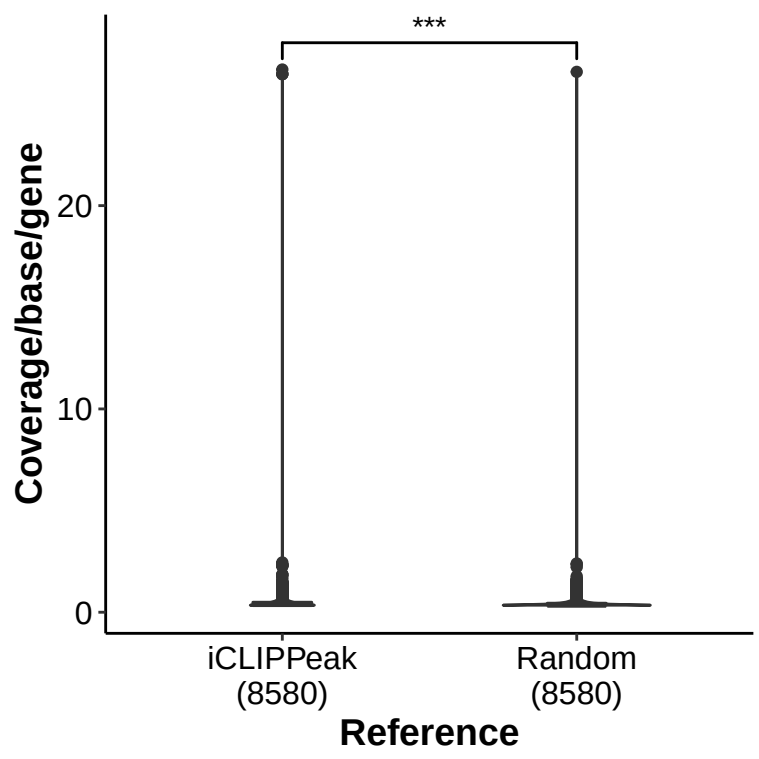
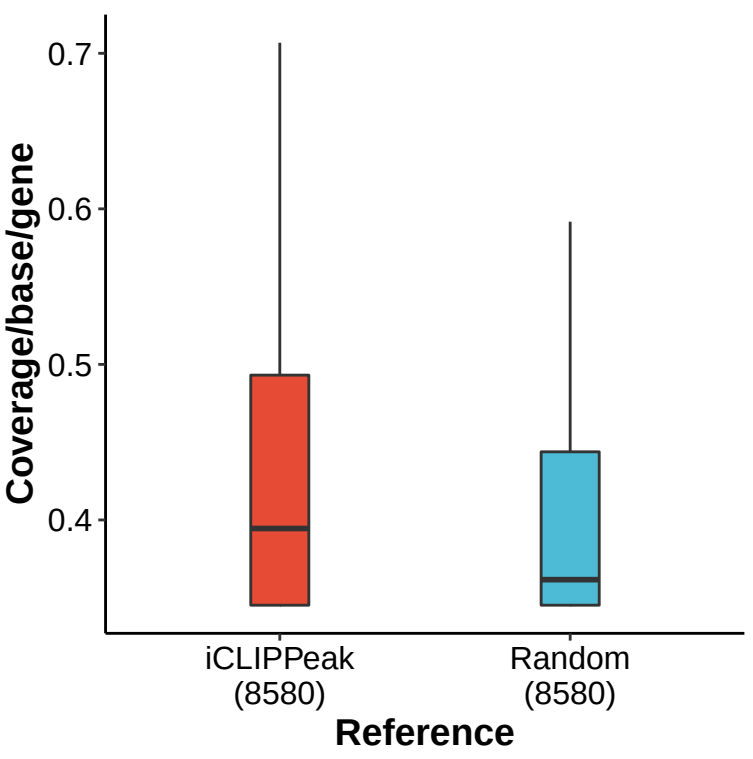
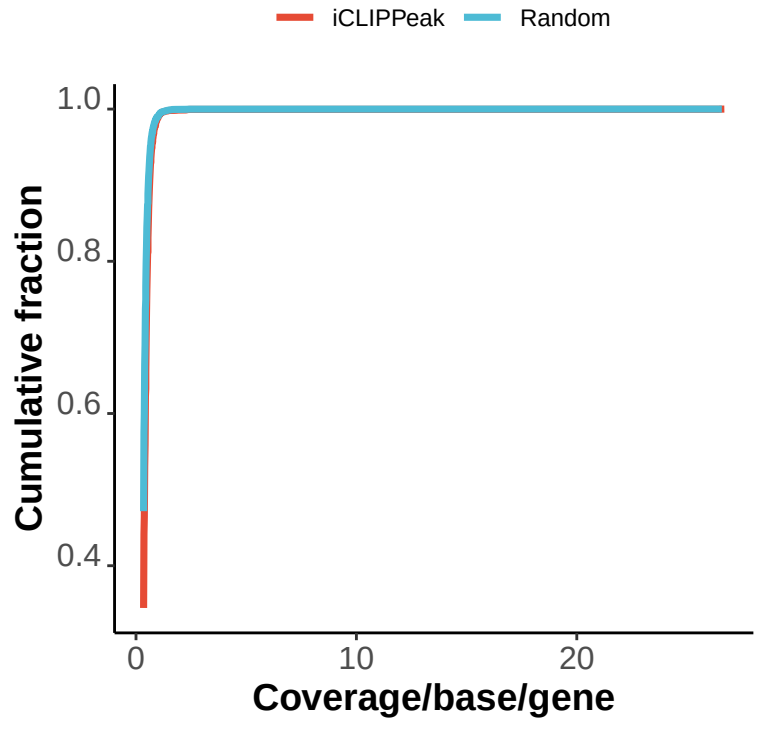
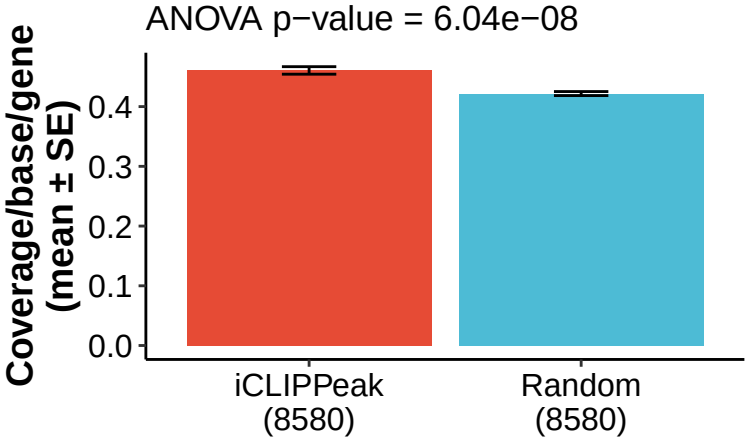
0.55
0.50
0.45
0.40
Coverage/base/gene
−500
−250
0
250
500
Center



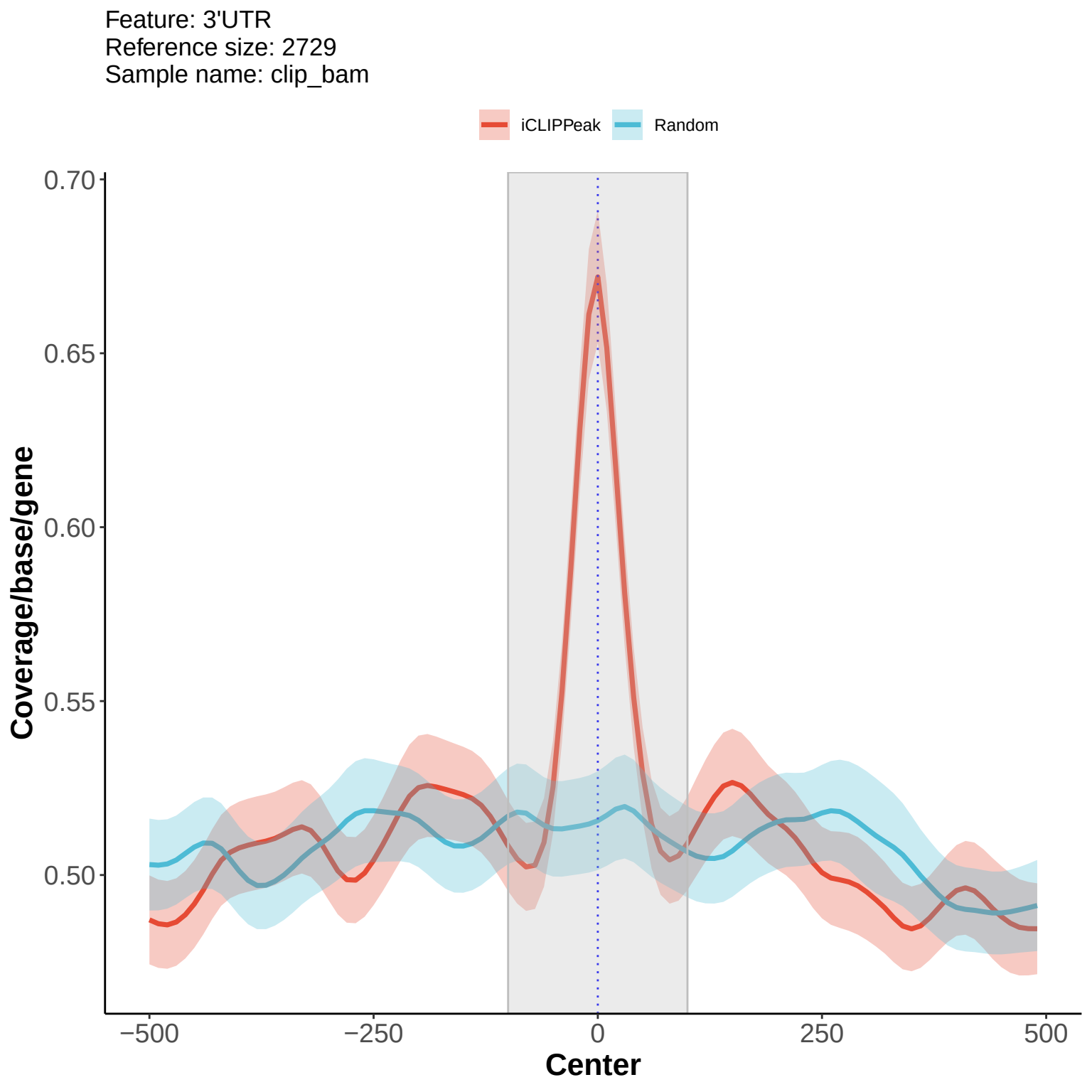






post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random−iCLIPPeak	−0.039	−0.053	−0.025	9.26e−08


Feature: 3'UTR
Reference size: 2729
Sample name: clip_bam
iCLIPPeak
Random
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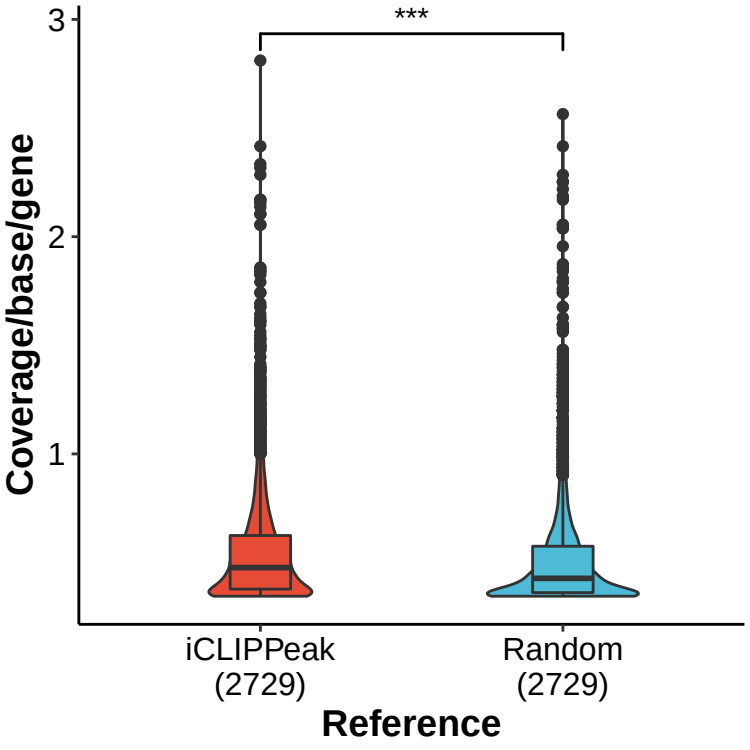
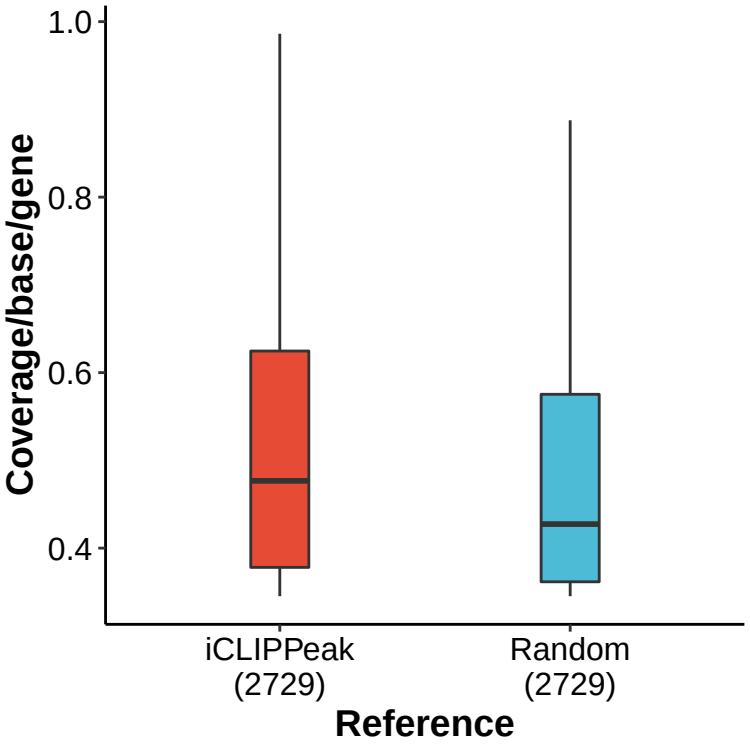
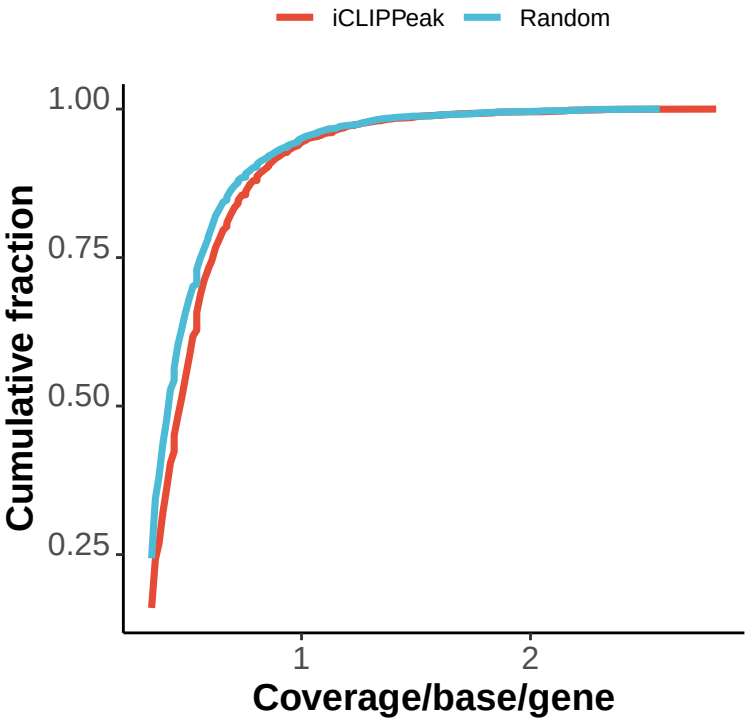
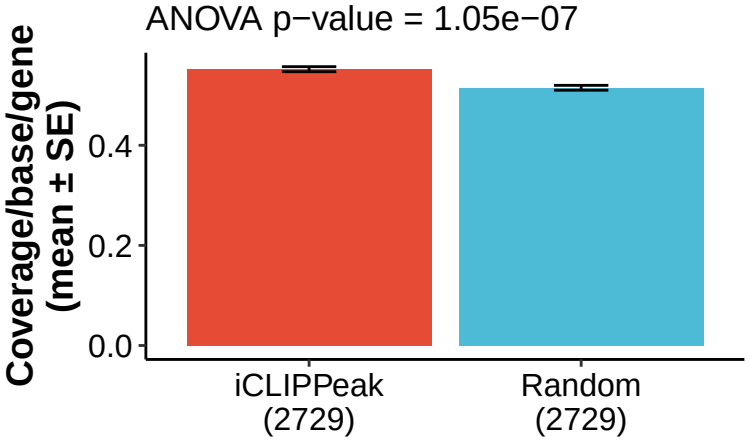
0.65
0.60
0.55
0.50
Coverage/base/gene
−500
−250
0
250
500
Center



