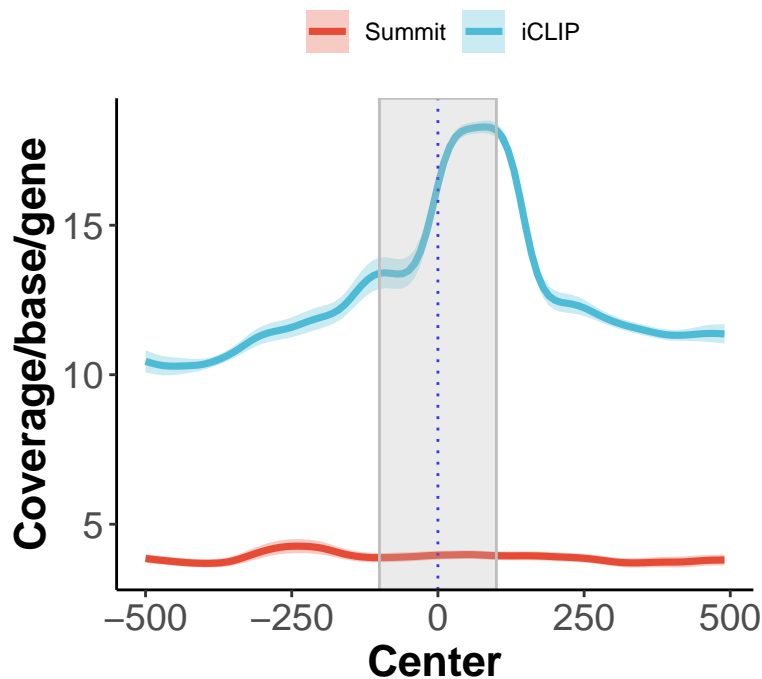
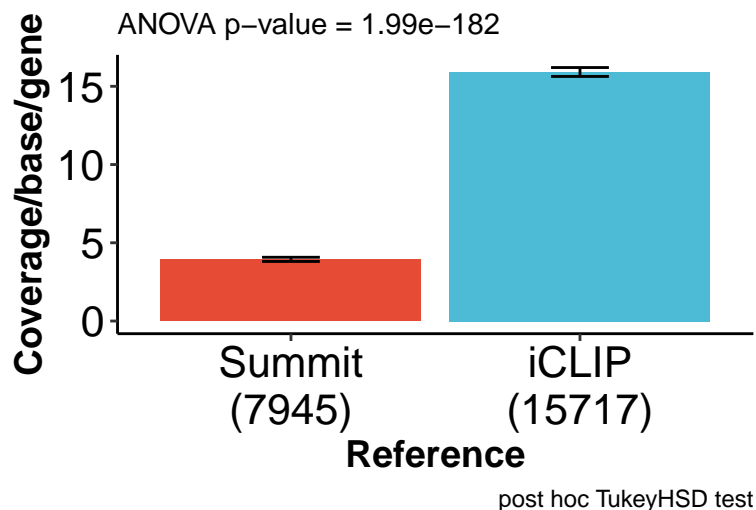


query



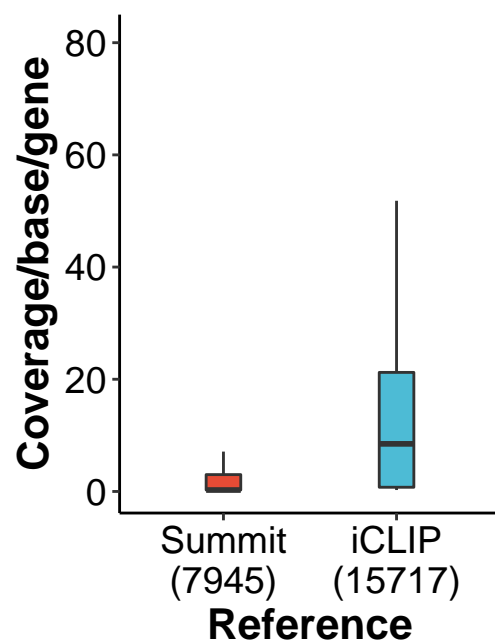
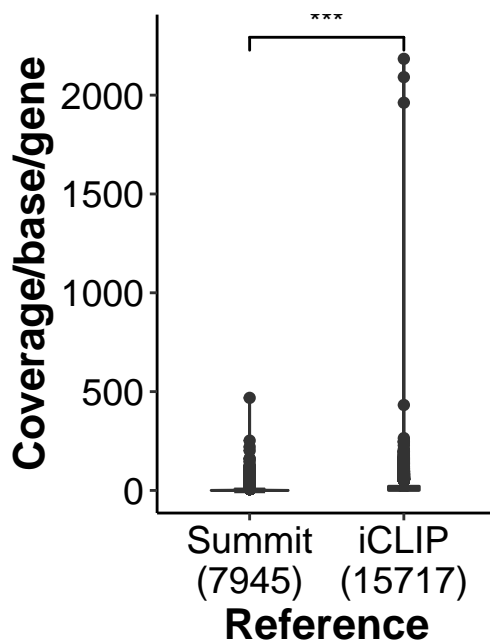
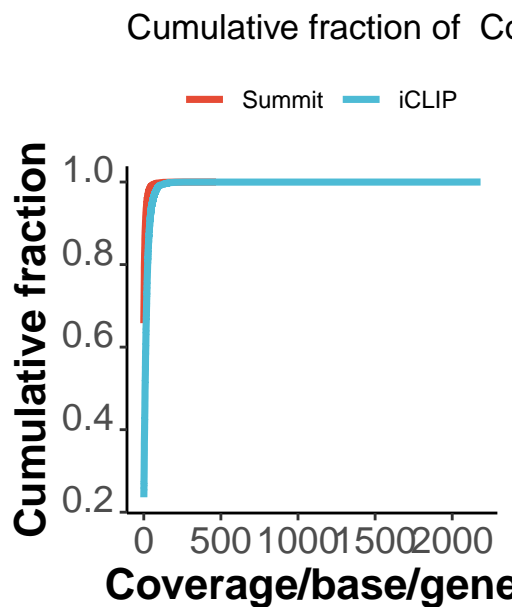
Mean + SE

ANOVA p-value = 1.99e-182



iCLIP-Summit

diff	lwr	upr	p adj
11.974	11.167	12.782	0

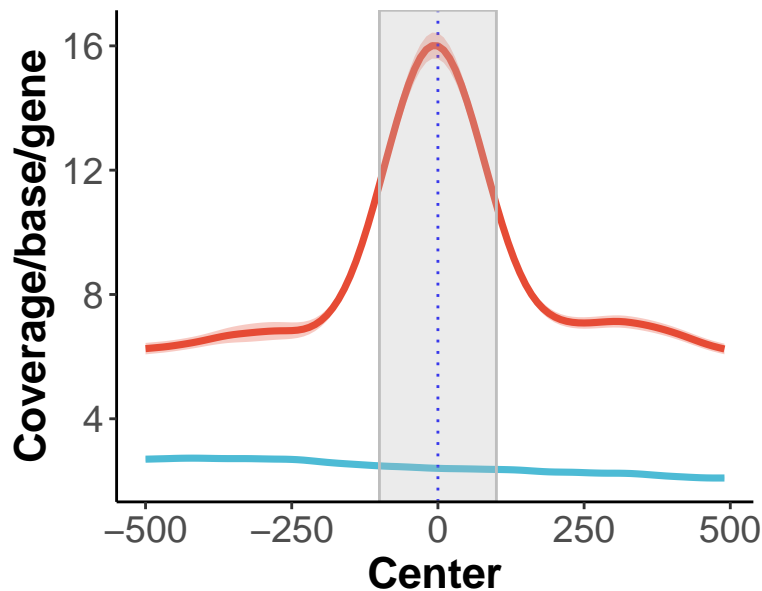


Reference Summit iCLIP

Reference Summit iCLIP

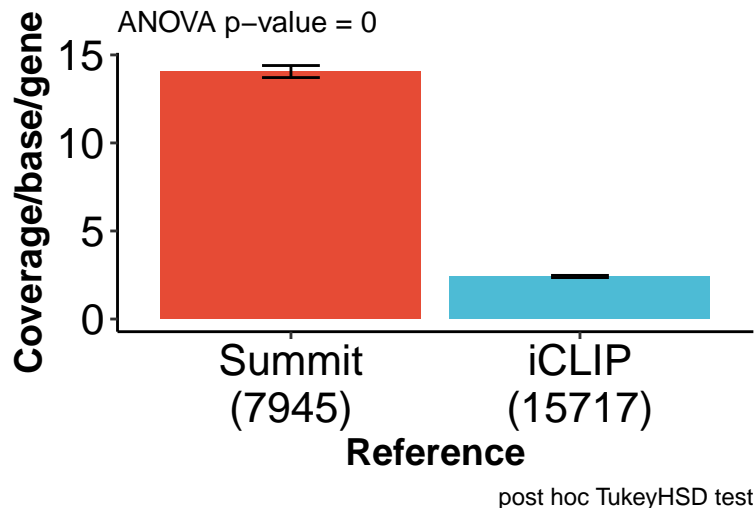
chip_query

Summit iCLIP



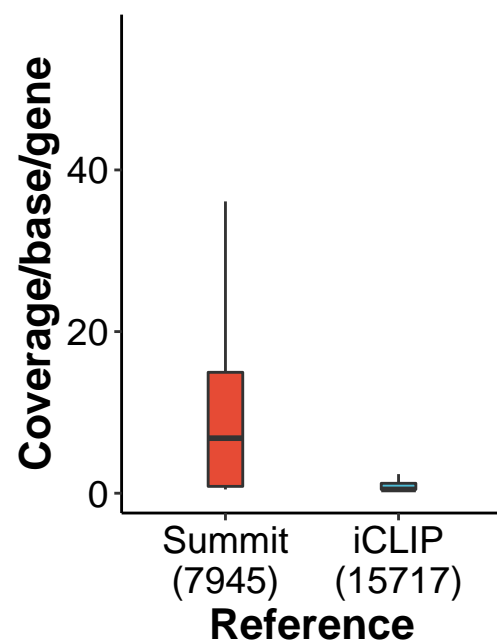
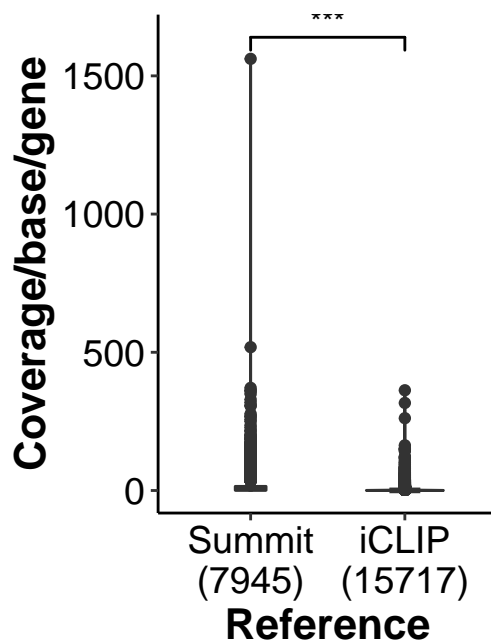
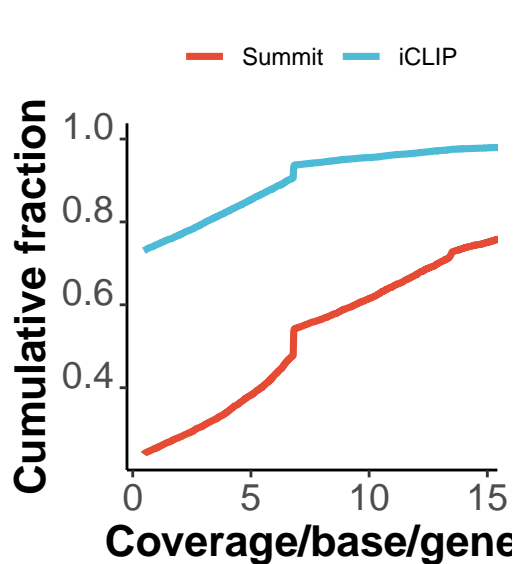
Mean + SE

