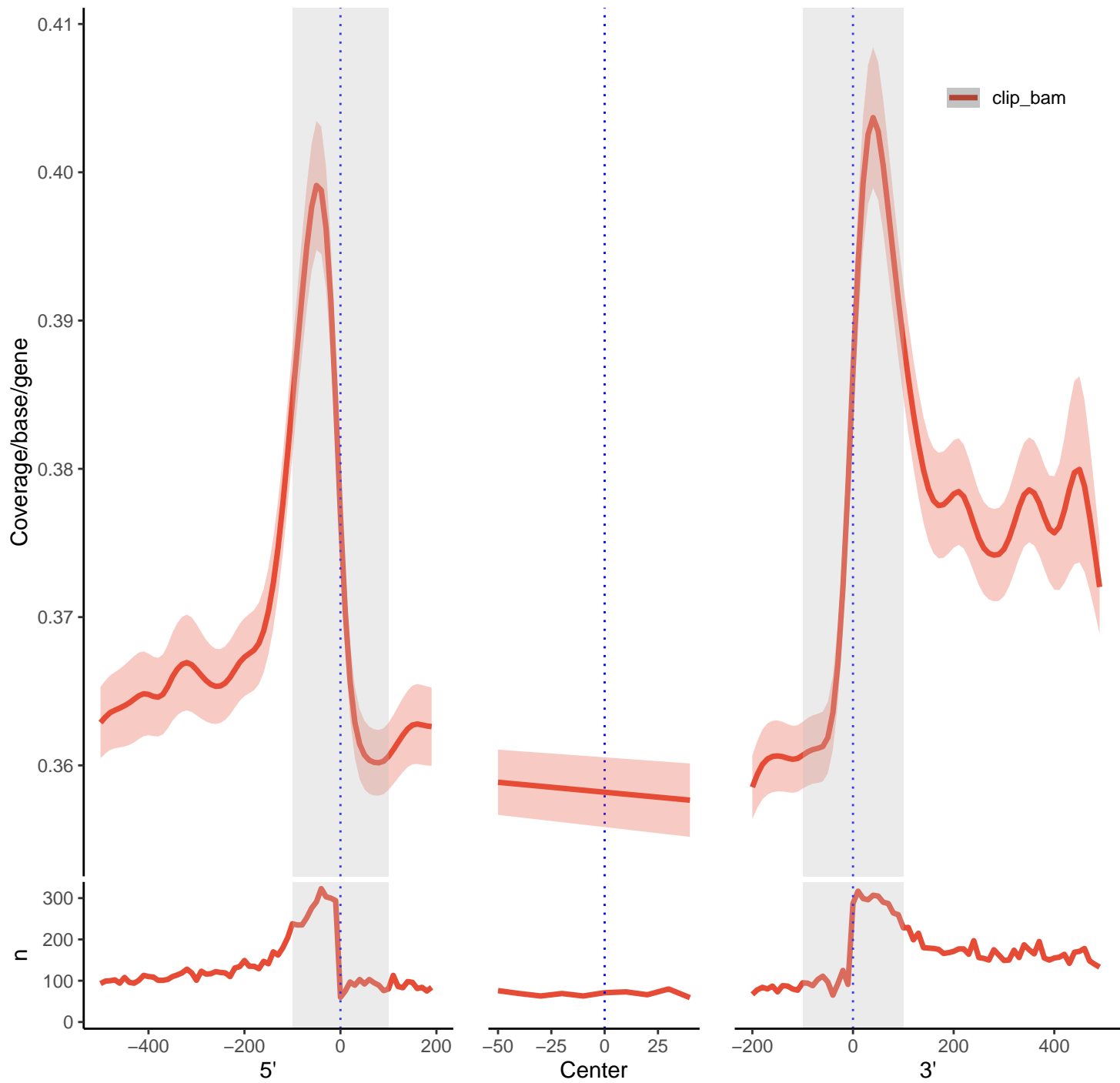
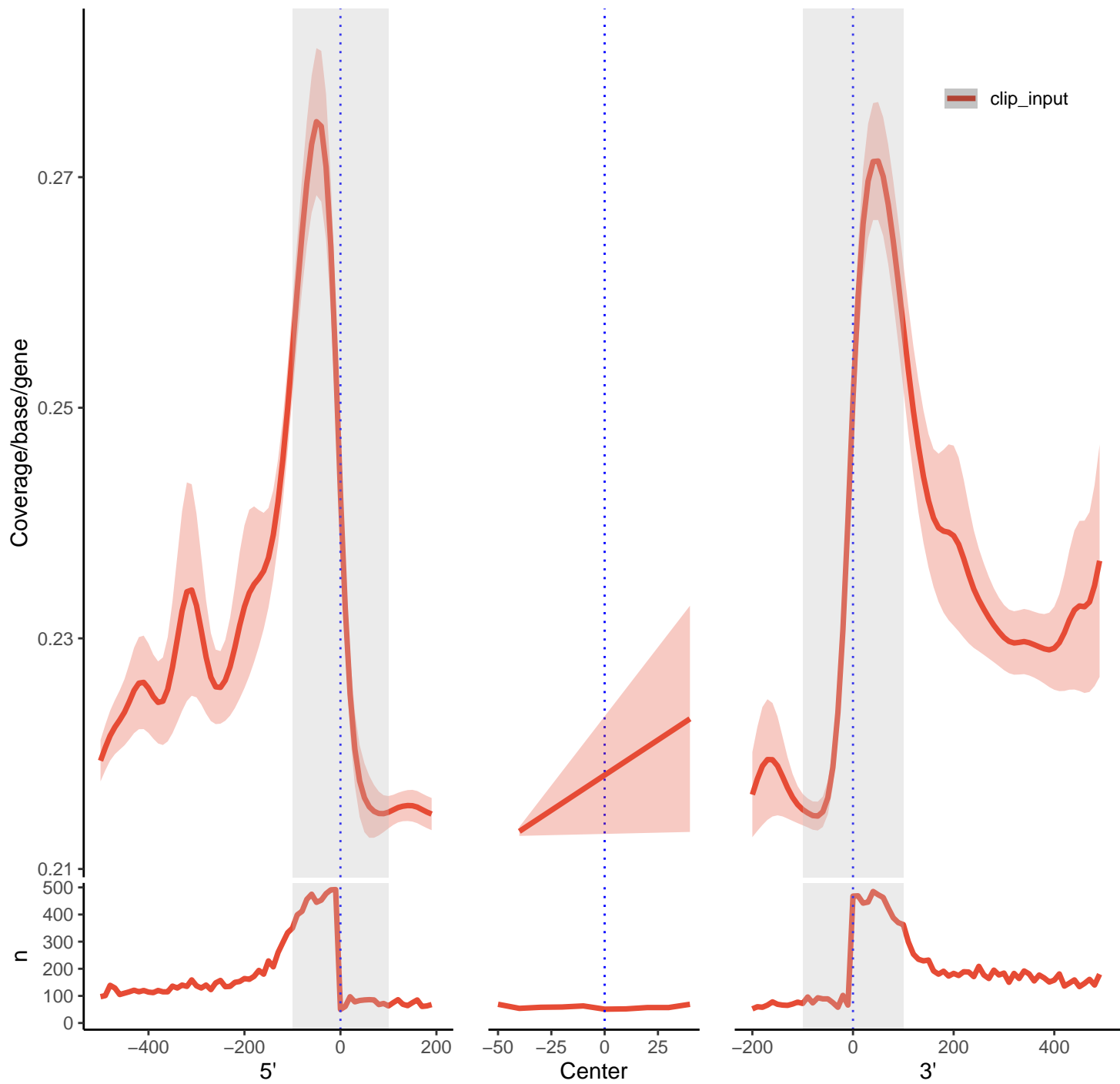


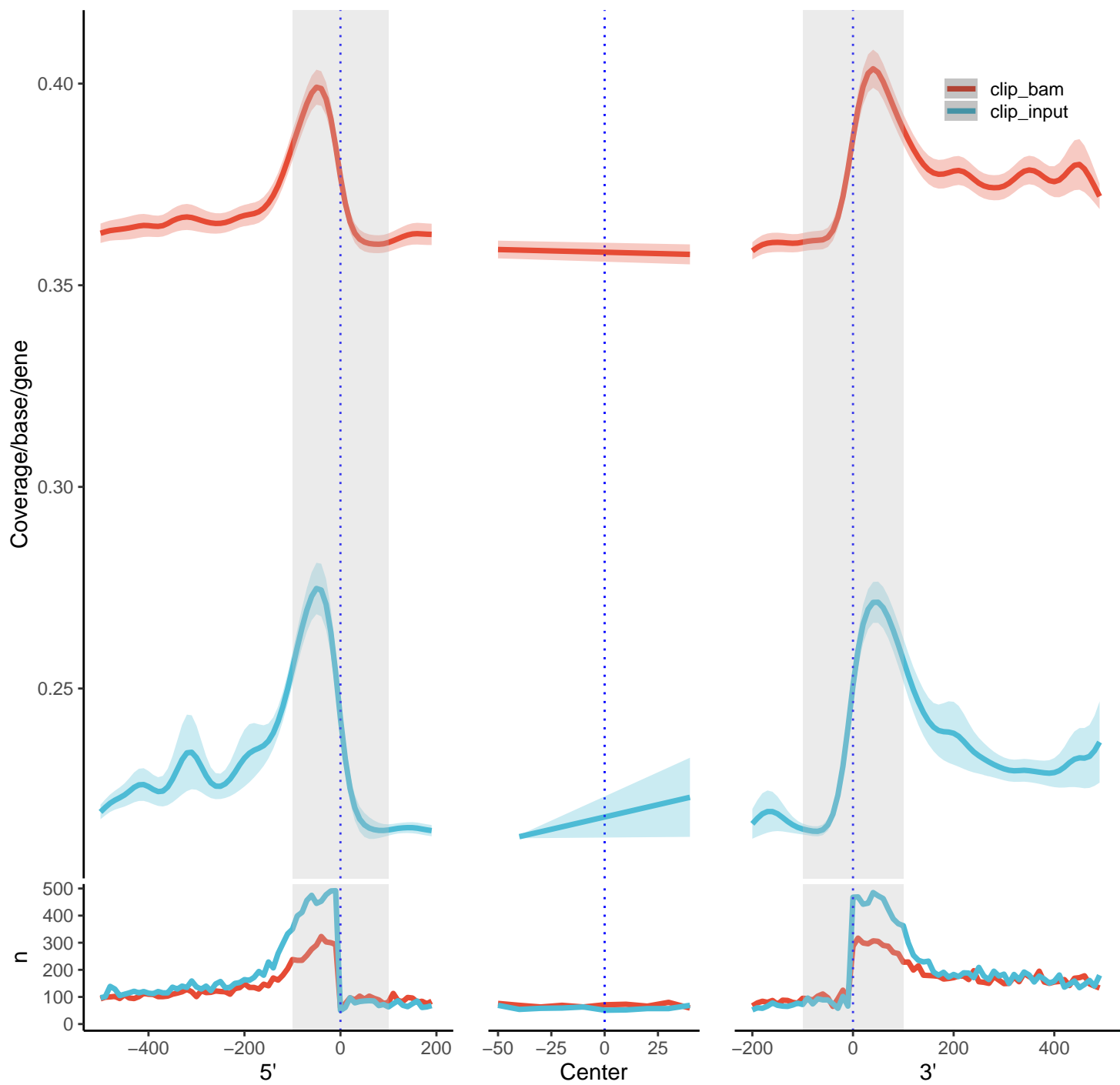
