





## Plotting parameters:

```
functionName: "plot_5parts_metagene"
                                 queryFiles: c(clip_bam =
"C:/Users/greenblatt/AppData/Local/R/win-library/4.3/GenomicPlot/extdata/treat_chr19.bam")
                  gFeatures_list: as.list(environment())[["gFeatures_list"]]
                                 inputFiles: c(clip_input =
"C:/Users/greenblatt/AppData/Local/R/win-library/4.3/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: "log2"
                                      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
```