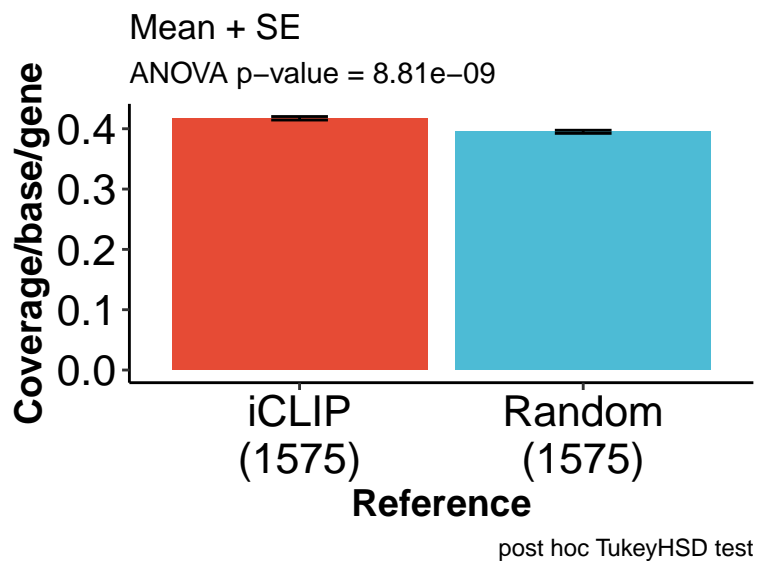
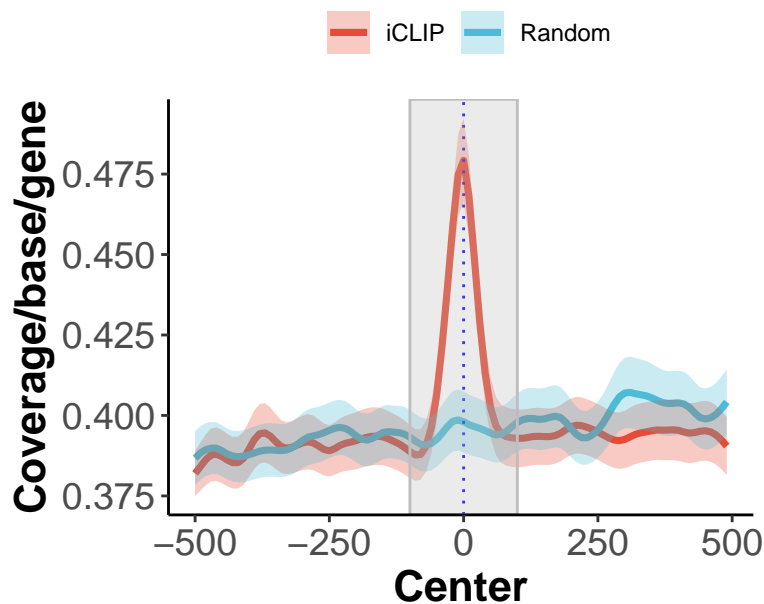
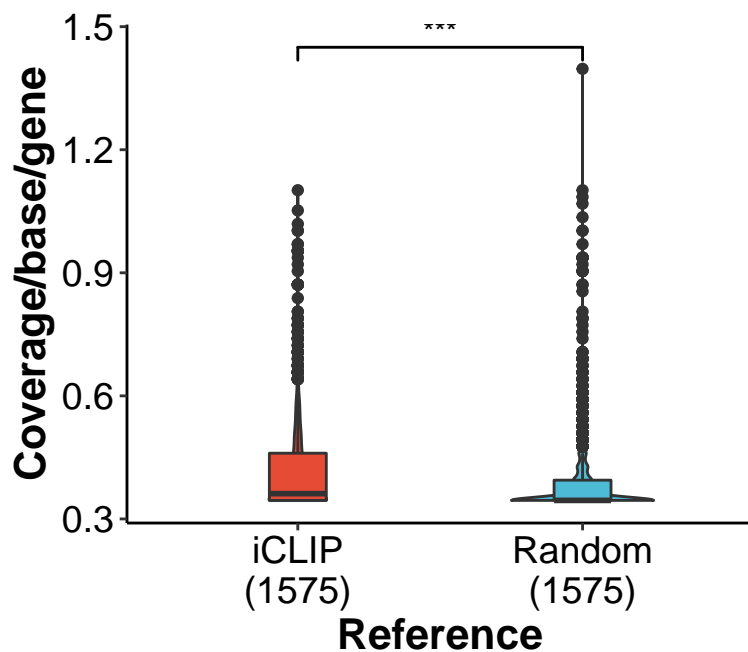


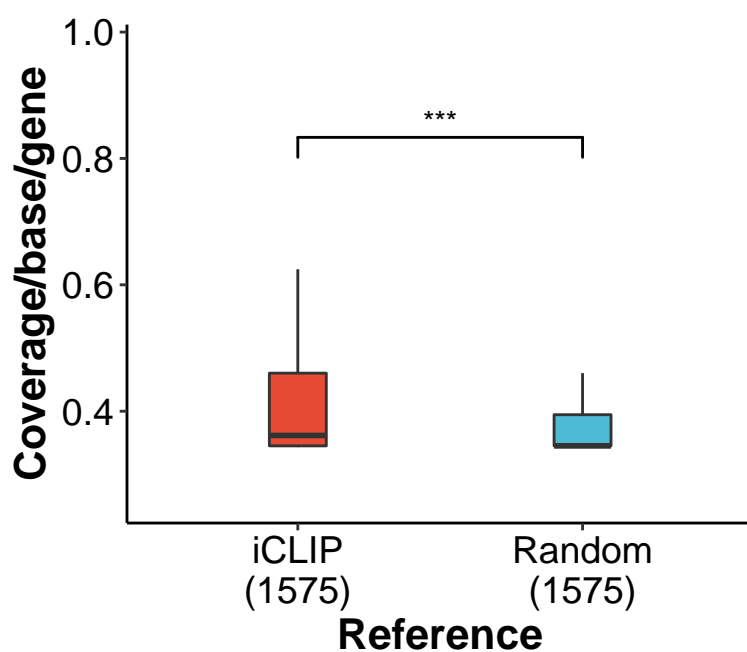
Feature: 5'UTR  
Reference size: 1575  
Sample name: query



	diff	lwr	upr	p adj
Random-iCLIP	-0.022	-0.03	-0.015	$6.9 \times 10^{-9}$

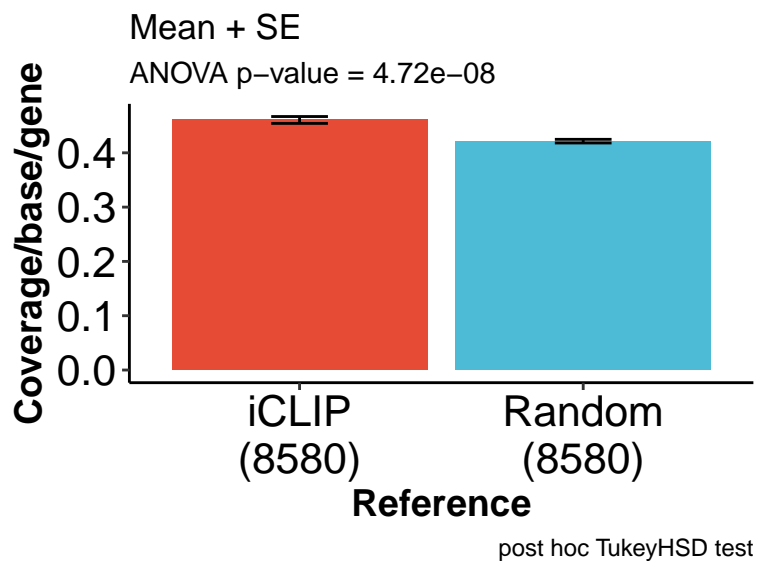
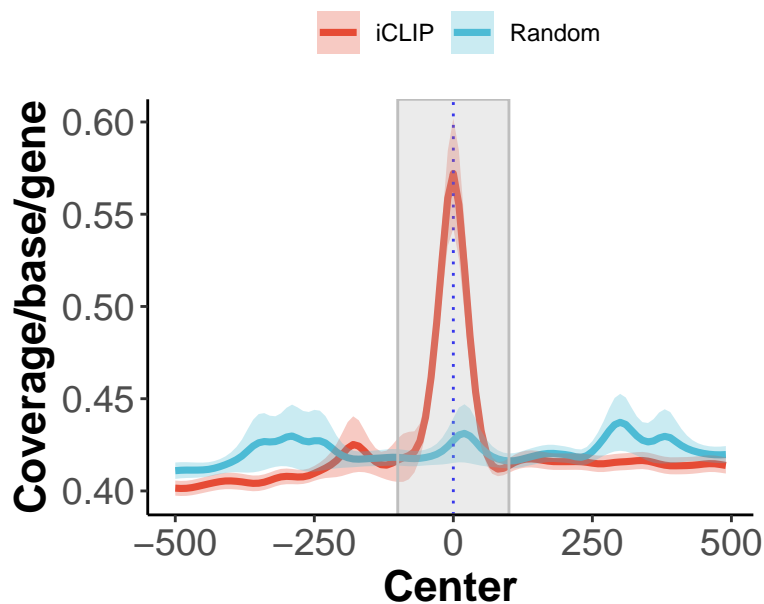


