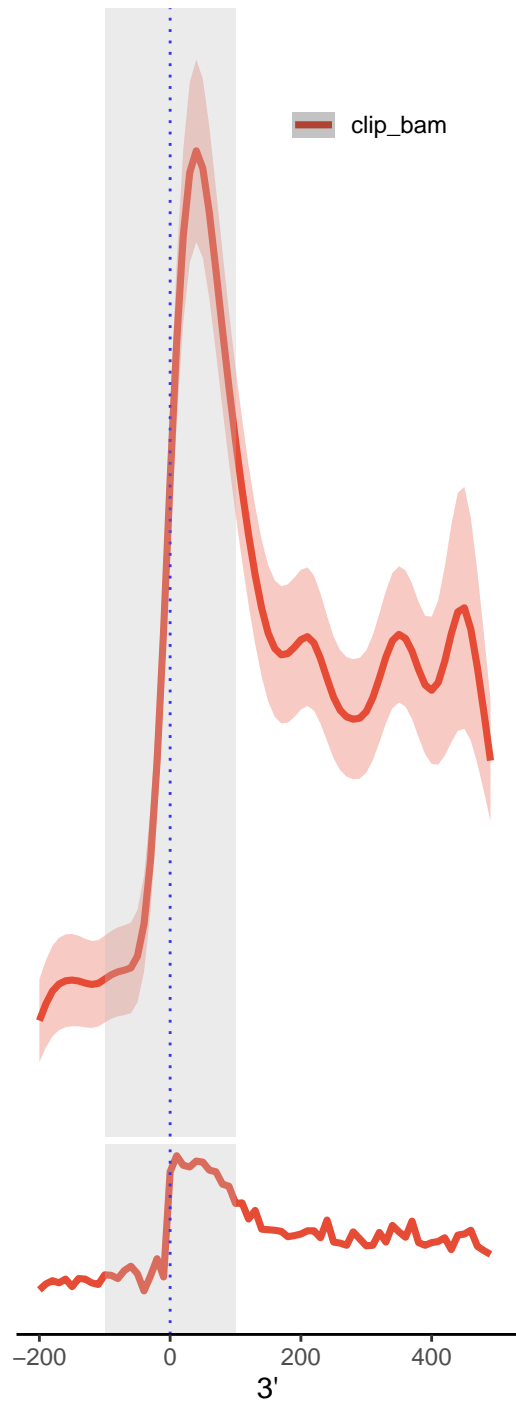
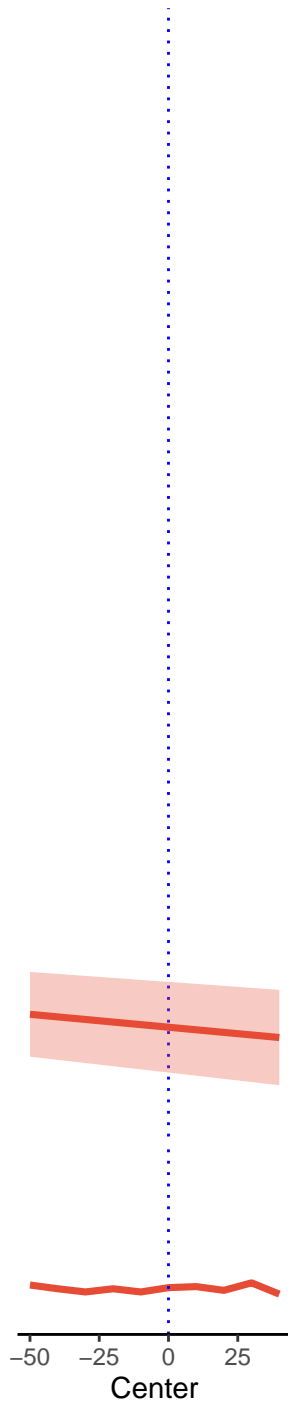
