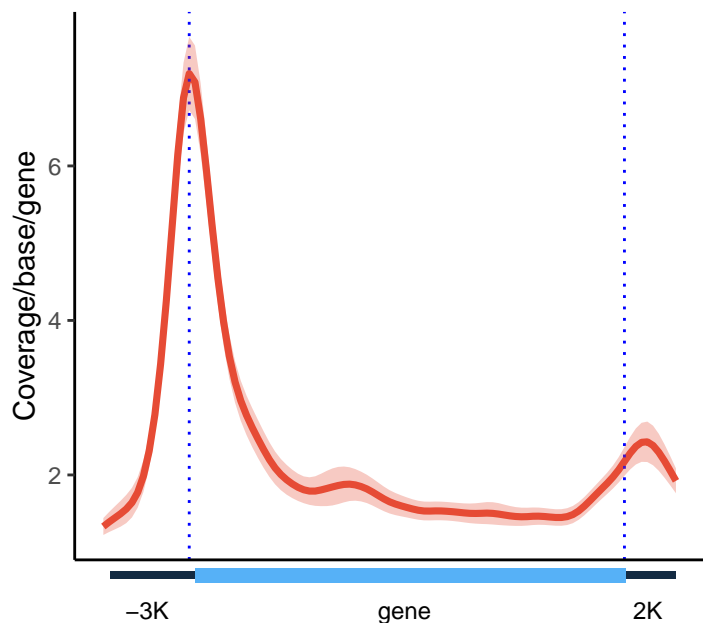
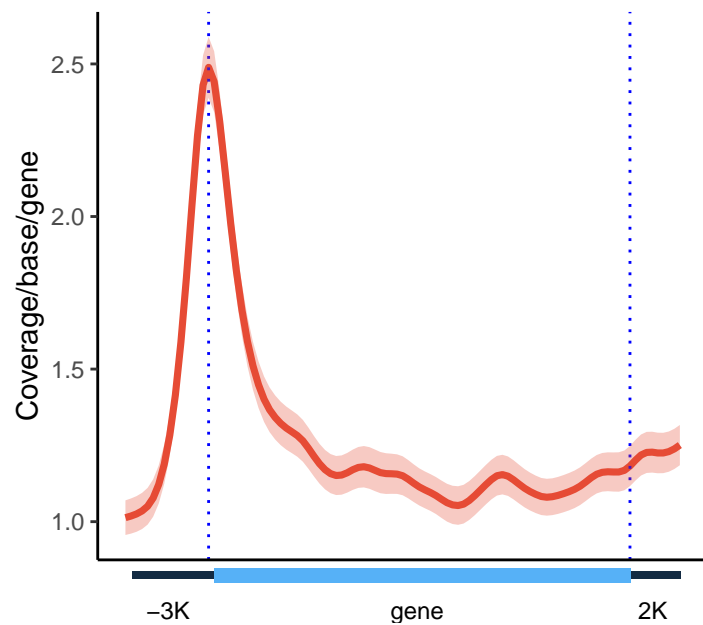


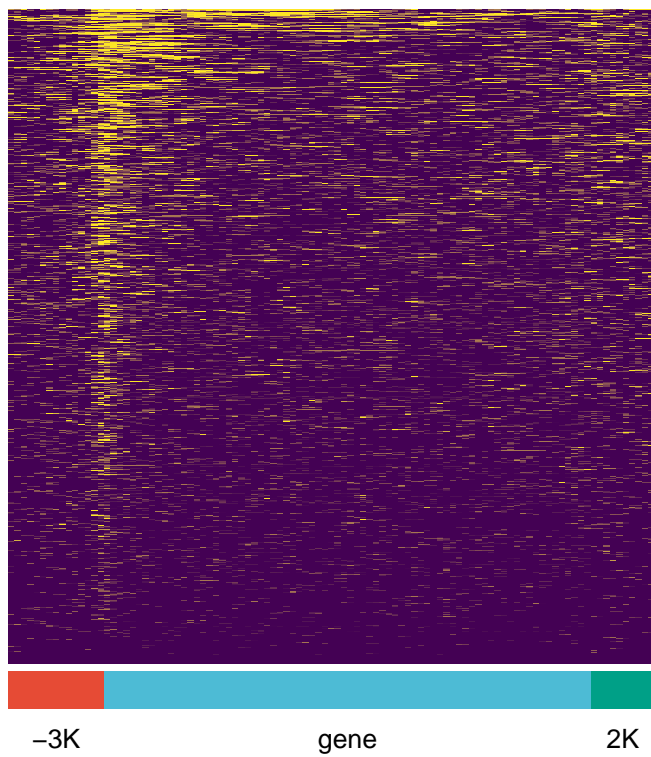
Query chip_bam



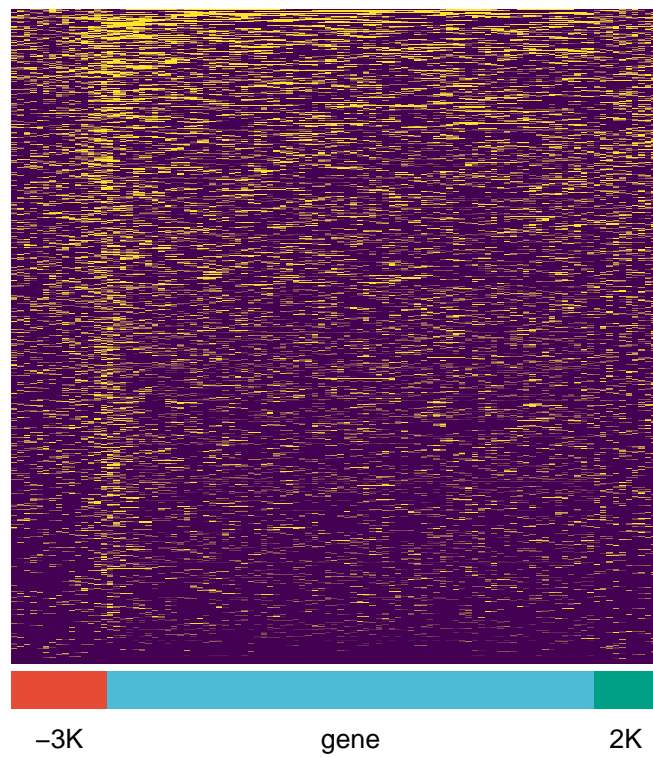
Query chip_input

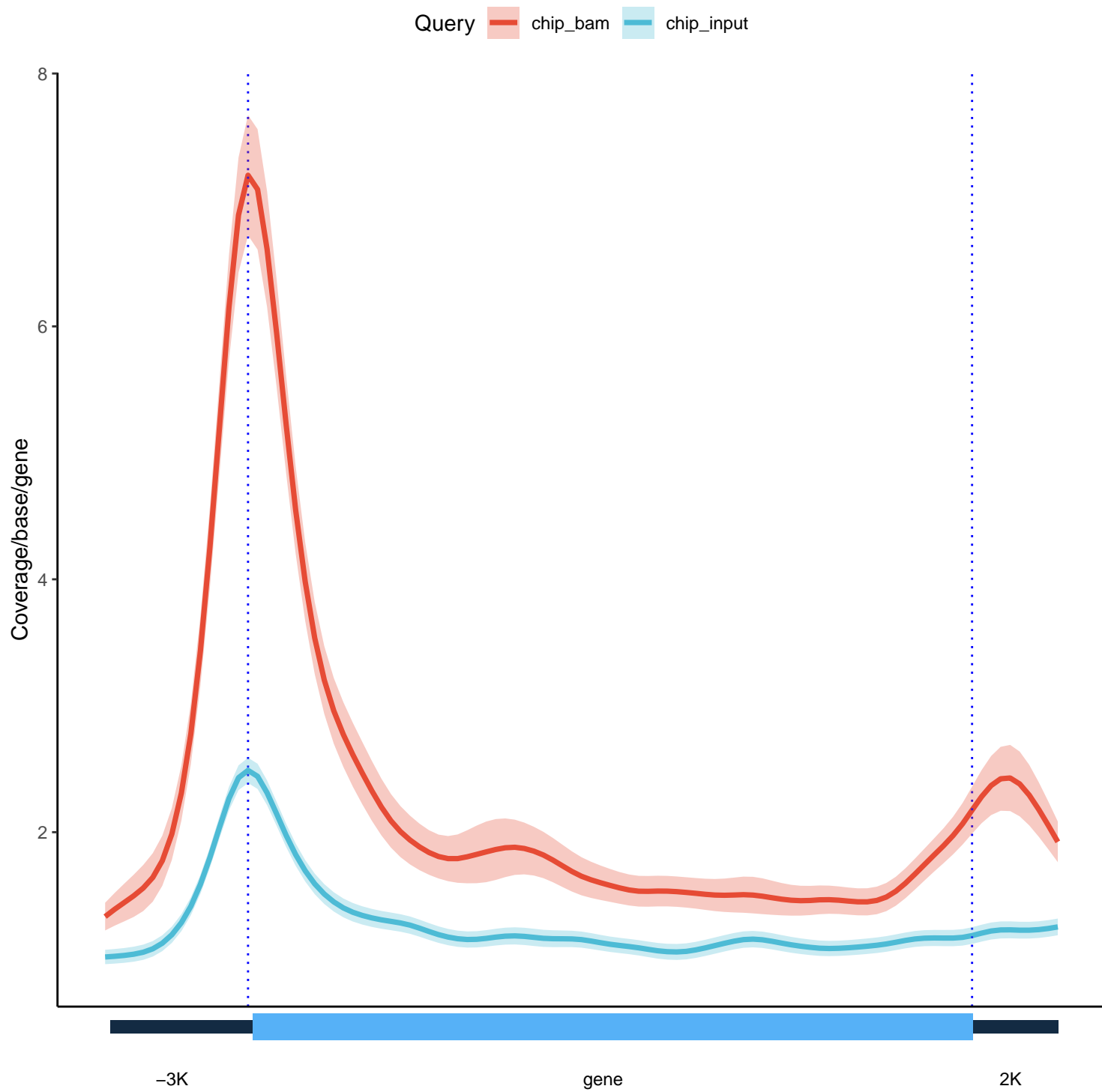