intron



intron



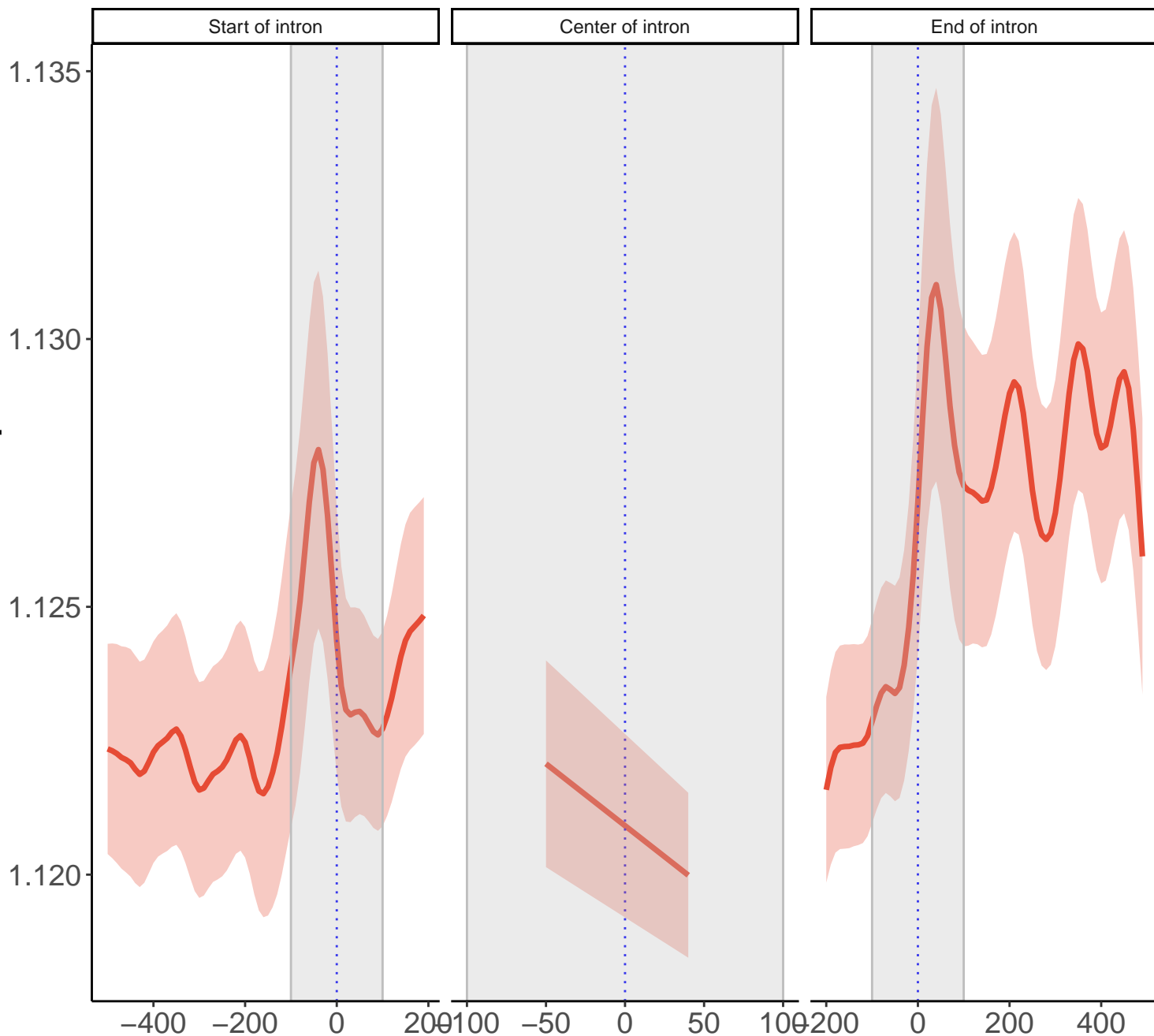
intron

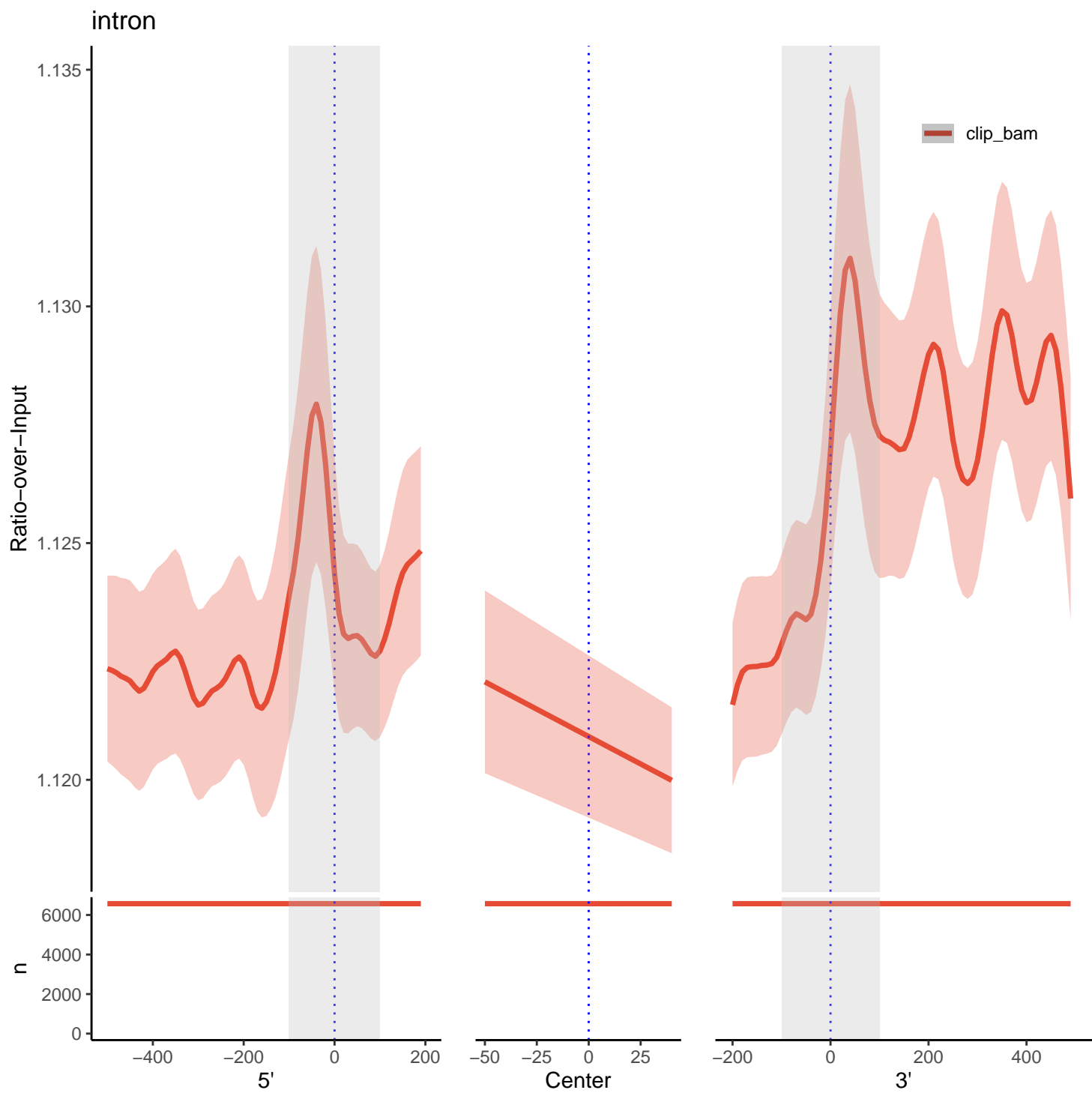


intron

clip_bam

Ratio-over-Input





Plotting parameters:

```
functionName: "plot_start_end_with_random"
  queryFiles: c(clip_bam =
"C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/treat_chr19.bam")
  inputFiles: c(clip_input =
"C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/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"
```