Reference  iCLIP  Random

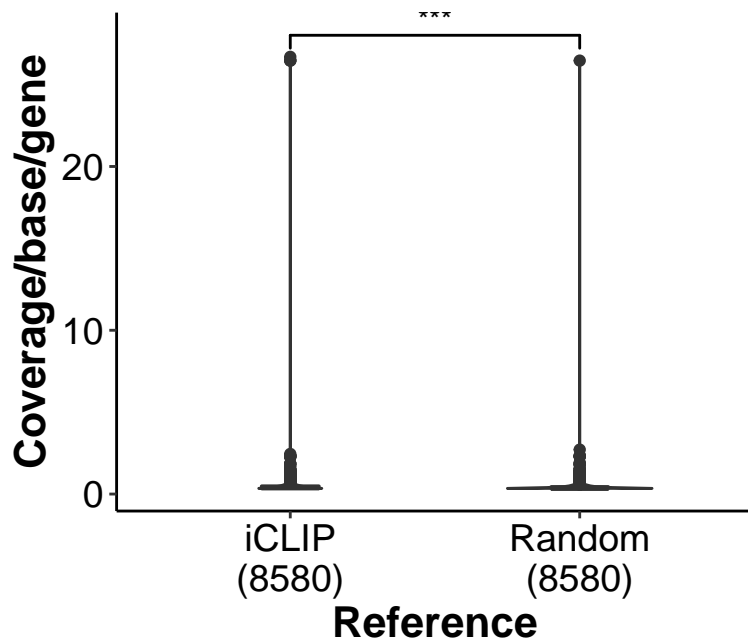


Reference  iCLIP  Random

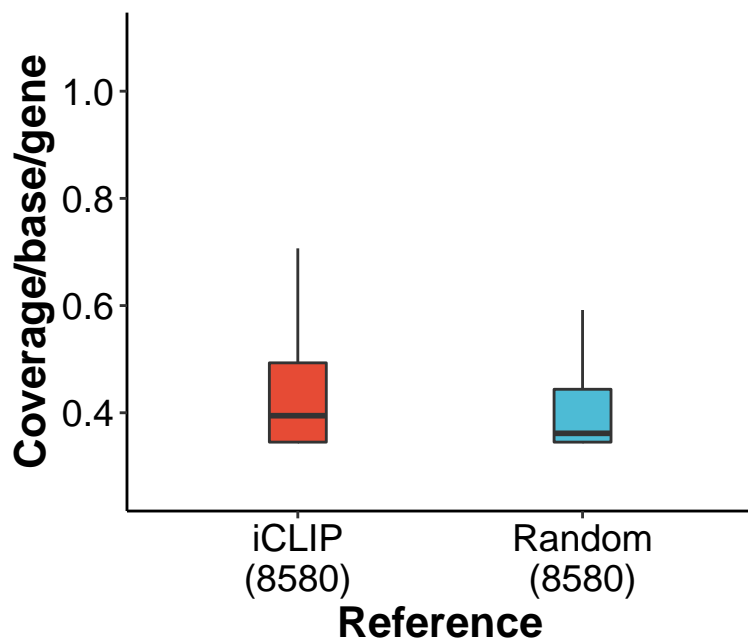
Feature: CDS  
Reference size: 8580  
Sample name: query



	diff	lwr	upr	p adj
<i>Random-iCLIP</i>	-0.039	-0.053	-0.025	$7.94e-08$

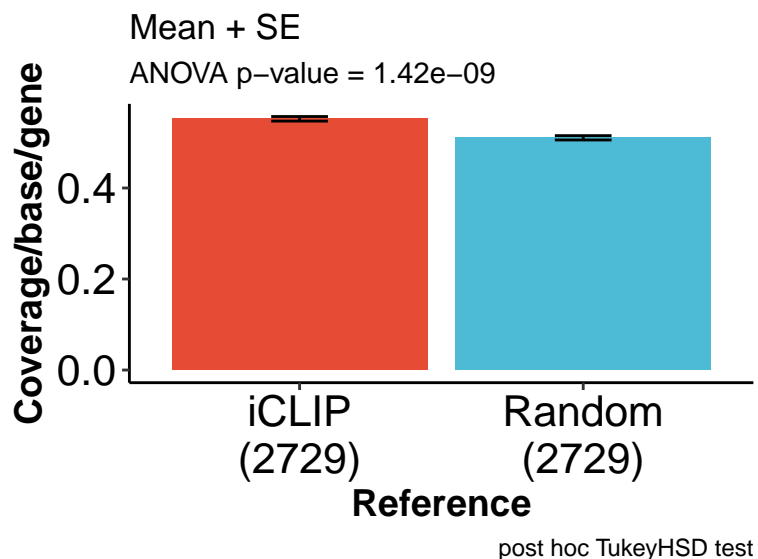
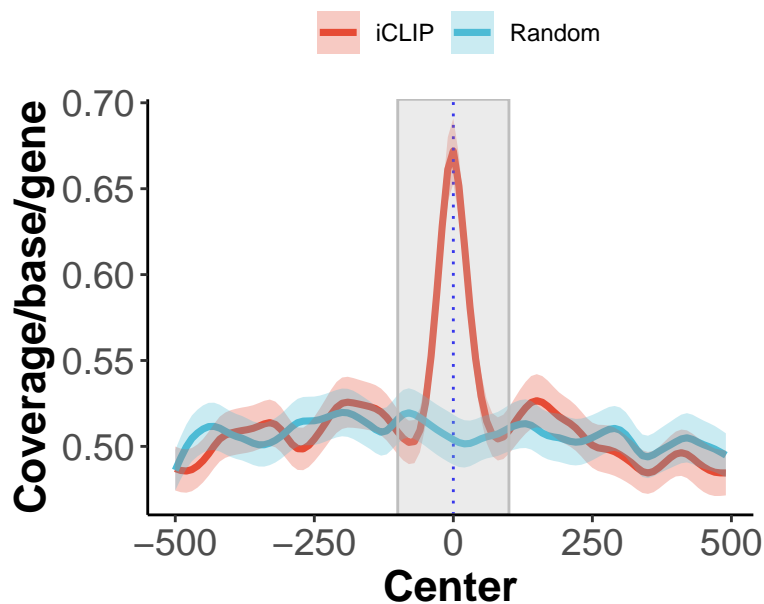


Reference  iCLIP  Random

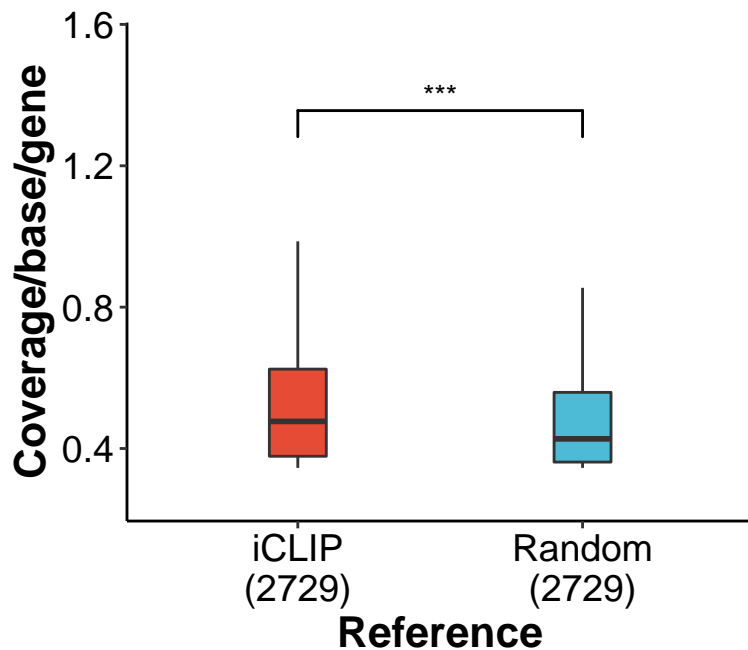
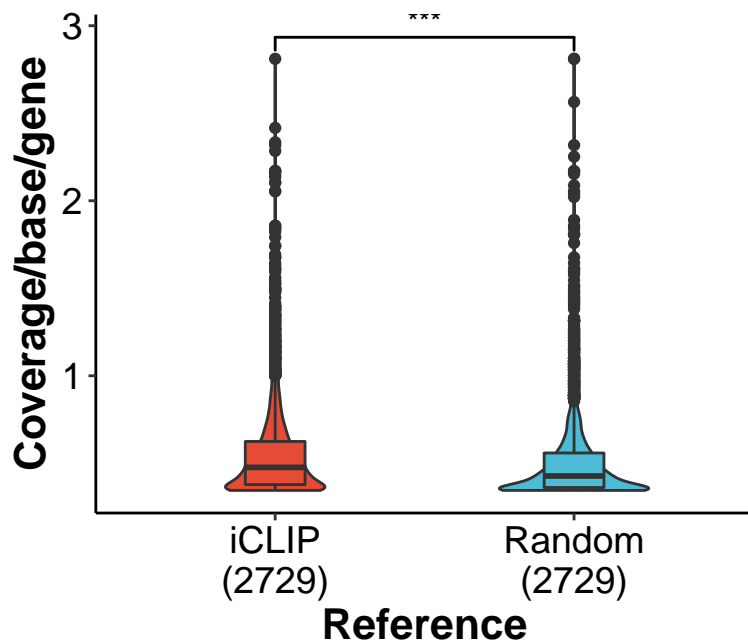