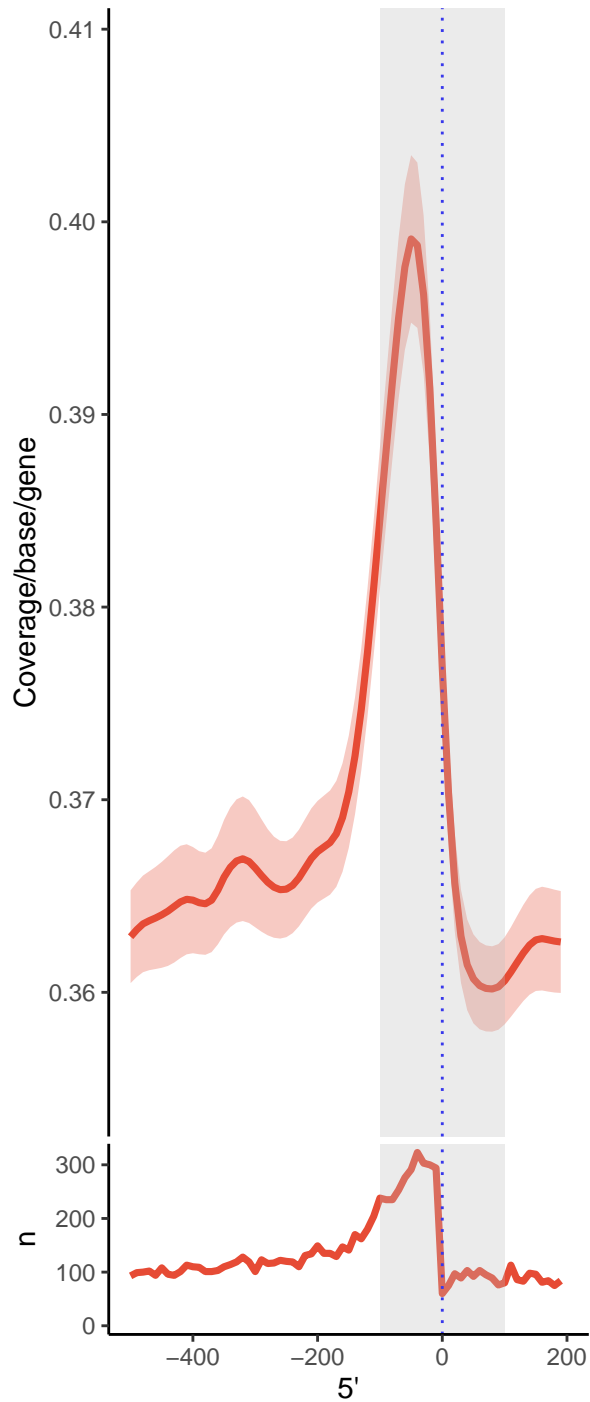
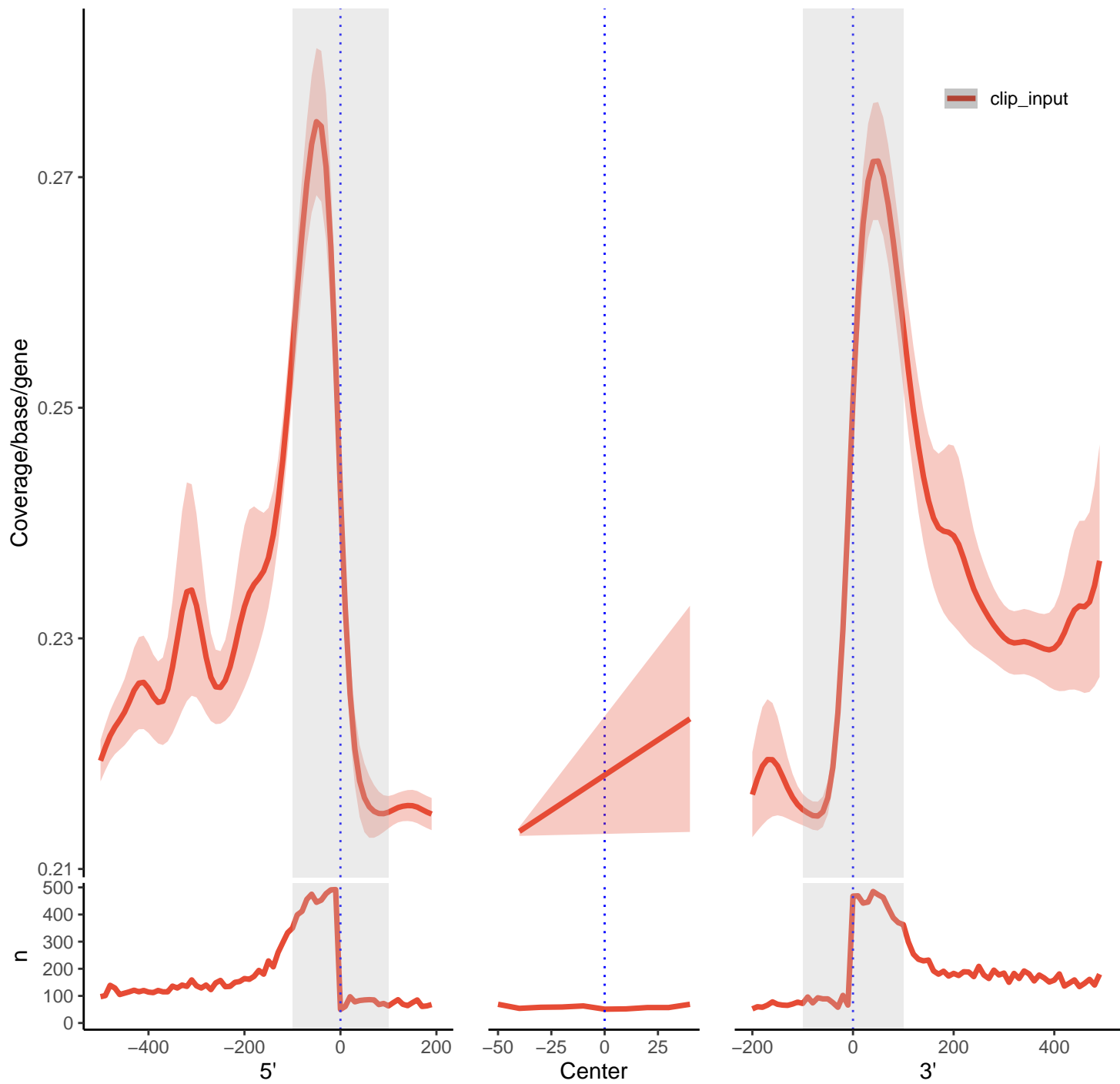