ANOVA p-value = 0

*iCLIP-Summit*

	diff	lwr	upr	p adj
<i>iCLIP-Summit</i>	-11.64	-12.146	-11.135	0

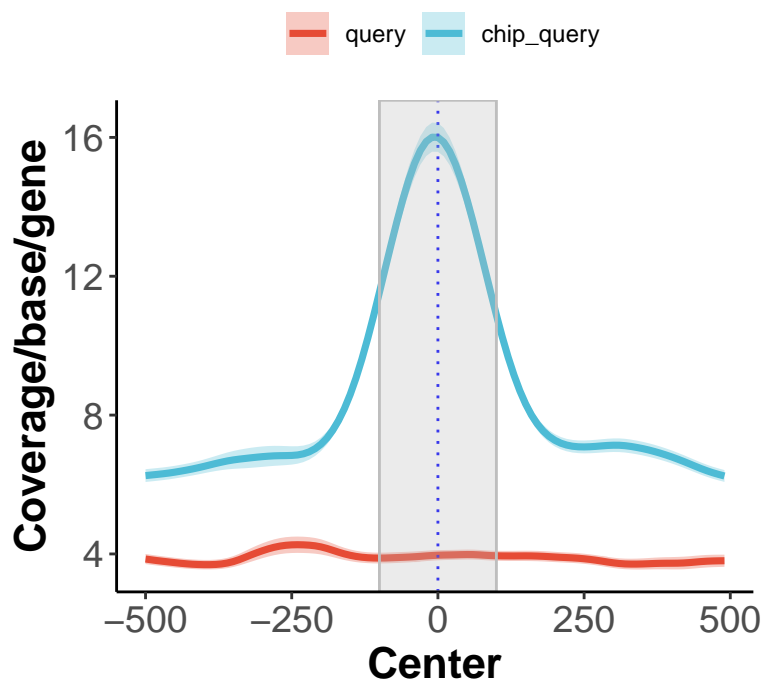
Cumulative fraction of C



Reference Summit iCLIP

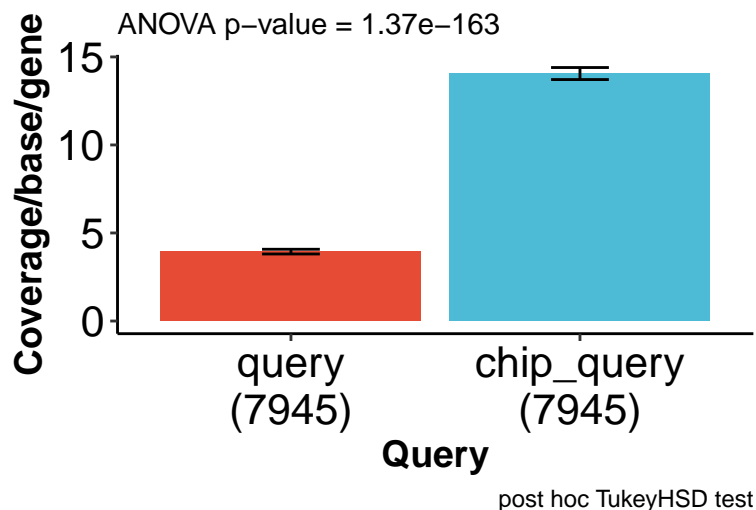
Reference Summit iCLIP

Summit



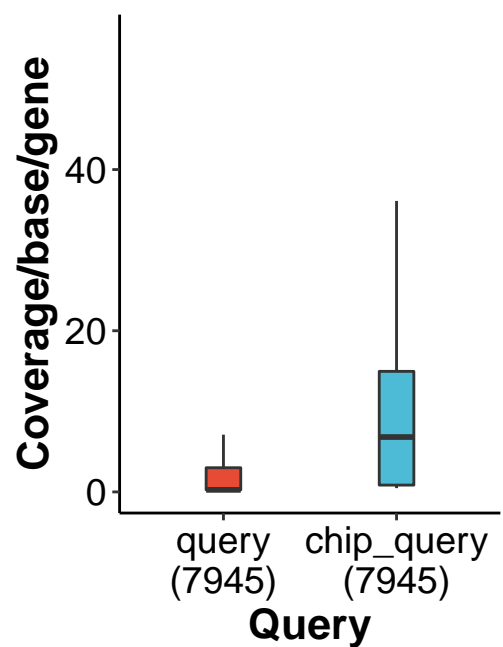
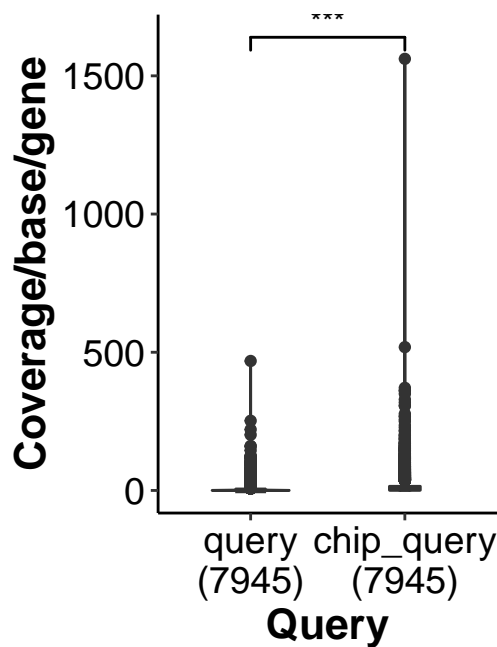
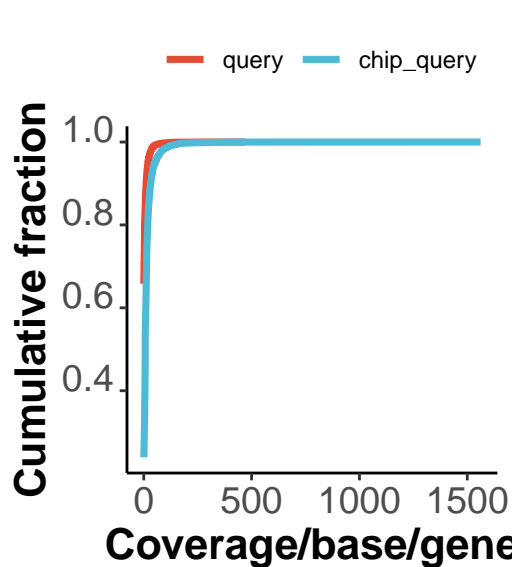




Mean + SE

ANOVA p-value = 1.37e-163

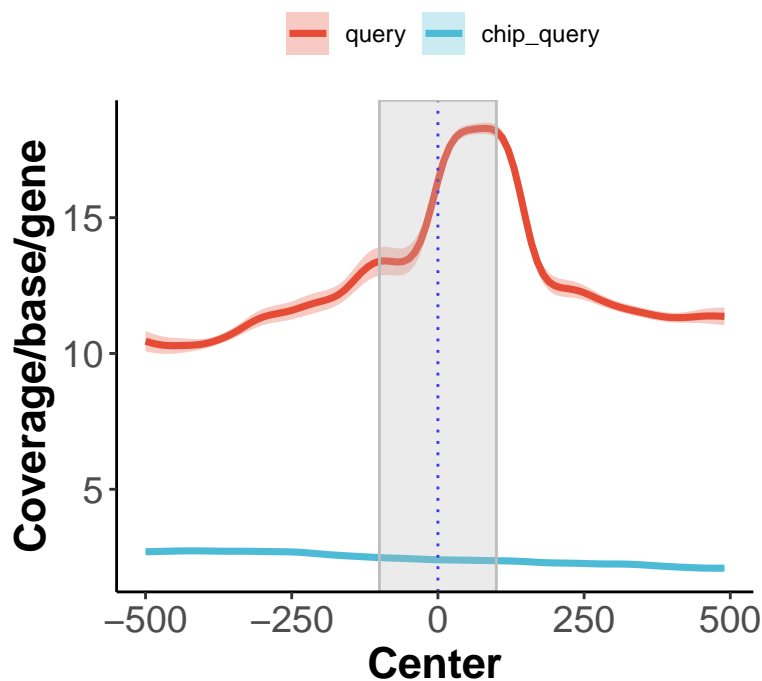


	diff	lwr	upr	p adj
chip_query-query	10.115	9.396	10.834	2.04e-08

Cumulative fraction of C

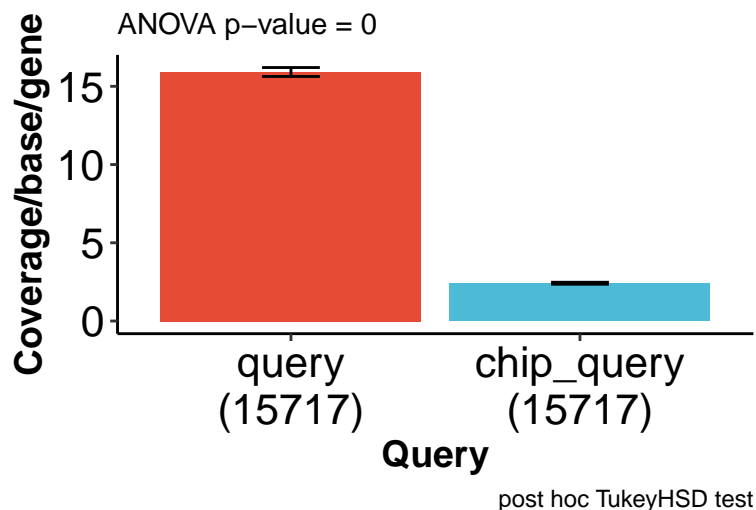
Query  query  chip_queQuery  query  chip_query

iCLIP

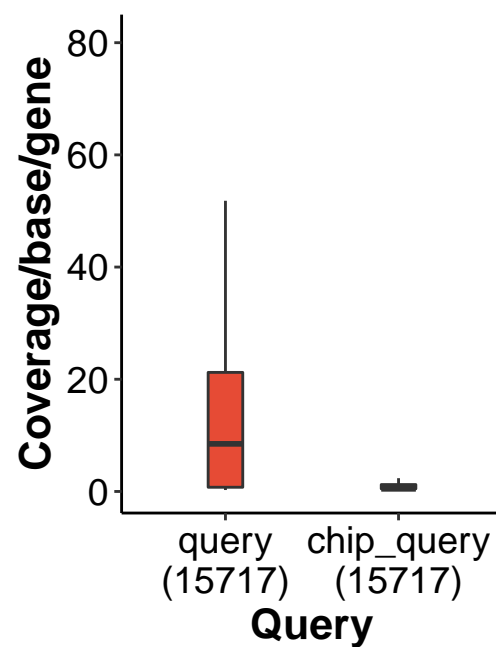
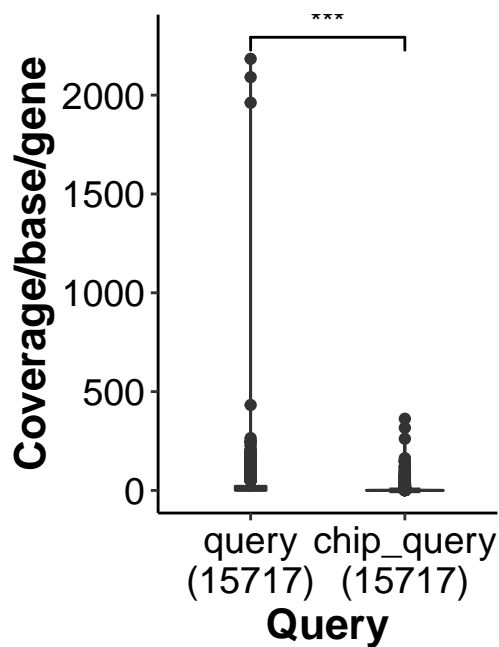
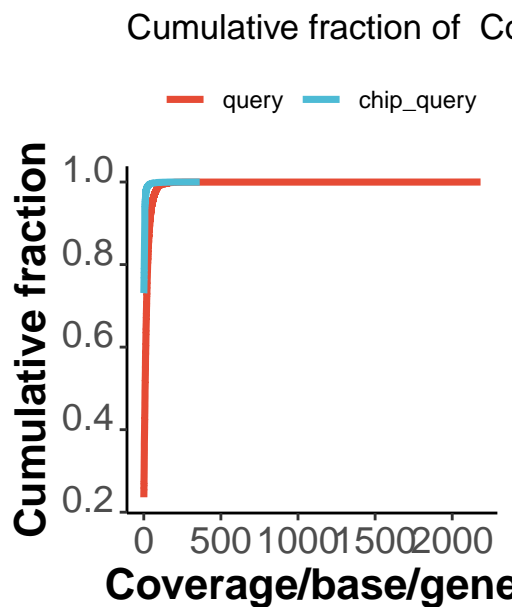