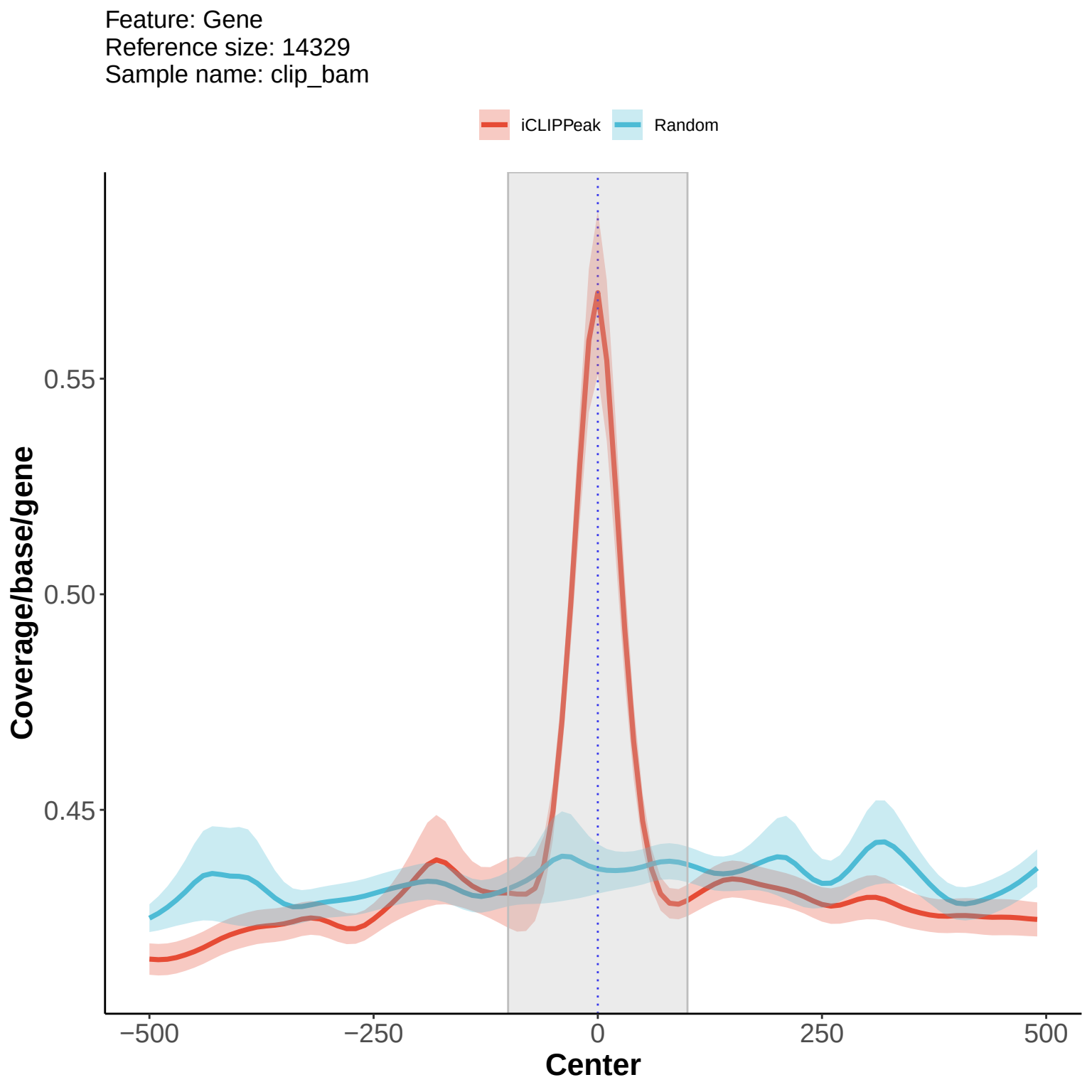


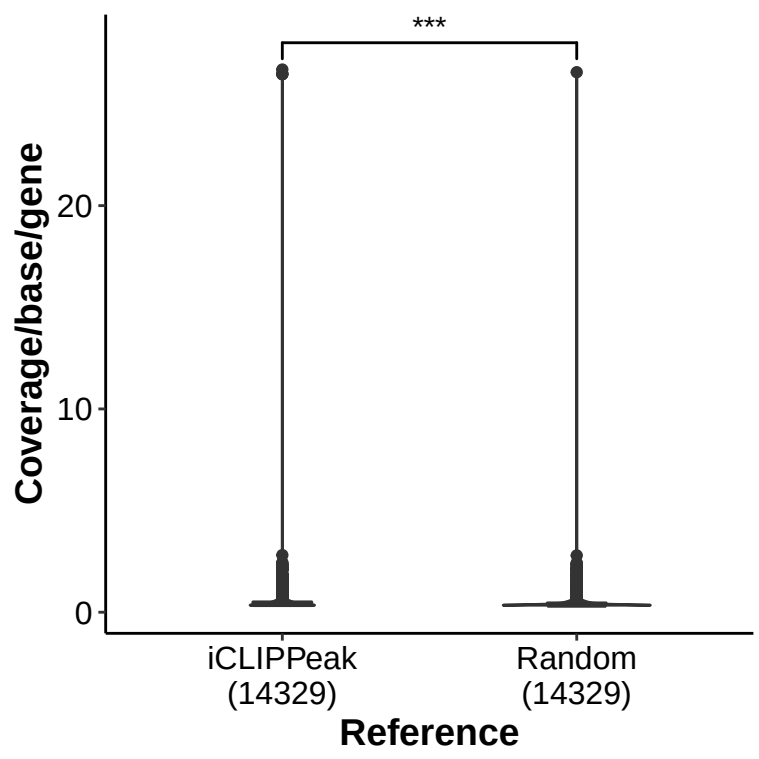


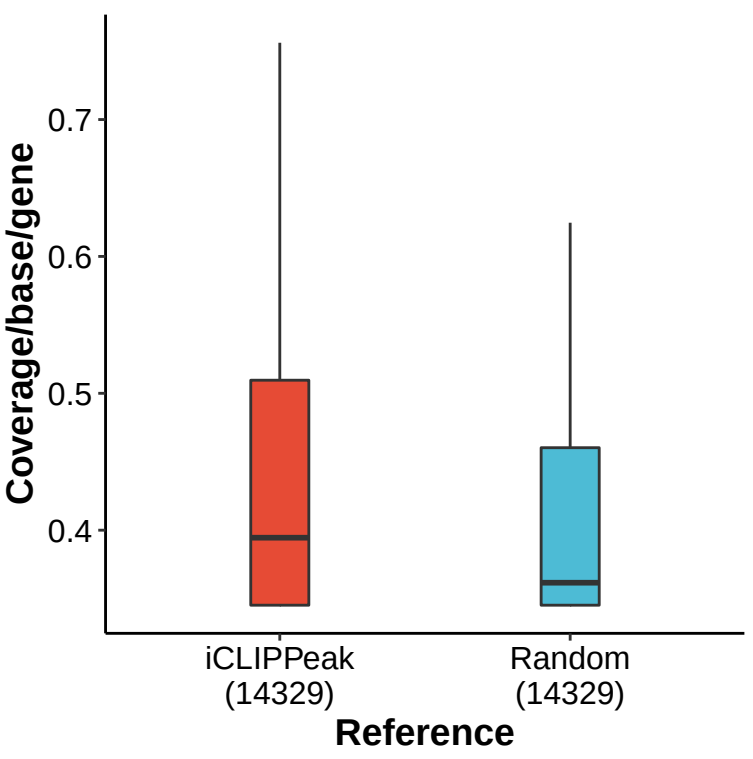


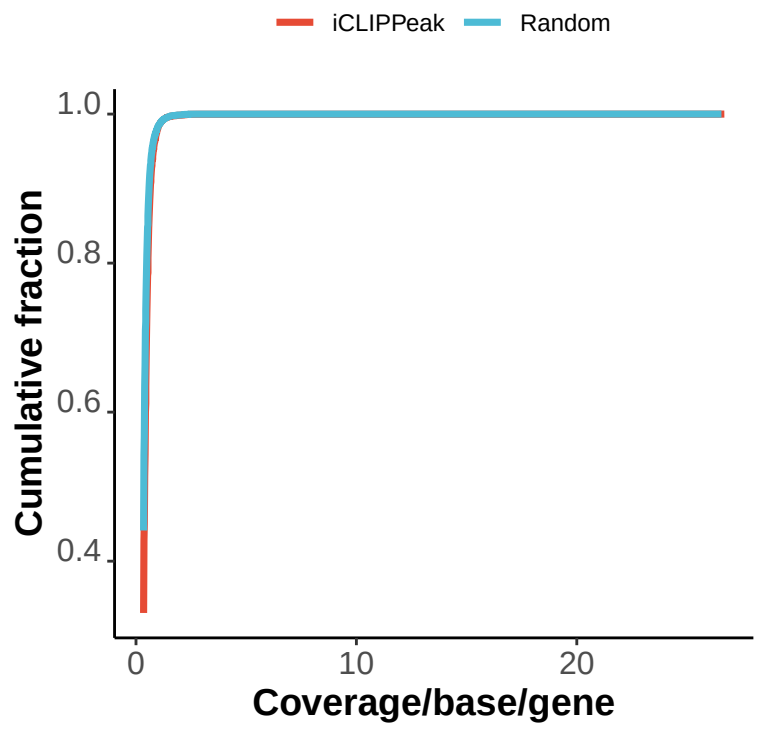
post hoc TukeyHSD test

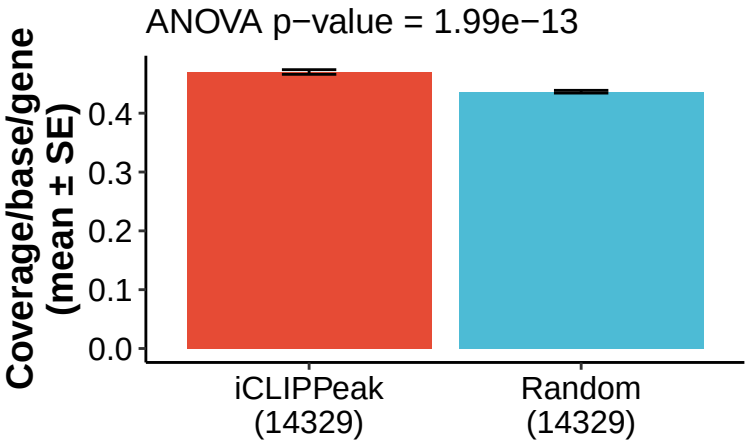
	diff	lwr	upr	p adj
Random−iCLIPPeak	−0.037	−0.051	−0.023	1.05e−07


Feature: Gene
Reference size: 14329
Sample name: clip_bam
iCLIPPeak
Random
Coverage/base/gene
0.55
0.50
0.45
−500
−250
0
250
500
Center



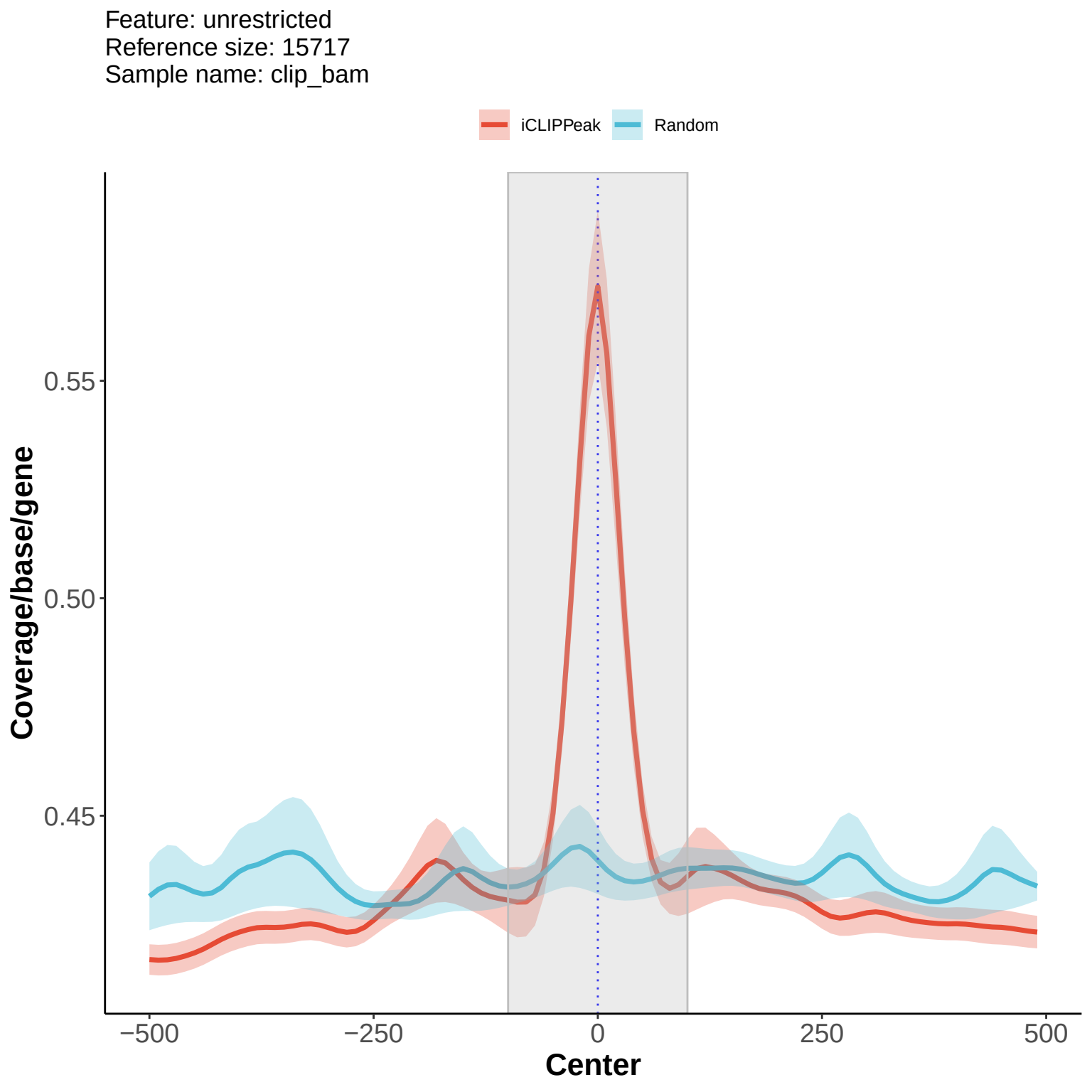


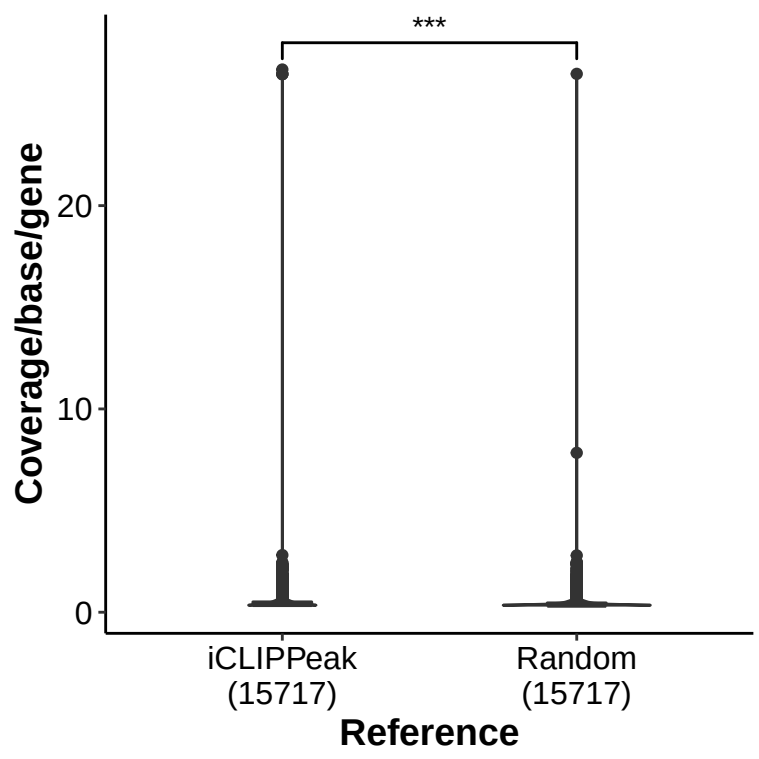


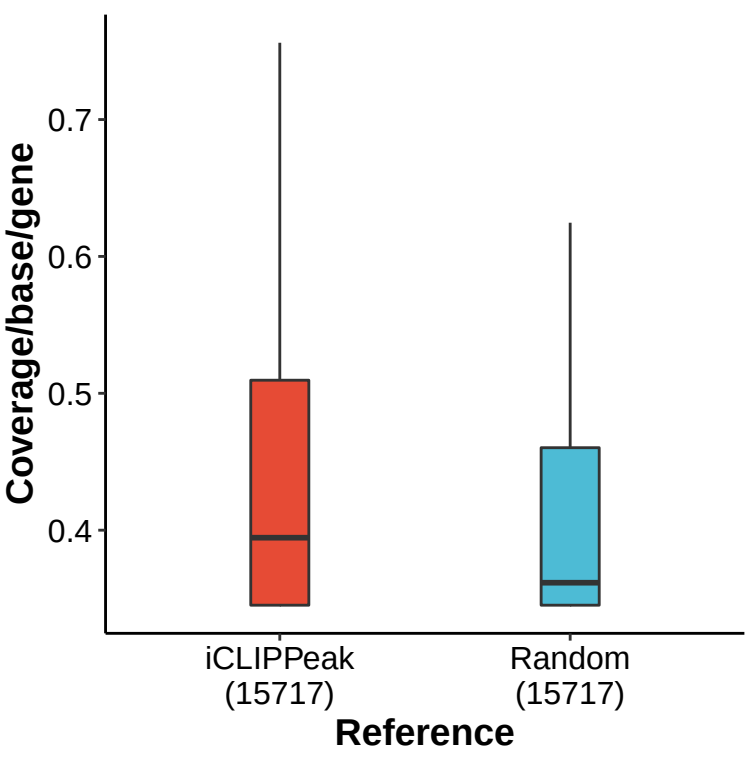


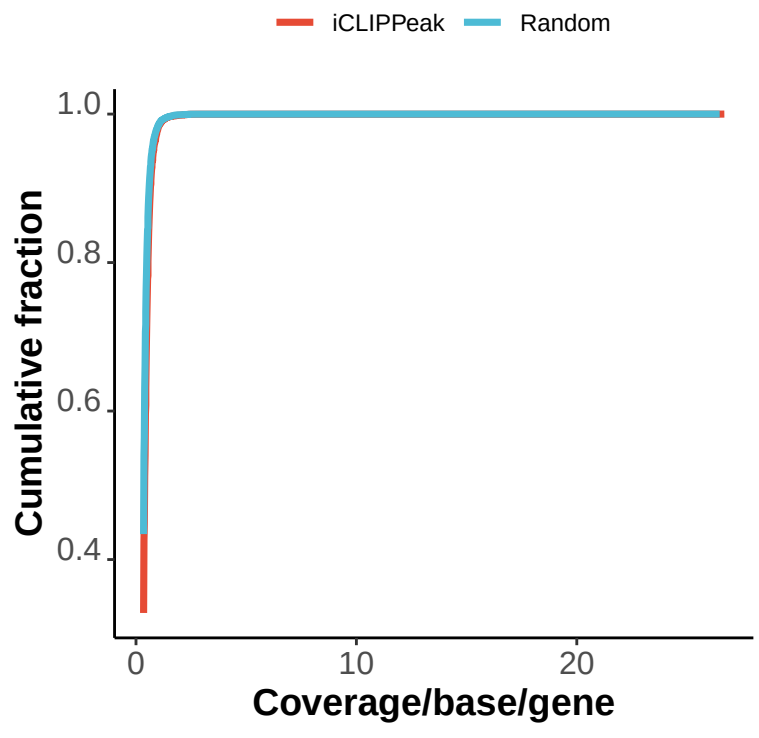
post hoc TukeyHSD test

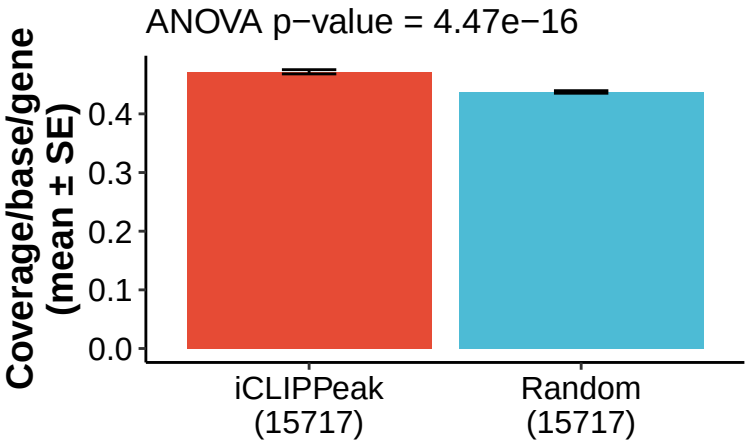
	diff	lwr	upr	p adj
Random−iCLIPPeak	−0.034	−0.042	−0.025	2.07e−13


Feature: unrestricted
Reference size: 15717
Sample name: clip_bam
iCLIPPeak
Random
Coverage/base/gene
0.55
0.50
0.45
−500
−250
0
250
500
Center



