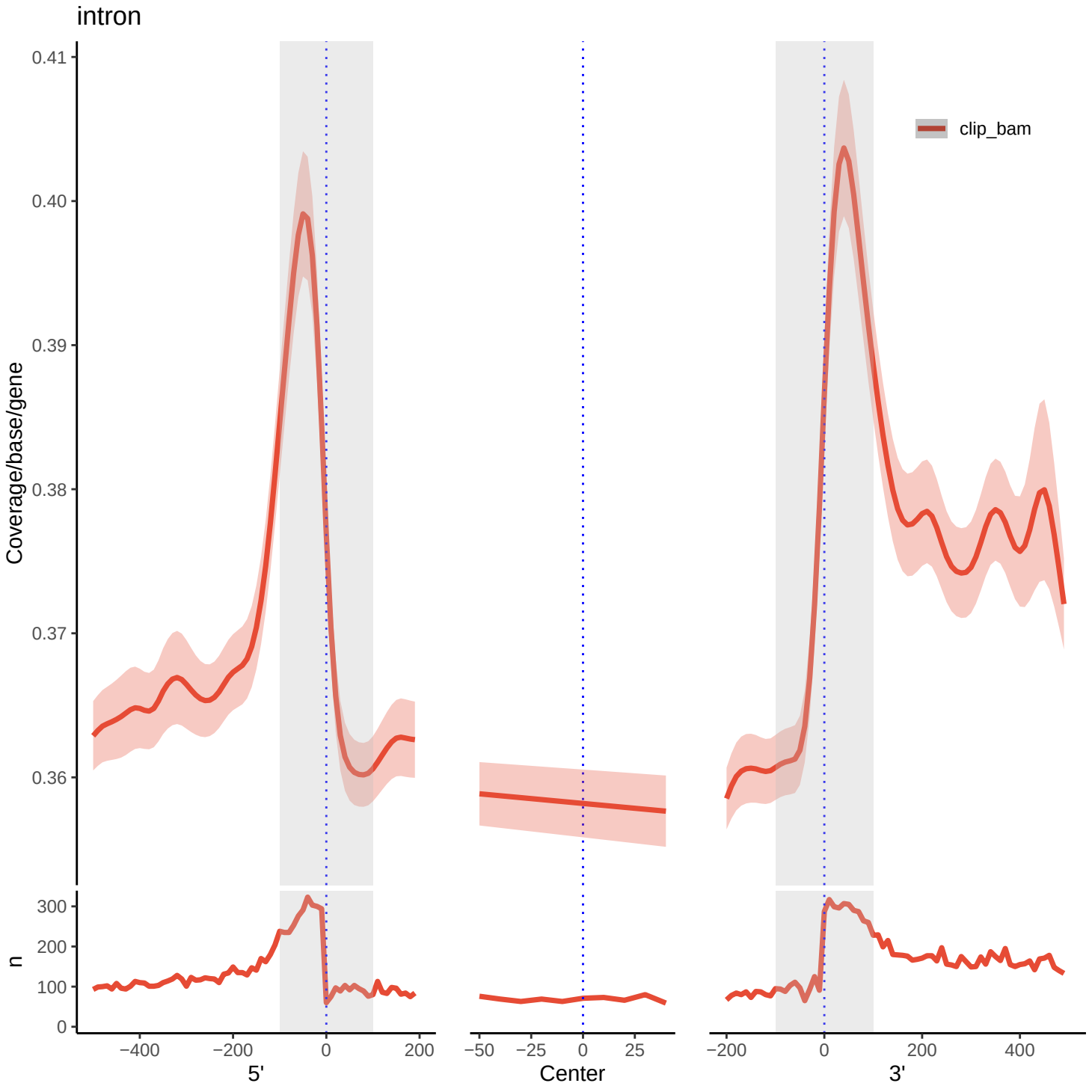
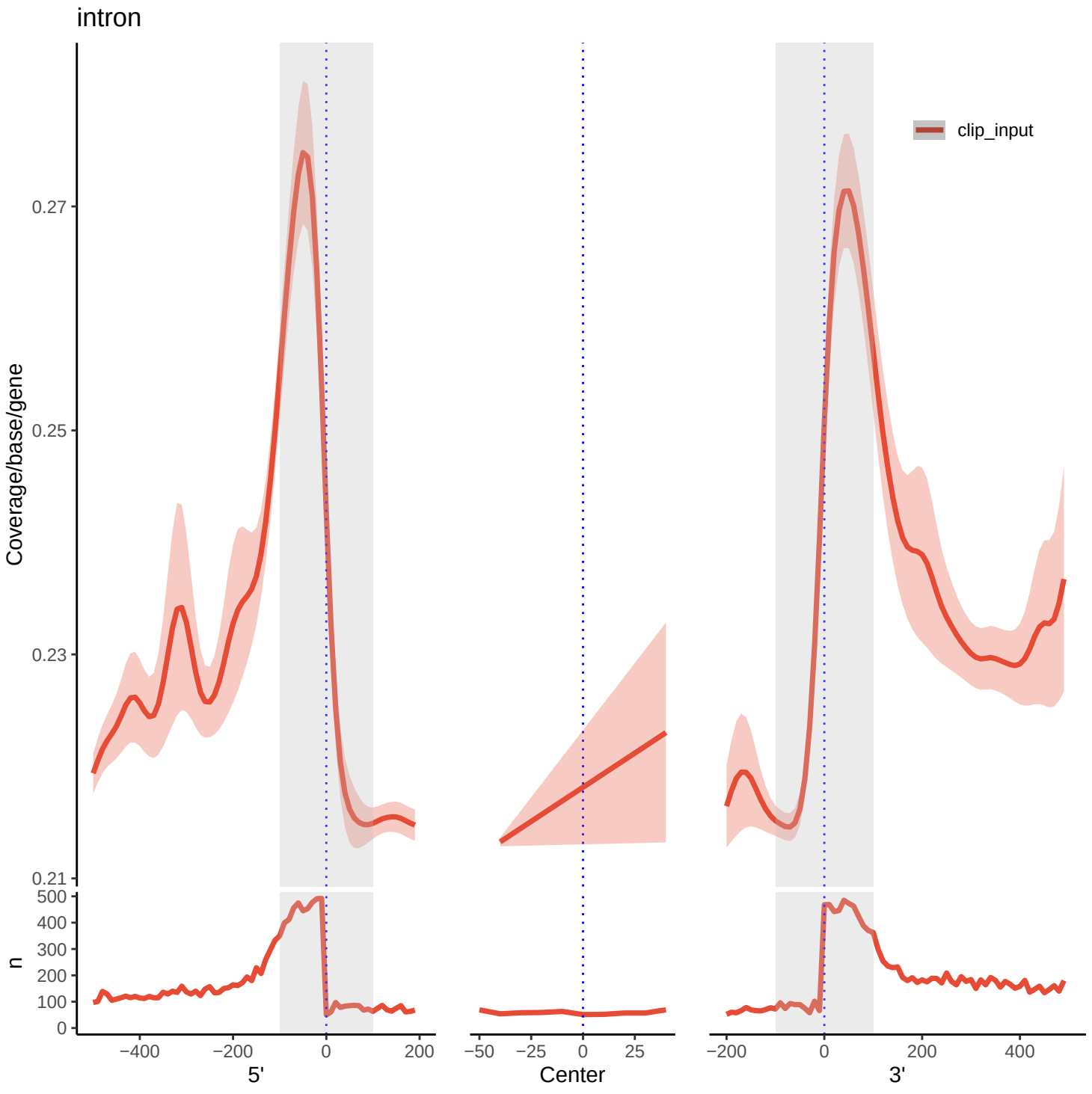
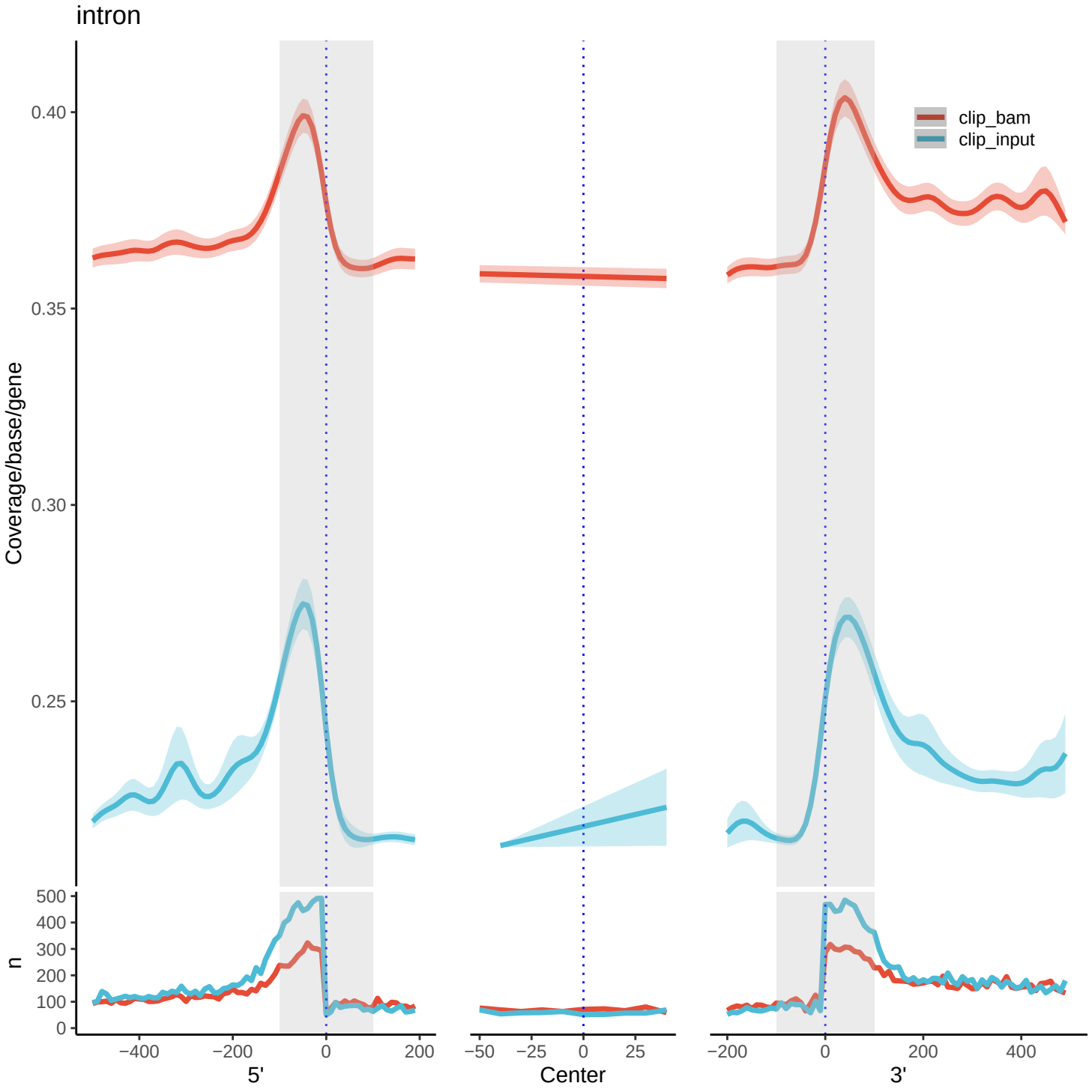
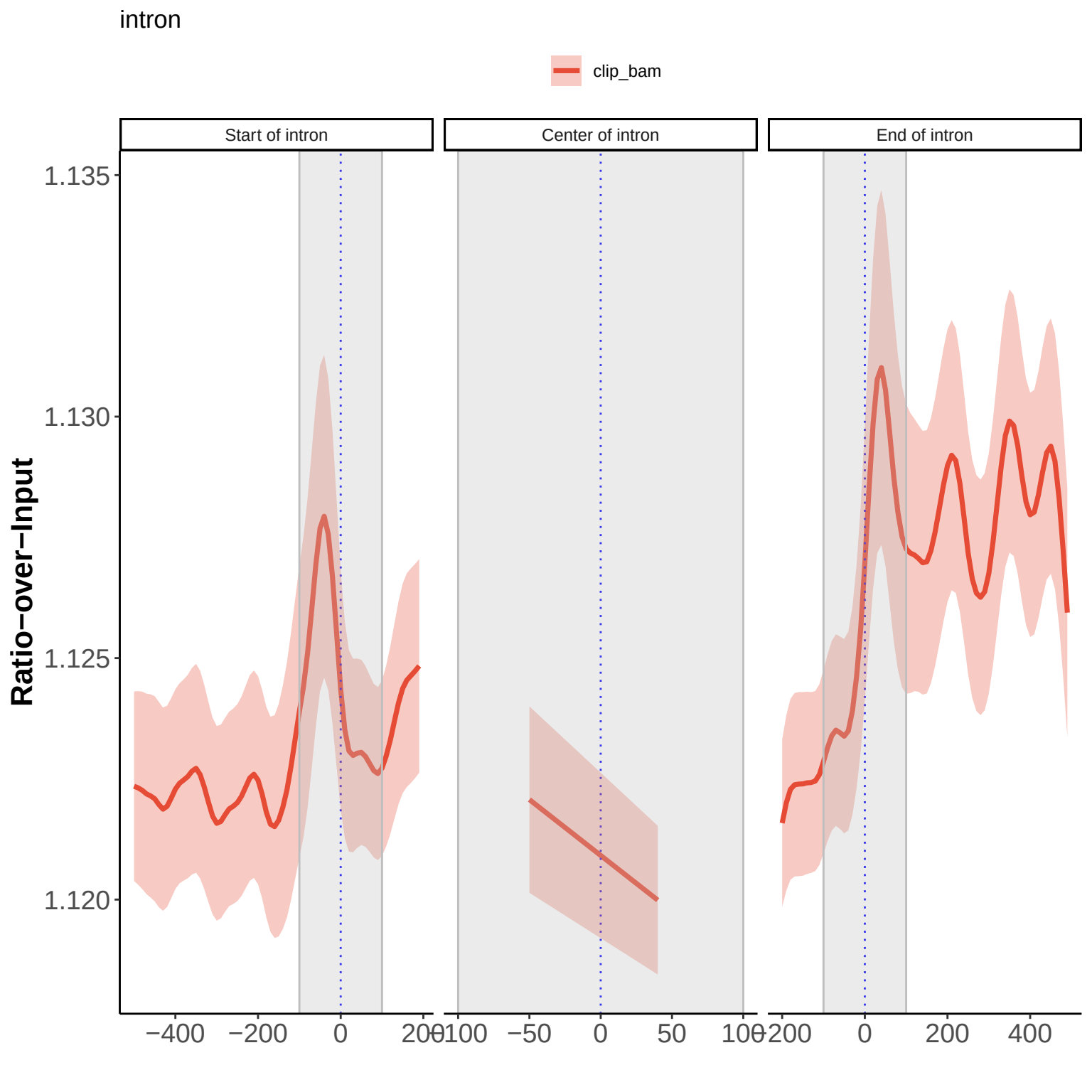
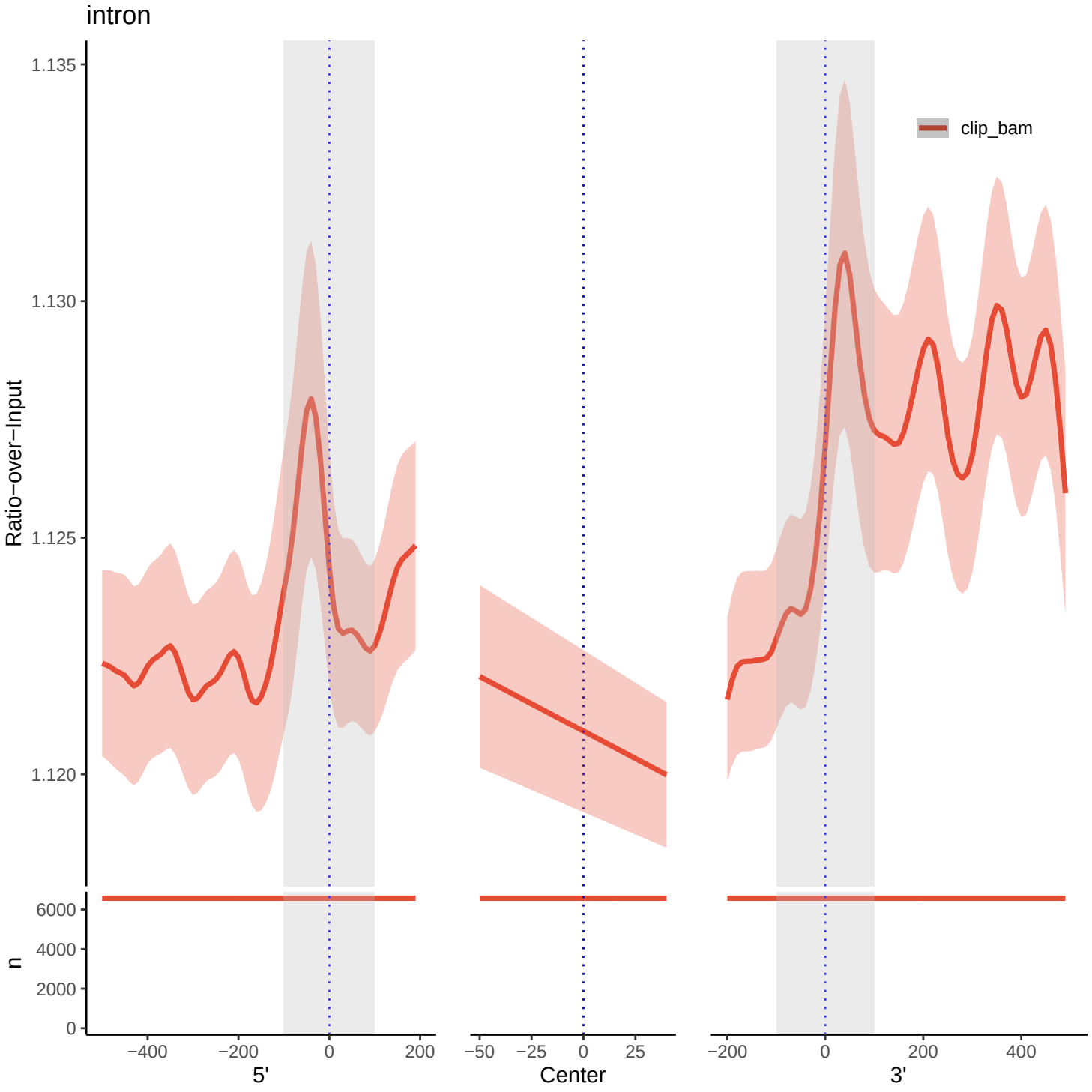

intron
clip_bam
Coverage/base/gene
0.41
0.40
0.39
0.38
0.37
0.36
n
300
200
100
0
−400
−200
0
200
5'
−50
−25
0
25
Center
−200
0
200
400
3'