Mean + SE

ANOVA p-value = 0



	diff	lwr	upr	p adj
chip_query-query	-13.5	-14.071	-12.928	0

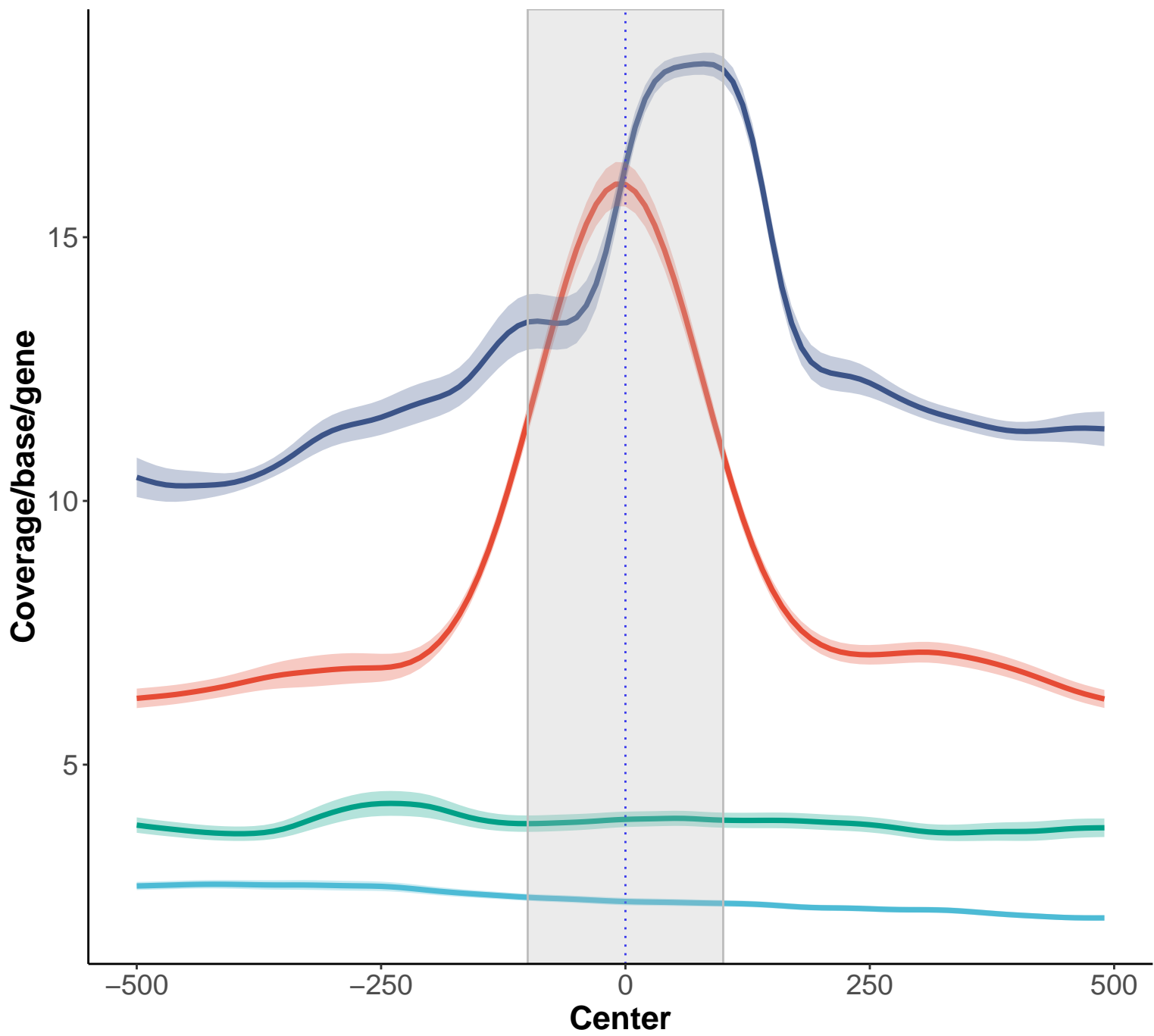


Query query chip_query

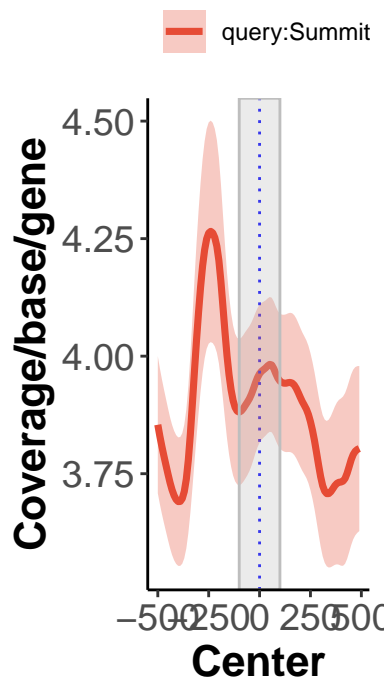
Query query chip_query

query:Summit

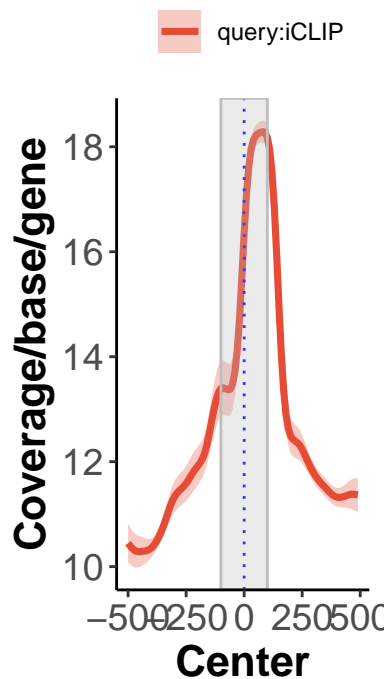
chip_query:Summit chip_query:iCLIP query:Summit query:iCLIP



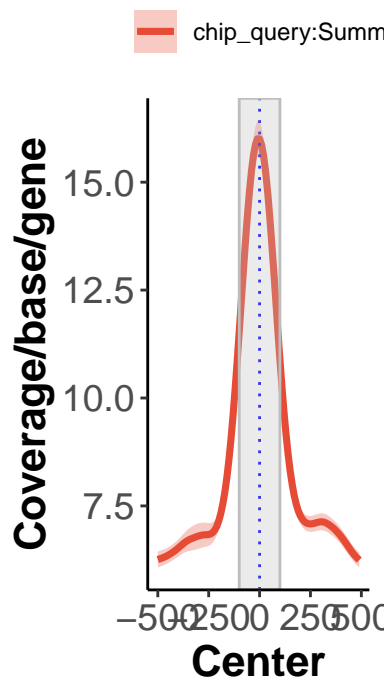
query:Summit



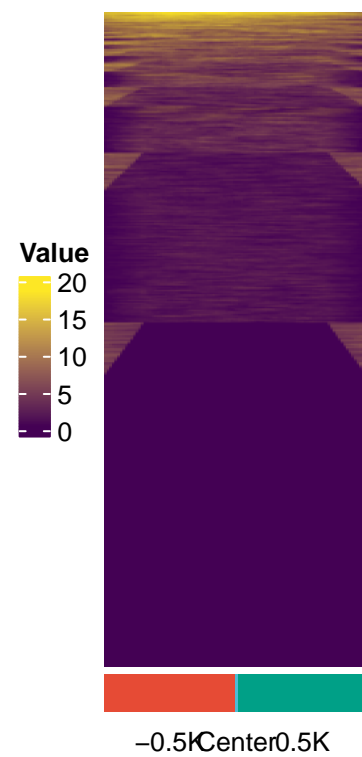
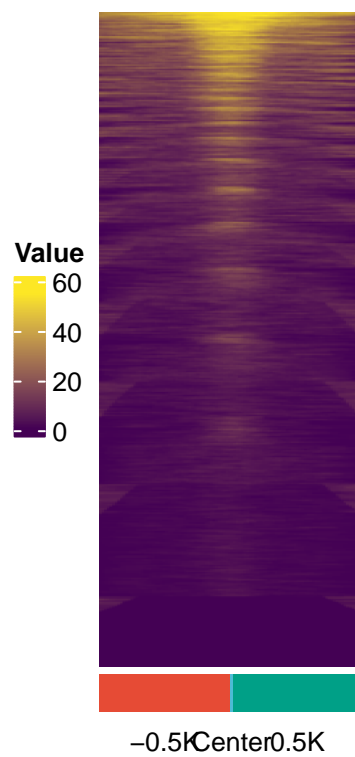
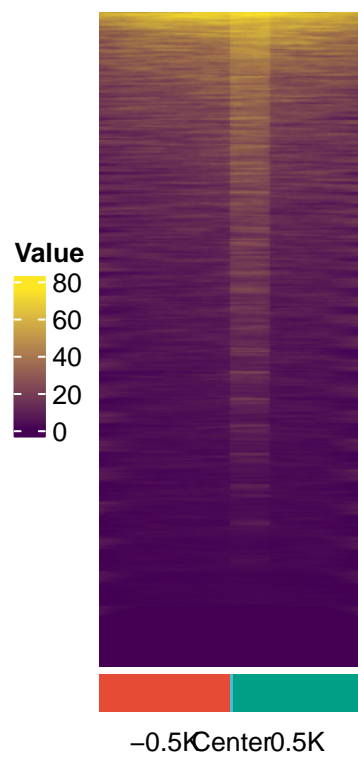
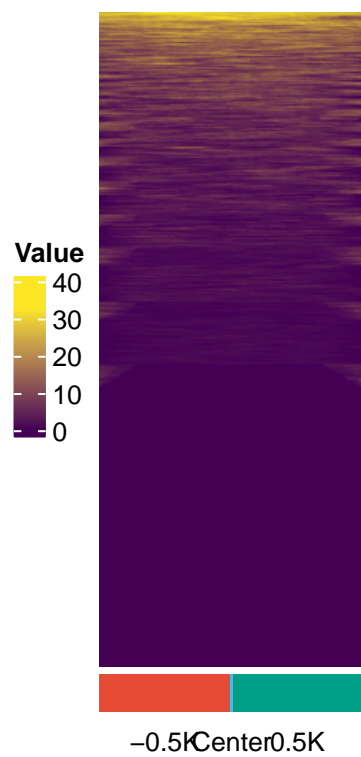
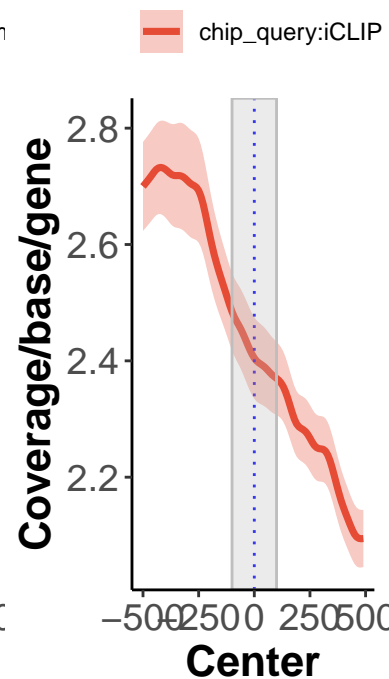
query:iCLIP



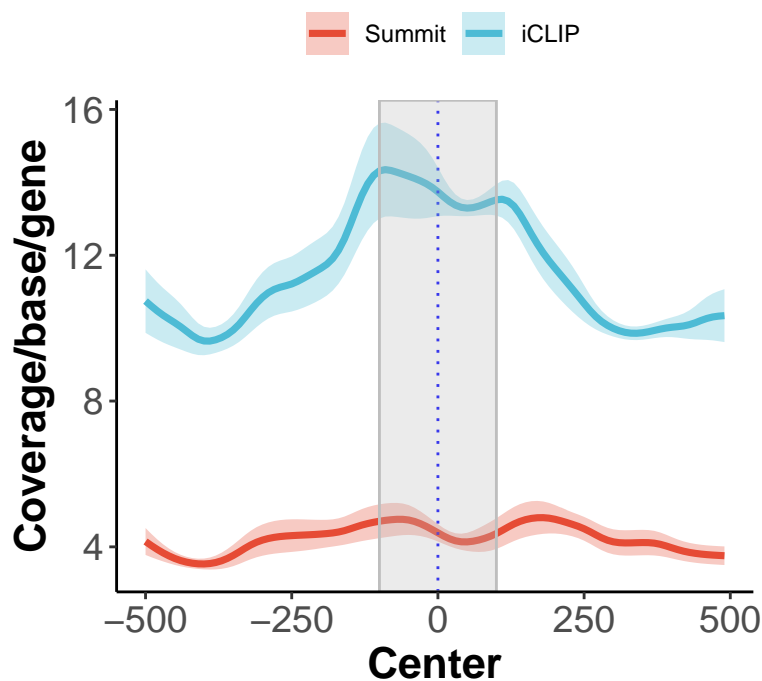
chip_query:Sun



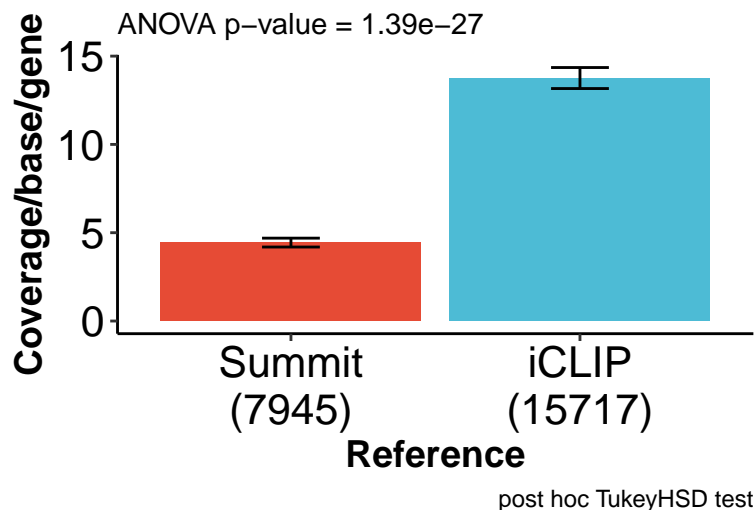
chip_query:iCLIP



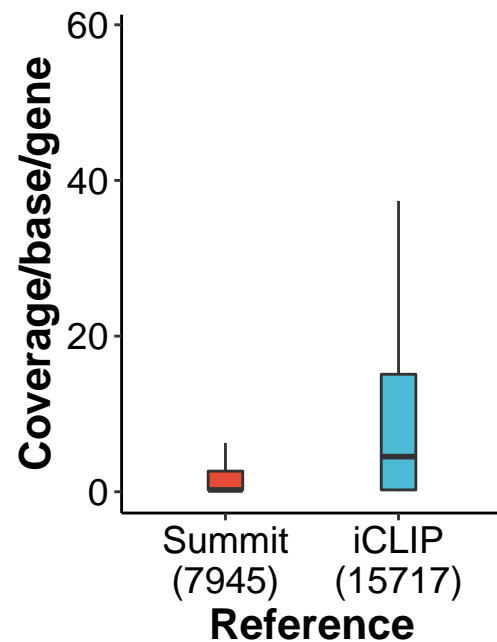
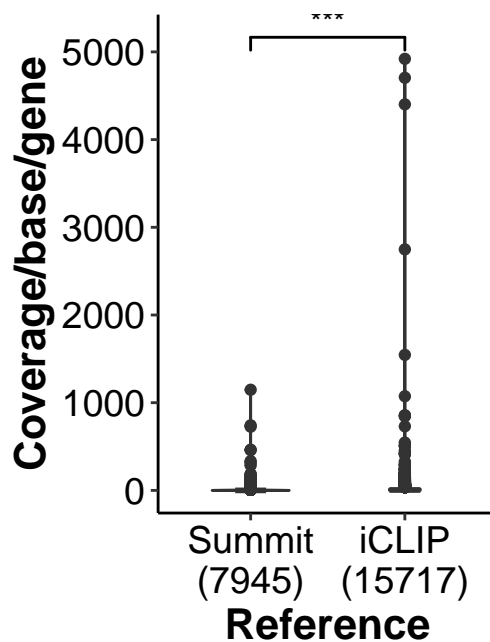
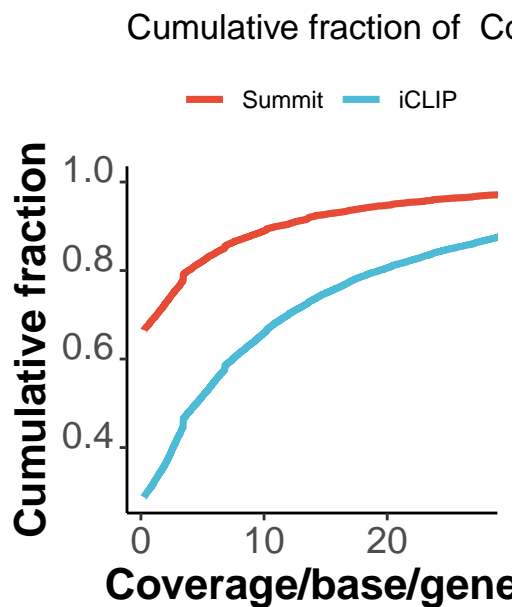
input