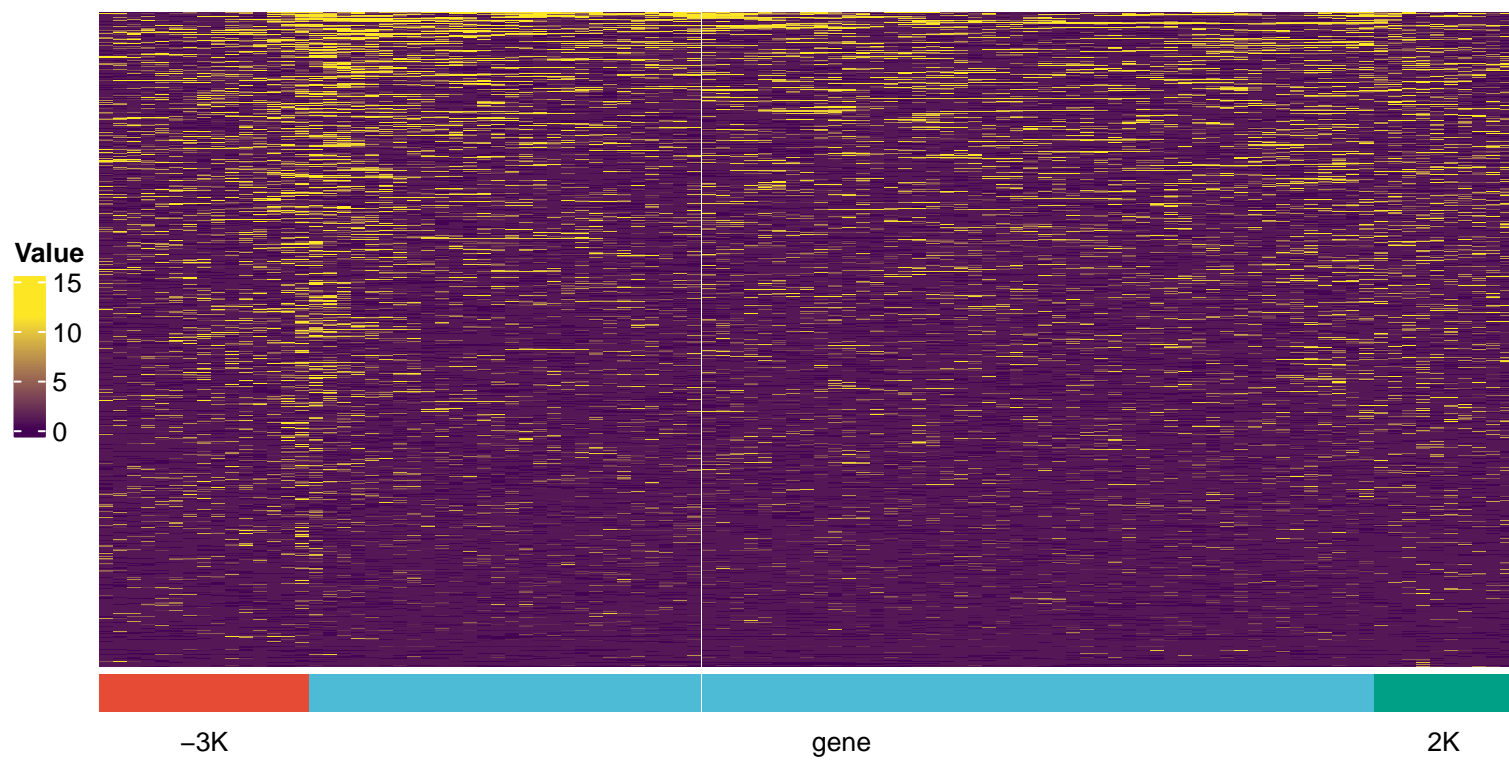
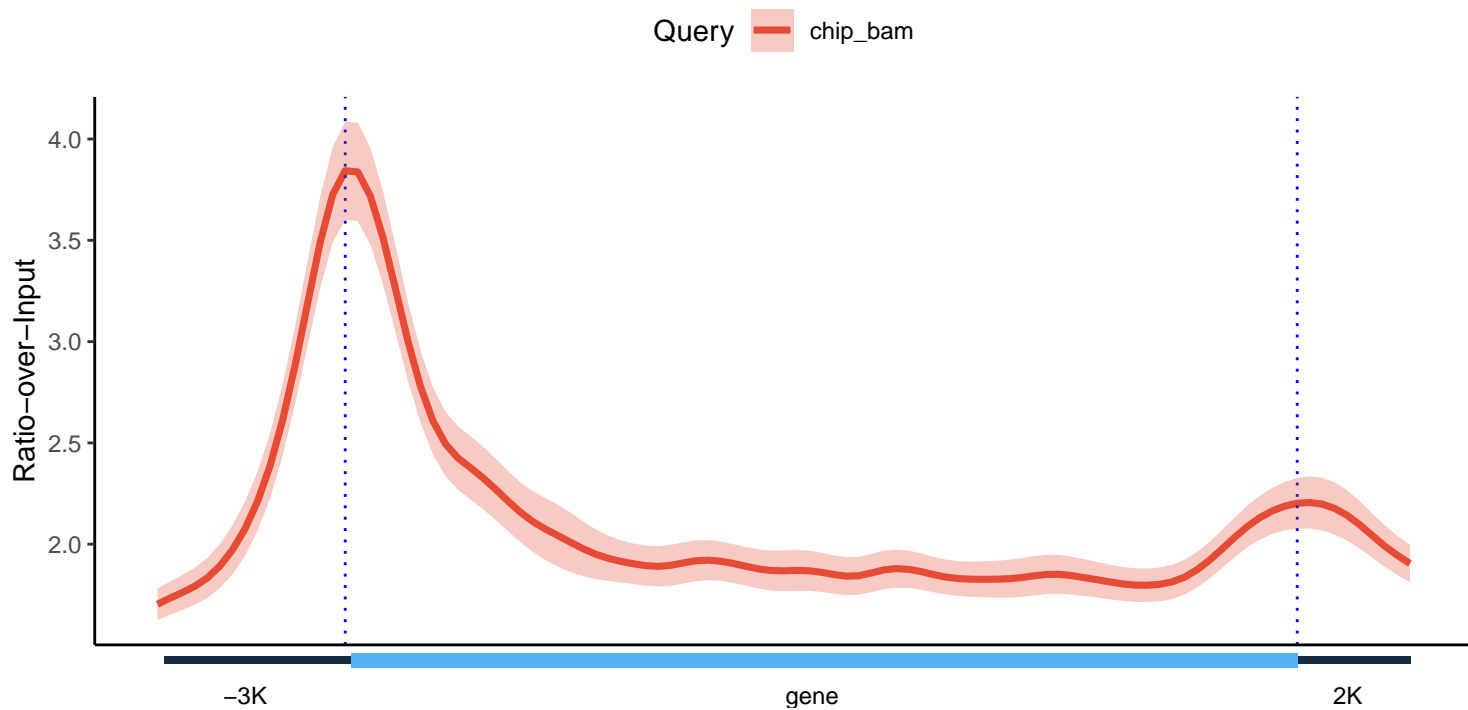
Value
20
15
10
5
0



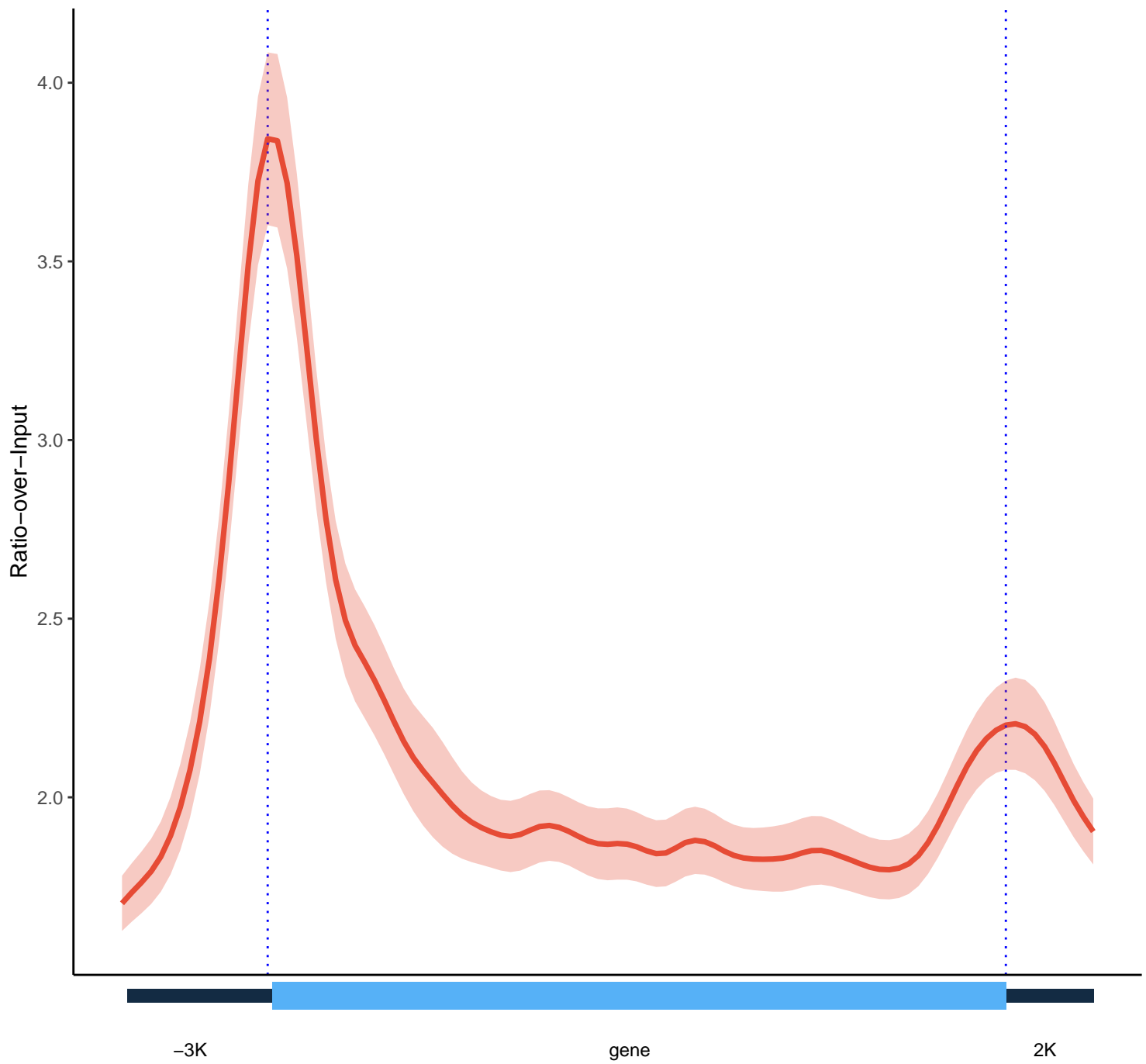
Value
8
6
4
2
0







Query chip_bam



Plotting parameters:

```
functionName: "plot_3parts_metagene"  
  queryFiles: c(chip_bam =  
    "C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/chip_treat_chr19.bam")  
    gFeatures: as.list(environment()[["gFeatures"]])  
    inputFiles: c(chip_input =  
      "C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/chip_input_chr19.bam")  
      scale: FALSE  
      verbose: FALSE  
      Ylab: "Coverage/base/gene"  
importParams: list(offset = 0, fix_width = 150, fix_point = "start", norm = TRUE, useScore =  
  FALSE, outRle = TRUE, useSizeFactor = TRUE, genome = "hg19")  
  smooth: TRUE  
  stranded: TRUE  
  outPrefix: "test_plot_3parts_metagene"  
  heatmap: TRUE  
  rmOutlier: 0  
  heatRange: NULL  
  transform: NA  
  hw: c(8, 8)  
  nc: 2
```