Reference  iCLIP  Random

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



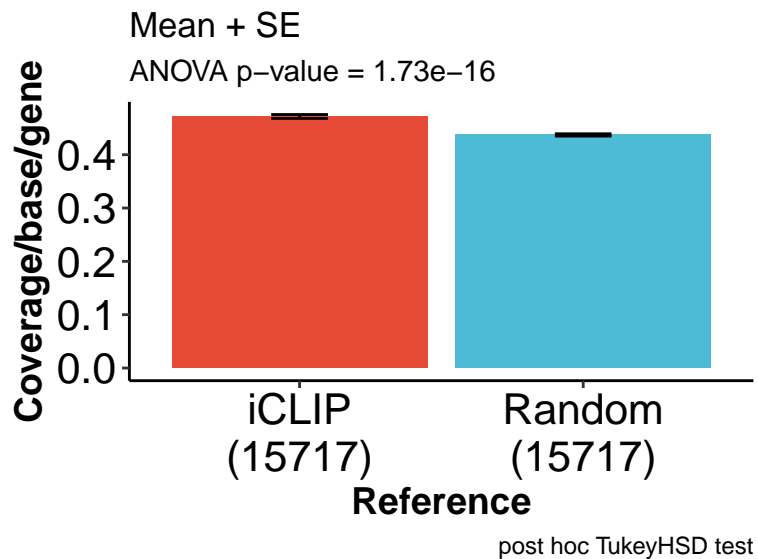
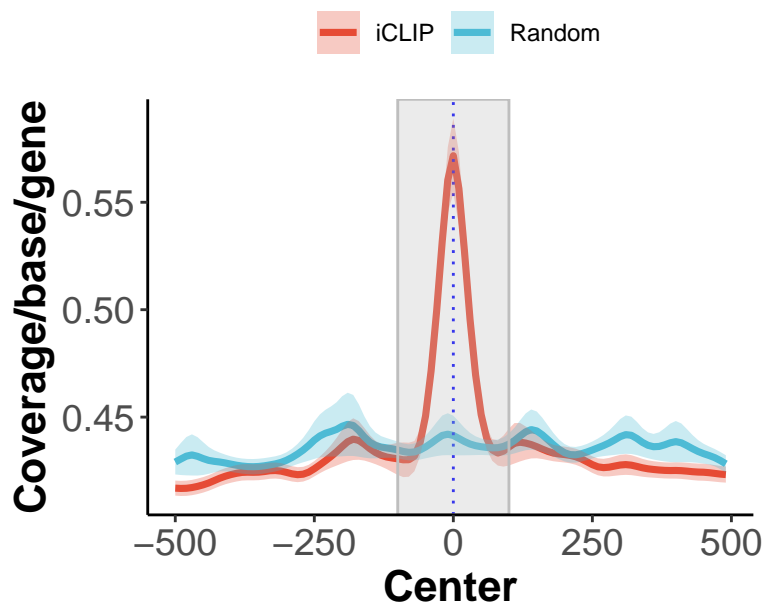
	diff	lwr	upr	p adj
Random-iCLIP	-0.042	-0.055	-0.028	$1.42\text{e-}09$



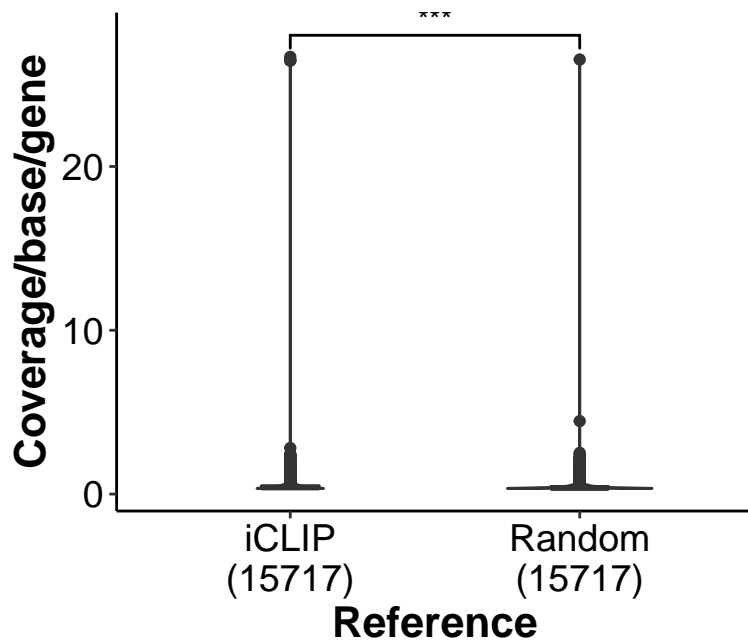
Reference iCLIP Random

Reference iCLIP Random

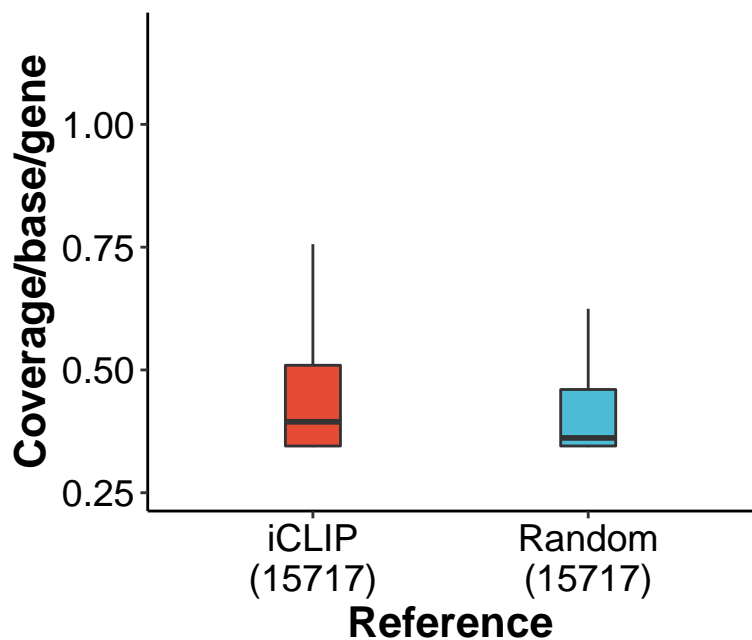
Feature: unrestricted  
Reference size: 15717  
Sample name: query



	diff	lwr	upr	p adj
<i>Random-iCLIP</i>	-0.035	-0.043	-0.026	2.29e-14

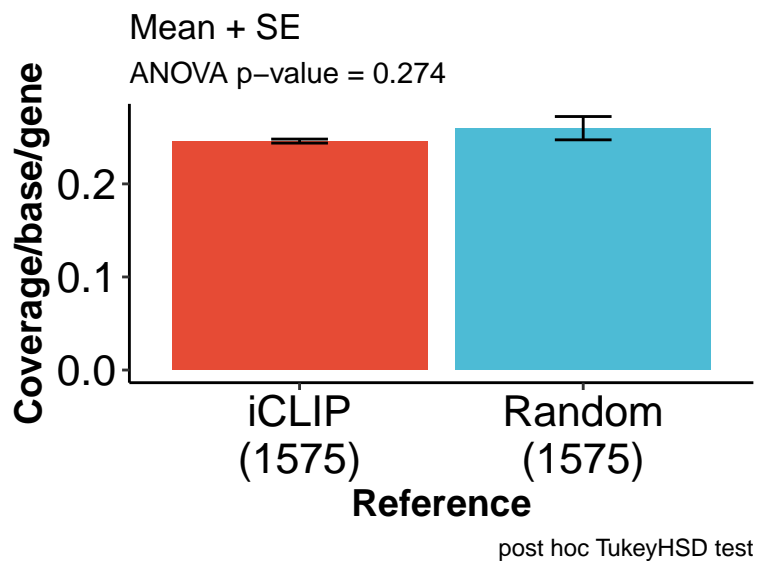
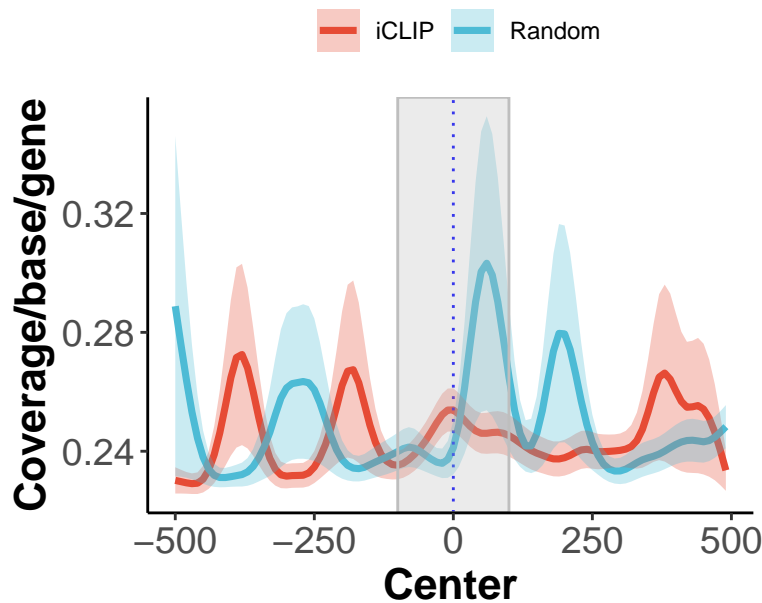