Mean + SE

ANOVA p-value = $1.39\text{e-}27$ 

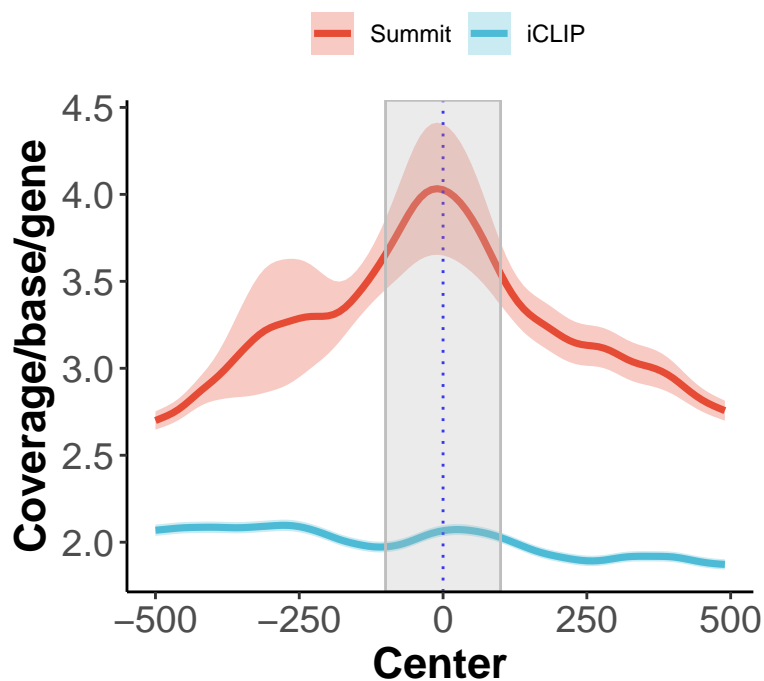
	diff	lwr	upr	p adj
<i>iCLIP-Summit</i>	9.317	7.641	10.993	0



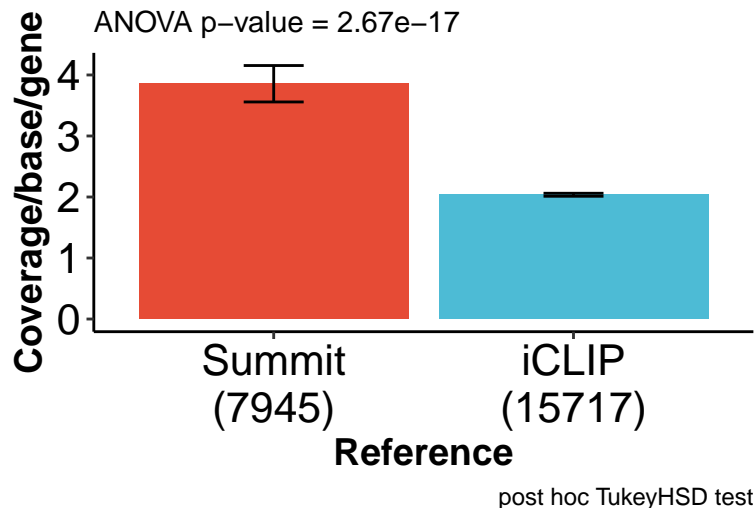
Reference Summit iCLIP

Reference Summit iCLIP

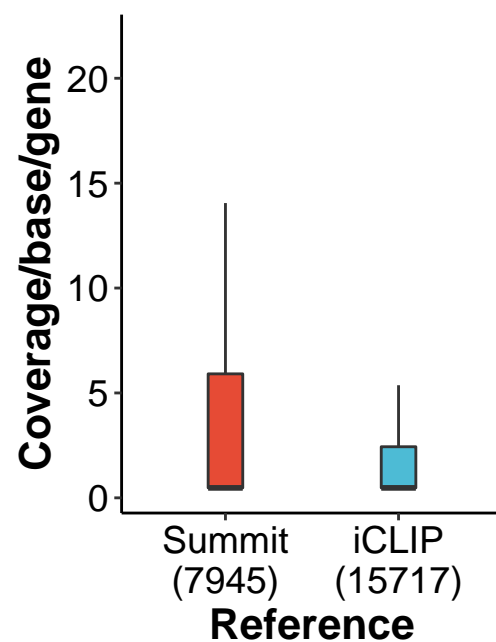
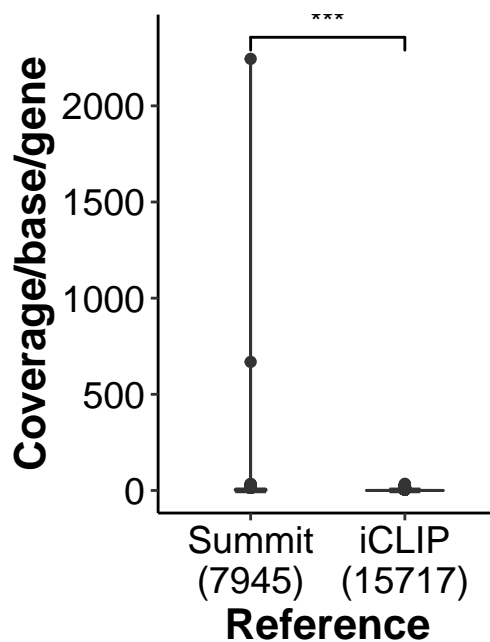
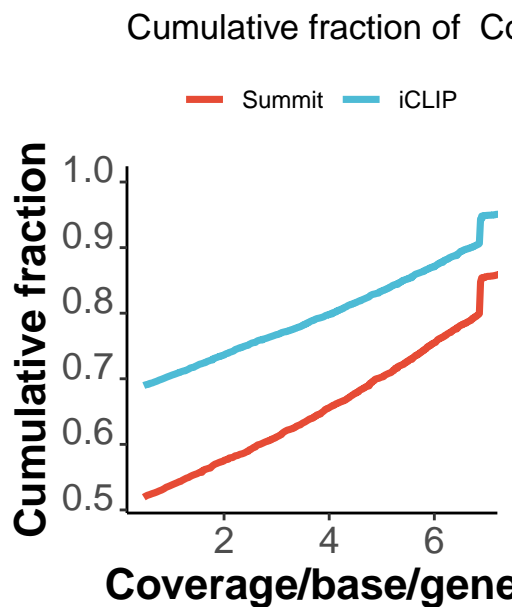
chip_input



Mean + SE

ANOVA p-value = 2.67×10^{-17} 

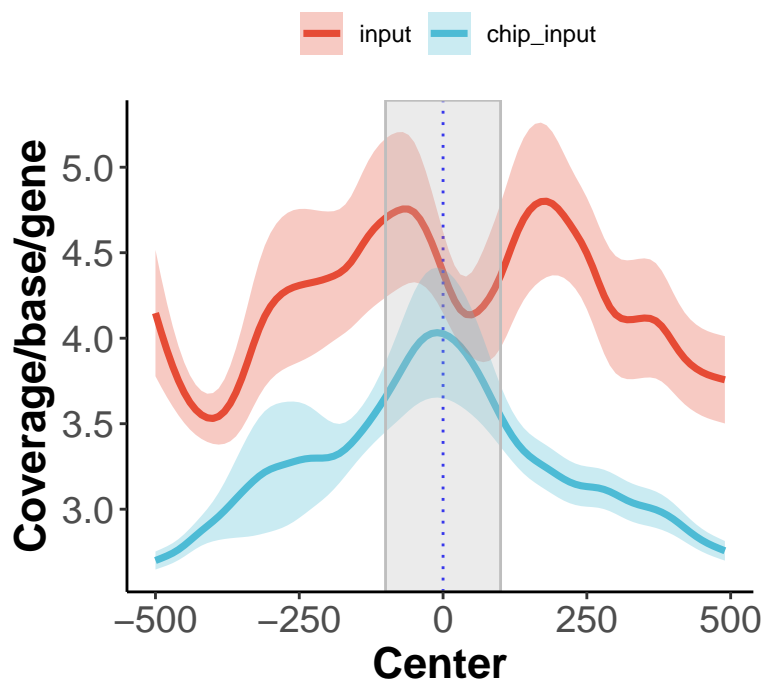
	diff	lwr	upr	p adj
<i>iCLIP-Summit</i>	-1.82	-2.241	-1.398	0



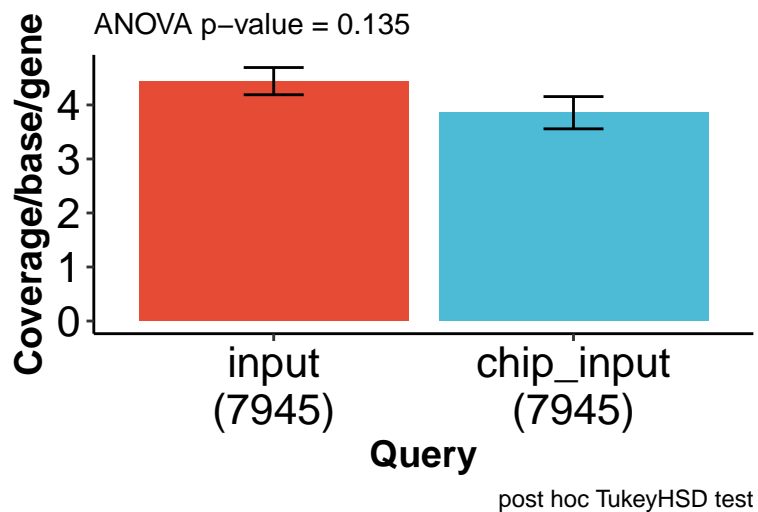
Reference Summit iCLIP

Reference Summit iCLIP

Summit



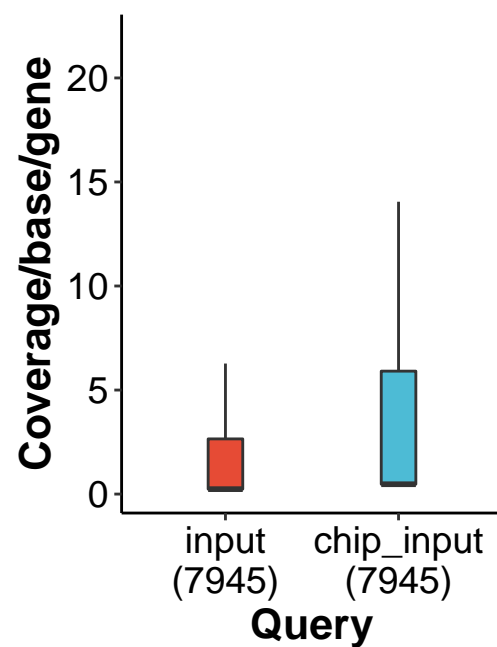
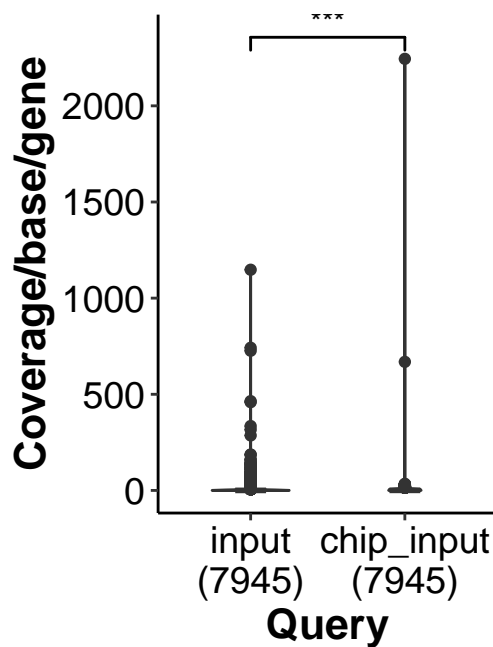
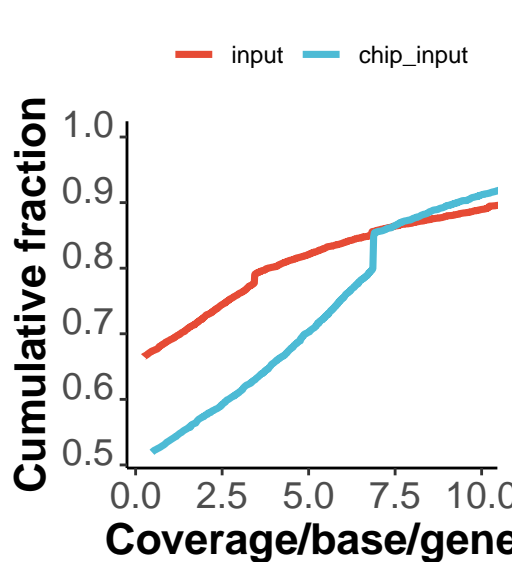
Mean + SE