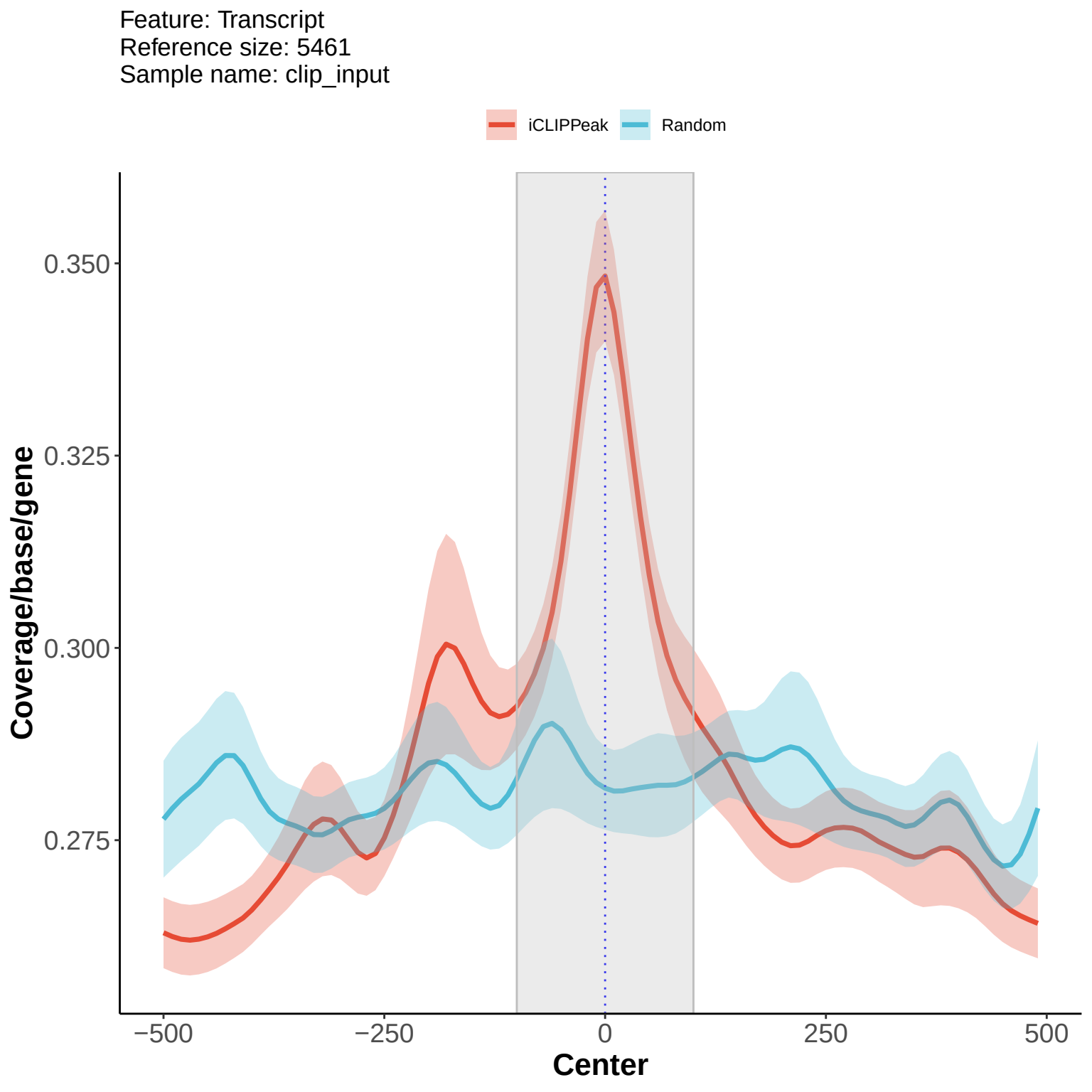


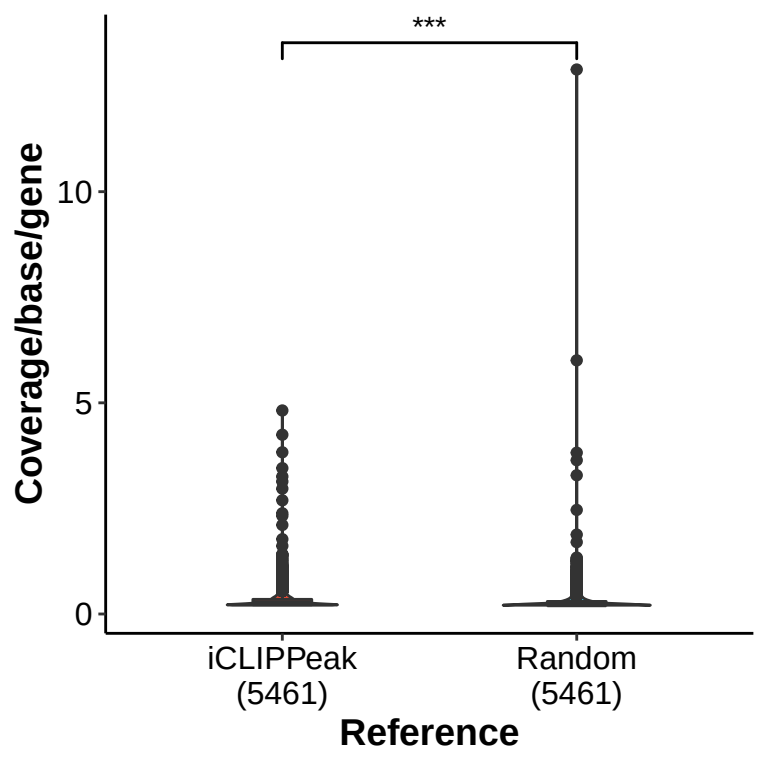


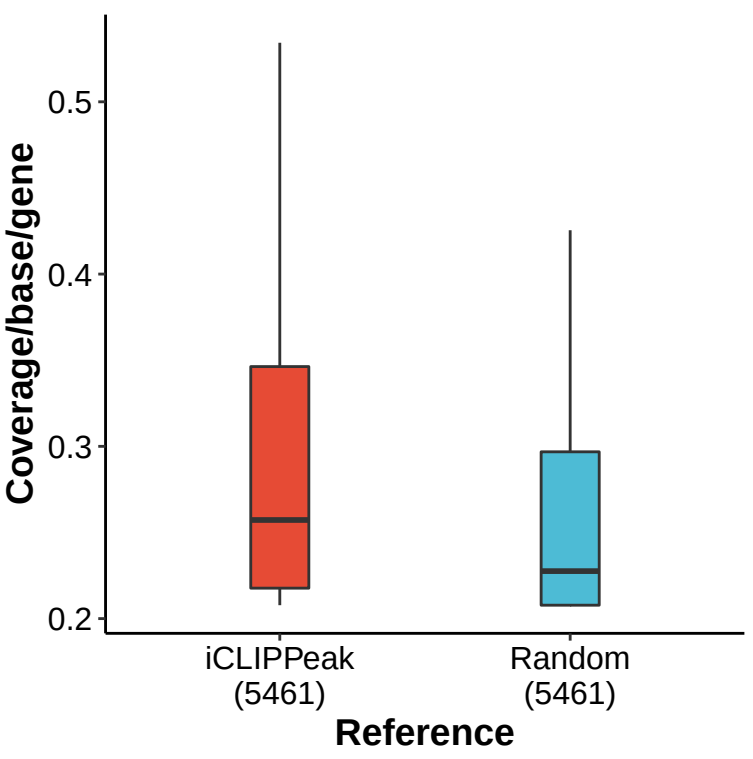


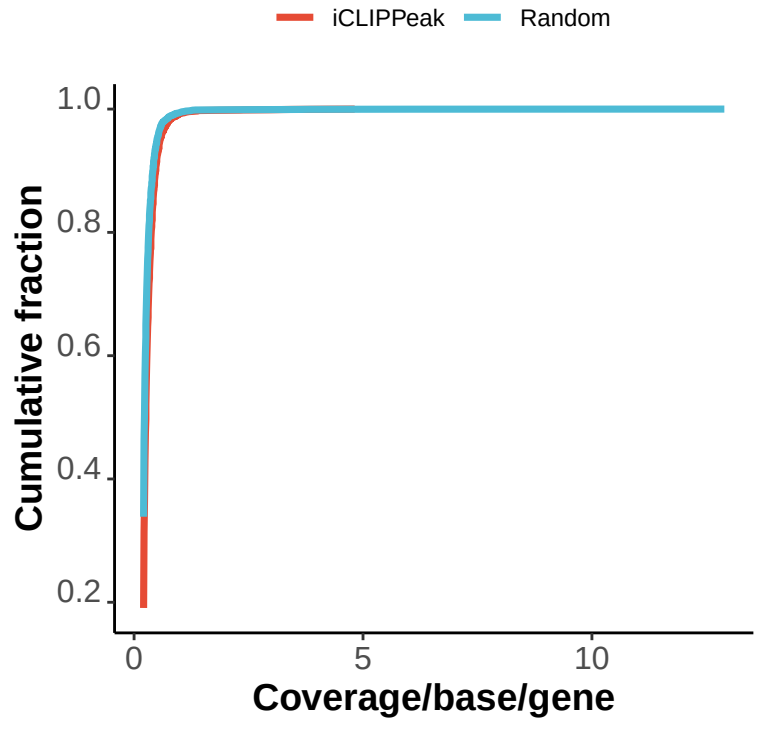
post hoc TukeyHSD test

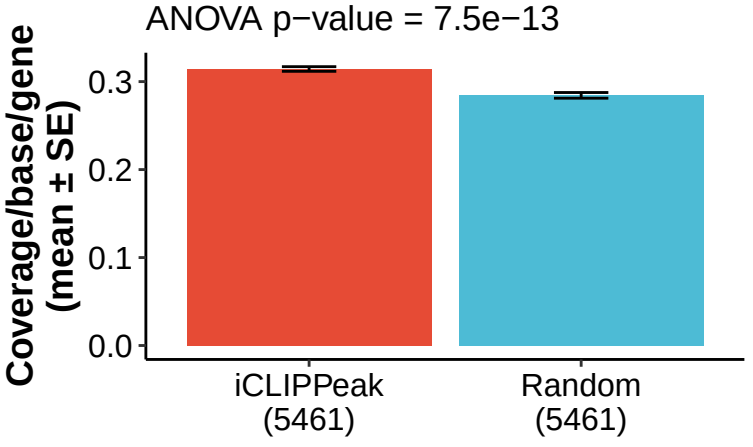
	diff	lwr	upr	p adj
Random−iCLIPPeak	−0.034	−0.043	−0.026	2.51e−14


Feature: Transcript
Reference size: 5461
Sample name: clip_input
iCLIPPeak
Random
0.350
0.325
0.300
0.275
Coverage/base/gene
−500
−250
0
250
500
Center



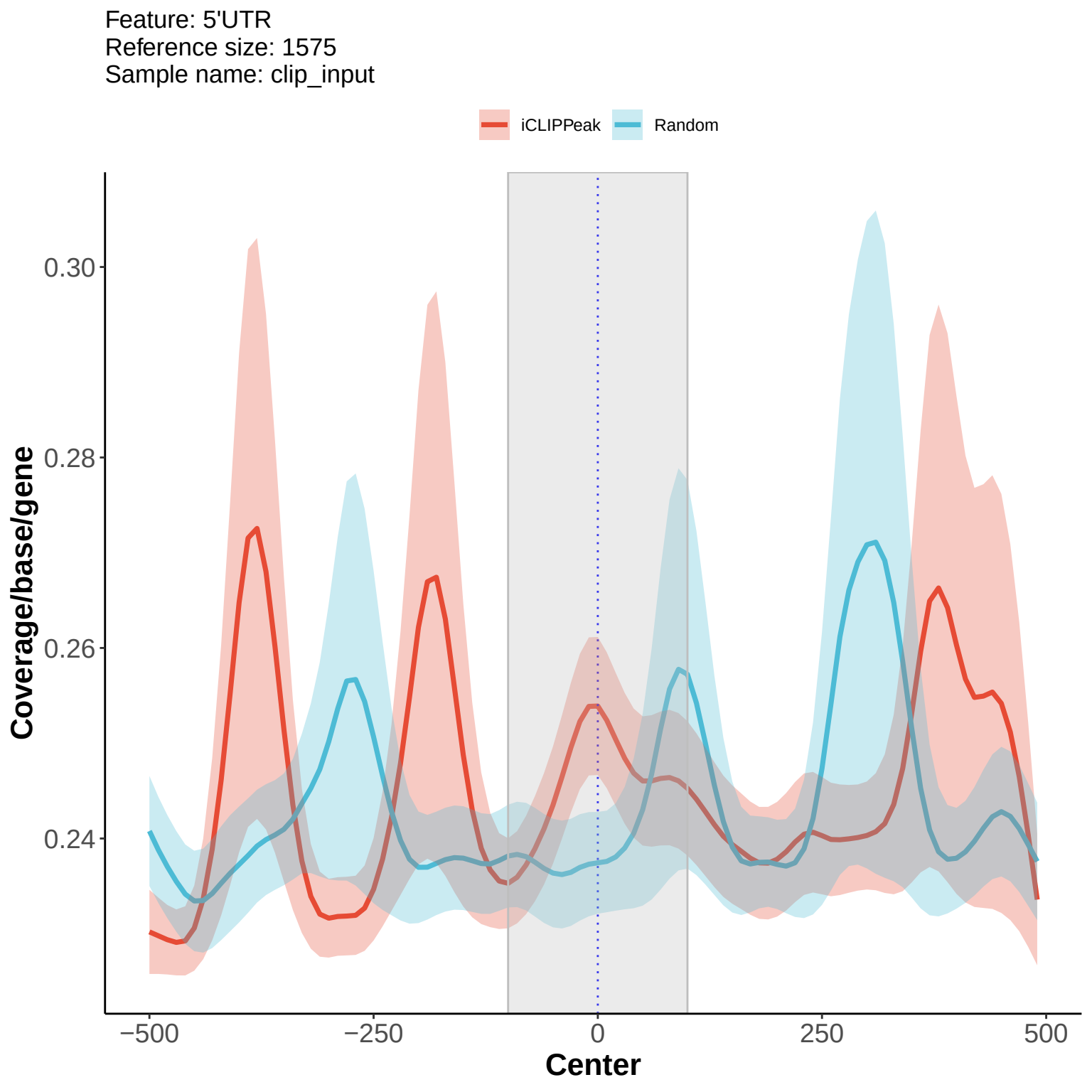






post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random−iCLIPPeak	−0.03	−0.038	−0.022	0


Feature: 5'UTR
Reference size: 1575
Sample name: clip_input
iCLIPPeak
Random
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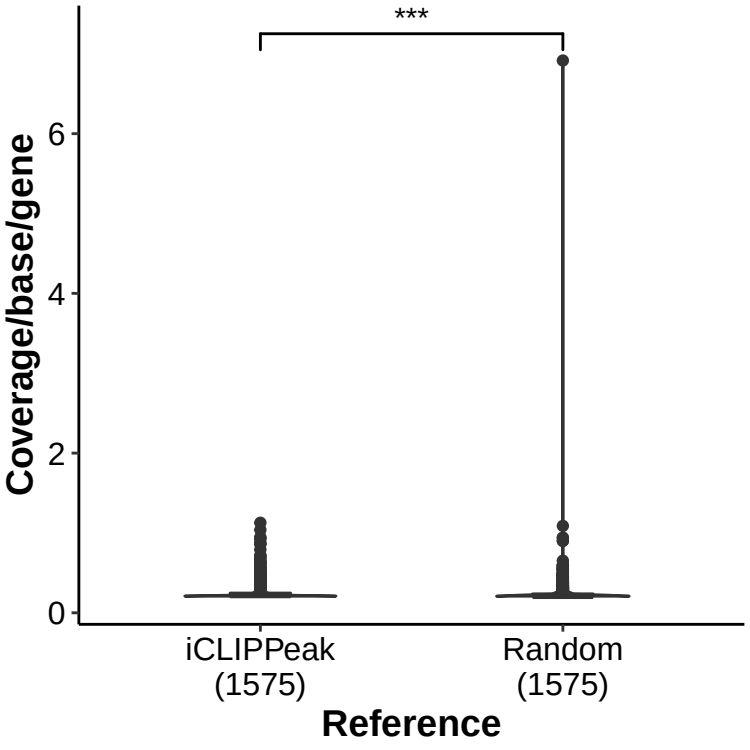
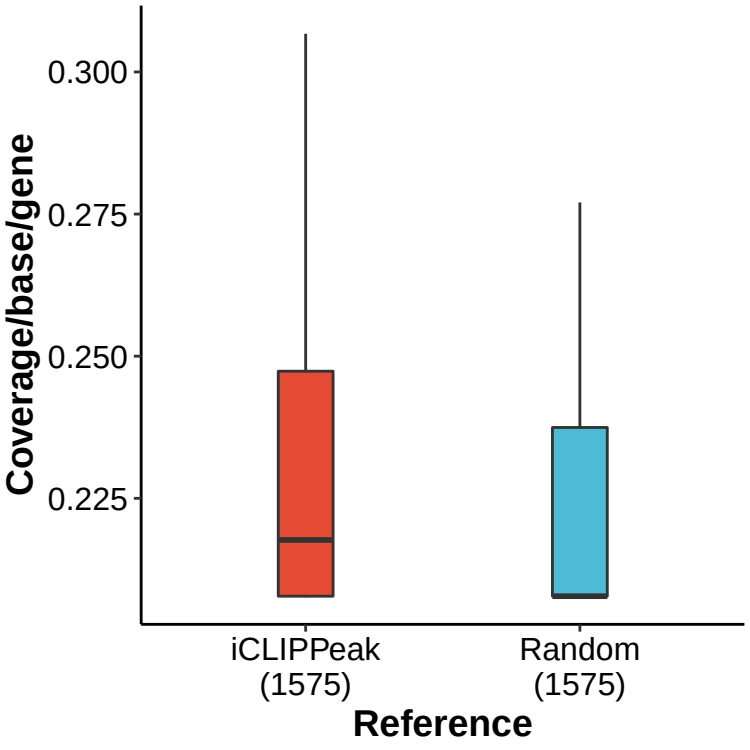
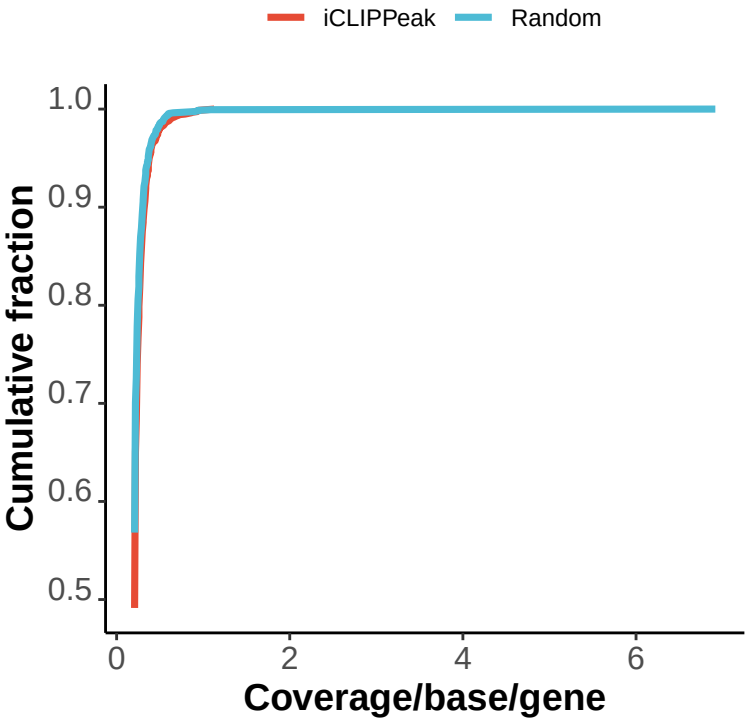
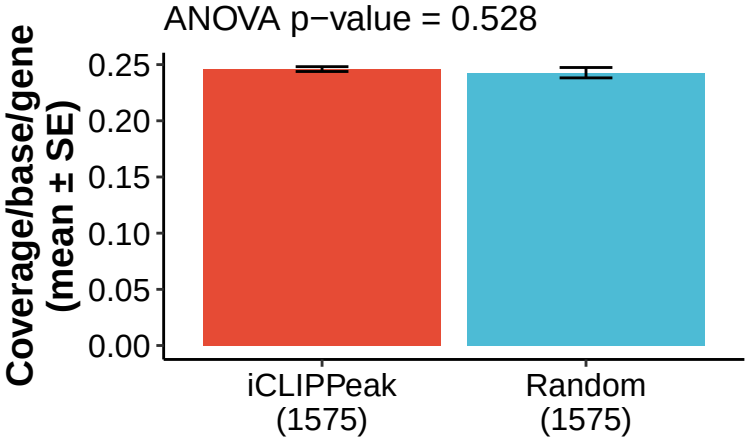
0.28
0.26
0.24
Coverage/base/gene
−500
−250
0
250
500
Center



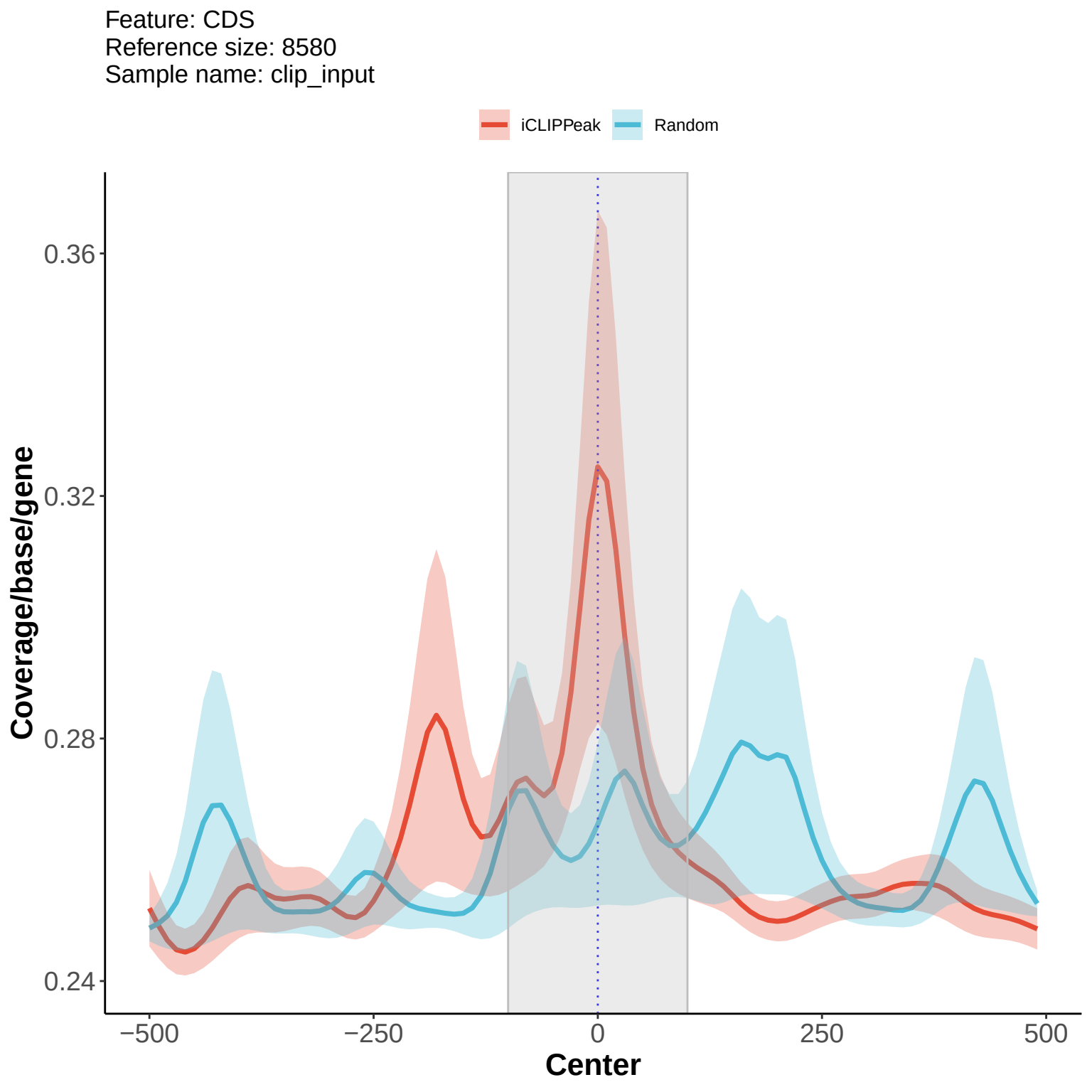






post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random−iCLIPPeak	−0.003	−0.013	0.007	0.528


