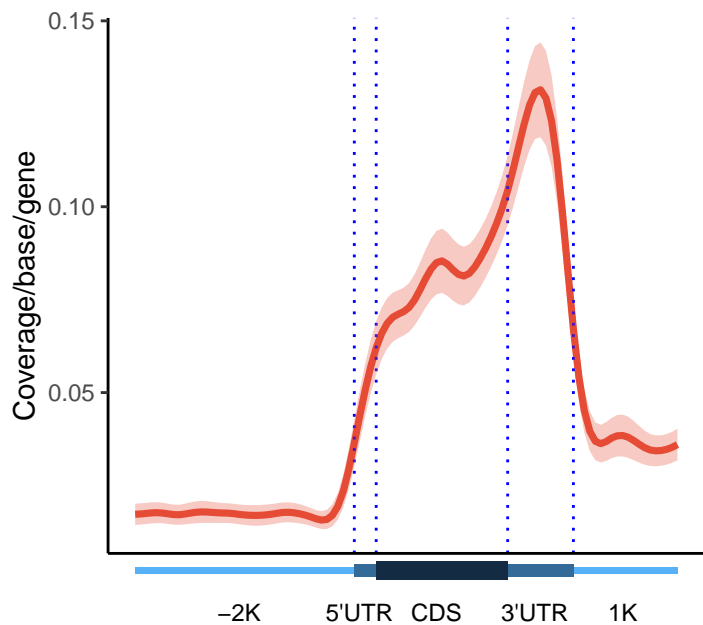
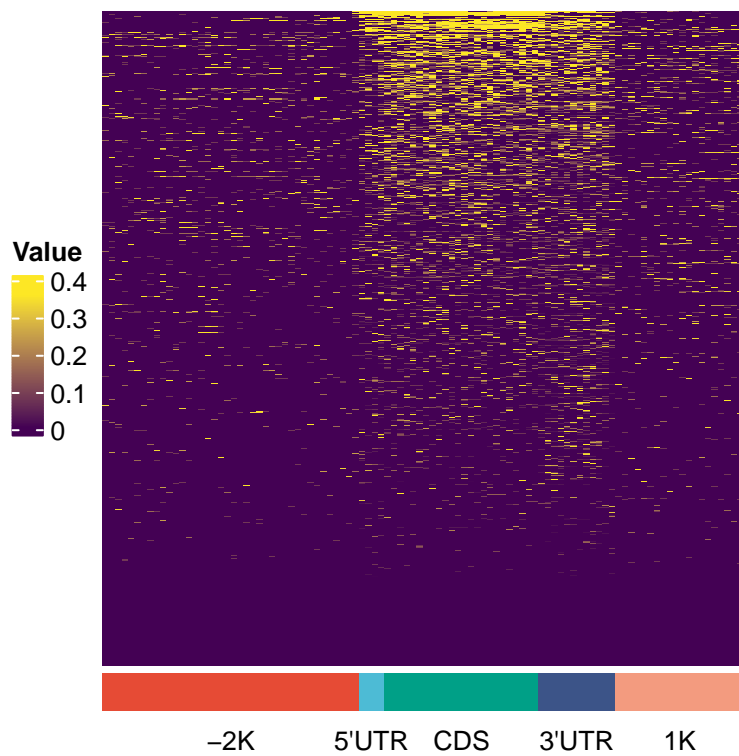
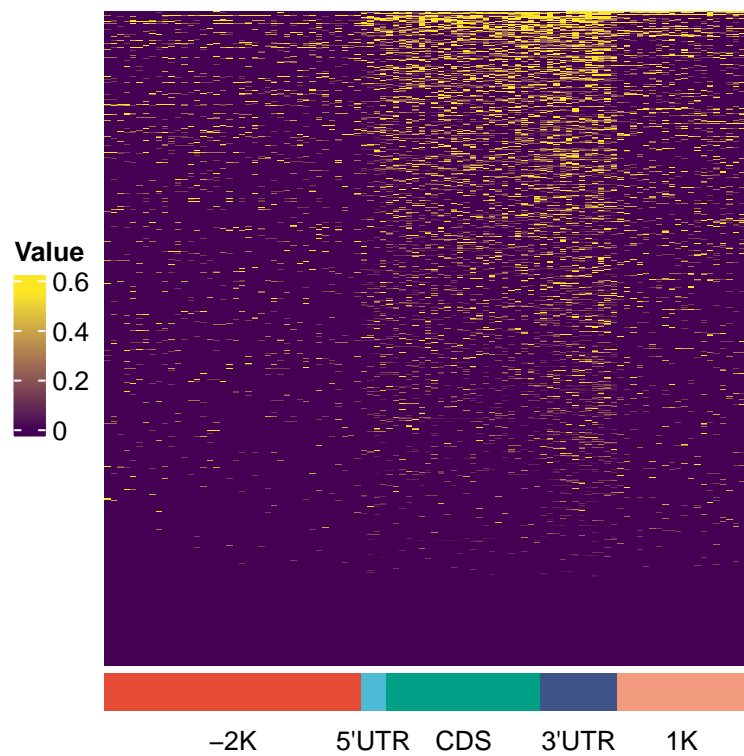
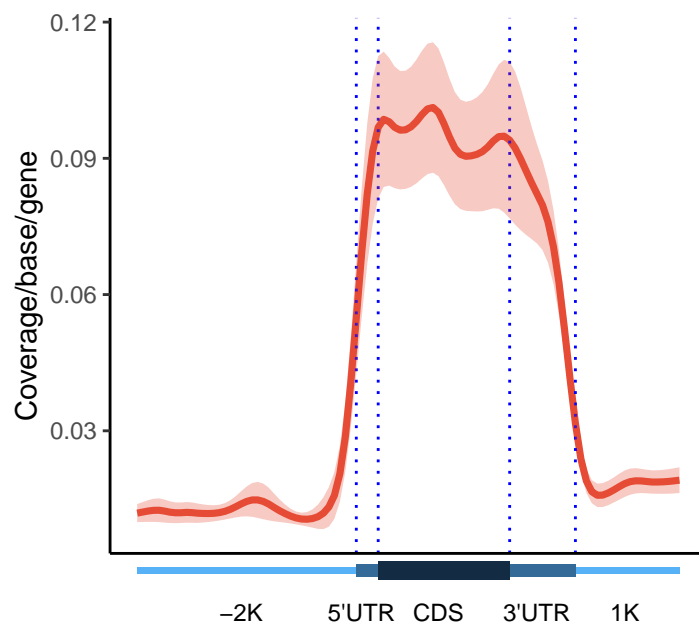


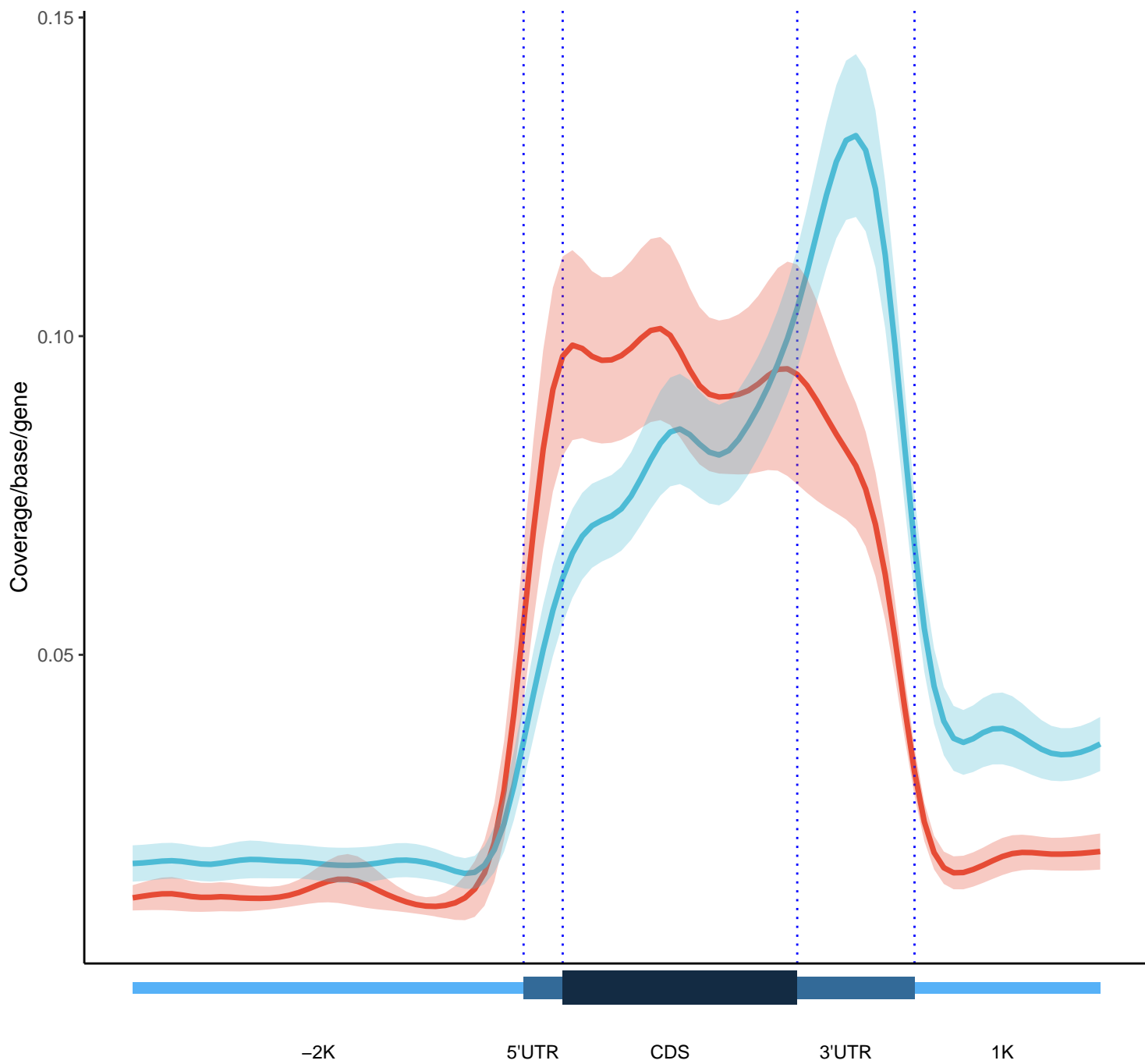