chip_input-input

diff	lwr	upr	p adj
-0.584	-1.35	0.181	0.135

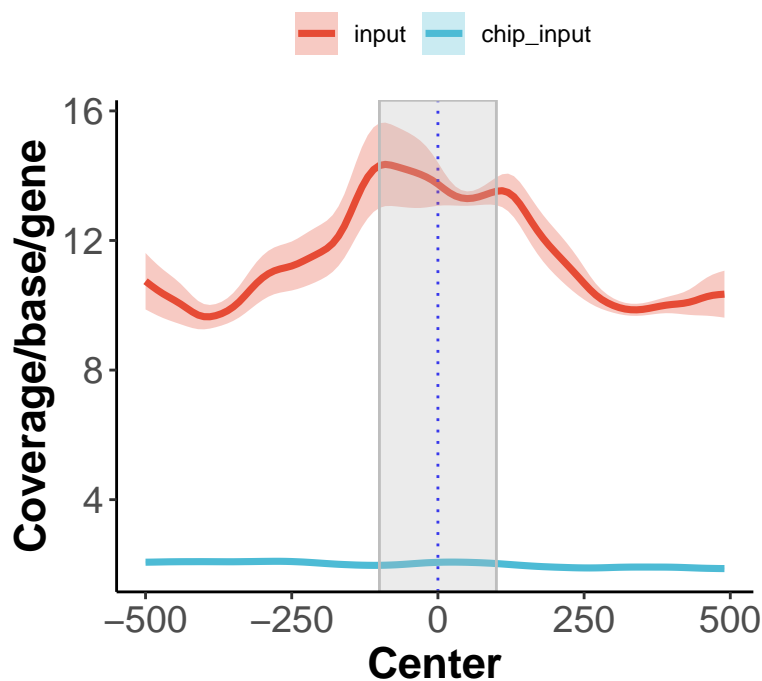
Cumulative fraction of C



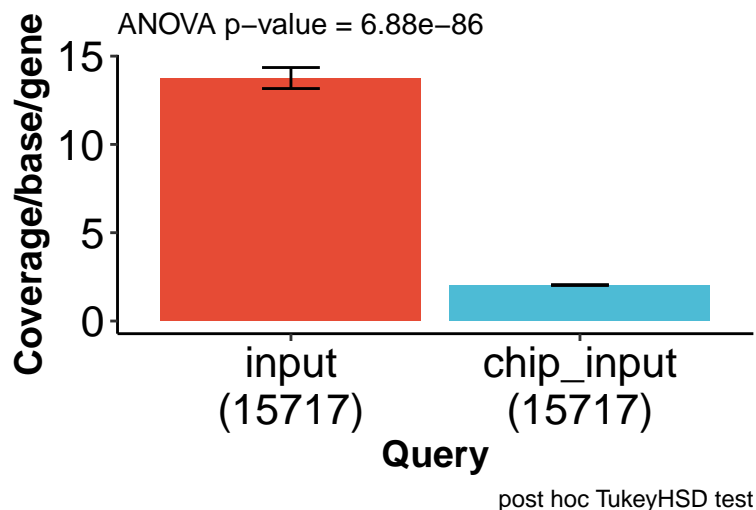
Query input chip_input

Query input chip_input

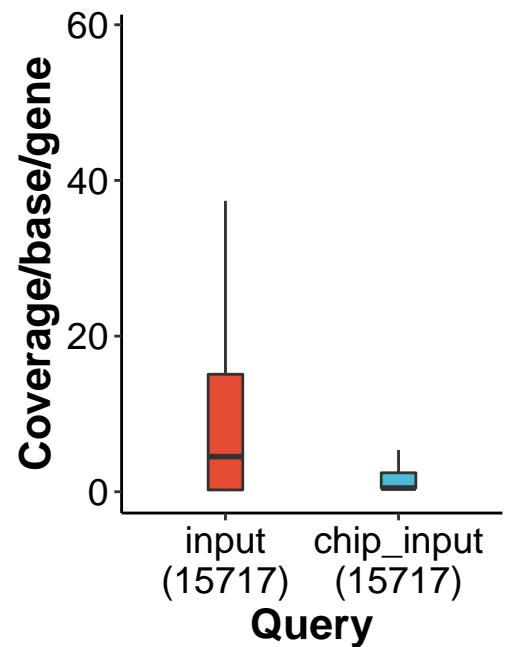
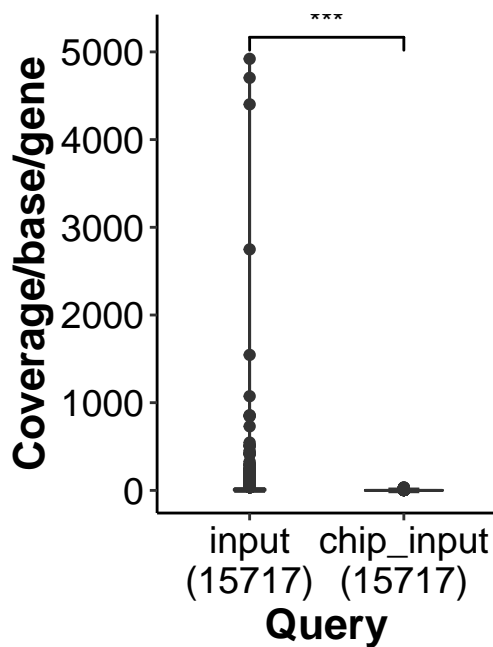
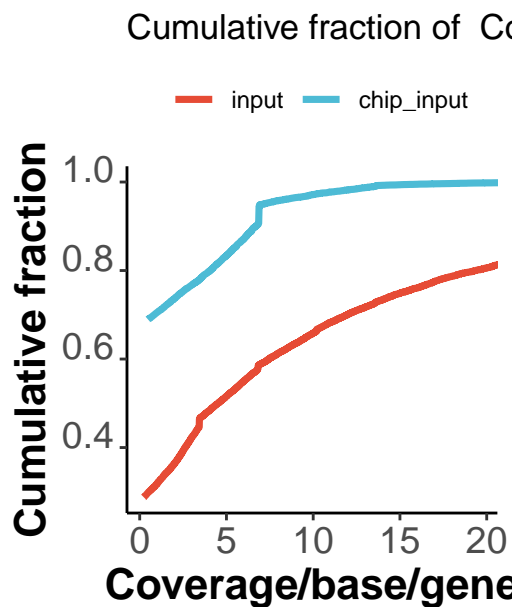
iCLIP



Mean + SE

ANOVA p-value = $6.88e-86$ 

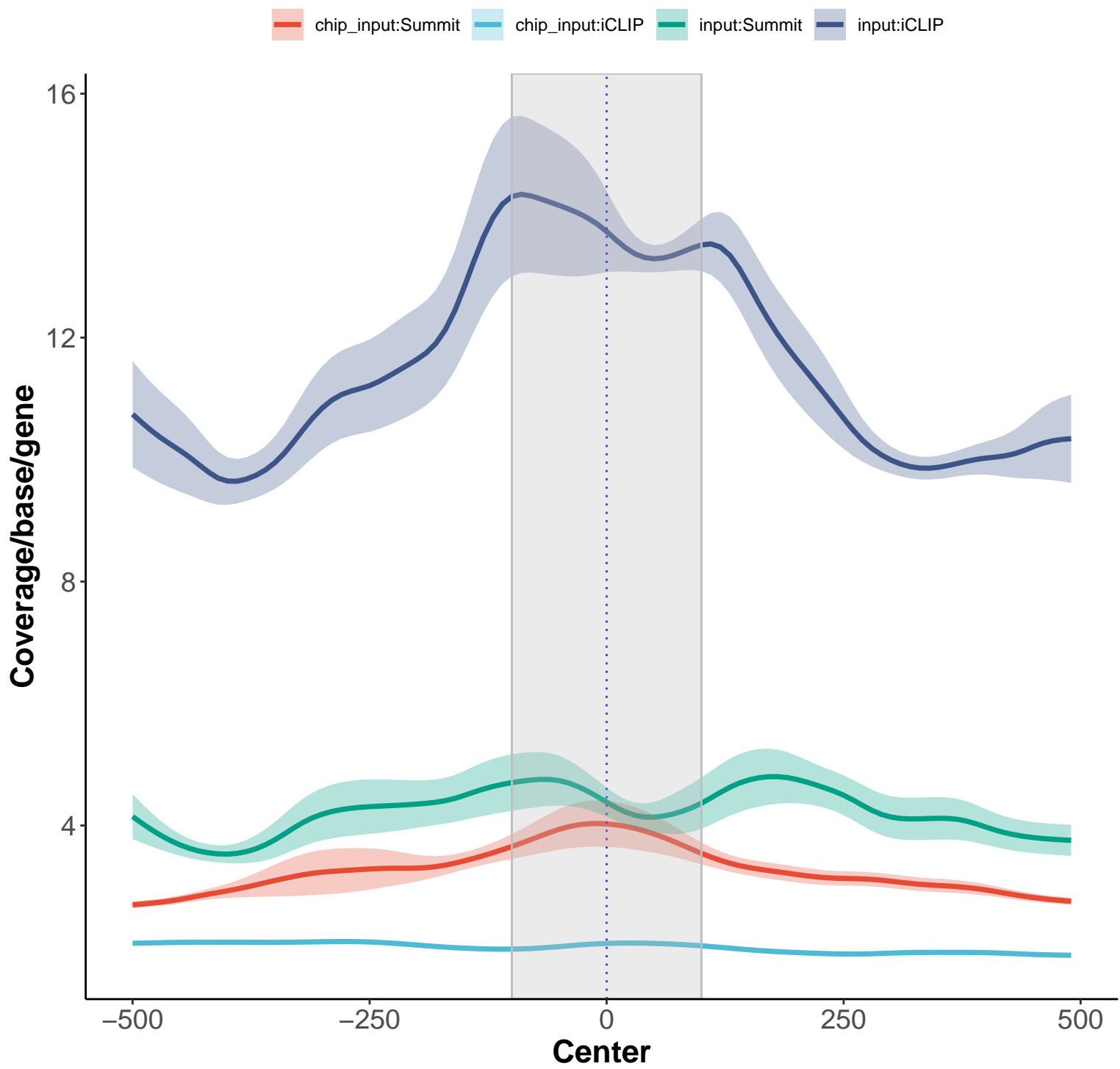
	diff	lwr	upr	p adj
chip_input-input	-11.722	-12.888	-10.556	0