Feature: CDS
Reference size: 8580
Sample name: clip_input
iCLIPPeak
Random
Coverage/base/gene
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0.32
0.28
0.24
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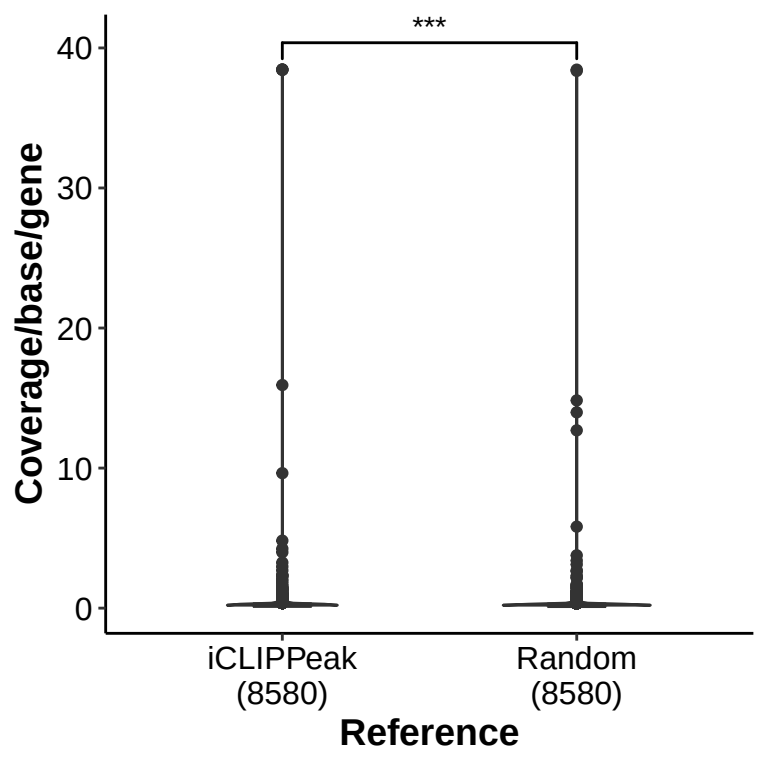
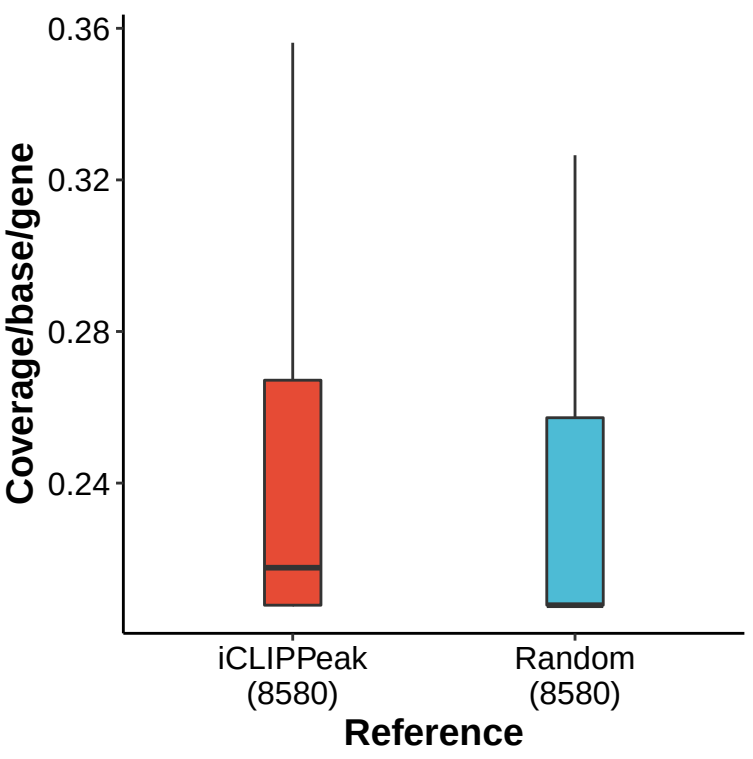
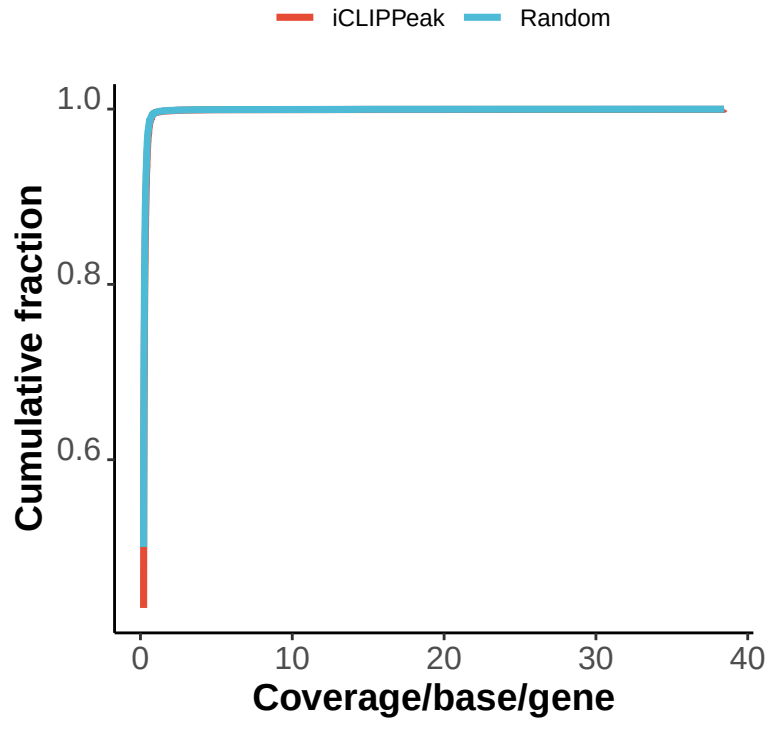
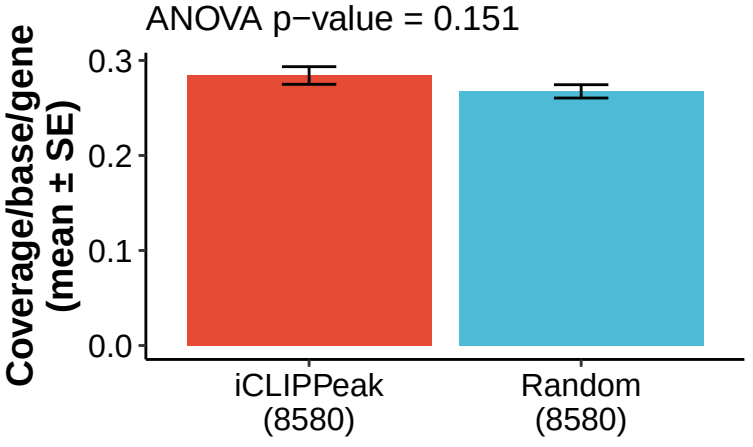
−250
0
250
500
Center



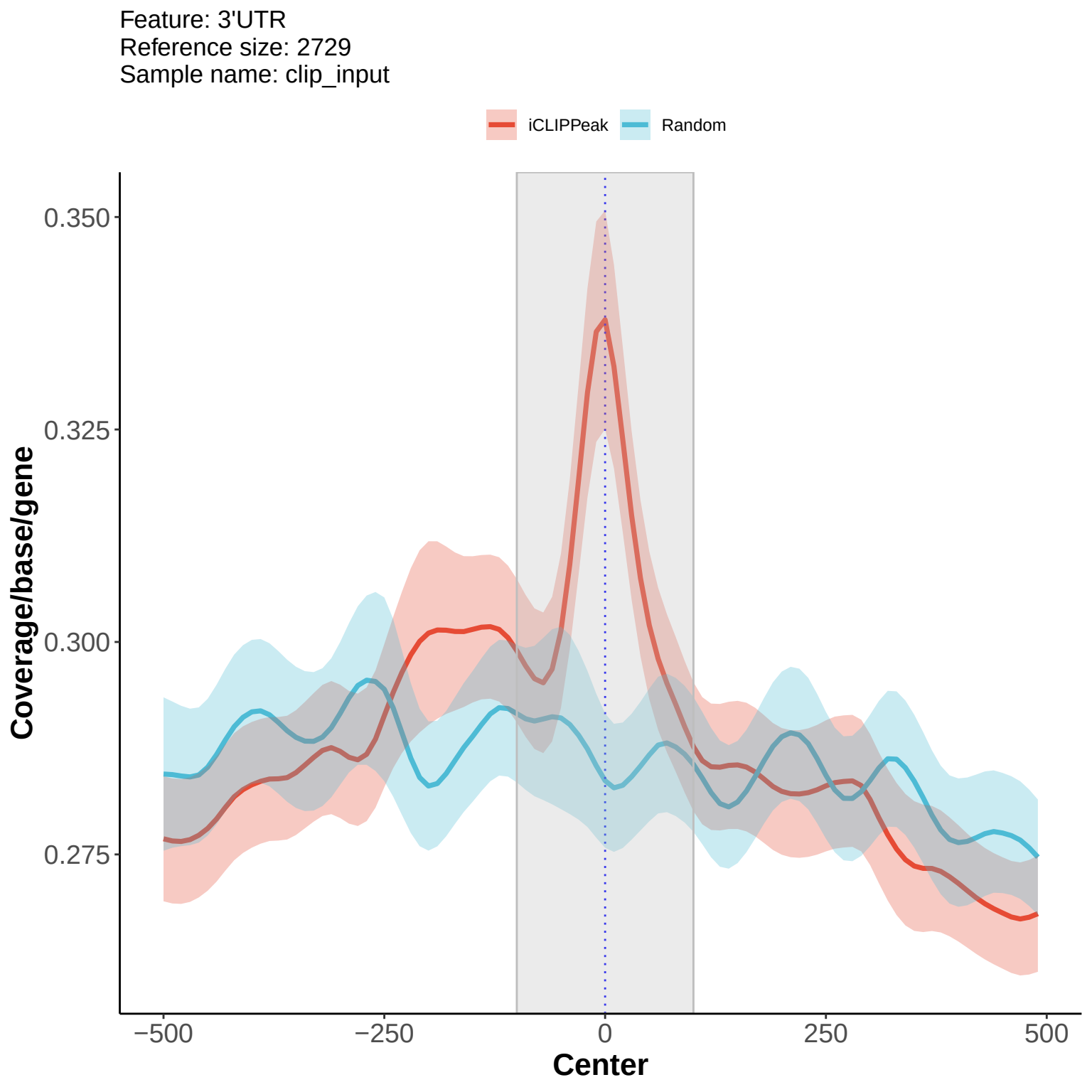


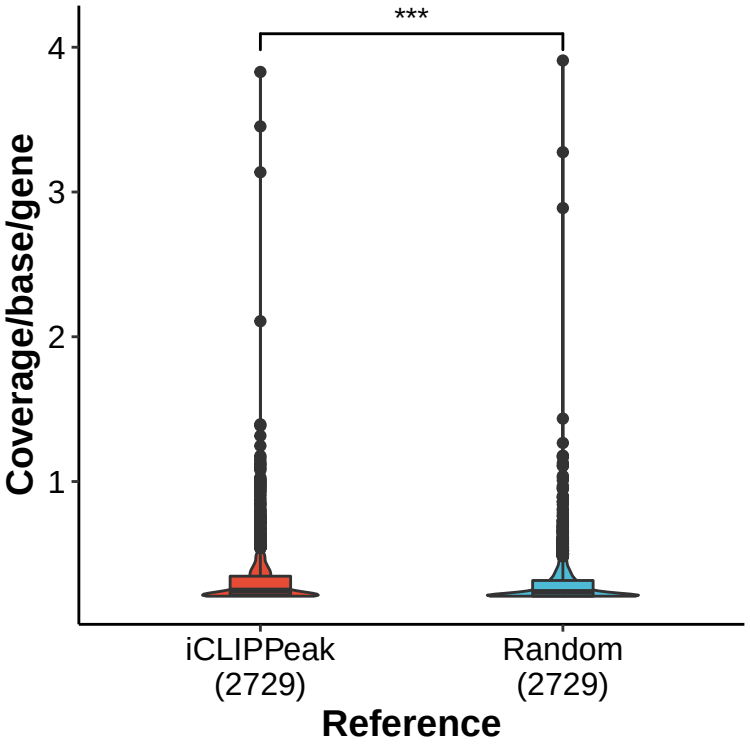


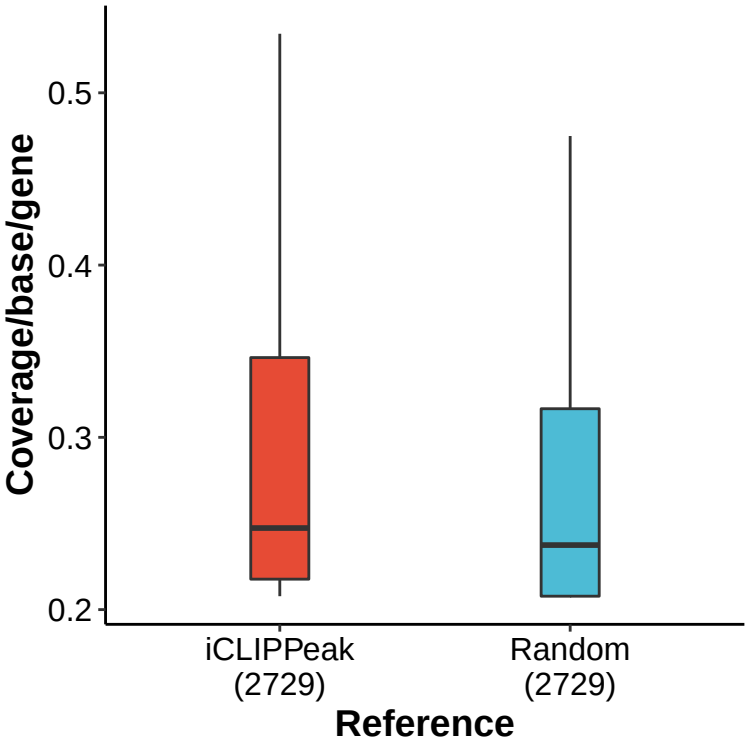


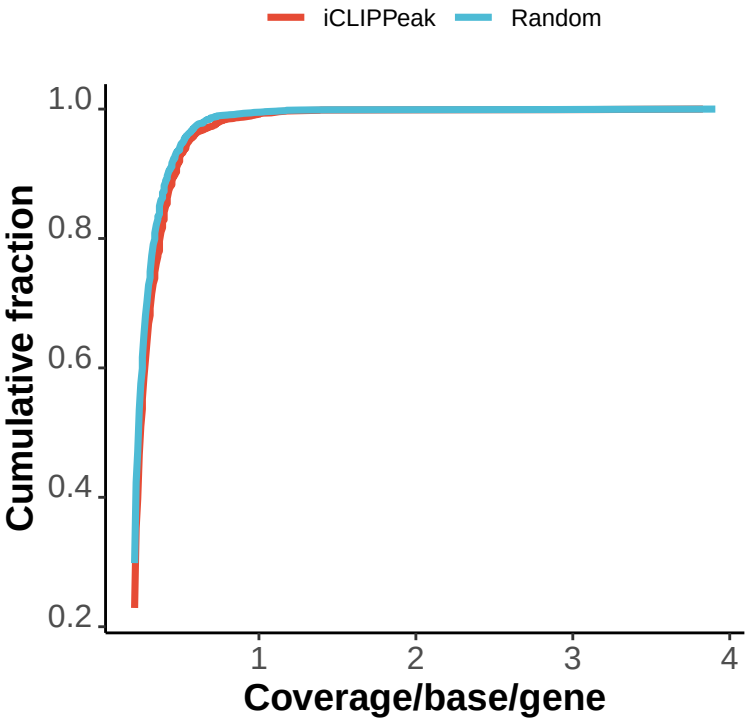
post hoc TukeyHSD test

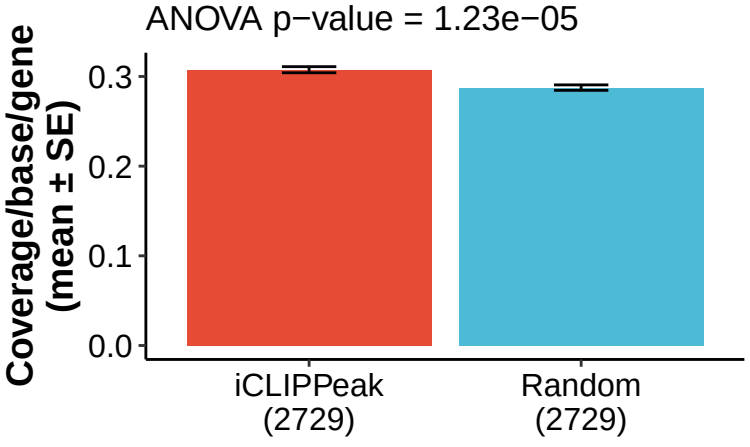
	diff	lwr	upr	p adj
Random−iCLIPPeak	−0.017	−0.04	0.006	0.151


Feature: 3'UTR
Reference size: 2729
Sample name: clip_input
iCLIPPeak
Random
0.350
0.325
0.300
0.275
Coverage/base/gene
−500
−250
0
250
500
Center