Query query:metagene

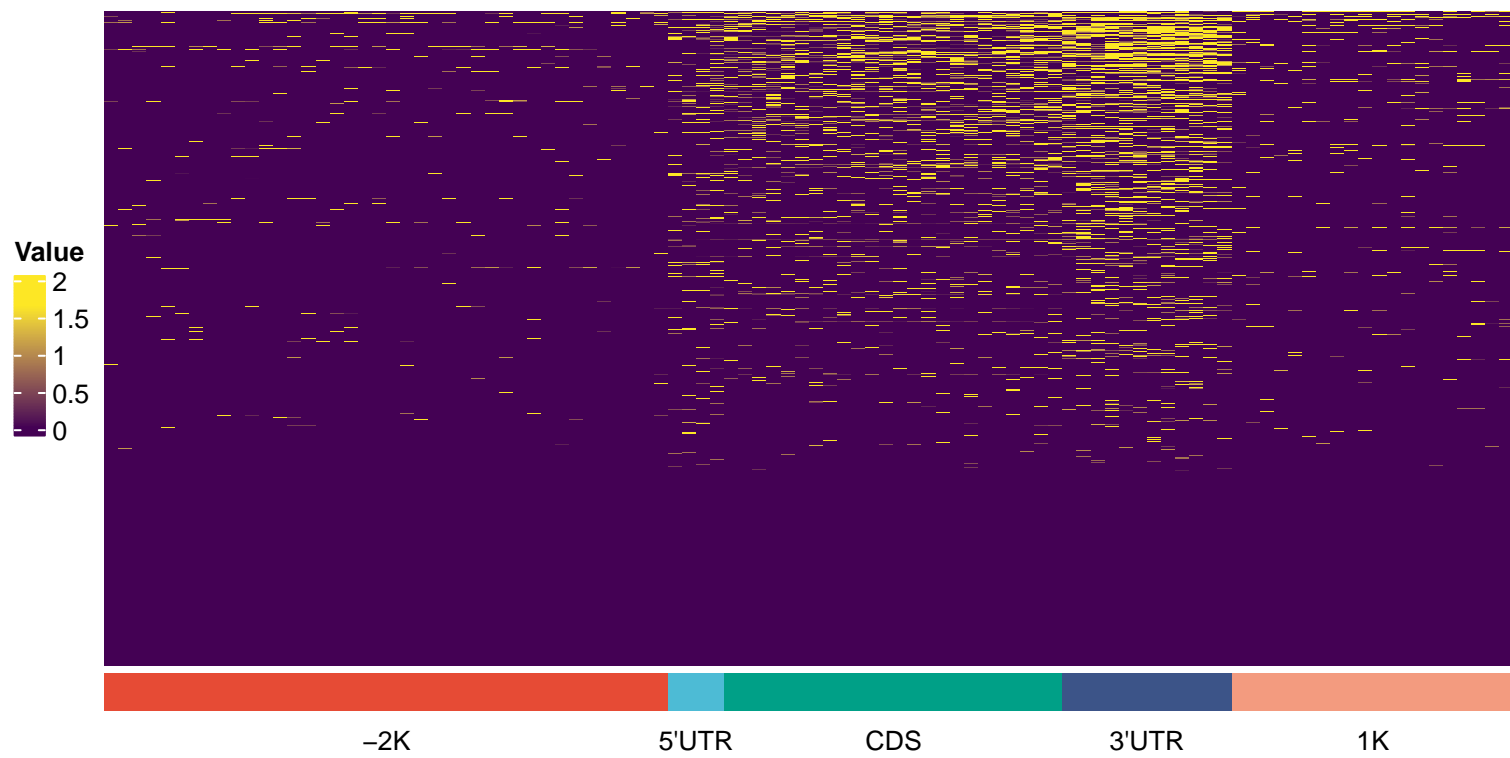
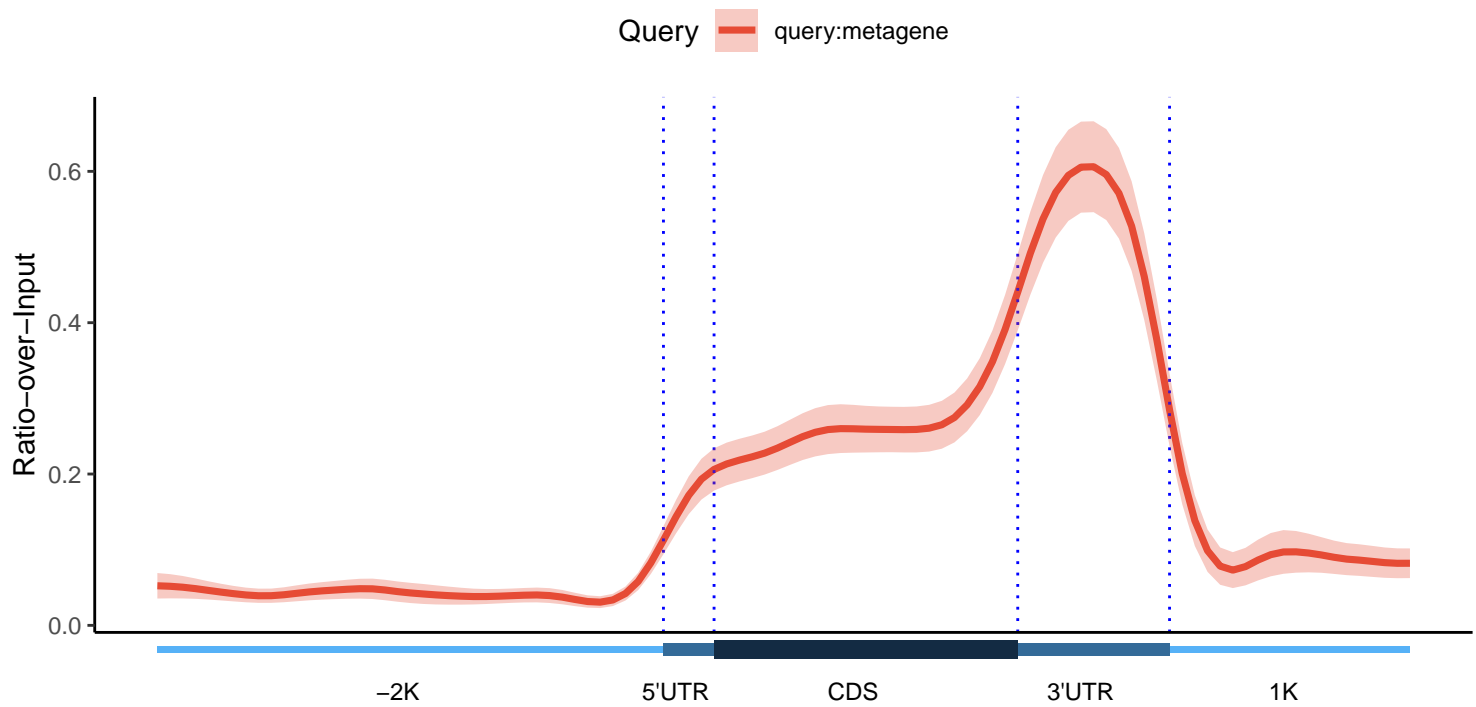


Query input:metagene



Query input:metagene query:metagene





Plotting parameters:

```
functionName: "plot_5parts_metagene"  
queryFiles: c(query = "C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/treat_chr19.bam")  
             gFeatures_list: as.list(environment())["gFeatures_list"]  
inputFiles: c(input = "C:/GREENBLATT/Rscripts/GenomicPlot_gh/inst/extdata/input_chr19.bam")  
handleInputParams: 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: TRUE  
Ylab: "Coverage/base/gene"  
      hw: c(8, 8)  
      nc: 2
```