Reference iCLIP Random

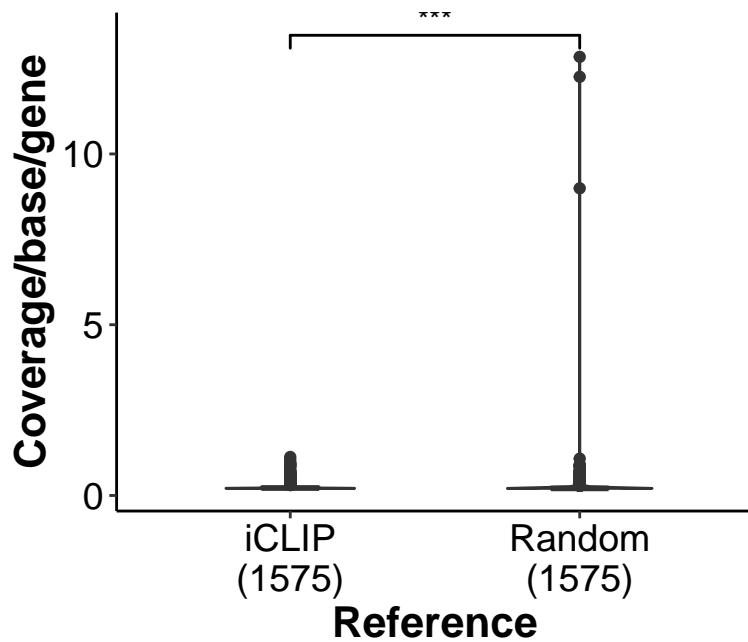


Reference iCLIP Random

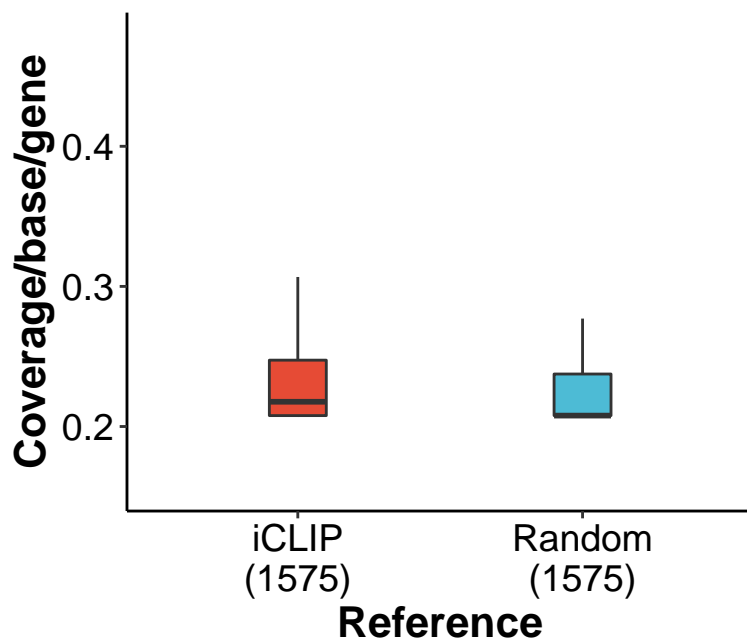
Feature: 5'UTR  
 Reference size: 1575  
 Sample name: input



	diff	lwr	upr	p adj
<i>Random-iCLIP</i>	0.014	-0.011	0.039	0.274

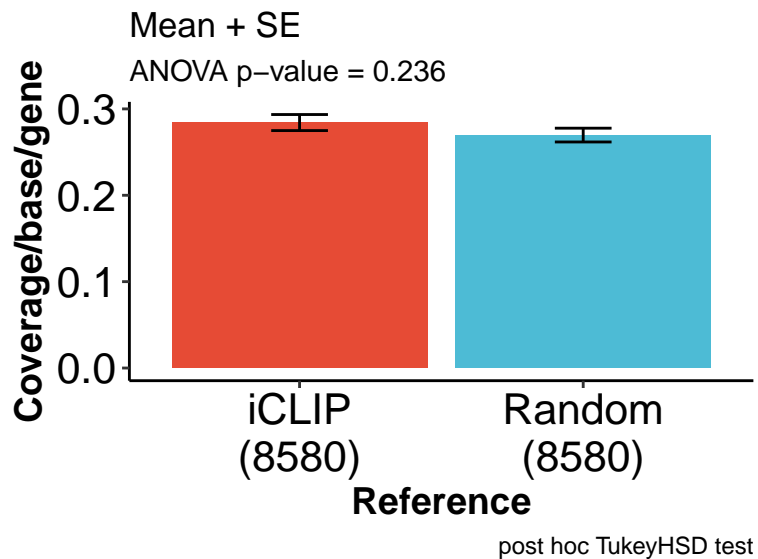
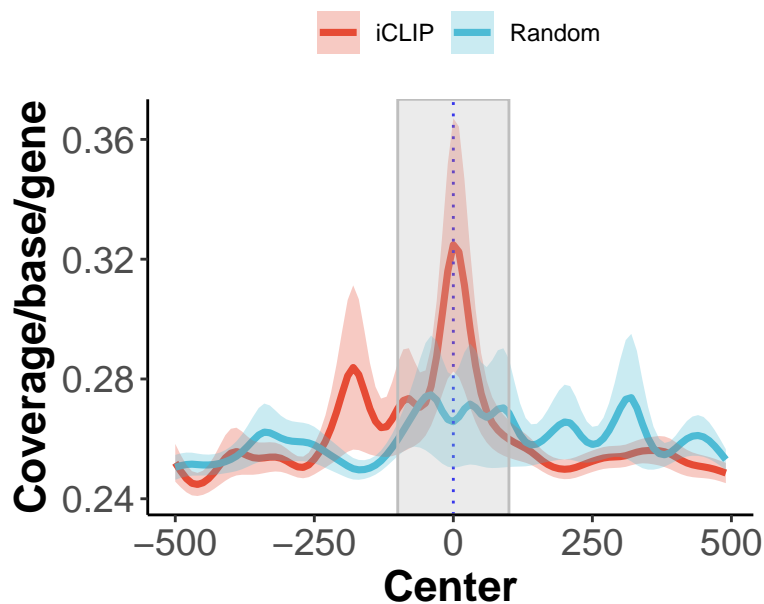


Reference iCLIP Random

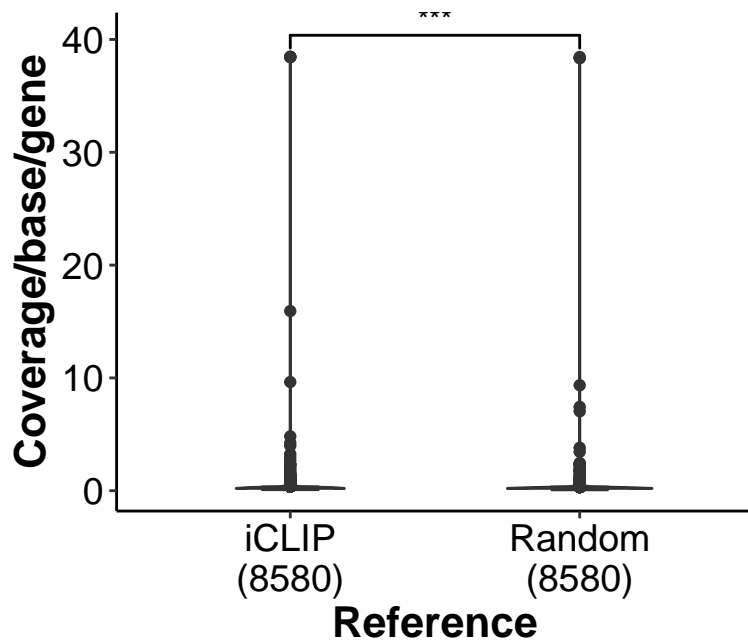


Reference iCLIP Random

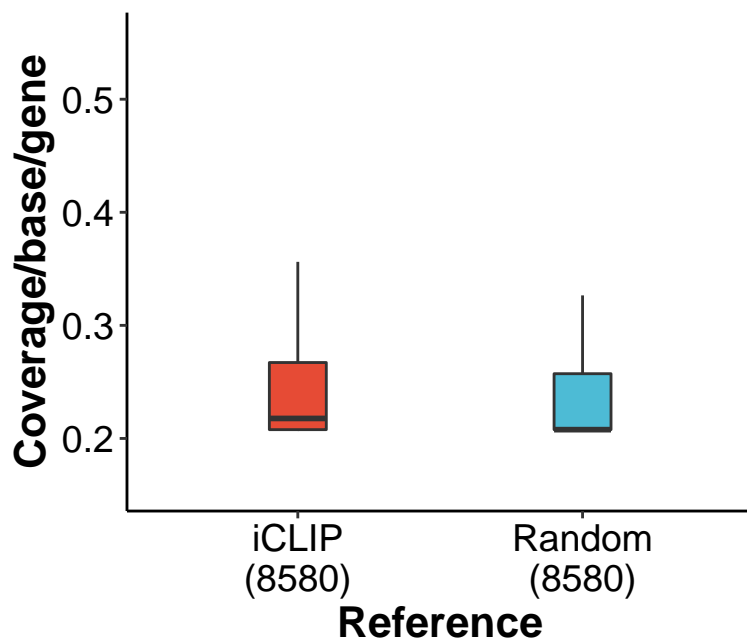
Feature: CDS  
Reference size: 8580  
Sample name: input