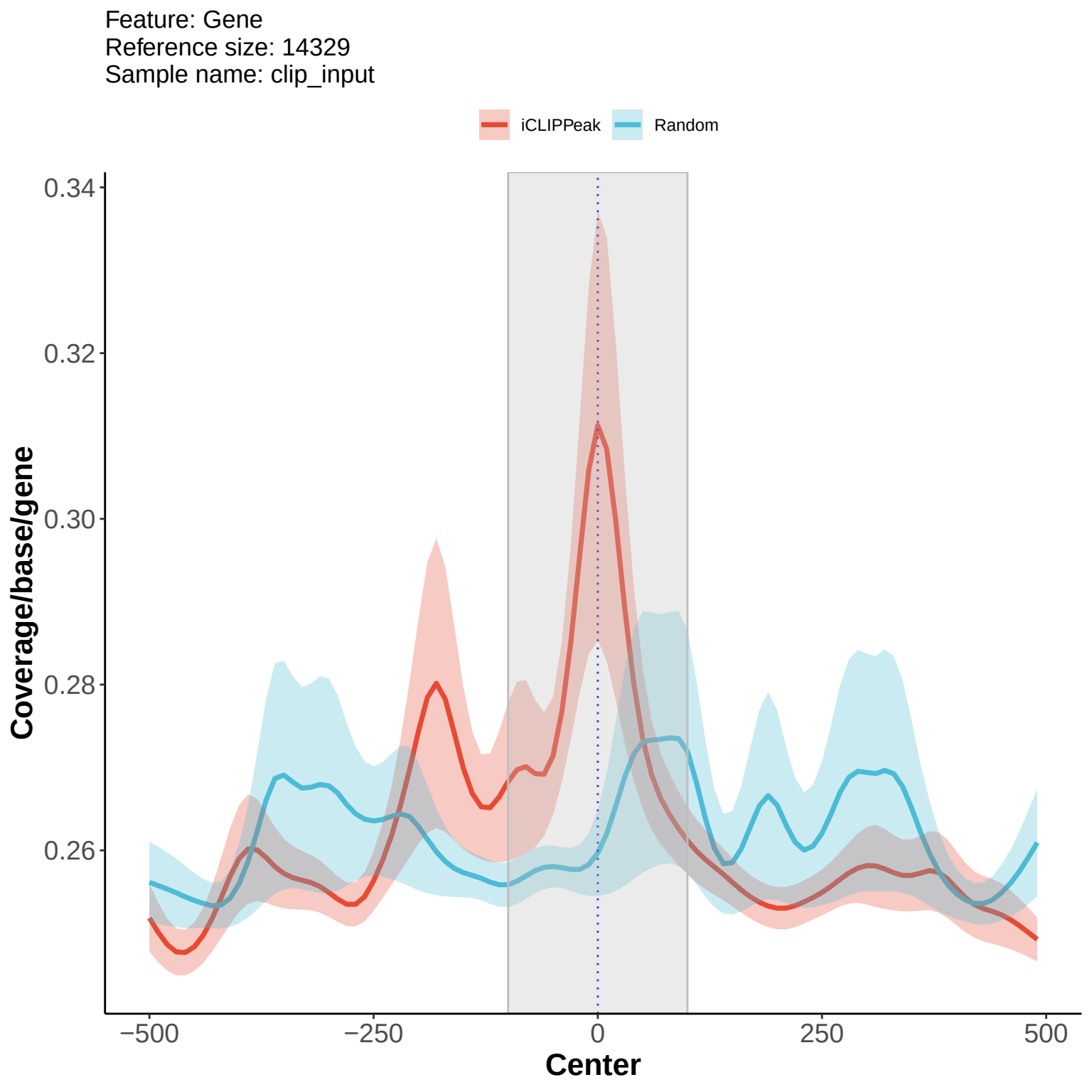


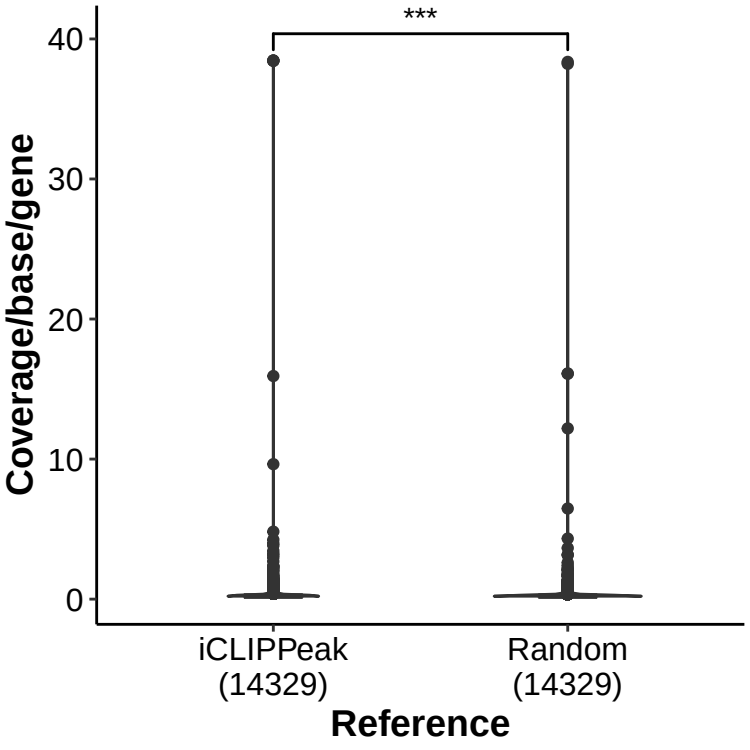


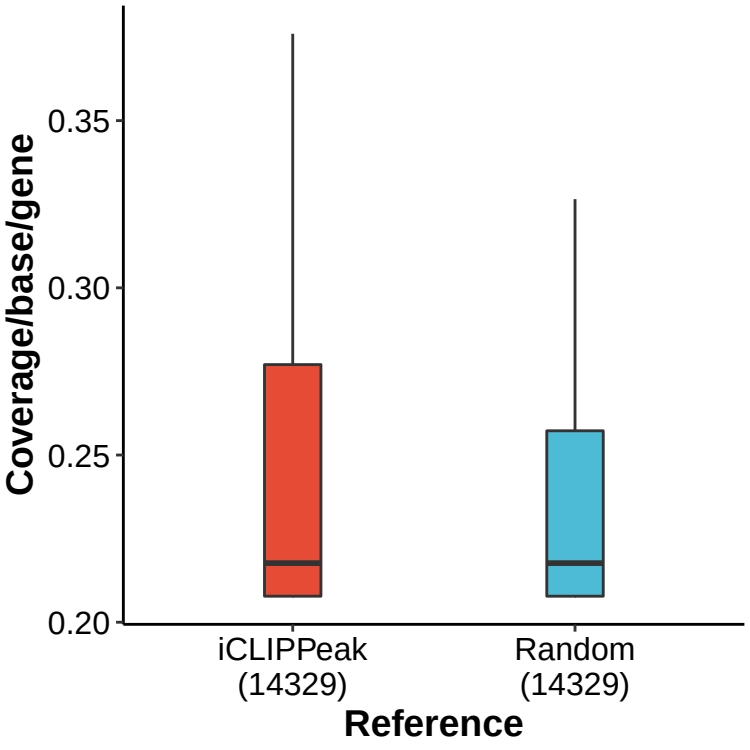


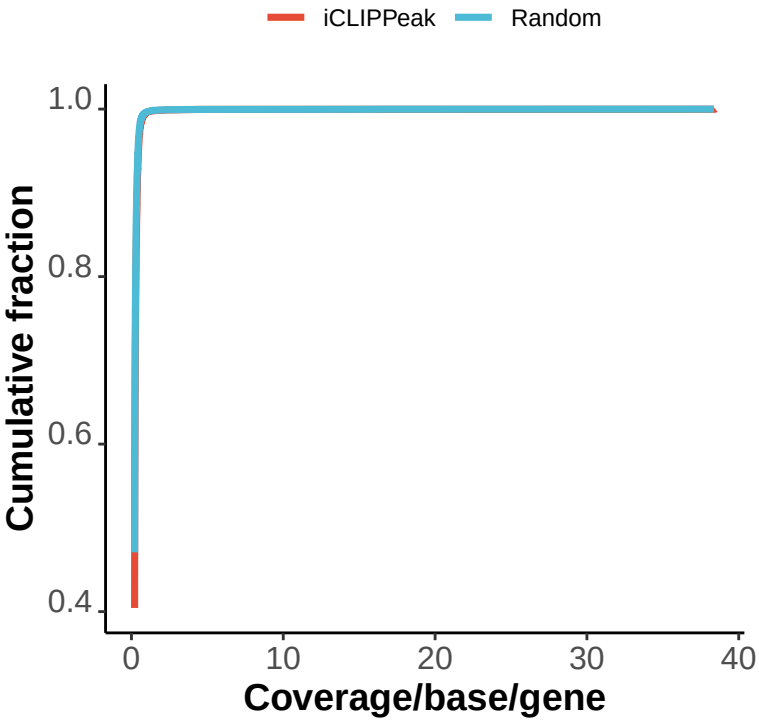
post hoc TukeyHSD test

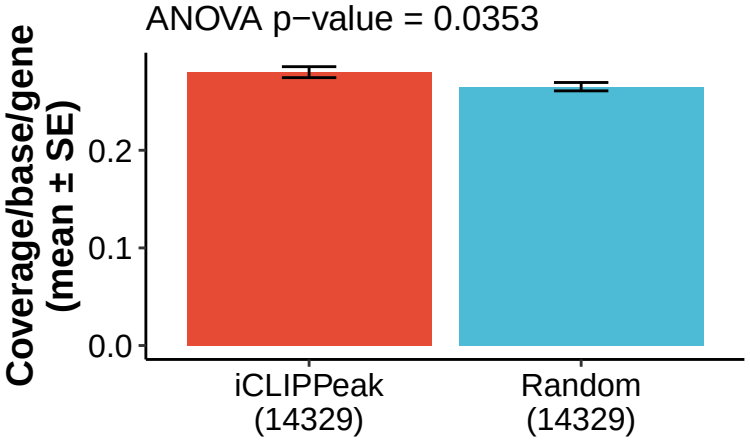
	diff	lwr	upr	p adj
Random−iCLIPPeak	−0.02	−0.029	−0.011	1.23e−05


Feature: Gene
Reference size: 14329
Sample name: clip_input
iCLIPPeak
Random
0.34
0.32
0.30
0.28
0.26
Coverage/base/gene
−500
−250
0
250
500
Center



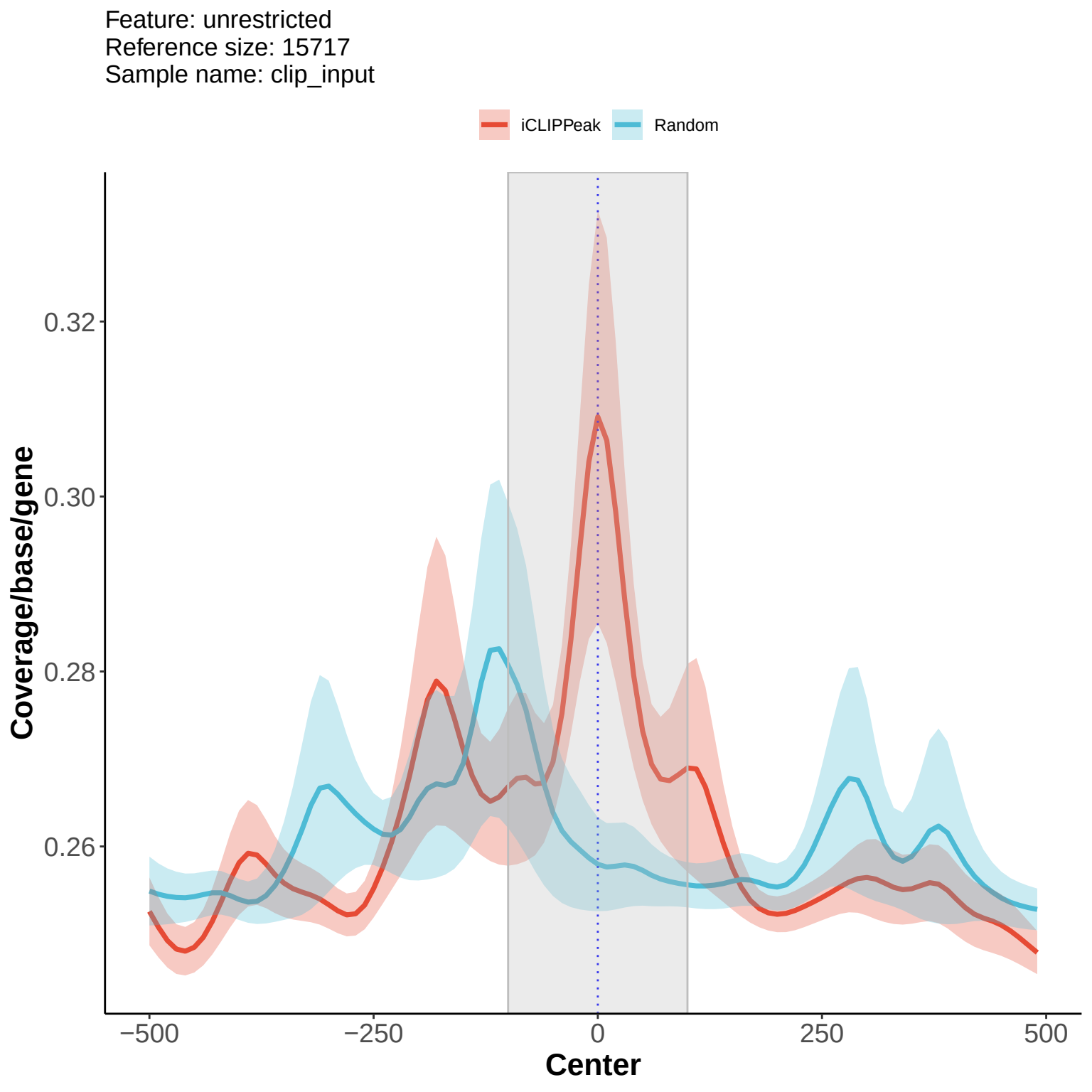


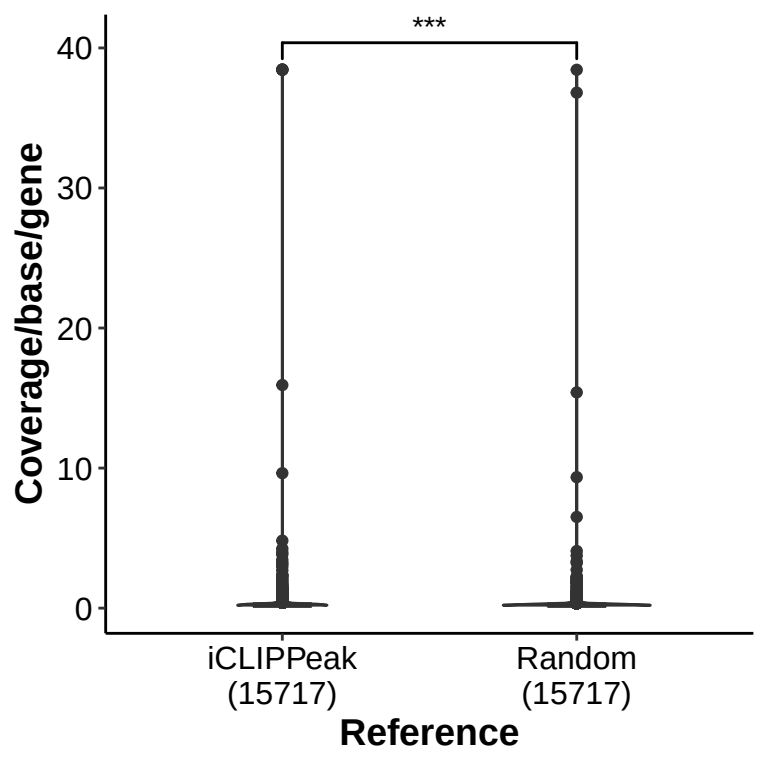


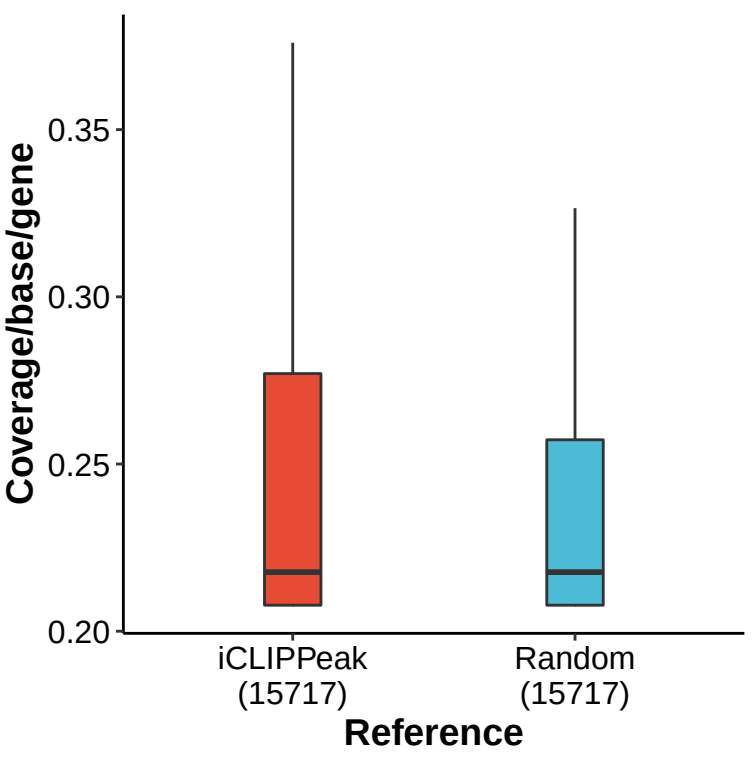


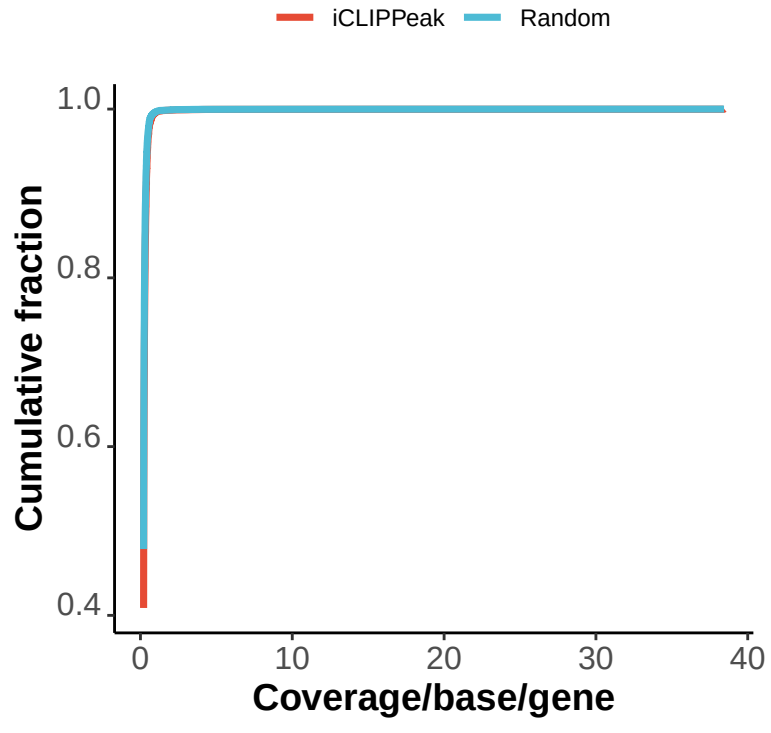
post hoc TukeyHSD test

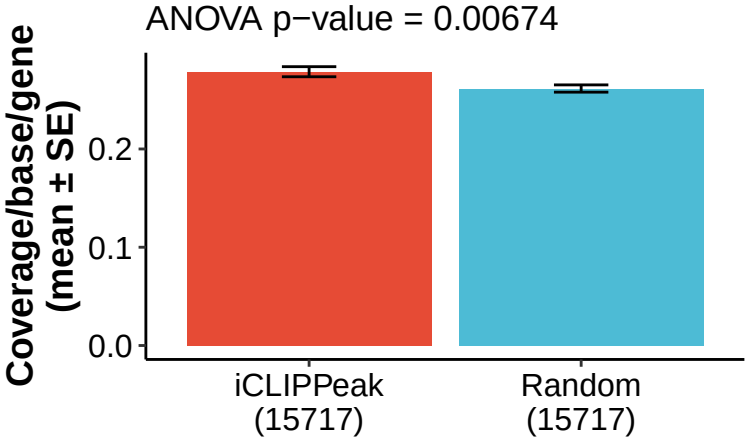
	diff	lwr	upr	p adj
Random−iCLIPPeak	−0.015	−0.029	−0.001	0.0353


Feature: unrestricted
Reference size: 15717
Sample name: clip_input
iCLIPPeak
Random
Coverage/base/gene
0.32
0.30
0.28
0.26
−500
−250
0
250
500
Center



