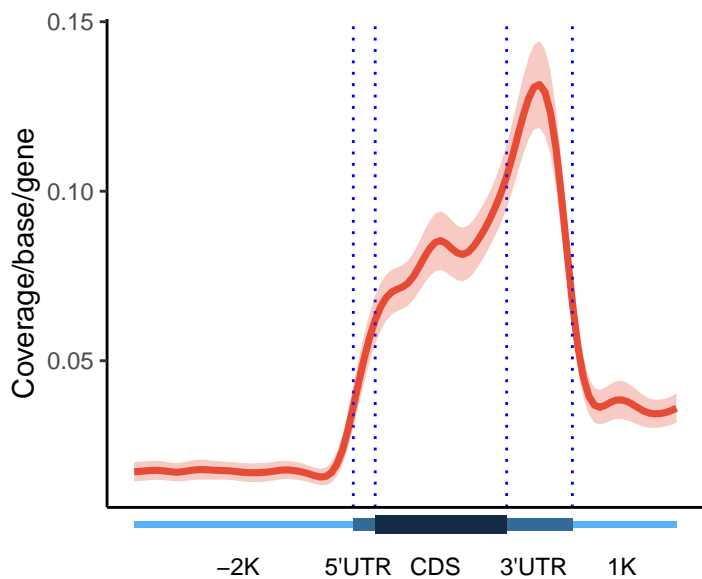
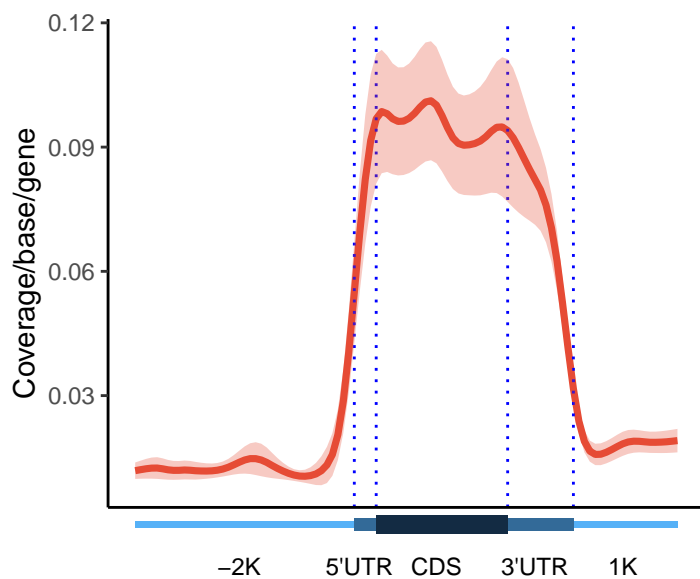


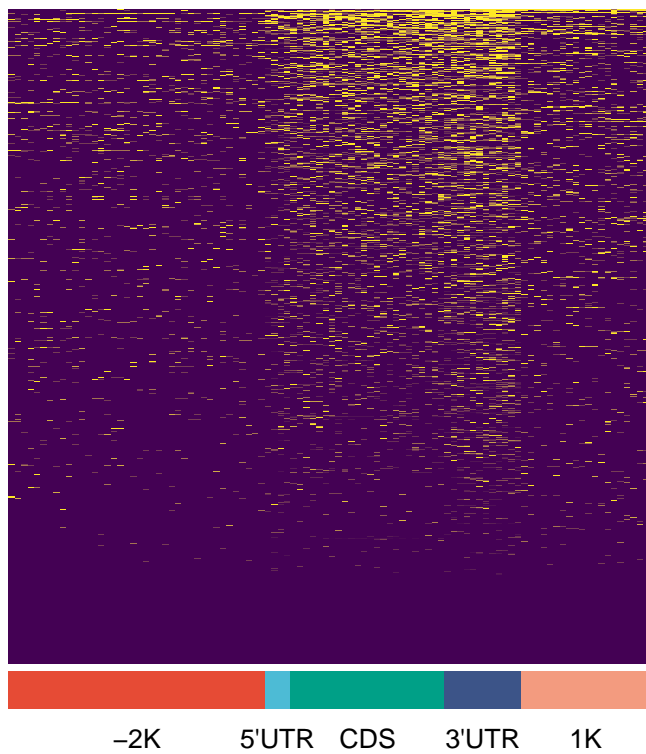
clip_bam:metagene



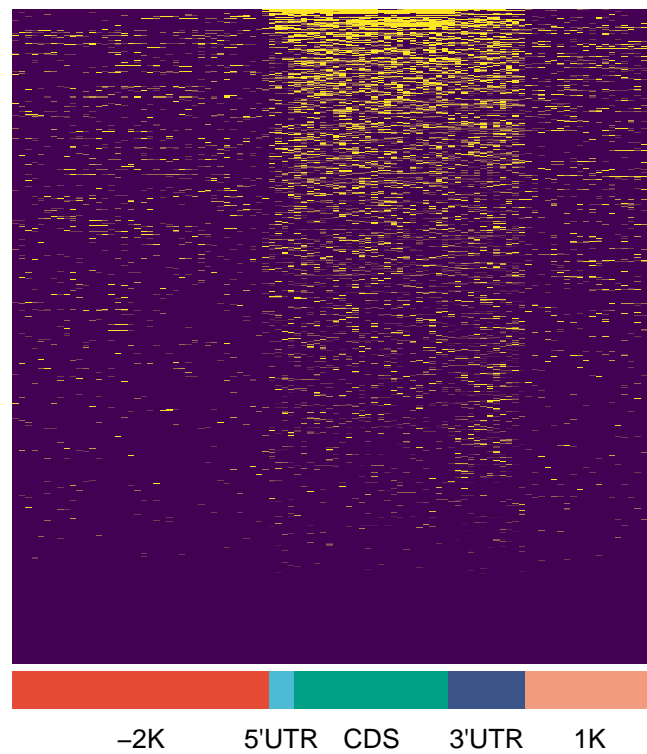
clip_input:metagene

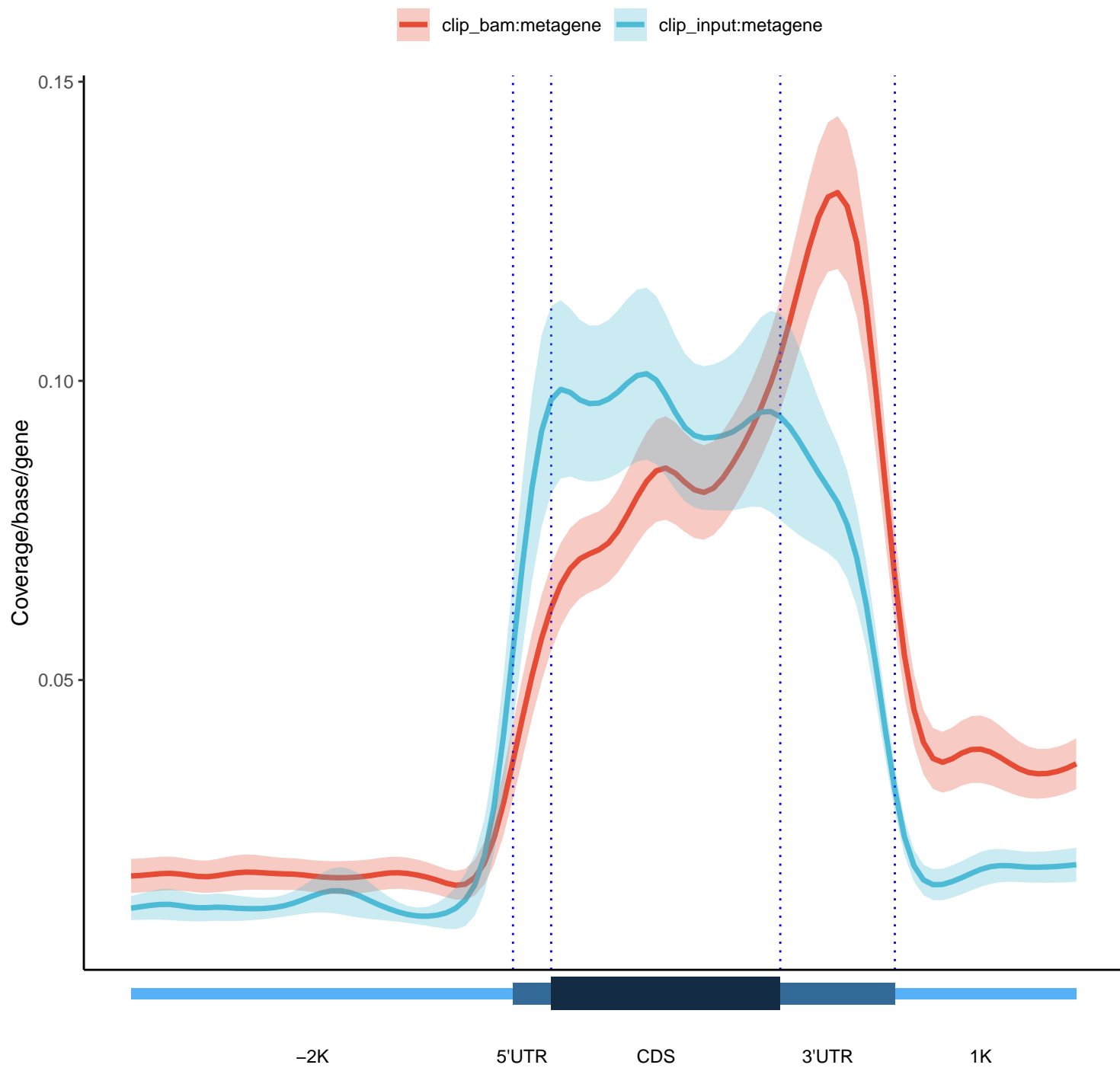


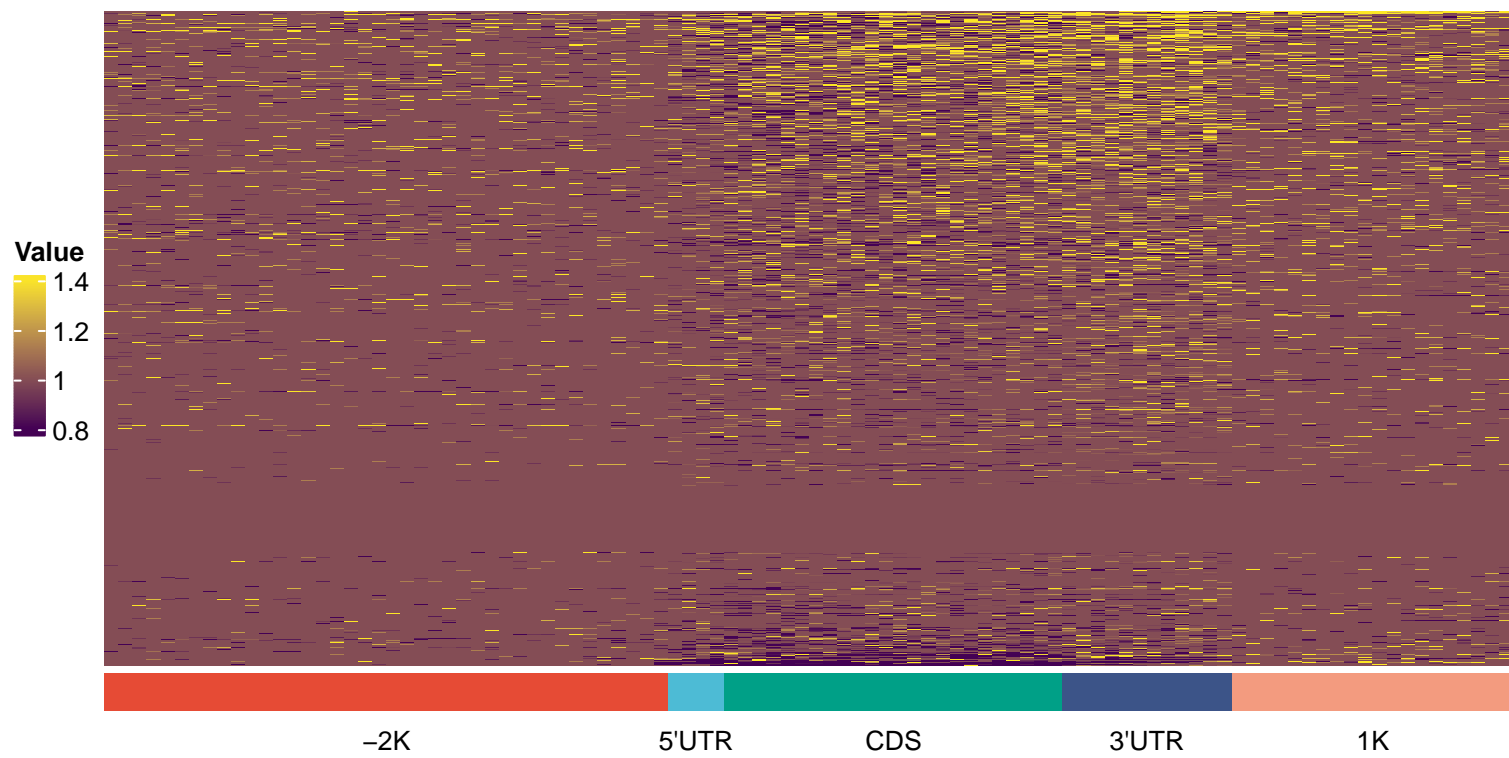