	diff	lwr	upr	p adj
<i>Random-iCLIP</i>	-0.014	-0.038	0.009	0.236

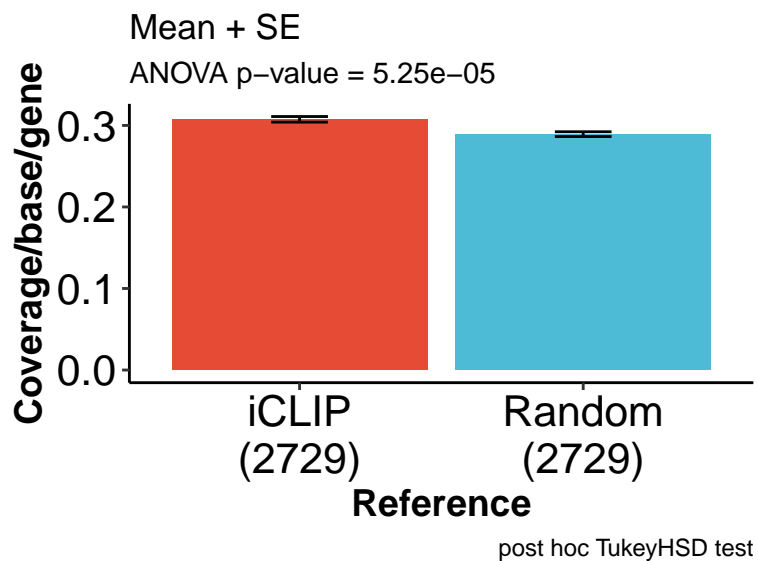
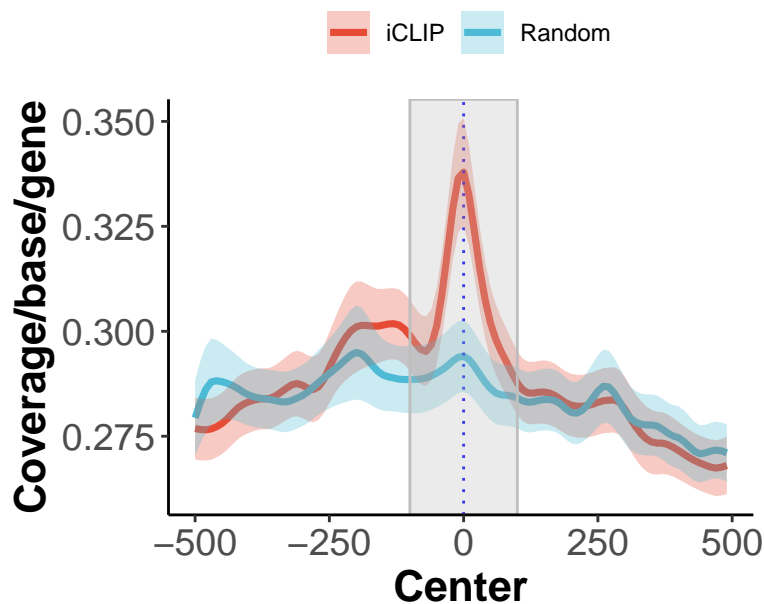


Reference iCLIP Random

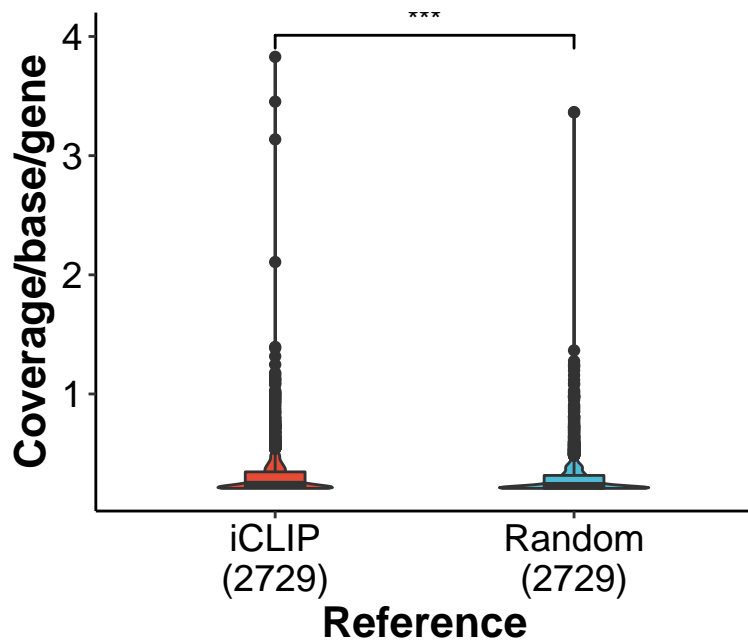


Reference iCLIP Random

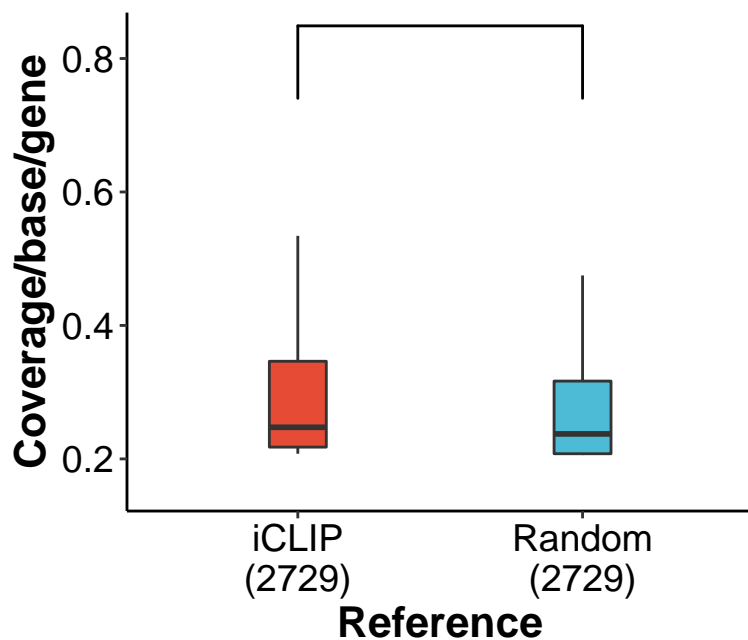
Feature: 3'UTR  
Reference size: 2729  
Sample name: input



	diff	lwr	upr	p adj
Random-iCLIP	-0.018	-0.027	-0.009	5.25e-05

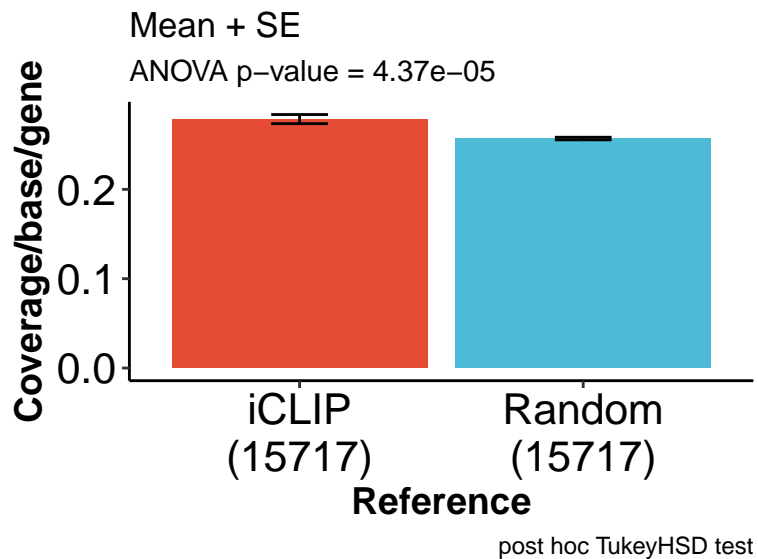
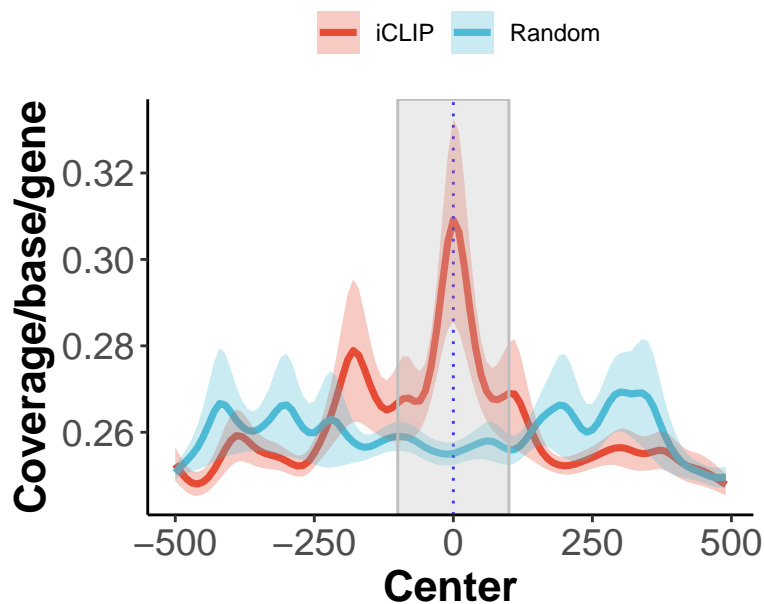