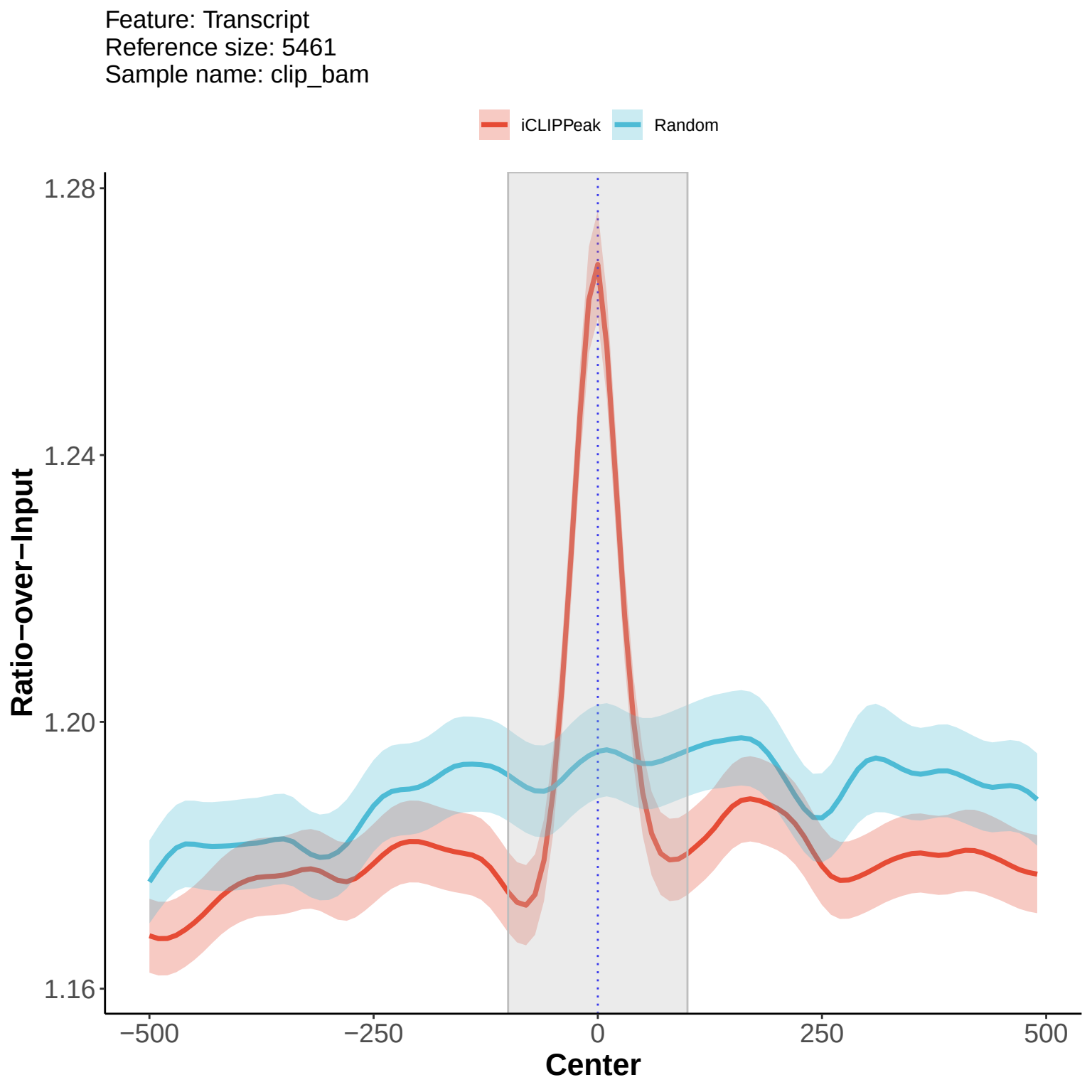


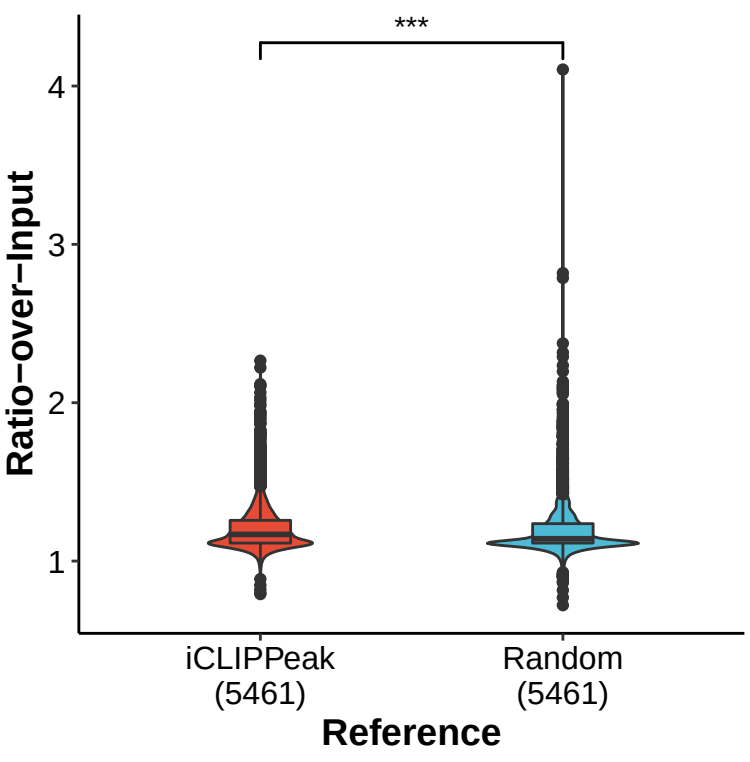


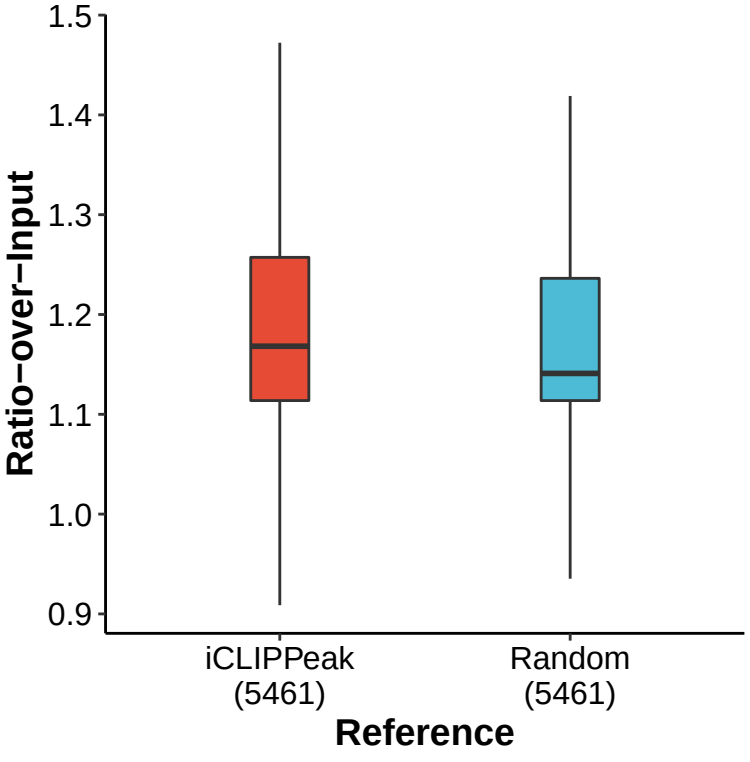


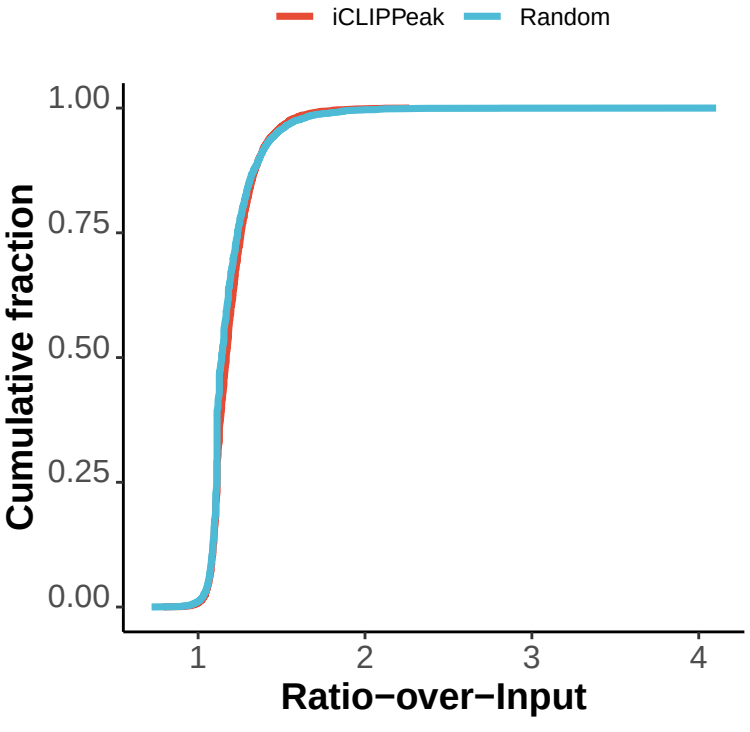
post hoc TukeyHSD test

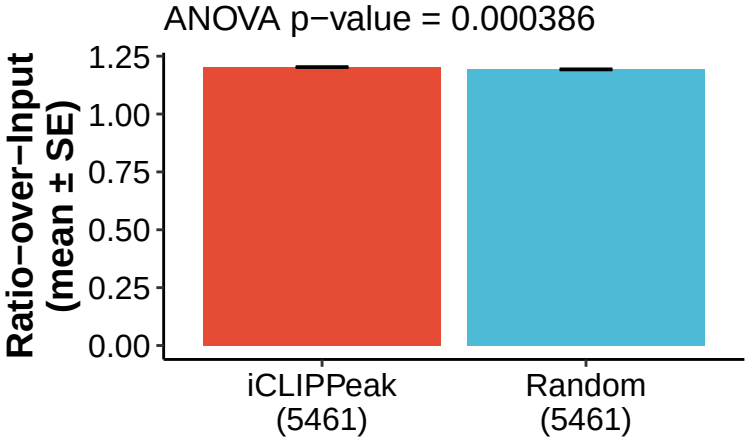
	diff	lwr	upr	p adj
Random−iCLIPPeak	−0.017	−0.029	−0.005	0.00674


Feature: Transcript
Reference size: 5461
Sample name: clip_bam
iCLIPPeak
Random
1.28
1.24
1.20
1.16
Ratio−over−Input
−500
−250
0
250
500
Center



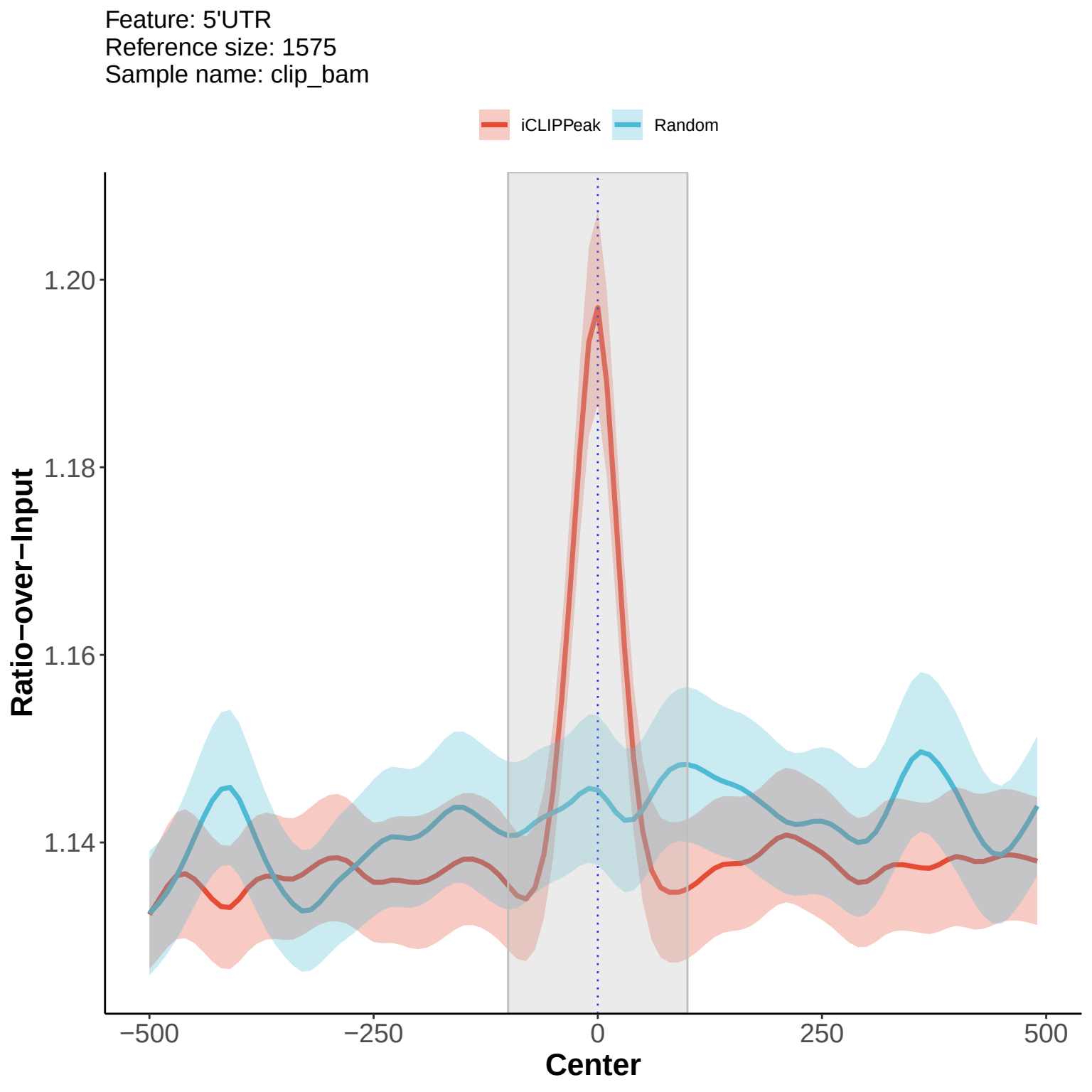


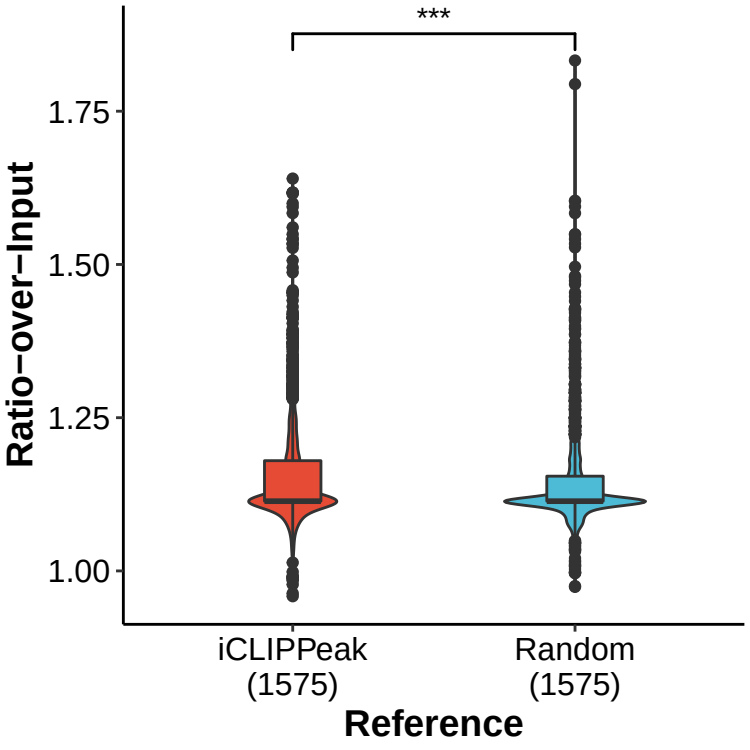


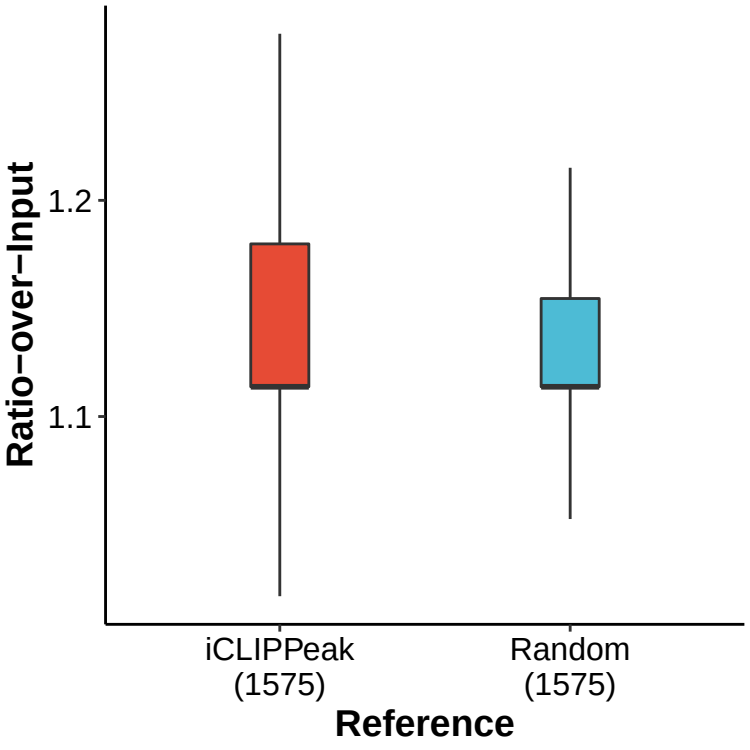


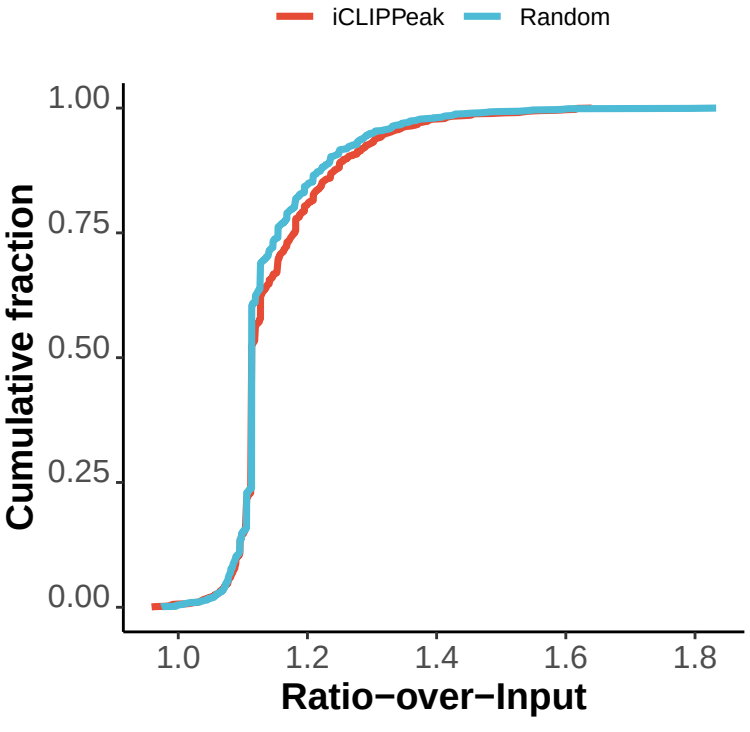
post hoc TukeyHSD test

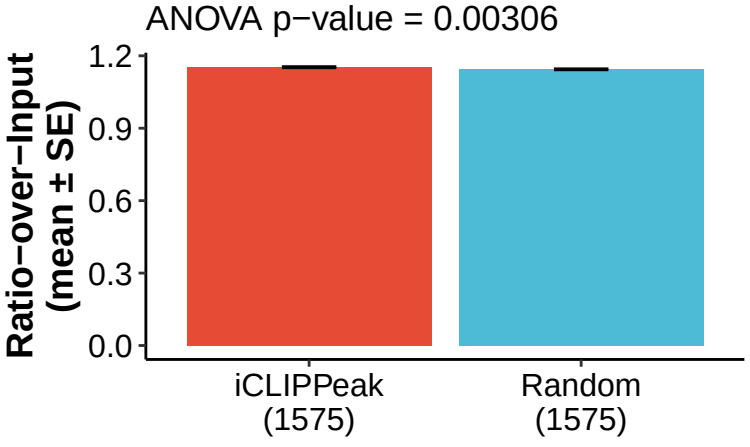
	diff	lwr	upr	p adj
Random−iCLIPPeak	−0.01	−0.015	−0.004	0.000386


Feature: 5'UTR
Reference size: 1575
Sample name: clip_bam
iCLIPPeak
Random
1.20
1.18
1.16
1.14
Ratio−over−Input
−500
−250
0
250
500
Center



