







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, outRIe = 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
```