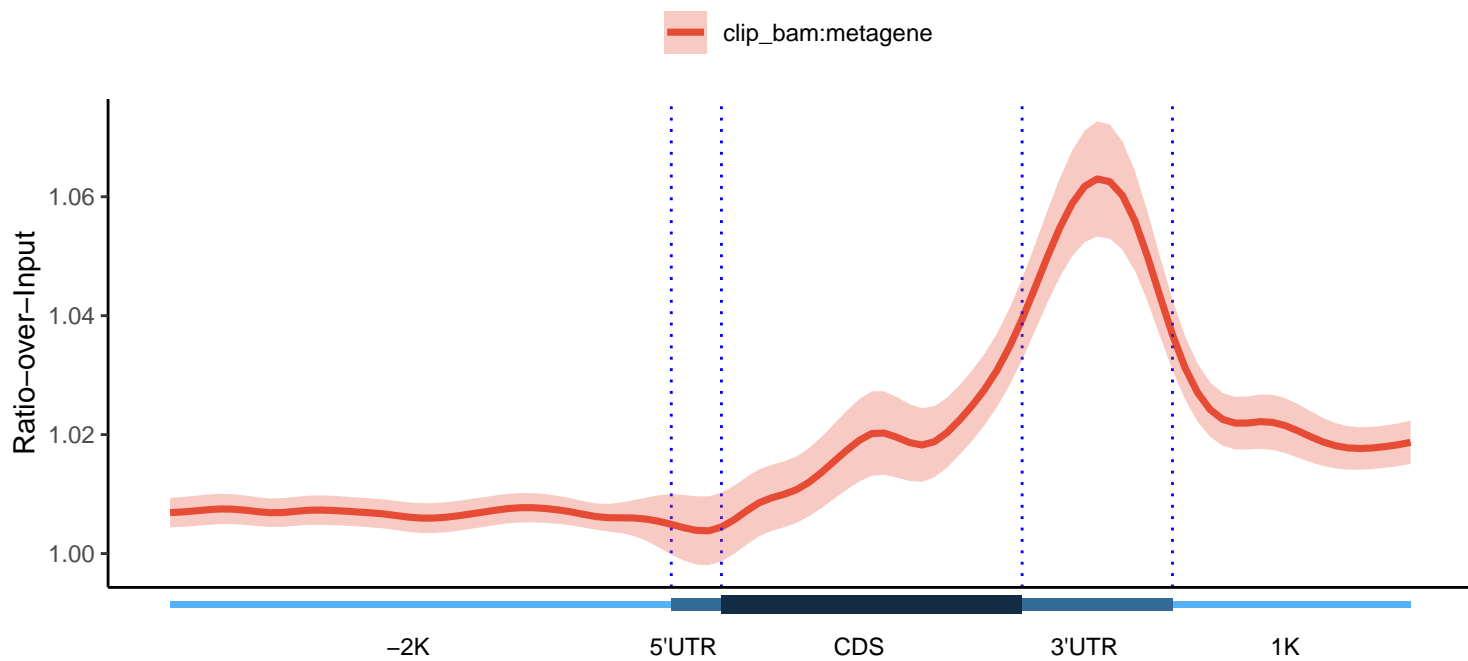
Value
0.6
0.4
0.2
0



Value
0.4
0.3
0.2
0.1
0







Plotting parameters:

```
functionName: "plot_5parts_metagene"  
  queryFiles: c(clip_bam =  
"C:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/GenomicPlot/extdata/treat_chr19.bam")  
    gFeatures_list: as.list(environment()[["gFeatures_list"]])  
    inputFiles: c(clip_input =  
"C:/Users/greenblatt/AppData/Local/Programs/R/R-4.2.1/library/GenomicPlot/extdata/input_chr19.bam")  
importParams: list(offset = -1, fix_width = 0, fix_point = "start", norm = TRUE, useScore =  
  FALSE, outRle = TRUE, useSizeFactor = FALSE, genome = "hg19")  
  verbose: FALSE  
  transform: NA  
  smooth: TRUE  
  scale: FALSE  
  stranded: TRUE  
outPrefix: "test_plot_5parts_metagene2"  
  heatmap: TRUE  
  heatRange: NULL  
  rmOutlier: 0  
Ylab: "Coverage/base/gene"  
  hw: c(8, 8)  
  nc: 2
```