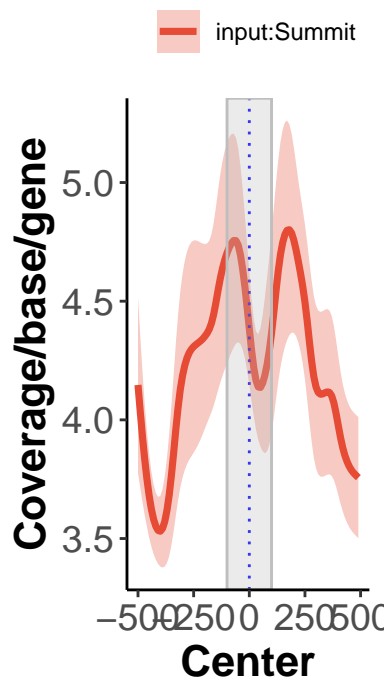
Query input chip_input

Query input chip_input

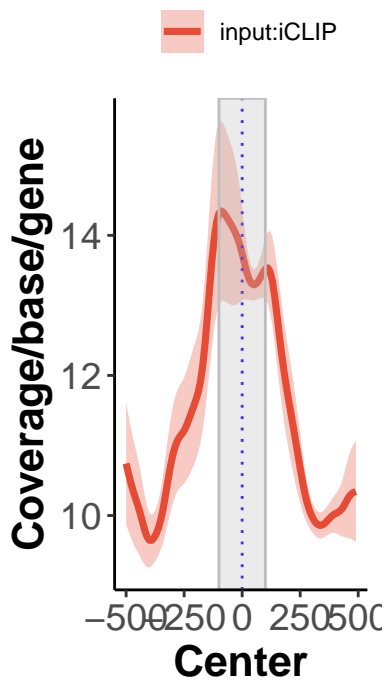
input:Summit



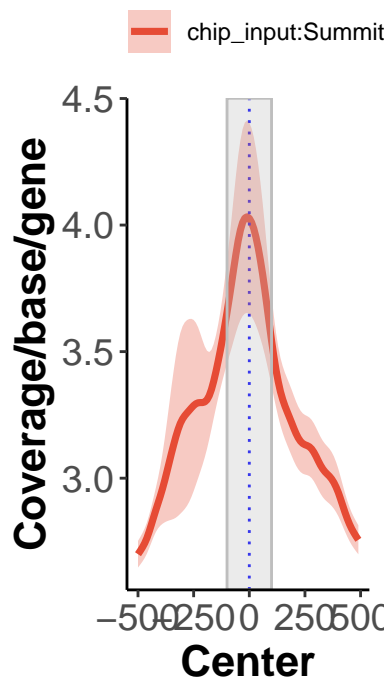
input:Summit



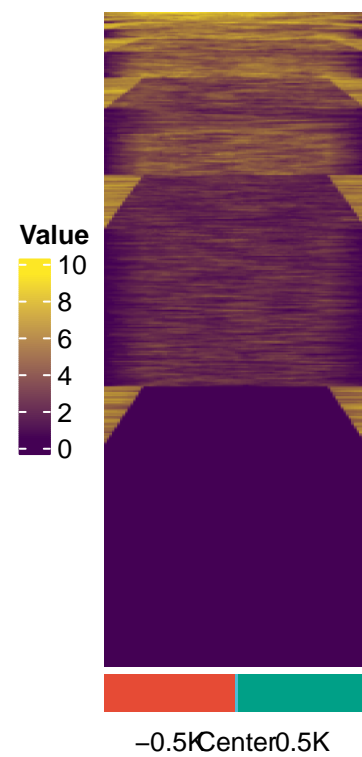
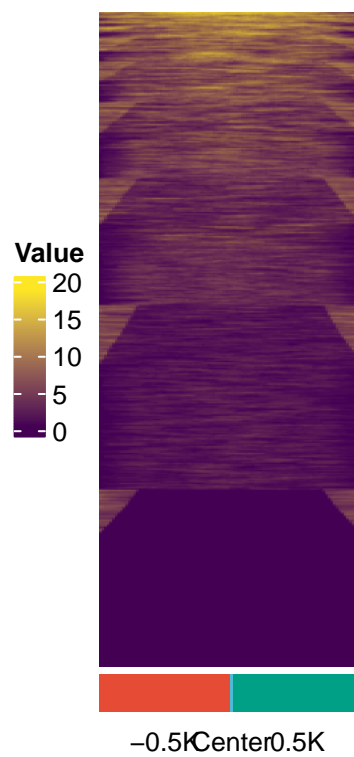
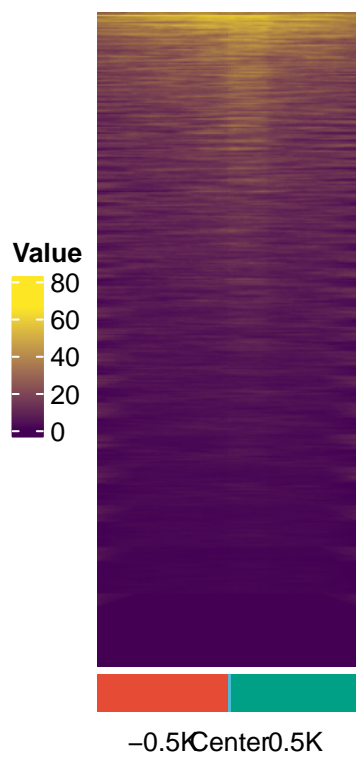
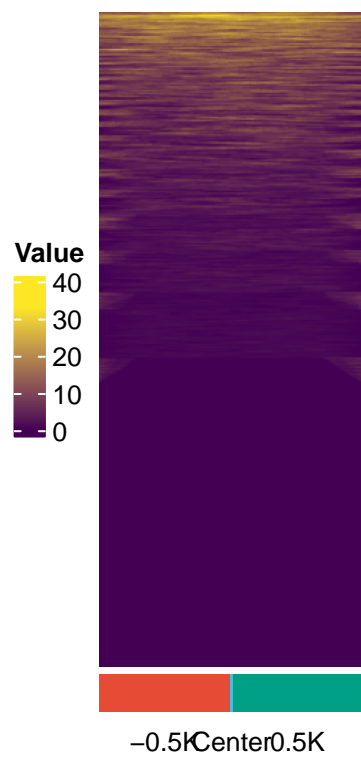
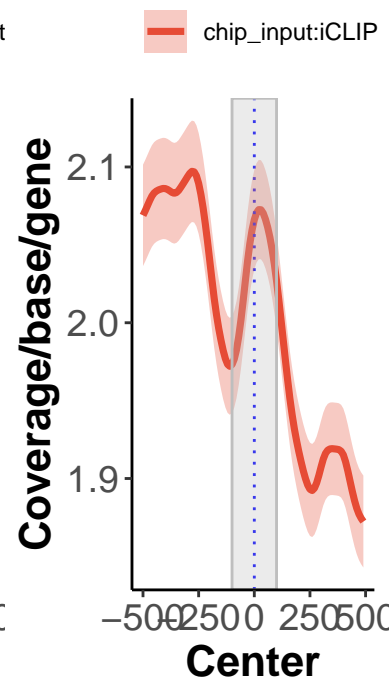
input:iCLIP



chip_input:Summr



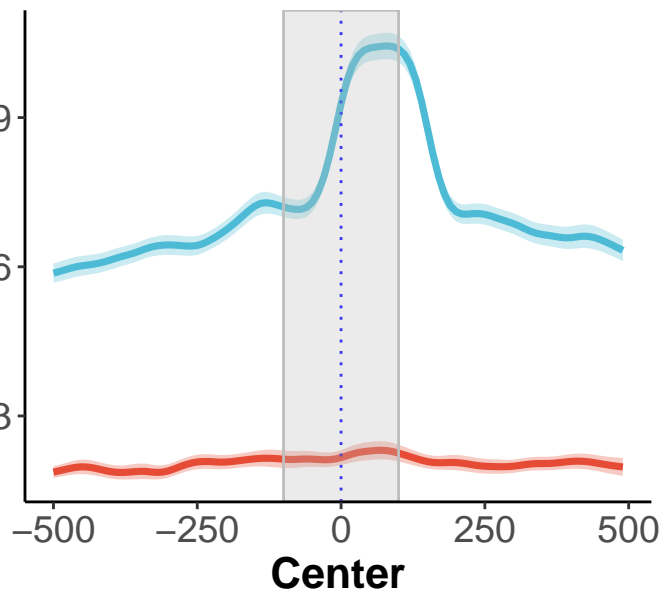
chip_input:iCLIP



query

Summit iCLIP

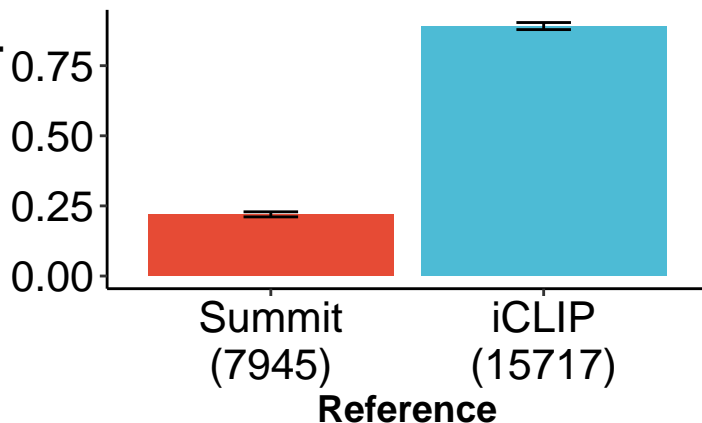
Ratio-over-Input



Mean + SE

ANOVA p-value = 3.18e-271

Ratio-over-Input



post hoc TukeyHSD test

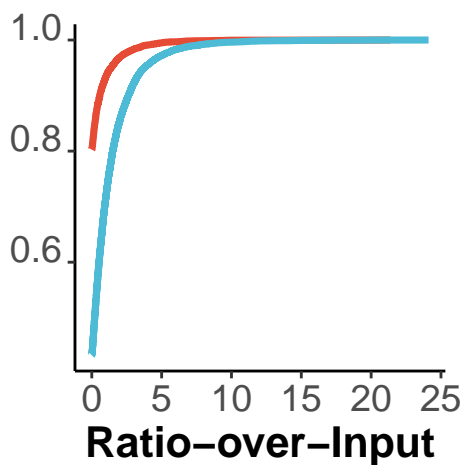
iCLIP-Summit

diff	lwr	upr	p adj
0.671	0.635	0.708	0

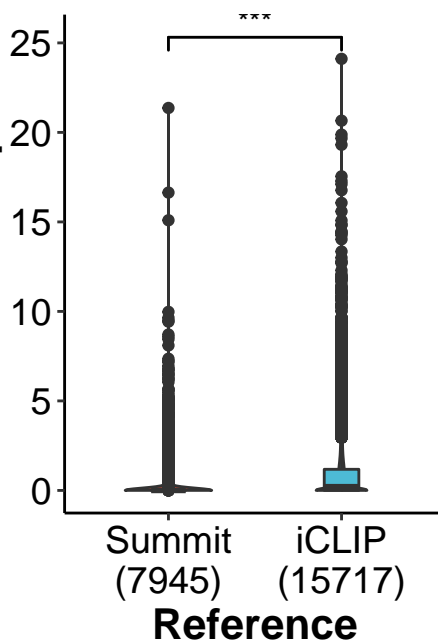
Cumulative fraction of R₀

Summit iCLIP

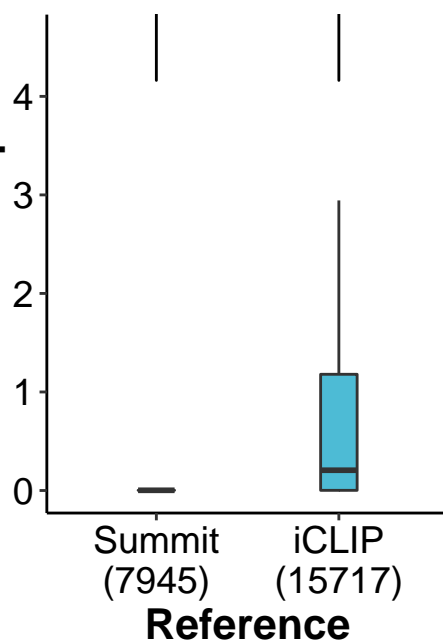
Cumulative fraction



Ratio-over-Input



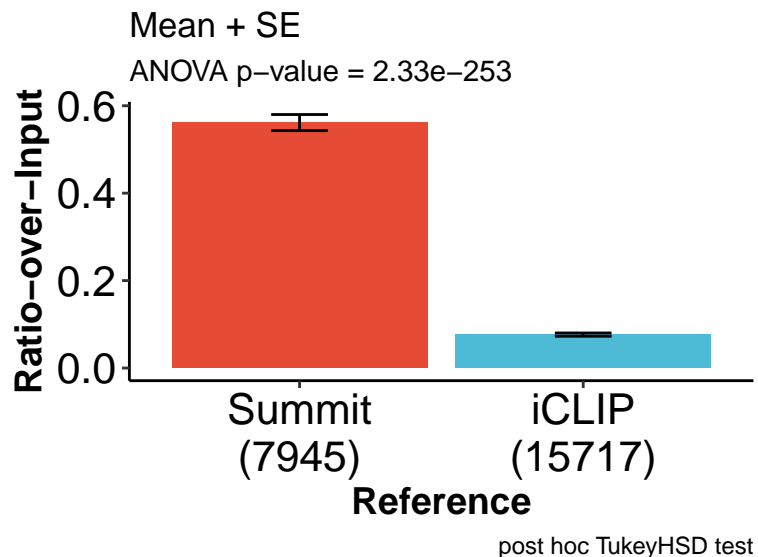
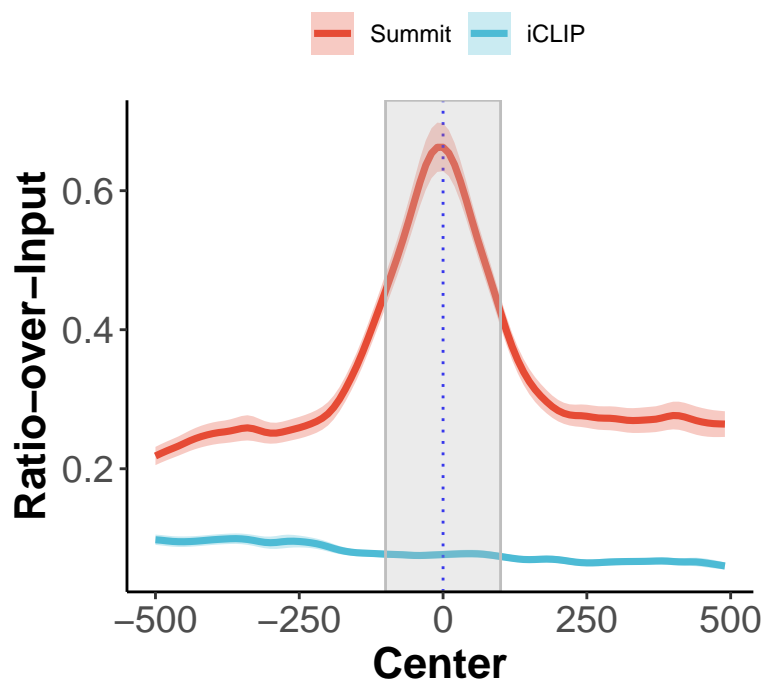
Ratio-over-Input