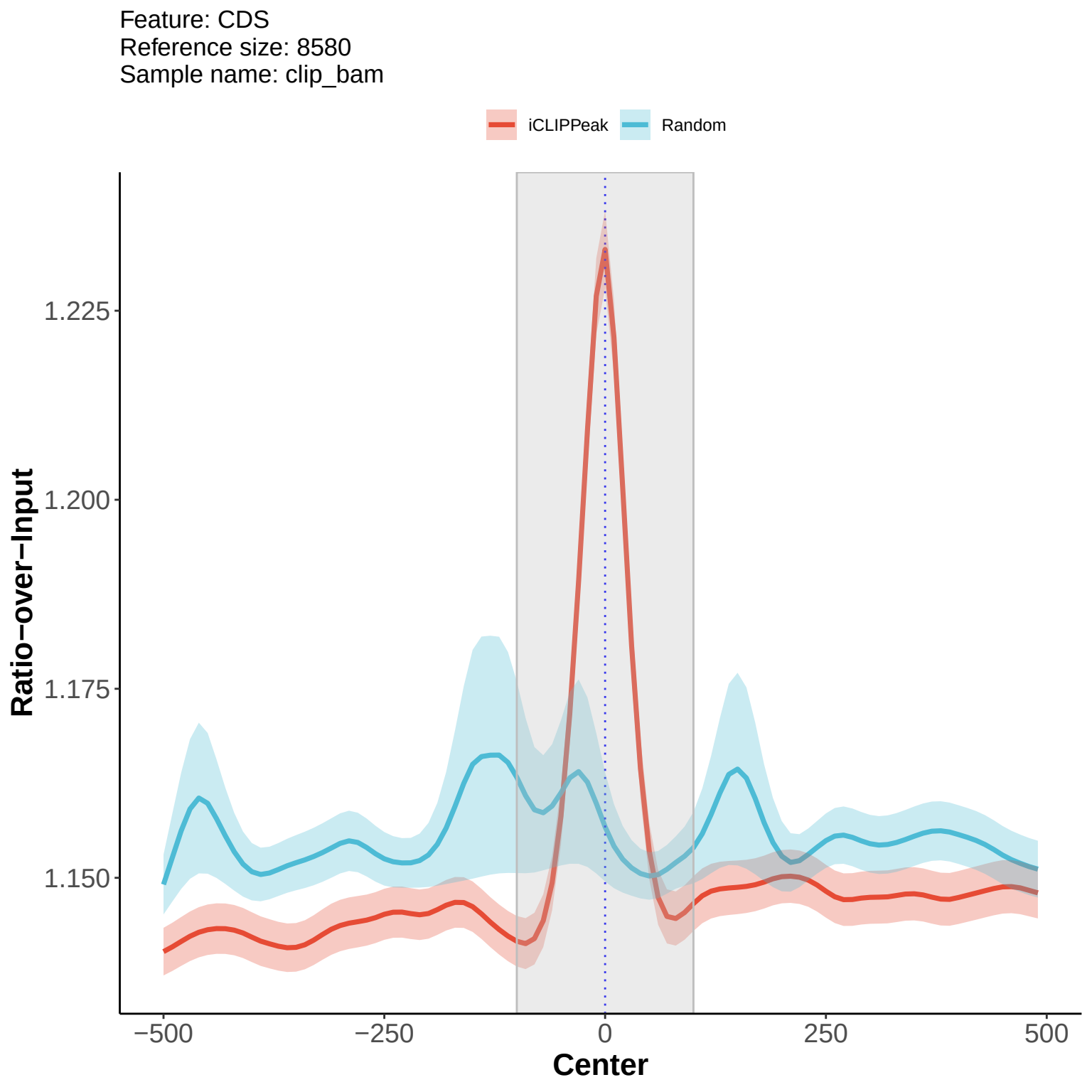


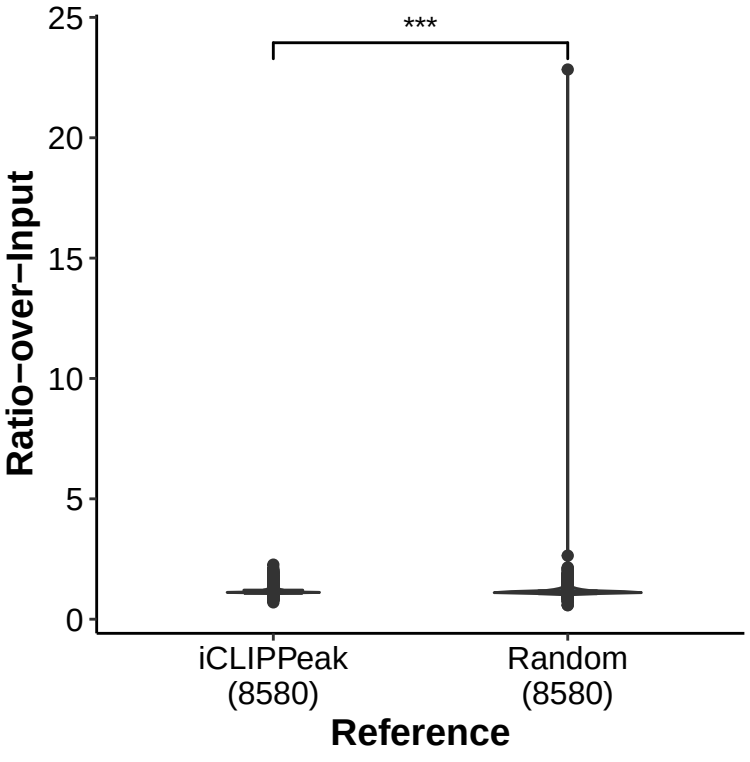


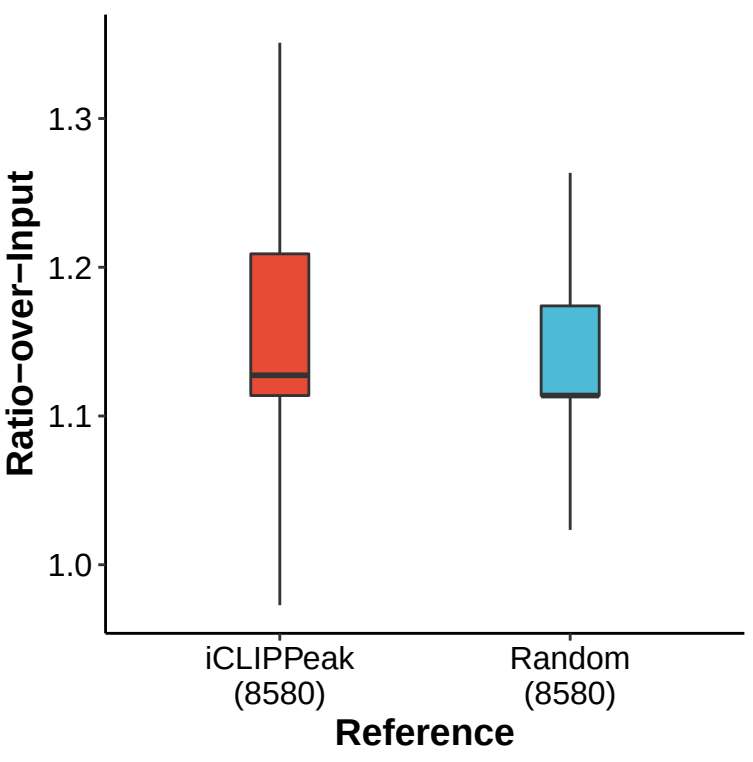


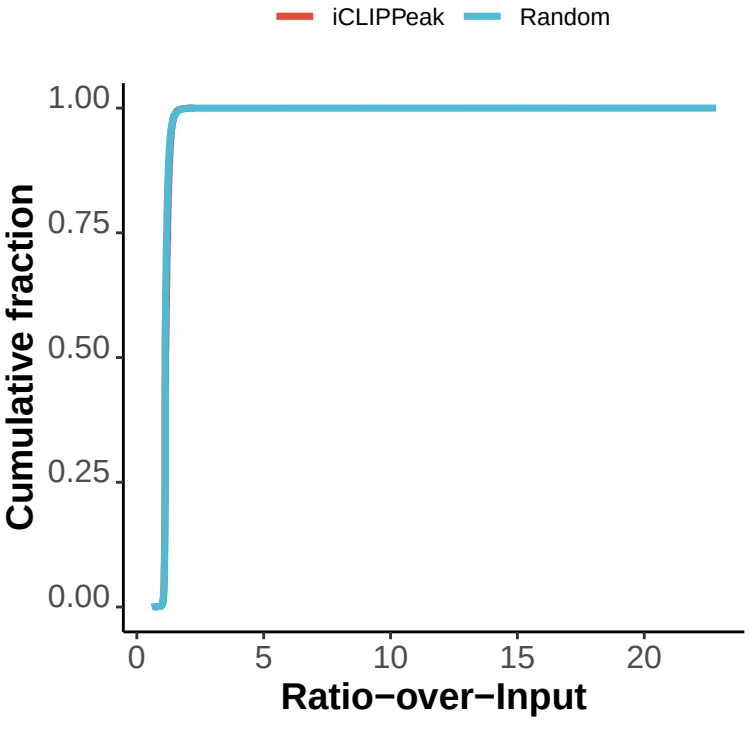
post hoc TukeyHSD test

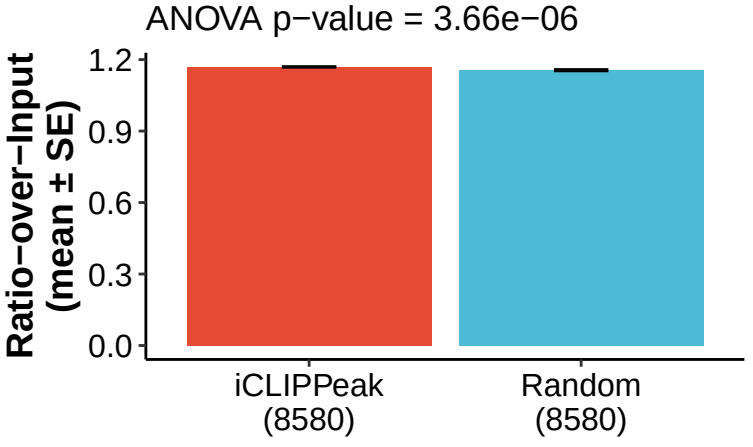
	diff	lwr	upr	p adj
Random−iCLIPPeak	−0.009	−0.015	−0.003	0.00306


Feature: CDS
Reference size: 8580
Sample name: clip_bam
iCLIPPeak
Random
Ratio−over−Input
1.225
1.200
1.175
1.150
−500
−250
0
250
500
Center



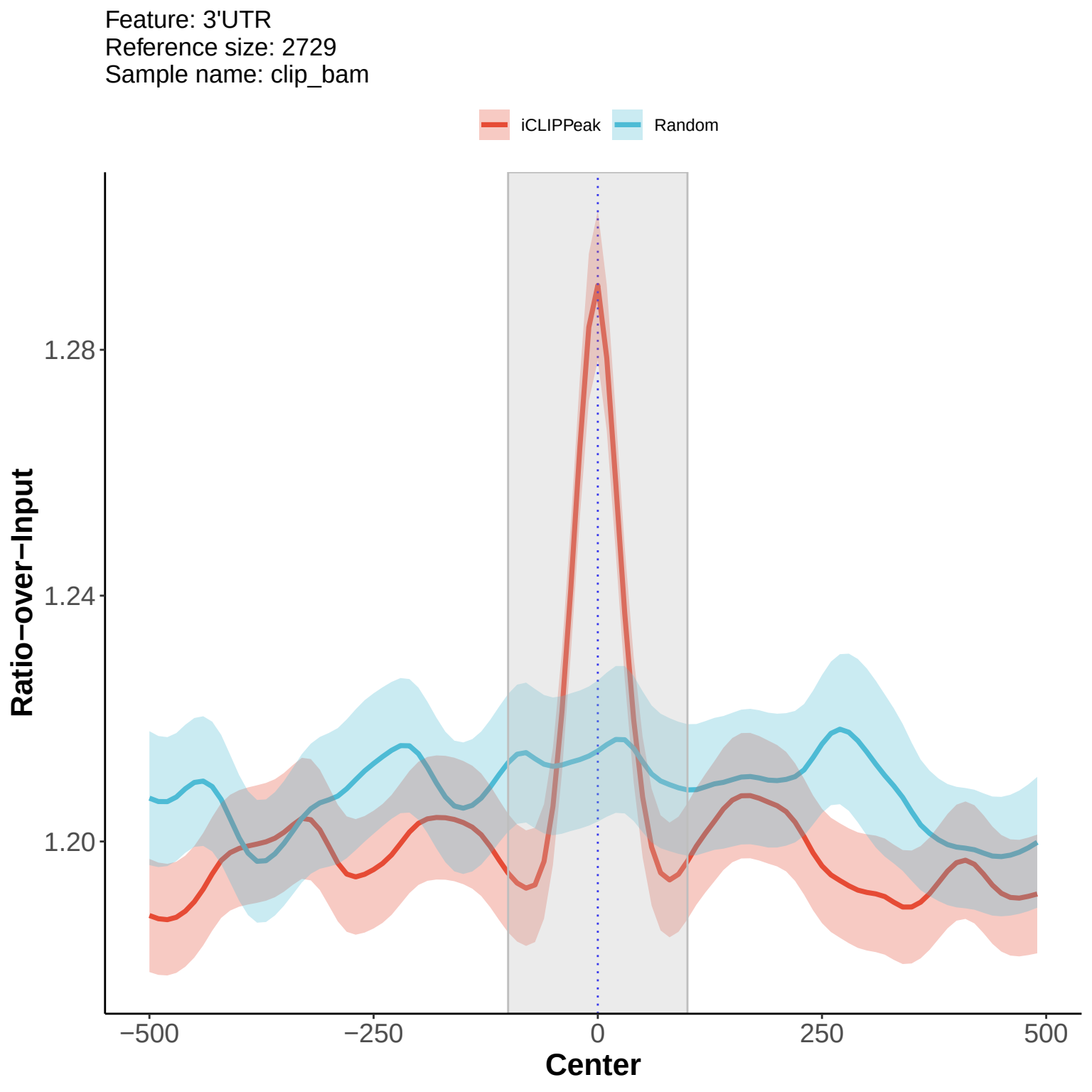






post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random−iCLIPPeak	−0.014	−0.019	−0.008	3.69e−06


Feature: 3'UTR
Reference size: 2729
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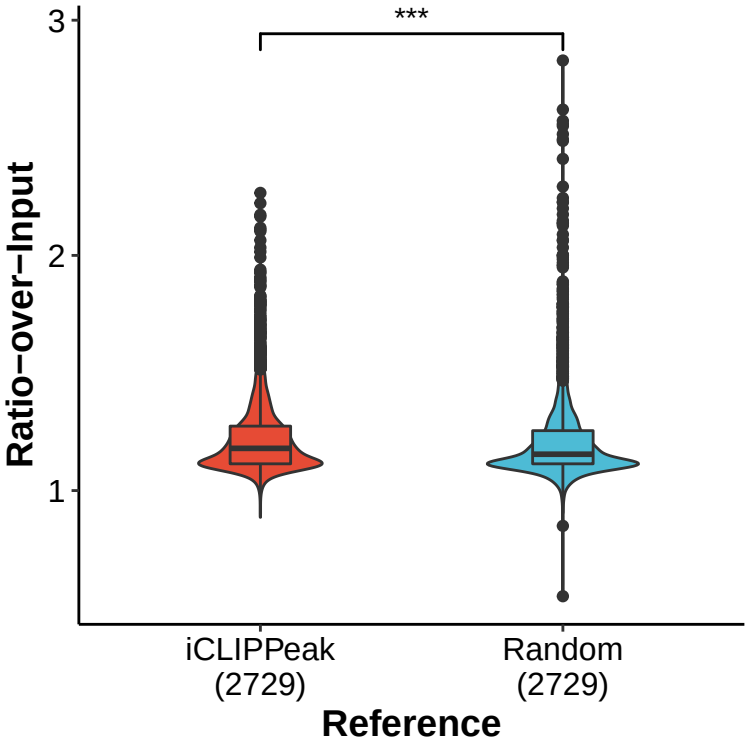
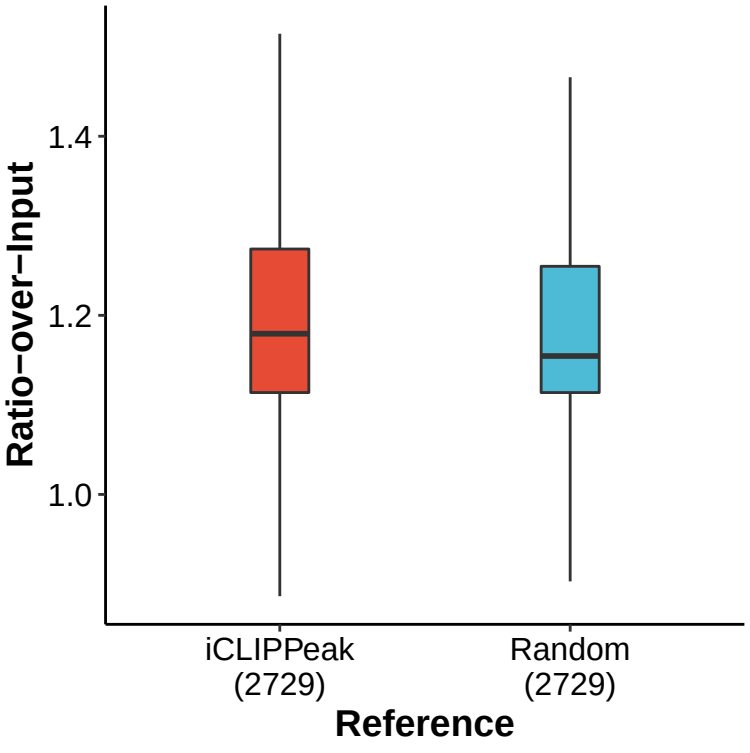
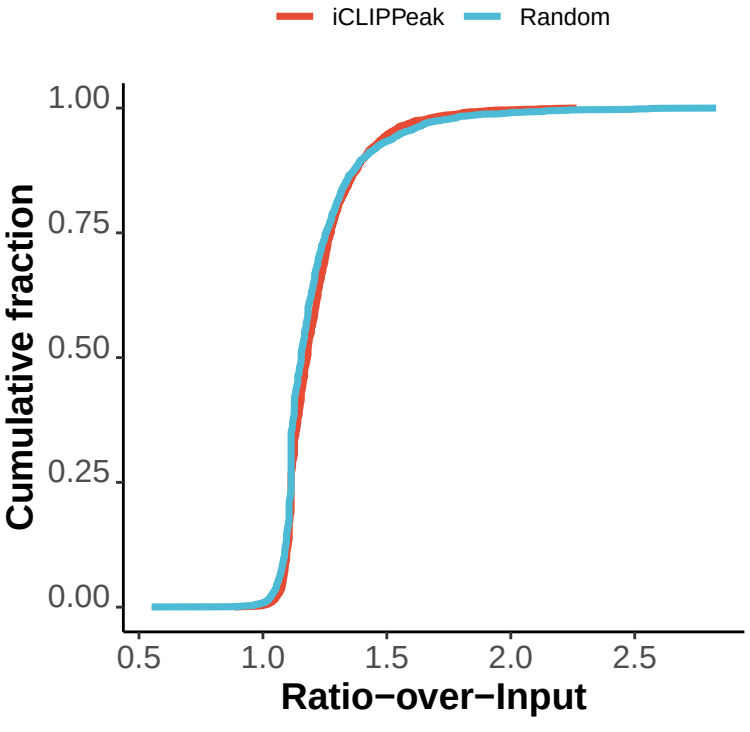
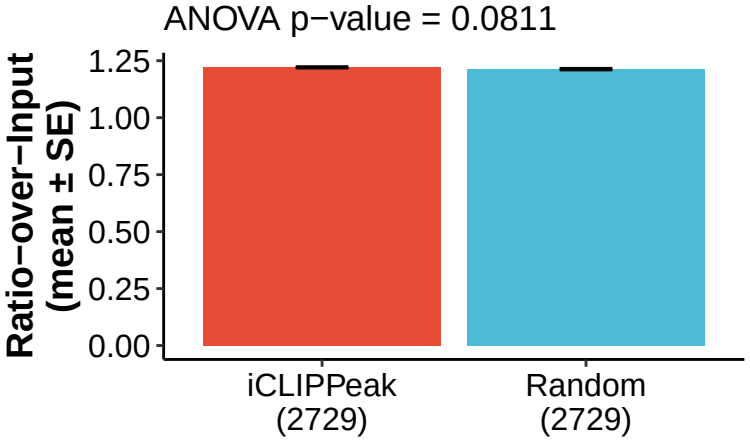
iCLIPPeak
Random
Ratio−over−Input
1.28
1.24
1.20
−500
−250
0
250
500
Center