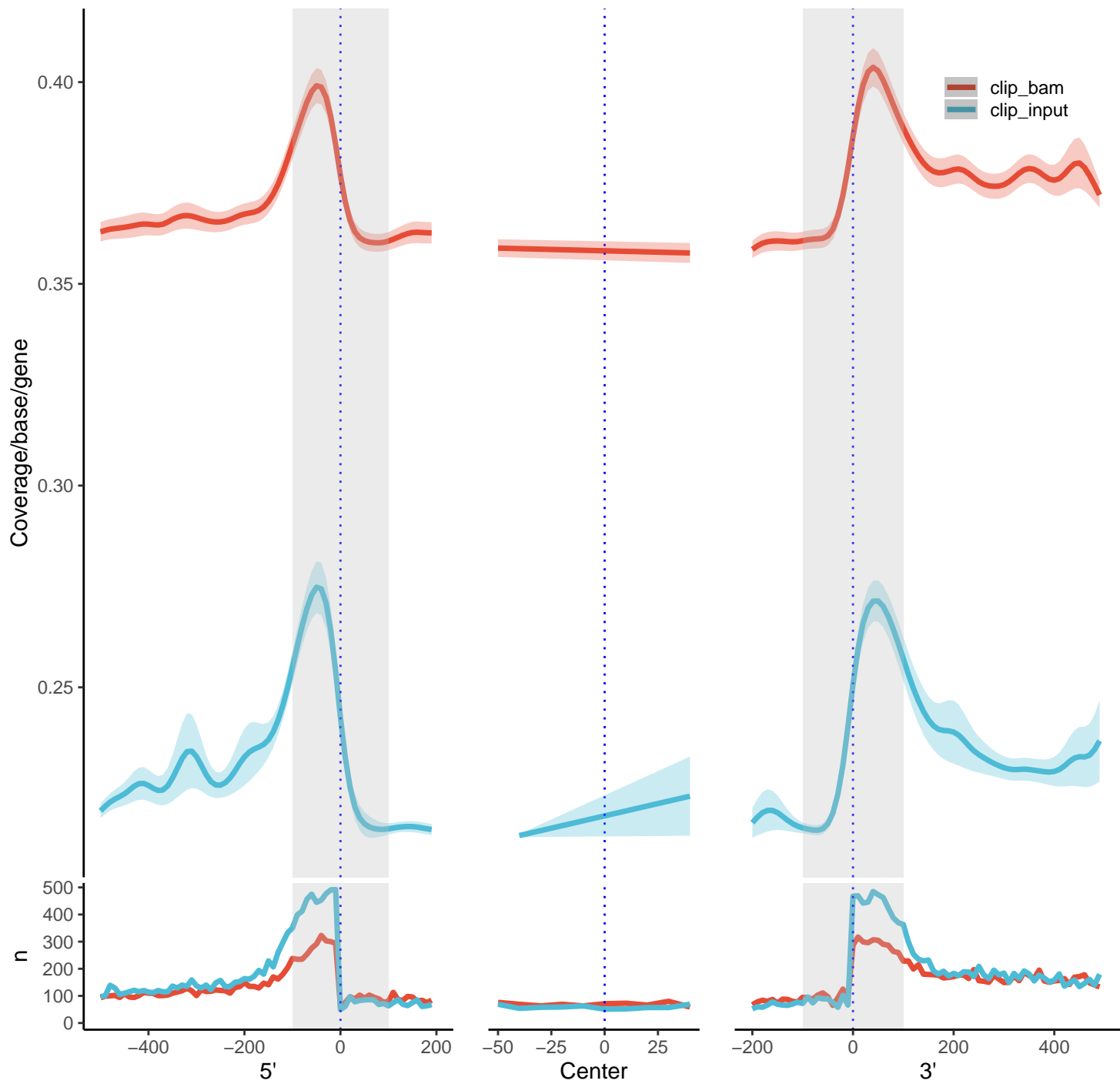
intron



intron



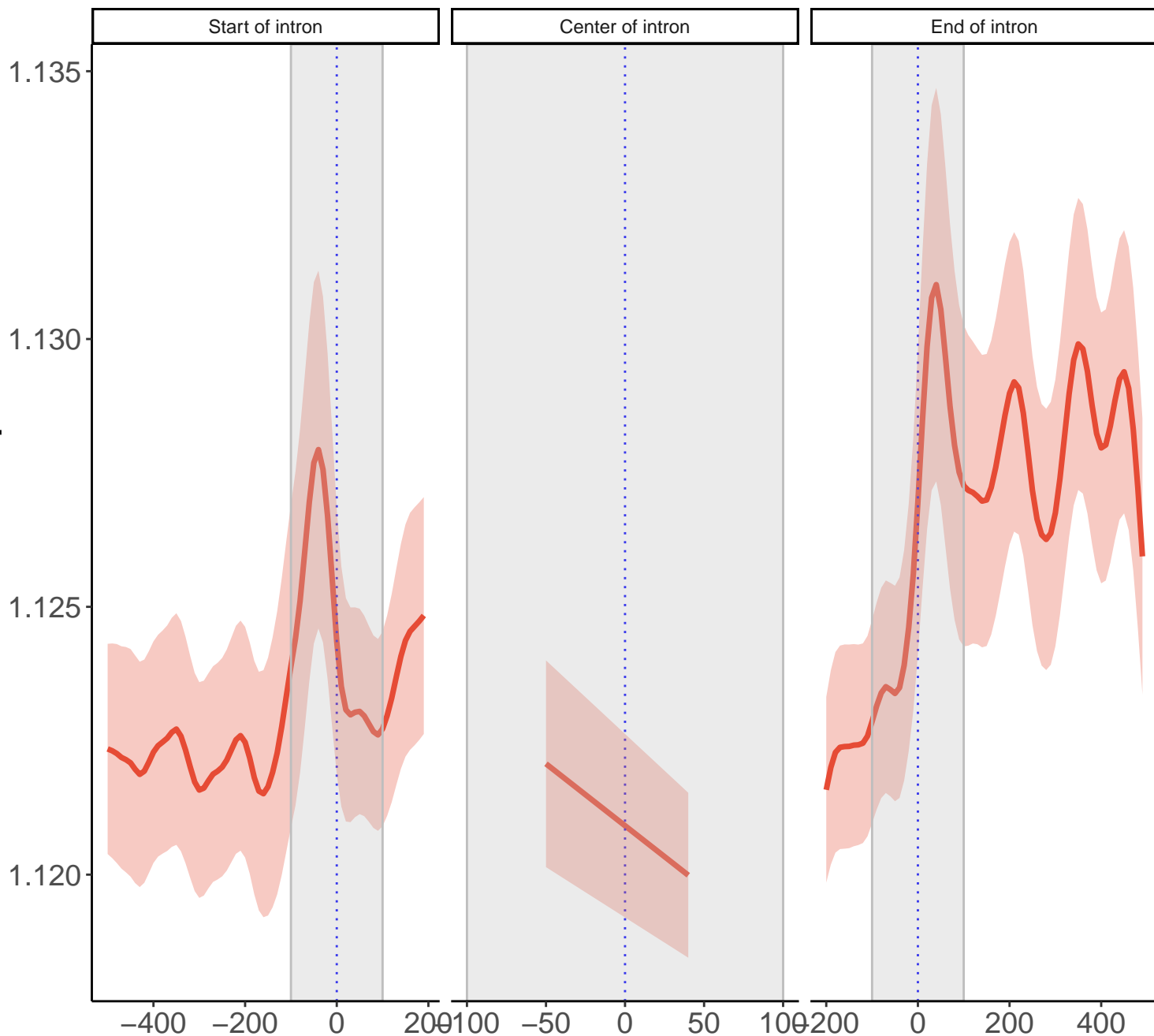