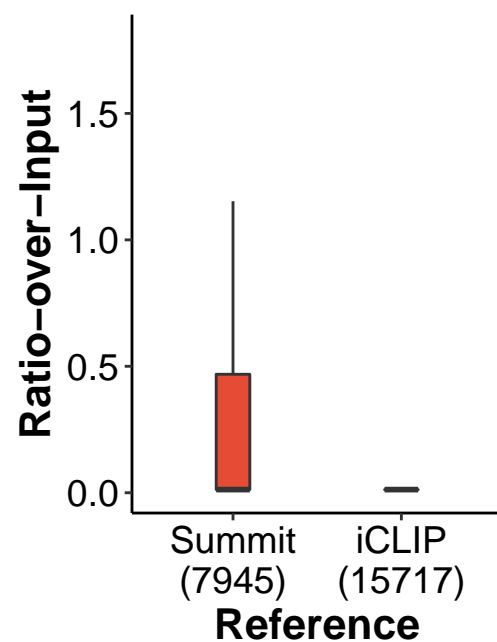
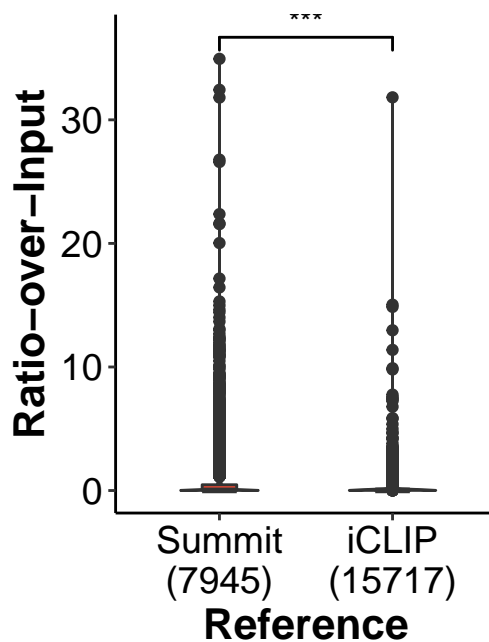
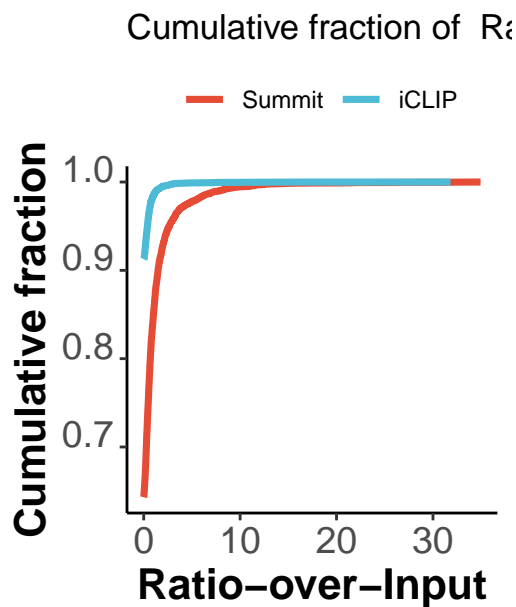
Reference Summit iCLIP

Reference Summit iCLIP

chip_query



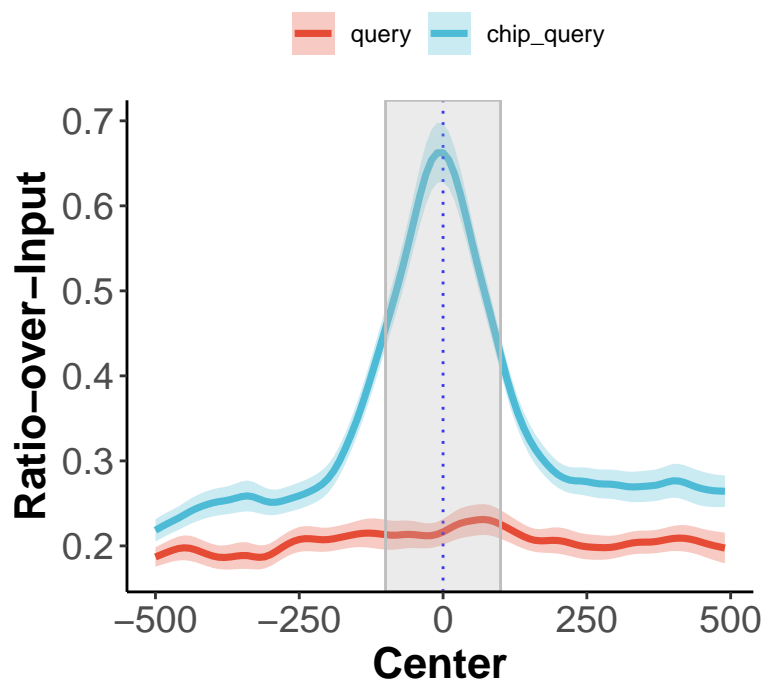
	diff	lwr	upr	p adj
iCLIP-Summit	-0.485	-0.513	-0.457	0



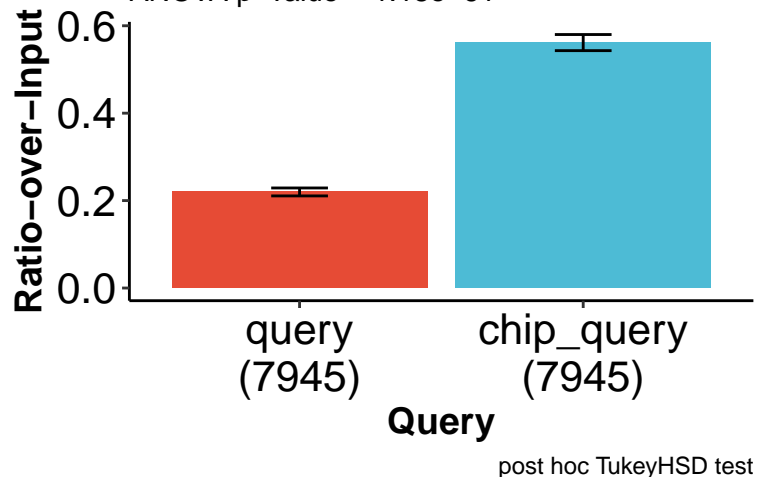
Reference Summit iCLIP

Reference Summit iCLIP

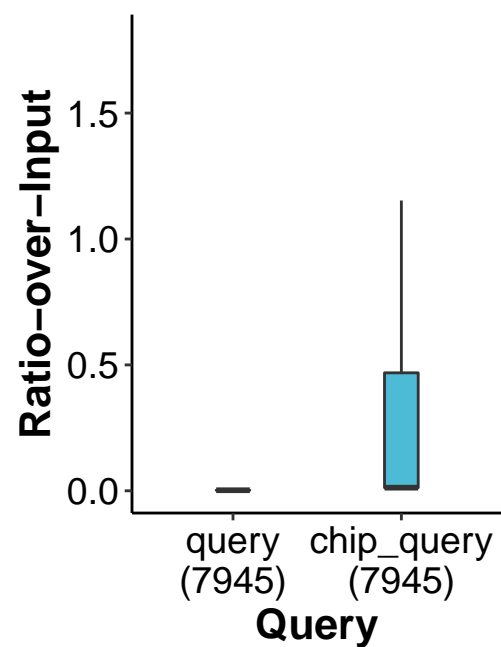
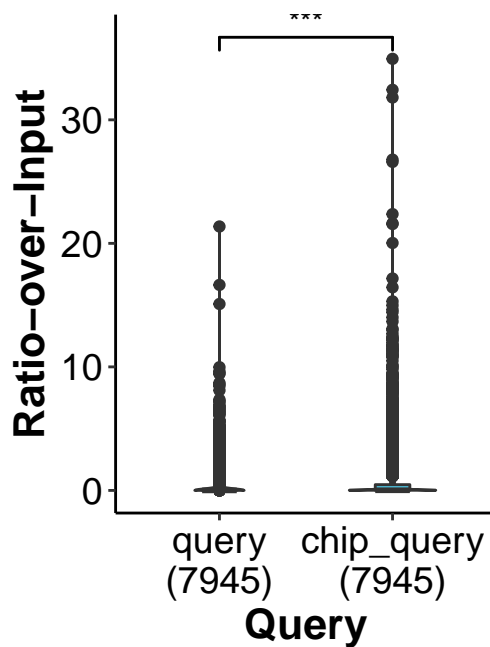
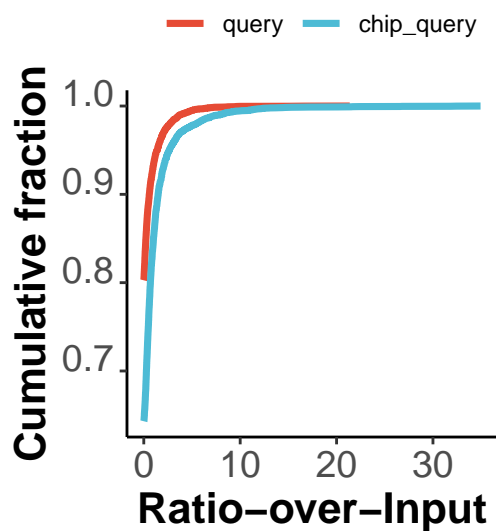




Summit



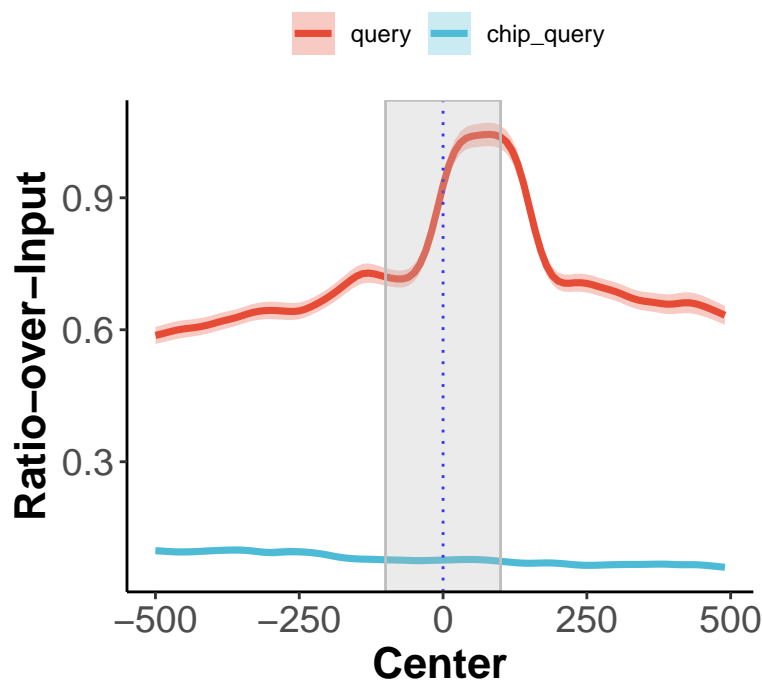
Mean + SE

ANOVA p-value = 1.18×10^{-61} 

	diff	lwr	upr	p adj
chip_query-query	0.342	0.301	0.382	2.04e-08

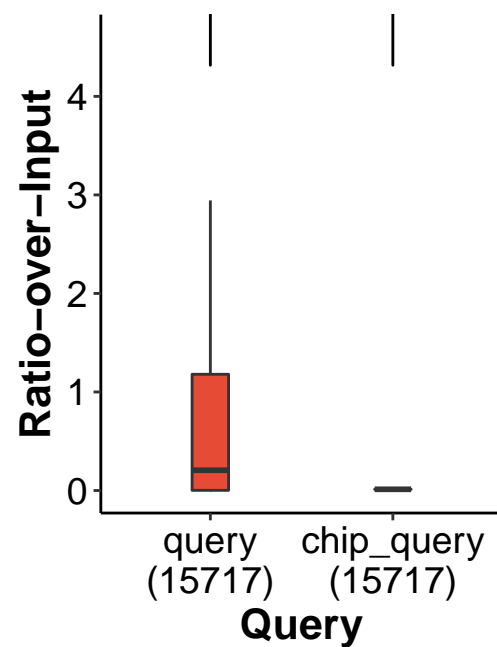
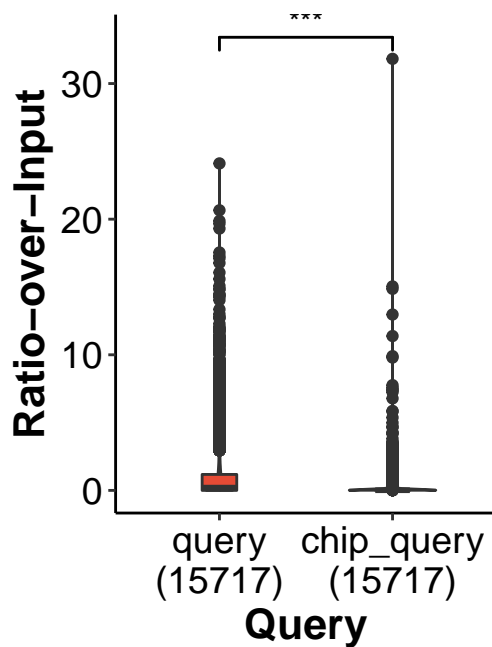
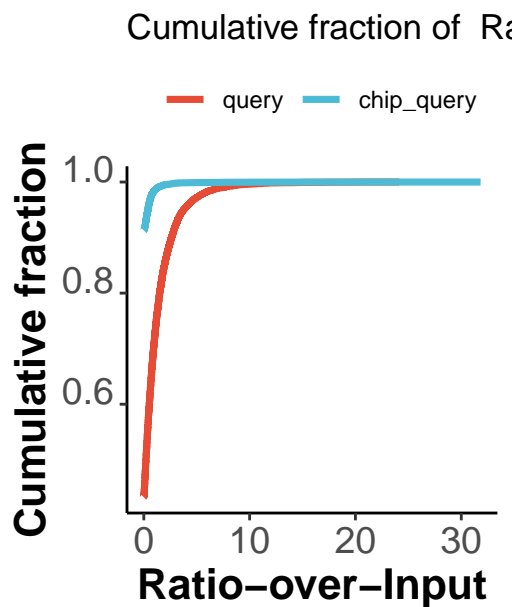
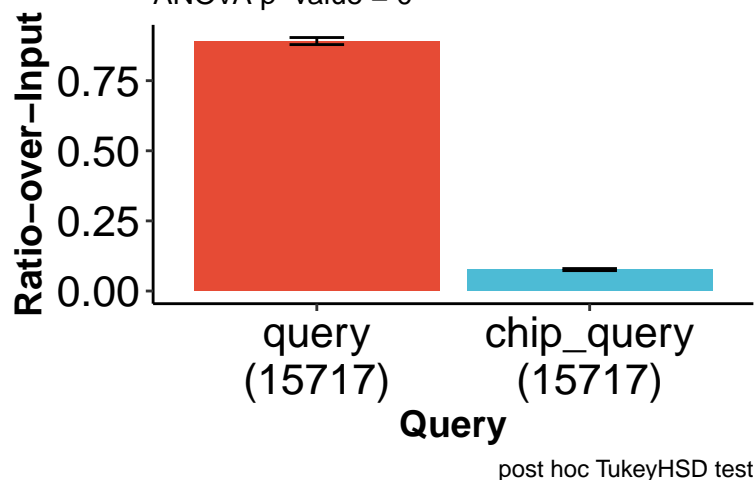