Reference  iCLIP  Random

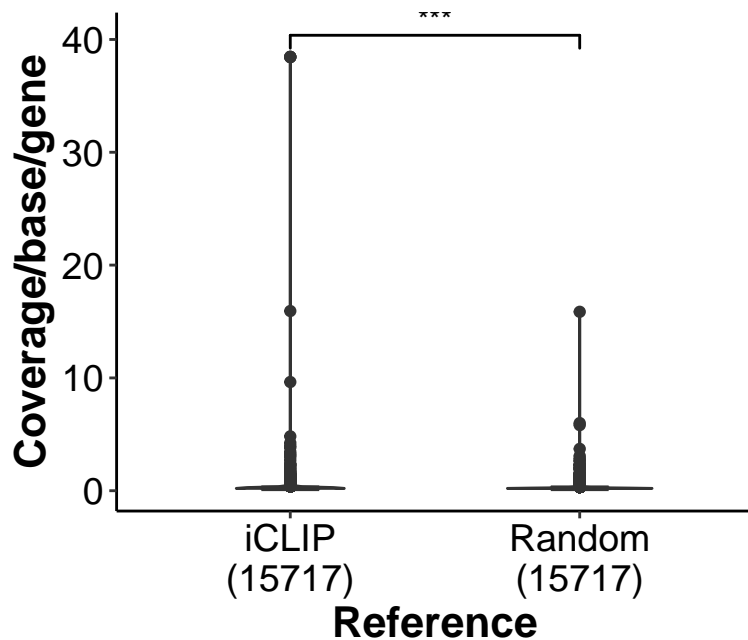


Reference  iCLIP  Random

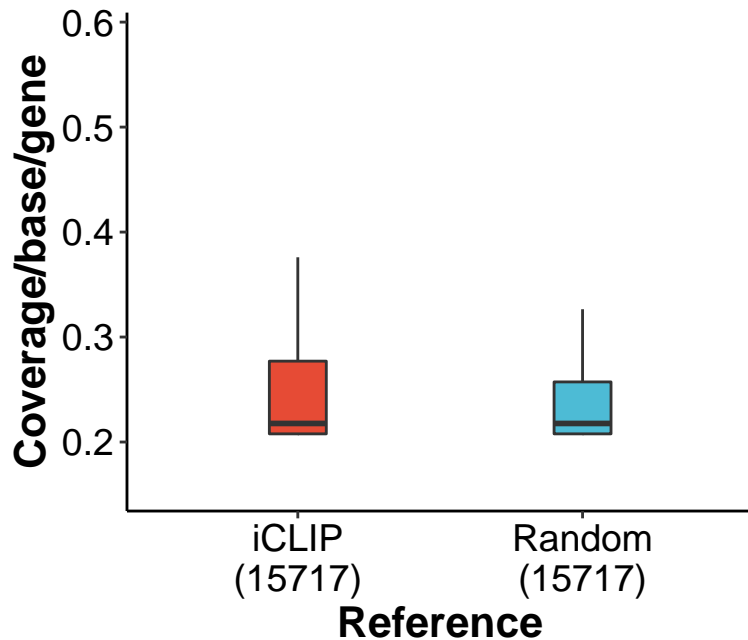
Feature: unrestricted  
Reference size: 15717  
Sample name: input



	diff	lwr	upr	p adj
Random-iCLIP	-0.022	-0.032	-0.011	4.36e-05



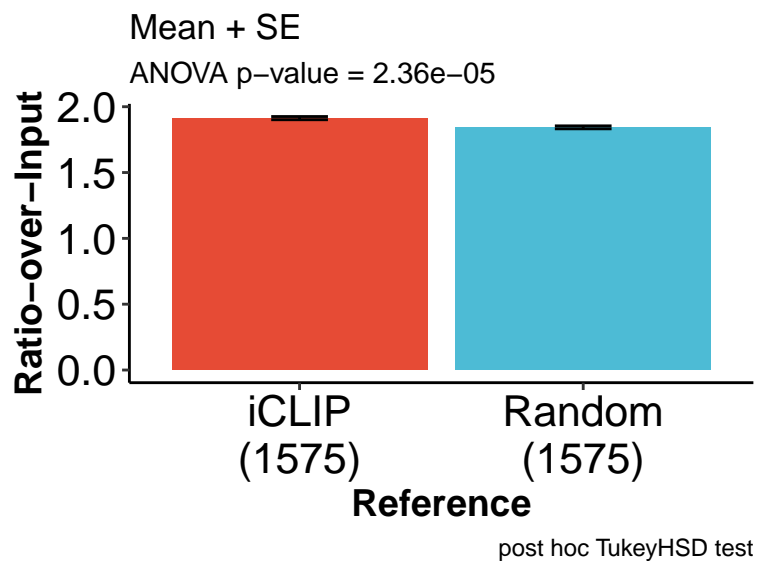
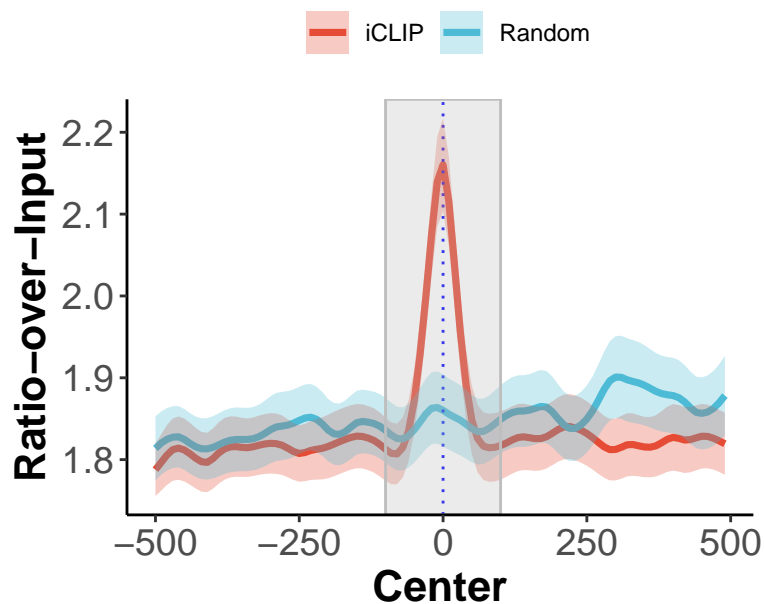
Reference  iCLIP  Random



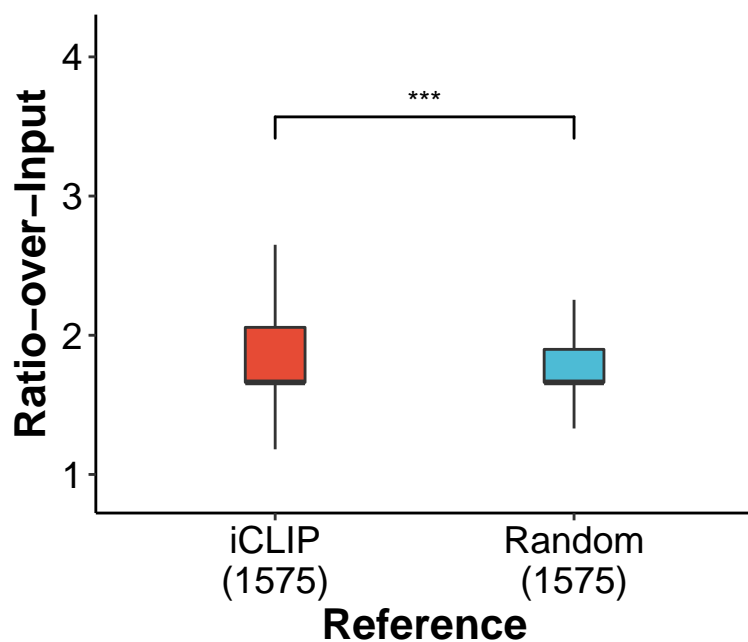
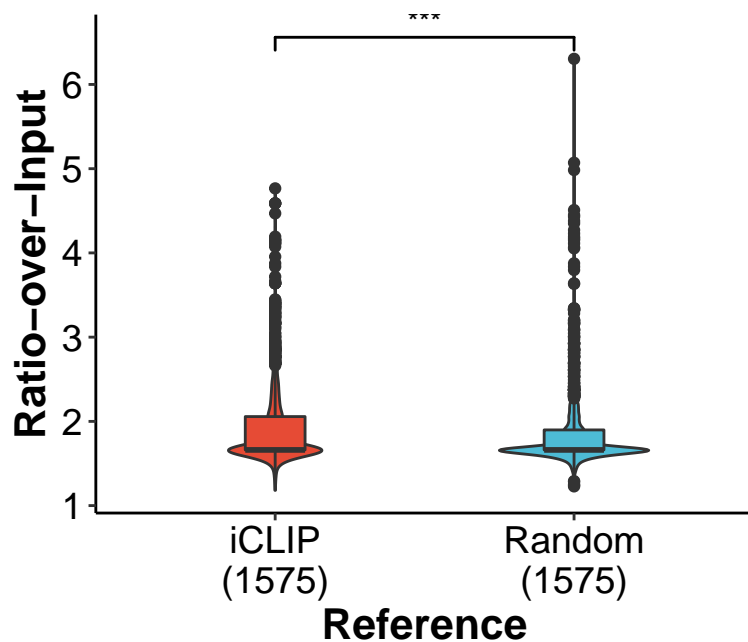
Reference  iCLIP  Random