intron
clip_input
Coverage/base/gene
0.27
0.25
0.23
0.21
n
500
400
300
200
100
0
−400
−200
0
200
5'
−50
−25
0
25
Center
−200
0
200
400
3'


intron
clip_bam
clip_input
Coverage/base/gene
0.40
0.35
0.30
0.25
n
500
400
300
200
100
0
−400
−200
0
200
5'
−50
−25
0
25
Center
−200
0
200
400
3'


intron
clip_bam
Start of intron
Center of intron
End of intron
Ratio−over−Input
1.135
1.130
1.125
1.120
−400
−200
0
200
−100
−50
0
50
100
−200
0
200
400


intron
clip_bam
Ratio−over−Input
1.135
1.130
1.125
1.120
n
6000
4000
2000
0
−400
−200
0
200
5'
−50
−25
0
25
Center
−200
0
200
400
3'

Plotting parameters:

functionName: "plot_start_end_with_random"
queryFiles: c(clip_bam =
"C:/Users/greenblatt/AppData/Local/Programs/R/R−4.2.1/library/GenomicPlot/extdata/treat_chr19.bam")
inputFiles: c(clip_input =
"C:/Users/greenblatt/AppData/Local/Programs/R/R−4.2.1/library/GenomicPlot/extdata/input_chr19.bam")
txdb: new("TxDb", .xData = <environment>)
centerFile: "intron"
importParams: list(offset = −1, fix_width = 0, fix_point = "start", norm = TRUE, useScore =
FALSE, outRle = TRUE, useSizeFactor = FALSE, genome = "hg19")
binSize: 10
insert: 100
verbose: FALSE
ext: c(−500, 200, −200, 500)
hl: c(−100, 100, −100, 100)
randomize: FALSE
stranded: TRUE
scale: FALSE
smooth: TRUE
rmOutlier: 0
outPrefix: "test_plot_start_end_with_random"
transform: NA
shade: TRUE
nc: 2
hw: c(8, 8)
Ylab: "Coverage/base/gene"