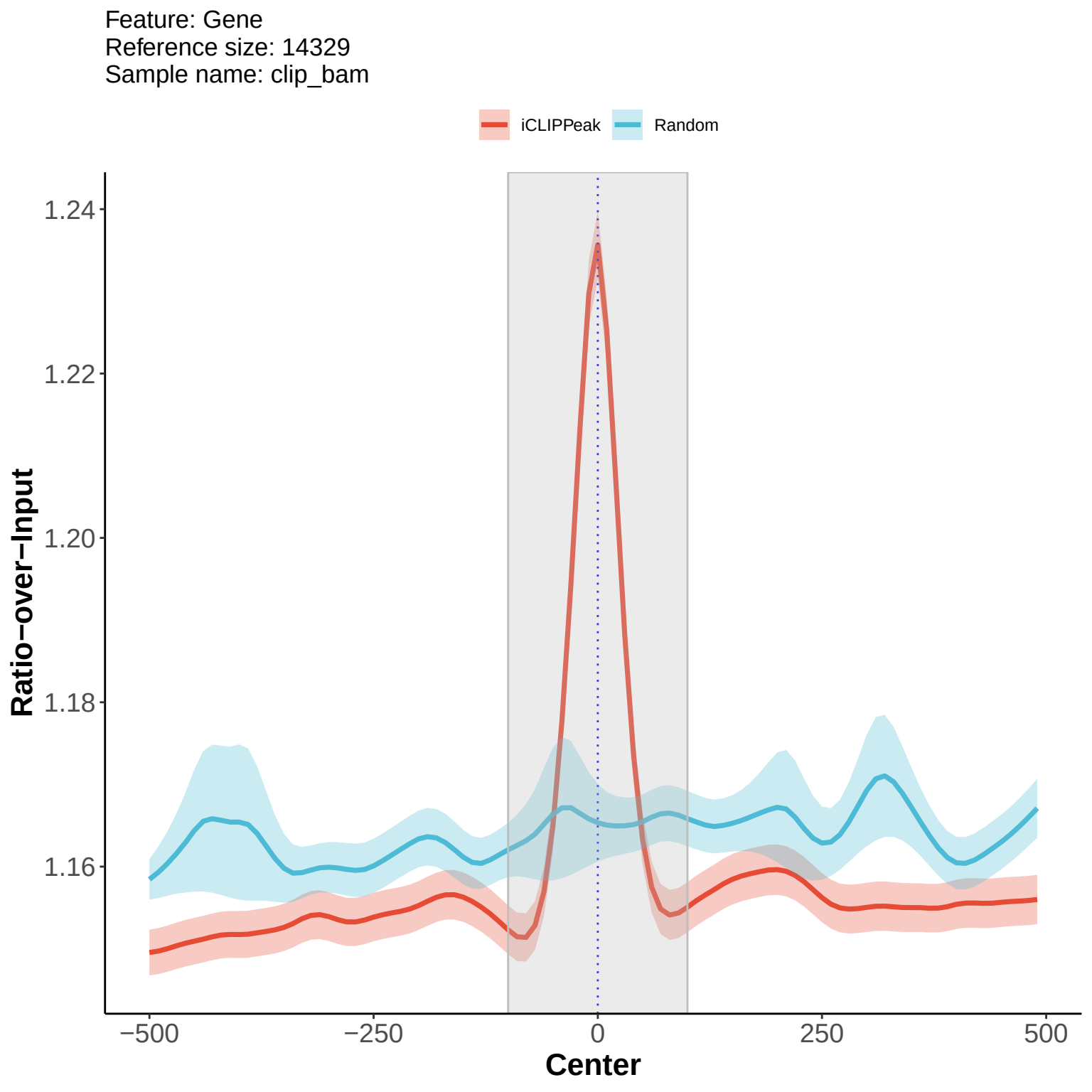


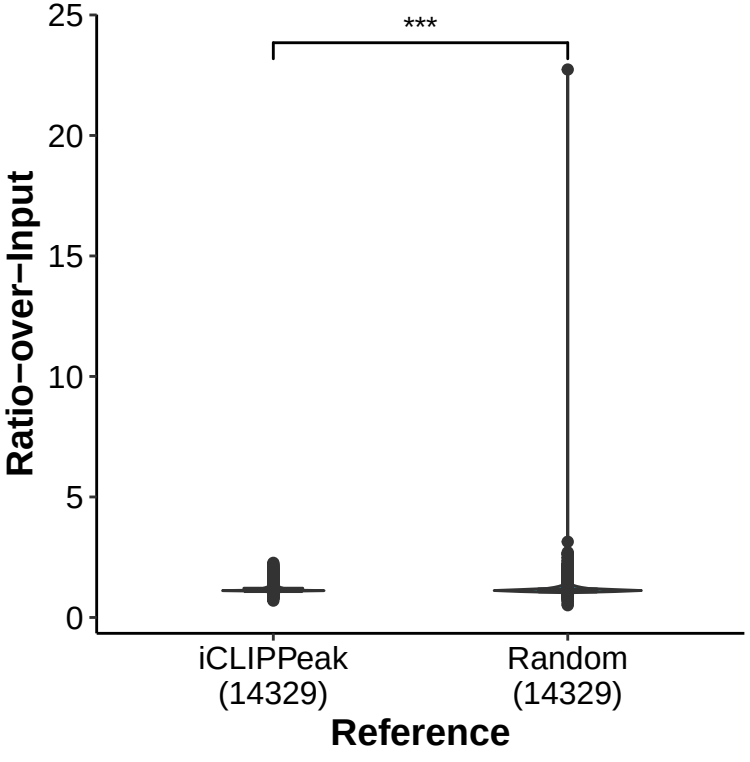


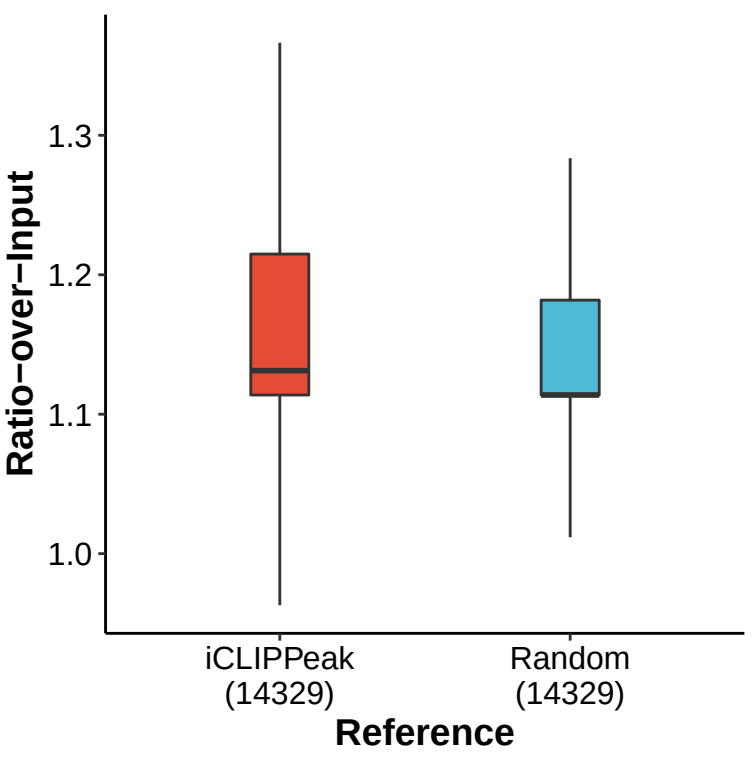


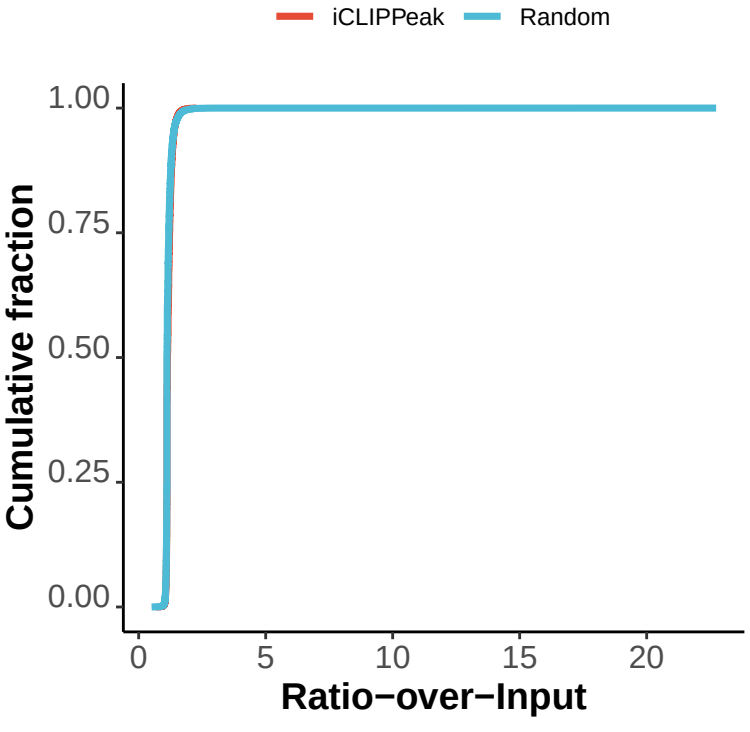
post hoc TukeyHSD test

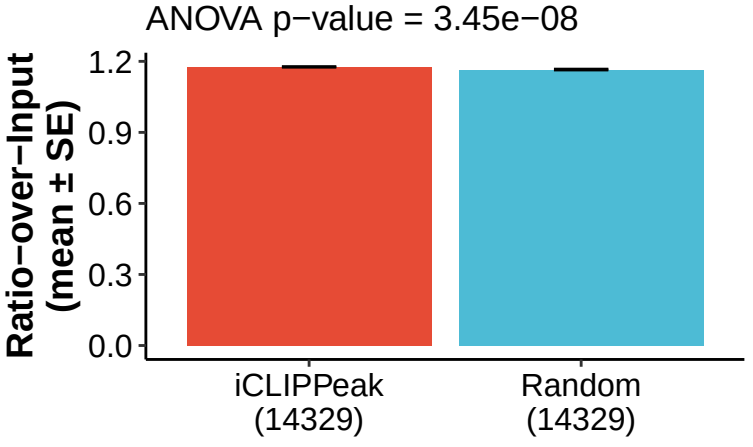
	diff	lwr	upr	p adj
Random−iCLIPPeak	−0.008	−0.017	0.001	0.0811


Feature: Gene
Reference size: 14329
Sample name: clip_bam
iCLIPPeak
Random
1.24
1.22
1.20
1.18
1.16
Ratio−over−Input
−500
−250
0
250
500
Center



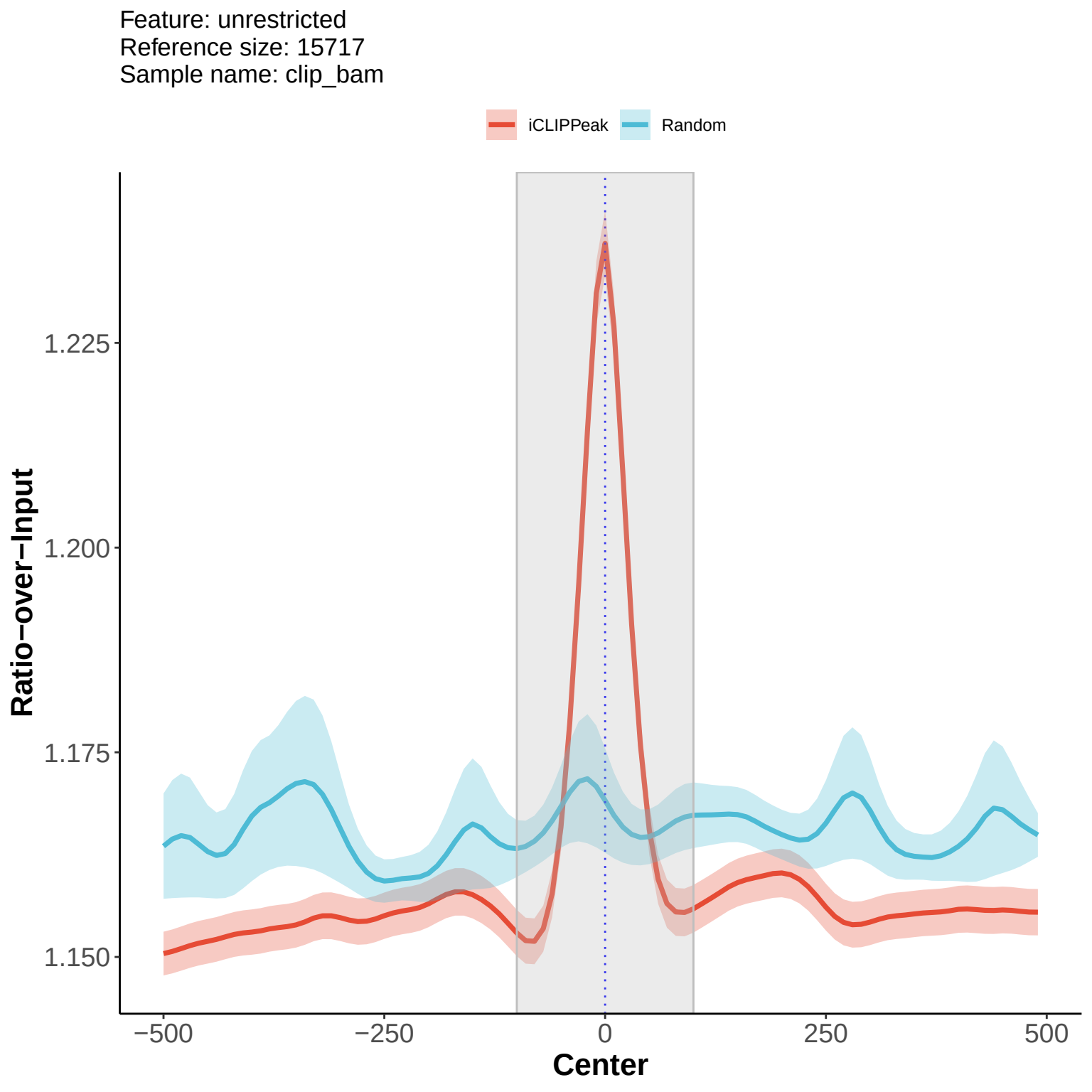


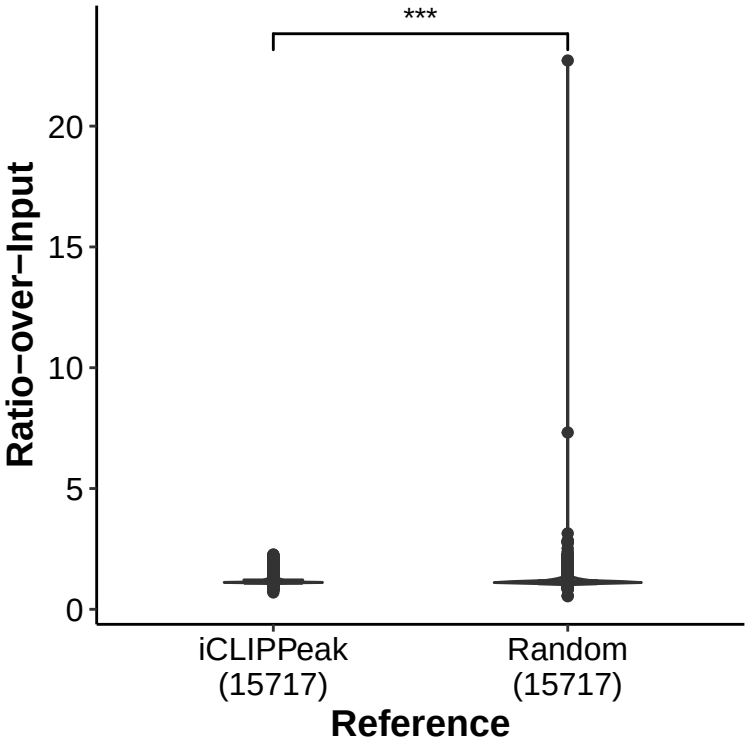


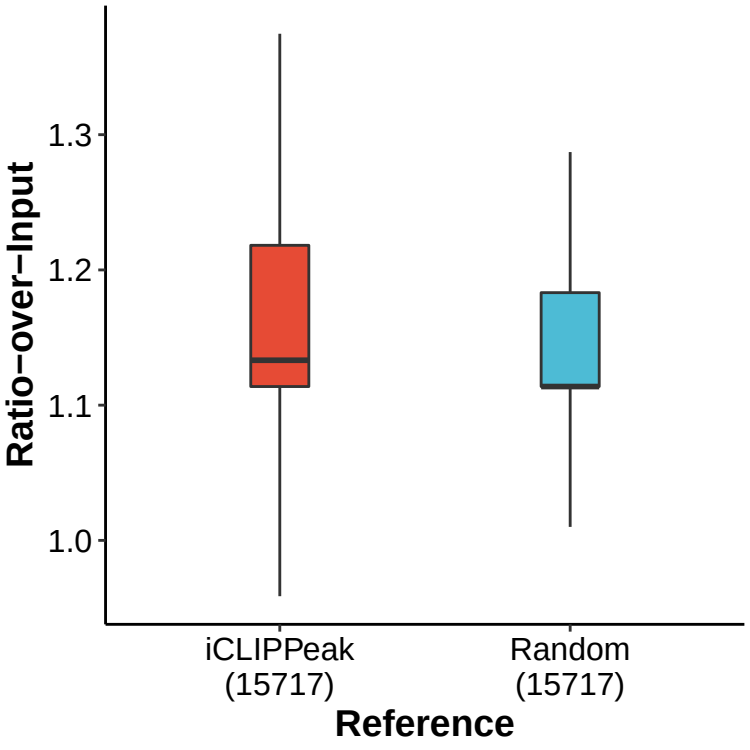


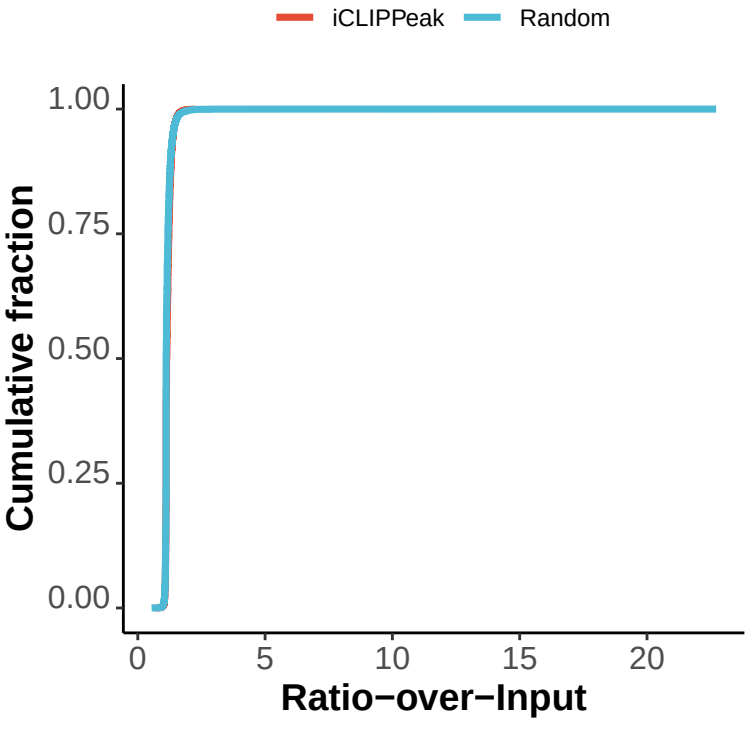
post hoc TukeyHSD test

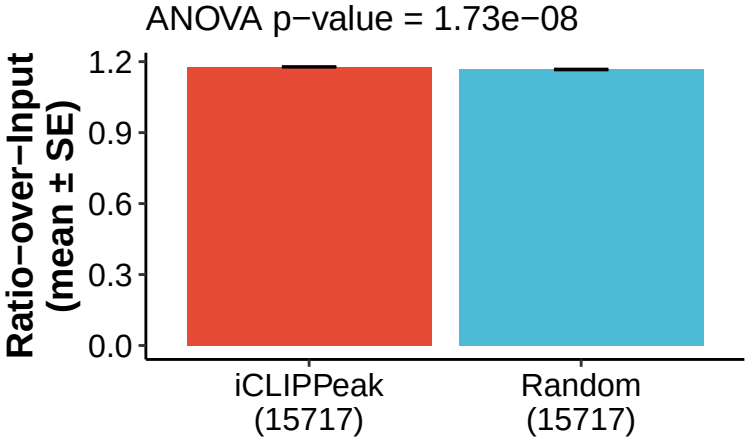
	diff	lwr	upr	p adj
Random−iCLIPPeak	−0.011	−0.015	−0.007	3.42e−08


Feature: unrestricted
Reference size: 15717
Sample name: clip_bam
iCLIPPeak
Random
Ratio−over−Input
1.225
1.200
1.175
1.150
−500
−250
0
250
500
Center









post hoc TukeyHSD test

	diff	lwr	upr	p adj
Random−iCLIPPeak	−0.011	−0.015	−0.007	1.71e−08

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