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



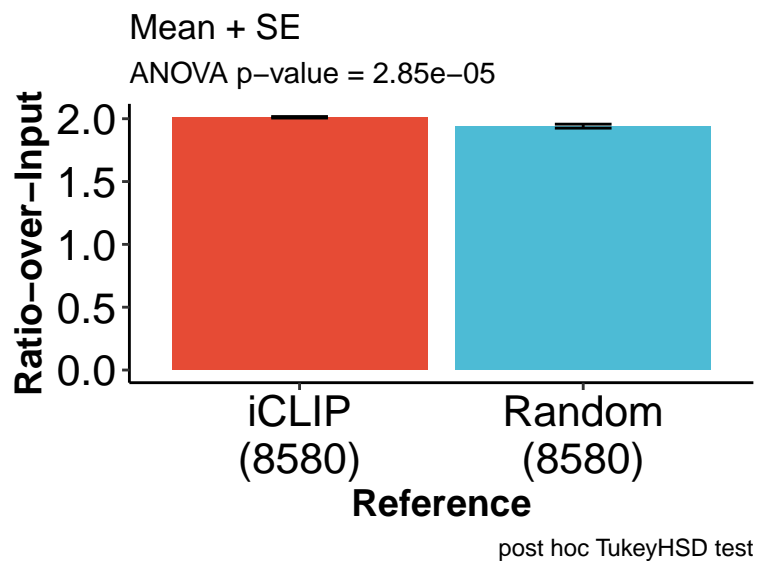
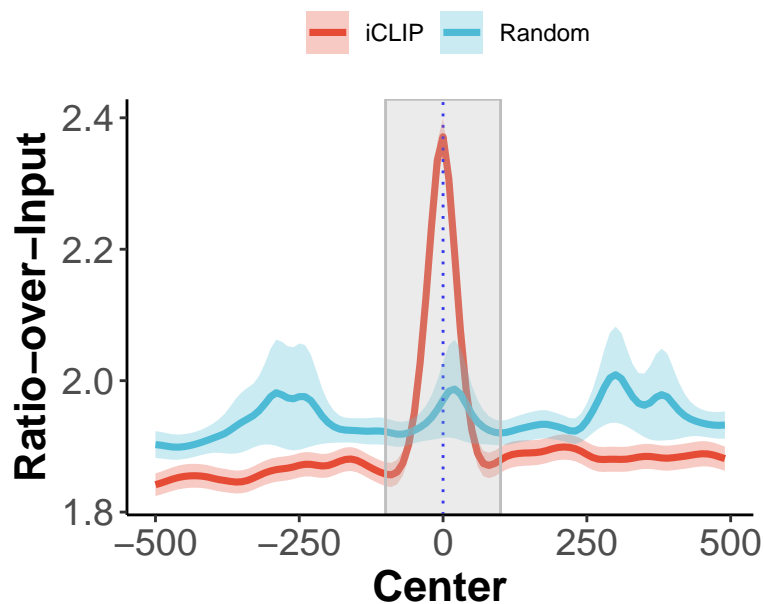
	diff	lwr	upr	p adj
<i>Random-iCLIP</i>	-0.07	-0.102	-0.038	$2.36e-05$



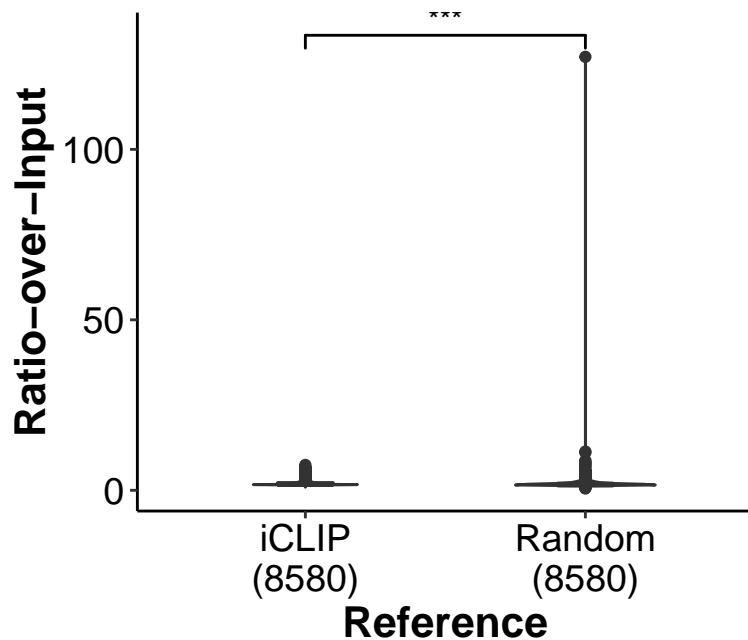
Reference  iCLIP  Random

Reference  iCLIP  Random

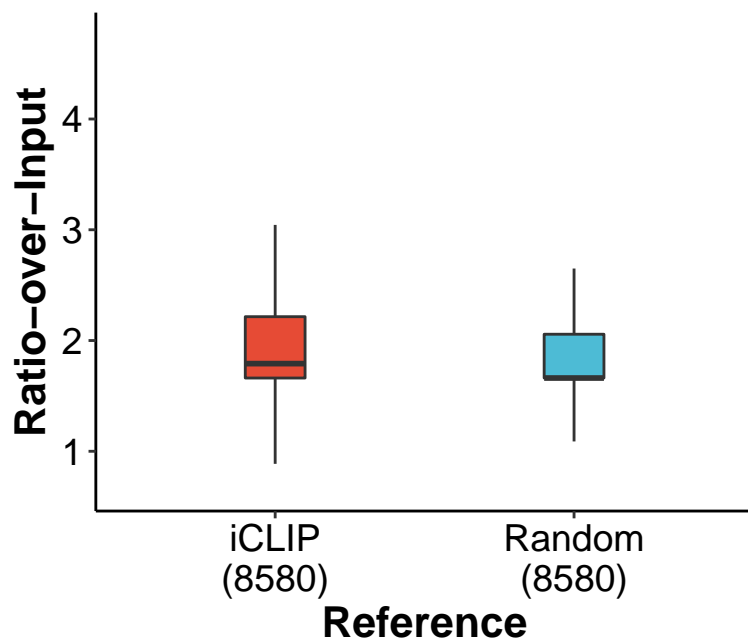
Feature: CDS  
Reference size: 8580  
Sample name: query



	diff	lwr	upr	p adj
Random-iCLIP	-0.071	-0.104	-0.038	2.86e-05

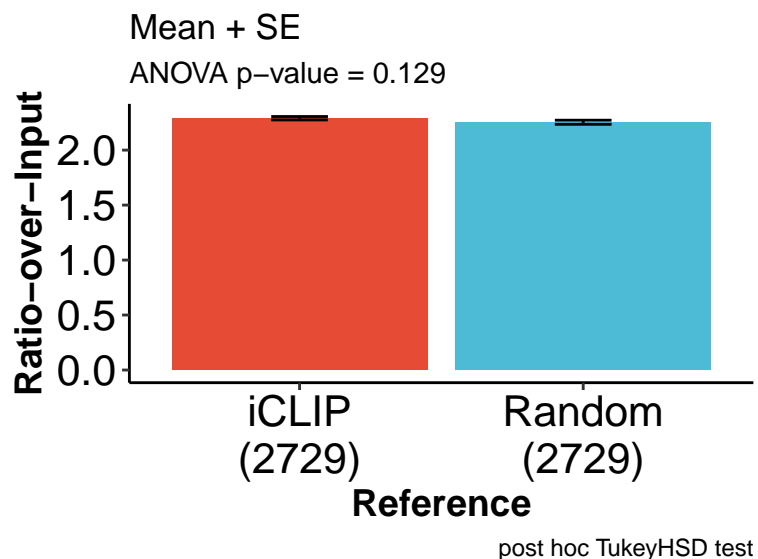
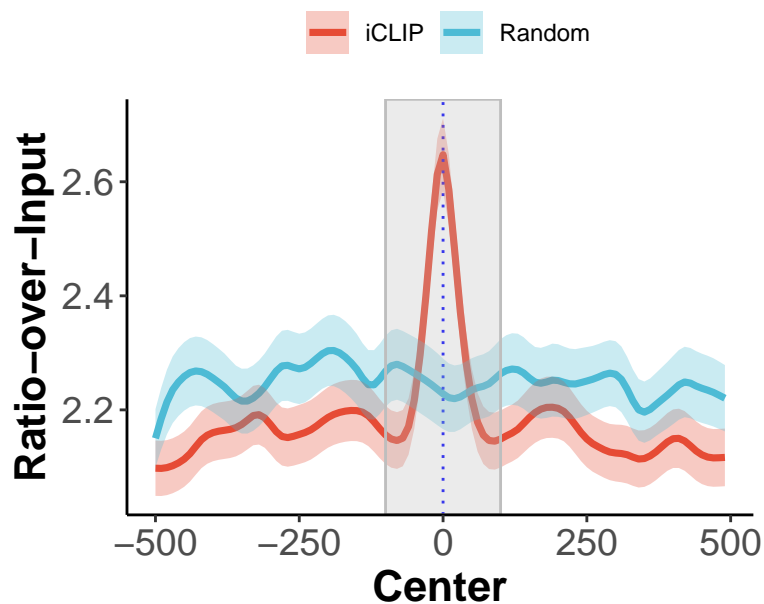