Cumulative fraction of R₀Query  query  chip_queryQuery  query  chip_query

iCLIP



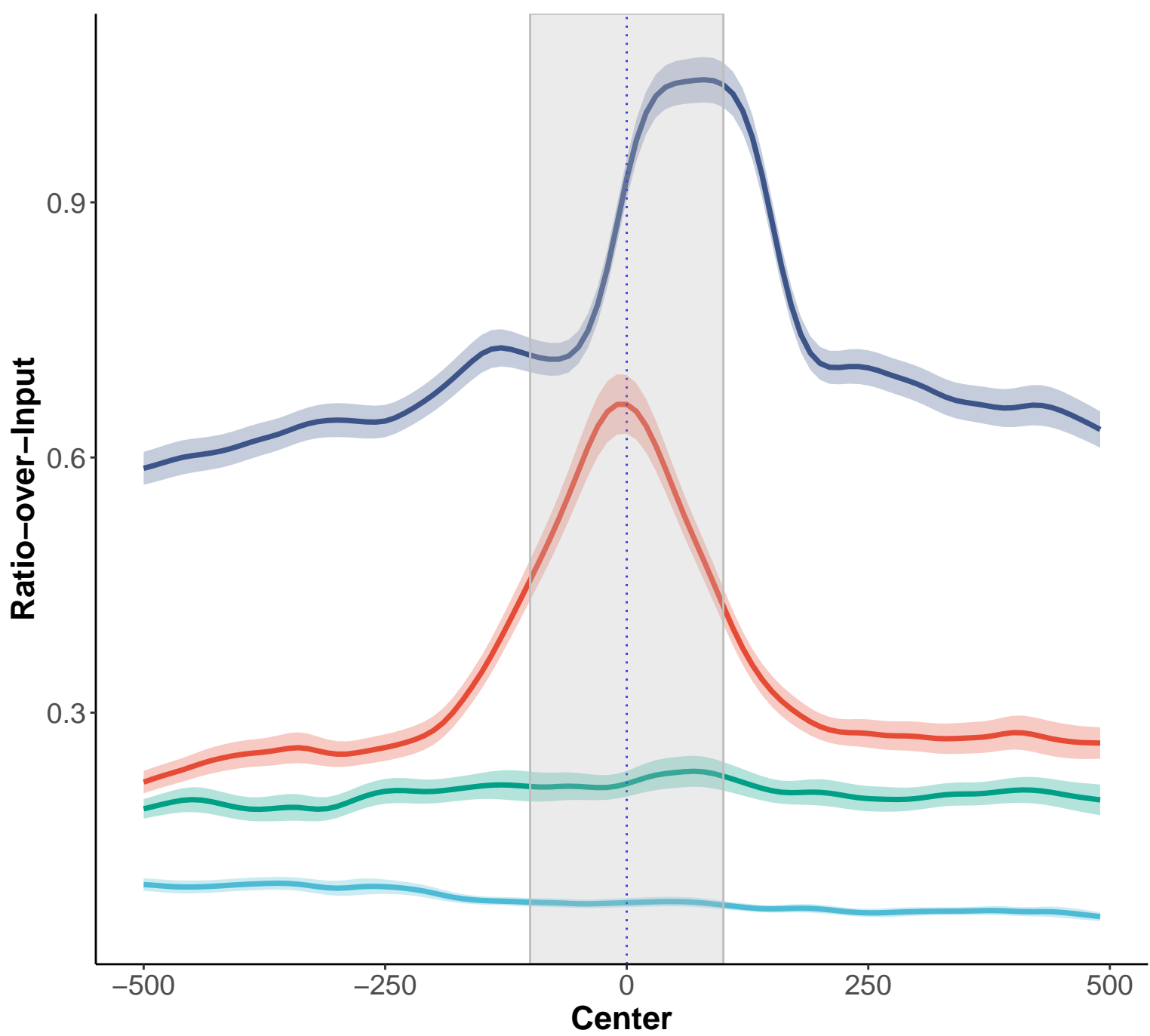
Mean + SE

ANOVA p-value = 0

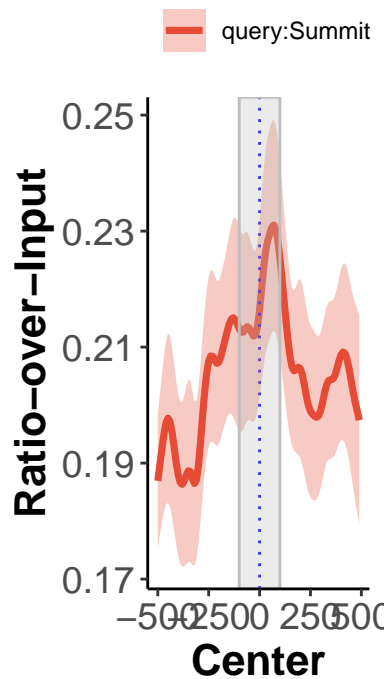
Query  query  chip_queryQuery  query  chip_query

query:Summit

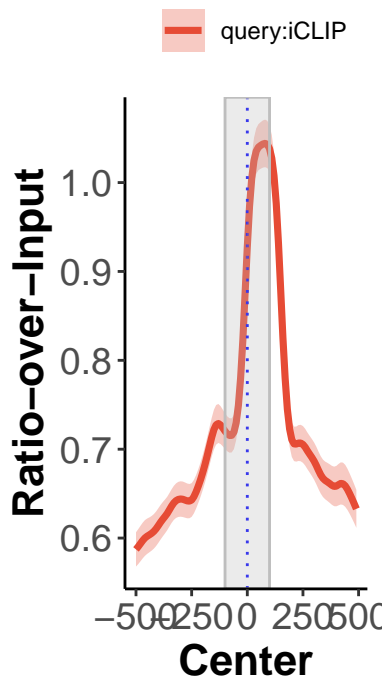
chip_query:Summit chip_query:iCLIP query:Summit query:iCLIP



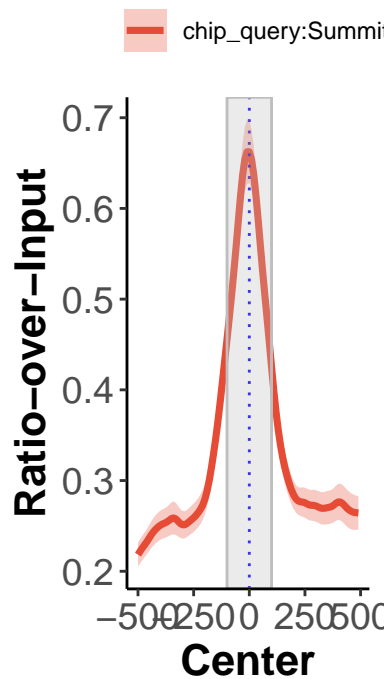
query:Summit



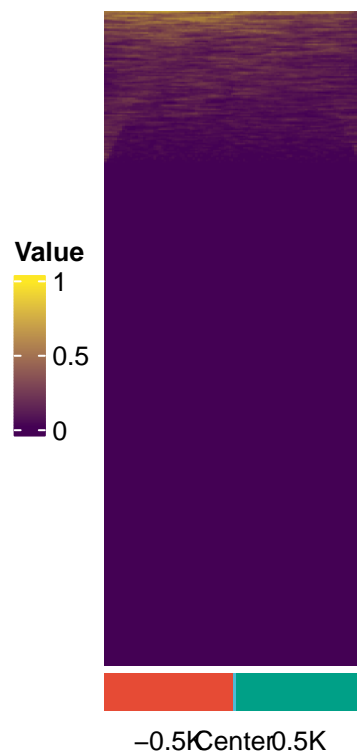
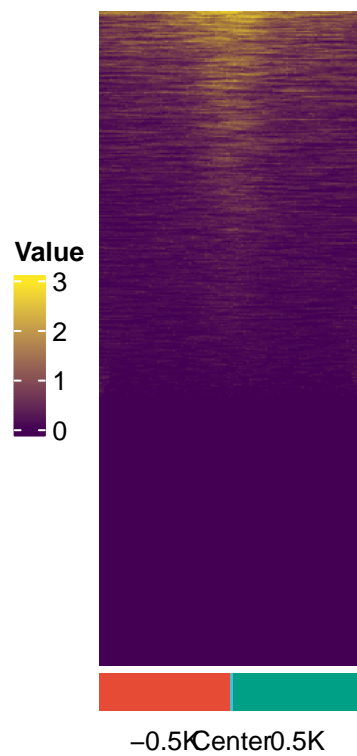
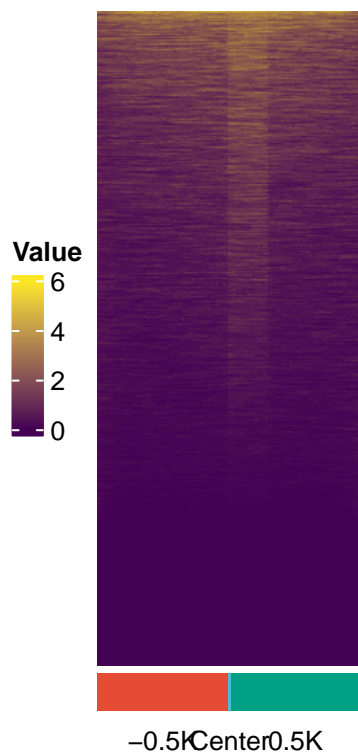
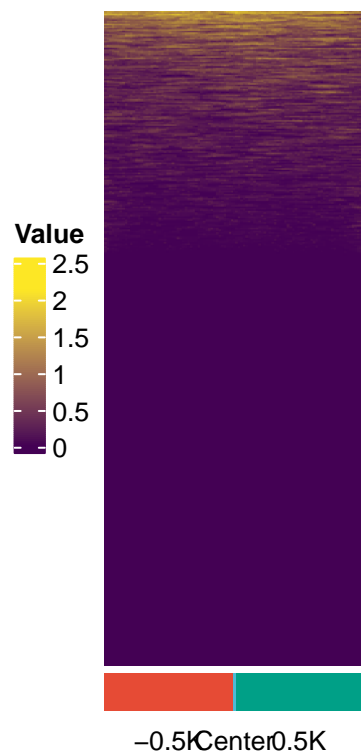
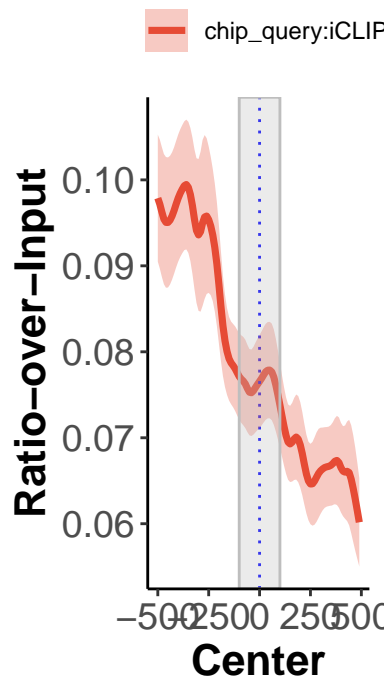
query:iCLIP



chip_query:Summit



chip_query:iCLIP



Plotting parameters:

```
functionName: "plot_locus"
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(Summit =
               "C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/test_chip_peak_chr19.bed",
               iCLIP =
               "C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/test_clip_peak_chr19.bed")
               txdb: NULL
               ext: c(-500, 500)
               hl: c(-100, 100)
               shade: TRUE
               smooth: TRUE
handleInputParams: list(offset = 0, fix_width = 150, fix_point = "start", norm = TRUE, useScore =
                          FALSE, outRle = TRUE, useSizeFactor = TRUE, genome = "hg19")
                          verbose: FALSE
                          binSize: 10
                          refPoint: "center"
                          Xlab: "Center"
                          Ylab: "Coverage/base/gene"
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")
               stranded: TRUE
               heatmap: TRUE
               scale: FALSE
outPrefix: "test_plot_locus2"
rmOutlier: FALSE
transform: NA
statsMethod: "wilcox.test"
heatRange: NULL
hw: c(8, 8)
nc: 2
```