intron

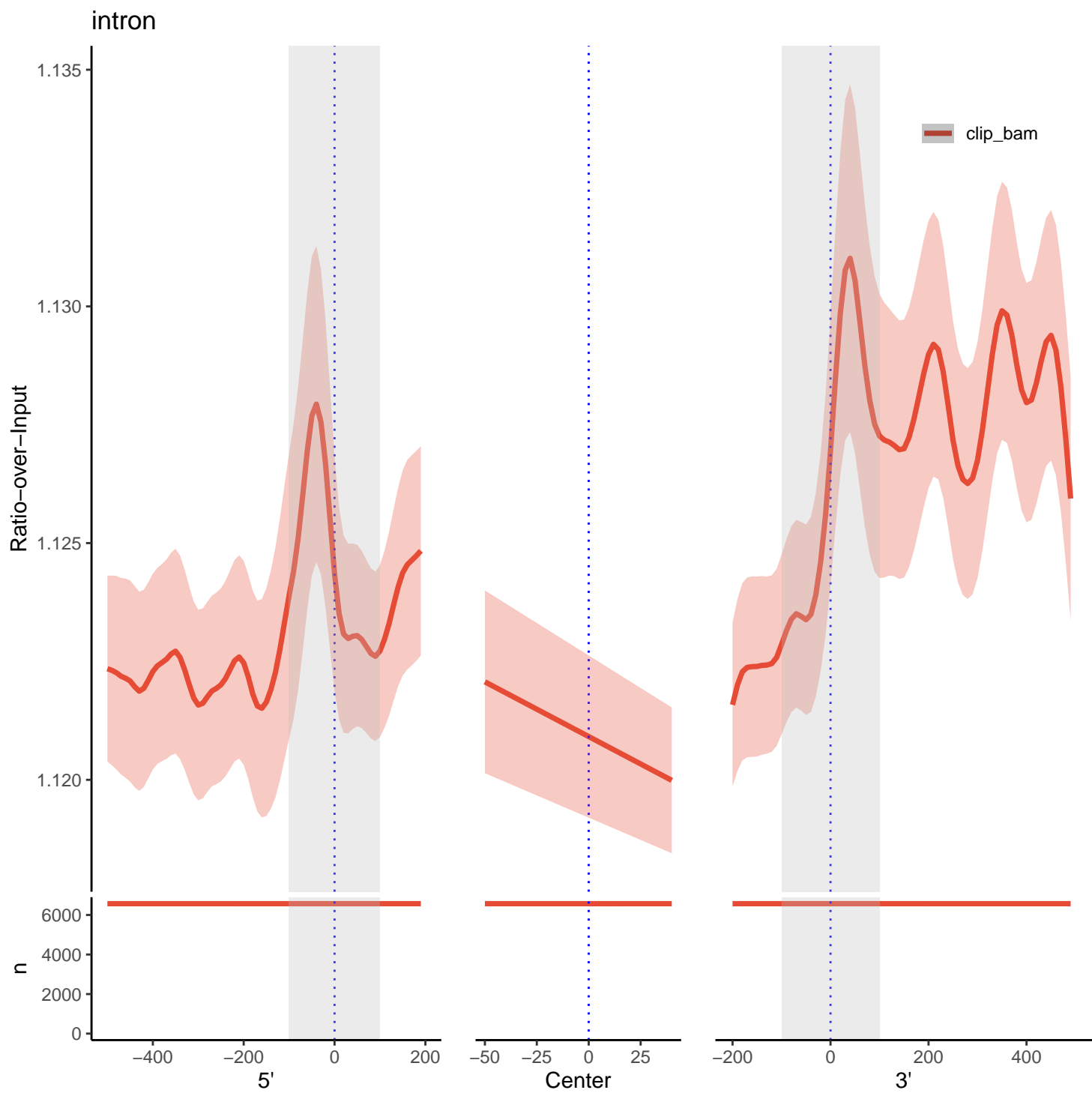


intron

clip_bam

Ratio-over-Input





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"
```