Reference  iCLIP  Random

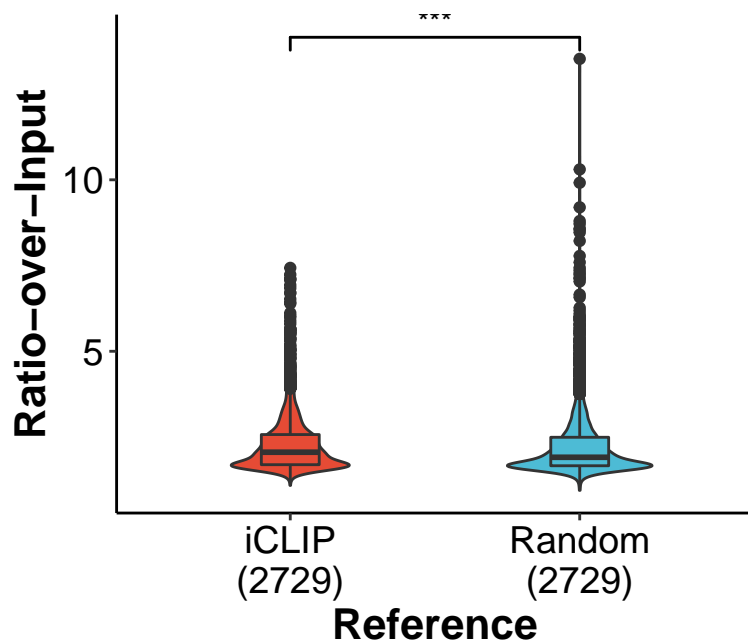


Reference  iCLIP  Random

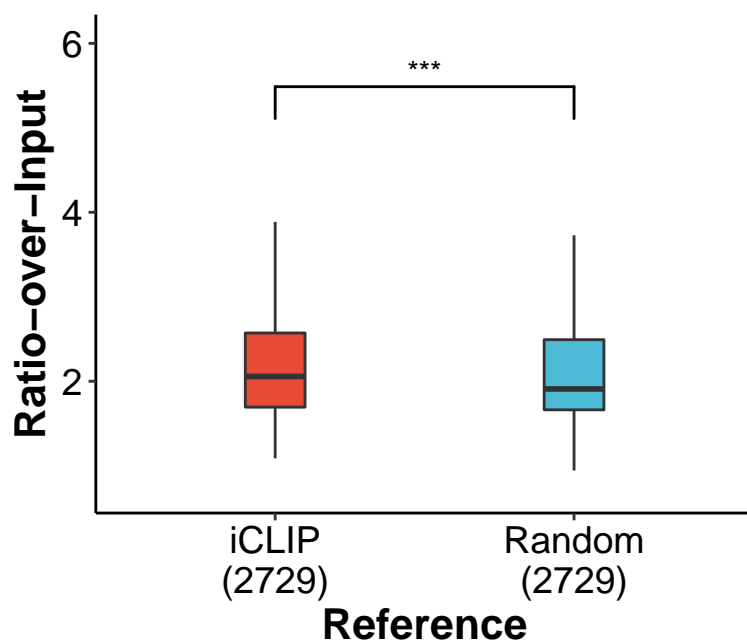
Feature: 3'UTR  
Reference size: 2729  
Sample name: query



	diff	lwr	upr	p adj
Random-iCLIP	-0.037	-0.084	0.011	0.129

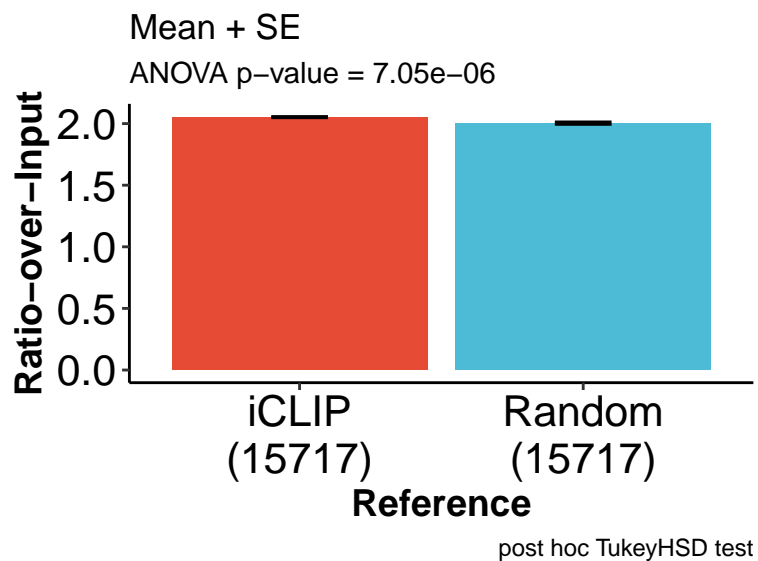
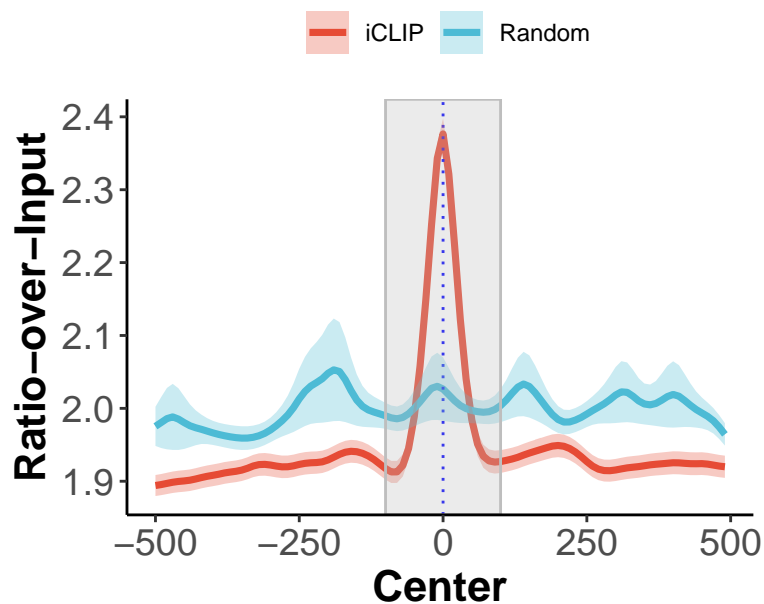


Reference iCLIP Random

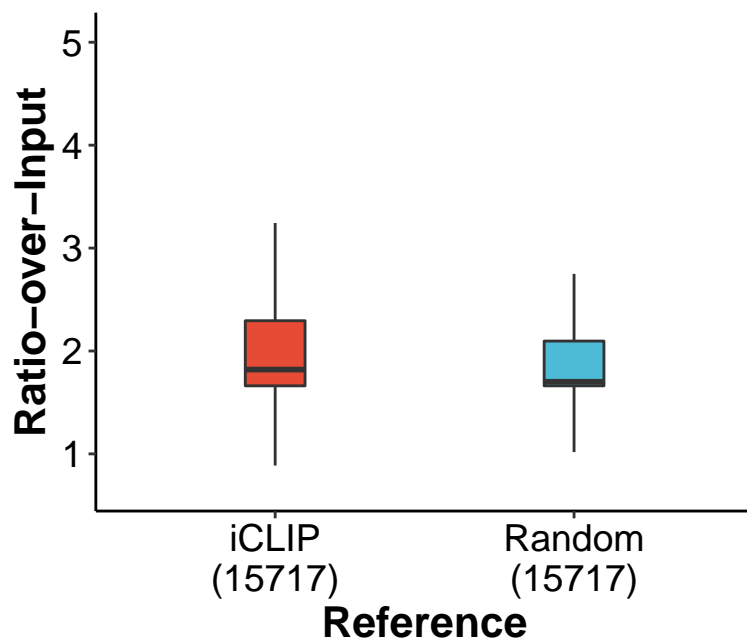
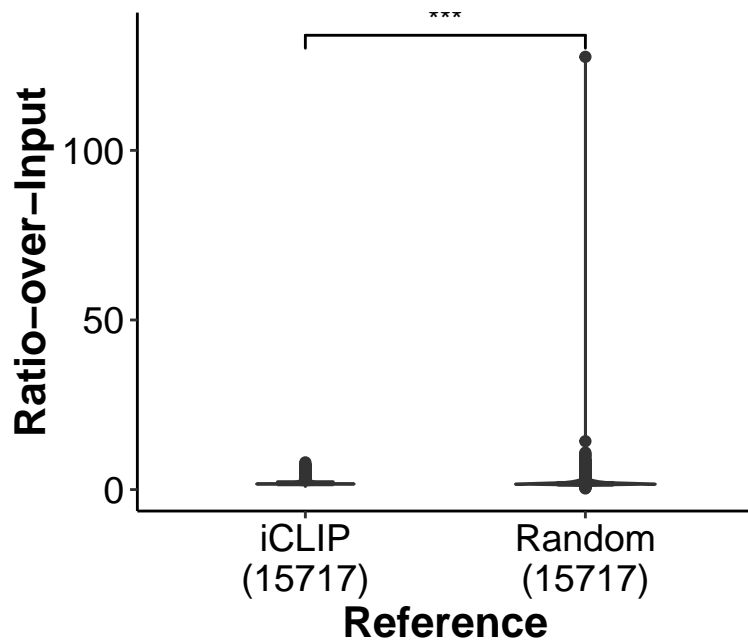


Reference iCLIP Random

Feature: unrestricted  
Reference size: 15717  
Sample name: query



	diff	lwr	upr	p adj
Random-iCLIP	-0.049	-0.07	-0.028	$7.02e-06$



Reference  iCLIP  Random

Reference  iCLIP  Random

Plotting parameters:

```
functionName: "plot_locus_with_random"
queryFiles: c(query = "C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/treat_chr19.bam")
centerFiles: c(iCLIP =
  "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
handleInputParams: 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(input = "C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/input_chr19.bam")
stranded: TRUE
scale: FALSE
outPrefix: "test_plot_locus_with_random"
rmOutlier: FALSE
n_random: 1
hw: c(8, 8)
statsMethod: "wilcox.test"
nc: 2
```